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Chapter 1

Introduction

QMCPACK is an open-source, high-performance electronic structure code that implements numerous Quantum Monte Carlo algorithms. Its main applications are electronic structure calculations of molecular, periodic 2D and periodic 3D solid-state systems. Variational Monte Carlo (VMC), diffusion Monte Carlo (DMC) and a number of other advanced QMC algorithms are implemented. By directly solving the Schrodinger equation, QMC methods offer greater accuracy than methods such as density functional theory, but at a trade-off of much greater computational expense. Distinct from many other correlated many-body methods, QMC methods are readily applicable to both bulk (periodic) and isolated molecular systems.

QMCPACK is written in C++ and designed with the modularity afforded by object-oriented programming. It makes extensive use of template metaprogramming to achieve high computational efficiency. Due to the modular architecture, the addition of new wavefunctions, algorithms, and observables is relatively straightforward. For parallelization QMCPACK utilizes a fully hybrid (OpenMP,CUDA)/MPI approach to optimize memory usage and to take advantage of the growing number of cores per SMP node or graphical processing units (GPUs) and accelerators. High parallel and computational efficiencies are achievable on the largest supercomputers. Finally, QMCPACK utilizes standard file formats for input and output in XML and HDF5 to facilitate data exchange.

This manual currently serves as an introduction to the essential features of QMCPACK and a guide to installing and running it. Over time this manual will be expanded to including a fuller introduction to QMC methods in general and to include more of the specialized features in QMCPACK.

1.1 Quickstart and a first QMCPACK calculation

If you are keen to get started this section describes how to quickly build and run QMCPACK on standard UNIX or Linux-like system. The autoconfiguring build system usually works without much fuss on these systems. If C++, MPI, BLAS/LAPACK, FFTW, HDF5, and CMake are already installed, QMCPACK can be built and run within five minutes. For supercomputers, cross-compilation systems, and other computer clusters the build system may require hints on the locations of libraries and which versions to use, typical of any code, see Chapter 3. Section 3.6 includes complete examples for common workstations and supercomputers that you can reuse.

To build QMCPACK:

1. Download the latest QMCPACK distribution from http://www.qmcpack.org
2. Untar the archive, e.g., tar xvf qmcpack_v1.3.tar.gz
3. Check the instructions in the README

4. Run CMake in a suitable build directory to configure QMCPACK for your system: 
   \texttt{cd qmcpack/build; cmake .}

5. If CMake is unable to find all needed libraries, see Chapter 3 for instructions and specific 
   build instructions for common systems.

6. Build QMCPACK: \texttt{make} or \texttt{make -j 16}, the latter for a faster parallel build on a system 
   using, e.g., 16 processes.

7. The QMCPACK executable is \texttt{bin/qmcpack}

QMCPACK is distributed with examples illustrating different capabilities. Most of the examples 
are designed to run quickly with modest resources. We'll run a short diffusion Monte Carlo 
calculation of a water molecule:

1. Go to the appropriate example directory: \texttt{cd ../examples/molecules}

2. (Optional) Put the QMCPACK binary on your path:
   \begin{verbatim}
   export PATH=$PATH:location-of-qmcpack/build/bin
   \end{verbatim}

3. Run QMCPACK: \texttt{./build/bin/qmcpack simple-H2O.xml} or \texttt{qmcpack simple-H2O.xml} 
   if you followed the step above.

4. The run will output to the screen and generate a number of files:

   \begin{verbatim}
   $ls H2O*
   H2O.HF.wfs.xml  H2O.s001.scalar.dat  H2O.s002.cont.xml
   H2O.s002.qmc.xml  H2O.s002.stat.h5  H2O.s001.qmc.xml
   H2O.s001.stat.h5  H2O.s002.dmc.dat  H2O.s002.scalar.dat
   \end{verbatim}

5. Partially summarized results are in the standard text files with the suffixes \texttt{scalar.dat} and 
   \texttt{dmc.dat}. They are viewable with any standard editor.

   If you have python and matplotlib installed, you can use the \texttt{qmca} analysis utility to produce 
   statistics and plots of the data. See Chapter 12 for information on analyzing QMCPACK data.

   \begin{verbatim}
   export PATH=$PATH:location-of-qmcpack/nexus/executables
   export PYTHONPATH=$PYTHONPATH:location-of-qmcpack/nexus/library
   qmca H2O.s002.scalar.dat  # For statistical analysis of the DMC data
   qmca -t -q e H2O.s002.scalar.dat  # Graphical plot of DMC energy
   \end{verbatim}

   The last command will produce a graph as per Fig. 1.1. This shows the average energy of 
   the DMC walkers at each timestep. In a real simulation we would have to check equilibration, 
   convergence with walker population, timestep etc.

   Congratulations, you have completed a DMC calculation with QMCPACK!
1.2 Authors and History

QMCPACK was initially written by Jeongnim Kim while in the group of Prof. David Ceperley at the University of Illinois at Urbana-Champaign, with later contributions at Oak Ridge National Laboratory. Over the years, many others have contributed, particularly students and researchers in the groups of Prof. David Ceperley and Prof. Richard M. Martin, as well as staff at Lawrence Livermore National Laboratory, Sandia National Laboratories, Argonne National Laboratory, and Oak Ridge National Laboratory.


If you should be added to this list please let us know.

Development of QMCPACK has been supported financially by several grants, including:

- “Network for ab initio many-body methods: development, education and training” supported through the Predictive Theory and Modeling for Materials and Chemical Science program by the U.S. Department of Energy Office of Science, Basic Energy Sciences.

- “QMC Endstation”, supported by Accelerating Delivery of Petascale Computing Environment at the DOE Leadership Computing Facility at ORNL.

- PetaApps, supported by the U. S. National Science Foundation.

- Materials Computational Center, supported by the U.S. National Science Foundation.
1.3 Support and Contacting the Developers

Questions about installing, applying or extending QMCPACK can be posted on the QMCPACK Google group [https://groups.google.com/forum/#!forum/qmcpack](https://groups.google.com/forum/#!forum/qmcpack). You may also email any of the developers, but we recommend checking the group first. Particular attention is given to any problem reports.

1.4 Performance

QMCPACK implements modern Monte Carlo algorithms, is highly parallel, and is also written using very efficient code for high per-CPU or on node performance. In particular the code is highly vectorizable, giving high performance on modern CPUs and GPUs. We believe QMCPACK delivers performance either comparable to or better than other QMC codes when similar calculations are run, particularly for the most common QMC methods and for large systems. If you find a calculation where this is not the case, or you simply find performance slower than expected, please post on the Google group or contact one of the developers. These reports are valuable. If your calculation is sufficiently mainstream we will optimize QMCPACK to improve the performance.

1.5 Open source license

QMCPACK is distributed under the University of Illinois/NCSA Open Source License.

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Materials computation Center, University of Illinois
http://www.mcc.uiuc.edu/qmc/

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Copyright is generally believed to remain with the authors of the individual sections of code. See the various notations in the source code as well as the code history.

### 1.6 Contributing to QMCPACK

QMCPACK is fully open source and we welcome contributions. Please post on the QMCPACK Google group or contact the developers. If you are planning a development, early discussions are encouraged. We will be able to tell you if anyone else is working on a similar feature or if any related work has been done in the past. Credit for your contribution can be obtained, e.g., through citation of a paper, or becoming one of the authors on the next version of the standard QMCPACK reference citation.

A guide to developing for QMCPACK, including instructions on how to work with GitHub and make pull requests (contributions) to the main source are listed on the QMCPACK GitHub wiki [https://github.com/QMCPACK/qmcpack/wiki](https://github.com/QMCPACK/qmcpack/wiki).

Contributions are made under the same license as QMCPACK, the UIUC/NCSA open source license. If this is problematic, please discuss with a developer.

Please note the following guidelines for contributions:

- Additions should be fully synchronized with the latest release version and ideally the latest develop branch on github. Merging of code developed on older versions is error prone.

- Code should be cleanly formatted, commented, portable, and accessible to other programmers. i.e. If you need to use any clever tricks, add a comment to note this, why the trick is needed, how it works etc. Although we like high performance, ease of maintenance and accessibility are also considerations.

- Comment your code. You are not only writing it for the compiler for also for other humans! (We know this is a repeat of the previous point, but it is important enough to repeat.)

- Write a brief description of the method, algorithms and inputs and outputs suitable for inclusion in this manual.

- Develop some short tests that exercise the functionality that can be used for validation and for examples. We can help with this and their integration into the test system.
1.7 QMCPACK Roadmap

A general outline of the QMCPACK roadmap is given below. Suggestions for improvements are welcome, particularly those that would facilitate new scientific applications. For example, if an interface to a particular quantum chemical or density functional code would help, this would be given strong consideration.

1.7.1 Code

We will continue improving the accessibility and usability of QMCPACK, by combinations of more convenient input parameters, improved workflow, integration with more quantum chemical and density functional codes, and a wider range of examples.

In terms of methodological development, we expect to significantly increase the range of QMC algorithms in QMCPACK in the near future.

Computationally, we are porting QMCPACK to the next generation of supercomputer systems. The internal changes required to run on these systems efficiently are expected to benefit all platforms due to improved vectorization, cache utilization and memory performance.

1.7.2 Documentation

This manual currently describes the core features of QMCPACK that are required for routine research calculations, i.e. the VMC and DMC methods, how to obtain and optimize trial wavefunctions, and simple observables. Over time this manual will be expanded to include a broader introduction to QMC methods and to describe more features of the code.

Due to its history as a research code, QMCPACK contains a variety of additional QMC methods, trial wavefunction forms, potentials (etc.) that, although not critical, may be very useful for specialized calculations or particular material or chemical systems. These “secret features” (every code has these) are not actually secret but simply lack descriptions, example inputs, and tests. You are encouraged to browse and read the source code to find them. New descriptions will be added over time, but can also be prioritized and added on request, e.g. if a specialized Jastrow factor would help or an historical Jastrow form is needed for benchmarking.
Chapter 2

Features of QMCPACK

2.1 Features in production

The following lists the main production level features of QMCPACK. If you do not see a specific feature that you are interested in listed, see the remainder of this manual and ask to see if specific feature is available or can be made full production level quickly.

- Variational Monte Carlo
- Diffusion Monte Carlo
- Reptation Monte Carlo
- Single and multi-determinant Slater Jastrow wavefunctions
- Wavefunction updates using optimized multi-determinant algorithm of Clark et al.
- Backflow wavefunctions
- One, two, and three-body Jastrow factors
- Excited state calculations via flexible occupancy assignment of Slater determinants
- All electron and non-local pseudopotential calculations
- Casula T-moves for variational evaluation of non-local pseudopotentials (non-size consistent and size-consistent variants)
- Wavefunction optimization using the “linear method” of Umrigar and co-workers, with arbitrary mix of variance and energy in the objective function
- Blocked, low memory adaptive shift optimizer of Zhao and Neuscamman.
- Gaussian, Slater, plane-wave and real-space spline basis sets for orbitals
- Interface and conversion utilities for plane-wave wavefunctions from Quantum Espresso (PWSCF)
- Interface and conversion utilities for Gaussian-basis wavefunctions from GAMESS
- Easy extension and interfacing to other electronic structure codes via standardized XML and HDF5 inputs
• MPI parallelism
• Fully threaded using OpenMP
• GPU (NVIDIA CUDA) implementation (limited functionality)
• HDF5 input/output for large data
• Nexus: advanced workflow tool to automate all aspects of QMC calculation from initial DFT calculations through to final analysis
• Analysis tools for minimal environments (perl only) through to python-based with graphs produced via matplotlib (included with Nexus).

2.1.1 Supported GPU features
The GPU implementation supports multiple GPUs per node, with MPI tasks assigned in a round-robin order to the GPUs. Currently, for large runs, 1 MPI task should be used per GPU per node. For smaller calculations, use of multiple MPI tasks per GPU may yield improved performance.

• VMC, wavefunction optimization, DMC.
• Periodic and open boundary conditions. Mixed boundary conditions are not yet supported.
• Wavefunctions:
  1. Single Slater determinants with 3D B-spline orbitals. Twist-averaged boundary conditions and complex wavefunctions are fully supported. Gaussian type orbitals are not supported yet.
  2. Hybrid Mixed basis representation in which orbitals are represented as 1D splines times spherical harmonics in spherical regions (muffin tins) around atoms, and 3D B-splines in the interstitial region.
  3. One-body and two-body Jastrows represented as 1D B-splines are supported. Three-body jastrow functions are not yet supported.
• Semilocal (nonlocal and local) pseudopotentials, Coulomb interaction (electron-electron, electron-ion) and Model periodic Coulomb (MPC) interaction.

2.2 Beta test features
This section describes developmental features in QMCPACK that might be ready for production, but require additional testing, features or documentation to be ready for general use. We describe them here because they offer significant benefits and are well tested in specific cases.

2.2.1 High performance CPU SoA optimizations
The Structure-of-Arrays (SoA) optimizations [16] are a set of improved data layouts facilitating vectorization on modern CPUs with wide SIMD units. For many calculations and architectures, the SoA implementation at least doubles the speed of the code. Meanwhile, the memory footprint is dramatically reduced by better algorithms. For full benefit, modern compilers supporting OpenMP 4.0 SIMD are recommended, e.g. GCC version $\geq$4.9 and Intel compiler
versions $\geq 15.0$. Users should check what is currently tested on cdash/ctest and make specific requests to expand the functionality that they need.

As described in 3.5.3, to enable the SoA implementation, QMCPACK should be configured with \\
-DENABLE_SOA=1.

SoA code path currently does NOT support:

- Backflow wavefunctions
- All electron calculations requiring cusp corrected orbitals
- Many observables

If using any non-core feature with the SoA code, please check carefully vs the conventional AoS (non-SOA enabled) code.

2.2.2 Auxiliary-Field Quantum Monte Carlo

The orbital-space Auxiliary-Field Quantum Monte Carlo (AFMQC) method is now available in QMCPACK. The main input for the code are the matrix elements of the Hamiltonian in a given single particle basis set, which must be produced from a mean-field calculations like Hartree-Fock or Density Functional Theory. The code is under active development and many features are currently in development. Check the latest version of QMCPACK for an up-to-date description of the available features. A partial list of the current capabilities of the code follows. For a detailed description of the currently available features, see chapter 15.

- Phaseless AFQMC algorithm of Zhang, et. al. (S. Zhang, H. Krakauer, "Quantum Monte Carlo Method using Phase-Free Random Walks with Slater Determinants", PRL 90, 136401 (2003)).
- "Hybrid" and "local energy" propagation schemes.
- Hamiltonian matrix elements from 1) Molpro’s FCIDUMP format (which can be produced by Molpro, PySCF and VASP) and from 2) internal HDF5 format produced by PySCF (see AFQMC section below).
- AFQMC calculations with RHF (closed shell doubly occupied), ROHF (open shell doubly occupied) and UHF (spin polarized broken symmetry) symmetry.
- Single and Multi-determinant trial wave-functions. Multi-determinant expansions with either orthogonal or non-orthogonal determinants allowed.
- Fast update scheme for orthogonal multi-determinant expansions.
- Distributed propagation algorithms for large systems. Enables calculations where the data structures do not fit on a single node.
- Complex implementation for PBC calculations with complex integrals.
- Sparse representation of large matrices for reduced memory usage.
Chapter 3

Obtaining, installing and validating QMCPACK

This chapter describes how to obtain, build and validate QMCPACK. This process is designed to be as simple as possible and should be no harder than building a modern plane-wave density functional theory code such as Quantum ESPRESSO, QBox, or VASP. Parallel builds enable a complete compilation in under 2 minutes on a fast multicore system. If you are unfamiliar with building codes we suggest working with your system administrator to install QMCPACK.

3.1 Installation steps

To install QMCPACK, follow the steps listed below. Full details of each step are given in the referenced sections.

1. Download the source code, Sections 3.2 or 3.3.

2. Verify that you have the required compilers, libraries and tools installed, Section 3.4.

3. Run the cmake configure step and build with make, Section 3.5 and 3.5.1. Some examples for common systems are given in Section 3.6.

4. Run the tests to verify QMCPACK, Section 3.8.

5. Build the ppconvert utility in QMCPACK, Section 3.10.

6. Download and patch Quantum ESPRESSO. This patch adds the pw2qmcpack utility, Section 3.11.

Hints for high performance are in Section 3.12. Troubleshooting suggestions are in Section 3.13.

Note that there are two different QMCPACK executables that can be produced: the general one, which is the default, and the “complex” version which support periodic calculations at arbitrary twist angles and k-points. This second version is enabled via a cmake configuration parameter, see Section 3.5.3. The general version only supports wavefunctions that can be made real. If you run a calculation that needs the complex version, QMCPACK will stop and inform you.
3.2 Obtaining the latest release version

Major releases of QMCPACK are distributed from http://www.qmcpack.org. These releases undergo the most testing. Unless there are specific reasons we encourage all production calculations to use the latest release versions.

Releases are usually compressed tar files indicating the version number, date, and often the source code revision control number corresponding to the release.

- Untar the archive, e.g., `tar xvf qmcpack_v1.3.tar.gz`

Releases can also be obtained from the 'master' branch of the QMCPACK git repository, similar to obtaining the development version (Sec. 3.3).

3.3 Obtaining the latest development version

The most recent development version of QMCPACK can be obtained anonymously via

```
git clone https://github.com/QMCPACK/qmcpack.git
```

Once checked-out, updates can be made via the standard `git pull`.

The 'develop' branch of the git repository contains the day-to-day development source with the latest updates, bugfixes etc. This may be useful for updates to the build system to support new machines, for support of the latest versions of Quantum ESPRESSO, or for updates to the documentation. Note that the development version may not be fully consistent with the online documentation. We attempt to keep the development version fully working. However, please be sure to run the tests and compare with previous release versions before using for any serious calculations. We try to keep bugs out, but occasionally they crawl in! Reports of any breakages are appreciated.

3.4 Prerequisites

The following are required to build QMCPACK. For workstations, these are available via the standard package manager. On shared supercomputers this software is usually installed by default and is often access via a modules environment - check your system documentation.

**Use of the latest versions of all compilers and libraries is strongly encouraged**, but not absolutely essential. Generally newer versions are faster - see Section 3.12 for performance suggestions.

- C/C++ compilers such as GNU, Clang, Intel, IBM XL. C++ compilers are required to support C++11 standard. Use of recent ("current year version") compilers is strongly encouraged.

- MPI library such as OpenMPI http://open-mpi.org or vendor optimized MPI.

- BLAS/LAPACK, numerical and linear algebra libraries. Use platform-optimized libraries where available, such as Intel MKL. ATLAS or other optimized open-source libraries may also be used http://math-atlas.sourceforge.net
• CMake, build utility, http://www.cmake.org
• Libxml2, XML parser, http://xmlsoft.org
• BOOST, peer-reviewed portable C++ source libraries, http://www.boost.org
• FFTW, FFT library, http://www.fftw.org/

To build the GPU accelerated version of QMCPACK an installation of NVIDIA CUDA development tools is required. Ensure that this is compatible with the C and C++ compiler versions you plan to use. Supported versions are included in the NVIDIA release notes.

Many of the utilities provided with QMCPACK use python (v2). The numpy and matplotlib libraries are required for full functionality.

Note that the standalone einspline library used by previous versions of QMCPACK is no longer required. A more optimized version is included inside. The standalone version should not be on any standard search paths because conflicts between the old and new include files can result.

3.5 Building with CMake

The build system for QMCPACK is based on CMake. It will autoconfigure based on the detected compilers and libraries. The most recent version of CMake has the best detection for the greatest variety of systems - at the time of writing this means CMake 3.4.3. The much older CMake 2.8 is known to work, but might not work optimally on your system.

Previously QMCPACK made extensive use of toolchains, but the build system has since been updated to eliminate the use of toolchain files for most cases. The build system is verified to work with GNU, Intel, and IBM XLC compilers. Specific compile options can be specified either through specific environmental or CMake variables. When the libraries are installed in standard locations, e.g., /usr, /usr/local, there is no need to set environmental or cmake variables for the packages.

3.5.1 Quick build instructions (try first)

If you are feeling lucky and are on a standard UNIX-like system such as a Linux workstation, the following might quickly give a working QMCPACK:

The safest quick build option is to specify the C and C++ compilers through their MPI wrappers. Here we use Intel MPI and Intel compilers. Move to the build directory, run cmake and make

```
cd build
make -j 8
```

You can increase the “8” to the number of cores on your system for faster builds. Substitute mpicc and mpicxx or other wrapped compiler names to suit your system. e.g. With OpenMPI use

```
cd build
make -j 8
```

If you are feeling particularly lucky, you can skip the compiler specification:
cd build
cmake ..
make -j 8

The complexities of modern computer hardware and software systems are such that you should check that the autoconfiguration system has made good choices and picked optimized libraries and compiler settings before doing significant production. i.e. Check the details below. We give examples for a number of common systems in Section 3.6.

3.5.2 Environment variables

A number of environmental variables affect the build. In particular they can control the default paths for libraries, the default compilers, etc. The list of environmental variables is given below:

- CXX: C++ compiler
- CC: C Compiler
- MKL_ROOT: Path for MKL
- LIBXML2_HOME: Path for libxml2
- HDF5_ROOT: Path for HDF5
- BOOST_ROOT: Path for Boost
- FFTW_HOME: Path for FFTW

3.5.3 Configuration options

In addition to reading the environmental variables, CMake provides a number of optional variables that can be set to control the build and configure steps. When passed to CMake, these variables will take precedence over the environmental and default variables. To set them add -D FLAG=VALUE to the configure line between the cmake command and the path to the source directory.

- Key QMCPACK build options
  - QMC_CUDA: Enable CUDA and GPU acceleration (1:yes, 0:no)
  - QMC_COMPLEX: Build the complex (general twist/k-point) version (1:yes, 0:no)
  - QMC_MIXED_PRECISION: Build the mixed precision (mixing double/float) version (1:yes (GPU default), 0:no (CPU default)).
    - The CPU support is experimental.
    - Use float and double for base and full precision.
    - The GPU support is quite mature.
    - Use always double for host side base and full precision and use float and double for CUDA base and full precision.
  - ENABLE_TIMERS: Enable fine-grained timers (1:yes, 0:no (default)).
    - Timers are off by default to avoid potential slowdown in small systems. For large systems (100+ electrons) there is no risk.
  - ENABLE_SOA: (Experimental) Enable CPU optimization and GPU support using Structure-of-Array (SoA) datatypes (1:yes, 0:no (default)).

- General build options
  - CMAKE_BUILD_TYPE: A variable which controls the type of build (defaults to Release). Possible values are:
    - None (Do not set debug/optimze flags, use CMAKE_C_FLAGS or CMAKE_CXX_FLAGS)
    - Debug (create a debug build)
    - Release (create a release/optimized build)
    - RelWithDebInfo (create a release/optimized build with debug info)
MinSizeRel (create an executable optimized for size)

CMAKE_C_COMPILER Set the C compiler
CMAKE_CXX_COMPILER Set the C++ compiler
CMAKE_C_FLAGS Set the C flags. Note: to prevent default
debug/release flags from being used, set the CMAKE_BUILD_TYPE=None
Also supported: CMAKE_C_FLAGS_DEBUG,
CMAKE_C_FLAGS_RELEASE, and CMAKE_C_FLAGS_RELWITHDEBINFO
CMAKE_CXX_FLAGS Set the C++ flags. Note: to prevent default
debug/release flags from being used, set the CMAKE_BUILD_TYPE=None
Also supported: CMAKE_CXX_FLAGS_DEBUG,
CMAKE_CXX_FLAGS_RELEASE, and CMAKE_CXX_FLAGS_RELWITHDEBINFO

- Additional QMCPACK build options

QMCLUDE Add extra include paths
QM_EXTRA_LIBS Add extra link libraries
QM_BUILD_STATIC Add -static flags to build
QM_DATA Specify data directory for QMCPACK performance and integration tests
QE_BIN Location of Quantum Espresso binaries including pw2qmcpack.x

- Intel MKL related

ENABLE_MKL Enable Intel MKL libraries (1:yes (default for intel compiler),
0:no (default otherwise)).
MKL_ROOT Path to MKL libraries (only necessary for non intel compilers
or intel without standard environment variables.)
One of the above environment variables can be used.

- Libxml2 related

Libxml2_INCLUDE_DIRS Specify include directories for libxml2
Libxml2_LIBRARY_DIRS Specify library directories for libxml2

- HDF5 related

ENABLE_PHDF5 1(default)/0, enables/disable parallel collective IO.

- FFTW related

FFTW_INCLUDE_DIRS Specify include directories for FFTW
FFTW_LIBRARY_DIRS Specify library directories for FFTW

- CTest related

MPIEXEC Specify the mpi wrapper, e.g. srun, aprun, mpirun, etc.
MPIEXEC_NUMPROC_FLAG Specify the number of mpi processes flag,
e.g. "-n", "-np", etc.

3.5.4 Role of QMC_DATA

QMCPACK includes a variety of optional performance and integration tests that use research
quality wavefunctions to obtain meaningful performance and to more thoroughly test the code.
The necessarily large input files are stored in the location pointed to by QMC_DATA, e.g. scratch
or long-lived project space on a supercomputer. These files are not included in the source code
distribution to minimize size. The tests are activated if cmake detects the files when configured. See

tests/performance/NiO/README, tests/solids/NiO_afqmc/README and tests/performance/C-

graphite/README for details of the current tests, input files, and downloading them.

Currently the files must be downloaded via

https://anl.box.com/s/pveyyzrc2wuvg5tmxjzzwxeo561vh3r0 and

https://anl.box.com/s/j5d6jeazpgx5441s04ajtv77iogoyjsh.

A complete set of files is currently:

QMC_DATA/C-graphite/lda.pwscf.h5
QMC_DATA/NiO/NiO-fcc-supertwist111-supershift000-S1.h5
QMC_DATA/NiO/NiO-fcc-supertwist111-supershift000-S2.h5
QMC_DATA/NiO/NiO-fcc-supertwist111-supershift000-S4.h5
QMC_DATA/NiO/NiO-fcc-supertwist111-supershift000-S8.h5
QMC_DATA/NiO/NiO-fcc-supertwist111-supershift000-S16.h5
QMC_DATA/NiO/NiO-fcc-supertwist111-supershift000-S32.h5
QMC_DATA/NiO/NiO-fcc-supertwist111-supershift000-S64.h5
QMC_DATA/NiO/NiO-fcc-supertwist111-supershift000-S128.h5
QMC_DATA/NiO/NiO-fcc-supertwist111-supershift000-S256.h5
QMC_DATA/NiO/NiO_fcc_fcidump.h5
QMC_DATA/NiO/NiO_fcc_wfn.dat
QMC_DATA/NiO/NiO_nm_choldump.h5

3.5.5 Configure and build using cmake and make

To configure and build QMCPACK, move to build directory, run cmake and make

cd build
cmake ..
make -j 8

As you will have gathered, cmake encourages “out of source” builds, where all the files for

a specific build configuration reside in their own directory separate from the source files. This

allows multiple builds to be created from the same source files which is very useful where the

filesystem is shared between different systems. You can also build versions with different settings

(e.g. QMC_COMPLEX) and different compiler settings. The build directory does not have to be
called build - use something descriptive such as build_machinename or build_complex. The “..” in
the cmake line refers to the directory containing CMakeLists.txt. Update the “..” for other build
directory locations.

3.5.6 Example configure and build

- Set the environments (the examples below assume bash, Intel compilers and MKL library)

    export CXX=icpc
    export CC=icc
    export LIBXML2_HOME=/usr/local
    export MKL_ROOT=/usr/local/intel/mkl/10.0.3.020
    export HDF5_ROOT=/usr/local
    export BOOST_ROOT=/usr/local/boost
    export FFTW_HOME=/usr/local/fftw

- Move to build directory, run cmake and make

    cd build
cmake -D CMAKE_BUILD_TYPE=Release ..
make -j 8

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3.5.7 Build scripts

It is recommended to create a helper script that contains the configure line for CMake. This is particularly useful when avoiding environmental variables, packages are installed in custom locations, or if the configure line is long or complex. In this case it is also recommended to add "rm -rf CMake*" before the configure line to remove existing CMake configure files to ensure a fresh configure each time that the script is called. Deleting all the files in the build directory is also acceptable. If you do so we recommend to add some sanity checks in case the script is run from the wrong directory, e.g., checking for the existence of some QMCPACK files.

Some build script examples for different systems are given in the config directory. For example, on Cray systems these scripts might load the appropriate modules to set the appropriate programming environment, specific library versions etc.

An example script build.sh is given below. It is much more complex than usually needed for comprehensiveness:

```bash
export CXX=mpic++
export CC=mpicc
export ACML_HOME=/opt/acml-5.3.1/gfortran64
export HDF5_ROOT=/opt/hdf5
export BOOST_ROOT=/opt/boost
rm -rf CMake*

cmake
  -D CMAKE_BUILD_TYPE=Debug
  -D Libxml2_INCLUDE_DIRS=/usr/include/libxml2
  -D Libxml2_LIBRARY_DIRS=/usr/lib/x86_64-linux-gnu
  -D FFTW_INCLUDE_DIRS=/usr/include
  -D FFTW_LIBRARY_DIRS=/usr/lib/x86_64-linux-gnu
  -D QMC_EXTRA_LIBS="-ldl ${ACML_HOME}/lib/libacml.a -lgfortran"
  -D QMC_DATA=/projects/QMCPACK/qmc-data
...
```

3.5.8 Using vendor optimized numerical libraries, e.g. Intel MKL

Although QMC does not make extensive use of linear algebra, use of vendor optimized libraries is strongly recommended for highest performance. BLAS routines are used in the Slater determinant update, the VMC wavefunction optimizer and to apply orbital coefficients in local basis calculations. Vectorized math functions are also beneficial, e.g. for the phase factor computation in solid state calculations. CMake is generally successful in finding these libraries, but specific combinations can require additional hints, as described below:

Using Intel MKL with non-Intel compilers

To use Intel MKL with, e.g. an MPICH wrapped gcc:

```bash
cmake
  -D CMAKE_C_COMPILER=mpicc
  -D CMAKE_CXX_COMPILER=mpicxx
  -D ENABLE_MKL=1
  -D MKL_ROOT=$MKLROOT/lib
...
```

MKLROOT is the directory containing the MKL binary, examples, and lib directories (etc.) and is often /opt/intel/mkl
3.5.9 Cross compiling

Cross-compiling is often difficult but is required on supercomputers with distinct host and compute processor generations or architectures. QMCPACK tried to do its best with CMake to facilitate cross-compiling.

- On a machine using Cray programming environment, we rely on compiler wrappers provided by Cray to set architecture specific flags correctly. The CMake configure log should indicate that a Cray machine was detected.
- If not on a Cray machine, by default we assume building for the host architecture. e.g. -xHost is added for the Intel compiler and -march=native is added for GNU/Clang compilers.
- If -x/-ax or -march is specified by the user in CMAKE_C_FLAGS and CMAKE_CXX_FLAGS, we respect user’s intention and do not add any architecture specific flags.

The general strategy for cross-compiling should therefore be to manually set CMAKE_C_FLAGS and CMAKE_CXX_FLAGS for the target archicture. Using `make VERBOSE=1` is a useful way to check the final compilation options. If on a Cray machine, selection of the appropriate programming environment should be sufficient.

3.6 Installation instructions for common workstations and supercomputers

This section describes how to build QMCPACK on various common systems including multiple Linux distributions, Apple OS X, and various supercomputers. The examples should serve as good starting points for building QMCPACK on similar machines. For example, the software environment on modern Crays is very consistent. Note that updates to operating systems and system software may require small modifications to these recipes. See Section 3.12 for key points to check to obtain highest performance and Section 3.13 for troubleshooting hints.

3.6.1 Installing on Ubuntu Linux or other apt-get based distributions

The following is designed to obtain a working QMCPACK build on e.g. a student laptop, starting from a basic Linux installation with none of the developer tools installed. Fortunately, all the required packages are available in the default repositories making for a quick installation. Note that for convenience we use a generic BLAS. For production a platform optimized BLAS should be used.

```
apt-get cmake g++ openmpi-bin libopenmpi-dev libboost-dev
apt-get libatlas-base-dev liblapack-dev libhdf5-dev libxml2-dev fftw3-dev
export CXX=mpiCC
cd build
cmake ..
make -j 8
ls -l bin/qmcpack
```

For qmca and other tools to function, we install some python libraries:

```
sudo apt-get install python-numpy python-matplotlib
```
3.6.2 Installing on CentOS Linux or other yum based distributions

The following is designed to obtain a working QMCPACK build on e.g. a student laptop, starting from a basic Linux installation with none of the developer tools installed. CentOS 7 (Red Hat compatible) is using gcc 4.8.2. The installation is only complicated by the need to install another repository to obtain HDF5 packages which are not available by default. Note that for convenience we use a generic BLAS. For production a platform optimized BLAS should be used.

```bash
sudo yum install make cmake gcc gcc-c++ openmpi openmpi-devel fftw fftw-devel 
       boost boost-devel libxml2 libxml2-devel
sudo yum install blas-devel lapack-devel atlas-devel
module load mpi
```

To setup repoforge as a source for the HDF5 package, go to [http://repoforge.org/use](http://repoforge.org/use). Install the appropriate up to date release package for your OS. By default the CentOS Firefox will offer to run the installer. The CentOS 6.5 settings were still usable for HDF5 on CentOS 7 in 2016, but use CentOS 7 versions when they become available.

```bash
sudo yum install hdf5 hdf5-devel
```

To build QMCPACK

```bash
module load mpi/openmpi-x86_64
which mpirun
# Sanity check; should print something like /usr/lib64/openmpi/bin/mpirun
export CXX=mpiCC
cd build
cmake ..
make -j 8
ls -l bin/qmcpack
```

3.6.3 Installing on Mac OS X using Macports

These instructions assume a fresh installation of macports and use the gcc 6.1 compiler. Older versions are fine, but it is vital to ensure matching compilers and libraries are used for all packages and to force use of what is installed in /opt/local. Performance should be very reasonable. Note that we utilize the Apple provided Accelerate framework for optimized BLAS.

Follow the Macports install instructions [https://www.macports.org/](https://www.macports.org/)

- Install Xcode and the Xcode Command Line Tools
- Agree to Xcode license in Terminal: sudo xcodebuild -license
- Install MacPorts for your version of OS X

Install the required tools:

```bash
sudo port install gcc6
sudo port select gcc mp-gcc6
sudo port install openmpi-devel-gcc6
sudo port select --set mpi openmpi-devel-gcc61-fortran

sudo port install fftw-3 +gcc6
sudo port install libxml2
sudo port install cmake
```
sudo post install boost +gcc6
sudo port install hdf5 +gcc6

sudo port select --set python python27
sudo port install py27-numpy +gcc6
sudo port install py27-matplotlib #For graphical plots with qmca

QMCPACK build:

```bash
cd build
cmake -DCMAKE_C_COMPILER=mpicc -DCMAKE_CXX_COMPILER=mpiCXX ..
make -j 6 # Adjust for available core count
ls -l bin/qmcpack
```

Cmake should pickup the versions of HDF5, libxml (etc.) installed in /opt/local by macports. If you have other copies of these libraries installed and wish to force use of a specific version, use the environment variables detailed in Sec. 3.5.2.

This recipe was verified on 1 July 2016 on a Mac running OS X 10.11.5 “El Capitain”.

### 3.6.4 Installing on Mac OS X using Homebrew (brew)

Homebrew is a package manager for OS X that provides a convenient route to install all the QMCPACK dependencies. The following recipe will install the latest available versions of each package. This was successfully tested under OS X 10.12 “Sierra” in December 2017. Note that it is necessary to build the MPI software from source to use the brew-provided gcc instead of Apple CLANG.

1. Install Homebrew from [http://brew.sh/](http://brew.sh/)

   ```bash
   /usr/bin/ruby -e "$(curl -fsSL https://raw.githubusercontent.com/Homebrew/install/master/install)"
   ```

2. Install the prerequisites

   ```bash
   brew install gcc # installs gcc 7.2.0 on 2017-12-19
   export HOMEBREW_CXX=g++-7
   export HOMEBREW_CC=gcc-7
   brew install mpich2 --build-from-source
   # Build from source required to use homebrew compiled compilers as
   # opposed to Apple CLANG. Check "mpicc -v" indicates Homebrew gcc
   brew install cmake
   brew install fftw
   brew install boost
   brew install homebrew/science/hdf5
   #Note: Libxml2 is not required via brew since OS X already includes it.
   ```

3. Configure and build QMCPACK

   ```bash
   cmake -DCMAKE_C_COMPILER=/usr/local/bin/mpicc \
   -DCMAKE_CXX_COMPILER=/usr/local/bin/mpicxx ..
   make -j 12
   ```

4. Run the short tests. When MPICH is used for the first time, OS X will request approval of the network connection for each executable.

   ```bash
   ctest -R short
   ```
3.6.5 Installing on ANL ALCF Mira/Cetus IBM Blue Gene/Q

Mira/Cetus is a Blue Gene/Q supercomputer at Argonne National Laboratory’s Argonne Leadership Computing Facility (ANL ALCF). Mira has 49152 compute nodes and each node has a 16-core PowerPC A2 processor with 16 GB DDR3 memory. Due to the fact that the login nodes and the compute nodes have different processors with distinct instruction sets, cross-compiling is required on this platform. See details about using Blue Gene/Q at [http://www.alcf.anl.gov/user-guides/compiling-linking](http://www.alcf.anl.gov/user-guides/compiling-linking). On Mira, compilers are loaded via softenv and users need to add +mpiwrapper-bgclang and +cmake in $HOME/.soft. In order to build QMCPACK, a toolchain file is provided for setting up CMake and the cmake command should be executed twice. **BGClang is required for C++11 support. IBM XL C/C++ compiler should not be used.**

```bash
cd build
cmake -DCMAKE_TOOLCHAIN_FILE=../config/BGQ_Clang++11_ToolChain.cmake ..
cmake -DCMAKE_TOOLCHAIN_FILE=../config/BGQ_Clang++11_ToolChain.cmake ..
make -j 16
ls -l bin/qmcpack
```

3.6.6 Installing on ALCF Theta, Cray XC40

Theta is a 9.65 petaflops system manufactured by Cray with 3624 compute nodes. Each node features a second-generation Intel Xeon Phi 7230 processor and 192 GB DDR4 RAM.

```bash
export CRAYPE_LINK_TYPE=dynamic
module unload cray-libsci
module load cray-hdf5-parallel
export BOOST_ROOT=/soft/libraries/boost/1.64.0/intel
cmake ..
make -j 24
ls -l bin/qmcpack
```

3.6.7 Installing on ORNL OLCF Titan Cray XK7 (NVIDIA GPU accelerated)

Titan is a GPU accelerated supercomputer at Oak Ridge National Laboratory’s Oak Ridge Leadership Computing Facility (ORNL OLCF). Each compute node has a 16 core AMD 2.2GHz Opteron 6274 (Interlagos) and an NVIDIA Kepler accelerator. The standard Cray software environment is available, with libraries accessed via modules. The only extra settings required to build the GPU version are the cudatoolkit module and specifying -DQMC_CUDA=1 on the cmake configure line. Note that on Crays the compiler wrappers “CC” and “cc” are used. The build system checks for these and does not (should not) use the compilers directly.

```bash
export CRAYPE_LINK_TYPE=dynamic
module swap PrgEnv-pgi PrgEnv-gnu # Use gnu compilers
module load cudatoolkit # CUDA for GPU build
module load cray-hdf5-parallel
module load cmake3
module load fftw
export FFTW_HOME=$FFTW_DIR/..
module load boost
mkdir build_titan_gpu
cd build_titan_gpu
export CC=cc
export CXX=CC
```
3.6.8 Installing on ORNL OLCF Titan Cray XK7 (CPU version)

As noted in Section 3.6.7 for the GPU, building on Crays requires only loading the appropriate library modules.

```bash
cmake -DQMC_CUDA=1 .. # Must enable CUDA capabilities
make -j 8
ls -l bin/qmcpack
```

3.6.9 Installing on ORNL OLCF Eos Cray XC30

Eos is a Cray XC30 with 16 core Intel Xeon E5-2670 processors connected by the Aries interconnect. The build process is identical to Titan, except that we use the default Intel programming environment. This is usually preferred to GNU.

```bash
export CRAYPE_LINK_TYPE=dynamic
module swap PrgEnv-pgi PrgEnv-gnu # Use gnu compilers
module unload cudatoolkit # No CUDA for CPU build
module load cray-hdf5-parallel
module load cmake3
module load fftw
export FFTW_HOME=$FFTW_DIR/..
module load boost
mkdir build_eos
cd build_eos
export CC=cc
export CXX=CC
cmake ..
make -j 8
ls -l bin/qmcpack
```

3.6.10 Installing on ORNL OLCF SummitDev

SummitDev is the development cluster for the next GPU accelerated supercomputer Summit at Oak Ridge National Laboratory’s Leadership Computing Facility (ORNL OLCF). It has IBM Power8 CPUs and NVIDIA Pascal GPUs.

Building QMCPACK

Please note that these build instructions are preliminary as the software environment is subject to change. QMCPACK can be build with the following commands:
module load xl
module load essl
module load netlib-lapack
module load hdf5/1.8.18
module load fftw
export FFTW_HOME=$OLCF_FFTW_ROOT
module load python
module load cmake
module load boost
module load cuda
mkdir build_summitdev
cd build_summitdev
cmake -DCMAKE_C_COMPILER="mpixlc" 
   -DCMAKE_CXX_COMPILER="mpixlC" 
   -DBUILD_LMYENGINE_INTERFACE=0 
   -DQMC_CUDA=1 \ 
   -DCUDA_ARCH="sm_60" \ 
   ..
make -j 8
ls -l bin/qmcpack

3.6.11 Installing on NERSC Edison Cray XC30

Edison is a Cray XC30 with dual 12-core Intel "Ivy Bridge" nodes installed at NERSC. The build settings are identical to eos.

export CRAYPE_LINK_TYPE=dynamic
module unload cray-libsci
module load boost
cmake ..
make -j 8
ls -l bin/qmcpack

When the above was tested on 15 September 2017, the following module and software versions were present:

qmcpack@edison04:trunk> module list
Currently Loaded Modulefiles:
  1) modules/3.2.10.6 14) rca/2.2.11-6.0.4.0_13.2__g84de67a.ari
  2) intel/17.0.2.174 15) atp/2.1.1
  3) craype-network-aries 16) PrgEnv-intel/6.0.4
  4) craype/2.5.12.3 17) craype-ivybridge
  5) udreg/2.3.2-6.0.4.0_12.2__g2f9c3ee.ari 18) cray-shmem/7.6.0
  6) ugni/6.0.14-6.0.4.0_14.1__ge?db4a2.ari 19) cray-mpich/7.6.0
  7) pmi/5.0.12 20) altld/2.0
  8) dmapp/7.1.1-6.0.4.0_46.2__q8b8abda2.ari 21) darshan/3.1.4
  9) gni-headers/5.0.11-6.0.4.0_7.2__g7136988.ari 22) boost/1.63
 10) xpmem/2.2.2-6.0.4.0_3.1__g43b0535.ari 23) cmake/3.8.1
 11) job/2.2.2-6.0.4.0_8.2__g3644b5.ari 24) cray-hdf5-parallel/1.10.0.3
 12) dvs/2.7.2.2.30-6.0.4.1_5.4__qd731684 25) libxml2/2.9.4
 13) alps/6.4.1-6.0.4.0_7.2__g86d8f3d.ari

3.6.12 Installing on NERSC Cori, Haswell Partition, Cray XC40

Cori is a Cray XC40 with 16-core Intel "Haswell" nodes installed at NERSC.
export CRAYPE_LINK_TYPE=dynamic
module unload cray-libsci
module load boost
module load cray-hdf5-parallel
module load cmake
mkdir build_cori_hsw
cd build_cori_hsw
cmake .
make -j 16
ls -l bin/qmcpack

When the above was tested on 29 August 2017, the following module and software versions were present:

build_cori_hsw> module list
Currently Loaded Modulefiles:
  1) modules/3.2.10.6
  2) nsg/1.2.0
  3) intel/17.0.2.174
  4) craype-network-aries
  5) craype/2.5.12
  6) udreg/2.3.2-6.0.4.0_16.2__g2f9c3ee.ari
  7) ugni/6.0.14-6.0.4.0_16.1__ge7db4a2.ari
  8) pmi/5.0.12
  9) dmmpp/7.1.1-6.0.4.0_46.2__gb8abda2.ari
 10) gni-headers/5.0.11-6.0.4.0_7.2__g7136988.ari
 11) xpmem/2.2.2-6.0.4.0_3.1__g43b0535.ari
 12) job/2.2.2-6.0.4.0_8.2__g3c644b5.ari
 13) dvs/2.7.2.2.31-6.0.4.1_6.1__gb3b87e6
 14) alps/6.4.1-6.0.4.0_7.2__g86d0f3d.ari
 15) rca/2.2.11-6.0.4.0_13.2__g84de67a.ari
 16) atp/2.1.1
 17) PrgEnv-intel/6.0.4
 18) craype-haswell
 19) cray-shmem/7.6.0
 20) cray-mpich/7.6.0
 21) altd/2.0
 22) darshan/3.1.4
 23) boost/1.61
 24) cmake/3.3.2
 25) cray-hdf5-parallel/1.10.0.3

3.6.13 Installing on NERSC Cori, Xeon Phi KNL partition, Cray XC40

The second phase of NERSC's Cori uses Intel Xeon Phi Knight's Landing (KNL) nodes. The following build recipe ensures that the code generation is appropriate for the KNL nodes:

export CRAYPE_LINK_TYPE=dynamic
module swap craype-haswell craype-mic-knl
module unload cray-libsci
module load boost
module load cray-hdf5-parallel
module load cmake
mkdir build_cori_knl
cd build_cori_knl
cmake ..
make -j 16
ls -l bin/qmcpack

When the above was tested on 29 August 2017, the following module and software versions were present:

build_cori_knl> module list
Currently Loaded Modulefiles:
  1) modules/3.2.10.6
  2) nsg/1.2.0
  3) intel/17.0.2.174
  4) craype-network-aries
  5) craype/2.5.12
  10) gni-headers/5.0.11-6.0.4.0_7.2__g7136988.ari
  11) xpmem/2.2.2-6.0.4.0_3.1__g43b0535.ari
  12) job/2.2.2-6.0.4.0_8.2__g3c644b5.ari
  13) dvs/2.7.2.2.31-6.0.4.1_6.1__gb3b87e6
  14) alps/6.4.1-6.0.4.0_7.2__g86d0f3d.ari
3.6.14 Installing on Windows

Install the Windows Subsystem for Linux and Bash on Windows. Open a bash shell and follow the install directions for Ubuntu in Section 3.6.1.

3.7 Installing via Spack (Beta)

Spack is a relatively new package manager for scientific software. One of goals of Spack is to reduce the barrier for the user to install scientific software. Spack is intended to work on everything from laptop computers to high-end supercomputers. More information about Spack can be found here https://spack.readthedocs.io/en/latest. The major advantage of installation with Spack is that all dependencies are automatically built, potentially including all the compilers and libraries, and different versions of QMCPACK can easily co-exist with each other. The QMCPACK Spack package also knows how to build and patch Quantum Espresso automatically. In principle QMCPACK may be installed with a single Spack command, but to use vendor optimized compilers and libraries requires additional configuration.

3.7.1 Setting up the Spack Environment

Begin by cloning Spack from GitHub and configuring your shell as described here: https://spack.readthedocs.io/en/latest/getting_started.html. The goal of the next several steps is to set-up the Spack environment for building. Firstly, it is highly recommended to limit the number of build jobs to a reasonable value for your machine. This can be accomplished by modifying your ~/.spack/config.yaml file as follows:

```yaml
config:
  build_jobs: 16
```

Next, make sure any existing compilers are properly detected. For many architectures, compilers are properly detected with no additional effort.

```
your-laptop> spack compilers
==> Available compilers
  gcc sierra-x86_64 --------------------------------------------
  gcc@7.2.0 gcc@6.4.0 gcc@5.5.0 gcc@4.9.4 gcc@4.8.5 gcc@4.7.4 gcc@4.6.4
```

However, if your compiler is not automatically detected, it is straightforward to add one:

```
your-laptop> spack compiler add <path-to-compiler>
```

This last step is the most troublesome. Pre-installed packages are not automatically detected. If vendor optimized libraries and already installed, you will need to manually add them to your ~/.spack/packages.yaml. For example, this works on Mac OS X for the Intel MKL package.

```
your-laptop> cat ~/.spack/packages.yaml
packages:
  intel-mkl:
    paths:
      intel-mkl@2018.0.128: /opt/intel/compilers_and_libraries_2018.0.104/mac
    buildable: False
```
Some trial-and-error may be involved to get the directory correct. If you do not include enough of the tree path, Spack will not be able to register the package in its database. More information about system packages can be found here

http://spack.readthedocs.io/en/latest/getting_started.html#system-packages

### 3.7.2 Building QMCPACK

The QMCPACK Spack package has a number of variants to support different compile time options and different versions of the application. A full list can be displayed by typing:

```
your laptop> spack info qmcpack
```

**Description:**
QMCPACK, is a modern high-performance open-source Quantum Monte Carlo (QMC) simulation code.

**Homepage:** [http://www.qmcpack.org/](http://www.qmcpack.org/)

**Tags:** None

**Preferred version:**
3.4.0 [git] https://github.com/QMCPACK/qmcpack.git

**Safe versions:**
develop [git] https://github.com/QMCPACK/qmcpack.git
3.4.0 [git] https://github.com/QMCPACK/qmcpack.git
3.3.0 [git] https://github.com/QMCPACK/qmcpack.git
3.2.0 [git] https://github.com/QMCPACK/qmcpack.git
3.1.1 [git] https://github.com/QMCPACK/qmcpack.git
3.1.0 [git] https://github.com/QMCPACK/qmcpack.git

**Variants:**

<table>
<thead>
<tr>
<th>Name</th>
<th>Default</th>
<th>Allowed values</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>build_type</td>
<td>[RelWithDebInfo]</td>
<td>Debug, Release, RelWithDebInfo, MinSizeRel</td>
<td>CMake build type</td>
</tr>
<tr>
<td>complex</td>
<td>[off]</td>
<td>True, False</td>
<td>Build the complex (general twist/k-point) version</td>
</tr>
<tr>
<td>cuda</td>
<td>[off]</td>
<td>True, False</td>
<td>Enable CUDA and GPU acceleration</td>
</tr>
<tr>
<td>da</td>
<td>[off]</td>
<td>True, False</td>
<td>Install with support for basic data analysis tools</td>
</tr>
<tr>
<td>debug</td>
<td>[off]</td>
<td>True, False</td>
<td>Build debug version</td>
</tr>
<tr>
<td>gui</td>
<td>[off]</td>
<td>True, False</td>
<td>Install with Matplotlib (long installation time)</td>
</tr>
<tr>
<td>mixed</td>
<td>[off]</td>
<td>True, False</td>
<td>Build the mixed precision (mixture of single and double precision) version for gpu and cpu</td>
</tr>
<tr>
<td>mpi</td>
<td>[on]</td>
<td>True, False</td>
<td>Build with MPI support</td>
</tr>
<tr>
<td>qe</td>
<td>[on]</td>
<td>True, False</td>
<td>Install with patched Quantum Espresso 5.3.0</td>
</tr>
<tr>
<td>soa</td>
<td>[off]</td>
<td>True, False</td>
<td>Build with Structure-of-Array instead of Array-of-Structure code. Only for CPU code and only in mixed precision</td>
</tr>
</tbody>
</table>
For example, to install the complex version of QMCPACK in mixed-precision use:

```bash
your-laptop> spack install qmcpack+mixed+complex%gcc@7.2.0 ^intel-mkl
```

where

```bash
%gcc@7.2.0
```
specifies the compiler version to be used and

```bash
^intel-mkl
```
specifies the Intel MKL should be used as the BLAS and LAPACK provider.

It is also possible to run the QMCPACK regression tests as part of the installation process, for example:

```bash
your-laptop> spack install --test=root qmcpack+mixed+complex%gcc@7.2.0 ^intel-mkl
```

will run the unit and short tests. The current behavior of the QMCPACK Spack package is to completed the install as long as all the unit tests pass. If the short tests fail, a warning is issued at the command prompt.

### 3.7.3 Loading QMCPACK into your environment

Spack does not set-up an environment to find its packages automatically. A few additional steps are needed. First, install the modules package by executing:

```bash
your-laptop> spack install environment-modules
```

Then modify your `.cshrc` file with something like

```bash
source ${HOME}/spack/opt/spack/darwin-sierra-x86_64/
    clang-7.3.0-apple/environment-modules-3.2.10-kenvhysdws4zw26tvbrj137fdyn7inhb/
    Modules/init/csh
```

You should then be able to load the qmcpack binary into your path by invoking

```bash
your-laptop> spack load qmcpack+mixed+complex%gcc@7.2.0
```

or more generally

```bash
your-laptop> spack load qmcpack+<spec>
```
3.7.4 Installing QMCPACK with Spack on Linux

Spack works robustly on the standard flavors of Linux (Ubuntu, CentOS, Ubuntu, etc.) using GCC or Intel compilers.

3.7.5 Installing QMCPACK with Spack on Mac OS X

Spack works on Mac OS X, but requires installation of a few packages using Homebrew. You will need to install at minimum the GCC compilers, CMake, and pkg-config. Intel compiler for Mac on OS X is not well supported by Spack packages and will most likely lead to a compile time failure in one of QMCPACK’s dependencies.

3.7.6 Installing QMCPACK with Spack on IBM Blue Gene

Untested at this time. In principle, it should work as long as each of package found in

Blue Gene prompt> spack spec qmcpack

can be compiled for the compute nodes.

3.7.7 Installing QMCPACK with Spack on Cray Supercomputers

There are a number of issues in the Cray module environment. Spack contributors are working to fix these problems. We will update this section once we have a recipe that works reliably.

3.7.8 Reporting Bugs

Bugs with the QMCPACK Spack package should be filed as a GitHub issue against this fork https://github.com/naromero77/spack

3.8 Testing and validation of QMCPACK

We strongly encourage running the included tests each time QMCPACK is built. These compare the results from the executable with known-good mean-field, quantum chemical, and other QMC results.

The tests included with QMCPACK currently mainly test the VMC code with single determinant wavefunction and simple spline Jastrow wavefunctions, and for gaussian and periodic spline basis sets. We check that the known mean field results are obtained with no Jastrow. When Jastrow functions are included we test against previous QMC data. The tests are statistical with a generous 3 $\sigma$ tolerance, however the system sizes are small, typically < 10 electrons, so the error bars are typically small. Limited DMC and optimizer tests included and are scheduled for expansion.

The “short” tests only take a few minutes on a 16 core machine. You can run these tests using the command below in the build directory:

ctest -R short # Run the tests with "short" in their name

The output should be similar to the following:

Test project build_gcc
  Start 1: short-LiH_dimer_ae-vmc_hf_noj-16-1
1/44 Test  #1: short-LiH_dimer_ae-vmc_hf_noj-16-1 .............. Passed  11.20 sec
  Start 2: short-LiH_dimer_ae-vmc_hf_noj-16-1-kinetic
Note that the number of tests that are run varies between the standard, complex, and GPU compilations.

The full set of tests consist of significantly longer versions of the short tests, as well as tests of the conversion utilities. The runs require several hours each for improved statistics and a much more stringent test of the code. To run all the tests simply run ctest in the build directory:

ctest # Run all the tests. This will take several hours.

You can also run verbose tests which direct the QMCPACK output to the standard output:

cctest -V -R short # Verbose short tests

The test system includes specific tests for the complex version of the code.

The input data files for the tests are located in the tests directory. The system-level test directories are grouped into heg, molecules, and solids, with particular physical systems under each (for example molecules/H4_ae). Under each physical system directory there may be tests for multiple QMC methods or parameter variations. The numerical comparisons and test definitions are in the CMakeLists.txt file in each physical system directory.

If all the QMC tests fail it is likely that the appropriate mpiexec (or aprun, srun) is not being called or found. If the QMC runs appear to work but all the other tests fail it is possible that python is not working on your system - we suggest checking some of the test console output in build/Testing/Temporary/LastTest.log or the output files under build/tests/.

Note that because most of these tests are very small, consisting of only a few electrons, the performance is not representative of larger calculations. For example, while the calculations might fit in cache, there will be essentially no vectorization due to the small electron counts. **These tests should therefore not be used for any benchmarking or performance analysis.**

Example runs that can be used for testing performance are described in Sec. 3.8.3

### 3.8.1 Unit tests

QMCPACK has a set of unit tests. All of the unit tests can be run with the following command (in the build directory):

cctest -L unit

The output should look similar to the following:

Test project qmcpack/build

Start 1: unit_test_numerics

1/11 Test #1: unit_test_numerics ............... Passed 0.06 sec

---

1The suffix ‘ae’ is short for ‘all-electron’ and ‘pp’ is short for ‘pseudopotential’
3.8.2 Integration tests with Quantum Espresso

As described in Sec. 3.11, it is possible to test entire workflows of trial wavefunction generation, conversion, and eventual QMC calculation. A patched QE must be installed so that the pw2qmcpack converter is available.

By adding 

```bash
-D QE_BIN=your_QE_binary_path
```

in the cmake command line when building your QMCPACK, tests named with “qe-” prefix will be included in the test set of your build. You can test the whole pw→pw2qmcpack→qmcpack workflow by

```bash
ctest -R qe
```

This provides a very solid test of the entire QMC toolchain for plane wave generated wavefunctions.

3.8.3 Performance tests

Performance tests representative of real research runs are included in the tests/performance directory. They can be used for benchmarking, comparing machine performance, or assessing optimizations. This is in contrast to the majority of the conventional integration tests where the particle counts are too small to be representative. Care is still needed to remove initialization, I/O, and compute a representative performance measure.

The ctest integration is sufficient to run the benchmarks and measure relative performance from version to version of QMCPACK and assess proposed code changes. Performance tests are prefixed with “performance”. To obtain highest performance on a particular platform, you must run the benchmarks in a standalone manner and tune thread counts, placement, walker count (etc.) This is essential to fairly compare different machines. Check with the developers if you are unsure of what is a fair change.

**NiO performance tests**

Follow the instructions in tests/performance/NiO/README to enable and run the NiO tests.

The NiO tests are for bulk supercells of varying size. The QMC runs consist of short blocks of (i) VMC without drift (ii) VMC with drift term included (iii) DMC with constant population. The tests use spline wavefunctions that must be downloaded as described in the README due to their large
size. You will need to set 

```
-DQMC_DATA=YOUR_DATA_FOLDER -DENABLE_TIMERS=1
```

when running cmake as described in the README.

Two sets of wavefunction are tested: spline orbitals with a one and two body Jastrow functions, and a more complex form with an additional three body Jastrow function. The Jastrows are the same for each run and are not reoptimized, as might be done for research purposes. Runs in the hundreds of electrons up to low thousands of electrons are representative of research runs performed in 2017. The largest runs target future machines and require very large memory.

<table>
<thead>
<tr>
<th>Performance Test Name</th>
<th>Historical name</th>
<th>Atoms</th>
<th>Electrons</th>
<th>Electrons/spin</th>
</tr>
</thead>
<tbody>
<tr>
<td>performance-NiO-cpu-a32-e384</td>
<td>S8</td>
<td>32</td>
<td>384</td>
<td>192</td>
</tr>
<tr>
<td>performance-NiO-cpu-a64-e768</td>
<td>S16</td>
<td>64</td>
<td>768</td>
<td>384</td>
</tr>
<tr>
<td>performance-NiO-cpu-a128-e1536</td>
<td>S32</td>
<td>128</td>
<td>1536</td>
<td>768</td>
</tr>
<tr>
<td>performance-NiO-cpu-a256-e3072</td>
<td>S64</td>
<td>256</td>
<td>3072</td>
<td>1536</td>
</tr>
<tr>
<td>performance-NiO-cpu-a512-e6144</td>
<td>S128</td>
<td>512</td>
<td>6144</td>
<td>3072</td>
</tr>
<tr>
<td>performance-NiO-cpu-a1024-e12288</td>
<td>S256</td>
<td>1024</td>
<td>12288</td>
<td>6144</td>
</tr>
</tbody>
</table>

Table 3.1: System sizes and names for NiO performance tests. GPU performance tests are named similarly but have different walker counts.

### 3.8.4 Troubleshooting tests

test reports briefly pass or fail of tests in printout and also collects all the standard outputs to help investigating how tests fail. If the test execution is completed, look at 

```
Testing/Temporary/LastTest.log
```

If you manually stop the testing (ctrl+c), look at 

```
Testing/Temporary/LastTest.log.tmp
```

You can locate the failing tests by searching for the key word ‘Fail’.

### 3.8.5 Slow testing with OpenMPI

OpenMPI has a default binding policy making all the threads running on a single core during testing when there are two or fewer MPI ranks. This significantly increases the testing time. If you are authorized to change the default setting, you can just add `hwloc_base_binding_policy=none` in 

```
/etc/openmpi/openmpi-mca-params.conf
```

### 3.9 Automated testing of QMCPACK

The QMCPACK developers run automatic tests of QMCPACK on several different computer systems, many on a continuous basis. See reports at


We currently test the following combinations nightly (workstations) and weekly (supercomputers):

- On a Linux Intel Xeon workstation:
  - GCC 4.8.5 with OpenMPI and CUDA 8.0 (GPU build, run on NVIDIA K40s)
  - GCC 4.8.5 with OpenMPI with Netlib BLAS
  - GCC 4.8.5 with OpenMPI with Intel MKL
  - Intel 2017 with Intel MPI and MKL
Figure 3.1: Example test results for QMCPACK, showing data for a workstation (Intel, GCC, both CPU and GPU builds) and for two ORNL supercomputers. In this example, 4 errors were found. This dashboard is accessible at https://cdash.qmcpack.org.

- Intel 2015 with Intel MPI and MKL and CUDA 8.0 (GPU build, run on NVIDIA K40s)
- Intel 2015 with Intel MPI and MKL

- On a Linux Intel Knight’s Landing workstation:
  - Intel 2017 with Intel MPI and MKL
  - GCC 4.8.5 with Intel MPI and MKL

- On Eos, a Cray XC30 Intel machine:
  - The default Intel programming environment and compiler with Cray MPI and Intel MKL

- On Titan, a Cray XK7 CPU+GPU machine:
  - The GCC programming environment and compiler with Cray MPI and CUDA
  - The GCC programming environment and compiler with Cray MPI

- On Cetus, an IBM Blue Gene Q machine:
  - Blue Gene Clang 4.0

3.10 Building ppconvert, a pseudopotential format converter

QMCPACK includes a utility, ppconvert, to convert between different pseudopotential formats. Examples include effective core potential formats (in Gaussians), the UPF format used by Quantum ESPRESSO, and the XML format used by QMCPACK itself. The utility also enables the
atomic orbitals to recomputed via a numerical density functional calculation if they need to be
reconstructed for use in an electronic structure calculation.

It is a stand along C++ executable that is not built by default but accessible via adding
-DBUILD_PPCONVERT=1 to cmake and then typing make ppconvert. Userguide is provided in
section 21.3.3.

3.11 Installing and patching Quantum ESPRESSO

For trial wavefunctions obtained in a plane-wave basis we mainly support Quantum ESPRESSO.
Note that ABINIT and QBox were supported historically and could be reactivated.

Quantum ESPRESSO currently stores wavefunctions in a non-standard internal “save” format.
To convert these to a conventional HDF5 format file we have developed a converter, pw2qmcpack.
This is an add on to the Quantum ESPRESSO distribution.

To simplify the process of patching Quantum ESPRESSO we have developed a script that will
automatically download and patch the source code. The patches are specific to each version. e.g.
To download and patch QE v6.3:

cd external_codes/quantum_espresso
./download_and_patch_qe6.3.sh

After running the patch, you must configure Quantum ESPRESSO with the HDF5 capability
enabled in either way:

* if your system already has HDF5 installed with Fortran, use the --with-hdf5 configuration
  option.

    cd qe-6.3
    ./configure --with-hdf5=/opt/local # Specify HDF5 base directory

    check the end of configure output if HDF5 libraries are found properly. If not, either install
    a complete library or use the other scheme. If using a parallel HDF5 library, be sure to use
    the same MPI with QE as used to build the parallel HDF5 library.

    Currently HDF5 support in QE itself is preliminary. To enable use of pw2qmcpack but use
    the old non-HDF5 I/O within QE, replace -D__HDF5 with -D__HDF5_C in make.inc.

    if your system has HDF5 with C only, manually edit make.inc by adding -D__HDF5_C
    and -DH5_USE_16_API in DFLAGS and provide include and library path in IFLAGS and
    HDF5_LIB

    The complete process is described in external_codes/quantum_espresso/README.

    The tests involving pw.x and pw2qmcpack.x have been integrated in the test suite of QMC-
    PACK. By adding -D QE_BIN=your QE_binary_path in the cmake command line when building
    your QMCPACK, tests named with “qe-” prefix will be included in the test set of your build.
    You can test the whole pw→pw2qmcpack→qmcpack workflow by

    ctest -R qe

    See Sec.3.8.2 and the testing section for more details.
3.12 How to build the fastest executable version of QMCPACK

To build the fastest version of QMCPACK we recommend the following:

- Use the latest C++ compilers available for your system. Substantial gains have been made optimizing C++ in recent years.

- Use a vendor optimized BLAS library such as Intel MKL and AMD ACML. Although QMC does not make extensive use of linear algebra, it is used in the VMC wavefunction optimizer, to apply the orbital coefficients in local basis calculations, and in the Slater determinant update.

- Use a vector math library such as Intel VML. For periodic calculations, the calculation of the structure factor and Ewald potential benefit from vectorized evaluation of sin and cos. Currently we only autodetect Intel VML, as provided with MKL, but support for MASSV and AMD LibM is included via #defines. See, e.g. src/Numerics/e2iphi.h. For large supercells, this optimization can gain 10% in performance.

Note that greater speedups of QMC calculations can usually be obtained by carefully choosing the required statistics for each investigation. i.e. Do not compute smaller error bars than necessary.

3.13 Troubleshooting the installation

Some tips to help troubleshoot installations of QMCPACK:

- First, build QMCPACK on a workstation that you control, or on any system that has a simple and up-to-date set of development tools. You can compare the results of cmake and QMCPACK on this system with any more difficult systems you encounter.

- Use up to date development software, particularly a recent CMake.

- Verify that the compilers and libraries that you expect are being configured. It is common to have multiple versions installed. The configure system will stop at the first version it finds which might not be the most recent. If this occurs, specify the appropriate directories and files directly (Section 3.5.3). e.g. cmake -DCMAKE_C_COMPILER=/full/path/to/mpicc -DCMAKE_CXX_COMPILER=/full/path/to/mpicxx ..

- To monitor the compiler and linker settings, use a verbose build, “make VERBOSE=1”. If an individual source file fails to compile you can experiment by hand using the output of the verbose build to reconstruct the full compilation line.

If you still have problems please post to the QMCPACK Google group with full details, or contact a developer.
Chapter 4

Running QMCPACK

QMCPACK requires at least one xml input file, and is invoked via:

qmcpack [command line options] <XML input file(s)>

4.1 Command line options

QMCPACK offers several command line options which affect how calculations are performed. If
the flag is absent, then the corresponding option is disabled.

--dryrun Validate the input file without performing the simulation. This is a good way to ensure
that QMCPACK will do what you think it will.

--help Print version information as well as a list of optional command-line arguments.

--noprint Do not print extra information on Jastrow or pseudopotential. If this flag is not
present, QMCPACK will create several .dat files that contain information about pseudopoten-
tials (one file per PP), and jastrow factors (one per jastrow factor). These file may be
useful for visual inspection of the jastrow, for example.

--save_wfs Write a .h5 file containing the real-space B-spline coefficients of the single particle
wave functions. See the manual §8.2.1 for more information.

--vacuum X deprecated, use ‘vacuum’ input tag described in §7.1.

--version Print version information and optional arguments. Same as --help.

4.2 Input files

The input is one or more XML file(s), documented in chapter §6.

4.3 Output files

QMCPACK generates multiple files, documented in chapter §11.
4.4 Running in parallel

4.4.1 MPI

QMCPACK is fully parallelized with MPI. When performing an ensemble job, all the MPI ranks are first equally divided into groups which perform individual QMC calculations. Within one calculation, all the walkers are fully distributed across all the MPI ranks in the group. Since MPI requires distributed memory, there must be at least one MPI per node. To maximize the efficiency, more facts should be taken into account. When using MPI+threads on compute nodes with more than one NUMA domain (e.g., AMD Interlagos CPU on Titan or a node with multiple CPU sockets), it is recommended to place as many MPI ranks as the number of NUMA domains if the memory is sufficient. On clusters with more than just one GPU per node (NVIDIA Tesla K80), it requires to use the same number of MPI ranks as the number of GPUs per node in order to let each MPI rank take one GPU.

4.4.2 Use of OpenMP threads

Modern processors integrate multiple identical cores even with hardware threads on a single die to increase the total performance and maintain a reasonable power draw. QMCPACK takes advantage of all that compute capability on a processor by using threads via OpenMP programming model as well as threaded linear algebra libraries. By default, QMCPACK is always built with OpenMP enabled. When launching calculations, users should instruct QMCPACK to create the right number of threads per MPI rank by specifying environmental variable OMP_NUM_THREADS. Even in the GPU accelerated version, using threads significantly reduces the time spent on the calculations performed by the CPU.

Performance consideration

As walkers are the basic units of workload in QMC algorithms, they are loosely coupled and distributed across all the threads. For this reason, the best strategy to run QMCPACK efficiently is to feed enough walkers to the available threads.

In a VMC calculation, the code automatically raises the actual number of walkers per MPI rank to the number of available threads if the user-specified number of walkers is smaller, see “walkers/mpi=XXX” in the VMC output. In a DMC calculation, the target number of walkers should be chosen to be slightly smaller than a multiple of the total number of available threads across all the MPI ranks belongs to this calculation. Since the number of walkers varies from generation to generation, its dynamical value should be slightly smaller or equal to that multiple most of the time.

To achieve better performance, mixed precision version (experimental) has been introduced to the CPU code. The mixed precision CPU code is more aggressive than the GPU version in using single precision (SP) operations. Current implementation utilizes SP on most calculations, except for matrix inversions and reductions where double precision is required to retain high accuracy. All the constant spline data in wavefunction, pseudopotentials and Coulomb potentials are initialized in double precision and later stored in single precision. The mixed precision code is as accurate as the double precision code up to a certain system size. Cross checking and verification of accuracy are encouraged for systems with more than approximately 1500 electrons. The mixed precision code has been tested on solids with real/complex builds with VMC, VMC using drift and DMC runs with wavefunction including single slater determinant and one- and two-body Jastrow factors. Wavefunction optimization will be fixed in the following updates.
Memory consideration

When using threads, some memory objects shared by all the threads. Usually these memory are read-only when the walkers are evolving, for instance the ionic distance table and wavefunction coefficients. If a wavefunction is represented by B-splines, the whole table is shared by all the threads. It usually takes a large chunk of memory when a large primitive cell was used in the simulation. Its actual size is reported as “MEMORY increase XXX MB BsplineSetReader” in the output file. See details about how to reduce it in section 8.2.1.

The other memory objects which are distinct for each walker during random walk need to be associated with individual walkers and can not be shared. This part of memory grows linearly as the number of walkers per MPI rank. Those objects include wavefunction values (Slater determinants) at given electronic configurations and electron related distance tables (electron-electron distance table). Those matrices dominate the $N^2$ scaling of the memory usage per walker.

4.4.3 Running on GPU machines

The GPU version on the NVIDIA CUDA platform is fully incorporated into the main source code. Commonly used functionalities for solid-state and molecular systems using B-spline single-particle orbitals are supported. Use of Gaussian basis sets and three-body Jastrow functions are not yet supported. A detailed description of the GPU implementation can be found in Ref. [6].

The current GPU implementation assumes one MPI process per GPU. To use nodes with multiple GPUs, use multiple MPI processes per node. Vectorization is achieved over walkers, that is, all walkers are propagated in parallel. In each GPU kernel, loops over electrons, atomic cores or orbitals are further vectorized to exploit an additional level of parallelism and to allow coalesced memory access.

Performance consideration

The relative speedup of the GPU implementation increases with both the number of electrons and the number of walkers running on a GPU. Typically, 128-256 walkers per GPU utilize sufficient number of threads to operate the GPU efficiently and to hide memory-access latency.

To achieve better performance, current implementation utilizes single precision operations on most GPU calculations, except for matrix inversions and Coulomb interaction where double precision is required to retain high accuracy. The mixed precision GPU code is as accurate as the double precision CPU code up to a certain system size. Cross checking and verification of accuracy are encouraged for systems with more than approximately 1500 electrons.

Memory consideration

In the GPU implementation, each walker has an anonymous buffer on the GPU’s global memory to store temporary data associated with the wavefunctions. Therefore, the amount of memory available on a GPU limits the number of walkers and eventually the system size that it can process.

If the GPU memory is exhausted, reduce the number of walkers per GPU. Coarsening the grids of the B-splines representation (by decreasing the value of meshfactor in the input file) can also lower the memory usage, at the expense (risk) of obtaining inaccurate results. Proceed with caution if this option has to be considered. It is also possible to distrubute the B-spline coefficients table between the host and GPU memory, see option Spline_Size_Limit_MB in Sec. 8.2.1.
Chapter 5

Units used in QMCPACK

Internally, QMCPACK uses atomic units throughout. Unless stated, all inputs and outputs are also in atomic units. For convenience the analysis tools offer conversions to eV, Ry, Angstrom, Bohr etc.
Chapter 6

Input file overview

This chapter introduces XML as it is used in QMCPACK’s input file. The focus is on the XML file format itself and the general structure of the input file rather than an exhaustive discussion of all keywords and structure elements.

QMCPACK uses XML to represent structured data in its input file. Instead of text blocks like

```
begin project
  id   = vmc
  series = 0
end project

begin vmc
  move   = pbyp
  blocks = 200
  steps  = 10
  timestep = 0.4
end vmc
```

QMCPACK input looks like

```
<project id="vmc" series="0">
</project>

<qmc method="vmc" move="pbyp">
  <parameter name="blocks" > 200 </parameter>
  <parameter name="steps" > 10 </parameter>
  <parameter name="timestep" > 0.4 </parameter>
</qmc>
```

XML elements start with `<element_name>`, end with `</element_name>`, and can be nested within each other to denote substructure (the trial wavefunction is composed of a Slater determinant and a Jastrow factor, which are each further composed of ...). `id` and `series` are attributes of the `<project/>` element. XML attributes are generally used to represent simple values, like names, integers, or real values. Similar functionality is also commonly provided by `<parameter/>` elements like those shown above.

The overall structure of the input file reflects different aspects of the QMC simulation: the simulation cell, particles, trial wavefunction, Hamiltonian, and QMC run parameters. A condensed version of the actual input file is shown below:
<?xml version="1.0"?>
<simulation>
  <project id="vmc" series="0">
    ...
  </project>

  <qmcsystem>
    <simulationcell>
      ...
    </simulationcell>

    <particleset name="e">
      ...
    </particleset>

    <particleset name="ion0">
      ...
    </particleset>

    <wavefunction name="psi0">
      ...
      <determinantset>
        <slaterdeterminant>
          ...
        </slaterdeterminant>
      </determinantset>
      <jastrow type="One-Body">
        ...
      </jastrow>
      <jastrow type="Two-Body">
        ...
      </jastrow>
    </wavefunction>

    <hamiltonian name="h0">
      <pairpot type="coulomb" name="ElecElec" />
      <pairpot type="coulomb" name="IonIon" />
      <pairpot type="pseudo" name="PseudoPot" />
    </hamiltonian>
  </qmcsystem>

  <qmc method="vmc" move="pbyp">47</qmc>
</simulation>
The omitted portions (…) are more fine-grained inputs such as the axes of the simulation cell, the number of up and down electrons, positions of atomic species, external orbital files, starting Jastrow parameters, and external pseudopotential files.

6.1 Project

The <project> tag uses the id and series attributes. The value of id is the first part of the prefix for output file names.

Output file names also contain the series number, starting at the value given by the series tag. After every <qmc> section the series value will increment, giving each section a unique prefix.

For the input file shown previously, the output files will start with vmc.s000, for example vmc.s000.scalar.dat. If there were another <qmc> section in the input file, the corresponding output files would use the prefix vmc.s001.

6.2 Random number initialization

The random number generator state is initialized from the random element using the seed attribute.

If the random element is not present, or the seed value is negative, the seed will be generated from the current time.

In order to initialize the many independent random number generators (one per thread and MPI process), the seed value is used (modulo 1024) as a starting index into a list of prime numbers. Entries in this offset list of prime numbers are then used as the seed for the random generator on each thread and process.

If checkpointing is enabled, the random number state is written to an HDF file at the end of each block (suffix: .random.h5). This file will be read if the mcwalkerset tag is present to perform a restart. For more information, see the checkpoint element in the QMC methods chapter [10] and the section on checkpoint and restart files in [11].
Chapter 7

Specifying the system to be simulated

7.1 Specifying the simulation cell

The simulationcell block specifies the geometry of the cell, how the boundary conditions should be handled, and how ewald summation should be broken up.

<table>
<thead>
<tr>
<th>parameter name</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>lattice</td>
<td>9 floats</td>
<td>any float</td>
<td>Must be specified</td>
<td>Specification of lattice vectors.</td>
</tr>
<tr>
<td>bconds</td>
<td>string</td>
<td>“p” or “n”</td>
<td>“n n n”</td>
<td>Boundary conditions for each axis.</td>
</tr>
<tr>
<td>vacuum</td>
<td>float</td>
<td>≥ 1.0</td>
<td>1.0</td>
<td>Vacuum scale.</td>
</tr>
<tr>
<td>LR_dim_cutoff</td>
<td>float</td>
<td>float</td>
<td>15</td>
<td>Ewald breakup distance.</td>
</tr>
</tbody>
</table>

An example of a simulationcell block is given below:

```xml
<simulationcell>
  <parameter name="lattice">
    3.8  0.0  0.0
    0.0  3.8  0.0
    0.0  0.0  3.8
  </parameter>
  <parameter name="bconds">
    p p p
  </parameter>
  <parameter name="LR_dim_cutoff"> 20 </parameter>
</simulationcell>
```

Here, a cubic cell 3.8 bohr on a side will be used. This simulation will use periodic boundary conditions, and the maximum $k$ vector will be $20/r_{wigner–seitz}$ of the cell.
7.1.1 Lattice
The cell is specified using 3 lattice vectors.

7.1.2 Boundary conditions
QMCPACK offers the capability to use a mixture of open and periodic boundary conditions. The bconds parameter expects a single string of three characters separated by spaces, e.g. “p p p” for purely periodic boundary conditions. These characters control the behavior of the x, y, and z, axes, respectively. Examples of valid bconds include:

“p p p” Periodic boundary conditions. Corresponds to a 3D crystal.

“n n n” Open boundary conditions. Corresponds to an isolated molecule in a vacuum.

“p p n” Slab geometry. Corresponds to a 2D crystal.

“p n n” Wire geometry. Corresponds to a 1D crystal.

7.1.3 Vacuum
The vacuum option allows adding a vacuum region in slab or wire boundary conditions (bconds= p p n or bconds= p n n, respectively). The main use is to save memory with spline or plane-wave basis trial wavefunctions, because no basis functions are required inside the vacuum region. For example, a large vacuum region can be added above and below a graphene sheet without having to generate the trial wavefunction in such a large box or to have as many splines as would otherwise be required. Note that the trial wavefunction must still be generated in a large enough box to sufficiently reduce periodic interactions in the underlying electronic structure calculation.

With the vacuum option, the box used for Ewald summation increases along the axis labeled n by a factor of vacuum. Note that all the particles remain in the original box without altering their positions. i.e. Bond lengths are not changed by this option. The default value is 1, no change to the specified axes.

An example of a simulationcell block using vacuum is given below. The size of the box along the z-axis increases from 12 to 18 by the vacuum scale of 1.5.

```
<simulationcell>
  <parameter name="lattice">
    3.8 0.0 0.0
    0.0 3.8 0.0
    0.0 0.0 12.0
  </parameter>
  <parameter name="bconds">
    p p n
  </parameter>
  <parameter name="vacuum"> 1.5 </parameter>
  <parameter name="LR_dim_cutoff"> 20 </parameter>
</simulationcell>
```
7.1.4 LR_dim_cutoff

When using periodic boundary conditions direct calculation of the Coulomb energy is not well behaved. As a result, QMCPACK uses an optimized Ewald summation technique to compute the Coulomb interaction.[9]

In the Ewald summation, the energy is broken into short- and long-ranged terms. The short-ranged term is computed directly in real space, while the long-ranged term is computed in reciprocal space. \( LR_{\text{dim}} \text{ cutoff} \) controls where the short-ranged term ends and the long-ranged term begins. The real-space cutoff, reciprocal-space cutoff, and \( LR_{\text{dim}} \text{ cutoff} \) are related via:

\[
LR_{\text{dim}} \text{ cutoff} = r_c \times k_c
\]

where \( r_c \) is the Wigner-Seitz radius, and \( k_c \) is the length of the maximum \( k \)-vector used in the long-ranged term.

7.2 Specifying the particle set

The `particleset` blocks specify the particles in the QMC simulations: their types, attributes (mass, charge, valence), and positions.

7.2.1 Input specification

<table>
<thead>
<tr>
<th>particleset element</th>
<th>parent elements:</th>
<th>simulation</th>
</tr>
</thead>
<tbody>
<tr>
<td>child elements:</td>
<td>group, attrib</td>
<td></td>
</tr>
<tr>
<td>attribute:</td>
<td></td>
<td></td>
</tr>
<tr>
<td>name/id</td>
<td>name/id</td>
<td>text</td>
</tr>
<tr>
<td>size(^o)</td>
<td>size</td>
<td>integer</td>
</tr>
<tr>
<td>random(^o)</td>
<td>random</td>
<td>text</td>
</tr>
<tr>
<td>randomsrc/</td>
<td>randomsrc/</td>
<td>text</td>
</tr>
<tr>
<td>random_source(^o)</td>
<td>random_source</td>
<td>text</td>
</tr>
</tbody>
</table>

**attribute**

<table>
<thead>
<tr>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>name/id</td>
<td>text</td>
<td>any</td>
<td>e</td>
<td>Name of particle set</td>
</tr>
<tr>
<td>size(^o)</td>
<td>integer</td>
<td>any</td>
<td>0</td>
<td>Number of particles in set</td>
</tr>
<tr>
<td>random(^o)</td>
<td>text</td>
<td>yes/no</td>
<td>no</td>
<td>Randomize starting positions</td>
</tr>
<tr>
<td>randomsrc/</td>
<td>text</td>
<td>particleset.name</td>
<td>none</td>
<td>Particle set to randomize</td>
</tr>
</tbody>
</table>

7.2.2 Detailed attribute description

**particleset required attributes**

- name/id
  Unique name for the particle set. Default is “e” for electrons. “i” or “ion0” is typically used for ions.

**particleset optional attributes**

- size
  Number of particles in set
random
Randomize starting positions of particles. Each component of each particle’s position is randomized independently in the range of the simulation cell in that component’s direction.

randomsrc/random_source
Specify source particle set around which to randomize the initial positions of this particle set.

name required attributes

• name/id
Unique name for the particle set group. Typically, element symbols are used for ions and “u” or “d” for spin-up and spin-down electron groups, respectively.

group optional attributes

• mass
Mass of particles in set.

• unit
Units for mass of particles in set (au$[m_e = 1]$ or amu$[\frac{1}{12}m_{12C} = 1]$).
7.2.3 Example use cases

Listing 7.1: particleset elements for ions and electrons randomizing electron start positions.

```xml
<particleset name="i" size="2">
  <group name="Li">
    <parameter name="charge">3.000000</parameter>
    <parameter name="valence">3.000000</parameter>
    <parameter name="atomicnumber">3.000000</parameter>
  </group>
  <group name="H">
    <parameter name="charge">1.000000</parameter>
    <parameter name="valence">1.000000</parameter>
    <parameter name="atomicnumber">1.000000</parameter>
  </group>
  <attrib name="position" datatype="posArray" condition="1">
    0.0 0.0 0.0
    0.5 0.5 0.5
  </attrib>
  <attrib name="ionid" datatype="stringArray">
    Li H
  </attrib>
</particleset>

<particleset name="e" random="yes" randomsrc="i">
  <group name="u" size="2">
    <parameter name="charge">-1</parameter>
  </group>
  <group name="d" size="2">
    <parameter name="charge">-1</parameter>
  </group>
</particleset>
```
Listing 7.2: particleset elements for ions and electrons specifying electron start positions

```
<particleset name="e">
  <group name="u" size="4">
    <parameter name="charge">-1</parameter>
    <attrib name="position" datatype="posArray">
      2.9151687332e-01 -6.5123272502e-01 -1.2188463918e-01
      5.8423636048e-01 4.2730406357e-01 -4.5964306231e-03
      3.5228575807e-01 -3.5027014639e-01 5.2644808295e-01
      -5.168625912e-01 -1.6648002292e+00 6.5837023441e-01
    </attrib>
  </group>
  <group name="d" size="4">
    <parameter name="charge">-1</parameter>
    <attrib name="position" datatype="posArray">
      3.1443445436e-01 6.5068682609e-01 -4.0983449009e-02
      -3.8686061749e-01 -9.3744432997e-02 -6.045005388e-01
      2.4978241724e-02 -3.2862514649e-02 -7.2266047173e-01
      -4.0352404772e-01 1.1927734805e+00 5.5610824921e-01
    </attrib>
  </group>
</particleset>

<particleset name="ion0" size="3">
  <group name="O">
    <parameter name="charge">6</parameter>
    <parameter name="valence">4</parameter>
    <parameter name="atomicnumber">8</parameter>
  </group>
  <group name="H">
    <parameter name="charge">1</parameter>
    <parameter name="valence">1</parameter>
    <parameter name="atomicnumber">1</parameter>
  </group>
  <attrib name="position" datatype="posArray">
    0.0000000000e+00 0.0000000000e+00 0.0000000000e+00
    0.0000000000e+00 -1.4308249289e+00 1.1078707576e+00
    0.0000000000e+00 1.4308249289e+00 1.1078707576e+00
  </attrib>
  <attrib name="ionid" datatype="stringArray">
    O H H
  </attrib>
</particleset>
```
Listing 7.3: particleset elements for ions specifying positions by ion type

```xml
<particleset name="ion0">
  <group name="O" size="1">
    <parameter name="charge">6</parameter>
    <parameter name="valence">4</parameter>
    <parameter name="atomicnumber">8</parameter>
    <attrib name="position" datatype="posArray">
      0.0000000000e+00 0.0000000000e+00 0.0000000000e+00
    </attrib>
  </group>
  <group name="H" size="2">
    <parameter name="charge">1</parameter>
    <parameter name="valence">1</parameter>
    <parameter name="atomicnumber">1</parameter>
    <attrib name="position" datatype="posArray">
      0.0000000000e+00 -1.4308249289e+00 1.1078707576e+00
      0.0000000000e+00 1.4308249289e+00 1.1078707576e+00
    </attrib>
  </group>
</particleset>
```
Chapter 8

Trial wavefunction specification

8.1 Introduction

This section describes the input blocks associated with the specification of the trial wavefunction in a QMCPACK calculation. These sections are contained within the <wavefunction> ... </wavefunction> xml blocks. Users are expected to rely on converters to generate the input blocks described in this section. The converters and the workflows are designed such that input blocks require minimum modifications from users. Unless the workflow requires modification of wavefunction blocks (e.g. setting the cutoff in a multi determinant calculation), only expert users should directly alter them.

The trial wavefunction in QMCPACK has a general product form:

\[ \Psi_T(\vec{r}) = \prod_k \Theta_k(\vec{r}) ; \]  

where each \( \Theta_k(\vec{r}) \) is a function of the electron coordinates (and possibly ionic coordinates and variational parameters). For problems involving electrons, the overall trial wavefunction must be antisymmetric with respect to electron exchange, so at least one of the functions in the product must be antisymmetric. Notice that, while QMCPACK allows for the construction of arbitrary trial wavefunctions based on the functions implemented in the code (e.g. slater determinants, jastrow functions, etc), the user must make sure that a correct wavefunction is used for the problem at hand. From here on, we assume a standard trial wavefunction for an electronic structure problem,

\[ \Psi_T(\vec{r}) = A(\vec{r}) \prod_k J_k(\vec{r}) ; \]  

where \( A(\vec{r}) \) is one of the antisymmetric functions: 1) slater determinant, 2) multi slater determinant, or 3) pfaffian, and \( J_k \) is any of the jastrow functions (described in section 8.3). The antisymmetric functions are built from a set of single particle orbitals (sposet). QMCPACK implements 4 different types of sposet, described in the section below. Each sposet is designed for a different type of calculation, so their definition and generation varies accordingly.

8.2 Single-particle orbitals
8.2.1 Spline basis sets

In this section we describe the use of spline basis sets to expand the sposet. Spline basis sets are designed to work seamlessly with plane wave DFT code, e.g. Quantum ESPRESSO as a trial wavefunction generator.

In QMC algorithms, all the SPOs \( \{ \phi(\vec{r}) \} \) need to be updated every time a single electron moves. Evaluating SPOs takes very large portion of computation time. In principle, PW basis set can be used to express SPOs directly in QMC like in DFT. but it introduces an unfavorable scaling due to the fact that the basis set size increases linearly as the system size. For this reason, it is efficient to use a localized basis with compact support and a good transferability from plane wave basis.

In particular, 3D tricubic B-splines provide a basis in which only 64 elements are nonzero at any given point in space [12]. The one-dimensional cubic B-spline is given by,

\[
f(x) = \sum_{i'=i-1}^{i+2} b^{i,3}(x) p_{i'},
\]

where \( b^{i}(x) \) are the piecewise cubic polynomial basis functions and \( i = \text{floor}(\Delta^{-1}x) \) is the index of the first grid point \( \leq x \). Constructing a tensor product in each Cartesian direction, we can represent a 3D orbital as

\[
\phi_n(x, y, z) = \sum_{i'=i-1}^{i+2} b^{i',3}_x(x) \sum_{j'=j-1}^{j+2} b^{j',3}_y(y) \sum_{k'=k-1}^{k+2} b^{k',3}_z(z) p_{i',j',k',n},
\]

This allows the rapid evaluation of each orbital in constant time. Furthermore, this basis is systematically improvable with a single spacing parameter, so that accuracy is not compromised compared with plane wave basis.

The use of 3D tricubic B-splines greatly improves the computational efficiency. The gain in computation time from plane wave basis set to an equivalent B-spline basis set becomes increasingly large as the system size grows. On the downside, this computational efficiency comes at the expense of increased memory use, which is easily overcome by the large aggregate memory available per node through OpenMP/MPI hybrid QMC.

The input xml block for the spline SPOs is give in Listing 8.1. A list of options is given in Table 8.1. QMCPACK has a very useful command line option \(--\text{save\_wfs}--\) which allows to dump the real space B-spline coefficient table into a h5 file on the disk. When the orbital transformation from k space to B-spline requires more than available amount of scratch memory on the compute nodes, users can perform this step on fat nodes and transfer back the h5 file for QMC calculations.

Listing 8.1: Determinant set XML element.

```xml
<determinantset type="bspline" source="i" href="pwscf.h5"
  tilematrix="1 1 3 1 2 -1 -2 1 0" twistnum="-1" gpu="yes"
  meshfactor="0.8"
  twist="0 0 0" precision="double">
  <slaterdeterminant>
    <determinant id="updet" size="208">
      <occupation mode="ground" spindataset="0"/>
    </determinant>
    <determinant id="downdet" size="208">
      <occupation mode="ground" spindataset="0"/>
    </determinant>
  </slaterdeterminant>
</determinantset>
```

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Table 8.1: Options for the determinanetset xml-block associated with B-spline single particle orbital sets.

Additional information:

- **precision**. Only effective on CPU version without mixed precision, ‘single’ is always imposed with mixed precision. Using single precision not only saves memory usage but also speeds up the B-spline evaluation. It is recommended to use single precision since we saw little chance of really compromising the accuracy of calculation.

- **meshfactor**. It is the ratio of actual grid spacing of B-splines used in QMC calculation with respect to the original one calculated from h5. Smaller meshfactor saves memory usage but reduces accuracy. The effects are similar to reducing plane wave cutoff in DFT calculation. Use with caution!

- **twistnum**. If positive, it is the index. It is recommended not to take this way since the indexing may show some uncertainty. If negative, the super twist is referred by `twist`.

- **Spline_Size_Limit_MB**. Allows to distribute the B-spline coefficient table between the host and GPU memory. The compute kernels access host memory via zero-copy. Though the performance penalty introduced by it is significant but allows large calculations to go.
8.2.2 Gaussian basis sets

In this section we describe the use of localized basis sets to expand the sposet. The general form of a single particle orbital in this case is given by:

\[ \psi_i(\vec{r}) = \sum_k C_{i,k} \eta_k(\vec{r}), \quad (8.5) \]

where \( \{\eta_k(\vec{r})\} \) is a set of M atom-centered basis functions and \( C_{i,k} \) is a coefficient matrix. This sposet should be used in calculations of finite systems employing an atom-centered basis set and is typically generated by the convert4qmc converter. Examples include calculations of molecules using gaussian basis sets or slater-type basis functions. Initial support for periodic systems is described in Sec. 13. Even though this section is called “Gaussian basis sets” (by far the most common atom-centered basis set), QMCPACK works with any atom-centered basis set built based on either spherical harmonic angular functions or cartesian angular expansions. The radial functions in the basis set can be expanded in either gaussian functions, slater-type functions or numerical radial functions.

In this section we describe the input sections for the atom-centered basis set and the sposet for a single slater determinant trial wavefunction. The input sections for multideterminant trial wavefunctions are described in section 8.4. The basic structure for the input block of a single slater determinant is given in Listing 8.2. A list of options for determinantset associated with this sposet is given in Table 8.2.

Listing 8.2: Basic input block for a single determinant trial wavefunction using a sposet expanded on an atom-centered basis set.

```xml
<wavefunction id="psi0" target="e">
  <determinantset>
    <basisset>
      ...
    </basisset>
    <slaterdeterminant>
      ...
    </slaterdeterminant>
  </determinantset>
</wavefunction>
```

The definition of the set of atom-centered basis functions is given by the basisset block, while the sposet is defined within slaterdeterminant. The basisset input block is composed from a collection of atomicBasisSet input blocks, one for each atomic species in the simulation where basis functions are centered. The general structure for basisset and atomicBasisSet are given in Listing 8.3, while the corresponding lists of options are given in Tables 8.3 and 8.4.
Table 8.2: Options for the determinantset xml-block associated with atom-centered single particle orbital sets.

Listing 8.3: Basic input block for basisset.

```xml
<basisset name="LCAOBSet">
  <atomicBasisSet name="Gaussian-G2" angular="cartesian" elementType="C" normalized="no">
    <grid type="log" ri="1.e-6" rf="1.e2" npts="1001"/>
    <basisGroup rid="C00" n="0" l="0" type="Gaussian">
      <radfunc exponent="5.134400000000e-02" contraction="1.399098787100e-02"/>
      ...
    </basisGroup>
  ...
</atomicBasisSet>
  ...
<atomicBasisSet name="Gaussian-G2" angular="cartesian" type="Gaussian" elementType="C" normalized="no">
  ...
</atomicBasisSet>
  ...
</basisset>
```

Table 8.3: Options for the basisset xml-block associated with atom-centered single particle orbital sets.

<table>
<thead>
<tr>
<th>attribute</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>name/id</td>
<td>text</td>
<td>any</td>
<td>&quot;&quot;</td>
<td>Name of atom-centered basis set.</td>
</tr>
<tr>
<td>type</td>
<td>text</td>
<td>see below</td>
<td>&quot;&quot;</td>
<td>Type of atomic basis set.</td>
</tr>
<tr>
<td>keyword</td>
<td>text</td>
<td>NMO,GTO,STO</td>
<td>NMO</td>
<td>Type of orbital set generated.</td>
</tr>
<tr>
<td>transform</td>
<td>text</td>
<td>yes/no</td>
<td>yes</td>
<td>Transform to numerical radial functions?</td>
</tr>
<tr>
<td>source</td>
<td>text</td>
<td>any</td>
<td>ion0</td>
<td>Particle set with the position of atom centers.</td>
</tr>
<tr>
<td>cuspCorrection</td>
<td>text</td>
<td>yes/no</td>
<td>no</td>
<td>Apply cusp correction scheme to splot?</td>
</tr>
</tbody>
</table>

---

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**Table 8.4: Options for the atomicBasisSet xml-block.**

<table>
<thead>
<tr>
<th>attribute</th>
<th>name/id</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>name/id</td>
<td>text</td>
<td>any</td>
<td></td>
<td>&quot;&quot;</td>
<td>Name of atomic basis set.</td>
</tr>
<tr>
<td>angular</td>
<td>text</td>
<td>see below</td>
<td></td>
<td>default</td>
<td>Type of angular functions.</td>
</tr>
<tr>
<td>expandYlm</td>
<td>text</td>
<td>see below</td>
<td></td>
<td>yes</td>
<td>Expand Ylm shells?</td>
</tr>
<tr>
<td>expM</td>
<td>text</td>
<td>see below</td>
<td></td>
<td>yes</td>
<td>Add sign for ((-1)^m)?</td>
</tr>
<tr>
<td>elementType/species</td>
<td>text</td>
<td>any</td>
<td>e</td>
<td></td>
<td>Atomic species where functions are centered.</td>
</tr>
<tr>
<td>normalized</td>
<td>text</td>
<td>yes/no</td>
<td>yes</td>
<td></td>
<td>Are single particle functions normalized?</td>
</tr>
</tbody>
</table>

**Table 8.5: Options for the basisGroup xml-block.**

<table>
<thead>
<tr>
<th>attribute</th>
<th>rid/id</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>name</td>
<td>text</td>
<td>any</td>
<td></td>
<td>&quot;&quot;</td>
<td>Name of the basisGroup.</td>
</tr>
<tr>
<td>type</td>
<td>text</td>
<td>any</td>
<td></td>
<td>&quot;&quot;</td>
<td>Type of basisGroup.</td>
</tr>
<tr>
<td>n/l/m/s</td>
<td>integer</td>
<td>any</td>
<td>0</td>
<td></td>
<td>Quantum numbers of basisGroup.</td>
</tr>
</tbody>
</table>

**Listing 8.4: Basic input block for slaterdeterminant with an atom-centered sposet.**

```xml
<slaterdeterminant>
</slaterdeterminant>
```

**Detailed description of attributes:**

In the following, we give a more detailed description of all the options presented in the various xml-blocks described in this section. Only non-trivial attributes are described below. Those with simple yes/no options and whose description above is enough to explain the intended behavior are not included.
determinantset attributes:

- **type**
  Type of sposet. For atom-centered based sposets, use type="MolecularOrbital" or type="MO". Other options describe elsewhere in this manual are "spline", "composite", "pw", "heg", "linearopt", etc.

- **keyword/key**
  Type of basis set generated, which doesn’t necessarily match the type of the basis set on the input block. The three possible options are: NMO (numerical molecular orbitals), GTO (gaussian-type orbitals), STO (slater-type orbitals). The default option is NMO. By default, QMCPACK will generate numerical orbitals from both GTO and STO types and use cubic or quintic spline interpolation to evaluate the radial functions. This is typically more efficient than evaluating the radial functions in the native basis (gaussians or exponents) and allows for arbitrarily large contractions without any additional cost. To force the use of the native expansion (not recommended), use GTO or STO for each type of input basis set.

- **transform**
  Request (or avoid) a transformation of the radial functions to NMO type. The default and recommended behavior is to transform to numerical radial functions. If transform is set to "yes", the option keyword is ignored.

- **cuspCorrection**
  Enable (disable) the use of the cusp correction algorithm (CASINO REFERENCE) for a basisset built with GTO functions. The algorithm is implemented as described in (CASINO REFERENCE) and only works with transform="yes" and an input GTO basis set. No further input is needed.

atomicBasisSet attributes:

- **name/id**
  Name of the basis set. Names should be unique.

- **angular**
  Type of angular functions used in the expansion. In general, two angular basis functions are allowed: "spherical" (for spherical Ylm functions) and "cartesian" (for functions of the type \(x^n y^m z^l\)).

- **expandYlm**
  Determines whether each basis group is expanded across the corresponding shell of m values (for spherical type) or consistent powers (for cartesian functions). Options:
  - "No": Do not expand angular functions across corresponding angular shell.
  - "Gaussian": Expand according to Gaussian03 format. This function is only compatible with angular="spherical". For a given input \((l,m)\), the resulting order of the angular functions becomes: \((1,-1,0)\) for \(l=1\) and \((0,1,-1,2,-2,...,l,-l)\) for general \(l\).
  - "Natural": Expand angular functions according to \((-l,-l+1,...,l-1,l)\).
- "Gamess": Expand according to Gamess’ format for cartesian functions. Notice that this option is only compatible with angular=“cartesian”. If angular=“cartesian” is used, this option is not necessary.

• \texttt{expM}
  Determines whether the sign of the spherical Ylm function associated with m \((-1^m)\) is included in the coefficient matrix or not.

• \texttt{elementType/species}
  Name of the species where basis functions are centered. Only one \texttt{atomicBasisSet} block is allowed per species. Additional blocks are ignored. The corresponding species must exist in the \texttt{particleset} given as the \texttt{source} option to \texttt{determinantset}. Basis functions for all the atoms of the corresponding species are included in the basis set, based on the order of atoms in the \texttt{particleset}.

\texttt{basisGroup} attributes:

• \texttt{type}
  Type of input basis radial function. Notice that this refers to the type of radial function in the input xml-block, which might not match the radial function generated internally and used in the calculation (if \texttt{transform} is set to "yes"). Also notice that different \texttt{basisGroup} blocks within a given \texttt{atomicBasisSet} can have different \texttt{type}.

• \texttt{n/l/m/s}
  Quantum numbers of the basis function. Notice that if \texttt{expandYlm} is set to "yes" in \texttt{atomicBasisSet}, a full shell of basis functions with the appropriate values of "m" will be defined for the corresponding value of "l". Otherwise a single basis function will be given for the specific combination of "(l,m)".

\texttt{radfunc} attributes for \texttt{type}="\texttt{Gaussian}"

• 

\texttt{slaterdeterminant} attributes:

• 

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8.2.3 Hybrid orbital representation

The hybrid representation of the single particle orbitals combines a localized atomic basis set around atomic cores and B-splines in the interstitial regions to reduce the memory usage while retaining high speed of evaluation and either retaining or increasing overall accuracy. Full details are provided in Ref. [39]. In practice, we have seen using meshfactor=0.5 is often possible and achieves huge memory saving. Figure 8.1 illustrates how the regions are assigned. Orbitals within region A are computed as

\[ \phi_n^A(r) = R_{n,l,m}(r)Y_{l,m}(\hat{r}) \]

Orbitals in region C are computed as the regular B-spline basis described in subsection 8.2.1 above. The region B interpolates between A and C as

\[ \phi_n^B(r) = S(r)\phi_n^A(r) + (1 - S(r))\phi_n^C(r) \]

\[ S(r) = \frac{1}{2} - \frac{1}{2} \tanh \left[ \alpha \left( \frac{r - r_{A/B}}{r_{B/C} - r_{A/B}} - \frac{1}{2} \right) \right] \]

To enable hybrid orbital representation, the input XML needs to see the tag hybridrep="yes" shown below.

Listing 8.5: Hybrid orbital representation input example.

```xml
<determinantset type="bspline" source="i" href="pwscf.h5"
    tilematrix="1 1 3 1 2 -1 -2 1 0" twistnum="-1" gpu="yes"
    meshfactor="0.8"
    twist="0 0 0" precision="single" hybridrep="yes">
    ...
</determinantset>
```

Second, the information describing the atomic regions is required in the particle set, shown below

Listing 8.6: particleset elements for ions with information needed by hybrid orbital representation.

```xml
<group name="Ni">
    <parameter name="charge">18</parameter>
    <parameter name="valence">18</parameter>
</group>
```
The parameters specific to hybrid representation are listed as

<table>
<thead>
<tr>
<th>attribute</th>
<th>element</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>name</strong></td>
<td><strong>datatype</strong></td>
</tr>
<tr>
<td>cutoff_radius</td>
<td>real</td>
</tr>
<tr>
<td>lmax</td>
<td>integer</td>
</tr>
<tr>
<td>inner_cutoff</td>
<td>real</td>
</tr>
<tr>
<td>spline_radius</td>
<td>real</td>
</tr>
<tr>
<td>spline_npuntos</td>
<td>integer</td>
</tr>
</tbody>
</table>

- **cutoff_radius** is required for every species. If a species is intended not being covered by atomic regions, setting the value 0.0 will put default values for all the reset parameters. A good value is usually a bit larger than the core radius listed in the pseudopotential file. After a parametric scan, pick the one from the flat energy region with the smallest potential variance.

- **lmax** is required if **cutoff_radius** > 0.0. The value usually needs to be at least the highest angular momentum plus 2.

- **inner_cutoff** is optional and set as **cutoff_radius** − 0.3 by default which is fine in most cases.

- **spline_radius** and **spline_npoints** are optional. By default, they are calculated based on **cutoff_radius** and a grid displacement 0.02 bohr. If users prefer inputing them, it is required that **cutoff_radius** <= **spline_radius**−2×**spline_radius**/(**spline_npoints**−1).

In addition, the hybrid orbital representation allows extra optimization to speed up the non-local pseudopotential evaluation using the batched algorithm listed in Sec. 9.2.2.
8.2.4 Plane-wave basis sets
8.2.5 Homogeneous electron gas

The interacting Fermi Liquid has its own special determinant set for filling up a Fermi surface. The shell number can be specified separately for both spin up and spin down. This determines how many electrons to include of each time, only closed shells are currently implemented. The shells are filled according to the rules of a square box, if other lattice vectors are used, the electrons may not fill up a complete shell.

This following example can also be used for Helium simulations too, by specifying the proper pair interaction in the Hamiltonian section.

Listing 8.7: 2D Fermi Liquid example: particle specification

```xml
<qmcsystem>
  <simulationcell name="global">
    <parameter name="rs" pol="0" condition="74">6.5</parameter>
    <parameter name="bconds">p p p</parameter>
    <parameter name="LR_dim_cutoff">15</parameter>
  </simulationcell>
  <particleset name="e" random="yes">
    <group name="u" size="37">
      <parameter name="charge">-1</parameter>
      <parameter name="mass">1</parameter>
    </group>
    <group name="d" size="37">
      <parameter name="charge">-1</parameter>
      <parameter name="mass">1</parameter>
    </group>
  </particleset>
</qmcsystem>
```

Listing 8.8: 2D Fermi Liquid example (Slater Jastrow wave function)

```xml
<qmcsystem>
  <wavefunction name="psi0" target="e">
    <determinantset type="electron-gas" shell="7" shell2="7" randomize="true">
    </determinantset>
    <jastrow name="J2" type="Two-Body" function="Bspline" print="no">
      <correlation speciesA="u" speciesB="u" size="8" cusp="0">
        <coefficients id="uu" type="Array" optimize="yes"/>
      </correlation>
      <correlation speciesA="u" speciesB="d" size="8" cusp="0">
        <coefficients id="ud" type="Array" optimize="yes"/>
      </correlation>
    </jastrow>
  </wavefunction>
</qmcsystem>
```
8.3 Jastrow Factors

Jastrow factors are among the simplest and most effective ways of including dynamical correlation in the trial many body wavefunction. The resulting many body wavefunction is expressed as the product of an antisymmetric (in the case of Fermions) or symmetric (for Bosons) part and a correlating Jastrow factor like so:

$$\Psi(\vec{R}) = A(\vec{R}) \exp[J(\vec{R})]$$

(8.8)

In this section we will detail the types and forms of Jastrow factor used in QMCPACK. Note that each type of Jastrow factor needs to be specified using its own individual jastrow XML element. For this reason, we have repeated the specification of the jastrow tag in each section, with specialization for the options available for that given type of Jastrow.

8.3.1 One-body Jastrow functions

The one-body Jastrow factor is a form that allows for the direct inclusion of correlations between particles that are included in the wavefunction with particles that are not explicitly part of it. The most common example of this are correlations between electrons and ions.

The Jastrow function is specified within a wavefunction element and must contain one or more correlation elements specifying additional parameters as well as the actual coefficients. Section 8.3.1 gives examples of the typical nesting of jastrow, correlation, and coefficient elements.

Input Specification

<table>
<thead>
<tr>
<th>Jastrow element</th>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>defaults</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>name</td>
<td>text</td>
<td></td>
<td>(required)</td>
<td></td>
<td>Unique name for this Jastrow function</td>
</tr>
<tr>
<td>type</td>
<td>text</td>
<td>One-body</td>
<td>(required)</td>
<td></td>
<td>Define a one-body function</td>
</tr>
<tr>
<td>function</td>
<td>text</td>
<td>B spline</td>
<td>(required)</td>
<td></td>
<td>BSpline Jastrow</td>
</tr>
<tr>
<td>source</td>
<td>text</td>
<td>name</td>
<td>(required)</td>
<td></td>
<td>Name of attribute of classical particle set</td>
</tr>
<tr>
<td>print</td>
<td>text</td>
<td>yes / no</td>
<td>yes</td>
<td></td>
<td>Jastrow factor printed in external file?</td>
</tr>
</tbody>
</table>

To be more concrete, the one-body Jastrow factors used to describe correlations between electrons and ions take the form below:

$$J_1 = \sum_i^{\text{ion}} \sum_i^{\text{e}} u_{ab}(|r_i - R_I|)$$

(8.9)

where I runs over all of the ions in the calculation, i runs over the electrons and $u_{ab}$ describes the functional form of the correlation between them. Many different forms of $u_{ab}$ are implemented in QMCPACK. We will detail two of the most common ones below.
Spline form

The one-body spline Jastrow function is the most commonly used one-body Jastrow for solids. This form was first described and used in [6]. Here \( u_{ab} \) is an interpolating 1D Bspline (tricubic spline on a linear grid) between zero distance and \( r_{cut} \). In 3D periodic systems the default cutoff distance is the Wigner Seitz cell radius. For other periodicities including isolated molecules the \( r_{cut} \) must be specified. The cusp can be set. \( r_i \) and \( R_I \) are most commonly the electron and ion positions, but any particlesets that can provide the needed centers can be used.

<table>
<thead>
<tr>
<th>Correlation element</th>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>defaults</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>elementType</td>
<td>text</td>
<td>name</td>
<td>see below</td>
<td>Classical particle target</td>
<td></td>
</tr>
<tr>
<td>speciesA</td>
<td>text</td>
<td>name</td>
<td>see below</td>
<td>Classical particle target</td>
<td></td>
</tr>
<tr>
<td>speciesB</td>
<td>text</td>
<td>name</td>
<td>see below</td>
<td>Quantum species target</td>
<td></td>
</tr>
<tr>
<td>size</td>
<td>integer</td>
<td>&gt; 0</td>
<td>(required)</td>
<td>Number of coefficients</td>
<td></td>
</tr>
<tr>
<td>rcut</td>
<td>real</td>
<td>&gt; 0</td>
<td>see below</td>
<td>Distance at which the correlation goes to 0</td>
<td></td>
</tr>
<tr>
<td>cusp</td>
<td>real</td>
<td>≥ 0</td>
<td>0</td>
<td>Value for use in Kato cusp condition</td>
<td></td>
</tr>
<tr>
<td>spin</td>
<td>text</td>
<td>yes or no</td>
<td>no</td>
<td>Spin dependent jastrow factor</td>
<td></td>
</tr>
</tbody>
</table>

**Input Specification**  Additional information:

- **elementType, speciesA, speciesB, spin.** For a spin independent Jastrow factor (spin = “no”) elementType should be the name of the group of ions in the classical particleset to which the quantum particles should be correlated. For a spin dependent Jastrow factor (spin = “yes”) set speciesA to the group name in the classical particleset and speciesB to the group name in the quantum particleset.

- **rcut.** The cutoff distance for the function in atomic units (bohr). For 3D fully periodic systems this parameter is optional and a default of the Wigner Seitz cell radius is used. Otherwise this parameter is required.

- **cusp.** The one body jastrow factor can be used to make the wavefunction satisfy the electron-ion cusp condition[4]. In this case, the derivative of the jastrow factor as the electron approaches the nucleus will be given by:

\[
\left( \frac{\partial J}{\partial r_{ii}} \right)_{r_{ii}=0} = -Z
\]  

(8.10)

Note that if the antisymmetric part of the wavefunction satisfies the electron-ion cusp condition (for instance by using single particle orbitals that respect the cusp condition) or if a non-divergent pseudopotential is used that the Jastrow should be cuspless at the nucleus and this value should be kept at its default of 0.
Example use cases  Specify a spin-independent function with four parameters. Because rcut is not specified, the default cutoff of the Wigner Seitz cell radius is used; this Jastrow must be used with a 3D periodic system such as a bulk solid. The name of the particleset holding the ionic positions is "i".

```xml
<jastrow name="J1" type="One-Body" function="Bspline" print="yes" source="i">
  <correlation elementType="C" cusp="0.0" size="4">
    <coefficients id="C" type="Array"> 0 0 0 0 </coefficients>
  </correlation>
</jastrow>
```

Specify a spin-dependent function with seven upspin and seven downspin parameters. The cutoff distance is set to 6 atomic units. Note here that the particleset holding the ions is labeled as ion0 rather than “i” in the other example. Also in this case the ion is Lithium with a coulomb potential, so the cusp condition is satisfied by setting cusp=“d”.

```xml
<jastrow name="J1" type="One-Body" function="Bspline" source="ion0" spin="yes">
  <correlation speciesA="Li" speciesB="u" size="7" rcut="6">
    <coefficients id="eLiu" cusp="3.0" type="Array"> 0.0 0.0 0.0 0.0 0.0 0.0 0.0 </coefficients>
  </correlation>
  <correlation speciesA="C" speciesB="d" size="7" rcut="6">
    <coefficients id="eLid" cusp="3.0" type="Array"> 0.0 0.0 0.0 0.0 0.0 0.0 0.0 </coefficients>
  </correlation>
</jastrow>
```
Pade form

While the spline Jastrow factor is the most flexible and most commonly used form implemented in QMCPACK, there are times where its flexibility can make it difficult to optimize. As an example, a spline jastrow with a very large cutoff may be difficult to optimize for isolated systems like molecules due to the small number of samples that will be present in the tail of the function. In such cases, a simpler functional form may be advantageous. The second order Pade jastrow factor, given in Eq. 8.11 is a good choice in such cases.

$$u_{ab}(r) = \frac{a \cdot r + c \cdot r^2}{1 + b \cdot r}$$ (8.11)

Unlike the spline jastrow factor which includes a cutoff, this form has an infinite range and for every particle pair (subject to the minimum image convention) it will be applied. It also is a cuspless jastrow factor, so it should either be used in combination with a single particle basis set that contains the proper cusp or with a smooth pseudopotential.

<table>
<thead>
<tr>
<th>Correlation element name</th>
<th>datatype</th>
<th>values</th>
<th>defaults</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>elementType text name</td>
<td>name</td>
<td>see below</td>
<td>Classical particle target</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Contents</th>
</tr>
</thead>
<tbody>
<tr>
<td>Coefficients</td>
</tr>
<tr>
<td>(None)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>parameter element name</th>
<th>datatype</th>
<th>values</th>
<th>defaults</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id string name (required)</td>
<td>name</td>
<td></td>
<td>name for variable</td>
<td></td>
</tr>
<tr>
<td>name string A or B or C</td>
<td></td>
<td>(required)</td>
<td>see Eq. 8.11</td>
<td></td>
</tr>
<tr>
<td>optimize text yes or no</td>
<td>yes</td>
<td>yes</td>
<td>if no, values are fixed in optimizations</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Contents</th>
</tr>
</thead>
<tbody>
<tr>
<td>(None)</td>
</tr>
</tbody>
</table>

Input Specification

Example use case Specify a spin independent function with independent jastrow factors for two different species (Li and H). The name of the particle set holding the ionic positions is "i".

```
<jastrow name="J1" function="pade2" type="One-Body" print="yes" source="i">
  <correlation elementType="Li">
    <var id="LiA" name="A"> 0.34 </var>
    <var id="LiB" name="B"> 12.78 </var>
    <var id="LiC" name="C"> 1.62 </var>
  </correlation>
</jastrow>
```
<correlation elementType="H">
    <var id="HA" name="A"> 0.14 </var>
    <var id="HB" name="B"> 6.88 </var>
    <var id="HC" name="C"> 0.237 </var>
</correlation>
8.3.2 Two-body Jastrow functions

The two-body Jastrow factor is a form that allows for the explicit inclusion of dynamic correlation between two particles included in the wavefunction. It is almost always given in a spin dependent form so as to satisfy the Kato cusp condition between electrons of different spins[4].

The two body Jastrow function is specified within a wavefunction element and must contain one or more correlation elements specifying additional parameters as well as the actual coefficients. Section 8.3.2 gives examples of the typical nesting of jastrow, correlation and coefficient elements.

Input Specification

<table>
<thead>
<tr>
<th>Jastrow element</th>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>defaults</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>name</td>
<td>text</td>
<td>(required)</td>
<td>Unique name for this Jastrow function</td>
<td></td>
<td></td>
</tr>
<tr>
<td>type</td>
<td>text</td>
<td>Two-body (required)</td>
<td>Define a one-body function</td>
<td></td>
<td></td>
</tr>
<tr>
<td>function</td>
<td>text</td>
<td>Bspline (required)</td>
<td>BSpline Jastrow</td>
<td></td>
<td></td>
</tr>
<tr>
<td>print</td>
<td>text</td>
<td>yes / no</td>
<td>yes</td>
<td>Jastrow factor printed in external file?</td>
<td></td>
</tr>
</tbody>
</table>

Contents

( None )

The two-body Jastrow factors used to describe correlations between electrons take the form

\[ J^2 = \sum_i^e \sum_{j>i}^e u_{ab}(|r_i - r_j|) \]  

(8.12)

The most commonly used form of two body Jastrow factor supported by the code is a splined Jastrow factor, with many similarities to the one body spline Jastrow.
Spline form

The two-body spline Jastrow function is the most commonly used two-body Jastrow for solids. This form was first described and used in [6]. Here $u_{ab}$ is an interpolating 1D Bspline (tricubic spline on a linear grid) between zero distance and $r_{\text{cut}}$. In 3D periodic systems the default cutoff distance is the Wigner Seitz cell radius. For other periodicities including isolated molecules the $r_{\text{cut}}$ must be specified. $r_i$ and $r_j$ are typically electron positions. The cusp condition as $r_i$ approaches $r_j$ is set by the relative spin of the electrons.

<table>
<thead>
<tr>
<th>Correlation element</th>
<th>values</th>
<th>defaults</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>speciesA</td>
<td>u or d</td>
<td>(required)</td>
<td>Quantum species target</td>
</tr>
<tr>
<td>speciesB</td>
<td>u or d</td>
<td>(required)</td>
<td>Quantum species target</td>
</tr>
<tr>
<td>size</td>
<td>&gt; 0</td>
<td>(required)</td>
<td>number of coefficients</td>
</tr>
<tr>
<td>rcut</td>
<td>&gt; 0</td>
<td>see below</td>
<td>distance at which the correlation goes to 0</td>
</tr>
<tr>
<td>spin</td>
<td>yes or no</td>
<td>no</td>
<td>spin dependent jastrow factor</td>
</tr>
</tbody>
</table>

Input Specification  Additional information:

- speciesA, speciesB The scale function $u(r)$ is defined for species pairs uu and ud. There is no need to define ud or dd since uu=dd and ud=du. The cusp condition is computed internally based on the charge of the quantum particles.

<table>
<thead>
<tr>
<th>Coefficients element</th>
<th>values</th>
<th>defaults</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id</td>
<td></td>
<td>(required)</td>
<td>Unique identifier</td>
</tr>
<tr>
<td>type</td>
<td>Array</td>
<td>(required)</td>
<td></td>
</tr>
<tr>
<td>optimize</td>
<td>yes or no</td>
<td>yes</td>
<td>if no, values are fixed in optimizations</td>
</tr>
</tbody>
</table>

Example use cases  Specify a spin-dependent function with 4 parameters for each channel. In this case, the cusp is set at a radius of 4.0 bohr (rather than to the default of the Wigner Seitz cell radius). Also, in this example, the coefficients are set to not be optimized during an optimization step.

```xml
<jastrow name="J2" type="Two-Body" function="Bspline" print="yes">
  <correlation speciesA="u" speciesB="u" size="8" rcut="4.0">
```
<correlation speciesA="u" speciesB="d" size="8" rcut="4.0">
  <coefficients id="ud" type="Array" optimize="no">
    0.4351561096 0.2377951747 0.1129144262 0.0356789236
  </coefficients>
</correlation>
</jastrow>
8.3.3 Long-ranged Jastrow factors

While short-ranged Jastrow factors capture the majority of the benefit for minimizing the total energy and the energy variance, long-ranged Jastrow factors are important to accurately reproduce the short-ranged (long wavelength) behavior of quantities such as the static structure factor, and are therefore essential for modern accurate finite size corrections in periodic systems.

Below two types of long-ranged Jastrow factors are described. The first (the k-space Jastrow) is simply an expansion of the one and/or two body correlation functions in plane waves, with the coefficients comprising the optimizable parameters. The second type have few variational parameters and use the optimized breakup method of Natoli and Ceperley[9] (the Yukawa and Gaskell RPA Jastrows).

Long-ranged Jastrow: k-space Jastrow

The k-space Jastrow introduces explicit long-ranged dependence commensurate with the periodic supercell. This Jastrow is to be used in periodic boundary conditions only.

The input for the k-space Jastrow fuses both one and two-body forms into a single element and so they are discussed together here. The one- and two-body terms in the k-Space Jastrow have the form:

\[
J_1 = \sum_{G \neq 0} b_G \rho_G^I \rho_{-G} \quad \text{(8.13)}
\]

\[
J_2 = \sum_{G \neq 0} a_G \rho_G \rho_{-G} \quad \text{(8.14)}
\]

Here \( \rho_G \) is the Fourier transform of the instantaneous electron density:

\[
\rho_G = \sum_{n \in \text{electrons}} e^{i G \cdot r_n} \quad \text{(8.15)}
\]

and \( \rho_G^I \) has the same form, but for the fixed ions. In both cases the coefficients are restricted to be real, though in general the coefficients for the one-body term need not be. See section 25.8 for more detail.

Input for the k-space Jastrow follows the familiar nesting of jastrow-correlation-coefficients elements, with attributes unique to the k-space Jastrow at the correlation input level.

<table>
<thead>
<tr>
<th>attributes</th>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>text</td>
<td>kSpace</td>
<td></td>
<td></td>
<td>Must be kSpace</td>
</tr>
<tr>
<td>name</td>
<td>text</td>
<td>anything</td>
<td></td>
<td>0</td>
<td>Unique name for Jastrow</td>
</tr>
<tr>
<td>source</td>
<td>text</td>
<td>particleset.name</td>
<td></td>
<td></td>
<td>Ion particleset name</td>
</tr>
</tbody>
</table>
correlation element

parent elements: jastrow type=kSpace
child elements: coefficients
attributes

<table>
<thead>
<tr>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>text</td>
<td>One-Body,Two-Body</td>
<td></td>
<td>Must be One-Body/Two-Body</td>
</tr>
<tr>
<td>kc</td>
<td>real</td>
<td>kc ≥ 0</td>
<td>0.0</td>
<td>k-space cutoff in a.u.</td>
</tr>
<tr>
<td>symmetry</td>
<td>text</td>
<td>crystal,isotropic,none</td>
<td>crystal</td>
<td>Symmetry of coefficients</td>
</tr>
<tr>
<td>spinDependent</td>
<td>boolean</td>
<td>yes,no</td>
<td>no</td>
<td>No current function</td>
</tr>
</tbody>
</table>

coefficients element

parent elements: correlation
child elements: None
attributes

<table>
<thead>
<tr>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id</td>
<td>text</td>
<td>anything</td>
<td>cG1/cG2</td>
<td>Label for coeffs</td>
</tr>
<tr>
<td>type</td>
<td>text</td>
<td>Array</td>
<td>0</td>
<td>Must be Array</td>
</tr>
</tbody>
</table>

body text

The body text is a list of real values for the parameters.

Additional information:

- It is normal to provide no coefficients as an initial guess. The number of coefficients will be automatically calculated according to the k-space cutoff + symmetry and set to zero.
- Providing an incorrect number of parameters also results in all parameters being set to zero.
- There is currently no way to turn optimization on/off for the k-space Jastrow. The coefficients are always optimized.
- Spin dependence is currently not implemented for this Jastrow.
- kc: Parameters with G vectors magnitudes less than kc are included in the Jastrow. If kc is zero, it is the same as excluding the k-space term.
- symmetry=crystal: Impose crystal symmetry on coefficients according to the structure factor.
- symmetry=isotropic: Impose spherical symmetry on coefficients according to G-vector magnitude.
- symmetry=none: Impose no symmetry on the coefficients.

Listing 8.9: k-space Jastrow with one- and two-body terms.

```xml
<jastrow type="kSpace" name="Jk" source="ion0">
  <correlation kc="4.0" type="One-Body" symmetry="crystal">
    <coefficients id="cG1" type="Array">
      <!-- Body text is a list of real values for the parameters. -->
    </coefficients>
  </correlation>
</jastrow>
```
Listing 8.10: k-space Jastrow with one-body term only.

```xml
<jastrow type="kSpace" name="Jk" source="ion0">
  <correlation kc="4.0" type="One-Body" symmetry="crystal">
    <coefficients id="cG1" type="Array">
    </coefficients>
  </correlation>
</jastrow>
```

Listing 8.11: k-space Jastrow with two-body term only.

```xml
<jastrow type="kSpace" name="Jk" source="ion0">
  <correlation kc="4.0" type="Two-Body" symmetry="crystal">
    <coefficients id="cG2" type="Array">
    </coefficients>
  </correlation>
</jastrow>
```

Long-ranged Jastrows: Gaskell RPA and Yukawa forms

NOTE: The Yukawa and RPA Jastrows do not work at present and are currently being revived. Please contact the developers if you are interested in using them.

The exact Jastrow correlation functions contain terms which have a form similar to the Coulomb pair potential. In periodic systems the Coulomb potential is replaced by an Ewald summation of the bare potential over all periodic image cells. This sum is often handled by the optimized breakup method[9] and this same approach is applied to the long-ranged Jastrow factors in QMCPACK.

There are two main long-ranged Jastrow factors of this type implemented in QMCPACK: the Gaskell RPA[37, 38] form and the Yukawa[1] form. Both of these forms were used by Ceperley in early studies of the electron gas[1], but they are also appropriate starting points for general solids.

The Yukawa form is defined in real space. It’s long-range form is formally defined as

\[
u_Y^{PBC}(r) = \sum_{L \neq 0} \sum_{i<j} u_Y(|r_i - r_j + L|)
\]

(8.16)

with \(u_Y(r)\) given by

\[
u_Y(r) = \frac{a}{r} \left( 1 - e^{-r/b} \right)
\]

(8.17)

In QMCPACK a slightly more restricted form is used:

\[
u_Y(r) = \frac{r_s}{r} \left( 1 - e^{-r/\sqrt{r_s}} \right)
\]

(8.18)

here “\(r_s\)” is understood to be a variational parameter.
The Gaskell RPA form—which contains correct short/long range limits and minimizes the total energy of the electron gas within the RPA—is defined directly in k-space:

\[ u_{RPA}(k) = -\frac{1}{2S_0(k)} + \frac{1}{2} \left( \frac{1}{S_0(k)^2} + \frac{4m_e v_k}{\hbar^2 k^2} \right)^{1/2} \]  

(8.19)

where \( v_k \) is the Fourier transform of the Coulomb potential and \( S_0(k) \) is the static structure factor of the non-interacting electron gas:

\[ S_0(k) = \begin{cases} \frac{1}{2k_F} - \frac{1}{2} \left( \frac{k}{2k_F} \right)^3 & k < 2k_F \\ \frac{1}{3} \frac{k^2}{k_F} - \frac{1}{2} \left( \frac{k}{2k_F} \right)^3 & k > 2k_F \end{cases} \]

When written in atomic units, RPA Jastrow implemented in QMCPACK has the form

\[ u_{RPA}(k) = \frac{1}{2N_e} \left( -\frac{1}{S_0(k)} + \left( \frac{1}{S_0(k)^2} + \frac{12}{r_s^3 k^4} \right) \right)^{1/2} \]  

(8.20)

Here “\( r_s \)” is again a variational parameter and \( k_F \equiv (\frac{9\pi}{4N_e})^{1/3} \).

For both the Yukawa and Gaskell RPA Jastrows, the default value for \( r_s \) is \( r_s = (\frac{3\Omega}{4\pi N_e})^{1/3} \).

Listing 8.12: Two body RPA Jastrow with long- and short-ranged parts.

```
jastrow type=Two-Body function=rpa/yukawa element
parent elements: wavefunction
child elements: correlation
attributes
name  datatype  values  default  description
  type  text  Two-Body  Must be Two-Body
  function  text  rpa/yukawa  Must be rpa or yukawa
  name  text  anything  RPA_Jee  Unique name for Jastrow
  longrange  boolean  yes/no  yes  Use long-range part
  shortrange  boolean  yes/no  yes  Use short-range part
 parameters
  rs  rs  \( r_s > 0 \)  \frac{3\Omega}{4\pi N_e}  Avg. elec-elec distance
  kc  kc  \( k_c > 0 \)  \( 2 \left( \frac{9\pi}{4} \right)^{1/3} \frac{4\pi N_e}{3\Omega} \)  K-space cutoff
```

8.3.4 Three-body Jastrow functions

Explicit three-body correlations can be included in the wavefunction via the three-body Jastrow factor. The three-body electron-electron-ion correlation function (\( u_{\sigma\sigma'1} \)) currently used in QMCPACK is identical to the one proposed in [2]:

\[ u_{\sigma\sigma'1}(r_{\sigma1}, r_{\sigma'1}, r_{\sigma''1}) = \sum_{\ell=0}^{M_{\sigma1}} \sum_{m=0}^{M_{\sigma1}} \sum_{n=0}^{M_{\sigma1}} \gamma_{\ell mn} r_{\sigma1}^\ell r_{\sigma'1}^m r_{\sigma''1}^n \times \left( r_{\sigma1} - \frac{r_c}{2} \right)^3 \Theta \left( r_{\sigma1} - \frac{r_c}{2} \right) \times \left( r_{\sigma'1} - \frac{r_c}{2} \right)^3 \Theta \left( r_{\sigma'1} - \frac{r_c}{2} \right) \]  

(8.21)
Here $M_{ei}$ and $M_{ee}$ are the maximum polynomial orders of the electron-ion and electron-electron distances, respectively, $\{\gamma_{\ell mn}\}$ are the optimizable parameters (modulo constraints), $r_c$ is a cutoff radius, and $r_{ab}$ are the distances between electrons or ions $a$ and $b$. i.e. The correlation function is only a function of the interparticle distances and not a more complex function of the particle positions, $r$. As indicated by the $\Theta$ functions, correlations are set to zero beyond a distance of $r_c/2$ in either of the electron-ion distances and the largest meaningful electron-electron distance is $r_c$. This is the highest-order Jastrow correlation function currently implemented.

Today, solid state applications of QMCPACK usually utilize one and two-body B-spline Jastrow functions, with calculations on heavier elements often also using the three-body term described above.

**Example use case**  Here is an example of H$_2$O molecule. After optimizing one and two body Jastrow factors, add the following block in the wavefunction. The coefficients will be filled zero automatically if not given.

```xml
<jastrow name="J3" type="eeI" function="polynomial" source="ion0" print="yes">
  <correlation ispecies="O" especies="u" isize="3" esize="3" rcut="10">
    <coefficients id="uuO" type="Array" optimize="yes" />
  </correlation>
  <correlation ispecies="O" especies1="u" especies2="d" isize="3" esize="3" rcut="10">
    <coefficients id="udO" type="Array" optimize="yes" />
  </correlation>
  <correlation ispecies="H" especies="u" isize="3" esize="3" rcut="10">
    <coefficients id="uuH" type="Array" optimize="yes" />
  </correlation>
  <correlation ispecies="H" especies1="u" especies2="d" isize="3" esize="3" rcut="10">
    <coefficients id="udH" type="Array" optimize="yes" />
  </correlation>
</jastrow>
```

### 8.4 Multideterminant wavefunctions

Multiple schemes to generate a multideterminant wavefunction are possible, from CASSF to full CI or selected CI. The QMCPACK converter can convert MCSCF multideterminant wavefunctions from GAMESS[33] and CIPSI[25] wavefunctions from Quantum Package[26] (QP). Full details of how to run a CIPSI calculation and convert the wavefunction for QMCPACK are given in Sec. 14.1.1.

### 8.5 Backflow wavefunctions

One can perturb the nodal surface of a single-slater/multi-slater wavefunction through use of a backflow-transformation. Specifically, if we have an antisymmetric function $D(x_{0\uparrow}, \cdots, x_{N\uparrow}, x_{0\downarrow}, \cdots, x_{N\downarrow})$, and if $i_\alpha$ is the $i$-th particle of species type $\alpha$, then the backflow transformation works by making the coordinate transformation $x_{i_\alpha} \rightarrow x'_{i_\alpha}$, and evaluating $D$ at these new “quasiparticle” coordinates. QMCPACK currently supports quasiparticle transformations given by:
\[
x'_{i\alpha} = x_{i\alpha} + \sum_{\alpha \leq \beta} \sum_{i_\alpha \neq j_\beta} \eta^{\alpha\beta}(|x_{i\alpha} - x_{j\beta}|)(x_{i\alpha} - x_{j\beta})
\]  
(8.22)

Here, \(\eta^{\alpha\beta}(|x_{i\alpha} - x_{j\beta}|)\) is a radially symmetric back flow transformation between species \(\alpha\) and \(\beta\). In QMCPACK, particle \(i_\alpha\) is known as the “target” particle and \(j_\beta\) is known as the “source”. The main types of transformations are so called one-body terms, which are between an electron and an ion \(T^{eI}(x_{i\alpha} - x_{j\beta})\), and two-body terms. Two body terms are distinguished as those between like and opposite spin electrons: \(T^{e\uparrow e\downarrow}(x_{i_\alpha\uparrow} - x_{j_\beta\downarrow})\) and \(T^{e\downarrow e\uparrow}(x_{i_\alpha\downarrow} - x_{j_\beta\uparrow})\). Henceforth, we will assume that \(T^{e\uparrow e\downarrow}(x) = T^{e\downarrow e\uparrow}(x)\).

In the following, we explain how to describe general terms like Eq. 8.22 in a QMCPACK XML file. For specificity, we will consider a particle set consisting of H and He (in that order). This ordering will be important when we build the XML file, so you can find this out either through your specific declaration of <particleset>, by looking at the hdf5 file in the case of plane waves, or by looking at the qmcpack output file in the section labelled “Summary of QMC systems”.

### 8.5.1 Input Specifications

All backflow declarations occur within a single <backflow> ... </backflow> block. Backflow transformations occur in <transformation> blocks, and have the following input parameters:

<table>
<thead>
<tr>
<th>Transformation element</th>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>defaults</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>name</td>
<td>text</td>
<td></td>
<td>(required)</td>
<td></td>
<td>Unique name for this Jastrow function</td>
</tr>
<tr>
<td>type</td>
<td>text</td>
<td></td>
<td>“e-I”</td>
<td>(required)</td>
<td>Define a one-body backflow transformation.</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>“e-e”</td>
<td></td>
<td>Define a two-body backflow transformation.</td>
</tr>
<tr>
<td>function</td>
<td>text</td>
<td></td>
<td>Bspline</td>
<td>(required)</td>
<td>B-spline type transformation. (No other types supported)</td>
</tr>
<tr>
<td>source</td>
<td>text</td>
<td></td>
<td>“e”</td>
<td></td>
<td>“e” if two-body, ion particle set if one-body.</td>
</tr>
</tbody>
</table>

Just like one and two-body jastrows, parameterization of the backflow transformations are specified within the <transformation> blocks by <correlation> blocks. Please refer to 8.3.1 for more information.

### 8.5.2 Example Use Case

Having specified the general form, we present a general example of one-body and two-body backflow transformations in a hydrogen-helium mixture. The H and He ions have independent backflow transformations, as do the like and unlike-spin two-body terms. One caveat is in order: ionic backflow transformations must be listed in the order that they appear in the particle set. If in our example, He is listed first, and H is listed second, the following example would be correct. However, switching backflow declaration to H first, then He, will result in an error. Outside of this, declaration of one-body blocks and two-body blocks aren’t sensitive to ordering.

```xml
<backflow>
<!--The One-Body term with independent e-He and e-H terms. IN THAT ORDER -->
<transformation name="eIonB" type="e-I" function="Bspline" source="ion0">
  <correlation cusp="0.0" size="8" type="shortrange" init="no" elementType="He" rcut="3.0">
    <coefficients id="eHeC" type="Array" optimize="yes">
```

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Currently, backflow only works with single-slater determinant wavefunctions. When a backflow transformation has been declared, it should be placed within the \texttt{<determinantset>} block, but outside of the \texttt{<slaterdeterminant>} blocks, like so:

\begin{verbatim}
<determinantset ... >
  <!--basis set declarations go here, if there are any -->

  <backflow>
    <transformation ...>
      <!--Here is where one and two-body terms are defined -->
    </transformation>
  </backflow>

  <slaterdeterminant>
    <!--Usual determinant definitions -->
  </slaterdeterminant>

</determinantset>
\end{verbatim}

### 8.5.3 Optimization Tips

Backflow is notoriously difficult to optimize—it’s extremely nonlinear in the variational parameters and also moves the nodal surface around. As such, it is likely that a full Jastrow+Backflow optimization with all parameters initialized to zero may not converge in a reasonable time. If you are experiencing this problem, the following pointers are suggested (in no particular order):

\begin{verbatim}
0 0 0 0 0 0 0 0
</coefficients>
</correlation>
<correlation cusp="0.0" size="8" type="shortrange" init="no" elementType="H" rcut="3.0">
  <coefficients id="eHC" type="Array" optimize="yes">
    0 0 0 0 0 0 0 0
  </coefficients>
</correlation>
</transformation>

<!--The Two-Body Term with Like and Unlike Spins -->
<transformation name="eeB" type="e-e" function="Bspline">
  <correlation cusp="0.0" size="7" type="shortrange" init="no" speciesA="u" speciesB="u" rcut="1.2">
    <coefficients id="uuB1" type="Array" optimize="yes">
      0 0 0 0 0 0 0
    </coefficients>
  </correlation>

  <correlation cusp="0.0" size="7" type="shortrange" init="no" speciesA="d" speciesB="u" rcut="1.2">
    <coefficients id="udB1" type="Array" optimize="yes">
      0 0 0 0 0 0 0
    </coefficients>
  </correlation>
</transformation>
</backflow>
\end{verbatim}
Get a good starting guess for $\Psi_T$
1. Try optimizing the Jastrow first without backflow.

2. Freeze the jastrow parameters, introduce only the e-e terms in the backflow transformation, and optimize these parameters.

3. Freeze the e-e backflow parameters, and now optimize the e-I terms.
   - If difficulty is encountered here, try optimizing each species independently.

4. Now, unfreeze all jastrow, e-e backflow, and e-I backflow parameters, and reoptimize.

Optimizing Backflow Terms
It is wholly possible that the above prescription might grind to a halt in steps 2 or 3 with the inability to optimize the e-e or e-I backflow transformation independently, especially if it is initialized to zero. To get around this, one suggestion is to build a good starting guess for the e-e or e-I backflow terms iteratively as follows.

1. Start off with a small number of knots initialized to zero. Set $r_{\text{cut}}$ to be small (much smaller than an interatomic distance).

2. Optimize the backflow function.

3. If this works, slowly increase $r_{\text{cut}}$ and/or the number of knots.

4. Repeat steps 2-3 until there is no noticeable change in energy or variance of $\Psi_T$.

Tweaking the Optimization Run
The following modifications are worth a try in the optimization block:

- Try setting “useDrift” to “no”. This eliminates the use of wavefunction gradients and force biasing in the VMC algorithm. This could be an issue for poorly optimized wavefunctions with pathological gradients.

- Try increasing “exp0” in the optimization block. Larger values of ”exp0” cause the search directions to more closely follow those predicted by steepest-descent than those by the linear method.

Note that the new adaptive shift optimizer has not yet been tried with backflow wavefunctions. It should perform better than the older optimizers, but a considered optimization process is still recommended.

8.6 Finite-difference linear response wave functions
The finite-difference linear response wave function (FDLR) is an experimental wave function type, described in detail in Ref.[22]. In this method, the wave function is formed as the linear response of some existing trial wave function in QMCPACK. This derivatives of this linear response are approximated by a simple finite-difference.
Forming a wave function within the linear response space of an existing ansatz can be very powerful. For example, a configuration interaction singles (CIS) wave function can be formed as a linear combination of the first derivatives of a Slater determinant (with respect to its orbital rotation parameters). Thus, in this sense, CIS is the linear response of Hartree–Fock theory.

Forming a CIS wave function as the linear response of an optimizable Slater determinant is where all testing of this wave function has been performed. In theory the implementation is flexible and it can be used with other trial wave functions in QMCPACK, but this has not been tested. The FDLR trial wave function is experimental.

Mathematically, the FDLR wave function has the form:

$$\Psi_{FDLR}(\mu, X) = \Psi(X + \mu) - \Psi(X - \mu),$$  \hspace{1cm} (8.23)

where $\Psi(P)$ is some trial wave function in QMCPACK, and $P$ are its optimizable parameters. $X$ are the “base” parameters about which the finite difference is performed (for example, an overall orbital rotation). $\mu$ are the “finite difference” parameters, which define the direction of the derivative, and whose magnitude determines the magnitude of the finite-difference. In the limit that the magnitude of $\mu$ goes to 0, the $\Psi_{FDLR}$ object defined above becomes equivalent to

$$\Psi_{FDLR}(\mu, X) = \sum_{pq} \mu_{pq} \frac{\partial \Psi_{det}(X)}{\partial X_{pq}},$$  \hspace{1cm} (8.24)

which is the desired linear response wave function that we are approximating. In the case that $\Psi(P)$ is a determinant with orbital rotation parameters $P$, the above is a CIS wave function with CIS expansion coefficients $\mu$ and orbital rotation $X$.

8.6.1 Input Specifications

An FDLR wave function is specified within a `<fdlr>` ... `</fdlr>` block.

To fully specify an FDLR wave function as above, we require the initial parameters for both $X$ and $\mu$ to be input. This therefore requires two trial wave functions to be provided on input. Each of these is best specified in its own XML file. The names of these two files are provided in an `<include>` tag via `<include wfn_x_href=`` ... '' wfn_d_href=`` ... ''>`.

`wfn_x_href` specifies the file that will hold the $X$ parameters. `wfn_d_href` specifies the file that will hold the $\mu$ parameters.

Other options inside the `<include>` tag are `opt_x` and `opt_d`, which specify whether or not $X$ and $\mu$ parameters are optimizable, respectively.

8.6.2 Example Use Case

```xml
<fdlrwfn name="FDLR">
  <include wfn_x_href="h2.wfn_x.xml" wfn_d_href="h2.wfn_d.xml" opt_x="yes" opt_d="yes"/>
</fdlrwfn>
```

with the h2.wfn_x.xml file containing one of the wave functions and corresponding set of $X$ parameters, such as:

```xml
<?xml version="1.0"?>
<wfn_x>
  <determinantset name="LCAOBSet" type="MolecularOrbital" transform="yes" source="ion0">
```

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<basisset name="LCAOBSet">
<atomicBasisSet name="Gaussian-G2" angular="cartesian" type="Gaussian"
  elementType="H" normalized="no">
  <grid type="log" ri="1.e-6" rf="1.e2" npts="1001"/>
  <basisGroup rid="H00" n="0" l="0" type="Gaussian">
    <radfunc exponent="1.923840000000e+01" contraction="3.282799101900e-02"/>
    <radfunc exponent="2.898720000000e+00" contraction="2.312039367510e-01"/>
    <radfunc exponent="6.534720000000e-01" contraction="8.172257764360e-01"/>
  </basisGroup>
  <basisGroup rid="H10" n="1" l="0" type="Gaussian">
    <radfunc exponent="1.630642000000e-01" contraction="1.000000000000e+00"/>
  </basisGroup>
</atomicBasisSet>
</basisset>

<sposet basisset="LCAOBSet" name="spo-up" size="4" optimize="yes">
  <occupation mode="ground"/>
  <coefficient size="4" id="updetC">
    2.83630000000000e-01 3.35683000000000e-01 2.83630000000000e-01
    3.35683000000000e-01 1.66206000000000e-01 1.22367400000000e+00
    -1.66206000000000e-01 -1.22367400000000e+00
    8.68279000000000e-01 -6.95081000000000e-01
    -6.95081000000000e-01 -9.77898000000000e-01
    9.77898000000000e-01 -1.19682400000000e+00
  </coefficient>
</sposet>

<sposet basisset="LCAOBSet" name="spo-dn" size="4" optimize="yes">
  <occupation mode="ground"/>
  <coefficient size="4" id="downdetC">
    2.83630000000000e-01 3.35683000000000e-01 2.83630000000000e-01
    3.35683000000000e-01 1.66206000000000e-01 1.22367400000000e+00
    -1.66206000000000e-01 -1.22367400000000e+00
    8.68279000000000e-01 -6.95081000000000e-01
    -6.95081000000000e-01 -9.77898000000000e-01
    9.77898000000000e-01 -1.19682400000000e+00
  </coefficient>
</sposet>

<sposet basisset="LCAOBSet" name="spo-up" size="4" optimize="yes">
  <occupation mode="ground"/>
  <coefficient size="4" id="updetC">
    2.83630000000000e-01 3.35683000000000e-01 2.83630000000000e-01
    3.35683000000000e-01 1.66206000000000e-01 1.22367400000000e+00
    -1.66206000000000e-01 -1.22367400000000e+00
    8.68279000000000e-01 -6.95081000000000e-01
    -6.95081000000000e-01 -9.77898000000000e-01
    9.77898000000000e-01 -1.19682400000000e+00
  </coefficient>
</sposet>

<sposet basisset="LCAOBSet" name="spo-dn" size="4" optimize="yes">
  <occupation mode="ground"/>
  <coefficient size="4" id="downdetC">
    2.83630000000000e-01 3.35683000000000e-01 2.83630000000000e-01
    3.35683000000000e-01 1.66206000000000e-01 1.22367400000000e+00
    -1.66206000000000e-01 -1.22367400000000e+00
    8.68279000000000e-01 -6.95081000000000e-01
    -6.95081000000000e-01 -9.77898000000000e-01
    9.77898000000000e-01 -1.19682400000000e+00
  </coefficient>
</sposet>
and similarly for the h2.wfn_d.xml file, which will hold the initial $\mu$ parameters.

The above is a wave function file for an optimizable determinant wave function for H$_2$, in a double zeta valence basis set. Thus, the FDLR wave function here would perform CIS on H$_2$ in a double zeta basis set.

### 8.7 Gaussian Product Wavefunction

The Gaussian Product wavefunction implements eq. 8.25

$$\Psi(\mathbf{R}) = \prod_{i=1}^{N} \exp \left[ -\frac{(\mathbf{R}_i - \mathbf{R}_O)^2}{2\sigma_i^2} \right], \quad (8.25)$$

where $\mathbf{R}_i$ is the position of the $i^{th}$ quantum particle and $\mathbf{R}_O$ is its center. $\sigma_i$ is the width of the Gaussian orbital around center $i$.

This variational wavefunction enhances single-particle density at chosen spatial locations with adjustable strengths. It is useful whenever such localization is physically relevant yet not captured by other parts of the trial wavefunction. For example, in an electron-ion simulation of a solid, the ions are localized around their crystal lattice sites. This single-particle localization is not captured by the ion-ion Jastrow. Therefore the addition of this localization term will improve the wavefunction. The simplest use case of this wavefunction is perhaps the quantum harmonic oscillator (please see the “tests/models/sho” folder for examples).

### Input Specification

<table>
<thead>
<tr>
<th>Gaussian Product Wavefunction (ionwf)</th>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>defaults</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>name</td>
<td>text</td>
<td>ionwf</td>
<td>(required)</td>
<td>Unique name for this wavefunction</td>
<td></td>
</tr>
<tr>
<td>width</td>
<td>floats</td>
<td>1.0 -1</td>
<td>(required)</td>
<td>Widths of Gaussian orbitals.</td>
<td></td>
</tr>
<tr>
<td>source</td>
<td>text</td>
<td>ion0</td>
<td>(required)</td>
<td>Name of classical particle set.</td>
<td></td>
</tr>
</tbody>
</table>

Additional information:

- **width** There must be one width provided for each quantum particle. If a negative width is given, then its corresponding Gaussian orbital is removed. Negative width is useful if one wants to use Gaussian wavefunction for a subset of the quantum particles.

- **source** The Gaussian centers must be specified in the form of a classical particle set. This classical particle set is likely the ion positions “ion0”, hence the name “ionwf”. However, one may define arbitrary centers using a different particle set. Please refer to examples in ‘tests/models/sho’.

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8.7.1 Example Use Case

<qmcsystem>
  <simulationcell>
    <parameter name="bconds">n n n</parameter>
  </simulationcell>
  <particleiset name="e">
    <group name="u" size="1">
      <parameter name="mass">5.0</parameter>
      <attrib name="position" datatype="posArray" condition="0">
        0.0001 -0.0001 0.0002
      </attrib>
    </group>
  </particleiset>
  <particleiset name="ion0" size="1">
    <group name="H">
      <attrib name="position" datatype="posArray" condition="0">
        0 0 0
      </attrib>
    </group>
  </particleiset>
  <wavefunction target="e" id="psi0">
    <ionwf name="iwf" source="ion0" width="0.8165"/>
  </wavefunction>
  <hamiltonian name="h0" type="generic" target="e">
    <extpot type="HarmonicExt" mass="5.0" energy="0.3"/>
    <estimator type="latticedeviation" name="latdev" target="e" tgroup="u"
    source="ion0" sgroup="H"/>
  </hamiltonian>
</qmcsystem>
Chapter 9

Hamiltonian and Observables

QMCPACK is capable of the simultaneous measurement of the Hamiltonian and many other quantum operators. The Hamiltonian attains a special status among the available operators (also referred to as observables) because it ultimately generates all available information regarding the quantum system. This is evident from an algorithmic standpoint as well since the Hamiltonian (embodied in the projector) generates the imaginary time dynamics of the walkers in DMC and RMC.

This section covers how the Hamiltonian can be specified, component by component, by the user in the XML format native to QMCPACK. It also covers the input structure of statistical estimators corresponding to quantum observables such as the density, the static structure factor, and forces.

9.1 The Hamiltonian

The many-body Hamiltonian in Hartree units is given by

\[
\hat{H} = -\sum_i \frac{1}{2m_i} \nabla_i^2 + \sum_i v^{ext}(r_i) + \sum_{i<j} v^{qq}(r_i, r_j) + \sum_{i<\ell} v^{qc}(r_i, r_\ell) + \sum_{\ell<m} v^{cc}(r_\ell, r_m). \tag{9.1}
\]

Here, the sums indexed by \(i/j\) are over quantum particles, while \(\ell/m\) are reserved for classical particles. Often the quantum particles are electrons and the classical particles are ions, though QMCPACK is not limited in this way. The mass of each quantum particle is denoted \(m_i\), \(v^{qq} / v^{qc} / v^{cc}\) are pair potentials between quantum-quantum/quantum-classical/classical-classical particles, and \(v^{ext}\) denotes a purely external potential.

QMCPACK is designed modularly so that any potential can be supported with minimal additions to the code base. Potentials currently supported include Coulomb interactions in open and periodic boundary conditions, the modified periodic coulomb (MPC) potential, non-local pseudopotentials, helium pair potentials, and various model potentials such as hard sphere, gaussian, and modified Poschl-Teller.

Reference information and examples for the \(<\text{hamiltonian}/>\) XML element is provided below. Detailed descriptions of the input for individual potentials is given in the sections that follow.
### hamiltonian element

**Parent elements:** simulation, qmcsystem  
**Child elements:** pairpot, extpot, estimator, constant (deprecated)

<table>
<thead>
<tr>
<th>attributes</th>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>name/id(^o)</td>
<td>text</td>
<td>anything</td>
<td></td>
<td>h0</td>
<td>Unique id for this Hamiltonian instance</td>
</tr>
<tr>
<td>type(^o)</td>
<td>text</td>
<td></td>
<td></td>
<td>generic</td>
<td>No current function</td>
</tr>
<tr>
<td>role(^o)</td>
<td>text</td>
<td>primary/extra</td>
<td>extra</td>
<td>extra</td>
<td>Designate as primary Hamiltonian or not</td>
</tr>
<tr>
<td>source(^o)</td>
<td>text</td>
<td>particleset.name</td>
<td>i</td>
<td></td>
<td>Identify classical particleset</td>
</tr>
<tr>
<td>target(^o)</td>
<td>text</td>
<td>particleset.name</td>
<td>e</td>
<td></td>
<td>Identify quantum particleset</td>
</tr>
<tr>
<td>default(^o)</td>
<td>boolean</td>
<td>yes/no</td>
<td>yes</td>
<td></td>
<td>Include kinetic energy term implicitly</td>
</tr>
</tbody>
</table>

Additional information:

- **target**: Must be set to the name of the quantum particleset. The default value is typically sufficient. In normal usage, no other attributes are provided.

### Listing 9.1: All electron Hamiltonian XML element.

```xml
<hamiltonian target="e">
  <pairpot name="ElecElec" type="coulomb" source="e" target="e"/>
  <pairpot name="ElecIon" type="coulomb" source="i" target="e"/>
  <pairpot name="IonIon" type="coulomb" source="i" target="i"/>
</hamiltonian>
```

### Listing 9.2: Pseudopotential Hamiltonian XML element.

```xml
<hamiltonian target="e">
  <pairpot name="ElecElec" type="coulomb" source="e" target="e"/>
  <pairpot name="ElecIon" type="coulomb" source="i" target="e"/>
  <pairpot name="IonIon" type="coulomb" source="i" target="i"/>
  <pairpot name="PseudoPot" type="pseudo" source="i" wavefunction="psi0" format="xml">
    <pseudo elementType="Li" href="Li.xml"/>
    <pseudo elementType="H" href="H.xml"/>
  </pairpot>
</hamiltonian>
```

### 9.2 Pair potentials

Many pair potentials are supported. Though only the most commonly used pair potentials are covered in detail in this section, all currently available potentials are listed briefly below. If a potential you desire is not covered below, or is not present at all, feel free to contact the developers.
Additional information:

- **type**: Used to select the desired pair potential. Must be selected from the list of type options above.

- **name**: A unique name used to identify this pair potential. Block averaged output data will appear under this name in scalar.dat and/or stat.h5 files.

- **source/target**: These specify the particles involved in a pair interaction. If an interaction is between classical (e.g. ions) and quantum (e.g. electrons), source/target should be the name of the classical/quantum particleset.

- Only **coulomb**, **pseudo**, **mpc** are described in detail below. The older or less used types (**cpp**, **skpot**) are not covered.

- Available only if **QMC_BUILD_LEVEL>2** and **QMC_CUDA** is not defined: **skpot**.

- Available only if **OHMMS_DIM==3**: mpc, vhxc, pseudo.

- Available only if **OHMMS_DIM==3** and **QMC_BUILD_LEVEL>2** and **QMC_CUDA** is not defined: **cpp**.

### 9.2.1 Coulomb potentials

The bare Coulomb potential is used in open boundary conditions:

\[
V_{c}^{\text{open}} = \sum_{i<j} \frac{q_i q_j}{|r_i - r_j|}
\]  

(9.2)

When periodic boundary conditions are selected, Ewald summation is used automatically:

\[
V_{c}^{\text{pbc}} = \sum_{i<j} \frac{q_i q_j}{|r_i - r_j|} + \frac{1}{2} \sum_{L \neq 0} \sum_{i,j} \frac{q_i q_j}{|r_i - r_j + L|}
\]  

(9.3)
The sum indexed by $L$ is over all non-zero simulation cell lattice vectors. In practice, the Ewald sum is broken into short and long ranged parts in a manner optimized for efficiency (see Ref. [9]) for details.

For information on how to set the boundary conditions, consult Sec. 7.1.

<table>
<thead>
<tr>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>text</td>
<td>coulomb</td>
<td></td>
<td>Must be coulomb</td>
</tr>
<tr>
<td>name/id</td>
<td>text</td>
<td>anything</td>
<td>ElecElec</td>
<td>Unique name for interaction</td>
</tr>
<tr>
<td>source</td>
<td>text</td>
<td>particleset.name</td>
<td>hamiltonian.target</td>
<td>Identify interacting particles</td>
</tr>
<tr>
<td>target</td>
<td>text</td>
<td>particleset.name</td>
<td>hamiltonian.target</td>
<td>Identify interacting particles</td>
</tr>
<tr>
<td>pbc</td>
<td>boolean</td>
<td>yes/no</td>
<td>yes</td>
<td>Use Ewald summation</td>
</tr>
<tr>
<td>physical</td>
<td>boolean</td>
<td>yes/no</td>
<td>yes</td>
<td>Hamiltonian(yes)/observable</td>
</tr>
<tr>
<td>forces</td>
<td>boolean</td>
<td>yes/no</td>
<td>no</td>
<td>Deprecated</td>
</tr>
</tbody>
</table>

Additional information

- **type/source/target** See description for the generic pairpot factory element above.

- **name**: Traditional user-specified names for electron-electron, electron-ion, and ion-ion terms are ElecElec, ElecIon, and IonIon, respectively. While any choice can be used, the data analysis tools expect to find columns in *.scalar.dat with these names.

- **pbc**: Ewald summation will not be performed if simulationcell.bconds== n n n, regardless of the value of pbc. Similarly, the pbc attribute can only be used to turn off Ewald summation if simulationcell.bconds!= n n n. The default value is recommended.

- **physical**: If physical==yes, this pair potential is included in the Hamiltonian and will factor into the LocalEnergy reported by QMCPACK and also in the DMC branching weight. If physical==no, then the pair potential is treated as a passive observable but not as part of the Hamiltonian itself. As such it does not contribute to the outputted LocalEnergy. Regardless of the value of physical output data will appear in scalar.dat in a column headed by name.

Listing 9.3: XML element for Coulomb interaction between electrons.

```xml
<pairpot name="ElecElec" type="coulomb" source="e" target="e"/>
```

Listing 9.4: XML element for Coulomb interaction between electrons and ions (all-electron only).

```xml
<pairpot name="ElecIon" type="coulomb" source="i" target="e"/>
```

Listing 9.5: XML element for Coulomb interaction between ions.

```xml
<pairpot name="IonIon" type="coulomb" source="i" target="i"/>
```
9.2.2 Pseudopotentials

QMCPACK supports pseudopotentials in semilocal form, which is local in the radial coordinate and non-local in angular coordinates. When all angular momentum channels above a certain threshold ($\ell_{\text{max}}$) are well approximated by the same potential ($V_\ell \equiv V_{\text{loc}}$), the pseudopotential separates into a fully local channel and an angularly-nonlocal component:

$$V^{PP} = \sum_{ij} \left( V_\ell(|r_i - \tilde{r}_j|) + \sum_{\ell \neq \ell} \sum_{m=-\ell}^{\ell} |Y_{\ell m}| \left( V_\ell(|r_i - \tilde{r}_j|) - V_\ell(|r_i - \tilde{r}_j|) \right) Y_{\ell m} \right)$$  \hspace{1cm} (9.4)

Here the electron/ion index is $i/j$ and only one type of ion is shown for simplicity.

Evaluation of the localized pseudopotential energy $\Psi_T^{-1} V^{PP} \Psi_T$ requires additional angular integrals. These integrals are evaluated on a randomly shifted angular grid. The size of this grid is determined by $\ell_{\text{max}}$. See Ref. [10] for further detail.

QMCPACK uses the FSAtom pseudopotential file format associated with the “Free Software Project for Atomic-scale Simulations” initiated in 2002 (see http://www.tddft.org/fsatom/manifest.php for general information). The FSAtom format uses XML for structured data. Files in this format do not use a specific identifying file extension; they are simply suffixed with “.xml”. The tabular data format of CASINO is also supported.

| parent elements: | hamiltonian |
| child elements:  | pseudo     |
| attributes       |            |
| name             | datatype   | values   | default | description                  |
| type$^*$         | text       | pseudo   |         | Must be pseudo               |
| name/id$^*$      | text       | anything | PseudoPot | No current function          |
| source$^*$       | text       | particleset.name | i | Ion particleset name         |
| target$^*$       | text       | particleset.name | hamiltonian.target | Electron particleset name   |
| pbc$^*$          | boolean    | yes/no   | yes     | Use Ewald summation          |
| forces           | boolean    | yes/no   | no      | Deprecated                   |
| wavefunction$^*$ | text       | wavefunction.name | invalid | Identify wavefunction       |
| format$^*$       | text       | xml/table | table   | Select file format           |
| algorithm$^*$    | text       | batched/default | default | Choose NLPP algorithm       |

Additional information:

- **type/source/target** See description for the generic pairpot factory element above.

- **name**: Ignored. Instead default names will be present in *scalar.dat output files when pseudopotentials are used. The field LocalECP refers to the local part of the pseudopotential. If non-local channels are present, a NonLocalECP field will be added that contains the non-local energy summed over all angular momentum channels.

- **pbc**: Ewald summation will not be performed if simulationcell.bconds== n n n, regardless of the value of pbc. Similarly, the pbc attribute can only be used to turn off Ewald summation if simulationcell.bconds!= n n n.
• **format**: If format==table, QMCPACK looks for *.psf files containing pseudopotential data in a tabular format. The files must be named after the ionic species provided in particleset (e.g. Li.psf and H.psf). If format==xml, additional pseudo child XML elements must be provided (see below). These elements specify individual file names and formats (both the FSAtom XML and CASINO tabular data formats are supported).

• **algorithm** The default algorithm evaluates the ratios of wavefunction components together for each quadrature point and then one point after another. The batched algorithm evaluates the ratios of quadrature points together for each wavefunction component and then one component after another. Internally, it uses VirtualParticleSet for quadrature points. Hybrid orbital representation has an extra optimization enabled when using the batched algorithm.

Listing 9.6: XML element for pseudopotential electron-ion interaction (psf files).

```xml
<pairpot name="PseudoPot" type="pseudo" source="i" wavefunction="psi0" format="psf"/>
```

Listing 9.7: XML element for pseudopotential electron-ion interaction (xml files).

```xml
<pairpot name="PseudoPot" type="pseudo" source="i" wavefunction="psi0" format="xml">
    <pseudo elementType="Li" href="Li.xml"/>
    <pseudo elementType="H" href="H.xml"/>
</pairpot>
```

Details of `<pseudo/>` input elements are given below. It is possible to include (or construct) a full pseudopotential directly in the input file without providing an external file via href. The full XML format for pseudopotentials is not yet covered.

<table>
<thead>
<tr>
<th>parent elements:</th>
<th>pairpot type=pseudo</th>
</tr>
</thead>
<tbody>
<tr>
<td>child elements:</td>
<td>header local grid</td>
</tr>
<tr>
<td>attributes</td>
<td></td>
</tr>
<tr>
<td><strong>name</strong></td>
<td><strong>datatype</strong></td>
</tr>
<tr>
<td>elementType/symbol</td>
<td>text</td>
</tr>
<tr>
<td>href</td>
<td>text</td>
</tr>
<tr>
<td>format</td>
<td>text</td>
</tr>
<tr>
<td>cutoff</td>
<td>real</td>
</tr>
<tr>
<td>lmax</td>
<td>integer</td>
</tr>
<tr>
<td>nrule</td>
<td>integer</td>
</tr>
</tbody>
</table>

Listing 9.8: XML element for pseudopotential of single ionic species.

```xml
<pseudo elementType="Li" href="Li.xml"/>
```

9.2.3 Modified periodic Coulomb interaction/correction

The modified periodic Coulomb (MPC) interaction is an alternative to direct Ewald summation. The MPC corrects the exchange correlation hole to more closely match its thermodynamic limit.
Because of this, the MPC exhibits smaller finite size errors than the bare Ewald interaction, though a few alternative and competitive finite size correction schemes now exist. The MPC is itself often used just as a finite size correction in postprocessing (set physical=false in the input).

<table>
<thead>
<tr>
<th>pairpot type=mpc element</th>
</tr>
</thead>
<tbody>
<tr>
<td>parent elements: Hamiltonian</td>
</tr>
<tr>
<td>attributes</td>
</tr>
<tr>
<td>name</td>
</tr>
<tr>
<td>type</td>
</tr>
<tr>
<td>name/id</td>
</tr>
<tr>
<td>source</td>
</tr>
<tr>
<td>target</td>
</tr>
<tr>
<td>physical</td>
</tr>
<tr>
<td>cutoff</td>
</tr>
</tbody>
</table>

Remarks

- physical: Typically set to no, meaning the standard Ewald interaction will be used during sampling and MPC will be measured as an observable for finite-size post correction. If physical is yes, the MPC interaction will be used during sampling. In this case an electron-electron Coulomb pairpot element should not be supplied.

- Developer note: Currently the name attribute for the mpc interaction is ignored. The name is always reset to MPC.

Listing 9.9: Modified periodic coulomb for finite size post-correction.

```xml
<pairpot type="MPC" name="MPC" source="e" target="e" ecut="60.0" physical="no"/>
```

### 9.3 General estimators

A broad range of estimators for physical observables are available in QMCPACK. The sections below contain input details for the total number density (density), number density resolved by particle spin (spindensity), spherically averaged pair correlation function (gofr), static structure factor (sk), energy density (energydensity), one body reduced density matrix (dm1b), $S(k)$ based kinetic energy correction (chiesa), forward walking (ForwardWalking), and force (Force) estimators. Other estimators are not yet covered.

When an <estimator/> element appears in <hamiltonian/>, it is evaluated for all applicable chained QMC runs (e.g. VMC→DMC→DMC). Estimators are generally not accumulated during wavefunction optimization sections. If an <estimator/> element is instead provided in a particular <qmc/> element, that estimator is only evaluated for that specific section (e.g. during VMC only).
### 9.3.1 Chiesa-Ceperley-Martin-Holzmann kinetic energy correction

This estimator calculates a finite size correction to the kinetic energy following the formalism laid out in Ref. [11]. The total energy can be corrected for finite size effects by using this estimator in conjunction with the MPC correction.

```
<estimator name="KEcorr" type="chiesa" source="e" psi="psi0"/>
```
9.3.2 Density estimator

The particle number density operator is given by

\[ \hat{n}_r = \sum_i \delta(r - r_i) \]  

(9.5)

The density estimator accumulates the number density on a uniform histogram grid over the simulation cell. The value obtained for a grid cell \( c \) with volume \( \Omega_c \) is then the average number of particles in that cell:

\[ n_c = \int dR |\Psi|^2 \int_{\Omega_c} dr \sum_i \delta(r - r_i) \]  

(9.6)

<table>
<thead>
<tr>
<th>estimator</th>
<th>type=density</th>
<th>element</th>
</tr>
</thead>
<tbody>
<tr>
<td>parent elements:</td>
<td>hamiltonian, qmc</td>
<td></td>
</tr>
<tr>
<td>child elements:</td>
<td>None</td>
<td></td>
</tr>
<tr>
<td>attributes</td>
<td></td>
<td></td>
</tr>
<tr>
<td>name</td>
<td>type</td>
<td>values</td>
</tr>
<tr>
<td>type</td>
<td>text</td>
<td>density</td>
</tr>
<tr>
<td>name</td>
<td>text</td>
<td>anything</td>
</tr>
<tr>
<td>delta</td>
<td>real array(3)</td>
<td>( 0 \leq v_i \leq 1 )</td>
</tr>
<tr>
<td>x_min</td>
<td>real</td>
<td>&gt; 0</td>
</tr>
<tr>
<td>x_max</td>
<td>real</td>
<td>&gt; 0</td>
</tr>
<tr>
<td>y_min</td>
<td>real</td>
<td>&gt; 0</td>
</tr>
<tr>
<td>y_max</td>
<td>real</td>
<td>&gt; 0</td>
</tr>
<tr>
<td>z_min</td>
<td>real</td>
<td>&gt; 0</td>
</tr>
<tr>
<td>z_max</td>
<td>real</td>
<td>&gt; 0</td>
</tr>
<tr>
<td>potential</td>
<td>boolean</td>
<td>yes/no</td>
</tr>
<tr>
<td>debug</td>
<td>boolean</td>
<td>yes/no</td>
</tr>
</tbody>
</table>

Additional information:

- **name**: The name provided will be used as a label in the stat.h5 file for the blocked output data. Post-processing tools expect name="Density".

- **delta**: This sets the histogram grid size used to accumulate the density: \( \text{delta}="0.1 0.1 0.05" \rightarrow 10 \times 10 \times 20 \) grid, \( \text{delta}="0.01 0.01 0.01" \rightarrow 100 \times 100 \times 100 \) grid. The density grid is written to a stat.h5 file at the end of each Monte Carlo block. If you request many blocks in a <qmc/> element, or select a large grid, the resulting stat.h5 file may be many GB in size.

- ***_min/*_max**: Can be used to select a subset of the simulation cell for the density histogram grid. For example if a (cubic) simulation cell is 20 Bohr on a side, setting \( *\_\text{min}=5.0 \) and \( *\_\text{max}=15.0 \) will result in a density histogram grid spanning a \( 10 \times 10 \times 10 \) Bohr cube about the center of the box. Use of \( x\_\text{min}, x\_\text{max}, y\_\text{min}, y\_\text{max}, z\_\text{min}, z\_\text{max} \) is only appropriate for orthorhombic simulation cells with open boundary conditions.
When open boundary conditions are used, a `<simulationcell/>` element must be explicitly provided as the first sub-element of `<qmcsystem/>` for the density estimator to work. In this case the molecule should be centered around the middle of the simulation cell \((L/2)\) and not the origin \((0,0,0)\) since the space within the cell, and hence the density grid, is defined from \(0\) to \(L\).

Listing 9.11: Density estimator (uniform grid).

```xml
<estimator name="Density" type="density" delta="0.05 0.05 0.05"/>
```

### 9.3.3 Spin density estimator

The spin density is similar to the total density described above. In this case, the sum over particles is performed independently for each spin component.

```
estimator type=spindensity element

parent elements:  hamiltonian, qmc
child elements:    None
attributes

<table>
<thead>
<tr>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>text</td>
<td>spindensity</td>
<td>any</td>
<td>Must be spindensity</td>
</tr>
<tr>
<td>name</td>
<td>text</td>
<td>anything</td>
<td>yes/no</td>
<td>Unique name for estimator</td>
</tr>
<tr>
<td>report</td>
<td>boolean</td>
<td></td>
<td>no</td>
<td>Write setup details to stdout</td>
</tr>
</tbody>
</table>

parameters

<table>
<thead>
<tr>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>grid</td>
<td>integer</td>
<td>(v_i &gt; 0)</td>
<td>Grid cell count</td>
<td></td>
</tr>
<tr>
<td>dr</td>
<td>real</td>
<td>(v_i &gt; 0)</td>
<td>Grid cell spacing (Bohr)</td>
<td></td>
</tr>
<tr>
<td>cell</td>
<td>real</td>
<td>anything</td>
<td>Volume grid exists in</td>
<td></td>
</tr>
<tr>
<td>corner</td>
<td>real</td>
<td>anything</td>
<td>Volume corner location</td>
<td></td>
</tr>
<tr>
<td>center</td>
<td>real</td>
<td>anything</td>
<td>Volume center/origin location</td>
<td></td>
</tr>
<tr>
<td>voronoi</td>
<td>text</td>
<td>particleset.name</td>
<td>Under development</td>
<td></td>
</tr>
<tr>
<td>test_moves</td>
<td>integer</td>
<td>(&gt;= 0)</td>
<td>0</td>
<td>Test estimator with random moves</td>
</tr>
</tbody>
</table>
```

Additional information:

- **name**: The name provided will be used as a label in the `stat.h5` file for the blocked output data. Post-processing tools expect `name="SpinDensity"`.

- **grid**: Sets the dimension of the histogram grid. Input like `<parameter name="grid">40 40 40</parameter>` requests a \(40 \times 40 \times 40\) grid. The shape of individual grid cells is commensurate with the supercell shape.

- **dr**: Real space dimensions of grid cell edges (Bohr units). Input like `<parameter name="dr">0.5 0.5 0.5</parameter>` in a supercell with axes of length 10 Bohr each (but of arbitrary shape) will produce a \(20 \times 20 \times 20\) grid. The inputted `dr` values are rounded to produce an integer number of grid cells along each supercell axis. Either `grid` or `dr` must be provided, but not both.
cell: When cell is provided, a user defined grid volume is used instead of the global supercell. This must be provided if open boundary conditions are used. Additionally, if cell is provided, the user must specify where the volume is located in space in addition to its size/shape (cell) using either the corner or center parameters.

corner: The grid volume is defined as \( \text{corner} + \sum_{d=1}^{3} u_d \text{cell}_d \) with \( 0 < u_d < 1 \) (“cell” refers to either the supercell or user provided cell).

center: The grid volume is defined as \( \text{center} + \sum_{d=1}^{3} u_d \text{cell}_d \) with \( -1/2 < u_d < 1/2 \) (“cell” refers to either the supercell or user provided cell). corner/center can be used to shift the grid even if cell is not specified. Simultaneous use of corner and center will cause QMCPACK to abort.

Listing 9.12: Spin density estimator (uniform grid).

```xml
<estimator type="spindensity" name="SpinDensity" report="yes">
  <parameter name="grid"> 40 40 40 </parameter>
</estimator>
```

Listing 9.13: Spin density estimator (uniform grid centered about origin).

```xml
<estimator type="spindensity" name="SpinDensity" report="yes">
  <parameter name="grid">
    20 20 20
  </parameter>
  <parameter name="center">
    0.0 0.0 0.0
  </parameter>
  <parameter name="cell">
    10.0 0.0 0.0
    0.0 10.0 0.0
    0.0 0.0 10.0
  </parameter>
</estimator>
```

9.3.4 Pair correlation function, \( g(r) \)

The functional form of the species resolved radial pair correlation function operator is

\[
g_{ss'}(r) = \frac{V}{4\pi r^2N_sN_{s'}} \sum_{i=1}^{N_s} \sum_{j'=1}^{N_{s'}} \delta(r - |r_{is} - r_{j's'}|). \tag{9.7}
\]

Here \( N_s \) is the number of particles of species \( s \) and \( V \) is the supercell volume. If \( s = s' \), then the sum is restricted so that \( i_s \neq j_s \).

In QMCPACK, an estimate of \( g_{ss'}(r) \) is obtained as a radial histogram with a set of \( N_b \) uniform bins of width \( \delta r \). This can be expressed analytically as

\[
g_{ss'}(r) = \frac{V}{4\pi r^2N_sN_{s'}} \sum_{i=1}^{N_s} \sum_{j=1}^{N_{s'}} \frac{1}{\delta r} \int_{r-\delta r/2}^{r+\delta r/2} dr' \delta(r' - |r_{si} - r_{s'j}|), \tag{9.8}
\]

where the radial coordinate \( r \) is restricted to reside at the bin centers, \( \delta r/2, 3\delta r/2, 5\delta r/2, \ldots \).
Additional information:

- **num_bin**: The number of bins in each species pair radial histogram.

- **rmax**: Maximum pair distance included in the histogram. The uniform bin width is \( \delta r = \frac{r_{\text{max}}}{\text{num} \_ \text{bin}} \). If periodic boundary conditions are used for any dimension of the simulation cell, then the default value of \( r_{\text{max}} \) is the simulation cell radius instead of 10 Bohr. For open boundary conditions the volume (\( V \)) used is 1.0 Bohr\(^3\).

- **source/sources**: If unspecified, only pair correlations between each species of quantum particle will be measured. For each classical particleset specified by source/sources, additional pair correlations between each quantum and classical species will be measured. Typically there is only one classical particleset (e.g. `source="ion0"`), but there can be several in principle (e.g. `sources="ion0 ion1 ion2"`).

- **target**: The default value is the preferred usage (i.e. `target` does not need to be provided).

- Data is outputted to the `stat.h5` for each QMC sub-run. Individual histograms are named according to the quantum particleset and index of the pair. For example, if the quantum particleset is named "e" and there are two species (up and down electrons, say), then there will be three sets of histogram data in each `stat.h5` file named `gofr_e_0_0`, `gofr_e_0_1`, and `gofr_e_1_1` for up-up, up-down, and down-down correlations, respectively.

**Listing 9.14**: Pair correlation function estimator element.

```xml
<estimator type="gofr" name="gofr" num_bin="200" rmax="3.0" />
```

**Listing 9.15**: Pair correlation function estimator element with additional electron-ion correlations.

```xml
<estimator type="gofr" name="gofr" num_bin="200" rmax="3.0" source="ion0" />
```

### 9.3.5 Static structure factor, \( S(k) \)

Let \( \rho^e_k = \sum_j e^{i \mathbf{k} \cdot \mathbf{r}_j^e} \) be the Fourier space electron density, with \( \mathbf{r}_j^e \) being the coordinate of the \( j \)-th electron. \( \mathbf{k} \) is a wavevector commensurate with the simulation cell. QMCPACK allows the
user to accumulate the static electron structure factor $S(k)$ at all commensurate $k$ such that $|k| \leq (LR\_DIM\_CUTOFF)r_e$. $N^e$ is the number of electrons, LR\_DIM\_CUTOFF is the optimized breakup parameter, and $r_e$ is the Wigner-Seitz radius. It is defined as follows:

$$S(k) = \frac{1}{N^e} \langle \rho^e \rho^e_k \rangle$$  \hspace{1cm} (9.9)

### estimator type=sk element

**parent elements:**  hamiltonian, qmc  
**child elements:**  None  
**attributes**

<table>
<thead>
<tr>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>text</td>
<td>sk</td>
<td>Must be sk</td>
<td>Unique name for estimator</td>
</tr>
<tr>
<td>name</td>
<td>text</td>
<td>anything</td>
<td>any</td>
<td>Output to stat.h5 (yes) or scalar.dat (no)</td>
</tr>
<tr>
<td>hdf5</td>
<td>boolean</td>
<td>yes/no</td>
<td>no</td>
<td></td>
</tr>
</tbody>
</table>

Additional information:

- **name**: Unique name for estimator instance. A data structure of the same name will appear in stat.h5 output files.
- **hdf5**: If hdf5==yes output data for $S(k)$ is directed to the stat.h5 file (recommended usage). If hdf5==no, the data is instead routed to the scalar.dat file resulting in many columns of data with headings prefixed by name and postfixed by the k-point index (e.g. sk_0 sk_1 ...sk_1037 ...).
- This estimator only works in periodic boundary conditions. Its presence in the input file is ignored otherwise.
- This is not a species resolved structure factor. Additionally, for $k$ vectors commensurate with the unit cell, $S(k)$ will include contributions from the static electronic density, thus meaning it won’t accurately measure the electron-electron density response.

Listing 9.16: Static structure factor estimator element.

```xml
<estimator type="sk" name="sk" hdf5="yes"/>
```

### 9.3.6 Species kinetic energy

Record species-resolved kinetic energy instead of the total kinetic energy in the Kinetic column of scalar.dat. SpeciesKineticEnergy is arguable the simplest estimator in QMCPACK. The implementation of this estimator is detailed in manual/estimator/estimator_implementation.pdf.
estimator type=specieskinetic element

<table>
<thead>
<tr>
<th>attributes</th>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>r</td>
<td>text</td>
<td>specieskinetic</td>
<td>any</td>
<td>Must be specieskinetic</td>
</tr>
<tr>
<td>name</td>
<td>r</td>
<td>text</td>
<td>anything</td>
<td>any</td>
<td>Unique name for estimator</td>
</tr>
<tr>
<td>hdf5</td>
<td>o</td>
<td>boolean</td>
<td>yes/no</td>
<td>no</td>
<td>Output to stat.h5 (yes)</td>
</tr>
</tbody>
</table>

Listing 9.17: Species kinetic energy estimator element.

<estimator type="specieskinetic" name="skinetic" hdf5="no"/>

9.3.7 Lattice deviation estimator

Record deviation of a group of particles in one particle set (target) from a group of particles in another particle set (source).

estimator type=latticedeviation element

<table>
<thead>
<tr>
<th>attributes</th>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>r</td>
<td>text</td>
<td>latticedeviation</td>
<td>any</td>
<td>Must be latticedeviation</td>
</tr>
<tr>
<td>name</td>
<td>r</td>
<td>text</td>
<td>anything</td>
<td>any</td>
<td>Unique name for estimator</td>
</tr>
<tr>
<td>hdf5</td>
<td>o</td>
<td>boolean</td>
<td>yes/no</td>
<td>no</td>
<td>Output to stat.h5 (yes)</td>
</tr>
<tr>
<td>per_xyz</td>
<td>o</td>
<td>boolean</td>
<td>yes/no</td>
<td>no</td>
<td>Directional-resolved (yes)</td>
</tr>
<tr>
<td>source</td>
<td>r</td>
<td>text</td>
<td>e/ion0/...</td>
<td>no</td>
<td>source particle set</td>
</tr>
<tr>
<td>sgroup</td>
<td>r</td>
<td>text</td>
<td>u/d/...</td>
<td>no</td>
<td>source particle group</td>
</tr>
<tr>
<td>target</td>
<td>r</td>
<td>text</td>
<td>e/ion0/...</td>
<td>no</td>
<td>target particle set</td>
</tr>
<tr>
<td>tgroup</td>
<td>r</td>
<td>text</td>
<td>u/d/...</td>
<td>no</td>
<td>target particle group</td>
</tr>
</tbody>
</table>

Additional information:

- **source**: The “reference” particle set to measure distances from, actual reference points are determined together with sgroup.

- **sgroup**: The “reference” particle group to measure distances from.

- **source**: The “target” particle set to measure distances to.

- **sgroup**: The “target” particle group to measure distances to. For example, in Listing 9.18, the distance from the up electron (“u”) to the origin of the coordinate system is recorded.

- **per_xyz**: Record direction-resolved distance. In Listing 9.18, the x,y,z coordinates of the up electron will be recorded separately if per_xyz=yes.

- **hdf5**: Record particle-resolved distances in the h5 file if hdf5=yes..
9.3.8 Energy density estimator

An energy density operator, $\hat{\mathcal{E}}_r$, satisfies

$$\int dr \hat{\mathcal{E}}_r = \hat{H}, \quad (9.10)$$

where the integral is over all space and $\hat{H}$ is the Hamiltonian. In QMCPACK, the energy density is split into kinetic and potential components

$$\hat{\mathcal{E}}_r = \hat{T}_r + \hat{V}_r \quad (9.11)$$

with each component given by

$$\hat{T}_r = \frac{1}{2} \sum_i \delta(r - r_i) p_i^2 \quad (9.12)$$

$$\hat{V}_r = \sum_{i<j} \frac{\delta(r - r_i) + \delta(r - r_j)}{2} \hat{v}^{ee}(r_i, r_j) + \sum_{i\ell} \frac{\delta(r - r_i) + \delta(r - \tilde{r}_\ell)}{2} \hat{v}^{eI}(r_i, \tilde{r}_\ell) + \sum_{\ell<m} \frac{\delta(r - \tilde{r}_\ell) + \delta(r - \tilde{r}_m)}{2} \hat{v}^{II}(\tilde{r}_\ell, \tilde{r}_m).$$

Here $r_i$ and $\tilde{r}_\ell$ represent electron and ion positions, respectively, $\hat{p}_i$ is a single electron momentum operator, and $\hat{v}^{ee}(r_i, r_j)$, $\hat{v}^{eI}(r_i, \tilde{r}_\ell)$, $\hat{v}^{II}(\tilde{r}_\ell, \tilde{r}_m)$ are the electron-electron, electron-ion, and ion-ion pair potential operators (including non-local pseudopotentials, if present). This form of the
energy density is size consistent, i.e. the partially integrated energy density operators of well separated atoms gives the isolated Hamiltonians of the respective atoms. For periodic systems with twist averaged boundary conditions, the energy density is formally correct only for either a set of supercell k-points that correspond to real valued wavefunctions, or a k-point set that has inversion symmetry around a k-point having a real valued wavefunction. For more information about the energy density, see Ref. [7].

In QMCPACK, the energy density can be accumulated on piecewise uniform three dimensional grids in generalized cartesian, cylindrical, or spherical coordinates. The energy density integrated within Voronoi volumes centered on ion positions is also available. The total particle number density is also accumulated on the same grids by the energy density estimator for convenience so that related quantities, such as the regional energy per particle, can be computed easily.

<table>
<thead>
<tr>
<th>estimator type=EnergyDensity element</th>
</tr>
</thead>
<tbody>
<tr>
<td>parent elements: hamiltonian, qmc</td>
</tr>
<tr>
<td>child elements: reference_points, spacegrid</td>
</tr>
<tr>
<td>attributes</td>
</tr>
<tr>
<td>name</td>
</tr>
<tr>
<td>type</td>
</tr>
<tr>
<td>name</td>
</tr>
<tr>
<td>dynamic</td>
</tr>
<tr>
<td>static</td>
</tr>
</tbody>
</table>

Additional information:

- name: Must be unique. A dataset with blocked statistical data for the energy density will appear in the stat.h5 files labeled as name.

Listing 9.19: Energy density estimator accumulated on a 20x10x10 grid over the simulation cell.

```xml
<estimator type="EnergyDensity" name="EDcell" dynamic="e" static="ion0">
  <spacegrid coord="cartesian">
    <origin p1="zero"/>
    <axis p1="a1" scale=".5" label="x" grid="-1 (.05) 1"/>
    <axis p1="a2" scale=".5" label="y" grid="-1 (.1) 1"/>
    <axis p1="a3" scale=".5" label="z" grid="-1 (.1) 1"/>
  </spacegrid>
</estimator>
```

Listing 9.20: Energy density estimator accumulated within spheres of radius 6.9 Bohr centered on the first and second atoms in the ion0 particleset.

```xml
<estimator type="EnergyDensity" name="EDatom" dynamic="e" static="ion0">
  <reference_points coord="cartesian">
    r1 1 0 0
    r2 0 1 0
    r3 0 0 1
  </reference_points>
  <spacegrid coord="spherical">
    <origin p1="ion01"/>
    <axis p1="r1" scale="6.9" label="r" grid="0 1"/>
  </spacegrid>
</estimator>
```
Listing 9.21: Energy density estimator accumulated within Voronoi polyhedra centered on the ions.

The <reference_points/> element provides a set of points for later use in specifying the origin and coordinate axes needed to construct a spatial histogramming grid. Several reference points on the surface of the simulation cell (see Table 9.1) as well as the positions of the ions (see the energydensity.static attribute) are made available by default. The reference points can be used, for example, to construct a cylindrical grid along a bond with the origin on the bond center.

### reference_points element

- **parent elements**: estimator type=EnergyDensity
- **child elements**: None
- **attributes**
  - name: text
  - datatype: cartesian/cell
  - default: Specify coordinate system

The body text is a line formatted list of points with labels

Additional information

- **coord**: If coord=cartesian, labeled points are in cartesian (x,y,z) format in units of Bohr. If coord=cell, then labeled points are in units of the simulation cell axes.

- **body text**: The list of points provided in the body text are line formatted, with four entries per line (label coord1 coord2 coord3). A set of points referenced to the simulation cell are available by default (see table 9.1). If energydensity.static is provided, the location of each individual ion is also available (e.g. if energydensity.static=ion0, then the location of the first atom is available with label ion01, the second with ion02, etc.). All points can be used by label when constructing spatial histogramming grids (see the spacegrid element below) used to collect energy densities.
Table 9.1: Reference points available by default. The vectors \(a_1\), \(a_2\), and \(a_3\) refer to the simulation cell axes. The representation of the cell is centered around \(000\).

The <spacegrid/> element is used to specify a spatial histogramming grid for the energy density. Grids are constructed based on a set of, potentially non-orthogonal, user provided coordinate axes. The axes are based on information available from reference_points. Voronoi grids are based only on nearest neighbor distances between electrons and ions. Any number of space grids can be provided to a single energy density estimator.

The <origin/> element gives the location of the origin for a non-Voronoi grid. Additional information:

- **p1/p2/fraction:** The location of the origin is set to \(p1+\text{fraction}*(p2-p1)\). If only \(p1\) is provided, the origin is at \(p1\).
The `<axis/>` element represents a coordinate axis used to construct the, possibly curved, coordinate system for the histogramming grid. Three `<axis/>` elements must be provided to a non-Voronoi `<spacegrid/>` element.

### Additional information:

- **label:** The allowed set of axis labels depends on the coordinate system (i.e. spacegrid.coord). Labels are x/y/z for coord=cartesian, r/phi/z for coord=cylindrical, r/phi/theta for coord=spherical.

- **p1/p2/scale:** The axis vector is set to \( p1 + \text{scale} \times (p2 - p1) \). If only \( p1 \) is provided, the axis vector is \( p1 \).

- **grid:** Specifies the histogram grid along the direction specified by label. The allowed grid points fall in the range \([-1,1]\) for label=x/y/z or \([0,1]\) for r/phi/theta. A grid of 10 evenly spaced points between 0 and 1 can be requested equivalently by `grid="0 (0.1) 1"` or `grid="0 (10) 1"`. Piecewise uniform grids covering portions of the range are supported, e.g. `grid="-0.7 (10) 0.0 (20) 0.5"`.

- Note that `grid` specifies the histogram grid along the (curved) coordinate given by `label`. The axis specified by `p1/p2/scale` does not correspond one-to-one with `label` unless `label=x/y/z`, but the full set of axes provided define the (sheared) space on top of which the curved (e.g. spherical) coordinate system is built.

### 9.3.9 One body density matrix

The N-body density matrix in DMC is \( \hat{\rho}_N = |\Psi_T\rangle \langle \Psi_{FN}| \) (for VMC, substitute \( \Psi_T \) for \( \Psi_{FN} \)). The one body reduced density matrix (1RDM) is obtained by tracing out all particle coordinates but
one:

\[ \hat{n}_1 = \sum_n Tr_{R_n} |\Psi_T\rangle \langle \Psi_{FN}| \]  

(9.13)

In the formula above, the sum is over all electron indices and \( Tr_{R_n}(\ast) = \int dR_n \langle R_n | \ast | R_n \rangle \) with \( R_n = [r_1, \ldots, r_{n-1}, r_{n+1}, \ldots, r_N] \). When the sum is restricted over spin up or down electrons, one obtains a density matrix for each spin species. The 1RDM computed by QMCPACK is partitioned in this way.

In real space, the matrix elements of the 1RDM are

\[ n_1(r, r') = \langle r | \hat{n}_1 | r' \rangle = \sum_n \int dR_n \Psi_T(r, R_n) \Psi^*_{FN}(r', R_n) \]  

(9.14)

A more efficient and compact representation of the 1RDM is obtained by expanding in the single particle orbitals obtained from a Hartree-Fock or DFT calculation, \( \{\phi_i\} \):

\[ n_1(i, j) = \langle \phi_i | \hat{n}_1 | \phi_j \rangle = \int dR \Psi^*_{FN}(R) \Psi_T(R) \sum_n \int dr'_n \frac{\Psi_T(r'_n, R_n)}{\Psi_T(r_n, R_n)} \phi_i(r'_n)^* \phi_j(r_n) \]  

(9.15)

The integration over \( r' \) in Eq. 9.15 is inefficient when one is also interested in obtaining matrices involving energetic quantities, such as the energy density matrix of Ref. [8] or the related (and more well known) Generalized Fock matrix. For this reason, an approximation is introduced as follows:

\[ n_1(i, j) \approx \int dR \Psi^*_{FN}(R) \Psi_T(R) \sum_n \int dr'_n \frac{\Psi_T(r'_n, R_n)}{\Psi_T(r_n, R_n)} \phi_i(r'_n)^* \phi_j(r_n) \]  

(9.16)

For VMC, FN-DMC, FP-DMC, and RN-DMC the formula above represents an exact sampling of the 1RDM corresponding to \( \hat{\rho}^1_N \) (see appendix A of Ref. [8] for more detail).
estimator type=dm1b element

parent elements: hamiltonian, qmc

child elements: none

definition:

name attributes

type: text dm1b

name: text anything

required parameters

name

type: array

basis: sposet.name

integrator:

type: uniform_grid

parameters

name

evaluator: text loop/matrix

scale: real 0 < scale < 1

center: real array(3)

points: integer > 0

samples: integer > 0

warmup: integer > 0

timestep: real > 0

use_drift: boolean yes/no

check_overlap: boolean yes/no

check_derivatives: boolean yes/no

acceptance_ratio: boolean yes/no

rstats: boolean yes/no

normalized: boolean yes/no

energy_matrix: boolean yes/no

description

name: Must be dm1b

name: Unique name for estimator

basis: Orbital basis

integrator: Integration method

evaluator: Evaluation method

scale: Scale integration cell

center: Center of cell

points: Grid points in each dim

samples: MC samples

warmup: MC warmup

timestep: MC time step

use_drift: Use drift in VMC

check_overlap: Print overlap matrix

check_derivatives: Check density derivatives

acceptance_ratio: Print accept ratio

rstats: Print spatial stats

normalized: basis comes norm’ed

energy_matrix: Energy density matrix

Additional information

• name: Density matrix results appear in stat.h5 files labeled according to name.

• basis: List of sposet.name’s. The total set of orbitals contained in all sposet’s comprises the basis (subspace) the one body density matrix is projected onto. This set of orbitals generally includes many virtual orbitals that are not occupied in a single reference Slater determinant.

• integrator: This selects the method used to perform the additional single particle integration. Options are uniform_grid (uniform grid of points over the cell), uniform (uniform random sampling over the cell), and density (Metropolis sampling of approximate density: \( \sum_{b \in \text{basis}} |\phi_b|^2 \), not well tested, please check results carefully!). Depending on the integrator selected, different subsets of the other input parameters are active.

• evaluator: Select for-loop or matrix multiply implementations. Matrix is preferred for speed. Both implementations should give the same results, but please check as this has not been exhaustively tested.

• scale: Resize the simulation cell by scale for use as an integration volume (active for integrator=uniform/uniform_grid).
• center: Translate the integration volume to center at this point (active for integrator=uniform/uniform_grid).
  If center is not provided, the scaled simulation cell is used as is.

• points: The number of grid points in each dimension for integrator=uniform_grid.
  For example, points=10 results in a uniform 10x10x10 grid over the cell.

• samples: Sets the number of Monte Carlo samples collected each step (active for integrator=uniform/density).

• warmup: Number of warmup Metropolis steps at the start of the run, prior to data collection
  (active for integrator=density).

• timestep: Drift-diffusion timestep used in Metropolis sampling (active for integrator=density).

• use_drift: Enable drift in Metropolis sampling (active for integrator=density).

• check_overlap: Print the overlap matrix (computed via simple Riemann sums) to the log
  and then abort. Note that subsequent analysis based on the 1RDM is simplest if the input
  orbitals are orthogonal.

• check_derivatives: Print analytic and numerical derivatives of the approximate (sam-
  pled) density for several sample points, then abort.

• acceptance_ratio: Print the acceptance ratio of the density sampling to the log each
  step.

• rstats: Print statistical information about the spatial motion of the sampled points to the
  log each step.

• normalized: Declare whether the inputted orbitals are normalized or not. If normalized=no,
  direct Riemann integration over a 200x200x200 grid will be used to compute the normaliza-
  tions prior to use.

• energy_matrix: Also accumulate the one body reduced energy density matrix and write
  it to stat.h5. This matrix is not covered in any detail here; the interested reader is referred
  to Ref. [8].

Listing 9.22: One body density matrix with uniform grid integration.

```
<estimator type="dm1b" name="DensityMatrices">
  <parameter name="basis" > spo_u spo_uv </parameter>
  <parameter name="evaluator" > matrix </parameter>
  <parameter name="integrator" > uniform_grid </parameter>
  <parameter name="points" > 4 </parameter>
  <parameter name="scale" > 1.0 </parameter>
  <parameter name="center" > 0 0 0 </parameter>
</estimator>
```

Listing 9.23: One body density matrix with uniform sampling.

```
<estimator type="dm1b" name="DensityMatrices">
  <parameter name="basis" > spo_u spo_uv </parameter>
  <parameter name="evaluator" > matrix </parameter>
  <parameter name="integrator" > uniform </parameter>
  <parameter name="samples" > 64 </parameter>
</estimator>
```
9.4 Forward Walking Estimators

Forward walking is a method by which one can sample the pure fixed-node distribution \( \langle \Phi_0 | \Phi_0 \rangle \). Specifically, one multiplies each walker’s DMC mixed estimate for the observable \( O, \frac{\langle \Phi_0 | \Phi_0 \rangle}{\sqrt{T(R)}} \), by the weighting factor \( \frac{\langle \Phi_0 | \Phi_0 \rangle}{\sqrt{T(R)}} \). As it turns out, this weighting factor for any walker \( R \) is proportional to the total number of descendants the walker will have after a sufficiently long projection time \( \beta \).

To forward walk on an observable, one declares a generic forward walking estimator within a \(<\text{hamiltonian}>\) block, and then specifies the observables to forward walk on and forward walking parameters. Here is a summary.

Additional information:

- **Cost:** Due to having to store histories of observables up to \( \text{max time-steps} \), one should multiply the memory cost of storing the non-forward walked observables variables by \( \text{max} \).
estimator type=ForwardWalking element

parent elements: hamiltonian, qmc
child elements: Observable

attributes

<table>
<thead>
<tr>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>text</td>
<td>ForwardWalking</td>
<td>any</td>
<td>Must be “ForwardWalking”</td>
</tr>
<tr>
<td>name</td>
<td>text</td>
<td>anything</td>
<td>any</td>
<td>Unique name for estimator</td>
</tr>
</tbody>
</table>

Observable element

parent elements: estimator, hamiltonian, qmc
child elements: None

attributes

<table>
<thead>
<tr>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>name</td>
<td>text</td>
<td>anything</td>
<td>any</td>
<td>Registered name of existing estimator on which to forward walk.</td>
</tr>
<tr>
<td>max</td>
<td>integer</td>
<td>&gt; 0</td>
<td></td>
<td>The maximum projection time in steps (max = ( \beta/\tau )).</td>
</tr>
<tr>
<td>frequency</td>
<td>text</td>
<td>≥ 1</td>
<td></td>
<td>Dump data only for every frequency-th scalar.dat file.</td>
</tr>
</tbody>
</table>

Not an issue for things like the potential energy, but can be prohibitive for observables like density, forces, etc.

- **Naming Convention:** Forward walked observables are automatically named FWE_name_i, where \( i \) is the forward walked expectation value at time step \( i \), and name is whatever name appears in the <Observable> block. This is also how it will appear in the scalar.dat file.

In the following example case, QMCPACK forward walks on the potential energy for 300 time steps, and dumps the forward walked value at every time step.

**Listing 9.27:** Forward walking estimator element.

```
<estimator name="fw" type="ForwardWalking">
  <Observable name="LocalPotential" max="300" frequency="1"/>
</estimator>
```

9.5 “Force” estimators

QMCPACK supports force estimation by use of the Chiesa-Ceperly-Zhang (CCZ) estimator. Currently, open and periodic boundary conditions are supported, but for all-electron calculations only.

Without loss of generality, the CCZ estimator for the z-component of the force on an ion centered at the origin is given by the following expression:

\[
F_z = -Z \sum_{i=1}^{N_e} \frac{z_i}{r_i^3} [\theta(r_i - R) + \theta(R - r_i)] \sum_{\ell=1}^{M} c_{\ell} r_i^\ell
\]  

(9.17)

\( Z \) is the ionic charge, \( M \) is the degree of the smoothing polynomial, \( \mathcal{R} \) is a real-space cutoff of the sphere within which the bare-force estimator is smoothed, and \( c_{\ell} \) are predetermined coefficients.
These coefficients are chosen to minimize the weighted mean square error between the bare force estimate and the s-wave filtered estimator. Specifically,

$$\chi^2 = \int_0^R dr \, r^m \left[ f_z(r) - \tilde{f}_z(r) \right]^2$$  \hspace{1cm} (9.18)

Here, $m$ is the weighting exponent, $f_z(r)$ is the unfiltered radial force density for the z force component, and $\tilde{f}_z(r)$ is the smoothed polynomial function for the same force density. The reader is invited to refer to the original paper for a more thorough explanation of the methodology, but with the notation in hand, QMCPACK takes the following parameters.

| estimator type=Force element |
|-----------------------------|-----------------------------|
| parent elements:            | hamiltonian, qmc             |
| child elements:             | parameter                   |

**attributes**

<table>
<thead>
<tr>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>mode</td>
<td>text</td>
<td>See above</td>
<td>bare</td>
<td>Select estimator type</td>
</tr>
<tr>
<td>type</td>
<td>text</td>
<td>Force</td>
<td>Force</td>
<td>Must be “Force”</td>
</tr>
<tr>
<td>name</td>
<td>text</td>
<td>anything</td>
<td>ForceBase</td>
<td>Unique name for this estimator</td>
</tr>
<tr>
<td>pbc</td>
<td>boolean</td>
<td>yes/no</td>
<td>yes</td>
<td>Using periodic BC’s or not</td>
</tr>
<tr>
<td>addionion</td>
<td>boolean</td>
<td>yes/no</td>
<td>no</td>
<td>Add the ion-ion force contribution to output force estimate</td>
</tr>
</tbody>
</table>

**parameters**

<table>
<thead>
<tr>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rcut</td>
<td>real</td>
<td>&gt; 0</td>
<td>1.0</td>
<td>Real space cutoff $R$ in bohr.</td>
</tr>
<tr>
<td>nbasis</td>
<td>integer</td>
<td>&gt; 0</td>
<td>2</td>
<td>Degree of smoothing polynomial $M$</td>
</tr>
<tr>
<td>weightexp</td>
<td>integer</td>
<td>&gt; 0</td>
<td>2</td>
<td>$\chi^2$ weighting exponent $m$.</td>
</tr>
</tbody>
</table>

Additional information:

- **Naming Convention**: The unique identifier name is appended with name_X_Y in the scalar.dat file, where $X$ is the ion ID number, and $Y$ is the component ID (an integer with $x=0$, $y=1$, $z=2$). All force components for all ions are computed and dumped to the scalar.dat file.

- **Miscellaneous**: Usually, the default choice of weightexp is sufficient. Different combinations of rcut and nbasis should be tested though to minimize variance and bias. There is of course a tradeoff, with larger nbasis and smaller rcut leading to smaller biases and larger variances.

The following is an example use case.

```xml
<estimator name="myforce" type="Force" mode="cep" addionion="yes">
  <parameter name="rcut">0.1</parameter>
  <parameter name="nbasis">4</parameter>
  <parameter name="weightexp">2</parameter>
</estimator>
```
Chapter 10

Quantum Monte Carlo Methods

<table>
<thead>
<tr>
<th>qmc factory element</th>
</tr>
</thead>
<tbody>
<tr>
<td>parent elements:</td>
</tr>
<tr>
<td>type selector:</td>
</tr>
<tr>
<td>type options:</td>
</tr>
<tr>
<td></td>
</tr>
<tr>
<td></td>
</tr>
<tr>
<td></td>
</tr>
</tbody>
</table>

shared attributes:

<table>
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<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>method</td>
<td>text</td>
<td>listed above</td>
<td>invalid</td>
<td>QMC driver</td>
</tr>
<tr>
<td>move</td>
<td>text</td>
<td>pbyp, alle</td>
<td>pbyp</td>
<td>method used to move electrons</td>
</tr>
<tr>
<td>gpu</td>
<td>text</td>
<td>yes, no</td>
<td>dep.</td>
<td>use the GPU</td>
</tr>
<tr>
<td>trace</td>
<td>text</td>
<td>no</td>
<td>??</td>
<td></td>
</tr>
<tr>
<td>checkpoint</td>
<td>integer</td>
<td>-1, 0, n</td>
<td>-1</td>
<td>checkpoint frequency</td>
</tr>
<tr>
<td>record</td>
<td>integer</td>
<td>n</td>
<td>0</td>
<td>save configuration every n steps</td>
</tr>
<tr>
<td>target</td>
<td>text</td>
<td>??</td>
<td></td>
<td></td>
</tr>
<tr>
<td>completed</td>
<td>text</td>
<td>??</td>
<td></td>
<td></td>
</tr>
<tr>
<td>append</td>
<td>text</td>
<td>yes, no</td>
<td>yes</td>
<td></td>
</tr>
</tbody>
</table>

Additional information:

- **move.** There are two ways implemented to move electrons. The more used method is the particle-by-particle move. In this method, only one electron is moved for acceptance or rejection. The other method is the all-electron move, namely all the electrons are moved once for testing acceptance or rejection.

- **gpu.** When the executable is compiled with CUDA, the target computing device can be chosen by this switch. With a regular CPU only compilation, this option is not effective.

- **checkpoint.** Enable or disable checkpointing and specify the frequency of output. Possible values are:

  - `-1` No checkpoint (default setting).
  - `0` Dump after the completion of a qmc section.
n Dump after every $n$ blocks. Also dump at the end of the run.

The particle configurations will be written to a .config.h5 file.

Listing 10.1: The following is an example of running a simulation that can be restarted.

```xml
<qmc method="dmc" move="pbyp" checkpoint="0">
  <parameter name="timestep">0.004</parameter>
  <parameter name="blocks">100</parameter>
  <parameter name="steps">400</parameter>
</qmc>
```

The checkpoint flag instructs qmcpack to output walker configurations. This also works in Variational Monte Carlo. This will output an h5 file with the name "projectid"."run-number".config.h5. Check that this file exists before attempting a restart.

To continue a run, specify the mcwalkerset element before your VMC/DMC block:

Listing 10.2: Restart (read walkers from previous run)

```xml
<mcwalkerset fileroot="BH.s002" version="0 6" collected="yes"/>
<qmc method="dmc" move="pbyp" checkpoint="0">
  <parameter name="timestep">0.004</parameter>
  <parameter name="blocks">100</parameter>
  <parameter name="steps">400</parameter>
</qmc>
```

BH is the project id and s002 is the calculation number to read in the walkers from the previous run.

In the project id section, make sure that the series number is different than any existing one to avoid overwriting it.

### 10.1 Variational Monte Carlo

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Type</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>walkers</td>
<td>integer</td>
<td>&gt; 0</td>
<td>number of walkers per node</td>
</tr>
<tr>
<td>blocks</td>
<td>integer</td>
<td>≥ 0</td>
<td>number of blocks</td>
</tr>
<tr>
<td>steps</td>
<td>integer</td>
<td>≥ 0</td>
<td>number of steps per block</td>
</tr>
<tr>
<td>warmupsteps</td>
<td>integer</td>
<td>≥ 0</td>
<td>number of steps for warming up</td>
</tr>
<tr>
<td>substeps</td>
<td>integer</td>
<td>≥ 0</td>
<td>number of substeps per step</td>
</tr>
<tr>
<td>usedrift</td>
<td>text</td>
<td>yes, no</td>
<td>use the algorithm with drift</td>
</tr>
<tr>
<td>timestep</td>
<td>real</td>
<td>&gt; 0</td>
<td>0.1</td>
</tr>
<tr>
<td>samples</td>
<td>integer</td>
<td>≥ 0</td>
<td>total number of samples</td>
</tr>
<tr>
<td>stepsbetweensamples</td>
<td>integer</td>
<td>&gt; 0</td>
<td>period of the sample accumulation</td>
</tr>
<tr>
<td>samplesperthread</td>
<td>integer</td>
<td>≥ 0</td>
<td>number of samples per thread</td>
</tr>
<tr>
<td>storeconfigs</td>
<td>integer</td>
<td>all values</td>
<td></td>
</tr>
<tr>
<td>blocks_between_recompute</td>
<td>integer</td>
<td>≥ 0</td>
<td>wavefunction recompute frequency</td>
</tr>
</tbody>
</table>

Additional information:
• **walkers.** The initial default number of walkers is 1 but in the CPU branch this number will be overwritten as the number of OpenMP threads if the user requested number is smaller than the number of threads.

• **blocks.** This parameter is universal for all the method. At the end of each block, all the statistics accumulated in the block is dumped into files, e.g. scalar.dat.

• **warmupsteps.** Warm-up steps are steps used only for equilibration. All the samples generated by warm-up steps are discarded. In practice, there’s no need to use many warm-up steps because we can always discard more statistics when we perform the post-process.

• **substeps.** In a substep, each of the electrons is moved only once by either particle-by-particle or all-electron move. Because the local energy is evaluated not at each substep but at each step, increasing the number of substeps doesn’t accumulate more samples. But in order to reduce the correlation between consecutive samples, increasing substeps is a very good option for its cheaper computational cost.

• **usedrift.** The VMC is implemented in two algorithms with or without drift. In the no-drift algorithm, the move of each electron is proposed with a Gaussian distribution. The standard deviation is chosen as the timestep input. In the drift algorithm, electrons are moved by langevin dynamics.

• **timestep.** The meaning of timestep depends on whether the drift is used or not. In general, larger timestep reduces the time correlation but might also reduces the accept ratio. Users are required to check the accept ratio of the calculation and make sure it’s larger than 0.9 or between 0.2 and 0.8 with or without the drift.

• **stepsbetweensamples.** Due to the fact that samples generated by consecutive steps might be still correlated. Having stepsbetweensamples larger than 1 reduces that correlation. In practice, using larger substeps is cheaper than using stepsbetweensamples to decorrelate samples.

• **samples.** This is the total amount of samples generated in the current VMC session. This parameter is not important for VMC only calculation but necessary if optimization or DMC follows.

\[
samples = \frac{\text{blocks} \cdot \text{steps} \cdot \text{walkers}}{\text{stepsbetweensamples}} \cdot \text{number of MPI tasks}
\]

• **samplesperthread.** This is an alternative way to set the target amount of samples. More useful in the VMC session preparing the population for the following DMC calculation.

\[
samplesperthread = \frac{\text{blocks} \cdot \text{steps}}{\text{stepsbetweensamples}}
\]

• **storeconfigs.** If storeconfigs is set to a non-zero value, then electron configurations during the VMC run will be saved to the files.

• **blocks between recompute.** For every few blocks, recompute the accuracy critical part of the wavefunction from scratch. =1 by default when using mixed precision. =0 (no recompute) by default when not using mixed precision. Recomputing introduces a performance penalty but it is small using >1 recompute period.

The following is an example of VMC section.

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10.2 Wavefunction Optimization

Optimizing wavefunction is critical in all kinds of real-space quantum Monte Carlo calculations because it significantly improves both the accuracy and efficiency of computation. However, it is very difficult to directly adopt deterministic minimization approaches due to the stochastic nature of evaluating quantities with Monte Carlo. Thanks to the algorithmic breakthrough during the first decade of this century and the tremendous computer power available, it becomes feasible to optimize tens of thousands of parameters in a wavefunction for a solid or molecule. QMCPACK has multiple optimizers implemented based on the state-of-the-art linear method. We are continually improving our optimizers for the robustness and friendliness and trying to provide a single solution. Due to the large variation of wavefunction types carrying distinct characteristics, using several optimizer may be needed in some cases. It is highly suggested to read the recommendation from the experts maintaining these optimizers.

A typical optimization block looks like the following. It starts with method="linear" and contains three blocks of parameters.

```
<loop max="10">
  <qmc method="linear" move="pbyp" gpu="yes">
    <!-- Specify the VMC options -->
    <parameter name="walkers"> 256 </parameter>
    <parameter name="samples"> 2867200 </parameter>
    <parameter name="stepsbetweensamples"> 1 </parameter>
    <parameter name="substeps"> 5 </parameter>
    <parameter name="warmupSteps"> 5 </parameter>
    <parameter name="blocks"> 70 </parameter>
    <parameter name="timestep"> 1.0 </parameter>
    <parameter name="usedrift"> no </parameter>
    <estimator name="LocalEnergy" hdf5="no"/>
  </qmc>
  ...
  <!-- Specify the correlated sampling options and define the cost function -->
  <parameter name="minwalkers"> 0.3 </parameter>
  <cost name="energy"> 0.95 </cost>
  <cost name="unreweightedvariance"> 0.00 </cost>
  <cost name="rewightedvariance"> 0.05 </cost>
  ...
  <!-- Specify the optimizer options -->
  <parameter name="MinMethod"> OneShiftOnly </parameter>
</loop>
```
• loop is helpful to execute identical optimization blocks repeatedly.
• The first part is highly identical to a regular VMC block.
• The second part is to specify the correlated sampling options and define the cost function.
• The last part is used to specify the options of different optimizers. They can be very distinct from one optimizer to another.

10.2.1 VMC run for the optimization

The VMC calculation for the wavefunction optimization has a strict requirement that samples or samplesperthread must be specified because of the optimizer needs for the stored samples. The input parameters of this part are identical to the VMC method.

Recommendations:
• Run the inclusive VMC calculation correctly and efficiently, because this part takes significant amount of time in optimization. For example, make sure the derived steps per block is 1 and use larger substeps to control the correlation between samples.
• A reasonable starting wavefunction is necessary. A lot of optimization fails because of a bad wavefunction starting point. The sign of a bad initial wavefunction includes but not limited to very long equilibration time, low acceptance ratio and huge variance. The first thing to do after a failed optimization is to check the information provided by the VMC calculation via *.scalar.dat files.

10.2.2 Correlated sampling and Cost function

After generating the samples with VMC, the derivatives of the wavefunction with respect to the parameters are computed for proposing a new set of parameters by optimizers. And later, a correlated sampling calculation is performed to quickly evaluate values of the cost function on the old set of parameters and the new set for the further decisions. The input parameters are listed in the following table.

<table>
<thead>
<tr>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>nonlocalpp</td>
<td>text</td>
<td>yes, no</td>
<td>no</td>
<td>include non-local PP energy in the cost function</td>
</tr>
<tr>
<td>minwalkers</td>
<td>real</td>
<td>0–1</td>
<td>0.3</td>
<td>lower bound of the effective weight</td>
</tr>
<tr>
<td>maxWeight</td>
<td>real</td>
<td>&gt; 1</td>
<td>1e6</td>
<td>Maximum weight allowed in reweighting</td>
</tr>
</tbody>
</table>

Additional information:
• maxWeight. The default should be good.
• **nonlocalpp.** Non-local PP contribution to the local energy depends on the wavefunction. When a new set of parameter is proposed, this contribution needs to be updated if the cost function consists of local energy. Fortunately, non-local contribution is chosen small when making a PP for small locality error. We can ignore its change and avoid the expensive computational cost. GPU code has a implementation issue that large amount of memory is consumed with this option.

• **minwalkers.** A CRITICAL parameter. When the ratio of effective samples to actual number of samples in a reweighting step goes lower than minwalkers, the proposed set of parameters is invalid.

The cost function consists of three components: energy, unreweighted variance and reweighted variance.

```
<cost name="energy"> 0.95 </cost>
<cost name="unreweightedvariance"> 0.00 </cost>
<cost name="reweightedvariance"> 0.05 </cost>
```

### 10.2.3 Optimizers

QMCPACK implements a few optimizers having different preference aiming for different priorities. They can be switched among ‘OneShiftOnly’ (default), ‘adaptive’ and ‘quartic’ (old) by the following line in the optimization block.

```
<parameter name="MinMethod"> THE METHOD YOU LIKE </parameter>
```

**OneShiftOnly**

The OneShiftOnly optimizer targets a fast optimization by moving parameters more aggressively. It works with OpenMP and GPU and can be considered for large systems. This method relies on the effective weight of correlated sampling rather than the cost function value to justify a new set of parameters. If effective weight is larger than minwalkers, the new set is taken no matter the cost function value decreases or not. If a proposed set is rejected, the standard output prints the measured ratio of effective samples to the total number of samples and adjustment on minwalkers can be made if needed.

<table>
<thead>
<tr>
<th>linear method</th>
<th>parameters</th>
</tr>
</thead>
<tbody>
<tr>
<td>name</td>
<td>datatype</td>
</tr>
<tr>
<td>shift_i</td>
<td>real</td>
</tr>
<tr>
<td>shift_s</td>
<td>real</td>
</tr>
</tbody>
</table>

Additional information:

• **shift_i.** This is the direct term added to the diagonal of the Hamiltonian matrix. More stable but slower optimization with a large value.

• **shift_s.** This is the initial value of the stabilizer based on the overlap matrix added to the Hamiltonian matrix. More stable but slower optimization with a large value. The used value is auto-adjusted by the optimizer.
Recommendations:

- Default shift_i, shift_s should be fine.

- For hard cases, increasing shift_i (factor of 5 or 10) can significantly stabilize the optimization by reducing the pace towards the optimal parameter set.

- If the VMC energy of the last optimization iterations grows significantly, increase minwalkers closer to 1 and make the optimization stable.

- If the first iterations of optimization are rejected on a reasonable initial wavefunction, lower the minwalkers value based on the measured value printed in the standard output to accept the move.

It is recommended to use this optimizer in two sections with a very small minwalkers in the first and a large value in the second like the following. In the very beginning, parameters are far away from optimal values and large changes are proposed by the optimizer. Having a small minwalkers allows accepting these changes much easier. When the energy gradually converges, we can have a large minwalkers to avoid risky parameter sets.

```
<loop max="6">
  <qmc method="linear" move="pbyp" gpu="yes">
    <!-- Specify the VMC options -->
    <parameter name="walkers"> 1 </parameter>
    <parameter name="samples"> 10000 </parameter>
    <parameter name="stepsbetweensamples"> 1 </parameter>
    <parameter name="substeps"> 5 </parameter>
    <parameter name="warmupSteps"> 5 </parameter>
    <parameter name="blocks"> 25 </parameter>
    <parameter name="timestep"> 1.0 </parameter>
    <parameter name="usedrift"> no </parameter>
    <estimator name="LocalEnergy" hdf5="no"/>
    <!-- Specify the optimizer options -->
    <parameter name="MinMethod"> OneShiftOnly </parameter>
    <parameter name="minwalkers"> 1e-4 </parameter>
  </qmc>
</loop>

<loop max="12">
  <qmc method="linear" move="pbyp" gpu="yes">
    <!-- Specify the VMC options -->
    <parameter name="walkers"> 1 </parameter>
    <parameter name="samples"> 20000 </parameter>
    <parameter name="stepsbetweensamples"> 1 </parameter>
    <parameter name="substeps"> 5 </parameter>
    <parameter name="warmupSteps"> 2 </parameter>
    <parameter name="blocks"> 50 </parameter>
    <parameter name="timestep"> 1.0 </parameter>
    <parameter name="usedrift"> no </parameter>
    <estimator name="LocalEnergy" hdf5="no"/>
    <!-- Specify the optimizer options -->
    <parameter name="MinMethod"> OneShiftOnly </parameter>
    <parameter name="minwalkers"> 0.5 </parameter>
  </qmc>
</loop>
```
For each optimization step, you will see

The new set of parameters is valid. Updating the trial wave function!

or

The new set of parameters is not valid. Revert to the old set!

Occasional rejection is fine. Frequent rejection indicates potential problems and users should inspect the VMC calculation or change optimization strategy. To track the progress of optimization, using command “qmca -q ev *.scalar.dat” to look at the VMC energy and variance for each optimization step.

**adaptive**

The default setting of the adaptive optimizer is to construct the linear method Hamiltonian and overlap matrices explicitly and add different shifts to the Hamiltonian matrix as “stabilizers”. The generalized eigenvalue problem is solved for each shift to obtain updates to the wave function parameters. Then a correlated sampling is performed for each shift’s updated wave function and the initial trial wave function using the middle shift’s updated wave function as the guiding function. The cost function for these wave functions is compared, and the update corresponding to the best cost function is selected. In the next iteration, the median magnitude of the stabilizers is set to that that generated the best update in the current iteration, thus adapting the magnitude of the stabilizers automatically.

When the trial wave function contains more than ten thousand parameters, constructing and storing the linear method matrices may become a memory bottleneck. To avoid explicit construction of these matrices, the adaptive optimizer implements the block linear method (BLM) approach. [14] The BLM tries to find an approximate solution \( \vec{c}_{opt} \) to the standard LM generalized eigenvalue problem by dividing the variable space into a number of blocks and making intelligent estimates for which directions within those blocks will be most important for constructing \( \vec{c}_{opt} \), which is then obtained by solving a smaller, more memory-efficient eigenproblem in the basis of these supposedly important block-wise directions.

<table>
<thead>
<tr>
<th><strong>linear method</strong> parameters</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>name</strong></td>
<td><strong>datatype</strong></td>
<td><strong>values</strong></td>
<td><strong>default</strong></td>
</tr>
<tr>
<td>max_relative_change</td>
<td>real</td>
<td>&gt; 0</td>
<td>10.0</td>
</tr>
<tr>
<td>max_param_change</td>
<td>real</td>
<td>&gt; 0</td>
<td>0.3</td>
</tr>
<tr>
<td>shift_i</td>
<td>real</td>
<td>&gt; 0</td>
<td>0.01</td>
</tr>
<tr>
<td>shift_s</td>
<td>real</td>
<td>&gt; 0</td>
<td>1.00</td>
</tr>
<tr>
<td>chase_lowest</td>
<td>text</td>
<td>yes, no</td>
<td>yes</td>
</tr>
<tr>
<td>chase_closest</td>
<td>text</td>
<td>yes, no</td>
<td>no</td>
</tr>
<tr>
<td>block_lm</td>
<td>text</td>
<td>yes, no</td>
<td>no</td>
</tr>
<tr>
<td>nblocks</td>
<td>integer</td>
<td>&gt; 0</td>
<td></td>
</tr>
<tr>
<td>nolds</td>
<td>integer</td>
<td>&gt; 0</td>
<td></td>
</tr>
<tr>
<td>nkept</td>
<td>integer</td>
<td>&gt; 0</td>
<td></td>
</tr>
</tbody>
</table>

Additional information:
- **shift_i**. This is the initial coefficient used to scale the diagonal stabilizer. More stable but slower optimization is expected with a large value. The adaptive method will automatically adjust this value after each linear method iteration.

- **shift_s**. This is the initial coefficient used to scale the overlap-based stabilizer. More stable but slower optimization is expected with a large value. The adaptive method will automatically adjust this value after each linear method iteration.

- **nblocks**. This is the number of blocks used in block LM. The amount of memory required to store LM matrices decreases with increased number of blocks. But the error introduced by BLM would increase with number of blocks.

- **nolds**. In BLM, the inter-block correlation is accounted for by including a small number of wave function update vectors outside the block. Larger nolds would include more inter-block correlation and more accurate results, but also higher memory requirements.

- **nkept**. This is the number of update directions retained from each block in the BLM. If all directions are retained in each block, then the BLM becomes equivalent to the standard LM. Retaining 5 or fewer directions per block is often sufficient.

Recommendations:
- Default shift_i, shift_s should be fine.
- When there are fewer than about 5,000 variables being optimized, the traditional LM is preferred as it has a lower overhead than the BLM when the number of variables is small.
- Initial experience with the BLM suggests that a few hundred blocks and a handful of nolds and nkept often provide a good balance between memory use and accuracy. In general, using fewer blocks should be more accurate but will require more memory.

```xml
<loop max="15">
  <qmc method="linear" move="pbyp">
    <!-- Specify the VMC options -->
    <parameter name="walkers"> 1 </parameter>
    <parameter name="samples"> 20000 </parameter>
    <parameter name="stepsbetweensamples"> 1 </parameter>
    <parameter name="substeps"> 5 </parameter>
    <parameter name="warmupSteps"> 5 </parameter>
    <parameter name="blocks"> 50 </parameter>
    <parameter name="timestep"> 1.0 </parameter>
    <parameter name="usedrift"> no </parameter>
    <estimator name="LocalEnergy" hdf5="no"/>
    <!-- Specify the correlated sampling options and define the cost function -->
    <cost name="energy"> 1.00 </cost>
    <cost name="unreweightedvariance"> 0.00 </cost>
    <cost name="reweightedvariance"> 0.00 </cost>
    <!-- Specify the optimizer options -->
    <parameter name="MinMethod">adaptive</parameter>
    <parameter name="max_relative_cost_change">10.0</parameter>
    <parameter name="shift_i"> 1.00 </parameter>
    <parameter name="shift_s"> 1.00 </parameter>
  </qmc>
</loop>
```
The adaptive optimizer is also able to optimize individual excited states directly. [13] In this case, it tries to minimize the following function:

$$\Omega[\Psi] = \frac{\langle \Psi | \omega - H | \Psi \rangle}{\langle \Psi | (\omega - H)^2 | \Psi \rangle}$$

The global minimum of this function corresponds to the state whose energy lies immediately above the shift parameter $\omega$ in the energy spectrum. For example, if $\omega$ were placed in between the ground state energy and the first excited state energy and the wave function ansatz was capable of a good description for the first excited state, then the wave function would be optimized for the first excited state. It is important to note that, if the ansatz is not capable of a good description of the excited state in question, the optimization may converge to a different state, as is known to occur in some circumstances for traditional ground state optimizations. Note also that the ground state can be targeted by this method by choosing $\omega$ to be below the ground state energy, although we should stress that this is not the same thing as a traditional ground state optimization and will in general give a slightly different wave function. Excited state targeting requires two additional parameters, as shown in this table.

<table>
<thead>
<tr>
<th>Excited State Targeting</th>
</tr>
</thead>
<tbody>
<tr>
<td>parameters</td>
</tr>
<tr>
<td>name</td>
</tr>
<tr>
<td>targetExcited</td>
</tr>
<tr>
<td>omega</td>
</tr>
</tbody>
</table>

Excited state recommendations:

- Due to the finite variance in any approximate wave function, it is recommended to set $\omega = \omega_0 - \sigma$, where $\omega_0$ is placed just below the energy of the targeted state and $\sigma^2$ is the energy variance.

- In order to obtain an unbiased excitation energy, one should optimize the ground state with the excited state variational principle as well by setting $\omega$ below the ground state energy. Note that using the ground state variational principle for the ground state and the excited state variational principle for the excited state creates a bias in favor of the ground state.

quartic

This is an older optimizer method retained for compatibility. We recommend starting with the newest OneShiftOnly or adaptive optimizers. The quartic optimizer fits a quartic
polynomial to 7 values of the cost function obtained using reweighting along chosen direction and determines the optimal move. This optimizer is very robust but a bit conservative to accept new steps especially when large parameters changes are proposed.

### Linear method

<table>
<thead>
<tr>
<th>Parameters</th>
<th>Datatype</th>
<th>Values</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>bigchange</td>
<td>real</td>
<td>&gt; 0</td>
<td>50.0</td>
<td>Largest parameter change allowed</td>
</tr>
<tr>
<td>alloweddifference</td>
<td>real</td>
<td>&gt; 0</td>
<td>1e-4</td>
<td>Allowed increased in energy</td>
</tr>
<tr>
<td>exp0</td>
<td>real</td>
<td>any value</td>
<td>-16.0</td>
<td>Initial value for stabilizer</td>
</tr>
<tr>
<td>stabilizerscale</td>
<td>real</td>
<td>&gt; 0</td>
<td>2.0</td>
<td>Increase in value of exp0 between iterations</td>
</tr>
<tr>
<td>nstabilizers</td>
<td>integer</td>
<td>&gt; 0</td>
<td>3</td>
<td>Number of stabilizers to try</td>
</tr>
<tr>
<td>max_its</td>
<td>integer</td>
<td>&gt; 0</td>
<td>1</td>
<td>Number of inner loops with same samples</td>
</tr>
</tbody>
</table>

Additional information:

- **exp0.** It is the initial value for stabilizer (shift to diagonal of H). The actual value of stabilizer is $10^{\exp0}$.

Recommendations:

- For hard cases (e.g. simultaneous optimization of long MSD and 3-Body J), set exp0 to 0 and do a single inner iteration (max its=1) per sample of configurations.

```xml
<parameter name="MinMethod">quartic</parameter>
<parameter name="exp0">-6</parameter>
<parameter name="alloweddifference"> 1.0e-4 </parameter>
<parameter name="nstabilizers"> 1 </parameter>
<parameter name="bigchange">15.0</parameter>
```

### 10.2.4 General recommendations

Here are a few recommendations to make wavefunction optimization easier.

- All electron wavefunctions are typically more difficult to optimize than pseudopotential ones due to the importance of the wavefunction near the nucleus.

- Two body Jastrow contributes the largest portion of correlation energy from bare Slater determinants. For this reason, the recommended order for optimizing wavefunction components is two-body, one-body, three-body Jastrow factors and MSD coefficients.

- For two-body spline Jastrows, always start from a reasonable one. The lack of physically-motivated constraints in the functional form at large distances can cause slow convergence if starting from zero.

- One-body spline Jastrow from old calculations can be a good starting point.

- Three-body polynomial Jastrow can start from zero. It is beneficial to first optimize one-body and two-body Jastrow factors without adding three-body terms in the calculation and then add the three-body Jastrow and optimize all the three components together.
10.3 Diffusion Monte Carlo
### DMC Method Parameters

<table>
<thead>
<tr>
<th>Name</th>
<th>Datatype</th>
<th>Values</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>targetwalkers</td>
<td>integer</td>
<td>$&gt; 0$</td>
<td>dep.</td>
<td>overall total number of walkers</td>
</tr>
<tr>
<td>blocks</td>
<td>integer</td>
<td>$\geq 0$</td>
<td>1</td>
<td>number of blocks</td>
</tr>
<tr>
<td>steps</td>
<td>integer</td>
<td>$\geq 0$</td>
<td>1</td>
<td>number of steps per block</td>
</tr>
<tr>
<td>warmupsteps</td>
<td>integer</td>
<td>$\geq 0$</td>
<td>0</td>
<td>number of steps for warming up</td>
</tr>
<tr>
<td>timestep</td>
<td>real</td>
<td>$&gt; 0$</td>
<td>0.1</td>
<td>time step for each electron move</td>
</tr>
<tr>
<td>checkproperties</td>
<td>integer</td>
<td>$\geq 0$</td>
<td>100</td>
<td>number of steps between walker updates</td>
</tr>
<tr>
<td>maxcpusecs</td>
<td>real</td>
<td>$\geq 0$</td>
<td>3.6e5</td>
<td>maximum allowed walltime in seconds</td>
</tr>
<tr>
<td>energyUpdateInterval</td>
<td>integer</td>
<td>$\geq 0$</td>
<td>0</td>
<td>trial energy update interval</td>
</tr>
<tr>
<td>refEnergy</td>
<td>AU</td>
<td>all values</td>
<td>dep.</td>
<td>reference energy</td>
</tr>
<tr>
<td>feedback</td>
<td>double</td>
<td>$\geq 0$</td>
<td>1.0</td>
<td>population feedback on the trial energy</td>
</tr>
<tr>
<td>useBareTau</td>
<td>option</td>
<td>yes,no</td>
<td>0</td>
<td>do not use effective time step</td>
</tr>
<tr>
<td>warmupByReconfiguration</td>
<td>option</td>
<td>yes,no</td>
<td>0</td>
<td>warm up with a fixed population</td>
</tr>
<tr>
<td>sigmaBound</td>
<td>double</td>
<td>$\geq 0$</td>
<td>10</td>
<td>parameter to cutoff large weights</td>
</tr>
<tr>
<td>killnode</td>
<td>string</td>
<td>yes/other</td>
<td>no</td>
<td>kill or reject walkers that cross nodes</td>
</tr>
<tr>
<td>reconfiguration</td>
<td>string</td>
<td>yes/pure/other</td>
<td>no</td>
<td>fixed population technique</td>
</tr>
<tr>
<td>branchInterval</td>
<td>integer</td>
<td>$\geq 0$</td>
<td>1</td>
<td>branching interval</td>
</tr>
<tr>
<td>substeps</td>
<td>integer</td>
<td>$\geq 0$</td>
<td>1</td>
<td>branching interval</td>
</tr>
<tr>
<td>nonlocalmoves</td>
<td>string</td>
<td>yes/no,v0,v1,v3</td>
<td>no</td>
<td>run with T-moves</td>
</tr>
<tr>
<td>scaleweight</td>
<td>string</td>
<td>yes/other</td>
<td>yes</td>
<td>scale weights (CUDA only)</td>
</tr>
<tr>
<td>MaxAge</td>
<td>double</td>
<td>$\geq 0$</td>
<td>10</td>
<td>kill persistent walkers</td>
</tr>
<tr>
<td>MaxCopy</td>
<td>double</td>
<td>$\geq 0$</td>
<td>2</td>
<td>limit population growth</td>
</tr>
<tr>
<td>fastgrad</td>
<td>text</td>
<td>yes/other</td>
<td>yes</td>
<td>fast gradients</td>
</tr>
<tr>
<td>maxDisplSq</td>
<td>real</td>
<td>all values</td>
<td>-1</td>
<td>maximum particle move</td>
</tr>
<tr>
<td>storeconfigs</td>
<td>integer</td>
<td>all values</td>
<td>0</td>
<td>store configurations</td>
</tr>
<tr>
<td>use_nonblocking</td>
<td>string</td>
<td>yes/no</td>
<td>yes</td>
<td>using non-blocking send/recv</td>
</tr>
<tr>
<td>blocks_between_recompute</td>
<td>integer</td>
<td>$\geq 0$</td>
<td>dep.</td>
<td>wavefunction recompute frequency</td>
</tr>
</tbody>
</table>

**Additional information:**

- **targetwalkers.** A DMC run can be considered a restart run or a new run. A restart run is considered to be any method block beyond the first one, such as when a DMC method block that follows a VMC block. Alternatively, if the user reads in configurations from disk it is also considered a restart run. In the case of a restart run, the DMC driver will use the configurations from the previous run, and this variable will not be used. For a new run, if the number of walkers is less than the number of threads, then the number of walkers will be set equal to the number of threads.

- **blocks.** Number of blocks run during an DMC method block. A block consists of a number of DMC steps (steps), after which all the statistics accumulated in the block are written to disk.

- **steps.** Number of diffusion Monte Carlo steps in a block.

- **warmupsteps.** Warm-up steps are steps at the beginning of a DMC run in which the instantaneous average energy is used to update the trial energy. During regular steps, $E_{\text{ref}}$ is used.
- **timestep.** The timestep determines the accuracy of the imaginary time propagator. Generally, multiple time steps are used to extrapolate to the infinite time step limit. A good range of timesteps in which to perform time step extrapolation will typically have a minimum of 99% acceptance probability for each step.

- **checkproperties.** When using particle by particle driver, this variable specifies how often to reset all the variables kept in the buffer.

- **maxcpusecs.** The default is 100 hours. Once the specified time has elapsed, the program will finalize the simulation even if not all blocks are completed.

- **energyUpdateInterval.** The default is to update the trial energy at every step. Otherwise the trial energy is updated every energyUpdateInterval steps.

  \[ E_{\text{trial}} = \text{refEnergy} + \text{feedback} \cdot (\ln \text{targetWalkers} - \ln N) \]

  where \( N \) is the current population.

- **refEnergy.** The default reference energy is taken from the VMC run that precedes the DMC run. This value is updated to the current mean whenever branching happens.

- **feedback.** Variable used to determine how strong to react to population fluctuations when doing population control. See the equation in energyUpdateInterval for more details.

- **useBareTau.** The same time step is used whether a move is rejected to not. The default is to use an effective time step when a move is rejected.

- **warmupByReconfiguration.** Warmup DMC is done with a fixed population

- **sigmaBound.** Determine the branch cutoff to limit wild weights based on the sigma and sigmaBound

- **killnode.** When running fixed-node, if a walker attempts to cross a node, the move will normally be rejected. If killnode = ”yes”, then walkers are destroyed when they cross a node.

- **reconfiguration.** If reconfiguration is ”yes”, then run with a fixed walker population using the reconfiguration technique.

- **branchInterval.** Number of steps between branching. The total number of DMC steps in a block will be BranchInterval*Steps.

- **substeps.** Same as BranchInterval.

- **nonlocalmoves.** Evaluate pseudopotentials using one of the nonlocal move algorithms such as T-moves.
  - **no**(default): imposes the locality approximation.
  - **yes/v0:** implements the algorithm in the 2006 Casula paper [23]
  - **v1:** implements the v1 algorithm in the 2010 Casula paper [24].
  - **v2:** is **not implemented** and **skipped** due to the existence of the v2 algorithm in the 2010 Casula paper [24].
v3: implements an algorithm similar to v1 but is much faster. v1 computes the transition probability before each single electron T-move selection due to the acceptance of previous T-moves. v3 reuses the transition probability computed in non-local pseudopotentials, namely before accepting any T-moves. This is an approximation to v1, and results in a different time step error, but significantly reduces the computational cost. v1 and v3 agrees at zero time step.

The v1 and v3 algorithms are size-consistent and important advances over the previous v0 non-size-consistent algorithm. Investigating the importance of size consistency is highly recommended.

- **scaleweight.** Scaling weight per Umrigar/Nightengale. CUDA only.
- **MaxAge.** Set the weight of a walker to \( \min(\text{currentweight},0.5) \) after a walker has not moved for MaxAge steps. Needed if persistent walkers appear during the course of a run.
- **MaxCopy.** When determining the number of copies of a walker to branch, set the number of copies equal to \( \min(\text{Multiplicity},\text{MaxCopy}) \).
- **fastgrad.** Calculates gradients with either the fast version or the full-ratio version.
- **maxDisplSq.** When running a DMC calculation with particle by particle, this sets the maximum displacement allowed for a single particle move. All distance displacements larger than the max is rejected. If initialized to a negative value, it becomes equal to Lattice(LR/rc).
- **sigmaBound.** Determine the branch cutoff to limit wild weights based on the sigma and sigmaBound
- **storeconfigs.** If storeconfigs is set to a non-zero value, then electron configurations during the DMC run will be saved. This option is disabled for the OpenMP version of DMC.
- **blocks_between_recompute.** See details in VMC section 10.1.

**Listing 10.3:** The following is an example of a very simple DMC section.

```xml
<qmc method="dmc" move="pbyp" target="e">
  <parameter name="blocks">100</parameter>
  <parameter name="steps">400</parameter>
  <parameter name="timestep">0.010</parameter>
  <parameter name="warmupsteps">100</parameter>
</qmc>
```

The time step should be adjusted for each problem individually. Please refer to the theory section on diffusion Monte Carlo.

**Listing 10.4:** The following is an example of running a simulation that can be restarted.

```xml
<qmc method="dmc" move="pbyp" checkpoint="0">
  <parameter name="timestep">0.004</parameter>
  <parameter name="blocks">100</parameter>
  <parameter name="steps">400</parameter>
</qmc>
```
The checkpoint flag instructs qmcpack to output walker configurations. This also works in Variational Monte Carlo. This will output an h5 file with the name "projectid'"run-number'.config.h5. Check that this file exists before attempting a restart. To read in this file for a continuation run, specify the following:

Listing 10.5: Restart (read walkers from previous run)

```xml
<mcwalkerset fileroot="BH.s002" version="0 6" collected="yes"/>
```

BH is the project id and s002 is the calculation number to read in the walkers from the previous run.

Combining VMC and DMC in a single run (and wave function optimization can be combined in this way too) is the standard way in which QMCPACK is typically run. There is no need to run two separate jobs, as method sections can be stacked, and walkers are transferred between them.

Listing 10.6: Combined VMC and DMC run

```xml
<qmc method="vmc" move="pbyp" target="e">
  <parameter name="blocks">100</parameter>
  <parameter name="steps">4000</parameter>
  <parameter name="warmupsteps">100</parameter>
  <parameter name="samples">1920</parameter>
  <parameter name="walkers">1</parameter>
  <parameter name="timestep">0.5</parameter>
</qmc>

<qmc method="dmc" move="pbyp" target="e">
  <parameter name="blocks">100</parameter>
  <parameter name="steps">400</parameter>
  <parameter name="timestep">0.010</parameter>
  <parameter name="warmupsteps">100</parameter>
</qmc>

<qmc method="dmc" move="pbyp" target="e">
  <parameter name="warmupsteps">500</parameter>
  <parameter name="blocks">50</parameter>
  <parameter name="steps">100</parameter>
  <parameter name="timestep">0.005</parameter>
</qmc>
```

10.4 Reptation Monte Carlo

Like diffusion monte carlo, reptation monte carlo (RMC) is a projector based method, allowing us the ability to sample the fixed-node wavefunction. However, by exploiting the path-integral formulation of Schrödinger’s equation, the RMC algorithm can offer some advantages over traditional DMC, such as sampling both the mixed and pure fixed-node distributions in polynomial time, as well as not having population fluctuations and biases. The current implementation does not work with T-moves.

There are two adjustable parameters that affect the quality of the RMC projection: imaginary projection time $\beta$ of the sampling path (commonly called a “reptile”), and the Trotter time step $\tau$. $\beta$ must be chosen to be large enough such that $e^{-\beta H} |\Psi_T\rangle \approx |\Phi_0\rangle$ for mixed observables, and $e^{-\frac{1}{2} H} |\Psi_T\rangle \approx |\Phi_0\rangle$ for pure observables. The reptile is discretized into $M = \beta/\tau$ beads at the cost of an $O(\tau)$ time-step error for observables arising from the Trotter-Suzuki breakup of the short-time propagator.
The following table lists some of the more practical

<table>
<thead>
<tr>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>beta</td>
<td>real</td>
<td>$&gt; 0$</td>
<td>dep.</td>
<td>reptile projection time $\beta$</td>
</tr>
<tr>
<td>timestep</td>
<td>real</td>
<td>$&gt; 0$</td>
<td>0.1</td>
<td>Trotter time step $\tau$ for each electron move</td>
</tr>
<tr>
<td>beads</td>
<td>int</td>
<td>$&gt; 0$</td>
<td>1</td>
<td>Number of reptile beads $M = \beta/\tau$</td>
</tr>
<tr>
<td>blocks</td>
<td>integer</td>
<td>$\geq 0$</td>
<td>1</td>
<td>number of blocks</td>
</tr>
<tr>
<td>steps</td>
<td>integer</td>
<td>$\geq 0$</td>
<td>1</td>
<td>number of steps per block</td>
</tr>
<tr>
<td>vmcpresteps</td>
<td>integer</td>
<td>$\geq 0$</td>
<td>0</td>
<td>propagates reptile using VMC for given number of steps</td>
</tr>
<tr>
<td>warmupsteps</td>
<td>integer</td>
<td>$\geq 0$</td>
<td>0</td>
<td>number of steps for warming up</td>
</tr>
<tr>
<td>MaxAge</td>
<td>integer</td>
<td>$\geq 0$</td>
<td>0</td>
<td>force accept for stuck reptile if age exceeds MaxAge.</td>
</tr>
</tbody>
</table>

Additional information:
Because of the sampling differences between DMC ensembles of walkers and RMC reptiles, the RMC block should contain the following estimator declaration to ensure correct sampling:

<estimator name="RMC" hdf5="no">.

- **beta** or **beads**? One can specify one or the other, and from the Trotter time-step, the code will construct an appropriately sized reptile. If both are given, beta overrides beads.

- **Mixed vs. Pure observables**? Configurations sampled by the endpoints of the reptile are distributed according to the mixed distribution $f(R) = \Psi_T(R)\Phi_0(R)$. Any observable that is computable within DMC and is dumped to the scalar.dat file will likewise be found in the scalar.dat file generated by RMC, except there will be an appended _m to alert the user that the observable was computed on the mixed distribution. For pure observables, care must be taken in the interpretation. If the observable is diagonal in the position basis (in layman’s terms, if it is entirely computable from a single electron configuration $R$, like the potential energy), and if the observable does not have an explicit dependence on the trial wavefunction (for example, the local energy has an explicit dependence on the trial wavefunction from the kinetic energy term), then pure estimates will be correctly computed. These observables will be found in either the scalar.dat file, where they will be appended with a _p suffix, or in the stat.h5 file. No mixed estimators will be dumped to the h5 file.

- **Sampling**. For pure estimators, one should check the traces of both pure and mixed estimates. Ergodicity is a known problem in RMC. Because we use the bounce algorithm, it is possible for the reptile to bounce back and forth without changing the electron coordinates of the central beads. This might not easily show up with mixed estimators, since these are accumulated at constantly regrown ends, but pure estimates are accumulated on these central beads, and so can exhibit strong autocorrelations in pure estimate traces.

- **Propagator**: Our implementation of RMC uses Moroni’s DMC link action (symmetrized), with Umrigar’s scaled drift near nodes. In this regard, the propagator is identical to the one QMCPACK uses in DMC.

- **Sampling**: We use Ceperley’s bounce algorithm. MaxAge is used in case the reptile gets stuck, at which point the code forces move acceptance, stops accumulating statistics, and requilibrates the reptile. Very rarely will this be required. For move proposals, we use
particle-by-particle VMC a total of \(N_e\) times to generate a new all-electron configuration, at which point the action is computed and the move is either accepted or rejected.
Chapter 11

Output overview

QMCPACK writes several output files which report information about the simulation (e.g. the physical properties such as the energy), as well as information about the computational aspects of the simulation, checkpoints, and restarts. The types of output files generated depend on the details of a calculation. The list below is not meant to be exhaustive, but rather to highlight some salient features of the more common filetypes. Further detail can be found in the description of the estimator one is interested in computing.

11.1 The .scalar.dat file

The most important output file is the .scalar.dat file. This file contains the output of block averaged properties of the system such as the local energy and other estimators. Each line corresponds to an average over $N_{walkers} \times N_{steps}$ samples. By default, the quantities reported in the .scalar.dat file include:

LocalEnergy  The local energy.
LocalEnergy\_sq  The local energy squared.
LocalPotential  The local potential energy.
Kinetic  The kinetic energy.
ElecElec  The electron-electron potential energy.
IonIon  The ion-ion potential energy.
LocalECP  The energy due to the pseudopotential/effective core potential.
NonLocalECP  The non-local energy due to the pseudopotential/effective core potential.
MPC  The modified periodic coulomb potential energy.
BlockWeight  The number of MC samples in the block.
BlockCPU  The number of seconds to compute the block.
AcceptRatio  The acceptance ratio.

QMCPACK includes a python utility, qmca, which can be used to process these files. Details and examples are given in chapter 12.
11.2 The .opt.xml file

This file is generated after a VMC wave function optimization, and contains the part of the input file which lists the optimized jastrow factors. Conveniently, this file is already formatted such it can easily be incorporated into a DMC input file.

11.3 The .qmc.xml file

This file contains information about the computational aspects of the simulation, for example, which parts of the code are being executed when. This file is only generated in an ensemble run in which qmcpack runs multiple input files.

11.4 The .dmc.dat file

This file contains information similar to the .scalar.dat file, but also includes extra information about the details of a DMC calculation. For example, information about the walker population.

Index The block number.
LocalEnergy The local energy.
Variance The variance.
Weight The number of samples in the block.
NumOfWalkers The number of walkers times the number of steps.
AvgSentWalkers The average number of walkers sent. During a DMC simulation walkers may be created or destroyed. At every step, QMCPACK will do some load balancing to ensure that the walkers are evenly distributed across nodes.
TrialEnergy The trial energy. See 10.3 for an explanation of the trial energy.
DiffEff The diffusion efficiency.
LivingFraction The fraction of the walker population from the previous step that survived to the current step.

11.5 The .bandinfo.dat file

This file contains information from the trial wavefunction about the band structure of the system, including the available \( k \)-points. This can be helpful in constructing trial wavefunctions.

11.6 Checkpoint and restart files

11.6.1 The .cont.xml file

This file enables continuation of the run. It is mostly a copy of the input XML file with the series number incremented, and the mcwalkerset element added to read the walkers from a config file. The .cont.xml file is always created, but other files it depends on are only present if checkpointing is enabled.
11.6.2 The .config.h5 file
This file contains stored walker configurations.

11.6.3 The .random.h5 file
This file contains the state of the random number generator to allow restarts. (Older versions used an XML file with a suffix of .random.xml).
Chapter 12

Analyzing QMCPACK data

12.1 Using the qmca tool to obtain total energies and related quantities

The qmca tool is the primary means of analyzing scalar valued data generated by QMCPACK. Output files that contain scalar valued data are *.scalar.dat and *.dmc.dat (see chapter 11 for a detailed description of these files). Quantities that are available for analysis in *.scalar.dat files include the local energy and its variance, the kinetic energy, the potential energy and its components, the acceptance ratio, and the average cpu time spent per block, among others. The *.dmc.dat files provide information regarding the DMC walker population in addition to the local energy.

Basic capabilities of qmca include calculating mean values and associated error bars, processing multiple files at once in batched fashion, performing twist averaging, plotting mean values by series, and plotting traces (per block or step) of the underlying data. These capabilities are explained with accompanying examples in the following subsections.

To use qmca, installations of Python and NumPy must be present on the local machine. For graphical plotting, the matplotlib module must also be available.

An overview of all supported input flags to qmca can be obtained by typing “qmca” at the command line with no other inputs (also try “qmca -x” for a short list of examples):

```
>qmca
no files provided, please see help info below

Usage: qmca [options] [file(s)]

Options:
  --version show program's version number and exit
  -v, --verbose Print detailed information (default=False).
  -q QUANTITIES, --quantities=QUANTITIES
      Quantity or list of quantities to analyze.
  See names and abbreviations below (default=all).
  -u UNITS, --units=UNITS Desired energy units. Can be Ha (Hartree), Ry
(Rydberg), eV (electron volts), kJ_mol (kJ.
```
joule/mole), K (Kelvin), J (Joules) (default=Ha).

-e EQUILIBRATION, --equilibration=EQUILIBRATION
Equilibration length in blocks (default=auto).

-a, --average
Average over files in each series (default=False).

-w WEIGHTS, --weights=WEIGHTS
List of weights for averaging (default=None).

-b, --reblock
(pending) Use reblocking to calculate statistics
(default=False).

-p, --plot
Plot quantities vs. series (default=False).

-t, --trace
Plot a trace of quantities (default=False).

-h, --histogram
(pending) Plot a histogram of quantities
(default=False).

-o, --overlay
Overlay plots (default=False).

--legend=LEGEND
Placement of legend. None for no legend,
outside for outside legend (default=upper right).

--noautocorr
Do not calculate autocorrelation. Warning:
error bars are no longer valid! (default=False).

--noac
Alias for --noautocorr (default=False).

--sv
Show autocorrelation of sample data (default=False).

--image
(pending) Save image files (default=False).

--report
(pending) Write a report (default=False).

--show_options
Print user provided options (default=False).

--examples
Print examples and exit (default=False).

--help
Print help information and exit (default=False).

-d DESIRED_ERROR, --desired_error=DESIZED_ERROR
Show number of samples needed for desired error bar
(default=none).

-n PARTICLE_NUMBER, --enlarge_system=PARTICLE_NUMBER
Show number of samples needed to maintain error bar on larger system: desired particle number first,
current particle number second (default=none)
12.1.1 Obtaining a statistically correct mean and error bar

A rough guess at the mean and error bar of the local energy can be obtained in the following way with qmca:

```
>qmca -q e qmc.s000.scalar.dat
qmc series 0 LocalEnergy = -45.876150 +/- 0.017688
```

In this case the VMC energy of an 8 atom cell of diamond is estimated to be $-45.876(2)$ Hartrees. This rough guess should not be used for production-level or publication quality estimates.

To obtain production-level results, the underlying data should first inspected visually to ensure that all data included in the averaging can be attributed to a distribution sharing the same mean. The first steps of essentially any Monte Carlo calculation (the “equilibration phase”) do not belong to the equilibrium distribution and should be excluded from estimates of the mean and its error bar.

We can plot a data trace (“-t”) of the local energy in the following way:

```
>qmca -t -q e -e 0 qmc.s000.scalar.dat
```

The “-e 0” part indicates that we do not want any data to be excluded from the calculation of averages initially. The resulting plot is shown in Fig. 12.1. The unphysical equilibration period is visible on the left side of the plot.

Most of the data fluctuates around a well defined mean (consistent variations around a flat line). This property is important to verify by plotting the trace for each QMC run.

If we exclude none of the equilibration data points, we get an erroneous estimate of $-45.870(2)$ Ha for the local energy:
The equilibration period is typically estimated by eye, though one should check a few conservative values to ensure that the mean remains unaffected. In this dataset, the equilibration appears to have been reached after 100 samples or so. After excluding the first 100 VMC blocks from the analysis we get:

```
> qmca -q e -e 100 qmc.s000.scalar.dat
qmc series 0 LocalEnergy = -45.877363 +/- 0.017432
```

This estimate (−45.877(2) Ha) differs significantly from the −45.870(2) Ha figure obtained from the full set of data, but it agrees with the rough estimate of −45.876(2) Hartrees obtained with the abbreviated command (“qmca -q e qmc.s000.scalar.dat”). This is because qmca makes a heuristic guess at the equilibration period and got it reasonably correct in this case. There are many cases where the heuristic guess fails and it should not be relied on for quality results.

We have so far obtained a statistically correct mean. To obtain a statistically correct error bar it is best to include ∼100 or more statistically independent samples. An estimate of the number of independent samples can be obtained by considering the autocorrelation time, which is essentially a measure of the number of samples that must be traversed before an uncorrelated/independent sample is reached. We can get an estimate of the autocorrelation time in the following way:

```
> qmca -q e -e 100 qmc.s000.scalar.dat --sac
qmc series 0 LocalEnergy = -45.877363 +/- 0.017432 4.8
```

The flag “--sac” stands for (s)how (a)uto(c)orrelation. In this case the autocorrelation estimate is 4.8 ≈ 5 samples. Since the total run contained 800 samples and we have excluded 100 of them, we can estimate the number of independent samples as (800 − 100)/5 = 140. In this case, the error bar is expected to be estimated reasonably well.

Please keep in mind that the error bar represents the expected range of the mean with a certainty of only ∼ 70%, i.e. it is a one sigma error bar. The actual mean value will lie outside the range indicated by the error bar in one out of every three runs and in a set of 20 runs one value can be expected to deviate from its estimate by twice the error bar.

### 12.1.2 Judging wavefunction optimization

Wavefunction optimization is a highly non-linear and sometimes sensitive process. As such, there is a risk that systematic errors encountered at this stage of the QMC process can be propagated into subsequent (expensive) DMC runs unless they are guarded against with vigilance.

In this section we again consider an 8 atom cell of diamond, but now in the context of Jastrow optimization (one- and two-body terms). In optimization runs it is often preferable to use a large number of warmup steps (∼ 100) so that equilibration bias does not propagate into the optimization process. We can check that the added warmup has had its intended effect by again checking the local energy trace:

```
> qmca -t -q e *scalar*
```

The resulting plot can be found in Fig. [12.2]. In this case sufficient warmup steps were used to exit the equilibration period before samples were collected and we can proceed without using the “−e” option with qmca.
After inspecting the trace, we should inspect the text output from qmca, now including the total energy and its variance:

```bash
>qmca -q ev opt*scalar.dat

<table>
<thead>
<tr>
<th>ratio</th>
<th>LocalEnergy</th>
<th>Variance</th>
</tr>
</thead>
<tbody>
<tr>
<td>opt series 0</td>
<td>-44.823616 +/- 0.007430</td>
<td>7.054219 +/- 0.041998</td>
</tr>
<tr>
<td>opt series 1</td>
<td>-45.877643 +/- 0.003329</td>
<td>1.095362 +/- 0.041154</td>
</tr>
<tr>
<td>opt series 2</td>
<td>-45.883191 +/- 0.004149</td>
<td>1.077942 +/- 0.021555</td>
</tr>
<tr>
<td>opt series 3</td>
<td>-45.877524 +/- 0.003094</td>
<td>1.074047 +/- 0.010491</td>
</tr>
<tr>
<td>opt series 4</td>
<td>-45.886062 +/- 0.003750</td>
<td>1.061707 +/- 0.014459</td>
</tr>
<tr>
<td>opt series 5</td>
<td>-45.877668 +/- 0.003475</td>
<td>1.091585 +/- 0.021637</td>
</tr>
<tr>
<td>opt series 6</td>
<td>-45.877109 +/- 0.003586</td>
<td>1.069205 +/- 0.008651</td>
</tr>
<tr>
<td>opt series 7</td>
<td>-45.882563 +/- 0.004324</td>
<td>1.058771 +/- 0.008651</td>
</tr>
</tbody>
</table>
```

The flags “-q ev” requested the energy (e) and the variance (v). For this combination of quantities, a third column (“ratio”) is printed containing the ratio of the variance and the absolute value of the local energy. The variance/energy ratio is an intensive quantity and is useful to inspect regardless of the system under study. Successful optimization of molecules and solids of any size generally result in comparable values for the variance/energy ratio.

The first line of the output (“series 0”) corresponds to the local energy and variance of the system without a Jastrow factor (all Jastrow coefficients were initialized to zero in this case), reflecting the quality of the orbitals alone. For pseudopotential systems, a variance/energy ratio
Figure 12.3: Energy and variance vs. optimization series for an 8 atom cell of diamond as plotted by qmca.

> 0.20 Ha generally indicates there is a problem with the input orbitals that needs to be resolved prior to performing wavefunction optimization.

The subsequent lines correspond to energies and variances of intermediate parameterizations of the trial wavefunction during the optimization process. The output line containing “opt series 1”, for example, corresponds to the trial wavefunction parameterized during the “series 0” step (the parameters of this wavefunction would be found in an output file matching *s000*opt.xml). The first thing to check about the resulting optimization is again the variance/energy ratio. For pseudopotential systems, a variance/energy ratio < 0.03 Ha is consistent with a trial wavefunction of production quality, and values of 0.01 Ha are rarely obtainable for standard Slater-Jastrow wavefunctions. By this metric, all parameterizations obtained for optimizations performed in series 0-6 are of comparable quality (note that the quality of the wavefunction obtained during optimization series 7 is effectively unknown).

A good way to further discriminate among the parameterizations is to plot the energy and variance as a function of series with qmca:

```
>qmca -p -q ev opt*scalar.dat
```

The “-p” option results in plots of means plus error bars vs. series for all requested quantities. The resulting plots for the local energy and variance are shown in Fig. 12.3. In this case the resulting energies and variances are statistically indistinguishable for all optimization cycles.

A good way to choose the optimal wavefunction for use in DMC is to select the one with lowest statistically significant energy within the set of optimized wavefunctions with reasonable variance (e.g. among those with variance/energy ratio < 0.03 Ha). For pseudopotential calculations, minimizing according to the total energy is recommended to reduce locality errors in DMC.

12.1.3 Judging diffusion Monte Carlo runs

Judging the quality of the DMC projection process requires more care than this needed in VMC. In order to reduce bias, a small timestep is required in the approximate projector but this also leads to slow equilibration and long autocorrelation times. Systematic errors in the projection process can also arise from statistical fluctuations due to pseudopotentials or from trial wavefunctions with larger than necessary variance.
Figure 12.4: Trace of the local energy for VMC followed by DMC with a small timestep (0.002 Ha$^{-1}$) for an 8 atom cell of diamond generated with qmca.

To illustrate the problems that can arise with respect to slow equilibration and long autocorrelation times, we consider the 8 atom diamond system with VMC (200 blocks of 160 steps) followed by DMC (400 blocks of 5 steps) with a small timestep (0.002 Ha$^{-1}$). A good first step in assessing the quality of any DMC run is to plot the trace of the local energy:

\[
\text{qmca -t -q e -e 0 *scalar*}
\]

The resulting trace plot is shown in Fig. 12.4. As always, the DMC local energy decreases exponentially away from the VMC value but in this case it takes a long time to do so. At least half of the DMC run is inefficiently consumed by equilibration. If we are not careful to inspect and remove the transient, the estimated DMC energy will be strongly biased by the transient as shown by the horizontal red line (estimated mean) in the figure. The autocorrelation time is also large (\(\sim 12\) blocks):

\[
\text{qmca -q e -e 200 --sac *s001.scalar*}
\]

Of the included 200 blocks, fewer than 20 contribute to the estimated error bar, indicating that we cannot trust the reported error bar. This can also be demonstrated directly from the data. If we halve the number of samples included to 100, we would expect from Gaussian statistics that the error bar would grow by a factor of \(\sqrt{2}\), but instead we get

\[
\text{qmca -q e -e 300 *s001.scalar*}
\]

Of the included 300 blocks, fewer than 20 contribute to the estimated error bar, indicating that we cannot trust the reported error bar. This can also be demonstrated directly from the data. If we halve the number of samples included to 100, we would expect from Gaussian statistics that the error bar would grow by a factor of \(\sqrt{2}\), but instead we get
Figure 12.5: Trace of the local energy for VMC followed by a short intermediate DMC with a large timestep (0.02 Ha$^{-1}$) and finally a production DMC run with a timestep of 0.01 Ha$^{-1}$. Calculations were performed in an 8 atom cell of diamond.

which erroneously shows an estimated increase in the error bar by a factor of about two. Overall this run is simply too short to gain meaningful information.

Consider the case where we are interested in the cohesive energy of diamond and, after having performed a timestep study of the cohesive energy, we have found that the energy difference between bulk diamond and atomic carbon converges to our required accuracy with a larger timestep of 0.01 Ha$^{-1}$. In a production setting, a small cell could be used to determine the appropriate timestep while a larger cell would subsequently be used to obtain a converged cohesive energy, though for purposes of demonstration we still proceed with the 8 atom cell here. The new timestep of 0.01 Ha$^{-1}$ will result in a shorter autocorrelation time than the smaller timestep used previously, but we would like to shorten the equilibration time further still. This can be achieved by using a larger timestep (say 0.02 Ha$^{-1}$) in a short intermediate DMC run used to walk down the transient. The rapidly achieved equilibrium with the 0.02 Ha$^{-1}$ timestep projector will be much nearer to the 0.01 Ha$^{-1}$ timestep one we seek than the original VMC equilibrium, and so we can expect a shortened secondary equilibration time in the production 0.01 Ha$^{-1}$ timestep run. Note that this procedure is fully general, even if one has to deal with an even shorter timestep—e.g. 0.002 Ha$^{-1}$—for a particular problem.

We now rerun the prior example but with an intermediate DMC calculation using 40 blocks of 5 steps with a timestep of 0.02 Ha$^{-1}$ followed by a production DMC calculation using 400 blocks of 10 steps with a timestep of 0.01 Ha$^{-1}$. We again plot the local energy trace using qmca

\[\texttt{qmca -t -q e -e 0 *scalar*}\]

with the result shown in Fig. 12.5. The projection transient has been effectively contained in the
short DMC run with a larger timestep. As expected, the production run contains only a short equilibration period. Removing the first 20 blocks as a precaution, we obtain an estimate of the total energy in VMC and DMC:

\[
\text{>qmca -q ev -e 20 --sac qmc.*.scalar.dat}
\]

<table>
<thead>
<tr>
<th>LocalEnergy</th>
<th>Variance</th>
</tr>
</thead>
<tbody>
<tr>
<td>ratio</td>
<td></td>
</tr>
<tr>
<td>qmc</td>
<td></td>
</tr>
<tr>
<td>series 0</td>
<td>-45.881042 +/- 0.001283</td>
</tr>
<tr>
<td>1.0</td>
<td>0.0235</td>
</tr>
<tr>
<td>qmc</td>
<td></td>
</tr>
<tr>
<td>series 1</td>
<td>-46.040814 +/- 0.005046</td>
</tr>
<tr>
<td>1.1</td>
<td>0.0220</td>
</tr>
<tr>
<td>qmc</td>
<td></td>
</tr>
<tr>
<td>series 2</td>
<td>-46.032960 +/- 0.002077</td>
</tr>
<tr>
<td>1.0</td>
<td>0.0220</td>
</tr>
</tbody>
</table>

Notice that the variance energy ratio in DMC (0.220 Ha) is similar to, but slightly smaller than, what is obtained with VMC (0.235 Ha). If the DMC variance/energy ratio is ever significantly larger than in VMC, this is cause to be concerned about the correctness of the DMC run. Also notice the estimated autocorrelation time (~ 5 blocks). This leaves us with an estimated ~ 76 independent samples, though we should recall that the autocorrelation time is also a statistical estimate which can be improved with more data. We can gain a better estimate of the autocorrelation time by using the *.dmc.dat files which contain output data resolved per step rather than per block (there are 10× more steps than blocks in this example case):

\[
\text{>qmca -q ev -e 200 --sac qmc.s002.dmc.dat}
\]

<table>
<thead>
<tr>
<th>LocalEnergy</th>
<th>Variance</th>
</tr>
</thead>
<tbody>
<tr>
<td>ratio</td>
<td></td>
</tr>
<tr>
<td>qmc</td>
<td></td>
</tr>
<tr>
<td>series 2</td>
<td>-46.032909 +/- 0.002068</td>
</tr>
<tr>
<td>1.4</td>
<td>0.0221</td>
</tr>
</tbody>
</table>

This results in an estimated autocorrelation time of ~ 31 steps, or ~ 3 blocks, indicating that we actually have ~ 122 independent samples which should be sufficient to obtain a trustworthy error bar. Our final DMC total energy is estimated to be -46.0329(2) Ha.

Another simulation property that should be explicitly monitored is the behavior of the DMC walker population. Data regarding the walker population is contained in the *.dmc.dat files. In Fig. 12.6 we show the trace of the DMC walker population for the current run:

\[
\text{>qmca -t -q nw *dmc.dat}
\]

<table>
<thead>
<tr>
<th>NumOfWalkers</th>
<th>Variance</th>
</tr>
</thead>
<tbody>
<tr>
<td>qmc</td>
<td></td>
</tr>
<tr>
<td>series 1</td>
<td>2056.905405 +/- 8.775527</td>
</tr>
<tr>
<td>qmc</td>
<td></td>
</tr>
<tr>
<td>series 2</td>
<td>2050.164160 +/- 4.954850</td>
</tr>
</tbody>
</table>

Following a DMC run the walker population should be checked for two qualities: 1) that the population is sufficiently large (a number > 2000 is generally sufficient to reduce population control bias) and 2) that the population fluctuates benignly around its intended target value. In this case the target walker count (provided in the input file) was 2048 and we can confirm from the plot that the population is simply fluctuating around this value. Also from the text output we have a dynamic population estimate of 2050(5) walkers. Rapid population reductions or increases—population explosions—are indicative of problems with a run. These issues sometimes result from using a considerably poor wavefunction (see comments regarding variance/energy ratio above and in the preceding subsections). QMCPACK has internal guards in place that prevent the population from exceeding certain maximum and minimum bounds, so in particularly faulty runs one might
Figure 12.6: Trace of the DMC walker population for an 8 atom cell of diamond obtained with qmca.

see the population “stabilize” to a constant value much larger or smaller than the target. In these cases the cause(s) for the divergent population behavior need to be investigated and resolved before proceeding further.

12.1.4 Obtaining other quantities

A number of other scalar valued quantities are available with qmca. To obtain text output for all quantities available, simply exclude the “-q” option used in the prior examples. Below is example output for a DMC calculation of the 8 atom diamond system from the scalar.dat file:

```
>qmca -e 20 qmc.s002.scalar.dat
qmca series 2
  LocalEnergy = -46.0330 +/- 0.0021
  Variance = 1.0149 +/- 0.0025
  Kinetic = 33.851 +/- 0.019
  LocalPotential = -79.884 +/- 0.020
  ElecElec = -11.4483 +/- 0.0083
  LocalECP = -22.615 +/- 0.029
  NonLocalECP = 5.2815 +/- 0.019
  IonIon = -51.10 +/- 0.00
  LocalEnergy_sq = 2120.05 +/- 0.19
  BlockWeight = 20514.27 +/- 48.38
  BlockCPU = 1.4890 +/- 0.0038
  AcceptRatio = 0.9963954 +/- 0.0000055
```
<table>
<thead>
<tr>
<th></th>
<th>Value</th>
<th>Error</th>
</tr>
</thead>
<tbody>
<tr>
<td>Efficiency</td>
<td>71.88</td>
<td>0.00</td>
</tr>
<tr>
<td>TotalTime</td>
<td>565.80</td>
<td>0.00</td>
</tr>
<tr>
<td>TotalSamples</td>
<td>7795421</td>
<td>0</td>
</tr>
</tbody>
</table>

Similarly, for the `dmc.dat` file we get

```
>qmca -e 20 qmc.s002.dmc.dat
qmc  series 2
LocalEnergy     = -46.0329 +/- 0.0020
Variance         = 1.0162 +/- 0.0025
TotalSamples     = 8201275 +/- 0
TrialEnergy      = -46.0343 +/- 0.0023
DiffEff          = 0.9939150 +/- 0.0000088
Weight           = 2050.23 +/- 4.82
NumOfWalkers     = 2050 +/- 5
LivingFraction   = 0.996427 +/- 0.000021
AvgSentWalkers   = 0.2625 +/- 0.0011
```

Any subset of desired quantities can be obtained by using the “-q” option with either the full names of the quantities listed above

```
>qmca -q 'LocalEnergy Kinetic LocalPotential' -e 20 qmc.s002.scalar.dat
qmc  series 2
LocalEnergy     = -46.0330 +/- 0.0021
Kinetic          = 33.851 +/- 0.019
LocalPotential   = -79.884 +/- 0.020
```

or with their corresponding abbreviations

```
>qmca -q ekp -e 20 qmc.s002.scalar.dat
qmc  series 2
LocalEnergy     = -46.0330 +/- 0.0021
Kinetic          = 33.851 +/- 0.019
LocalPotential   = -79.884 +/- 0.020
```

Abbreviations for each quantity can be found by typing `qmca` at the command line with no other input. A current list is provided below:

```
Abbreviations and full names for quantities:
  ar = AcceptRatio
  bc = BlockCPU
  bw = BlockWeight
  ce = CorrectedEnergy
  de = DiffEff
  e  = LocalEnergy
  ee = ElecElec
  eff = Efficiency
  ii = IonIon
  k  = Kinetic
  kc = KEcorr
  l  = LocalECP
```
Please see the output overview for `scalar.dat` (Sec. 11.1) and `dmc.dat` (Sec. 11.4) for more information about these quantities. The data analysis aspects for these quantities is essentially the same as for the local energy as covered in the preceding subsections. Quantities that do not belong to an equilibrium distribution (e.g. BlockCPU) are somewhat different, though they still exhibit statistical fluctuations.

### 12.1.5 Processing multiple files

Batch file processing is a common use case for `qmca`. If we consider an “equation of state” calculation involving the 8 atom diamond cell we have used so far, we might be interested in the total energy for the various supercell volumes along the trajectory from compression to expansion. After checking the traces (“`qmca -t -q e scale_*/vmc/*scalar*`”) to settle on a sensible equilibration cutoff as discussed in the preceding subsections we can obtain the total energies all at once:

```
>qmca -q ev -e 40 scale_*/vmc/*scalar*
```

<table>
<thead>
<tr>
<th>ratio</th>
<th>LocalEnergy</th>
<th>Variance</th>
</tr>
</thead>
<tbody>
<tr>
<td>scale_0.80/vmc/qmc</td>
<td>series 0 -44.670984 +/- 0.006051 2.542384 +/-</td>
<td></td>
</tr>
<tr>
<td>0.019902 0.0569</td>
<td></td>
<td></td>
</tr>
<tr>
<td>scale_0.82/vmc/qmc</td>
<td>series 0 -44.982818 +/- 0.005757 2.413011 +/-</td>
<td></td>
</tr>
<tr>
<td>0.022626 0.0536</td>
<td></td>
<td></td>
</tr>
<tr>
<td>scale_0.84/vmc/qmc</td>
<td>series 0 -45.228257 +/- 0.005374 2.258577 +/-</td>
<td></td>
</tr>
<tr>
<td>0.019322 0.0499</td>
<td></td>
<td></td>
</tr>
<tr>
<td>scale_0.86/vmc/qmc</td>
<td>series 0 -45.415842 +/- 0.005532 2.204980 +/-</td>
<td></td>
</tr>
<tr>
<td>0.052978 0.0486</td>
<td></td>
<td></td>
</tr>
<tr>
<td>scale_0.88/vmc/qmc</td>
<td>series 0 -45.570215 +/- 0.004651 2.061374 +/-</td>
<td></td>
</tr>
<tr>
<td>0.014359 0.0452</td>
<td></td>
<td></td>
</tr>
<tr>
<td>scale_0.90/vmc/qmc</td>
<td>series 0 -45.683684 +/- 0.005009 1.988539 +/-</td>
<td></td>
</tr>
<tr>
<td>0.018267 0.0435</td>
<td></td>
<td></td>
</tr>
<tr>
<td>scale_0.92/vmc/qmc</td>
<td>series 0 -45.751359 +/- 0.004928 1.913282 +/-</td>
<td></td>
</tr>
<tr>
<td>0.013998 0.0418</td>
<td></td>
<td></td>
</tr>
<tr>
<td>scale_0.94/vmc/qmc</td>
<td>series 0 -45.791622 +/- 0.005026 1.843704 +/-</td>
<td></td>
</tr>
<tr>
<td>0.014460 0.0403</td>
<td></td>
<td></td>
</tr>
<tr>
<td>scale_0.96/vmc/qmc</td>
<td>series 0 -45.809256 +/- 0.005053 1.829103 +/-</td>
<td></td>
</tr>
<tr>
<td>0.014536 0.0399</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

In this case, we are using a Jastrow factor optimized only at the equilibrium geometry ("scale_1.00") but with radial cutoffs restricted to the Wigner-Seitz radius of the most compressed supercell ("scale_0.80") to avoid introducing wavefunction cusps at the cell boundary (QMCPACK would have aborted with a warning in this case, had we tried). It is clear that this restricted Jastrow factor is not an optimal choice as it yields variance/energy ratios between $0.036$ and $0.057$ Ha. This issue is largely a result of our undersized (8 atom) supercell and larger cells should always be used in real production calculations.

Batch processing is also possible for multiple quantities. If multiple quantities are requested, an additional line is inserted to separate results from different runs:

```
>qmca -q 'e bc eff' -e 40 scale_*/vmc/*scalar*
```

<table>
<thead>
<tr>
<th>Scale</th>
<th>Local Energy</th>
<th>Block CPU</th>
<th>Efficiency</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.98/vmc/qmc</td>
<td>-45.806235 +/- 0.004963</td>
<td>1.775391 +/- 0.015199</td>
<td>0.015199 0.0388</td>
</tr>
<tr>
<td>1.00/vmc/qmc</td>
<td>-45.783481 +/- 0.005293</td>
<td>1.726869 +/- 0.012001</td>
<td>0.012001 0.0377</td>
</tr>
<tr>
<td>1.02/vmc/qmc</td>
<td>-45.741655 +/- 0.005627</td>
<td>1.681776 +/- 0.011496</td>
<td>0.011496 0.0368</td>
</tr>
<tr>
<td>1.04/vmc/qmc</td>
<td>-45.685101 +/- 0.005353</td>
<td>1.682608 +/- 0.015423</td>
<td>0.015423 0.0368</td>
</tr>
<tr>
<td>1.06/vmc/qmc</td>
<td>-45.615164 +/- 0.005978</td>
<td>1.652155 +/- 0.048186</td>
<td>0.048186 0.0376</td>
</tr>
<tr>
<td>1.08/vmc/qmc</td>
<td>-45.543037 +/- 0.005191</td>
<td>1.646375 +/- 0.035920</td>
<td>0.035920 0.0372</td>
</tr>
<tr>
<td>1.10/vmc/qmc</td>
<td>-45.450976 +/- 0.004794</td>
<td>1.707649 +/- 0.012381</td>
<td>0.012381 0.0360</td>
</tr>
<tr>
<td>1.12/vmc/qmc</td>
<td>-45.371851 +/- 0.005103</td>
<td>1.686997 +/- 0.014788</td>
<td>0.014788 0.0367</td>
</tr>
<tr>
<td>1.14/vmc/qmc</td>
<td>-45.265490 +/- 0.005311</td>
<td>1.631614 +/- 0.019942</td>
<td>0.019942 0.0371</td>
</tr>
<tr>
<td>1.16/vmc/qmc</td>
<td>-45.161961 +/- 0.004868</td>
<td>1.656586 +/- 0.009756</td>
<td>0.009756 0.0367</td>
</tr>
<tr>
<td>1.18/vmc/qmc</td>
<td>-45.062579 +/- 0.005971</td>
<td>1.671998 +/- 0.007546</td>
<td>0.007546 0.0363</td>
</tr>
<tr>
<td>1.20/vmc/qmc</td>
<td>-44.960477 +/- 0.004888</td>
<td>1.651864 +/- 0.009756</td>
<td>0.009756 0.0367</td>
</tr>
</tbody>
</table>

**In this case,** we are using a Jastrow factor optimized only at the equilibrium geometry ("scale_1.00") but with radial cutoffs restricted to the Wigner-Seitz radius of the most compressed supercell ("scale_0.80") to avoid introducing wavefunction cusps at the cell boundary (QMCPACK would have aborted with a warning in this case, had we tried). It is clear that this restricted Jastrow factor is not an optimal choice as it yields variance/energy ratios between 0.036 and 0.057 Ha. This issue is largely a result of our undersized (8 atom) supercell and larger cells should always be used in real production calculations.

Batch processing is also possible for multiple quantities. If multiple quantities are requested, an additional line is inserted to separate results from different runs: 

>qmca -q 'e bc eff' -e 40 scale_*/vmc/*scalar*

<table>
<thead>
<tr>
<th>Scale</th>
<th>Local Energy</th>
<th>Block CPU</th>
<th>Efficiency</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.80/vmc/qmc</td>
<td>-44.6710 +/- 0.0061</td>
<td>0.00038</td>
<td>38104.00 +/- 0.00</td>
</tr>
<tr>
<td>0.82/vmc/qmc</td>
<td>-44.9828 +/- 0.0058</td>
<td>0.00013</td>
<td>44483.91 +/- 0.00</td>
</tr>
<tr>
<td>0.84/vmc/qmc</td>
<td>-45.2283 +/- 0.0054</td>
<td>0.00030</td>
<td>0.00030</td>
</tr>
</tbody>
</table>

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12.1.6 Twist averaging

Twist averaging can be performed straightforwardly for any output quantity listed in Sec. 12.1.4 with `qmca`. We illustrate these capabilities by repeating the 8 atom diamond DMC runs performed in Sec. 12.1.3 at eight real valued supercell twist angles (a $2 \times 2 \times 2$ Monkhorst-Pack grid centered at the $\Gamma$-point). Data traces for each twist can be overlapped on the same plot:

```
>qmca -to -q e -e '30 20 30' *scalar* --legend outside
```

The “-o” option requests the plots be overlapped; eight separate plots would be generated otherwise. The equilibration input “-e '30 20 30'” cuts out from the analyzed data the first 30 blocks for series 0 (VMC), 20 blocks for series 1 (intermediate DMC), and 30 blocks for series 2 (production DMC). The resulting plot is shown in Fig. 12.7.

Twist averaging is performed by providing the “-a” option. If provided on its own, uniform weights are applied to each twist angle. To obtain a trace plot with twist averaging enforced, use a command similar to the following:

```
>qmca -a -t -q e -e '30 20 30' *scalar*
```

The resulting plot is shown in Fig. 12.8. As can be seen from the trace plot, the chosen equilibration lengths are appropriate and we proceed to obtain the twist averaged total energy from the `scalar.dat` files

```
>qmca -a -q ev --sac *s002.scalar*
```

and also from the `dmc.dat` files

<table>
<thead>
<tr>
<th>ratio</th>
<th>LocalEnergy</th>
<th>Variance</th>
</tr>
</thead>
<tbody>
<tr>
<td>avg</td>
<td>-45.873369 +/- 0.000753</td>
<td>5.3</td>
</tr>
<tr>
<td>1.3</td>
<td>0.0224</td>
<td>1.028751 +/- 0.001056</td>
</tr>
</tbody>
</table>
Figure 12.7: Overlapped energy traces from VMC to DMC for an 8 supercell of diamond obtained with qmca. Data for each twist appears in a different color.

yielding a twist averaged total energy of $-45.8733(8)$ Ha.

As can be seen from the Fig. 12.7, some of the twist angles are degenerate. This is seen more clearly in the text output:

<table>
<thead>
<tr>
<th>ratio</th>
<th>LocalEnergy</th>
<th>Variance</th>
</tr>
</thead>
<tbody>
<tr>
<td>avg</td>
<td>-45.873371 +/- 0.000741</td>
<td>30.5 1.028843 +/- 0.000972</td>
</tr>
<tr>
<td>1.6</td>
<td>0.0224</td>
<td></td>
</tr>
</tbody>
</table>

| qmc.g000 | series 2 | -45.264510 +/- 0.001942 | 1.057065 +/- 0.002318 |
| qmc.g001 | series 2 | -46.035511 +/- 0.001806 | 1.015992 +/- 0.002836 |
| qmc.g002 | series 2 | -46.034225 +/- 0.002539 | 1.013420 +/- 0.002835 |
| qmc.g003 | series 2 | -46.035410 +/- 0.001538 | 1.015039 +/- 0.002661 |
| qmc.g004 | series 2 | -46.047285 +/- 0.001898 | 1.018219 +/- 0.002588 |
| qmc.g005 | series 2 | -46.035511 +/- 0.001806 | 1.015992 +/- 0.002836 |
| qmc.g006 | series 2 | -46.034225 +/- 0.002539 | 1.013420 +/- 0.002835 |
| qmc.g007 | series 2 | -46.035511 +/- 0.001806 | 1.015992 +/- 0.002836 |
Figure 12.8: Twist averaged energy trace from VMC to DMC for an 8 supercell of diamond obtained with qmca.

The degenerate twists grouped by set are \{0\}, \{1, 2, 4\}, \{3, 5, 6\}, \{7\}.

Alternatively, the run could have been performed at only the four unique (irreducible) twist angles. We will emulate this situation by analyzing data for twists 0, 1, 3, and 7 only. In a production setting with irreducibly weighted twists, run would be performed on these twists alone; we reuse the uniform twist data for illustration purposes only.

We can use qmca to perform twist averaging with different weights applied to each twist

```
>qmca -a -w '1 3 3 1' -q ev -e 30 *g000*2*sc* *g001*2*sc* *g003*2*sc* *g007*2*sc*
```

yielding a total energy value of $-45.874(1)$ Ha, in agreement with the uniform weighted twist average performed above.

The decision of whether or not to perform irreducible weighted twist averaging should be made on the basis of efficiency. The relative efficiency of irreducible vs. uniform weighted twist averaging
depends on the irreducible weights and the ratio of the lengths of the available sampling and
equilibration periods. A formula for the relative efficiency of these two cases is derived and discussed
in more detail in Appendix A.

12.1.7 Setting output units

Estimates outputted by qmca are in Hartree units by default. The output units for energetic
quantities can be changed by using the “-u” option.

Energy in Hartrees:

```bash
>qmca -q e -u Ha -e 20 qmc.s002.scalar.dat
qmca series 2 LocalEnergy = -46.032960 +/- 0.002077
```

Energy in electron volts:

```bash
>qmca -q e -u eV -e 20 qmc.s002.scalar.dat
qmca series 2 LocalEnergy = -1252.620565 +/- 0.056521
```

Energy in Rydbergs:

```bash
>qmca -q e -u rydberg -e 20 qmc.s002.scalar.dat
qmca series 2 LocalEnergy = -92.065919 +/- 0.004154
```

Energy in kilojoules per mole:

```bash
>qmca -q e -u kj_mol -e 20 qmc.s002.scalar.dat
qmca series 2 LocalEnergy = -120859.512998 +/- 5.453431
```

12.1.8 Speeding up trace plotting

When working with many files or files with many entries, qmca may take a long time to produce
plots. The time delay is actually due to the autocorrelation time estimate used to calculate error
bars. The calculation time for the autocorrelation scales as $O(M^2)$, with $M$ being the number of
statistical samples. If you are only interested in plotting traces and not in the estimated error bars,
the autocorrelation time estimation can be turned off with the “--noac” option:

```bash
>qmca -t -q e -e 20 --noac qmc.s002.scalar.dat
```

Please note that the resulting error bars printed to the console will be underestimated and are not
meaningful. Do not use “--noac” in conjunction with the “-p” plotting option as these plots are
of no use without meaningful error bars.

12.1.9 Short usage examples

Plotting a trace of the local energy:

```bash
>qmca -t -q e *scalar*
```

Applying an equilibration cutoff to VMC data (series 0):

```bash
>qmca -q e -e 30 *s000.scalar*
```

Applying the same equilibration cutoff to VMC and DMC data (series 0, 1, 2):
Applying different equilibration cutoffs to VMC and DMC data (series 0, 1, 2):

```
>qmca -q e -e 20 *scalar*
```

Obtaining the energy, variance, and variance/energy ratio for all series:

```
>qmca -q ev -e 30 *scalar*
```

Overlaying plots of mean + error bar for energy and variance for separate two- and three- body Jastrow optimization runs:

```
>qmca -po -q ev ./optJ2/*scalar* ./optJ3/*scalar*
```

Obtaining the acceptance ratio:

```
>qmca -q ar -e 30 *scalar*
```

Obtaining the average DMC walker population:

```
>qmca -q nw -e 400 *s002.dmc.dat
```

Obtaining the Monte Carlo efficiency:

```
>qmca -q eff -e 30 *scalar*
```

Obtaining the total wallclock time per series:

```
>qmca -q tt -e 0 *scalar*
```

Obtaining the average wallclock time spent per block:

```
>qmca -q bc -e 0 *scalar*
```

Obtaining a subset of desired quantities:

```
>qmca -q 'e v ar eff' -e 30 *scalar*
```

Obtaining all available quantities:

```
>qmca -e 30 *scalar*
```

Obtaining the twist averaged total energy with uniform weights:

```
>qmca -a -q e -e 40 *g*s002.scalar.dat
```

Obtaining the twist averaged total energy with specific weights:

```
>qmca -a -w '1 3 3 1' -q e -e 40 *g*s002.scalar.dat
```

Obtaining the local, kinetic, and potential energies in eV:

```
>qmca -q ekp -e 30 -u eV *scalar*
```
12.1.10 Production quality checklist

1. Inspect the trace plots ("-t" option) for any oddities in the data. Typical behavior is a short equilibration period followed by benign fluctuations around a clear mean value. There should not be any large spikes in the data. This applies to all runs (VMC, optimization, DMC, etc.).

2. Remove all equilibration steps ("-e" option) from the data by inspecting the trace plot.

3. Check the quality of the orbitals (standalone Jastrow-less VMC or sometimes the first scalar file produced during optimization) by inspecting the variance/energy ratio "qmca -q ev *scalar*". For pseudopotential systems without a Jastrow, the variance/energy ratio should not exceed 0.2 Ha, otherwise there is a problem with the orbitals.

4. Check the quality of the optimized Jastrow factor by inspecting the variance/energy ratio. For pseudopotential systems with a Jastrow, the variance/energy ratio should not exceed 0.04 Ha for pseudopotential systems. A good Jastrow is indicated by a variance/energy ratio in the range 0.01 – 0.03 Ha. A value less than 0.01 Ha is difficult to achieve.

5. Confirm that the optimization has converged by plotting the energy and variance vs. optimization series ("qmca -p -q ev *scalar*"). Do not assume that optimization has converged in only a few cycles. Use at least 10 cycles of with around 100,000 samples unless you already have experience with the system in question.

6. Optimize Jastrow factors according to energy minimization to reduce locality errors arising from the use of non-local pseudopotentials in DMC. A good approach is to optimize with a few cycles of variance minimization followed by several cycles of energy minimization.

7. Occasionally try optimizing with more samples and/or cycles to see if improved results are obtained.

8. If using a B-spline representation of the orbitals, converge the VMC energy and variance with respect to the mesh size (controlled via meshfactor). This is best done in the presence of any Jastrow factor to reduce noise. Consider using the hybrid LMTO representation of the orbitals as this can reduce both the VMC/DMC variance and DMC timestep error in addition to saving memory.

9. Check the variance/energy ratio of all production VMC and DMC calculations. In all cases the DMC ratio should be slightly less than the VMC one and both should abide the guidelines above, i.e. the ratio should be less than 0.04 Ha for pseudopotential systems. The production ratio should also be consistent with what is observed during wavefunction optimization.

10. Be aware of population control bias in DMC. Run with a population of ~ 2000 or greater. Occasionally repeat a run using a larger population to explicitly confirm that population control bias is small.

11. Check the stability of the DMC walker population by plotting the trace of the population size ("qmca -t -q nw *dmc.dat"). Verify that the average walker population is consistent with the requested value provided in the input.

12. In DMC, perform a timestep study to either 1) obtain extrapolated results, or 2) obtain a timestep for future production where an energy difference shows convergence (e.g. a band gap or defect formation energy). For pseudopotential systems, converged timesteps for many
systems are in the range $0.002 - 0.01 \text{ Ha}^{-1}$, but the actual converged timestep must be explicitly checked.

13. In periodic systems, converge the total energy with respect to the size of the twist/k-point grid. Results for smaller systems can easily be transferred to larger ones (e.g. a 2x2x2 twist grid in a 2x2x2 tiled cell is equivalent to a 1x1x1 twist grid in a 4x4x4 tiled cell).

14. In periodic systems, perform finite size extrapolation including two body corrections (needed for cohesive energy/phase stability studies) unless it can be shown that finite size effects cancel for the energy difference in question (e.g. some defect formation energies).

12.2 Using the qfit tool for statistical timestep extrapolation and curve fitting

The qfit tool is used to provide statistical estimates of curve fitting parameters based on QMC-PACK data. While qfit will eventually support many types of fitted curves (e.g. Morse potential binding curves, various equation of state fitting curves, etc.), it is currently limited to estimating fitting parameters related to timestep extrapolation.

12.2.1 The jack-knife statistical technique

The qfit tool obtains estimates of fitting parameter means and associated error bars via the “jack-knife” technique. The jack-knife method is a powerful and general tool to obtain meaningful error bars for any quantity that is related in a non-linear fashion to an underlying set of statistical data. For this reason, we give a brief overview of the jack-knife technique before proceeding with usage instructions for the qfit tool.

Consider $N$ statistical variables $\{x_n\}_{n=1}^N$ that have been outputted by one or more simulation runs. If we have $M$ samples of each of the $N$ variables, then the mean values of each of these variables can be estimated in the standard way, i.e. $\bar{x}_n \approx \frac{1}{M} \sum_{m=1}^{M} x_{nm}$.

Suppose we are interested in $P$ statistical quantities $\{y_p\}_{p=1}^P$ that are related to the original $N$ variables by a known multidimensional function $F$:

$$y_1, y_2, \ldots, y_P = F(x_1, x_2, \ldots, x_N) \quad \text{or} \quad \bar{y} = F(\bar{x}) \quad (12.1)$$

The relationship implied by $F$ is completely general. For example the $\{x_n\}$ might be elements of a matrix with $\{y_p\}$ being the eigenvalues, or $F$ might be a fitting procedure for $N$ energies at different timesteps with $P$ fitting parameters. An approximate guess at the mean value of $\bar{y}$ can be obtained by evaluating $F$ at the mean value of $\bar{x}$ (i.e. $F(\bar{x}_1 \ldots \bar{x}_N)$), but with this approach we have no way to estimate the statistical error bar of any $\bar{y}_p$.

In the jack-knife procedure, the statistical variability intrinsic to the underlying data $\{x_n\}$ is used to obtain estimates of the mean and error bar of $\{y_p\}$. We first construct a new set of $x$ statistical data by taking the average over all samples but one:

$$\bar{x}_{nm} = \frac{1}{N-1} (N \bar{x}_n - x_{nm}) \quad m \in [1, M] \quad (12.2)$$

The result is a distribution of approximate $x$ mean values. These are used to construct a distribution of approximate means for $y$:

$$\bar{y}_{1m}, \ldots, \bar{y}_{Pm} = F(\bar{x}_{1m}, \ldots, \bar{x}_{Nm}) \quad m \in [1, M] \quad (12.3)$$
Estimates for the mean and error bar of the quantities of interest can finally be obtained using the formulas below:

\[ \bar{y}_p = \frac{1}{M} \sum_{m=1}^{M} \bar{y}_{pm} \] (12.4)

\[ \sigma_{y_p} = \sqrt{\frac{M-1}{M} \left( \sum_{m=1}^{M} \bar{y}_{pm}^2 - M \bar{y}_p^2 \right)} \] (12.5)

### 12.2.2 Performing timestep extrapolation

In this section, we use a 32 atom supercell of MnO as an example system for timestep extrapolation. Data for this system has been collected in DMC using the following sequence of timesteps: 0.04, 0.02, 0.01, 0.005, 0.0025, 0.00125 Ha\(^{-1}\). For a typical production pseudopotential study, timesteps in the range 0.02 – 0.002 Ha\(^{-1}\) are usually sufficient and it is recommended to increase the number of steps/blocks by a factor of two when the timestep is halved. In order to perform accurate statistical fitting, we must first understand the equilibration and autocorrelation properties of the inputted local energy data. After plotting the local energy traces (qmca \(-t\ \-q\ \-e\ \-e\ \-e\ \-e\ \ 0\ \ . /qmc*/+scalar*) it is clear that an equilibration period of 30 blocks is reasonable. Approximate autocorrelation lengths are also obtained with qmca:

```
> qmca -e 30 -q e --sac ./qmc*/qmc.g000.s002.scalar.dat
./qmc_tm_0.00125/qmc.g000 series 2 LocalEnergy = -3848.234513 +/-
   0.055754  1.7
./qmc_tm_0.00250/qmc.g000 series 2 LocalEnergy = -3848.237614 +/-
   0.055432  2.2
./qmc_tm_0.00500/qmc.g000 series 2 LocalEnergy = -3848.349741 +/-
   0.069729  2.8
./qmc_tm_0.01000/qmc.g000 series 2 LocalEnergy = -3848.274596 +/-
   0.126407  3.9
./qmc_tm_0.02000/qmc.g000 series 2 LocalEnergy = -3848.539017 +/-
   0.075740  2.4
./qmc_tm_0.04000/qmc.g000 series 2 LocalEnergy = -3848.976424 +/-
   0.075305  1.8
```

The autocorrelation must be removed from the data prior to jack-knifing and so we will reblock the data by a factor of 4.

The `qfit` tool can be used in the following way to obtain a linear timestep fit of the data:

```
> qfit ts -e 30 -b 4 -s 2 -t '0.00125 0.0025 0.005 0.01 0.02 0.04' . /qmc*/+scalar*
fit function : linear
fitted formula: (-3848.193 +/- 0.037) + (-18.95 +/- 1.95)*t
intercept : -3848.193 +/- 0.037 Ha
```

The input arguments are as follows: `ts` indicates we are performing a timestep fit, “-e 30” is the equilibration period removed from each set of scalar data, “-b 4” indicates the data will be reblocked by a factor of 4 (e.g. a file containing 400 entries will be block averaged into a new set of 100 prior to jack-knife fitting), “-s 2” indicates that the timestep data begins with series 2 (scalar files matching *s000* or *s001* are to be excluded), and “-t ’0.00125 0.0025 0.005 0.01 0.02 0.04”
Figure 12.9: Linear (left) and quadratic (right) timestep fits to DMC data for a 32 atom supercell of MnO obtained with qfit. Zero timestep estimates are indicated by the red data point on the left side of either panel.

0.04’ ” provides a list of timestep values corresponding to the inputted scalar files. The “-e” and “-b” options can receive a list of file-specific values (same format as “-t”) if desired. As can be seen from the text output, the parameters for the linear fit are printed with error bars obtained with jack-knife resampling and the zero timestep “intercept” is $-3848.19(4)$ Ha. In addition to text output, the command above will result in a plot of the fit with the zero timestep value shown as a red dot, as shown in the left panel of Fig. 12.9.

Different fitting functions are supported via the “-f” option. Currently supported options include linear ($a + bt$), quadratic ($a + bt + ct^2$), and sqrt ($a + bt + ct$). Results for a quadratic fit are shown below as well as in the right panel of Fig. 12.9.

```
>qfit ts -f quadratic -e30 -b4 -s2 -t '0.00125 0.0025 0.005 0.01 0.02 0.04' ./qmc/*/*scalar*
fit function : quadratic
fitted formula: (-3848.245 +/- 0.047) + (-7.25 +/- 8.33)*t + (-285.00 +/- 202.39)*t^2
intercept : -3848.245 +/- 0.047 Ha
```

In this case we find a zero timestep estimate of $-3848.25(5)$ Ha$^{-1}$. A timestep of 0.04 Ha$^{-1}$ might be on the large side to include in timestep extrapolation and it is likely to have an outsize influence in the case of linear extrapolation. Upon excluding this point, linear extrapolation yields a zero timestep value of $-3848.22(4)$ Ha$^{-1}$. It should be noted that quadratic extrapolation can result in intrinsically larger uncertainty in the extrapolated value. For example, when the 0.04 Ha$^{-1}$ point is excluded the uncertainty grows by 50% and we obtain an estimated value of $-3848.28(7)$ instead.

### 12.3 Densities and spin-densities

TBD.
Chapter 13

Periodic LCAO for solids

13.1 Introduction

QMCPACK implements linear combination of atomic orbitals (LCAO) and Gaussian basis sets in periodic boundary conditions. This method uses orders of magnitude less memory than the real space spline wavefunction. While the spline scheme enables very fast evaluation of the wavefunction, it may require too much on-node memory for a large complex cell. The periodic Gaussian evaluation provides a fallback that will definitely fit in available memory, but at significantly increased computational expense. Well designed Gaussian basis sets should be used to accurately represent the wavefunction, typically including both diffuse and high angular momentum functions.

The initial implementation is limited to the Γ-point using trial wavefunctions generated by PySCF[34], but other codes such as Crystal can be interfaced on request.

LCAO schemes use physical considerations to construct a highly efficient basis set compared to plane waves. Typically only a few tens of basis functions per atom are required compared to thousands of plane-waves. Many forms of LCAO schemes exist and are being implemented in QMCPACK. The details of the already implemented methods will be described in the following section of the manual.

Gaussian Trial Orbitals (GTOs): The Gaussian basis functions follow a radial-angular decomposition

$$\phi(r) = R_l(r)Y_{lm}(\theta, \phi)$$  \hspace{1cm} (13.1)

where $Y_{lm}(\theta, \phi)$ is a spherical harmonic, $l$ and $m$ are the angular momentum and its $z$ component, and $r, \theta, \phi$ are spherical coordinates. In practice they are atom centered and the $l$ expansion typically includes 1-3 additional channels compared to the formally occupied states of the atom, e.g. 4-6 for a nickel atom with occupied $s$, $p$, and $d$ electron shells.

The evaluation of GTOs within PBC differs slightly from evaluating GTOs in Open Boundary Conditions (OBC). The orbitals are evaluated at a distance $r$ in the primitive cell (similar to OBC) and then the contributions of the periodic images are added by evaluating the orbital at a distance $r + T$ where $T$ is a translation of the cell lattice vector. This requires loops over the periodic images until the contributions are orbitals $\Phi$. In the current implementation, the number of periodic images is an input parameter named $PBCimages$, which takes three integers corresponding to the number of periodic images along the supercell axes (X, Y and Z axes for a cubic cell). By default these parameters are set to $PBCimages= 5 5 5$ but they require manual convergence checks. Convergence checks can be performed by checking the total energy convergence with respect to $PBCimages$, similar to checks performed for plane wave cutoff energy and b-spline grids. Use of diffuse Gaussians may require these parameters to be increased, while sharply localized Gaussians
may permit a decrease. The cost of evaluating the wavefunction increases sharply as $PBCimages$
is increased. This input parameter will be replaced by a tolerance factor and numerical screening
in future.

13.2 Generating and using periodic gaussian trial wavefunctions using PySCF

Similar to any QMC calculation, using periodic GTOs requires the generation of a periodic trial
wavefunction. QMCPACK is currently interfaced to PySCF which is a multipurpose electronic
structure written mainly in Python with key numerical functionality implemented via optimized C
and C++ libraries[34]. Such a wavefunction can be generated following the example for a 2x1x1
supercell, below. Note that the current implementation and example covers only the use of the
Gamma (Γ) point. More general and multiple k-points (real and complex) will be supported in
future releases.

Listing 13.1: Example PySCF input for single k-point calculation for a 2x1x1 Carbon supercell.

```python
#!/usr/bin/env python
import numpy
from pyscf.pbc import gto, scf, dft
from mpi4pyscf.pbc import df
from pyscf.pbc.tools.pbc import super_cell

nmp = [2, 1, 1]
cell = gto.Cell()
cell.a = 
     3.37316115 3.37316115 0.00000000
     0.00000000 3.37316115 3.37316115
     3.37316115 0.00000000 3.37316115

cell.atom = 
     C 0.00000000 0.00000000 0.00000000
     C 1.686580575 1.686580575 1.686580575

cell.basis='bfd-vtz'
cell.ecp = 'bfd'
cell.unit='B'
cell.drop_exponent=0.1
cell.verbose = 5
cell.build()

supcell = super_cell(cell, nmp)
mydf = df.FFTDF(supcell)
mydf.auxbasis = 'weigend'

mf = dft.RKS(supcell)
mf.xc = 'lda'
```
mf.exxdiv = 'ewald'
mf.with_df = mydf

e_scf=mf.kernel()

print 'e_scf', e_scf

kpts=[]
title="C_Diamond"
from PyscfToQmcpack import savetoqmcpack
savetoqmcpack(supcell,mf,title=title,kpts=kpts)

Note that the last 4 lines of the file

contains an empty list of k-points (since this is a gamma point calculation) and a title. The title
variable will be the name of the HDF5 file where all the data needed by QMCPACK will be stored.
The function savetoqmcpack will be called at the end of the calculation and will generate the HDF5
similarly to the non-periodic PySCF calculation in section 21.3.1 (convert4qmc). The function is
distributed with QMCPACK and located in the qmcpack/src/QMCTools directory under the name
PyscfToQmcpack.py. In order for the script to work, you need to specify the path to the file in
your PYTHONPATH such as

export PYTHONPATH=QMCPACK_PATH/src/QMCTools:$PYTHONPATH

In order to generate QMCPACK input files, you will need to run convert4qmc exactly as specified
in section 21.3.1;

convert4qmc -pyscf C_Diamond.h5

This tool can be used with any option described in convert4qmc. Since the HDF5 contains
all the information needed for a QMC run, there is no need to specify any other specific tag for
periodicity. Running such a command will generate 3 input files;

Listing 13.2: CDiamond.structure.xml. This file contains the geometry of the system.
As one can see, the cell has been extended to contain 4 atoms in a 2x1x1 Carbon Cell.

Listing 13.3: CDiamond.wfj-Twist0.xml. This file contains the trial wavefunction.

```
<wavefunction name="psi0" target="e">
  <determinantset type="MolecularOrbital" name="LCAOBSet" source="ion0"
    transform="yes" twist="0 0 0" href="C_Diamond.h5" PBCimages="5 5 5">
    <slaterdeterminant>
      <determinant id="updet" size="8">
        <occupation mode="ground"/>
        <coefficient size="116" spindataset="0"/>
      </determinant>
      <determinant id="downdet" size="8">
        <occupation mode="ground"/>
        <coefficient size="116" spindataset="0"/>
      </determinant>
    </slaterdeterminant>
  </determinantset>
  <jastrow name="J2" type="Two-Body" function="Bspline" print="yes">
    <correlation size="10" speciesA="u" speciesB="u">
      <coefficients id="uu" type="Array" 0 0 0 0 0 0 0 0 0 0</coefficients>
    </correlation>
    <correlation size="10" speciesA="u" speciesB="d">
      <coefficients id="ud" type="Array" 0 0 0 0 0 0 0 0 0 0</coefficients>
    </correlation>
  </jastrow>
  <jastrow name="J1" type="One-Body" function="Bspline" source="ion0" print="159">
```

159
This file contains information related to the trial wavefunction. It is identical to the input file from an Open Boundary Conditions calculation to the exception of the following tags:

<table>
<thead>
<tr>
<th>tag</th>
<th>tag type</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>twist</td>
<td>3 doubles</td>
<td>Gamma (0 0 0)</td>
<td>coordinate of the twist to compute</td>
</tr>
<tr>
<td>href</td>
<td>string</td>
<td>default</td>
<td>name of the HDF5 file generated by PySCF and used for convert4qmc</td>
</tr>
<tr>
<td>PBCimages</td>
<td>3 Integer</td>
<td>5 5 5</td>
<td>Number of periodic images to evaluate the orbitals</td>
</tr>
</tbody>
</table>

Other files containing QMC methods (such as optimization, VMC and DMC blocks) will be generated and will behave in a similar fashion regardless of the type of SPO in the trial wavefunction.
Chapter 14

Selected Configuration Interaction

A direct path towards improving the accuracy of a QMC calculation is through a better trial wavefunction. While using a multireference wavefunction can be straightforward in theory, in actual practice methods such as CASSCF are not always intuitive and often require being an expert in either the method or the code generating the wavefunction. An alternative is to use a Selected Configuration of Interaction method (selected CI) such as CIPSI (Configuration Interaction using a Perturbative Selection done Iteratively). This provides a direct route to systematically improving the wavefunction.

14.1 Theoretical Background

The principle behind selected CI is rather simple and was first published in 1955 by R.K. Nesbet[28]. The first calculations on atoms were performed by Diner, Malrieu and Claverie[27] in 1967, and it became computationally viable for larger molecules in 2013 by Caffarel et al.[25]

As described by Caffarel et al in Ref. [25], multi-determinantal expansions of the ground-state wavefunction $\Psi_T$ are written as a linear combination of Slater determinants

$$
\sum_k c_k \sum_q d_{k,q} D_k,q^{\dagger}(r^\dagger)D_k,q(r^\dagger)
$$

(14.1)

where each determinant corresponds to a given occupation by the $N_\alpha$ and $N_\beta$ electrons of $N = N_\alpha + N_\beta$ orbitals among a set of $M$ spin-orbitals $\{\phi_1,..,\phi_M\}$ (restricted case). When no symmetries are considered, the maximum number of such determinants is

$$
\binom{M}{N_\alpha} \cdot \binom{M}{N_\beta}
$$

(14.2)

a number that grows factorially with $M$ and $N$. The best representation of the exact wavefunction in the determinantal basis is the full configuration interaction (FCI) wave function written as

$$
|\Psi_0\rangle = \sum_i c_i |D_i\rangle
$$

(14.3)

where $c_i$ are the ground-state coefficients obtained by diagonalizing the matrix, $H_{ij} = \langle D_i | H | D_j \rangle$, within the full orthonormalized set $\langle D_i | D_j \rangle = \delta_{ij}$, of determinants $|D_i\rangle$. CIPSI provides a convenient method to build up to this full wavefunction with a single criteria.

A CIPSI wavefunction is built iteratively starting from a reference wavefunction, usually Hartree-Fock or CASSCF, by adding all single and double excitations and then iteratively selecting relevant
determinants according to some criteria. Detailed iterative steps can be found in the reference by Caffarel et al. and references within[25, 32, 29, 31] but are summarized below:

- **Step 1:** Define a reference wavefunction:
  \[ |\Psi\rangle = \sum_{i \in D} c_i |i\rangle \quad E_{var} = \frac{\langle \Psi | \hat{H} | \Psi \rangle}{\langle \Psi | \Psi \rangle} \]  
  \[ (14.4) \]

- **Step 2:** Generate external determinants \( |\alpha\rangle \):
  New determinants are added by generating all single and double excitations from determinants \( i \in D \) such as:
  \[ \langle \Psi^{(\alpha)}_a | H | D_{c_i} \rangle \neq 0 \]  
  \[ (14.5) \]

- **Step 3:** Evaluate second order perturbative contribution to each determinant \( |\alpha\rangle \):
  \[ \Delta E = \frac{\langle \Psi | \hat{H} | \alpha \rangle \langle \alpha | \hat{H} | \Psi \rangle}{E_{var} - \langle \alpha | \hat{H} | \alpha \rangle} \]  
  \[ (14.6) \]

- **Step 4:** Select the determinants with the largest contributions and add them to the Hamiltonian.

- **Step 5:** Diagonalize the Hamiltonian within the new added determinants and update the wavefunction and the the value of \( E_{var} \).

- **Step 6:** Iterate until reaching convergence.

Repeating this process leads to a multi-reference trial wavefunction of high quality that can be used in QMC.

\[ \Psi_T(r) = e^{J(r)} \sum_k c_k \sum_q d_{k,q} D_{k,q}(r^\dagger) D_{k,q}(r^\dagger) \]  
\[ (14.7) \]

The linear coefficients \( c_k \) are then optimized with the presence of the Jastrow function.

It is important to note that:

- When all determinants \( |\alpha\rangle \) are selected, the full configuration interaction result is obtained.

- CIPSI can be seen as a deterministic counter part of FCIQMC.

- In practice, any wavefunction method can be made multireference with CIPSI. For instance, a multireference Coupled Cluster (MRCC) with CIPSI is implemented in QP.[30]

- At any time, with CIPSI selection, \( E_{PT2} = \sum_{\alpha} \Delta E_{\alpha} \) estimates the distance to the FCI solution.
14.1.1 CIPSI wavefunction interface

The CIPSI method is implemented in the *Quantum Package* (QP) code[26] developed by the Caffarel group. Once the trial wavefunction is generated, QP is able to produce output readable by the QMCPACK converter as described in section 21.3.1. QP can be installed with multiple plugins for different levels of theory in quantum chemistry. When installing the "QMC" plugin, QP can save the wavefunction in a format readable by the QMCPACK converter.

In the following we use the $C_2O_2H_3N$ molecule (Fig 14.1) as an example of how to run a multireference calculation with CIPSI as a trial wavefunction for QMCPACK. The choice of this molecule is motivated by its multireference nature. While the molecule remains small enough for CCSD(T) calculations with aug-cc-pVTZ basis set, the D1 diagnostic shows a very high value for $C_2O_2H_3N$, suggesting a multireference character. Therefore, an accurate reference for the system is not available and it becomes difficult to trust the quality of a single-determinant wavefunction, even when using the DFT-B3LYP exchange and correlation functional. Therefore, in the following, we show an example of how to systematically improve the nodal surface by increasing the number of determinants in the trial wavefunction.

The following steps show how to run from Hartree-Fock to selected CI using QP, convert the wavefunction to a QMCPACK trial wavefunction and finally how to analyze the result.

- **Step 1: Generate the QP input file:**
  QP takes for input an XYZ file containing the geometry of the molecule such as:

<table>
<thead>
<tr>
<th>Element</th>
<th>x</th>
<th>y</th>
<th>z</th>
</tr>
</thead>
<tbody>
<tr>
<td>C</td>
<td>1.067070</td>
<td>-0.370798</td>
<td>0.020324</td>
</tr>
<tr>
<td>C</td>
<td>-1.115770</td>
<td>-0.239135</td>
<td>0.081860</td>
</tr>
<tr>
<td>O</td>
<td>-0.537581</td>
<td>1.047619</td>
<td>-0.091020</td>
</tr>
<tr>
<td>N</td>
<td>0.879629</td>
<td>0.882518</td>
<td>0.046830</td>
</tr>
<tr>
<td>H</td>
<td>-1.525096</td>
<td>-0.354103</td>
<td>1.092299</td>
</tr>
<tr>
<td>H</td>
<td>-1.868807</td>
<td>-0.416543</td>
<td>-0.683862</td>
</tr>
<tr>
<td>H</td>
<td>2.035229</td>
<td>-0.841662</td>
<td>0.053363</td>
</tr>
<tr>
<td>O</td>
<td>-0.025736</td>
<td>-1.160835</td>
<td>-0.084319</td>
</tr>
</tbody>
</table>
The input file is generated through the following command line:

```
qp_create_ezfio_from_xyz C2O2H3N.xyz -b cc-pvtz
```

This means that we will be simulating the molecule in all-electrons within the cc-pVTZ basis set. Other options are of course possible such as using ECPs, different spin multiplicities etc. For more details, see the Quantum Package tutorial [https://github.com/LCPQ/quantum_package/wiki/Tutorial](https://github.com/LCPQ/quantum_package/wiki/Tutorial).

A directory called `C2O2H3N.ezfio` is created and contains all the relevant data to run the SCF Hartree-Fock calculation. Note that due to the large size of molecular orbitals (220), it is preferable to run QP in parallel. QP parallelization is based on a Master/Slave process allowing a master node to manage the work load between multiple MPI processes through the LibZMQ library. In practice one submits the run to one master node, then submits as many nodes as necessary to speed up the calculations. If a "slave" node dies before the end of its task, the master node will resubmit the workload to another available node. If more nodes are added at any time during the simulation, the master node will use them to reduce the time to solution.

- **Step 2: Running Hartree-Fock:**

  To save the integrals on disk and avoid recomputing them later, edit the ezfio directory with the following command:

  ```
  qp_edit C2O2H3N.ezfio
  ```

  This will generate a temporary file showing all the contents of the simulation and opens an editor to allow modification of their values. Look for `disk_access_ao_integrals` and modify its value from `None` to `Write`.

  To run a simulation with QP, use the binary `qp_run` with the desired level of theory, in this case Hartree-Fock (SCF).

  ```
  mpirun -np 1 qp_run SCF C2O2H3N.ezfio &> C2O2H3N-SCF.out
  ```

  If run in serial, the evaluation of the integrals and the Hamiltonian diagonalization would take a substantial amount of computer time. It is recommended to add a few more `slave-nodes` to help speed up the calculation.

  ```
  mpirun -np 20 qp_run -slave qp_ao_ints C2O2H3N.ezfio &> C2O2H3N-SCF-Slave.out
  ```

  The total Hartree-Fock energy of the system in cc-pVTZ is \( E_{HF} = −283.0992 \text{Ha} \).

- **Step 2: Freeze Core electrons:**

  In order to avoid making excitation from the core electrons, freeze the core electrons and only
do the excitations from the valence electrons.

```
qp_set_frozen_core.py C2O2H3N.ezfio
```

This will will automatically freeze the orbitals from 1 to 5, and leave the remaining active.

- **Step 3: Atomic orbitals to Molecular Orbital transformation**
  This step, transforming the atomic orbitals to molecular orbitals, is the most costly, especially given that its implementation in Quantum Package is serial. It is recommended to do it in a separate run and on one node.

```
qp_run four_idx_transform C2O2H3N.ezfio
```

The MO integrals are now saved on disk and unless the orbitals are changed, they will not be recomputed.

- **Step 4: CIPSI**
  At this point the wavefunction is ready for the selected CI. By default QP has 2 convergence criteria. The number of determinants (set by default to 1M) or the value of PT2 (set by default to 1.10^{-4} Ha). For this molecule, the total number of determinants in the FCI space is 207e + 88 determinants. While his number is completely out of range of what is possible to compute, we will set the limit of determinants in QP to 5M determinants and see if the nodal surface of the wavefunction is converged enough for the DMC. It is important to remember at this point that the main value of CIPSI compared to other selected CI method, is that the value of PT2 is evaluated directly at each step giving a good estimated of the error to the FCI energy. This allows us to conclude that when the E+PT2 energy is converged, the nodal surface is probably also converged.

Similar to the SCF runs, FCI runs have to be submitted in parallel with a *Master/Slave* process:

```
mpirun -np 1 qp_run fci_zmq C2O2H3N.ezfio &> C2O2H3N-FCI.out
mpirun -np 199 qp_run -slave selection_davidson_slave C2O2H3N.ezfio
```

- **Step 5 (optional): Natural orbitals**
  While this step is optional, it is important to note that using natural orbitals instead of Hartree Fock orbitals will always improve the quality of the wavefunction and improve the quality of the nodal surface by reducing the number of needed determinants for the same accuracy. When a full convergence to the FCI limit is attainable, this step will not lead to any change in the energy but will only reduce the total number of determinants. However, if a full convergence is not possible, this step can increase significantly the accuracy of the calculation at the same number of determinants.
Figure 14.2: Evolution of the variational energy and the Energy + PT2 as a function of the number of determinants for the \(C_2O_2H_3N\) molecule.

Table 14.1: Energies of \(C_2O_2H_3N\) using orbitals from Hartree-Fock, natural orbitals, 0.4M and 4M determinants

<table>
<thead>
<tr>
<th>Method</th>
<th>N_det</th>
<th>Energy</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hartree-Fock</td>
<td>1</td>
<td>-281.6729</td>
</tr>
<tr>
<td>Natural Orbitals</td>
<td>1</td>
<td>-281.6735</td>
</tr>
<tr>
<td>E_Variational</td>
<td>438,753</td>
<td>-282.2951</td>
</tr>
<tr>
<td>E_Variational</td>
<td>4,068,271</td>
<td>-282.4882</td>
</tr>
<tr>
<td>E+PT2</td>
<td>438,753</td>
<td>-282.6809</td>
</tr>
<tr>
<td>E+PT2</td>
<td>4,068,271</td>
<td>-282.6805</td>
</tr>
</tbody>
</table>

At this point, the orbitals are modified, a new AO→MO transformation is required and Steps 3 and 4 need to be run again.

- Step 6: Analysis of the CIPSI results
  Figure 14.2 shows the evolution of the variational energy and the energy corrected with PT2 as a function of the number of determinants up to 4M determinants. While it is clear that the raw variational energy is far from being converged, the Energy + PT2 appears converged around 0.4M determinants.

- Step 7: Truncation of the number of determinants.
  While using all the 4M determinants from CIPSI always guarantees that all important de-
terminants are kept in the wavefunction, practically, such a large number of determinants would make any QMC calculation prohibitively expensive, as the cost of evaluating a determinant in DMC grows as $\sqrt{N_{\text{det}}}$ where $N_{\text{det}}$ is the number of determinants in the trial wavefunction. To truncate the number of determinants, we follow the method described by Scemama et. al [29] where the wavefunction is truncated by removing independently spin-up and spin-down determinants whose contribution to the norm of the wavefunction is below a user-defined threshold, $\epsilon$. For this step, we choose to truncate the determinants whose coefficients are below, $1.10^{-3}$, $1.10^{-4}$, $1.10^{-5}$ and $1.10^{-6}$, translating to 239, 44539, 541380 and 908128 determinants, respectively.

To truncate the determinants in QP, edit the ezfio file as follows:

```
qp_edit C2O2H3N.ezfio
```

then look for `ci_threshold` and modify the value according to the desired threshold. Use the following run to truncate the determinants:

```
qp_run truncate_wf_spin C2O2H3N.ezfio
```

- **Step 7: Save the wavefunction for QMCPACK**

  The wavefunction in QP is now ready to be converted to QMCPACK format. Save the wavefunction into QMCPACK format and then convert the wavefunction using the `convert4qmc` tool

  ```
  qp_run save_for_qmcpack C2O2H3N.ezfio &> C2O2H3N.dump
  convert4qmc -QP C2O2H3N.dump -addCusp -production
  ```

  Since we are running all-electron calculations, orbitals in QMC need to be corrected for the electron-nuclearcusp condition. This is done by adding the option `-addCusp` to `convert4qmc`, which adds a tag forcing QMCPACK to run the correction or read them from a file if pre-computed. When running multiple DMC runs with different truncation thresholds, only the number of determinants is varied and the orbitals remain unchanged from one calculation to another and the cusp correction needs only be run once.

- **Step 7: Running QMCPACK**

  At this point, running a multideterminant DMC becomes identical to running a regular DMC with QMCPACK; After correcting the orbitals for the cusp, optimize the Jastrow functions and then run the DMC. It is however important to mention a few remarks:

  1. QMCPACK allows reoptimization of the coefficients of the determinants during the Jastrow optimization step. While this has proven to lower the energy significantly when the number of determinants is below 10k, a large number of determinants from CIPSI is often too large to optimize conveniently. Keeping the coefficients of the determinants from CIPSI unoptimized is an alternative strategy.

  2. The large determinant expansion and the Jastrows are both trying to recover the missing correlations from the system. When optimizing the Jastrows, we recommend to first optimize J1 and J2 without the J3, and then with the added J3. Trying to initially optimize J1, J2
Table 14.2: DMC Energies and CIPSI(E+PT2) of $C_2O_2H_3N$ in function of the number of determinants in the trial wavefunction.

<table>
<thead>
<tr>
<th>N_det</th>
<th>DMC</th>
<th>CISPI</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>-283.0696 (6)</td>
<td>-283.0063</td>
</tr>
<tr>
<td>239</td>
<td>-283.0730 (9)</td>
<td>-282.9063</td>
</tr>
<tr>
<td>44,539</td>
<td>-283.078 (1)</td>
<td>-282.7339</td>
</tr>
<tr>
<td>541,380</td>
<td>-283.088 (1)</td>
<td>-282.6772</td>
</tr>
<tr>
<td>908,128</td>
<td>-283.089 (1)</td>
<td>-282.6775</td>
</tr>
</tbody>
</table>

Step 8: Analyzing DMC results from QMCPACK

From Table 14.2, we can see that increasing the number of determinants from 0.5M to almost 1M determinant keeps the energy within error bars and does not improve the quality of the nodal surface. We can conclude that the DMC energy is converged at 0.54M determinants. It is important to note that this number of determinants also corresponds to the convergence of E+PT2 in CIPSI calculations, confirming for this case that the convergence of the nodal surface can follow the convergence of E+PT2 instead of the more difficult variational energy.

As mentioned in previous sections, DMC is variational relative to the exact nodal surface. A nodal surface is "better" if it lowers the DMC energy. To assess the quality of the nodal surface from CIPSI, we compare these DMC results to other single determinant calculations from multiple nodal surfaces and theories. Figure 14.3 shows the energy of the $C_2O_2H_3N$ molecule as a function of different single-determinant (SD) trial wavefunctions with an aug-cc-pVTZ basis set, including Hartree-Fock (HF), DFT-PBE and hybrid functionals B3LYP and PBE0. The last 4 points in the plot show the systematic improvement of the nodal surface as a function of the number of determinants.

When the DMC-CIPSI energy is converged with respect to the number of determinants, its nodal surface is still lower than the best SD-DMC (B3LYP) by 6(1)mHa. When compared to CCSD(T) with the same basis set, $E_{CCSD(T)}$ is 4mHa higher than DMC-CIPSI and 2mHa lower than DMC-B3LYP. While 6 (1) mHa can seem very small, it is however important to remember that CCSD(T) cannot describe correctly multireference systems and therefore it is impossible to assess the correctness of the SD-DMC result, making CIPSI-DMC calculations an ideal benchmark tool for multireference systems.
Figure 14.3: DMC energy of $C_2O_2H_3N$ molecule as a function of different single determinant trial wavefunctions with aug-ccp-VTZ basis set using nodal surfaces from Hartree-Fock (HF), DFT-PBE and DFT with hybrid functionals PBE0 and P3LYP. The CIPSI trial wavefunction contains as indicated 239, 44539, 514380 and 908128 determinants (D).
Chapter 15

Auxiliary-Field Quantum Monte Carlo

The Auxiliary-Field Quantum Monte Carlo (AFQMC) method is an orbital-space formulation of the imaginary-time propagation algorithm. We refer the reader to one of the review articles on the method [21, 19, 20], for a detailed description of the algorithm. It uses the Hubbard-Stratonovich transformation to express the imaginary-time propagator, which is inherently a 2-body operator, as an integral over 1-body propagators which can be efficiently applied to an arbitrary Slater determinant. This transformation allows us to represent the interacting many-body system as an average over a non-interacting system (e.g. Slater determinants) in a time-dependent fluctuating external field (the Auxiliary fields). The walkers in this case represent non-orthogonal Slater determinants, whose time average represent the desired quantum state. QMCPACK currently implements the phaseless AFQMC algorithm of Zhang and Krakauer [19], where a trial wave-function is used to project the simulation to the real axis, controlling the fermionic sign problem at the expense of a bias. This approximation is similar in spirit to the fixed-node approximation in real-space DMC, but applied in the Hilbert space where the AFQMC random walk occurs.

15.1 Theoretical Background

... Coming Soon ...

15.2 Input

The input for an AFQMC calculation is fundamentally different to the input for other real-space algorithms in QMCPACK. The main source of input comes from the Hamiltonian matrix elements in an appropriate single particle basis. This must be evaluated by an external code and saved in a format that QMCPACK can read. More details about file formats are found below. The input file has six basic xml-blocks: AFQMCInfo, Hamiltonian, Wavefunction, WalkerSet, Propagator, and execute. The first five define input structures required for various types of calculations. The execute block represents actual calculations and takes as input the other blocks. Non-execution blocks are parsed first, followed by a second pass where execution blocks are parsed (and executed) in order. Listing 13.1 shows an example of a minimal input file for an AFQMC calculation. Table 15.1 shows a brief description of the most important parameters in the calculation. All xml sections contain a “name” argument used to identify the resulting object within
QMCPACK. For example, in the example, multiple Hamiltonian objects with different names can be defined. The one actually used in the calculation is the one passed to “execute” as ham.

Listing 15.1: Sample input file for AFQMC.

```xml
<?xml version="1.0"?>
<simulation method="afqmc">
  <project id="Carbon" series="0"/>

  <AFQMCInfo name="info0">
    <parameter name="NMO">32</parameter>
    <parameter name="NAEA">16</parameter>
    <parameter name="NAEB">16</parameter>
  </AFQMCInfo>

  <Hamiltonian name="ham0" type="SparseGeneral" info="info0">
    <parameter name="filetype">hdf5</parameter>
    <parameter name="filename">../fcidump.h5</parameter>
  </Hamiltonian>

  <Wavefunction name="wfn0" info="info0">
    <ImpSamp name="impsamp0" type="PureSD" init="ground">
      <parameter name="filetype">none</parameter>
    </ImpSamp>
  </Wavefunction>

  <WalkerSet name="wset0" type="distributed"/>

  <Propagator name="prop0" info="info0"/>

  <execute wset="wset0" ham="ham0" wfn="wfn0" prop="prop0" info="info0">
    <parameter name="timestep">0.005</parameter>
    <parameter name="blocks">10000</parameter>
    <parameter name="nWalkers">20</parameter>
  </execute>
</simulation>
```

Below is a list of all input sections for AFQMC calculations, along with a detailed explanation of accepted parameters. Since the code is under active development, the list of parameters and their interpretation can change in the future.

**AFQMCInfo**: input block that defines basic information about the calculation. It is passed to all other input blocks to propagate the basic information: `<AFQMCInfo name="info0">

- **NMO**. Number of molecular orbitals, i.e., number of states in the single particle basis.
- **NAEA**. Number of Active Electrons-Alpha, i.e., number of spin-up electrons.
- **NAEB**. Number of Active Electrons-Beta, i.e., number of spin-down electrons.
- **NCA**. number of core electrons of spin up (only meaningful if reading ASCII FCIDUMPs). Default: 0.
- **NCB.** Number of core electrons of spin down (only meaningful if reading ASCII FCIDUMPs). Default: 0.

Hamiltonian: controls the object that reads, stores and manages the hamiltonian. `<Hamiltonian name="ham0" type="SparseGeneral" info="info0">`

- **filename.** Name of file with the Hamiltonian. This is a required parameter.

- **filetype.** The type of file found in filename. Options are: fcidump, hdf5. fcidump is the ASCII-based format of Molpro, VASP, PySCF, etc.; hdf5 is the native HDF5-based format of QMCPACK and can also be generated by modified versions of PySCF and VASP. This is a required parameter.

- **cutoff_1bar.** Cutoff applied to integrals during reading. Any term in the hamiltonian smaller than this value is set to zero. (For filetype=“hdf5”, the cutoff is only applied to the 2-electron integrals). Default: 1e-8

- **cutoff_decomposition.** Cutoff used to stop the iterative cycle in the generation of the Cholesky decomposition of the 2-electron integrals. The generation of Cholesky vectors is stopped when the maximum error in the diagonal reaches this value. In case of an eigenvalue factorization, this becomes the cutoff applied to the eigenvalues. Only eigenvalues above this value are kept. Default: 1e-6

- **hdf_write_file.** If a value is given, an hdf5 restart file for the Hamiltonian is generated. Default: “” (no file is generated)

- **hdf_write_type.** What to store in the restart file. Options: “integrals”: write directly the 1- and 2-electron integrals; “factorized”: write the cholesky decomposition of the integrals; “default”: Default value, write the type found in filetype.

- **ascii_write_file** If a value is given, an ASCII restart file for the Hamiltonian is generated. Default: “” (no file is generated)

- **nblocks.** This parameter controls the distribution of the 2-electron integrals among processors. In the default behavior (nblocks=1), all nodes contain the entire list of integrals. If nblocks > 1, the of nodes in the calculation will be split in nblocks groups. Each node in a given group contains the same subset of integrals and subsequently operates on this subset during any further operation that requires the hamiltonian. The maximum number of groups is NMO. Currently only works for filetype=“hdf5” and the file must contain integrals. Not yet implemented for input hamiltonians in the form of Cholesky vectors or for ASCII input. Coming soon! Default: No distribution

- **printEig.** If “yes”, prints additional information during the Cholesky decomposition. Default: no

- **fix_2eint.** If this is set to “yes”, orbital pairs that are found not to be positive definite are ignored in the generation of the Cholesky factorization. This is necessary if the 2-electron integrals are not positive definite due to round-off errors in their generation. Default: no
Wavefunction: controls the object that manages the trial wave-functions. This block expects a list of xml-blocks defining actual trial-wave functions for various roles. 

```xml
<Wavefunction name="wfn0" info="info0">
  <ImpSamp name="impsamp0" type="PureSD">
    • init. Argument in ImpSamp. Selects pre-defined trial wave-functions if desired. Value: ground. Only for PureSD. Sets the trial wave-function to a block diagonal form. Diagonal in the occupied-occupied block and zero outside. This option corresponds to a ground state determinant (assuming orbitals ordered by increasing eigenvalue) in the orbital space that defines the hamiltonian. For a Hamiltonian generates based on HF orbitals, this generates a HF trial wave-function. (Only useful situation.)
    • filename. Name of file with wave-function information.
    • cutoff. cutoff applied to the terms in the calculation of the local energy. Only terms in the hamiltonian above this cutoff are included in the evaluation of the energy. Default: 1e-6
    • nnodes. Defines the parallelization of the local energy evaluation and the distribution of the Hamiltonian matrix (not to be confused with the list of 2-electron integrals managed by Hamiltonian. These are not the same.) If nnodes > 1, the nodes in the simulation are split into groups of nnodes, each group works collectively in the evaluation of the local energy of their walkers. This helps distribute the effort involved in the evaluation of the local energy among the nodes in the group, but also distributes the memory associated with the wave-function among the nodes in the group. Default: No distribution
    • hdf_write_file. If provided, a restart file for the wave-function will be generated. Default: ""
    • runtype. Unique to MultiPureSD with orthogonal expansions. Values: 0. Use low memory algorithm. Much slower but has small memory requirements; 1. Use high-memory algorithm. Faster but with significant memory requirements.
    • fast. Unique to MultiPureSD. If “yes”, use fast-update algorithm with orthogonal expansions. Default: No
    • Estimator. Optional xml-block which defines a trial wave-function used for the calculation of energy averages. It is used only during the collection of averages and doesn’t influence the propagation. Note that this block must be set if an Estimator xml-block in the execute xml-block is specified. This must also be defined in order to calculate and print the energy in the case of hybrid propagation (see below).
  </ImpSamp>
</Wavefunction>
```

WalkerSet: Controls the object that handles the set of walkers. 

```xml
<WalkerSet name="wset0" type="distributed">
  • pop_control. Population control algorithm. Options: “simple”: Uses a simple branching scheme with a fluctuating population. Walkers with weight above max_weight are split into multiple walkers of weight reset_weight. Walkers with weight below min_weight are killed with probability (weight/min_weight); “pair”: Fixed-population branching algorithm, based on QWalk’s branching algorithm. Pairs of walkers with weight above/below max_weight/min_weight are combined into 2 walkers with weights equal to (w1 + w2)/2. The probability of replicating walker w1 (larger weight) occurs with probability w1/(w1 + w2), otherwise walker w2 (lower weight) is replicated; “comb”: Fixed-population branching algorithm based on the Comb method. Will be available in the next release. Default: “pair”
</WalkerSet>
```
- **min_weight.** Weight at which walkers are possibly killed (with probability weight/min_weight). Default: 0.05
- **max_weight.** Weight at which walkers are replicated. Default: 4.0
- **reset_weight.** Weight to which replicated walkers are reset to. Default: 1.0
- **extra_spaces.** Number of empty spaces kept in the list. Useful to avoid constant reallocation. Default: 10

**Propagator:** Controls the object that manages the propagators. `<Propagator name="prop0" info="info0">

- **cutoff.** Cutoff applied to Cholesky vectors. Elements of the Cholesky vectors below this value are set to zero. Default: 1e-6
- **substractMF.** If “yes”, apply mean-field subtraction based on the ImpSamp trial wavefunction. Must set to “no” to turn it off. Default: yes
- **useCholesky.** If “yes”, use iterative Cholesky decomposition to factorize 2-electron integral matrix. If “no”, use eigenvalue decomposition (which is very slow and memory intensive). Default: yes
- **vbias_bound.** Upper bound applied to the vias potential. Components of the vias potential above this value are truncated there. The bound is currently applied to $\sqrt{\tau_{bias}}$, so a larger value must be used as either the time-step or the fluctuations increase (e.g. from running a larger system or using a poor trial wave-function). Default: 3.0
- **apply_constrain.** If “yes”, apply the phaseless constrain to the walker propagation. Currently, setting this to “no” produces unknown behavior, since free propagation algorithm has not been tested. Default: yes
- **hybrid.** If “yes”, use hybrid propagation algorithm. This propagation scheme doesn’t use the local energy during propagation, leading to significant speed ups when its evaluation cost is high. The local energy of the ImpSamp trial wave-function is never evaluated. To obtain energy estimates in this case, you must define an Estimator xml-block with the *Wavefunction* block. The local energy of this trial wave-function is evaluated and printed. It is possible to use a previously defined trial wave-function in the Estimator block, just set its “name” argument to the name of a previously defined wave-function. In this case, the same object is used for both roles. Default: no
- **nnodes.** Controls the parallel propagation algorithm. If nnodes > 1, the nodes in the simulation are split into groups of nnodes nodes, each group working collectively to propagate their walkers. Default: 1 (Serial algorithm)
- **hdf_read_file.** If provided, initializes the object from the given file. Default: “”
- **hdf_write_file.** If provided, generates a restart file. Default: “”
- **parallel_factorization.** If “yes”, calculates Cholesky decomposition in parallel. Mostly for testing purposes. Default: yes
- **parallel_propagation.** If “yes”, uses parallel propagation algorithm even with nnodes=1. This is set to “yes” if nnodes > 1. If “no”, uses a serial propagation algorithm. Only possible if nnodes=1 and ncores=1 (in execute block). Default: yes

- **dense.** If “yes”, use a dense representation of the factorized hamiltonian. The default behavior uses a sparse representation. Which option is better depends on the sparsity of the problem. Default: no

```
eexecute: Defines an execution region. <execute wset="wset0" ham="ham0" wfn="wfn0"
prop="prop0" info="info0">
```

- **nWalkers.** initial number of walkers per core group (see ncores). This sets the number of walkers for a given gorup of “ncores” on a node, the total number of walkers in the simulation depends on the total number of nodes and on the total number of cores on a node in the following way: \( #_{\text{walkers}}^{\text{total}} = n_{\text{Walkers}} \times #_{\text{nodes}} \times #_{\text{cores}}^{\text{total}} / n_{\text{cores}} \).
  Default: 5

- **timestep.** time step in 1/a.u.
  Default: 0.01

- **blocks.** number of blocks. Slow operations occur once per block, e.g. write to file, slow observables, checkpoints, etc.
  Default: 100

- **step.** number of steps within a block. Operations that occur at the step level include: load balance, orthogonalization, branching, etc.
  Default: 1

- **substep.** number of substeps within a step. Only walker propagation occurs in a substep.
  Default: 1

- **ortho.** number of steps between orthogonalization. Default: 1

- **ncores.** Number of nodes in a task group. This number defines the number of cores on a node that share the parallel work associated with a distributed task. This number is used in the Wavefunction and Propagator task groups. The walker sets are shares by the ncores on a given node in the task group.

- **checkpoint.** Number of blocks between checkpoint files are generated. If a value smaller than 1 is given, no file is generated. If hdf_write_file is not set, a default name is used.
  Default: 0

- **samplePeriod.** Number of blocks between sample collection. Default: 0

- **hdf_write_file.** If set (and checkpoint>0), a checkpoint file with this name will be written.

- **hdf_read_file.** If set, the simulation will be restarted from the given file.

Within the Estimators xml block has an argument name: the type of estimator we want to measure. Currently only “basic” or “Basic” or “standard” are allowed, which are synonymous with one another. The basic estimator has the following optional parameters:
• **EstimEloc** or **estim_eloc** or **estimeloc**. print the local energy of the “Estimator” wave-function. Default: false

• **timers.** print timing information. Default: true

• **nwalk.** print population control information (**max # branching events etc?**). Default: false

### 15.3 File formats

... Coming Soon ...

### 15.4 Advice/Useful Information

AFQMC calculations are computationally expensive and require some care in order to obtain reasonable performance. Below is a growing list of useful advice for new users followed by a sample input for a large calculation.

• Generate Cholesky-decomposed integrals with external codes instead of the 2-electron integrals directly. The generation of the Cholesky factorization is faster and consumes less memory.

• Use the hybrid algorithm for walker propagation. Set steps/substeps to adequate values to reduce the number of energy evaluations. This is essential when using large multi-determinant expansions.

• Adjust cutoffs in the wave-function and propagator blocks until desired accuracy is reached. The cost of the calculation will depend on these cutoffs.

• Adjust ncores/nWalkers to obtain better efficiency. Larger nWalkers will lead to more efficient linear algebra operations, but will increase the time per step. Larger ncores will reduce the time per step, but will reduce efficiency due to inefficiencies in the parallel implementation. For large calculations, values between 6-12 for both quantities should be reasonable, depending on architecture.

Listing 15.2: Example of sections of an AFQMC input file for a large calculation.

```xml
<Hamiltonian name="ham0" type="SparseGeneral" info="info0">
  <parameter name="filetype">hdf5</parameter>
  <parameter name="filename">fcidump.h5</parameter>
  <parameter name="cutoff_1bar">1e-6</parameter>
  <parameter name="cutoff_decomposition">1e-5</parameter>
</Hamiltonian>

<Wavefunction name="wfn0" info="info0">
  <ImpSamp name="impsamp0" type="PureSD" init="ground" >
    <parameter name="filetype">none</parameter>
    <parameter name="cutoff">1e-6</parameter>
  </ImpSamp>
</Wavefunction>
```
15.5 Using PySCF to generate integrals for AFQMC

PySCF (https://github.com/sunqm/pyscf) is a collection of electronic structure programs powered by Python. It is the recommended program for the generation of input for AFQMC calculations in QMCPACK. We refer the reader to the documentation of the code (http://sunqm.github.io/pyscf/) for a detailed description of the features and the functionality of the code. While the notes below are not meant to replace a detailed study of the PySCF documentation, these notes describe useful knowledge and tips in the use of pyscf for the generation of input for QMCPACK.

For molecular systems or periodic calculations at the Gamma point, PySCF provides a routine that generates the integral file in Molpro’s FCIDUMP format, which contains all the information needed to run AFQMC with a single determinant trial wave-function. Below is an example using this routine to generate the FCIDUMP file for an 8-atom unit cell of carbon in the diamond structure with HF orbitals. For a detailed description, see PySCF’s documentation.

Listing 15.3: Simple example showing how to generate FCIDUMP files with PySCF

```python
import numpy
from pyscf.tools import fcidump
from pyscf.pbc import gto, scf, tools

cell = gto.Cell()
cell.a = '"
  3.5668  0  0
  0  3.5668  0
  0  0  3.5668"
cell.atom = '"
  C  0.  0.  0.
  C  0.8917  0.8917  0.8917
  C  1.7834  1.7834  0.
  C  2.6751  2.6751  0.8917
  C  1.7834  0.  1.7834
  C  2.6751  0.8917  2.6751"
```
C 0.1.7834 1.7834
C 0.8917 2.6751 2.6751'''
cell.basis = 'gth-szv'
cell.pseudo = 'gth-pade'
cell.gs = [10]*3 # for testing purposes, must be increased for converged results
cell.verbose = 4
cell.build()

mf = scf.RHF(cell)
ehf = mf.kernel()
print("HF energy (per unit cell) = %.17g" % ehf)

c = mf.mo_coeff
h1e = reduce(numpy.dot, (c.T, mf.get_hcore(), c))
eri = mf.with_df.ao2mo(c, compact=True)

# nuclear energy + electronic ewald
e0 = cell.energy_nuc() + tools.pbc.madelung(cell, numpy.zeros(3))*cell.nelectron*-.5
fcidump.from_integrals('fcidump.dat', h1e, eri, c.shape[1], cell.nelectron, ms=0, tol=1e-8, nuc=e0)
<table>
<thead>
<tr>
<th>Name</th>
<th>Data Type</th>
<th>Values</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>NMO</td>
<td>integer</td>
<td>≥ 0</td>
<td>no</td>
<td>number of molecular orbitals</td>
</tr>
<tr>
<td>NAEA</td>
<td>integer</td>
<td>≥ 0</td>
<td>no</td>
<td>number of active electrons of spin up</td>
</tr>
<tr>
<td>NAEB</td>
<td>integer</td>
<td>≥ 0</td>
<td>no</td>
<td>number of active electrons of spin down</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Parameters in Hamiltonian</th>
<th>Name</th>
<th>Data Type</th>
<th>Values</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>type</td>
<td>argument</td>
<td>SparseGeneral</td>
<td>no</td>
<td>type of Hamiltonian</td>
</tr>
<tr>
<td>info</td>
<td>info</td>
<td>argument</td>
<td></td>
<td></td>
<td>name of AFQMCInfo block</td>
</tr>
<tr>
<td>filename</td>
<td>filename</td>
<td>string</td>
<td></td>
<td>no</td>
<td>name of file with the hamiltonian</td>
</tr>
<tr>
<td>filetype</td>
<td>filetype</td>
<td>string</td>
<td>fcidump</td>
<td>no</td>
<td>ASCII based format of Molpro, VASP, PySCF, etc.</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>hdf5</td>
<td></td>
<td>native HDF5-based format of QMCPACK</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Parameters in Wavefunction</th>
<th>Name</th>
<th>Data Type</th>
<th>Values</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>info</td>
<td>info</td>
<td>argument</td>
<td></td>
<td></td>
<td>name of AFQMCInfo block</td>
</tr>
<tr>
<td>ImpSamp</td>
<td>ImpSamp</td>
<td>xml-block</td>
<td></td>
<td>no</td>
<td>defines the trial wave-function</td>
</tr>
<tr>
<td>type</td>
<td>type</td>
<td>argument</td>
<td>PureSD</td>
<td>no</td>
<td>single slater determinant trial wave-function</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>MultiPureSD</td>
<td></td>
<td>linear combination of Slater Determinants</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>GenSD</td>
<td></td>
<td>single determinant w/o rotated 2-e integrals</td>
</tr>
<tr>
<td>filetype</td>
<td>filetype</td>
<td>string</td>
<td>ascii</td>
<td>no</td>
<td>ASCII data file type</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>hdf5</td>
<td></td>
<td>HDF5 data file type</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>none</td>
<td></td>
<td>no input file needed, requires init=“ground”</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Parameters in WalkerSet</th>
<th>Name</th>
<th>Data Type</th>
<th>Values</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>type</td>
<td>argument</td>
<td>distributed</td>
<td>no</td>
<td>type of walker container: standard</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Parameters in Propagator</th>
<th>Name</th>
<th>Data Type</th>
<th>Values</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>type</td>
<td>type</td>
<td>argument</td>
<td>afqmc</td>
<td>afqmc</td>
<td>type of propgator</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>vmc</td>
<td></td>
<td>not yet functioning</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Parameters in execute</th>
<th>Name</th>
<th>Data Type</th>
<th>Values</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>info</td>
<td>info</td>
<td>argument</td>
<td></td>
<td></td>
<td>name of AFQMCInfo block</td>
</tr>
<tr>
<td>nWalkers</td>
<td>nWalkers</td>
<td>integer</td>
<td>≥ 0</td>
<td>5</td>
<td>initial number of walkers per task group</td>
</tr>
<tr>
<td>timestep</td>
<td>timestep</td>
<td>real</td>
<td>&gt; 0</td>
<td>0.01</td>
<td>time step in 1/a.u.</td>
</tr>
<tr>
<td>blocks</td>
<td>blocks</td>
<td>integer</td>
<td>≥ 0</td>
<td>100</td>
<td>number of blocks</td>
</tr>
<tr>
<td>step</td>
<td>step</td>
<td>integer</td>
<td>&gt; 0</td>
<td>1</td>
<td>number of steps within a block</td>
</tr>
<tr>
<td>substep</td>
<td>substep</td>
<td>integer</td>
<td>&gt; 0</td>
<td>1</td>
<td>number of substeps within a step</td>
</tr>
</tbody>
</table>

Table 15.1: Input options for AFQMC in QMCPACK
Chapter 16

Examples

WARNING: THESE EXAMPLES ARE NOT CONVERGED! YOU MUST CONVERGE PARAMETERS (SIMULATION CELL SIZE, JASTROW PARAMETER NUMBER/CUTOFF, TWIST NUMBER, DMC TIME STEP, DFT PLANE WAVE CUTOFF, DFT K-POINT MESH, ETC.) FOR REAL CALCULATIONS!

The following examples should run in serial on a modern workstation in a few hours.

16.1 Using QMCPACK directly

In examples/molecules, there are the following examples. Each directory also contains a README file with more details.

<table>
<thead>
<tr>
<th>Directory</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>H2O</td>
<td>H2O molecule from GAMESS orbitals</td>
</tr>
<tr>
<td>He</td>
<td>Helium atom with simple wavefunctions</td>
</tr>
</tbody>
</table>

16.2 Using Nexus

For more information about Nexus, see the User Guide in nexus/documentation.

For Python to find the Nexus library, the PYTHONPATH environment variable should be set to <QMCPACK source>/nexus/library. For these examples to work properly, the executables for Quantum ESPRESSO and QMCPACK either need to be on the path, or the paths in the script should be adjusted.

These examples can be found under the nexus/examples/qmcpack directory.

<table>
<thead>
<tr>
<th>Directory</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>diamond</td>
<td>Bulk diamond with VMC</td>
</tr>
<tr>
<td>graphene</td>
<td>Graphene sheet with DMC</td>
</tr>
<tr>
<td>c20</td>
<td>C20 cage molecule</td>
</tr>
<tr>
<td>oxygen_dimer</td>
<td>Binding curve for O2 molecule</td>
</tr>
<tr>
<td>H2O</td>
<td>H2O molecule with Quantum ESPRESSO orbitals</td>
</tr>
<tr>
<td>LiH</td>
<td>LiH crystal with Quantum ESPRESSO orbitals</td>
</tr>
</tbody>
</table>
Chapter 17

Lab 1: Monte Carlo Statistical Analysis

17.1 Topics covered in this Lab

This lab focuses on the basics of analyzing data from Monte Carlo (MC) calculations. In this
lab, participants will use data from VMC calculations of a simple one-electron system with an
analytically soluble system (the ground state of the hydrogen atom) to understand how to interpret
a MC situation. Most of these analyses will also carry over to diffusion Monte Carlo (DMC)
simulations. Topics covered include:

- averaging Monte Carlo variables
- the statistical error bar of mean values
- effects of autocorrelation and variance on the error bar
- the relationship between Monte Carlo timestep and autocorrelation
- the use of blocking to reduce autocorrelation
- the significance of the acceptance ratio
- the significance of the sample size
- how to determine whether a Monte Carlo run was successful
- the relationship between wavefunction quality and variance
- gauging the efficiency of Monte Carlo runs
- the cost of scaling up to larger system sizes

17.2 Lab directories and files

labs/lab1_qmc_statistics/

atom
├── H.s000.scalar.dat
└── H.xml

- H atom VMC calculation
- H atom VMC data
- H atom VMC input file
autocorrelation - varying autocorrelation
- H.dat - data for gnuplot
- H.plt - gnuplot for time step vs. E_L, tau_c
- H.s000.scalar.dat - H atom VMC data: time step = 10
- H.s001.scalar.dat - H atom VMC data: time step = 5
- H.s002.scalar.dat - H atom VMC data: time step = 2
- H.s003.scalar.dat - H atom VMC data: time step = 1
- H.s004.scalar.dat - H atom VMC data: time step = 0.5
- H.s005.scalar.dat - H atom VMC data: time step = 0.2
- H.s006.scalar.dat - H atom VMC data: time step = 0.1
- H.s007.scalar.dat - H atom VMC data: time step = 0.05
- H.s008.scalar.dat - H atom VMC data: time step = 0.02
- H.s009.scalar.dat - H atom VMC data: time step = 0.01
- H.s010.scalar.dat - H atom VMC data: time step = 0.005
- H.s011.scalar.dat - H atom VMC data: time step = 0.002
- H.s012.scalar.dat - H atom VMC data: time step = 0.001
- H.s013.scalar.dat - H atom VMC data: time step = 0.0005
- H.s014.scalar.dat - H atom VMC data: time step = 0.0002
- H.s015.scalar.dat - H atom VMC data: time step = 0.0001
- H.xml - H atom VMC input file

average
- Python scripts for average/std. dev.
  - average.py - average five E_L from H atom VMC
  - stddev2.py - standard deviation using (E_L)^2
  - stddev.py - standard deviation around the mean

basis - varying basis set for orbitals
- H__exact.s000.scalar.dat - H atom VMC data using STO basis
- H_STO-2G.s000.scalar.dat - H atom VMC data using STO-2G basis
- H_STO-3G.s000.scalar.dat - H atom VMC data using STO-3G basis
- H_STO-6G.s000.scalar.dat - H atom VMC data using STO-6G basis

blocking - varying block/step ratio
- H.dat - data for gnuplot
- H.plt - gnuplot for N_block vs. E, tau_c
- H.s000.scalar.dat - H atom VMC data 50000:1 blocks:steps
- H.s001.scalar.dat - " " " " 25000:2 blocks:steps
- H.s002.scalar.dat - " " " " 12500:4 blocks:steps
- H.s003.scalar.dat - " " " " 6250: 8 blocks:steps
- H.s004.scalar.dat - " " " " 3125:16 blocks:steps
- H.s005.scalar.dat - " " " " 250:20 blocks:steps
- H.s006.scalar.dat - " " " " 125:40 blocks:steps
- H.s007.scalar.dat - " " " " 100:50 blocks:steps
- H.s008.scalar.dat - " " " " 50:100 blocks:steps
- H.s009.scalar.dat - " " " " 25:200 blocks:steps
- H.s010.scalar.dat - " " " " 12.5:400 blocks:steps
- H.s011.scalar.dat - " " " " 100:500 blocks:steps
- H.s012.scalar.dat - " " " " 50:1000 blocks:steps
- H.s013.scalar.dat - " " " " 40:1250 blocks:steps
- H.s014.scalar.dat - " " " " 20:2500 blocks:steps
- H.s015.scalar.dat - " " " " 10:5000 blocks:steps
- H.xml - H atom VMC input file

blocks - varying total number of blocks
- H.dat - data for gnuplot
- H.plt - gnuplot for N_block vs. E
- H.s000.scalar.dat - H atom VMC data 500 blocks
- H.s001.scalar.dat - " " " " 2000 blocks
17.3 Atomic units

QMCPACK operates in Hartree atomic units to reduce the number of factors in the Schrödinger equation. Thus, the unit of length is the bohr (5.291772 × 10⁻¹¹ m = 0.529177 Å); the unit of energy is the hartree (4.359744 × 10⁻¹⁸ J = 27.211385 eV). The energy of the ground state of the hydrogen atom in these units is -0.5 hartrees.

17.4 Reviewing statistics

We will practice taking the average (mean) and standard deviation of some Monte Carlo data by hand to review the basic definitions.

Enter Python’s command line by typing `python [Enter]`. You will see a prompt “>>”.

The mean of a data set is given by:

\[
\bar{x} = \frac{1}{N} \sum_{i=1}^{N} x_i \quad (17.1)
\]

To calculate the average of five local energies from a MC calculation of the ground state of an
electron in the hydrogen atom, input (truncate at the thousandths place if you cannot copy and
paste; script versions are also available in the average directory):

\[
\left( (-0.45298911858) + (-0.45481953564) + (-0.48066105923) + (-0.47316713469) \\
+ (-0.4620473302) \right)/5.
\]

Then, press [Enter] to get:

```python
>>> ((-0.45298911858) + (-0.45481953564) + (-0.48066105923) + \\
(-0.47316713469) + (-0.4620473302))/5.
-0.46473683566800006
```

To understand the significance of the mean, we also need the standard deviation around the
mean of the data (also called the error bar), given by:

\[
\sigma = \sqrt{\frac{1}{N(N-1)} \sum_{i=1}^{N} (x_i - \bar{x})^2}
\]

(17.2)

To calculate the standard deviation around the mean (-0.464736835668) of these five data points,
put in:

\[
(\frac{1}{5 \times (5 - 1)}) \times (\left(-0.45298911858 - (-0.464736835668)\right)^2 + \\
\left(-0.45481953564 - (-0.464736835668)\right)^2 + \left(-0.48066105923 - (-0.464736835668)\right)^2 + \\
\left(-0.47316713469 - (-0.464736835668)\right)^2 + \left(-0.4620473302 - (-0.464736835668)\right)^2) \right)^{0.5}
\]

Then, press [Enter] to get:

```python
>>> ( (1./(5.*(5.-1.))) * ( (-0.45298911858-(-0.464736835668))**2 + \\
(-0.45481953564-(-0.464736835668))**2 + (-0.48066105923-(-0.464736835668))**2 + \\
(-0.47316713469-(-0.464736835668))**2 + (-0.4620473302-(-0.464736835668))**2 ) )**0.5
0.0053303187464332066
```

Thus, we might report this data as having a value -0.465 +/- 0.005 hartrees. This calculation
of the standard deviation assumes that the average for this data is fixed, but we may continually
add Monte Carlo samples to the data so it is better to use an estimate of the error bar that does
not rely on the overall average. Such an estimate is given by:

\[
\tilde{\sigma} = \sqrt{\frac{1}{N - 1} \sum_{i=1}^{N} [(x_i^2) - (x_i)^2]}
\]

(17.3)

To calculate the standard deviation with this formula, input the following, which includes the
square of the local energy calculated with each corresponding local energy:

\[
(1./(5.-1.)) \times (0.60984565298-(-0.45298911858)**2) + \\
(0.61641291630-(-0.45481953564)**2) + (1.35860151160-(-0.48066105923)**2) + \\
(0.78720769003-(-0.47316713469)**2) + (0.56393677687-(-0.4620473302)**2) \right) \right)^{0.5}
\]

and press [Enter] to get:
This much larger standard deviation, acknowledging that the mean of this small data set is not the average in the limit of infinite sampling more accurately, reports the value of the local energy as -0.5 +/- 0.8 hartrees.

Type `quit()` and press `[Enter]` to exit the Python command line.

17.5 Inspecting Monte Carlo data

QMCPACK outputs data from MC calculations into files ending in scalar.dat. Several quantities are calculated and written for each block of Monte Carlo steps in successive columns to the right of the step index.

Change directories to `atom`, and open the file ending in scalar.dat with a text editor (e.g., `vi *scalar.dat` or `emacs *scalar.dat`). If possible, adjust the terminal so that lines do not wrap. The data will begin as follows (broken into three groups to fit on this page):

<table>
<thead>
<tr>
<th>#</th>
<th>index</th>
<th>LocalEnergy</th>
<th>LocalEnergy_sq</th>
<th>LocalPotential</th>
</tr>
</thead>
<tbody>
<tr>
<td>...</td>
<td>0</td>
<td>-4.5298911858e-01</td>
<td>6.0984565298e-01</td>
<td>-1.1708693521e+00</td>
</tr>
<tr>
<td>1</td>
<td>-4.5481953564e-01</td>
<td>6.1641291630e-01</td>
<td>-1.1863425644e+00</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>-4.8066105923e-01</td>
<td>1.3586015116e+00</td>
<td>-1.176646209e+00</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>-4.7316713469e-01</td>
<td>7.8720769003e-01</td>
<td>-1.1799481122e+00</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>-4.6204733002e-01</td>
<td>5.6393677687e-01</td>
<td>-1.1619244081e+00</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>-4.4313854290e-01</td>
<td>6.0831516179e-01</td>
<td>-1.2064503401e+00</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>-4.5064926960e-01</td>
<td>5.9891422196e-01</td>
<td>-1.1521370176e+00</td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>-4.5687452611e-01</td>
<td>5.8139614676e-01</td>
<td>-1.1423627617e+00</td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>-4.5018503739e-01</td>
<td>8.417849706e-01</td>
<td>-1.1842075439e+00</td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>-4.3862013841e-01</td>
<td>5.547715836e-01</td>
<td>-1.2080979177e+00</td>
<td></td>
</tr>
</tbody>
</table>

The first line begins with a `#`, indicating that this line does not contain MC data but rather the labels of the columns. After a blank line, the remaining lines consist of the MC data. The first column, labeled index, is an integer indicating which block of MC data is on that line. The second column contains the quantity usually of greatest interest from the simulation, the local energy. Since this simulation did not use the exact ground state wave function, it does not produce -0.5 hartrees as the local energy although the value lies within about 10%. The value of the local energy fluctuates from block to block and the closer the trial wave function is to the ground state, the smaller these fluctuations will be. The next column contains an important ingredient in estimating the error in the MC average—the square of the local energy—found by evaluating the square of the Hamiltonian.

<table>
<thead>
<tr>
<th>...</th>
<th>Kinetic</th>
<th>Coulomb</th>
<th>BlockWeight</th>
<th>...</th>
</tr>
</thead>
<tbody>
<tr>
<td>7.1788023352e-01</td>
<td>-1.1708693521e+00</td>
<td>1.28000000000e+04</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
The fourth column from the left consists of the values of the local potential energy. In this simulation, it is identical to the Coulomb potential (contained in the sixth column) because the one electron in the simulation has only the potential energy coming from its interaction with the nucleus. In many-electron simulations, the local potential energy contains contributions from the electron-electron Coulomb interactions and the nuclear potential or pseudopotential. The fifth column contains the local kinetic energy value for each MC block, obtained from the Laplacian of the wave function. The sixth column shows the local Coulomb interaction energy. The seventh column displays the weight each line of data has in the average (the weights are identical in this simulation).

The eighth column shows the CPU time (in seconds) to calculate the data in that line. The ninth column from the left contains the acceptance ratio (1 being full acceptance) for Monte Carlo steps in that line’s data. Other than the block weight, all quantities vary from line to line.

Exit the text editor (\[Esc\] :q! \[Enter\] in vi, [Ctrl]-x [Ctrl]-c in emacs).

### 17.6  Averaging quantities in the MC data

QMCPACK includes the qmca Python tool to average quantities in the scalar.dat file (and also the dmc.dat file of DMC simulations). Without any flags, qmca will output the average of each column with a quantity in the scalar.dat file as follows.

Execute qmca by `qmca *.scalar.dat`, which for this data outputs:

```
H series 0
LocalEnergy = -0.45446 +/- 0.00057  0.00057
Variance = 0.8625000000e-01  0.018
Kinetic = 0.8625000000e-01  0.0020
```
<table>
<thead>
<tr>
<th>Quantity</th>
<th>Value</th>
<th>Error</th>
</tr>
</thead>
<tbody>
<tr>
<td>LocalPotential</td>
<td>-1.1910 +/- 0.0016</td>
<td></td>
</tr>
<tr>
<td>Coulomb</td>
<td>-1.1910 +/- 0.0016</td>
<td></td>
</tr>
<tr>
<td>LocalEnergy_sq</td>
<td>0.736 +/- 0.018</td>
<td></td>
</tr>
<tr>
<td>BlockWeight</td>
<td>12800.00000000 +/- 0.00000000</td>
<td></td>
</tr>
<tr>
<td>BlockCPU</td>
<td>0.00582002 +/- 0.00000067</td>
<td></td>
</tr>
<tr>
<td>AcceptRatio</td>
<td>0.985508 +/- 0.000048</td>
<td></td>
</tr>
<tr>
<td>Efficiency</td>
<td>0.00000000 +/- 0.00000000</td>
<td></td>
</tr>
</tbody>
</table>

After one blank, qmca prints the title of the subsequent data, gleaned from the data file name. In this case, H.s000.scalar.dat became “H series 0”. Everything before the first “." will be interpreted as the title, and the number between “.” and the next “.”” will be interpreted as the series number.

The first column under the title is the name of each quantity qmca averaged. The column to the right of the equal signs contains the average for the quantity of that line, and the column to the right of the plus-slash-minus is the statistical error bar on the quantity. All quantities calculated from MC simulations have and must be reported with a statistical error bar!

Two new quantities not present in the scalar.dat file are computed by qmca from the data–variance and efficiency. We will look at these later in this lab.

To view only one value, qmca takes the -q (quantity) flag. For example, the output of `qmc -q LocalEnergy *.scalar.dat` in this directory produces a single line of output:

```
H series 0 LocalEnergy = -0.454460 +/- 0.000568
```

Type `qmc --help` to see the list of all quantities and their abbreviations.

### 17.7 Evaluating MC simulation quality

There are several aspects of a MC simulation to consider in deciding how well it went. Besides the deviation of the average from an expected value (if there is one), the stability of the simulation in its sampling, the autocorrelation between MC steps, the value of the acceptance ratio (accepted steps over total proposed steps), and the variance in the local energy all indicate the quality of a MC simulation. We will look at these one by one.

#### 17.7.1 Tracing MC quantities

Visualizing the evolution of MC quantities over the course of the simulation by a trace offers a quick picture of whether the random walk had expected behavior. qmca plots traces with the -t flag.

Type `qmc -q e -t H.s000.scalar.dat`, which produces a graph of the trace of the local energy:
The solid black line connects the values of the local energy at each MC block (labeled “samples”). The average value is marked with a horizontal, solid red line. One standard deviation above and below the average are marked with horizontal, dashed red lines.

The trace of this run is largely centered around the average with no large-scale oscillations or major shifts, indicating a good quality MC run.

Try tracing the kinetic and potential energies, seeing that their behavior is comparable to the total local energy.

Change to directory problematic and type `qmca -q e -t H.s000.scalar.dat` to produce this graph:
Here, the local energy samples cluster around the expected -0.5 hartrees for the first 150 samples or so and then begin to oscillate more wildly and increase erratically toward 0, indicating a poor quality MC run.

Again, trace the kinetic and potential energies in this run and see how their behavior compares to the total local energy.

17.7.2 Blocking away autocorrelation

*Autocorrelation* occurs when a given MC step biases subsequent MC steps, leading to samples that are not statistically independent. We must take this autocorrelation into account in order to obtain accurate statistics. *qmca* outputs autocorrelation when given the --sac flag.

Change to directory autocorrelation and type `qmca -q e --sac H.s000.scalar.dat`.

```
H series 0  LocalEnergy = -0.454982 +/- 0.000430  1.0
```

The value after the error bar on the quantity is the autocorrelation (1.0 in this case).

Proposing too small a step in configuration space, the MC time step, can lead to autocorrelation since the new samples will be in the neighborhood of previous samples. Type `grep timestep H.xml` to see the varying time step values in this QMCPACK input file (H.xml):

```
<parameter name="timestep">10</parameter>
<parameter name="timestep">5</parameter>
<parameter name="timestep">2</parameter>
<parameter name="timestep">1</parameter>
<parameter name="timestep">0.5</parameter>
<parameter name="timestep">0.2</parameter>
<parameter name="timestep">0.1</parameter>
<parameter name="timestep">0.05</parameter>
```
Generally, as the time step decreases, the autocorrelation will increase (caveat: very large time steps will also have increasing autocorrelation). To see this, type `qmca -q e --sac *.scalar.dat` to see the energies and autocorrelation times, then plot with gnuplot by inputting `gnuplot H.plt`:

![Graph showing autocorrelation and error bars increasing with time step](image.png)

The error bar also increases with the autocorrelation. Press `q [Enter]` to quit gnuplot.

To get around the bias of autocorrelation, we group the MC steps into blocks, take the average of the data in the steps of each block, and then finally average the averages in all the blocks. QMCPACK outputs the block averages as each line in the scalar.dat file. (For DMC simulations, in addition to the scalar.dat, QMCPACK outputs the quantities at each step to the dmc.dat file, which permits reblocking the data differently from the specification in the input file.)

Change directories to `blocking`. Here we look at the time step of the last data set in the autocorrelation directory. Verify this by typing `grep timestep H.xml` to see that all values are set to 0.001. Now to see how we will vary the blocking, type `grep -A1 blocks H.xml`. The parameter “steps” indicates the number of steps per block, and the parameter “blocks” gives the number of blocks. For this comparison, the total number of MC steps (equal to the product of “steps” and “blocks”) is fixed at 50000. Now check the effect of blocking on autocorrelation–type `qmca -q e --sac *scalar.dat` to see the data and `gnuplot H.plt` to visualize the data:
The greatest number of steps per block produces the smallest autocorrelation time. The larger number of blocks over which to average at small step-per-block number masks the corresponding increase in error bar with increasing autocorrelation.

Press \texttt{q \[Enter]} to quit gnuplot.

### 17.7.3 Balancing autocorrelation and acceptance ratio

Adjusting the time step value also affects the ratio of accepted steps to proposed steps. Stepping nearby in configuration space implies that the probability distribution is similar and thus more likely to result in an accepted move. Keeping the acceptance ratio high means the algorithm is efficiently exploring configuration space and not sticking at particular configurations. Return to the autocorrelation directory. Refresh your memory on the time steps in this set of simulations by \texttt{grep timestep H.xml}. Then, type \texttt{qmca \ -q ar *scalar.dat} to see the acceptance ratio as it varies with decreasing time step:

<table>
<thead>
<tr>
<th>H series</th>
<th>AcceptRatio</th>
<th>+/-</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>0.047646</td>
<td>0.000206</td>
</tr>
<tr>
<td>1</td>
<td>0.125361</td>
<td>0.000308</td>
</tr>
<tr>
<td>2</td>
<td>0.328590</td>
<td>0.000340</td>
</tr>
<tr>
<td>3</td>
<td>0.535708</td>
<td>0.000313</td>
</tr>
<tr>
<td>4</td>
<td>0.732537</td>
<td>0.000234</td>
</tr>
<tr>
<td>5</td>
<td>0.903498</td>
<td>0.000156</td>
</tr>
<tr>
<td>6</td>
<td>0.961506</td>
<td>0.000083</td>
</tr>
<tr>
<td>7</td>
<td>0.985499</td>
<td>0.000051</td>
</tr>
<tr>
<td>8</td>
<td>0.996251</td>
<td>0.000025</td>
</tr>
<tr>
<td>9</td>
<td>0.998638</td>
<td>0.000014</td>
</tr>
<tr>
<td>10</td>
<td>0.999515</td>
<td>0.000009</td>
</tr>
<tr>
<td>11</td>
<td>0.999884</td>
<td>0.000004</td>
</tr>
</tbody>
</table>
By series 8 (time step = 0.02), the acceptance ratio is in excess of 99%.

Considering the increase in autocorrelation and subsequent increase in error bar as time step decreases, it is important to choose a time step that trades off appropriately between acceptance ratio and autocorrelation. In this example, a time step of 0.02 occupies a spot where acceptance ratio is high (99.6%), and autocorrelation is not appreciably larger than the minimum value (1.4 vs. 1.0).

### 17.7.4 Considering variance

Besides autocorrelation, the dominant contributor to the error bar is the variance in the local energy. The variance measures the fluctuations around the average local energy, and, as the fluctuations go to zero, the wave function reaches an exact eigenstate of the Hamiltonian. *qmca* calculates this from the local energy and local energy squared columns of the scalar.dat.

Type `qmca -q v H.s009.scalar.dat` to calculate the variance on the run with time step balancing autocorrelation and acceptance ratio:

| H series 9 Variance = 0.513570 +/- 0.010589 |

Just as the total energy doesn’t tell us much by itself, neither does the variance. However, comparing the ratio of the variance to the energy indicates how the magnitude of the fluctuations compares to the energy itself. Type `qmca -q ev H.s009.scalar.dat` to calculate the energy and variance on the run side by side with the ratio:

<table>
<thead>
<tr>
<th>LocalEnergy</th>
<th>Variance</th>
<th>ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>-0.454460 +/- 0.000568</td>
<td>0.529496 +/- 0.018445</td>
<td>1.1651</td>
</tr>
</tbody>
</table>

1.1651 is a very high ratio indicating the square of the fluctuations is on average larger than the value itself. In the next section, we will approach ways to improve the variance that subsequent labs will build upon.

### 17.8 Reducing statistical error bars

#### 17.8.1 Increasing MC sampling

Increasing the number of MC samples in a data set reduces the error bar as the inverse of the square root of the number of samples. There are two ways to increase the number of MC samples in a simulation: running more samples in parallel and increasing the number of blocks (with fixed number of steps per block, this increases the total number of MC steps).

To see the effect of the running more samples in parallel, change to the directory nodes. The series here increases the number of nodes by factors of four from 32 to 128 to 512. Type `qmca -q ev *scalar.dat` and note the change in the error bar on the local energy as the number of nodes. Visualize this with gnuplot H.plt:
Increasing the number of blocks, unlike running in parallel, increases the total CPU time of the simulation.

Press q [Enter] to quit gnuplot.

To see the effect of increasing the block number, change to the directory blocks. To see how we will vary the number of blocks, type `grep -A1 blocks H.xml`. The number of steps remains fixed, thus increasing the total number of samples. Visualize the tradeoff by inputting `gnuplot H.plt`:
Press `q [Enter]` to quit gnuplot.

### 17.8.2 Improving the basis set

In all of the above examples, we are using the sum of two gaussian functions (STO-2G) to approximate what should be a simple decaying exponential (STO = Slater-type orbital) for the wave function of the ground state of the hydrogen atom. The sum of multiple copies of a function varying each copy’s width and amplitude with coefficients is called a **basis set**. As we add gaussians to the basis set, the approximation improves, the variance goes toward zero and the energy goes to -0.5 hartrees. In nearly every other case, the exact function is unknown, and we add basis functions until the total energy does not change within some threshold.

Change to the directory `basis` and look at the total energy and variance as we change the wave function by typing `qmca -q ev H_*`:

<table>
<thead>
<tr>
<th>ratio</th>
<th>LocalEnergy</th>
<th>Variance</th>
</tr>
</thead>
<tbody>
<tr>
<td>H_STO-2G</td>
<td>series 0 -0.454460 +/- 0.000568</td>
<td>0.529496 +/- 0.018445</td>
</tr>
<tr>
<td></td>
<td>1.1651</td>
<td></td>
</tr>
<tr>
<td>H_STO-3G</td>
<td>series 0 -0.465386 +/- 0.000502</td>
<td>0.410491 +/- 0.010051</td>
</tr>
<tr>
<td></td>
<td>0.8820</td>
<td></td>
</tr>
<tr>
<td>H_STO-6G</td>
<td>series 0 -0.471332 +/- 0.000491</td>
<td>0.213919 +/- 0.012954</td>
</tr>
<tr>
<td></td>
<td>0.4539</td>
<td></td>
</tr>
<tr>
<td>H_exact</td>
<td>series 0 -0.500000 +/- 0.000000</td>
<td>0.000000 +/- 0.000000</td>
</tr>
<tr>
<td></td>
<td>-0.0000</td>
<td></td>
</tr>
</tbody>
</table>

`qmca` also puts out the ratio of the variance to the local energy in a column to the right of the variance error bar. A typical high quality value for this ratio is lower than 0.1 or so—none of these
few-gaussian wave functions satisfy that rule of thumb.

Use qmca to plot the trace of the local energy, kinetic energy, and potential energy of H\textsubscript{2}\textsubscript{exact} – the total energy is constantly -0.5 hartree even though the kinetic and potential energies fluctuate from configuration to configuration.

### 17.8.3 Adding a Jastrow factor

Another route to reducing the variance is the introduction of a Jastrow factor to account for electron-electron correlation (not the statistical autocorrelation of Monte Carlo steps but the physical avoidance that electrons have of one another). To do this, we will switch to the hydrogen dimer with the exact ground state wave function of the atom (STO basis) – this will not be exact for the dimer. The ground state energy of the hydrogen dimer is -1.174 hartrees.

Change directories to `dimer` and put in `qmca -q ev *scalar.dat` to see the result of adding a simple, one-parameter Jastrow to the STO basis for the hydrogen dimer at experimental bond length:

<table>
<thead>
<tr>
<th>LocalEnergy</th>
<th>Variance</th>
</tr>
</thead>
<tbody>
<tr>
<td>H\textsubscript{2}_STO_no_jastrow</td>
<td>-0.876548 +/- 0.005313</td>
</tr>
<tr>
<td>H\textsubscript{2}_STO_with_jastrow</td>
<td>-0.912763 +/- 0.004470</td>
</tr>
</tbody>
</table>

The energy reduces by 0.044 +/- 0.006 hartrees and the variance by 0.19 +/- 0.02. This is still 20% above the ground state energy, and subsequent labs will cover how to improve on this with improved forms of the wave function that capture more of the physics.

### 17.9 Scaling to larger numbers of electrons

#### 17.9.1 Calculating the efficiency

The inverse of the product of CPU time and the variance measures the efficiency of an MC calculation. Use qmca to calculate efficiency by typing `qmca -q eff *scalar.dat` to see the efficiency of these two H\textsubscript{2} calculations:

<p>| | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>H\textsubscript{2}_STO_no_jastrow</td>
<td>Efficiency = 16698.725453 +/- 0.000000</td>
<td></td>
</tr>
<tr>
<td>H\textsubscript{2}_STO_with_jastrow</td>
<td>Efficiency = 52912.365609 +/- 0.000000</td>
<td></td>
</tr>
</tbody>
</table>

The Jastrow factor increased the efficiency in these calculations by a factor of three, largely through the reduction in variance (check the average block CPU time to verify this claim).

#### 17.9.2 Scaling up

To see how MC scales with increasing particle number, change directories to `size`. Here are the data from runs of increasing number of electrons for H, H\textsubscript{2}, C, CH\textsubscript{4}, C\textsubscript{2}, C\textsubscript{2}H\textsubscript{4}, (CH\textsubscript{4})\textsubscript{2}, and (C\textsubscript{2}H\textsubscript{4})\textsubscript{2} using the STO-6G basis set for the orbitals of the Slater determinant. The file names begin with the number of electrons simulated for those data.

Use `qmca -q bc *scalar.dat` to see that the CPU time per block increases with number of electrons in the simulation, then plot the total CPU time of the simulation by `gnuplot Nelectron_tCPU.plt`:
The green pluses represent the CPU time per block at each electron number. The red line is a quadratic fit to those data. For a fixed basis set size, we expect the time to scale quadratically up to 1000s of electrons, at which point a cubic scaling term may become dominant. Knowing the scaling allows you to roughly project the calculation time for a larger number of electrons.

Press [q] [Enter] to quit gnuplot.

This isn’t the whole story, however. The variance of the energy also increases with a fixed basis set as the number of particles increases at a faster rate than the energy decreases. To see this, type `qmca -q ev *scalar.dat`:

<table>
<thead>
<tr>
<th>LocalEnergy</th>
<th>Variance</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.471352 +/- 0.000493</td>
<td>0.213020 +/-</td>
</tr>
<tr>
<td>0.898875 +/- 0.000998</td>
<td>0.545717 +/-</td>
</tr>
<tr>
<td>-37.608586 +/- 0.020453</td>
<td>184.322000 +/-</td>
</tr>
<tr>
<td>-38.821513 +/- 0.022740</td>
<td>169.797871 +/-</td>
</tr>
<tr>
<td>-72.302390 +/- 0.037691</td>
<td>491.416711 +/-</td>
</tr>
<tr>
<td>-75.488701 +/- 0.042919</td>
<td>404.218115 +/-</td>
</tr>
<tr>
<td>-58.459857 +/- 0.039309</td>
<td>498.579645 +/-</td>
</tr>
<tr>
<td>-91.567283 +/- 0.048392</td>
<td>632.114026 +/-</td>
</tr>
</tbody>
</table>
The increase in variance is not uniform, but the general trend is upward with a fixed wave function form and basis set. Subsequent labs will address how to improve the wave function in order to keep the variance manageable.
Chapter 18

Lab 2: QMC Basics

18.1 Topics covered in this Lab

This lab focuses on the basics of performing quality QMC calculations. As an example participants test an oxygen pseudopotential within DMC by calculating atomic and dimer properties, a common step prior to production runs. Topics covered include:

- converting pseudopotentials into QMCPACK’s FSATOM format
- generating orbitals with Quantum ESPRESSO
- converting orbitals into QMCPACK’s ESHDF format with pw2qmcpack
- optimizing Jastrow factors with QMCPACK
- removing DMC timestep error via extrapolation
- automating QMC workflows with Nexus
- testing pseudopotentials for accuracy

18.2 Lab outline

1. download and conversion of oxygen atom pseudopotential
2. DMC timestep study of the neutral oxygen atom
   (a) DFT orbital generation with Quantum ESPRESSO
   (b) orbital conversion with pw2qmcpack.x
   (c) optimization of Jastrow correlation factor with QMCPACK
   (d) DMC run with multiple timesteps
3. DMC timestep study of the first ionization potential of oxygen
   (a) repetition of a-d above for ionized oxygen atom
4. automated DMC calculations of the oxygen dimer binding curve
18.3 Lab directories and files

% labs/lab2_qmc_basics/

- oxygen_atom  - oxygen atom calculations
  ├── 0.q0.dft.in  - Quantum ESPRESSO input for DFT run
  ├── 0.q0.p2q.in  - pw2qmcpack.x input for orbital conversion run
  ├── 0.q0.opt.in.xml  - QMCPACK input for Jastrow optimization run
  ├── 0.q0.dmc.in.xml  - QMCPACK input file for neutral O DMC
  └── ip_conv.py  - tool to fit oxygen IP vs timestep
      └── reference  - directory w/ completed runs

- oxygen_dimer  - oxygen dimer calculations
  ├── dimer_fit.py  - tool to fit dimer binding curve
  ├── 0.dimer.py  - automation script for dimer calculations
  │ └── pseudopotentials  - directory for pseudopotentials
  │     └── reference  - directory w/ completed runs
  └── your_system  - performing calculations for an arbitrary system (yours)
    ├── example.py  - example nexus file for periodic diamond
    │ └── pseudopotentials  - directory containing C pseudopotentials
    │     └── reference  - directory w/ completed runs

18.4 Obtaining and converting a pseudopotential for oxygen

First enter the oxygen_atom directory:

```
cd labs/lab2_qmc_basics/oxygen_atom/
```

Throughout the rest of the lab, locations will be specified with respect to labs/lab2_qmc_basics (e.g. oxygen_atom).

We will use a potential from the Burkatzki-Filippi-Dolg pseudopotential database. Although the full database is available in QMCPACK distribution (trunk/pseudopotentials/BFD/), we use a BFD pseudopotential to illustrate the process of converting and testing an external potential for use with QMCPACK. To obtain the pseudopotential, go to [http://www.burkatzki.com/pseudos/index.2.html](http://www.burkatzki.com/pseudos/index.2.html) and click on the “Select Pseudopotential” button. Next click on oxygen in the periodic table. Click on the empty circle next to “V5Z” (a large gaussian basis set) and click on “Next”. Select the Gamess format and click on “Retrieve Potential”. Helpful information about the pseudopotential will be displayed. The desired portion is at the bottom (the last 7 lines). Copy this text into the editor of your choice (e.g. emacs or vi) and save it as O.BFD.gamess (be sure to include a newline at the end of the file). To transform the pseudopotential into the FSATOM XML format used by QMCPACK, use the ppconvert tool:

```
ppconvert --gamess_pot O.BFD.gamess --s_ref "1s(2)2p(4)" --p_ref "1s(2)2p(4)" --d_ref "1s(2)2p(4)" --xml O.BFD.xml
```

Observe the notation used to describe the reference valence configuration for this helium-core PP: 1s(2)2p(4). The ppconvert tool uses the following convention for the valence states: the first s state is labeled 1s (1s, 2s, 3s, ...), the first p state is labeled 2p (2p, 3p, ...), the first d state is labeled 3d (3d, 4d, ...). Copy the resulting xml file into the oxygen_atom directory.

Note: the command to convert the PP into QM Espresso’s UPF format is similar (both formats are required):
For reference, the text of O.BFD.gamess should be:

```
O-QMC GEN 2 1
3
6.00000000 1 9.29793903
55.78763416 3 8.86492204
-38.81978498 2 8.62925665
1
38.41914135 2 8.71924452
```

The full QMCPACK pseudopotential is also included in oxygen_atom/reference/O.BFD.*.

### 18.5 DFT with Quantum ESPRESSO to obtain the orbital part of the wavefunction

With the pseudopotential in hand, the next step toward a QMC calculation is to obtain the Fermionic part of the wavefunction, in this case a single Slater determinant constructed from DFT-LDA orbitals for a neutral oxygen atom. If you had trouble with the pseudopotential conversion step, pre-converted pseudopotential files are located in the oxygen_atom/reference directory.

Quantum ESPRESSO input for the DFT-LDA ground state of the neutral oxygen atom can be found in `O.q0.dft.in` and also listing 18.1 below. Setting `wf_collect=.true.` instructs Quantum Espresso to write the orbitals to disk at the end of the run. Option `wf_collect=.true.` may be a potential problem in large simulations, it is recommended to avoid it and use the converter `pw2qmcpack` in parallel, see details in Sec. 21.3.2. Note that the plane-wave energy cutoff has been set to a reasonable value of 300 Ry here (`ecutwfc=300`). This value depends on the pseudopotentials used, and in general should be selected by running DFT→(orbital conversion)→VMC with increasing energy cutoffs until the lowest VMC total energy and variance is reached.

**Listing 18.1: Quantum ESPRESSO input file for the neutral oxygen atom (O.q0.dft.in)**

```bash
&CONTROL
  calculation = 'scf'
  restart_mode = 'from_scratch'
  prefix = 'O.q0'
  outdir = './'
  pseudo_dir = './'
  disk_io = 'low'
  wf_collect = .true.
/

&SYSTEM
  cell = (1.0 0.0 0.0, 0.0 1.0 0.0, 0.0 0.0 1.0)
  ibrav = 0
  nat = 1
  ntyp = 1
  nspin = 2
  tot_charge = 0
  tot_magnetization = 2
  input_dft = 'lda'
```
Run Quantum ESPRESSO by typing

```
mpirun -np 4 pw.x -input O.q0.dft.in >&O.q0.dft.out&
```

The DFT run should take a few minutes to complete. If desired, you can track the progress of
the DFT run by typing “tail -f O.q0.dft.out”. Once finished, you should check the LDA total
energy in O.q0.dft.out by typing “grep '! ' O.q0.dft.out”. The result should be close to

```
! total energy = -31.57553905 Ry
```

The orbitals have been written in a format native to Quantum ESPRESSO in the O.q0.save
directory. We will convert them into the ESHDF format expected by QMCPACK by using the
pw2qmcpack.x tool. The input for pw2qmcpack.x can be found in the file O.q0.p2q.in and
also in listing 18.2 below.

Listing 18.2: pw2qmcpack.x input file for orbital conversion (O.q0.p2q.in)

```
&inputpp
  prefix = 'O.q0'
  outdir = './'
  write_psir = .false.
/
```

Perform the orbital conversion now by typing the following:
Upon completion of the run, a new file should be present containing the orbitals for QMC-PACK: O.q0.pwscf.h5. Template XML files for particle (O.q0.ptcl.xml) and wavefunction (O.q0.wfs.xml) inputs to QMCPACK should also be present.

18.6 Optimization with QMCPACK to obtain the correlated part of the wavefunction

The wavefunction we have obtained to this point corresponds to a non-interacting Hamiltonian. Once the Coulomb pair potential is switched on between particles, it is known analytically that the exact wavefunction has cusps whenever two particles meet spatially and in general the electrons become correlated. This is represented in the wavefunction by introducing a Jastrow factor containing at least pair correlations

\[
\Psi_{\text{Slater-Jastrow}} = e^{-J} \Psi_{\text{Slater}}
\]

(18.1)

\[
J = \sum_{\sigma \sigma'} \sum_{i<j} u^{\sigma \sigma'}_2 (|r_i - r_j|) + \sum_{ij} u^I_1 (|r_i - r_I|)
\]

(18.2)

Here \( \sigma \) is a spin variable while \( r_i \) and \( r_I \) represent electron and ion coordinates, respectively. The introduction of \( J \) into the wavefunction is similar to F12 methods in quantum chemistry, though it has been present in essentially all QMC studies since the first applications of the method (circa 1965).

How are the functions \( u^{\sigma \sigma'}_2 \) and \( u^I_1 \) obtained? Generally, they are approximated by analytical functions with several unknown parameters that are determined by minimizing the energy or variance directly within VMC. This is effective because the energy and variance reach a global minimum only for the true ground state wavefunction (Energy = \( E \equiv \langle \Psi | H | \Psi \rangle \), Variance = \( V \equiv \langle \Psi | (H - E)^2 | \Psi \rangle \)). For this exercise, we will focus on minimizing the variance.

First, we need to update the template particle and wavefunction information in O.q0.ptcl.xml and O.q0.wfs.xml. We want to simulate the O atom in open boundary conditions (the default is periodic). To do this open O.q0.ptcl.xml with your favorite text editor (e.g. emacs or vi) and replace

```xml
<parameter name="bconds">
  n n n
</parameter>
```

with

```xml
<parameter name="bconds">
  p p p
</parameter>
```

Next we will select Jastrow factors appropriate for an atom. In open boundary conditions, the B-spline Jastrow correlation functions should cut off to zero at some distance away from the atom. Open O.q0.wfs.xml and add the following cutoffs (rcut in Bohr radii) to the correlation factors:

```xml

...
These terms correspond to \( \frac{u_2^{\uparrow\downarrow}}{u_2^{\uparrow\downarrow}} \), \( u_2^{\uparrow\downarrow} \), and \( \frac{u_1^O}{u_1^I O} \), respectively. In each case, the correlation function \( (u) \) is represented by piecewise continuous cubic B-splines. Each correlation function has eight parameters which are just the values of \( u \) on a uniformly spaced grid up to \( rcut \). Initially the parameters \( (\text{coefficients}) \) are set to zero:

<table>
<thead>
<tr>
<th>coefficients id=&quot;uu&quot; type=&quot;Array&quot;</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0</td>
</tr>
</tbody>
</table>

Finally, we need to assemble particle, wavefunction, and pseudopotential information into the main QMCPACK input file (0.q0.opt.in.xml) and specify inputs for the Jastrow optimization process. Open 0.q0.opt.in.xml and write in the location of the particle, wavefunction, and pseudopotential files (“<!-- ... -->” are comments):

...  
<!-- include simulationcell and particle information from pw2qmcpqack -->  
<include href="O.q0.ptcl.xml"/>  
...  
<!-- include wavefunction information from pw2qmcpqack -->  
<include href="O.q0.wfs.xml"/>  
...  
<!-- O pseudopotential read from "O.BFD.xml" -->  
<pseudo elementType="O" href="O.BFD.xml"/>  
...

The relevant portion of the input describing the linear optimization process is

```
<loop max="MAX">
  <qmc method="linear" move="pbyp" checkpoint="-1">
    <cost name="energy"     > ECOST  </cost>
    <cost name="unreweightedvariance" > UVCOST </cost>
    <cost name="reweightedvariance" > RVCOST </cost>
    <parameter name="timestep" > TS  </parameter>
    <parameter name="samples" > SAMPLES </parameter>
    <parameter name="warmupSteps" > 50  </parameter>
    <parameter name="blocks" > 200  </parameter>
    <parameter name="subSteps" > 1    </parameter>
    <parameter name="nonlocalpp" > yes  </parameter>
    <parameter name="useBuffer" > yes  </parameter>
  </qmc>
</loop>
```

An explanation of each input variable can be found below. The remaining variables control specialized internal details of the linear optimization algorithm. The meaning of these inputs is beyond the scope of this lab and reasonable results are often obtained keeping these values fixed.
energy  Fraction of trial energy in the cost function.

unreweightedvariance  Fraction of unreweighted trial variance in the cost function. Neglecting the weights can be more robust.

rewightedvariance  Fraction of trial variance (including the full weights) in the cost function.

timestep  Timestep of the VMC random walk, determines spatial distance moved by each electron during MC steps. Should be chosen such that the acceptance ratio of MC moves is around 50% (30-70% is often acceptable). Reasonable values are often between 0.2 and 0.6 Ha$^{-1}$.

samples  Total number of MC samples collected for optimization, determines statistical error bar of cost function. Often efficient to start with a modest number of samples (50k) and then increase as needed. More samples may be required if the wavefunction contains a large number of variational parameters. MUST be be a multiple of the number of threads/cores.

warmupSteps  Number of MC steps discarded as a warmup or equilibration period of the random walk. If this is too small, it will bias the optimization procedure.

blocks  Number of average energy values written to output files. Should be greater than 200 for meaningful statistical analysis of output data (e.g. via qmca).

subSteps  Number of MC steps in between energy evaluations. Each energy evaluation is expensive so taking a few steps to decorrelate between measurements can be more efficient. Will be less efficient with many substeps.

nonlocalpp,useBuffer  If nonlocalpp="no", then nonlocal part of the pseudopotential is not included when computing the cost function. If useBuffer="yes", then temporary data is stored to speed up nonlocal pseudopotential evaluation at the expense of memory consumption.

loop max  Number of times to repeat the optimization. Using the resulting wavefunction from the previous optimization in the next one improves the results. Typical choices range between 8 and 16.

The cost function defines the quantity to be minimized during optimization. The three components of the cost function, energy, unreweighted variance, and reweighted variance should sum to one. Dedicating 100% of the cost function to unreweighted variance is often a good choice. Another common choice is to try 90/10 or 80/20 mixtures of reweighted variance and energy. Using 100% energy minimization is desirable for reducing DMC pseudopotential localization errors, but the optimization process is less stable and should only be attempted after performing several cycles of e.g. variance minimization first (the entire loop section can be duplicated with a different cost function each time).

Replace MAX, EVCOST, UVCOST, RVCOST, TS, and SAMPLES in the loop with appropriate starting values in the 0.q0.opt.in.xml input file. Perform the optimization run by typing

```
mpirun -np 4 qmcpack 0.q0.opt.in.xml >&0.q0.opt.out&
```

The run should only take a few minutes for reasonable values of loop max and samples.

Log file output will appear in 0.q0.opt.out. The beginning of each linear optimization will be marked with text similar to

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At the end of each optimization section the change in cost function, new values for the Jastrow parameters, and elapsed wallclock time are reported:

```
...
<optVariables href="O.q0.opt.s011.opt.xml">
  uu_0 6.9392504232e-01 1 1 ON 0
  uu_1 4.9690781460e-01 1 1 ON 1
  uu_2 4.0934542375e-01 1 1 ON 2
  uu_3 3.785640157e-01 1 1 ON 3
  uu_4 3.7308380014e-01 1 1 ON 4
  uu_5 3.5419786809e-01 1 1 ON 5
  uu_6 4.3139019377e-01 1 1 ON 6
  uu_7 1.9344371667e-01 1 1 ON 7
  ud_0 3.9219009713e-01 1 1 ON 8
  ud_1 1.2352664647e-01 1 1 ON 9
  ud_2 4.4048945133e-02 1 1 ON 10
  ud_3 2.1415676741e-02 1 1 ON 11
  ud_4 1.5201803731e-02 1 1 ON 12
  ud_5 2.3708169445e-02 1 1 ON 13
  ud_6 3.4279064930e-02 1 1 ON 14
  ud_7 4.334583596e-02 1 1 ON 15
  eO_0 -7.8490123937e-01 1 1 ON 16
  eO_1 -6.6726618338e-01 1 1 ON 17
  eO_2 -4.8753453838e-01 1 1 ON 18
  eO_3 -3.0913993774e-01 1 1 ON 19
  eO_4 -1.7901872177e-01 1 1 ON 20
  eO_5 -8.6199000697e-02 1 1 ON 21
  eO_6 -4.060116841e-02 1 1 ON 22
  eO_7 -4.1358075061e-03 1 1 ON 23
</optVariables>
...
```

The cost function should decrease during each linear optimization (Delta cost < 0). Try “grep OldCost *opt.out”. You should see something like this:

```
OldCost: 1.2655186572e+00 NewCost: 7.2443875597e-01 Delta Cost: -5.4107990118e-01
```
Blocked averages of energy data, including the kinetic energy and components of the potential energy, are written to scalar.dat files. The first is named “O.q0.opt.s000.scalar.dat”, with a series number of zero (s000). In the end there will be MAX of them, one for each series.

When the job has finished, use the qmca tool to assess the effectiveness of the optimization process. To look at just the total energy and the variance, type “qmca -q ev O.q0.opt*scalar*”. This will print the energy, variance, and the variance/energy ratio in Hartree units:

<table>
<thead>
<tr>
<th>ratio</th>
<th>LocalEnergy</th>
<th>Variance</th>
</tr>
</thead>
<tbody>
<tr>
<td>O.q0.opt</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.0564</td>
<td>-15.739585 +/- 0.007656</td>
<td>0.887412 +/- 0.010728</td>
</tr>
<tr>
<td>O.q0.opt</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.0201</td>
<td>-15.848347 +/- 0.004089</td>
<td>0.318490 +/- 0.006404</td>
</tr>
<tr>
<td>O.q0.opt</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.0184</td>
<td>-15.867494 +/- 0.004831</td>
<td>0.292309 +/- 0.007786</td>
</tr>
<tr>
<td>O.q0.opt</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.0173</td>
<td>-15.871508 +/- 0.003025</td>
<td>0.275364 +/- 0.006045</td>
</tr>
<tr>
<td>O.q0.opt</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.0175</td>
<td>-15.865512 +/- 0.002997</td>
<td>0.278056 +/- 0.006523</td>
</tr>
<tr>
<td>O.q0.opt</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.0175</td>
<td>-15.864967 +/- 0.002733</td>
<td>0.278065 +/- 0.004413</td>
</tr>
<tr>
<td>O.q0.opt</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.0172</td>
<td>-15.869644 +/- 0.002949</td>
<td>0.273497 +/- 0.006141</td>
</tr>
<tr>
<td>O.q0.opt</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.0180</td>
<td>-15.868397 +/- 0.003838</td>
<td>0.285451 +/- 0.007570</td>
</tr>
</tbody>
</table>

Plots of the data can also be obtained with the “-p” option (“qmca -p -q ev O.q0.opt*scalar*”). Identify which optimization series is the “best” according to your cost function. It is likely that multiple series are similar in quality. Note the opt.xml file corresponding to this series. This file
contains the final value of the optimized Jastrow parameters to be used in the DMC calculations of the next section of the lab.

Questions and Exercises

1. What is the acceptance ratio of your optimization runs? (use “qmca -q ar 0.q0.opt*scalar*”) Do you expect the Monte Carlo sampling to be efficient?

2. How do you know when the optimization process has converged?

3. (optional) Optimization is sometimes sensitive to initial guesses of the parameters. If you have time, try varying the initial parameters, including the cutoff radius (rcut) of the Jastrow factors (remember to change id in the <project/> element). Do you arrive at a similar set of final Jastrow parameters? What is the lowest variance you are able to achieve?

18.7 DMC timestep extrapolation I: neutral O atom

The diffusion Monte Carlo (DMC) algorithm contains two biases in addition to the fixed node and pseudopotential approximations that are important to control: timestep and population control bias. In this section we will focus on estimating and removing timestep bias from DMC calculations. The essential fact to remember is that the bias vanishes as the timestep goes to zero while the needed computer time increases inversely with the timestep.

In the same directory you used to perform wavefunction optimization (oxygen_atom) you will find a sample DMC input file for the neutral oxygen atom named 0.q0.dmc.in.xml. Open this file in a text editor and note the differences from the optimization case. Wavefunction information is no longer included from pw2qmcpack, but instead should come from the optimization run:

```xml
<!-- OPT_XML is from optimization, e.g. 0.q0.opt.s008.opt.xml -->
<include href="OPT_XML"/>
```

Replace “OPT_XML” with the opt.xml file corresponding to the best Jastrow parameters you found in the last section (this is a file name similar to 0.q0.opt.s008.opt.xml).

The QMC calculation section at the bottom is also different. The linear optimization blocks have been replaced with XML describing a VMC run followed by DMC. The input keywords are described below.

- **timestep** Timestep of the VMC/DMC random walk. In VMC choose a timestep corresponding to an acceptance ratio of about 50%. In DMC the acceptance ratio is often above 99%.

- **warmupSteps** Number of MC steps discarded as a warmup or equilibration period of the random walk.

- **steps** Number of MC steps per block. Physical quantities, such as the total energy, are averaged over walkers and steps.

- **blocks** Number of blocks. This is also the number of average energy values written to output files. Should be greater than 200 for meaningful statistical analysis of output data (e.g. via qmca). The total number of MC steps each walker takes is blocks×steps.
samples VMC only. This is the number of walkers used in subsequent DMC runs. Each DMC walker is initialized with electron positions sampled from the VMC random walk.

nonlocalmoves DMC only. If yes/no, use the locality approximation/T-moves for non-local pseudopotentials. T-moves generally improve the stability of the algorithm and restore the variational principle for small systems (T-moves version 1).

The purpose of the VMC run is to provide initial electron positions for each DMC walker. Setting walkers = 1 in the VMC block ensures there will be only one VMC walker per execution thread. There will be a total of 4 VMC walkers in this case (see O.q0.dmc.qsub.in). We want the electron positions used to initialize the DMC walkers to be decorrelated from one another. A VMC walker will often decorrelate from its current position after propagating for a few Ha\(^{-1}\) in imaginary time (in general this is system dependent). This leads to a rough rule of thumb for choosing blocks and steps for the VMC run (VWALKERS = 4 here):

\[
\text{VBLOCKS} \times \text{VSTEPS} \geq \frac{\text{DWALKERS}}{\text{VWALKERS}} \frac{5 \text{ Ha}\^{-1}}{\text{VTIMESTEP}}
\]  
(18.3)

Fill in the VMC XML block with appropriate values for these parameters. There should be more than one DMC walker per thread and enough walkers in total to avoid population control bias. The general rule of thumb is to have more than \(~2000\) walkers, although the dependence of the total energy on population size should be explicitly checked from time to time.

To study timestep bias, we will perform a sequence of DMC runs over a range of timesteps (0.1 Ha\(^{-1}\) is too large and timesteps below 0.002 Ha\(^{-1}\) are probably too small). A common approach is to select a fairly large timestep to begin with and then decrease the timestep by a factor of two in each subsequent DMC run. The total amount of imaginary time the walker population propagates should be the same for each run. A simple way to accomplish this is to choose input parameters in the following way

\[
\text{timestep}_n = \text{timestep}_{n-1}/2 \\
\text{warmupSteps}_n = \text{warmupSteps}_{n-1} \times 2 \\
\text{blocks}_n = \text{blocks}_{n-1} \\
\text{steps}_n = \text{steps}_{n-1} \times 2
\]  
(18.4)

Each DMC run will require about twice as much computer time as the one preceeding it. Note that the number of blocks is kept fixed for uniform statistical analysis. \(\text{blocks} \times \text{steps} \times \text{timestep} \sim 60 \text{ Ha}^{-1}\) is sufficient for this system.

Choose an initial DMC timestep and create a sequence of \(N\) timesteps according to [18.4]. Make \(N\) copies of the DMC XML block in the input file

```xml
<qmc method="dmc" move="pbyp">
  <parameter name="warmupSteps" > DWARMUP </parameter>
  <parameter name="blocks" > DBLOCKS </parameter>
  <parameter name="steps" > DSTEPS </parameter>
  <parameter name="timestep" > DTIMESTEP </parameter>
  <parameter name="nonlocalmoves" > yes </parameter>
</qmc>
```

Fill in DWARMUP, DBLOCKS, DSTEPS, and DTIMESTEP for each DMC run according to [18.4]. Start the DMC timestep extrapolation run by typing:
The run should take only a few minutes to complete.

QMCPACK will create files prefixed with 0.q0.dmc. The log file is 0.q0.dmc.out. As before, block averaged data is written to scalar.dat files. In addition, DMC runs produce dmc.dat files which contain energy data averaged only over the walker population (one line per DMC step). The dmc.dat files also provide a record of the walker population at each step.

Use the PlotTstepConv.pl to obtain a linear fit to the timestep data (type “PlotTstepConv.pl 0.q0.dmc.in.xml 40”). You should see a plot similar to fig. 18.1. The tail end of the text output displays the parameters for the linear fit. The “a” parameter is the total energy extrapolated to zero timestep in Hartree units.

```
mpirun -np 4 qmcpack 0.q0.dmc.in.xml >&0.q0.dmc.out&
```

![Figure 18.1: Linear fit to DMC timestep data from PlotTstepConv.pl.](image)

### Questions and Exercises

1. What is the $\tau \to 0$ extrapolated value for the total energy?
2. What is the maximum timestep you should use if you want to calculate the total energy to an accuracy of 0.05 eV? For convenience, 1 Ha = 27.2113846 eV.

3. What is the acceptance ratio for this (bias< 0.05 eV) run? Does it follow the rule of thumb for sensible DMC (acceptance ratio > 99%)?

4. Check the fluctuations in the walker population (qmca -t -q nw 0.q0.dmc*dmc.dat --noac). Does the population seem to be stable?

5. (Optional) Study population control bias for the oxygen atom. Select a few population sizes. Copy 0.q0.dmc.in.xml to a new file and remove all but one DMC run (select a single timestep). Make one copy of the new file for each population, set "samples", and choose a unique id in <project/>. Use qmca to study the dependence of the DMC total energy on the walker population. How large is the bias compared to timestep error? What bias is incurred by following the “rule of thumb” of a couple thousand walkers? Will population control bias generally be an issue for production runs on modern parallel machines?

### 18.8 DMC timestep extrapolation II: O atom ionization potential

In this section, we will repeat the calculations of the prior two sections (optimization, timestep extrapolation) for the +1 charge state of the oxygen atom. Comparing the resulting 1st ionization potential (IP) with experimental data will complete our first test of the BFD oxygen pseudopotential. In actual practice, higher IP’s could also be tested prior to performing production runs.

Obtaining the timestep extrapolated DMC total energy for ionized oxygen should take much less (human) time than for the neutral case. For convenience, the necessary steps are briefly summarized below.

1. Obtain DFT orbitals with Quantum ESPRESSO
   (a) Copy the DFT input (0.q0.dft.in) to 0.q1.dft.in
   (b) Edit 0.q1.dft.in to match the +1 charge state of the oxygen atom
       ```
       ...
       prefix = '0.q1'
       ...
       tot_charge = 1
       tot_magnetization = 3
       ...
       ```
   (c) Perform the DFT run: mpirun -np 4 pw.x -input 0.q1.dft.in >&0.q1.dft.out&

2. Convert the orbitals to ESHDF format
   (a) Copy the pw2qmcpack input (0.q0.p2q.in) to 0.q1.p2q.in
   (b) Edit 0.q1.p2q.in to match the file prefix used in DFT
       ```
       ...
       prefix = '0.q1'
       ...
       ```
   (c) Perform the orbital conversion run: mpirun -np 1 pw2qmcpack.x<0.q1.p2q.in>&0.q1.p2q.out&
3. Optimize the Jastrow factor with QMCPACK

(a) Copy the optimization input (O.q0.opt.in.xml) to O.q1.opt.in.xml
(b) Edit O.q1.opt.in.xml to match the file prefix used in DFT

```xml
...<project id="O.q1.opt" series="0">...
...<include href="O.q1.ptcl.xml"/>
...<include href="O.q1.wfs.xml"/>
...```

(c) Edit the particle XML file (O.q1.ptcl.xml) to have open boundary conditions

```xml
<parameter name="bconds">n n n</parameter>
```

(d) Add cutoffs to the Jastrow factors in the wavefunction XML file (O.q1.wfs.xml)

```xml
...<correlation speciesA="u" speciesB="u" size="8" rcut="10.0">
...<correlation speciesA="u" speciesB="d" size="8" rcut="10.0">
...<correlation elementType="O" size="8" rcut="5.0">
...```

(e) Perform the Jastrow optimization run: `mpirun -np 4 qmcpack O.q1.opt.in.xml > O.q1.opt.out`
(f) Identify the optimal set of parameters with `qmca ([your opt.xml])`.

4. DMC timestep study with QMCPACK

(a) Copy the DMC input (O.q0.dmc.in.xml) to O.q1.dmc.in.xml
(b) Edit O.q1.dmc.in.xml to use the DFT prefix and the optimal Jastrow

```xml
...<project id="O.q1.dmc" series="0">...
...<include href="O.q1.ptcl.xml"/>
...<include href="[your opt.xml]"/>
...```

(c) Perform the DMC run: `mpirun -np 4 qmcpack O.q1.dmc.in.xml > O.q1.dmc.out`
(d) Obtain the DMC total energy extrapolated to zero timestep with `PlotTstepConv.pl`.
The process listed above, which excludes additional steps for orbital generation and conversion, can become tedious to perform by hand in production settings where many calculations are often required. For this reason automation tools are introduced for calculations involving the oxygen dimer in section 18.10 of the lab.

Questions and Exercises

1. What is the $\tau \rightarrow 0$ extrapolated DMC value for the 1st ionization potential of oxygen?


3. What can we conclude about the accuracy of the pseudopotential? What factors complicate this assessment?

4. Explore the sensitivity of the IP to the choice of timestep. Type “./ip_conv.py” to view three timestep extrapolation plots: two for the $q = 0, 1$ total energies and one for the IP. Is the IP more, less, or similarly sensitive to timestep than the total energy?

5. What is the maximum timestep you should use if you want to calculate the ionization potential to an accuracy of 0.05 eV? What factor of cpu time is saved by assessing timestep convergence on the IP (a total energy difference) vs. a single total energy?

6. Are the acceptance ratio and population fluctuations reasonable for the $q = 1$ calculations?

18.9 DMC workflow automation with Nexus

Production QMC projects are often composed of many similar workflows. The simplest of these is a single DMC calculation involving four different compute jobs:

1. Orbital generation via Quantum ESPRESSO or GAMESS.
2. Conversion of orbital data via pw2qmcpack.x or convert4qmc.
3. Optimization of Jastrow factors via QMCPACK.
4. DMC calculation via QMCPACK.

Simulation workflows quickly become more complex with increasing costs in terms of human time for the researcher. Automation tools can decrease both human time and error if used well. The set of automation tools we will be using is known as Nexus [15], which is distributed with QMCPACK. Nexus is capable of generating input files, submitting and monitoring compute jobs, passing data between simulations (such as relaxed structures, orbital files, optimized Jastrow parameters, etc.), and data analysis. The user interface to Nexus is through a set of functions defined in the Python programming language. User scripts that execute simple workflows resemble input files and do not require programming experience. More complex workflows require only basic programming constructs (e.g. for loops and if statements). Nexus input files/scripts should be easier to navigate than QMCPACK input files and more efficient than submitting all the jobs by hand.
Nexus is driven by simple user-defined scripts that resemble keyword-driven input files. An example Nexus input file that performs a single VMC calculation (with pre-generated orbitals) is shown below. Take a moment to read it over and especially note the comments (prefixed with “#”) explaining most of the contents. If the input syntax is unclear you may want to consult portions of appendix 18.12, which gives a condensed summary of Python constructs. An additional example and details about the inner workings of Nexus can be found in the reference publication [15].

```
#!/usr/bin/env python

# import Nexus functions
from nexus import settings, job, get_machine, run_project
from nexus import generate_physical_system
from nexus import generate_qmcpack, vmc

settings(  # Nexus settings
    pseudo_dir = './pseudopotentials',  # location of PP files
    runs = '',  # root directory for simulations
    results = '',  # root directory for simulation results
    status_only = 0,  # show simulation status, then exit
    generate_only = 0,  # generate input files, then exit
    sleep = 3,  # seconds between checks on sim. progress
    machine = 'ws4',  # workstation with 4 cores
)

qmcjob = job(  # specify job parameters
    cores = 4,  # use 4 MPI tasks
    threads = 1,  # 1 OpenMP thread per node
    app = 'qmcpack',  # use QMCPACK executable (assumed in PATH)
)

qmc_calcs = [  # list QMC calculation methods
    vmc(  # VMC
        walkers = 1,  # 1 walker
        warmupsteps = 50,  # 50 MC steps for warmup
        blocks = 200,  # 200 blocks
        steps = 10,  # 10 steps per block
        timestep = .4  # 0.4 1/Ha timestep
    )
]

dimer = generate_physical_system(  # make a dimer system
    type = 'dimer',  # system type is dimer
    dimer = ('O', 'O'),  # dimer is two oxygen atoms
    separation = 1.2074,  # separated by 1.2074 Angstrom
    Lbox = 15.0,  # simulation box is 15 Angstrom
    units = 'A',  # Angstrom is dist. unit
    net_spin = 2,  # nup-ndown is 2
    O = 6  # pseudo-oxygen has 6 valence el.
)

qmc = generate_qmcpack(  # make a qmcpack simulation
    identifier = 'example',  # prefix files with 'example'
)
```
path = 'scale_1.0',          # run in ./scale_1.0 directory
system = 'dimer',           # run the dimer system
job = 'qmcjob',             # set job parameters
input_type = 'basic',       # basic qmcpack inputs given below
pseudos = ['O.BFD.xml'],    # list of PP's to use
orbitals_h5 = ['O2.pwscf.h5'], # file with orbitals from DFT
bconds = 'nnn',             # open boundary conditions
jastrows = [],              # no jastrow factors
calculations = qmc_calcs    # QMC calculations to perform
}
run_project(qmc)     # write input file and submit job

18.10 Automated binding curve of the oxygen dimer

In this section we will use Nexus to calculate the DMC total energy of the oxygen dimer over a series of bond lengths. The equilibrium bond length and binding energy of the dimer will be determined by performing a polynomial fit to the data (Morse potential fits should be preferred in production tests). Comparing these values with corresponding experimental data provides a second test of the BFD pseudopotential for oxygen.

Enter the oxygen_dimer directory. Copy your BFD pseudopotential from the atom runs into oxygen_dimer/pseudopotentials (be sure to move both files: .upf and .xml). Open O_dimer.py with a text editor. The overall format is similar to the example file shown in the last section. The main difference is that a full workflow of runs (DFT orbital generation, orbital conversion, optimization and DMC) are being performed rather than a single VMC run.

As in the example in the last section, the oxygen dimer is generated with the generate_physical_system function:

```python
dimer = generate_physical_system(
    type = 'dimer',
    dimer = ('O', 'O'),
    separation = 1.2074*scale,
    Lbox = 10.0,
    units = 'A',
    net_spin = 2,
    0 = 6
)
```

Similar syntax can be used to generate crystal structures or to specify systems with arbitrary atomic configurations and simulation cells. Notice that a “scale” variable has been introduced to stretch or compress the dimer.

Next, objects representing a Quantum ESPRESSO (PWSCF) run and subsequent orbital conversion step are constructed with respective generate_* functions:

```python
dft = generate_pwscf(
    identifier = 'dft',
    ...
    input_dft = 'lda',
    ...
)
sims.append(dft)
```
# describe orbital conversion run
p2q = generate_pw2qmcpack(
    identifier = 'p2q',
    ...
    dependencies = (dft,'orbitals'),
)  
sims.append(p2q)

Note the dependencies keyword. This keyword is used to construct workflows out of otherwise separate runs. In this case, the dependency indicates that the orbital conversion run must wait for the DFT to finish prior to starting.

Objects representing QMCPACK simulations are then constructed with the generate_qmcpack function:

```python
opt = generate_qmcpack(
    identifier = 'opt',
    ...
    jastrows = [('J1','bspline',8,5.0),
                 ('J2','bspline',8,10.0)],
    calculations = [
        loop(max=12,
             qmc=linear(
                 energy = 0.0,
                 unreweightedvariance = 1.0,
                 reweightedvariance = 0.0,
                 timestep = 0.3,
                 samples = 61440,
                 warmupsteps = 50,
                 blocks = 200,
                 substeps = 1,
                 nonlocalpp = True,
                 usebuffer = True,
                 walkers = 1,
                 minwalkers = 0.5,
                 maxweight = 1e9,
                 usedrift = False,
                 minmethod = 'quartic',
                 beta = 0.025,
                 exp0 = -16,
                 bigchange = 15.0,
                 alloweddifference = 1e-4,
                 stepsize = 0.2,
                 stabilizerscale = 1.0,
                 nstabilizers = 3,
                 )
        ),
    dependencies = (p2q,'orbitals'),
)  
sims.append(opt)

qmc = generate_qmcpack(
    identifier = 'qmc',
    ...
jastrows = [],
calculations = [
    vmc(
        walkers = 1,
        warmupsteps = 30,
        blocks = 20,
        steps = 10,
        substeps = 2,
        timestep = .4,
        samples = 2048
    ),
    dmc(
        warmupsteps = 100,
        blocks = 400,
        steps = 32,
        timestep = 0.01,
        nonlocalmoves = True,
    ),
],
dependencies = [(p2q,'orbitals'),(opt,'jastrow')],
sims.append(qmc)

Shared details such as the run directory, job, pseudopotentials, and orbital file have been omitted (...). The “opt” run will optimize a 1-body B-spline Jastrow with 8 knots having a cutoff of 5.0 Bohr and a B-spline Jastrow (for up-up and up-down correlations) with 8 knots and cutoffs of 10.0 Bohr. The Jastrow list for the DMC run is empty and the usage of dependencies above indicates that the DMC run depends on the optimization run for the Jastrow factor. Nexus will submit the “opt” run first and upon completion it will scan the output, select the optimal set of parameters, pass the Jastrow information to the “qmc” run and then submit the DMC job. Independent job workflows are submitted in parallel when permitted. No input files are written or job submissions made until the “run_project” function is reached:

```python
run_project(sims)
```

All of the simulations objects have been collected into a list (sims) for submission.

As written, O_dimer.py will only perform calculations at the equilibrium separation distance of 1.2074 Angstrom, since the list of scaling factors (representing stretching or compressing the dimer) only contains one value (scales = [1.00]). Modify the file now to perform DMC calculations across a range of separation distances with each DMC run using the Jastrow factor optimized at the equilibrium separation distance. Specifically, you will want to change the list of scaling factors to include both compression (scale<1.0) and stretch (scale>1.0):

```python
scales = [1.00,0.90,0.95,1.05,1.10]
```

Note that “1.00” is left in front because we are going to optimize the Jastrow factor first at the equilibrium separation and reuse this Jastrow factor for all other separation distances. This procedure is used because it can reduce variations in localization errors (due to pseudopotentials in DMC) along the binding curve.

Change the “status_only” parameter in the “settings” function to 1 and type “/O_dimer.py” at the command line. This will print the status of all simulations:
In this case, five simulation “cascades” (workflows) have been identified, each one starting and ending with “dft” and “qmc” runs, respectively. The six status flags (setup, sent_files, submitted, finished, got_output, analyzed) each show 0, indicating that no work has been done yet.

Now change “status_only” back to 0, set “generate_only” to 1, and run 0_dimer.py again. This will perform a dry-run of all simulations. The dry-run should finish in about 20 seconds:
starting runs:

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
poll 0  memory 91.03 MB
   Entering ./scale_1.0 0
       writing input files 0 dft
   Entering ./scale_1.0 0
       sending required files 0 dft
       submitting job 0 dft
...
poll 1  memory 91.10 MB
...
   Entering ./scale_1.0 0
       Would have executed:
           export OMP_NUM_THREADS=1
           mpirun -np 4 pw.x -input dft.in

poll 2  memory 91.10 MB
   Entering ./scale_1.0 0
       copying results 0 dft
   Entering ./scale_1.0 0
       analyzing 0 dft
...

poll 3  memory 91.10 MB
   Entering ./scale_1.0 1
       writing input files 1 p2q
   Entering ./scale_1.0 1
       sending required files 1 p2q
       submitting job 1 p2q
...
   Entering ./scale_1.0 1
       Would have executed:
           export OMP_NUM_THREADS=1
           mpirun -np 1 pw2qmcpack.x<p2q.in

poll 4  memory 91.10 MB
   Entering ./scale_1.0 1
       copying results 1 p2q
   Entering ./scale_1.0 1
       analyzing 1 p2q
...

poll 5  memory 91.10 MB
   Entering ./scale_1.0 2
       writing input files 2 opt
   Entering ./scale_1.0 2
       sending required files 2 opt
       submitting job 2 opt
...
Nexus polls the simulation status every 3 seconds and sleeps in between. The “scale_*” directories should now contain several files:

```
scale_1.0
dft.in
  O.BFD.upf
  O.BFD.xml
opt.in.xml
p2q.in
pwscf_output
qmc.in.xml
  sim_dft/
    analyzer.p
    input.p
    sim.p
  sim_opt/
    analyzer.p
    input.p
    sim.p
  sim_p2q/
    analyzer.p
    input.p
    sim.p
```
Take a minute to inspect the generated input (dft.in, p2q.in, opt.in.xml, qmc.in.xml) files. The pseudopotential files (O.BFD.upf and O.BFD.xml) have been copied into each local directory. Four additional directories have been created: sim_dft, sim_p2q, sim_opt and sim_qmc. The sim.p files in each directory contain the current status of each simulation. If you run O_dimer.py again, it should not attempt to rerun any of the simulations:

```
Project starting
  checking for file collisions
  loading cascade images
    cascade 0 checking in
    cascade 10 checking in
    cascade 4 checking in
    cascade 13 checking in
    cascade 7 checking in
  checking cascade dependencies
    all simulation dependencies satisfied

starting runs:
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
poll 0  memory 64.25 MB
Project finished
```

This way one can continue to add to the O_dimer.py file (e.g. adding more separation distances) without worrying about duplicate job submissions.

Let's actually submit the jobs in the dimer workflow now. Reset the state of the simulations by removing the sim.p files (“rm ./scale*/sim*/sim.p”), set “generate_only” to 0, and rerun O_dimer.py. It should take about 20 minutes for all the jobs to complete. You may wish to open another terminal to monitor the progress of the individual jobs while the current terminal runs O_dimer.py in the foreground. You can begin the first exercise below once the optimization job completes.

**Questions and Exercises**

1. Evaluate the quality of the optimization at scale=1.0 using the qmca tool. Did the optimization succeed? How does the variance compare with the neutral oxygen atom? Is the wavefunction of similar quality to the atomic case?

2. Evaluate the traces of the local energy and the DMC walker population for each separation
distance with the qmca tool. Are there any anomalies in the runs? Is the acceptance ratio reasonable? Is the wavefunction of similar quality across all separation distances?

3. Use the dimer_fit.py tool located in oxygen_dimer to fit the oxygen dimer binding curve. To get the binding energy of the dimer, we will need the DMC energy of the atom. Before performing the fit, answer: What DMC timestep should be used for the oxygen atom results? The tool accepts three arguments ("./dimer_fit.py P N E Eerr"), P is the prefix of the DMC input files (should be "qmc" at this point), N is the order of the fit (use 2 to start), E and Eerr are your DMC total energy and error bar, respectively for the oxygen atom (in eV). A plot of the dimer data will be displayed and text output will show the DMC equilibrium bond length and binding energy as well as experimental values. How accurately does your fit to the DMC data reproduce the experimental values? What factors affect the accuracy of your results?

4. Refit your data with a fourth-order polynomial. How do your predictions change with a fourth-order fit? Is a fourth-order fit appropriate for the available data?

5. Add new “scale” values to the list in O_dimer.py that interpolate between the original set (e.g. expand to [1.00, 0.90, 0.925, 0.95, 0.975, 1.025, 1.05, 1.075, 1.10]). Perform the DMC calculations and redo the fits. How accurately does your fit to the DMC data reproduce the experimental values? Should this pseudopotential be used in production calculations?

6. (Optional) Perform optimization runs at the extremal separation distances corresponding to scale=[0.90, 1.10]. Are the individually optimized wavefunctions of significantly better quality than the one imported from scale=1.00? Why? What form of Jastrow factor might give an even better improvement?

18.11 (Optional) Running your system with QMCPACK

This section covers a fairly simple route to get started on QMC calculations of an arbitrary system of interest using the Nexus workflow management system to setup input files and optionally perform the runs. The example provided in this section uses QM Espresso (PWSCF) to generate the orbitals forming the Slater determinant part of the trial wavefunction. PWSCF is a natural choice for solid state systems and it can be used for surface/slab and molecular systems as well, albeit at the price of describing additional vacuum space with plane waves.

To start out with, you will need pseudopotentials (PP’s) for each element in your system in both the UPF (PWSCF) and FSATOM/XML (QMCPACK) formats. A good place to start is the Burkatzki-Filippi-Dolg (BFD) pseudopotential database (http://www.burkatzki.com/pseudos/index.2.html), which we have already used in our study of the oxygen atom. The database does not contain PP’s for the 4th and 5th row transition metals or any of the lanthanides or actinides. If you need a PP that is not in the BFD database, you may need to generate and test one manually (e.g. with OPIUM, http://opium.sourceforge.net/). Otherwise, use ppconvert as outlined in section 18.4 to obtain PP’s in the formats used by PWSCF and QMCPACK. Enter the your_system lab directory and place the converted PP’s in your_system/pseudopotentials.

Before performing production calculations (more than just the initial setup in this section) be sure to converge the plane wave energy cutoff in PWSCF as these PP’s can be rather hard, sometimes requiring cutoffs in excess of 300 Ry. Depending on the system under study, the amount
of memory required to represent the orbitals (QMCPACK uses 3D B-splines) becomes prohibitive and one may be forced to search for softer PP’s.

Beyond pseudopotentials, all that is required to get started are the atomic positions and the dimensions/shape of the simulation cell. The Nexus file example.py illustrates how to setup PWSCF and QMCPACK input files by providing minimal information regarding the physical system (an 8-atom cubic cell of diamond in the example). Most of the contents should be familiar from your experience with the automated calculations of the oxygen dimer binding curve in section 18.10 (if you’ve skipped ahead you may want to skim that section for relevant information). The most important change is the expanded description of the physical system:

```python
# details of your physical system (diamond conventional cell below)
my_project_name = 'diamond_vmc' # directory to perform runs
my_dft_pps = ['C.BFD.upf'] # pwscf pseudopotentials
my_qmc_pps = ['C.BFD.xml'] # qmcpack pseudopotentials

# generate your system
# units : 'A'/'B' for Angstrom/Bohr
# axes : simulation cell axes in cartesian coordinates (a1,a2,a3)
# elem : list of atoms in the system
# pos : corresponding atomic positions in cartesian coordinates
# kgrid : Monkhorst-Pack grid
# kshift : Monkhorst-Pack shift (between 0 and 0.5)
# net_charge : system charge in units of e
# net_spin : # of up spins - # of down spins
# C = 4 : (pseudo) carbon has 4 valence electrons
my_system = generate_physical_system(
    units = 'A',
    axes = [[3.57000000e+00, 0.00000000e+00, 0.00000000e+00],
            [0.00000000e+00, 3.57000000e+00, 0.00000000e+00],
            [0.00000000e+00, 0.00000000e+00, 3.57000000e+00]],
    elem = ['C','C','C','C','C','C'],
    pos = [[0.00000000e+00, 0.00000000e+00, 0.00000000e+00],
           [8.92500000e-01, 8.92500000e-01, 8.92500000e-01],
           [0.00000000e+00, 1.78500000e+00, 1.78500000e+00],
           [8.92500000e-01, 2.67750000e+00, 2.67750000e+00],
           [1.78500000e+00, 0.00000000e+00, 1.78500000e+00],
           [2.67750000e+00, 8.92500000e-01, 2.67750000e+00],
           [1.78500000e+00, 1.78500000e+00, 0.00000000e+00],
           [2.67750000e+00, 2.67750000e+00, 8.92500000e-01]],
    kgrid = (1,1,1),
    kshift = (0,0,0),
    net_charge = 0,
    net_spin = 0,
    C = 4 # one line like this for each atomic species
)

my_bconds = 'ppp' # ppp/nnn for periodic/open BC's in QMC
# if nnn, center atoms about (a1+a2+a3)/2
```

If you have a system you would like to try with QMC, make a copy of example.py and fill in the relevant information about the pseudopotentials, simulation cell axes, and atomic species/positions. Otherwise, you can proceed with example.py as it is.

Set “generate_only” to 1 and type “./example.py” or similar to generate the input files.
All files will be written to “./diamond_vmc” (“./[my_project_name]” if you have changed “my_project_name” in the file). The input files for PWSCF, pw2qmcpack, and QMCPACK are scf.in, pw2qmcpack.in, and vmc.in.xml, respectively. Take some time to inspect the generated input files. If you have questions about the file contents, or run into issues with the generation process, feel free to consult with a lab instructor.

If desired, you can submit the runs directly with example.py. To do this, first reset the Nexus simulation record by typing “rm ./diamond_vmc/sim*/sim.p” or similar and set “generate_only” back to 0. Next rerun example.py (you may want to redirect the text output).

Alternatively the runs can be submitted by hand:

```
mpirun -np 4 pw.x<scf.in>&scf.out

(wait until JOB DONE appears in scf.out)

mpirun -np 1 pw2qmcpack.x<p2q.in>&p2q.out
```

Once the conversion process has finished the orbitals should be located in the file diamond_vmc/pwscf_output/pwscf.pwscf.h5. Open diamond_vmc/vmc.in.xml and replace “MISSING.h5” with “./pwscf_output/pwscf.pwscf.h5”. Next submit the VMC run:

```
mpirun -np 4 qmcpack vmc.in.xml>&vmc.out
```

Note: If your system is large, the above process may not complete within the time frame of this lab. Working with a stripped down (but relevant) example is a good idea for exploratory runs.

Once the runs have finished, you may want to begin exploring Jastrow optimization and DMC for your system. Example calculations are provided at the end of example.py in the commented out text.

### 18.12 Appendix A: Basic Python constructs

Basic Python data types (int, float, str, tuple, list, array, dict, obj) and programming constructs (if statements, for loops, functions w/ keyword arguments) are briefly overviewed below. All examples can be executed interactively in Python. To do this, type “python” at the command line and paste any of the shaded text below at the “>>>” prompt. For more information about effective use of Python, consult the detailed online documentation: [https://docs.python.org/2/](https://docs.python.org/2/).

#### Intrinsic types: int, float, str

```
# this is a comment
i=5           # integer
f=3.6         # float
s='quantum/montecarlo' # string
n=None        # represents "nothing"

f+=1.4        # add-assign (-,*,/ also): 5.0
2**3          # raise to a power: 8
str(i)        # int to string: '5'
```
Container types: **tuple, list, array, dict, obj**

```python
from numpy import array  # get array from numpy module
from generic import obj  # get obj from Nexus' generic module

t=('A',42,56,123.0)    # tuple
l=['B',3.14,196]      # list
a=array([1,2,3])     # array
d={'a':5,'b':6}       # dict

# printing
print t                # ('A', 42, 56, 123.0)
print l               # ['B', 3.1400000000000001, 196]
print a               # [1 2 3]
print d               # {'a': 5, 'b': 6}
print o               # a = 5
                       # b = 6
len(t),len(l),len(a),len(d),len(o) # number of elements: (4, 3, 3, 2, 2)

t[0],l[0],a[0],d['a'],o.a # element access: ('A', 'B', 1, 5, 5)

s = array([0,1,2,3,4]) # slices: works for tuple, list, array
s[:]                  # array([0, 1, 2, 3, 4])
s[2:]                 # array([2, 3, 4])
s[:2]                 # array([0, 1])
s[1:4]                # array([1, 2, 3])
s[0:5:2]              # array([0, 2, 4])

# list operations
l2 = list(l)    # make independent copy
l.append(4)     # add new element: ['B', 3.14, 196, 4]
l+[5,6,7]       # addition: ['B', 3.14, 196, 4, 5, 6, 7]
3*[0,1]         # multiplication: [0, 1, 0, 1, 0, 1]

b=array([5,6,7])  # array operations
a2 = a.copy()     # make independent copy
a+b                # addition: array([ 6, 8, 10])
```
a+3  # addition: array([ 4, 5, 6])
a*b  # multiplication: array([ 5, 12, 21])
3*a  # multiplication: array([3, 6, 9])

# dict/obj operations
d2 = d.copy()  # make independent copy
d['c'] = 7  # add/assign element
d.keys()  # get element names: ['a', 'c', 'b']
d.values()  # get element values: [5, 7, 6]

# obj-specific operations
o.c = 7  # add/assign element
o.set(c=7,d=8)  # add/assign multiple elements

An important feature of Python to be aware of is that assignment is most often by reference, i.e. new values are not always created. This point is illustrated below with an obj instance, but it also holds for list, array, dict, and others.

```python
>>> o = obj(a=5,b=6)
... >>> p=o
... >>> p.a=7
... >>> print o
  a = 7
  b = 6

>>> q=o.copy()
... >>> q.a=9
... >>> print o
  a = 7
  b = 6
```

Here p is just another name for o, while q is a fully independent copy of it.

**Conditional Statements: if/elif/else**

```python
a = 5
if a is None:
    print 'a is None'
elif a==4:
    print 'a is 4'
elif a<=6 and a>2:
    print 'a is in the range (2,6)'
elif a<-1 or a>26:
    print 'a is not in the range [-1,26]'
```
elif a!=10:
    print 'a is not 10'
else:
    print 'a is 10'
#end if

The “#end if” is not part of Python syntax, but you will see text like this throughout Nexus for clear encapsulation.

**Iteration: for**

```python
from generic import obj

l = [1,2,3]
m = [4,5,6]
s = 0
for i in range(len(l)):  # loop over list indices
    s += l[i] + m[i]
#end for

print s  # s is 21

s = 0
for v in l:  # loop over list elements
    s += v
#end for

print s  # s is 6

o = obj(a=5,b=6)
s = 0
for v in o:  # loop over obj elements
    s += v
#end for

print s  # s is 11

d = {'a':5,'b':4}
for n,v in o.iteritems():# loop over name/value pairs in obj
    d[n] += v
#end for

print d  # d is {'a': 10, 'b': 10}
```

**Functions: def, argument syntax**

```python
def f(a,b,c=5):  # basic function, c has a default value
```
print a, b, c
# end def f

f(1, b=2)  # prints: 1 2 5

def f(*args, **kwargs):  # general function, returns nothing
    print args  # args: tuple of positional arguments
    print kwargs  # kwargs: dict of keyword arguments
# end def f

f('s', (1, 2), a=3, b='t')  # 2 pos., 2 kw. args, prints:
    # ('s', (1, 2))
    # {'a': 3, 'b': 't'}

l = [0, 1, 2]
f(*l, a=6)  # pos. args from list, 1 kw. arg, prints:
    # (0, 1, 2)
    # {'a': 6}
o = obj(a=5, b=6)
f(*l, **o)  # pos./kw. args from list/obj, prints:
    # (0, 1, 2)
    # {'a': 5, 'b': 6}

f(  
    blocks = 200,
    steps = 10,
    timestep = 0.01
)  # indented kw. args, prints
    # ()
    # {'steps': 10, 'blocks': 200, 'timestep': 0.01}
o = obj(
    blocks = 100,
    steps = 5,
    timestep = 0.02
)  # obj w/ indented kw. args
f(**o)  # kw. args from obj, prints:
    # ()
    # {'timestep': 0.02, 'blocks': 100, 'steps': 5}
Chapter 19

Lab 3: Advanced Molecular Calculations

19.1 Topics covered in this Lab

This lab covers molecular QMC calculations with wavefunctions of increasing sophistication. All of the trial wavefunctions are initially generated with the GAMESS code. Topics covered include:

- Generating single determinant trial wavefunctions with GAMESS (HF and DFT)
- Generating multi-determinant trial wavefunctions with GAMESS (CISD, CASCI, SOCI)
- Optimizing wavefunctions (Jastrow factors and CSF coefficients) with QMC
- DMC timestep and walker population convergence studies
- Systematic progressions of Jastrow factors in VMC
- Systematic convergence of DMC energies with multi-determinant wavefunctions
- Influence of orbitals basis choice on DMC energy

19.2 Lab directories and files

labs/lab3_advanced_molecules/exercises

```bash
  ├── ex1_first-run-hartree-fock
  │     ├── gms
  │     │     ├── h2o.hf.inp
  │     │     └── h2o.hf.out
  │     └── convert
  │         ├── h2o.hf.out
  │         ├── h2o.ptcl.xml
  │         └── h2o.wfs.xml
  │     └── opt
  │         └── optm.xml
  │     ├── dmc_timestep
  │     │     └── dmc_ts.xml
  │     └── dmc_walkers
  │         └── dmc_wk.xml
  └── dmc_walkers
```

- `ex1_first-run-hartree-fock`: basic work flow from Hartree-Fock to DMC
- `gms`: Hartree-Fock calculation using GAMESS
- `h2o.hf.inp`: GAMESS input
- `h2o.hf.dat`: GAMESS punch file containing orbitals
- `h2o.hf.out`: GAMESS output with orbitals and other info
- `convert`: Convert GAMESS wavefunction to QMCPACK format
- `h2o.hf.out`: GAMESS output
- `h2o.ptcl.xml`: converted particle positions
- `h2o.wfs.xml`: converted wave function
- `opt`: VMC optimization
- `optm.xml`: QMCPACK VMC optimization input
- `dmc_timestep`: Check DMC timestep bias
- `dmc_ts.xml`: QMCPACK DMC input
- `dmc_walkers`: Check DMC population control bias
- `dmc_wk.xml`: QMCPACK DMC input template
19.3 Exercise #1: Basics

The purpose of this exercise is to show how to generate wave-functions for QMCPACK using GAMESS and to optimize the resulting wave-functions using VMC. This will be followed by a study of the time-step and walker population dependence of DMC energies. The exercise will be performed on a water molecule at the equilibrium geometry.

19.3.1 Generation of a Hartree-Fock wave-function with GAMESS

From the top directory, go to “ex1_first-run-hartree-fock/gms”. This directory contains an input file for a HF calculation of a water molecule using BFD ECPs and the corresponding cc-pVTZ basis set. The input file should be named: “h2o.hf.inp”. Study the input file. If the student wishes, he can refer to section A for a more detailed description of the GAMESS input syntax. There will be a better time to do this soon, so we recommend that the student continues with the exercise at this point. After you are done, execute GAMESS with this input and store the standard output in a file named “h2o.hf.output”. Finally, in the “convert” folder, use convert4qmc to generate the QMCPACK particleset and wavefunction files. It is always useful to rename the files generated by convert4qmc to something meaningful, since by default they are called sample.Gaussian-G2.xml and sample.Gaussian-G2.ptcl.xml. In a standard computer (without cross-compilation), these tasks
could be accomplished by the following commands.

```bash
cd ${TRAINING TOP}/ex1_first-run-hartree-fock/gms
go_run_vesta rungms h2o.hf
cd ../convert
cpy ../gms/h2o.hf.output
go_run_vesta convert4qmc -gamessAscii h2o.hf.output -add3BodyJ
mv sample.Gaussian-G2.xml h2o.wfs.xml
mv sample.Gaussian-G2.ptcl.xml h2o.ptcl.xml
```

The HF energy of the system is -16.9600590022 Ha. To search for the energy in the output file quickly, you can use

```
grep "TOTAL ENERGY =" h2o.hf.output
```

As the job runs on VESTA, it is a good time to review section B, which contains a description on the use of the converter.

### 19.3.2 Optimize the wave-function

When the execution of the previous steps is completed, there should be 2 new files called h2o.wfs.xml and h2o.ptcl.xml. Now we will use VMC to optimize the Jastrow parameters in the wave-function. From the top directory, go to “ex1_first-run-hartree-fock/opt”. Copy the xml files generated in the previous step to the current directory. This directory should already contain a basic QMCPACK input file for an optimization calculation (optm.xml) Open optm.xml with your favorite text editor and modify the name of the files that contain the wavefunction and particleset XML blocks. These files are included with the commands:

```xml
<include href=ptcl.xml/>
<include href=wfs.xml/>
```

(the particle set must be defined before the wave-function). The name of the particle set and wave-function files should now be h2o.ptcl.xml and h2o.wfs.xml, respectively. Study both files and submit when you are ready. Notice that the location of the ECPs has been set for you, in your own calculations you have to make sure you obtain the ECPs from the appropriate libraries and convert them to QMCPACK format using ppconvert. This is a good time to study section C, which contains a review of the main parameters in the optimization XML block, while this calculation finishes. The previous steps can be accomplished by the following commands:

```bash
cd ${TRAINING TOP}/ex1_first-run-hartree-fock/opt
cpy ../convert/h2o.wfs.xml ./
cpy ../convert/h2o.ptcl.xml ./
# edit optm.xml to include the correct ptcl.xml and wfs.xml
go_run_vesta qmcpack optm.xml
```

Use the analysis tool qmca to analyze the results of the calculation. Obtain the VMC energy and variance for each step in the optimization and plot it using your favorite program. Remember that qmca has built-in functions to plot the analyzed data.

```
qmca -q e *scalar.dat -p
```

The resulting energy as a function of optimization step should look qualitatively similar to figure [19.1]. The energy should decrease quickly as a function of the number of optimization steps.
After 6-8 steps, the energy should be converged to ≈2-3mHa. To improve convergence, we would need to increase the number of samples used during the optimization. You can check this for yourself on your free time. With optimized wave-functions we are in a position to perform VMC and DMC calculations. The modified wave-function files after each step are written in a file named ID.sNNN.opt.xml, where ID is the identifier of the calculation defined in the input file (this is defined in the project XML block with parameter “id”) and NNN is a series number which increases with every executable xml block in the input file.

### 19.3.3 Time-step Study

Now we will study the dependence of the DMC energy with time-step. From the top directory, go to “ex1_first-run-hartree-fock/dmc_timestep”. This folder contains a basic xml input file (dmc_ts.xml) that performs a short VMC calculation and three DMC calculations with varying time-steps (0.1, 0.05, 0.01). Link the particle set and the last optimization file from the previous folder (the file called jopt-h2o.sNNNN.opt.xml with the largest value of NNN). Rename the optimized wave-function to any suitable name if you wish, for example h2o.opt.xml, and change the name of the particle set and wave-function files in the input file. An optimized wave-function can be found in the reference files (same location) in case it is needed.

The main steps needed to perform this exercise are:

```bash
cd ${TRAINING TOP}/ex1_first-run-hartree-fock/dmc_timestep
cp ../opt/h2o.ptcl.xml ./
cp ../opt/jopt-h2o.s007.opt.xml h2o.opt.wfs.xml
# edit dmc_ts.xml to include the correct ptcl.xml and wfs.xml
jobrun_vesta qmcpack dmc_ts.xml
```
While these runs complete, go to section D and review the basic VMC and DMC input blocks. Notice that in the current DMC blocks, as the time-step is decreased the number of blocks is also increased. Why is this?

When the simulations are finished, use qmca to analyze the output files and to plot the DMC energy as a function of time-step. Results should be qualitatively similar to those presented in figure 19.2, in this case we present more time-steps with well converged results to better illustrate the time-step dependence. In realistic calculations, the time-step must be chosen small enough so that the resulting error is below the desire accuracy. Alternatively, various calculations can be performed and the results extrapolated to the zero time-step limit.

19.3.4 Walker Population Study

Now we will study the dependence of the DMC energy with the number of walkers in the simulation. Remember that, in principle, the DMC distribution is reached in the limit of an infinite number of walkers. In practice, the energy and most properties converge to high accuracy with \(\sim\)100-1000 walkers. The actual number of walkers needed in a calculation will depend on the accuracy of the VMC wave-function and on the complexity and size of the system. Also notice that using too many walkers is not a problem, at worse it will be inefficient since it will cost more computer time than necessary. In fact, this is the strategy used when running QMC calculations on large parallel computers since we can reduce the statistical error bars efficiently by running with large walker populations distributed across all processors.

From the top directory, go to “ex1_first-run-hartree-fock/dmc_walkers”. Copy the optimized wave-function and particle set files used in the previous calculations to the current folder, these are the ones generated on step 2 of this exercise. An optimized wave-function can be found in the reference files (same location) in case it is needed. The directory contains a sample DMC
input file and submission script. Make 3 directories named NWx, with x values 120, 240, 480 and copy the input file to each one. Go to “NW120”, and, in the input file, change the name of the wave-function and particle set files (in this case they will be located one directory above, so use “..\dmc_timestep\h2.opt.xml” for example), change the pseudopotential directory to point to one directory above, change “targetWalkers” to 120, change the number of steps to 100, the time-step to 0.01 and the number of blocks to 400. Notice that “targetWalkers” is one way to set the desired (average) number of walkers in a DMC calculation. One can alternatively set “samples” in the <qmc method="\vmc" block to carry over de-correlated VMC configurations as DMC walkers. For your own simulations we generally recommend setting setting \( \sim 2^*(\text{#threads}) \) walkers per node (slightly smaller than this value).

The main steps needed to perform this exercise are:

cd $(TRAINING TOP)/ex1_first-run-hartree-fock/dmc_walkers
cp ../opt/h2o.ptcl.xml ./
cp ../opt/jopt-h2o.s007.opt.xml h2o.opt.wfs.xml
# edit dmc_wk.xml to include the correct ptcl.xml and wfs.xml and
# use the correct pseudopotential directory
mkdir NW120
cp dmc_wk.xml NW120
# edit dmc_wk.xml to use the desired number of walkers,
# and collect the desired amount of statistics
jobrun_vesta qmcpack dmc_wk.xml
# repeat for NW240, NW480

Repeat the same procedure in the other folders by setting (targetWalkers=240, steps=100, timestep=0.01, blocks=200) in NW240 and (targetWalkers=480, steps=100, timestep=0.01, blocks=100)
in NW480. When the simulations complete, use qmca to analyze and plot the energy as a function of the number of walkers in the calculation. As always, figure 19.3 shows representative results of the dependence of the energy on the number of walkers for a single water molecule. As shown, less than 240 walkers are needed to obtain an accuracy of 0.1 mHa.

19.4 Exercise #2 Slater-Jastrow Wave-Function Options

From this point on in the tutorial we assume familiarity with the basic parameters in the optimization, VMC and DMC XML input blocks of QMCPACK. In addition, we assume familiarity with the submission system. As a result, the folder structure will not contain any prepared input or submission files, the student will generate them using input files from exercise 1. In the case of QMCPACK sample files, you will find optm.xml, vmc.dmc.xml and submit.csh files. Some of the options in these files can be left unaltered, but many of them will need to be tailored to the particular calculation.

In this exercise we will study the dependence of the DMC energy on the choices made in the wave-function ansatz. In particular, we will study the influence/dependence of the VMC energy with the various terms in the Jastrow. We will also study the influence of the VMC and DMC energies on the single particle orbitals used to form the Slater determinant in single determinant wave-functions. For this we will use wave-functions generated with various exchange-correlation functionals in DFT. Finally, we will optimize a simple multi-determinant wave-function and study the dependence of the energy on the number of configurations used in the expansion. All of these exercises will be performed on the water molecule at equilibrium.

19.4.1 Influence of Jastrow on VMC energy with HF wave-function

In this section we will study the dependence of the VMC energy on the various Jastrow terms, e.g. one-body, two-body and three-body. From the top directory, go to “ex2_slater-jastrow-wf-options/jastrow”. We will compare the single determinant VMC energy using a two-body Jastrow term, both one- and two-body terms and finally one-, two- and three-body terms. Since we are interested in the influence of the Jastrow, we will use the HF orbitals calculated in exercise #1. Make three folders named 2j,12j,123j. For both 2j and 12j, copy the input file optm.xml from “ex1_first-run-hartree-fock/opt”. This input file performs both wave-function optimization and a VMC calculation. Remember to correct relative paths to the pseudopotential directory. Copy the un-optimized HF wave-function and particle set files from “ex1_first-run-hartree-fock/convert”, if you followed the instructions in exercise #1 these should be named h2o.wfs.xml and h2o.ptcl.xml. Otherwise, you can obtained them from the REFERENCE files. Modify the file h2o.wfs.xml to remove the appropriate jastrow blocks. For example, for a two-body Jastrow (only), you need to eliminate the jastrow blocks named <jastrow name="J1" and <jastrow name="J3". In the case of 12j, remove only <jastrow name="J3". Recommended settings for the optimization run are: nodes=32, threads=16, blocks=250, samples=128000, time-step=0.5, 8 optimization loops, and in the VMC section we recommend walkers=16, blocks=1000, steps=1, substeps=100. Notice that samples should always be set to blocks*threads per node*nodes = 32*16*250=128000. Repeat the process in both 2j and 12j cases. For the 123j case, the wave-function has already been optimized in the previous exercise. Copy the optimized HF wave-function and the particle set from “ex1_first-run-hartree-fock/opt”. Copy the input file from any of the previous runs and remove the optimization block from the input, just leave the VMC step. In all three cases, modify the submission script and submit the run.
These simulations will take several minutes to complete. This is an excellent opportunity to go to section E and review the wavefunction XML block used by QMCPACK. When the simulation are completed, use qmca to analyze the output files. Using your favorite plotting program (e.g. gnuplot), plot the energy and variance as a function of the Jastrow form. Figure 19.4 shows a typical result for this calculation. As can be seen, the VMC energy and variance depends strongly on the form of the Jastrow. Since the DMC error bar is directly related to the variance of the VMC energy, improving the Jastrow will always lead to a reduction in the DMC effort. In addition, systematic approximations (time-step, number of walkers, etc) are also reduced with improved wave-functions.

19.4.2 Generation of wave-functions from DFT using GAMESS

In this section we will use GAMESS to generate wave-functions for QMCPACK from DFT calculations. From the top folder, go to “ex2_slater-jastrow-wf-options/orbitals”. In order to demonstrate the variation in DMC energies with the choice of DFT orbitals, we will choose the following set of exchange-correlation functionals (PBE, PBE0, BLYP, B3LYP). For each functional, make a directory using your preferred naming convention (e.g. the name of the functional). Go into each folder and copy a GAMESS input file from “ex1_first-run-hartree-fock/gms” .Rename the file with your preferred naming convention, we suggest using h2o.[dft].inp, where [dft] is the name of the functional used in the calculation. At this point, this input file should be identical to the one used to generate the HF wave-function in exercise #1. In order to perform a DFT calculation we only need to add “DFTTYP” to the $CONTRL . . . $END section and set it to the desired functional type, for example “DFTTYP=PBE” for a PBE functional. This variable must be set to (PBE, PBE0, BLYP, B3LYP) to obtain the appropriate functional in GAMESS. For a complete list of implemented functionals, see the GAMESS input manual.
19.4.3 Optimization and DMC calculations with DFT wave-functions

In this section we will optimize the wave-function generated in the previous step and perform DMC calculations. From the top directory, go to “ex2_slater-jastrow-wf-options/orbitals”. The steps required to achieve this are identical to those used to optimize the wave-function with HF orbitals. Make individual folders for each calculation and obtain the necessary files to perform optimization, VMC and DMC calculations from “ex1_first-run-hartree-fock/opt” and “ex1_first-run-hartree-fock/dmc_ts”, for example. For each functional, make the appropriate modifications to the input files and copy the particle set and wave-function files from the appropriate directory in “ex2_slater-jastrow-wf-options/orbitals/[dft]”. We recommend the following settings: nodes=32, threads=16, (in optimization) blocks=250, samples=128000, timestep=0.5, 8 optimization loops, (in VMC) walkers=16, blocks=100, steps=1, substeps=100, (in DMC) blocks 400, targetWalkers=960, timestep=0.01. Submit the runs and analyze the results using qmca.

How do the energies compare against each other? How do they compare against DMC energies with HF orbitals?

19.5 Exercise #3: Multi-Determinant Wave-Functions

In this exercise we will study the dependence of the DMC energy on the set of orbitals and the type of configurations included in a multi-determinant wave-function.

19.5.1 Generation of a CISD wave-functions using GAMESS

In this section we will use GAMESS to generate a multi-determinant wave-function with Configuration Interaction with Single and Double excitations (CISD). In CISD, the Schrodinger equation is solved exactly in a basis of determinants including the HF determinant and all its single and double excitations.

Go to “ex3_multi-slater-jastrow/cisd/gms” and you’ll see input and output files named h2o.cisd.inp and h2o.cisd.out. Due to technical problems with GAMESS in the BGQ architecture of VESTA, we are unable to use CISD properly in GAMESS. For this reason, the output of the calculation is already provided in the directory.

There will be time in the next step to study the GAMESS input files and the description in section A. Since the output is already provided, the only thing needed is to use the converter to generate the appropriate QMCPACK files.

```
jobrun_vesta convert4qmc h2o.cisd.out -ci h2o.cisd.out \
-readInitialGuess 57 -threshold 0.0075
```

We used the PRTMO=.T. flag in the GUESS section to include orbitals in the output file. You should read these orbitals from the output (-readInitialGuess 40). The highest occupied orbital in any determinant should be 34, so reading 40 orbitals is a safe choice. In this case, it is important to rename the xml files with meaningful names, for example h2o.cisd.wfs.xml. A threshold of 0.0075 is sufficient for the calculations in the training.

19.5.2 Optimization of Multi-Determinant wave-function

In this section we will optimize the wave-function generated in the previous step. There is no difference in the optimization steps if a single determinant and a multi-determinant wave-function. QMCPACK will recognize the presence of a multi-determinant wavefunction and will automatically
optimize the linear coefficients by default. Go to “ex3_multi-slater-jastrow/cisd” and make a folder called thres0.01. Copy the particle set and wavefunction files created in the previous step to the current directory. With your favorite text editor, open the wave-function file h2o.wfs.xml. Look for the multideterminant XML block and change the “cutoff” parameter in detlist to 0.01. Then follow the same steps used in the subsection “Optimization and DMC calculations with DFT wave-functions” to optimize the wave-function. Similar to this case, design a QMCPACK input file that performs wave-function optimization followed by VMC and DMC calculations. Submit the calculation.

This is a good time to review the GAMESS input file description in Appendix section A. When the run is completed, go to the previous directory and make a new folder named thres0.0075. Repeat the steps performed above to optimize the wave-function with a cutoff of 0.01, but use a cutoff of 0.0075 this time. This will increase the number of determinants used in the calculation. Notice the “cutoff” parameter in the XML should be less than the “-threshold 0.0075” flag passed to the converted, which is further bounded by the PRTTOL flag in the GAMESS input.

After the wave-function is generated, we are ready to optimize. Instead of starting from an un-optimized wave-function, we can start from optimized wave-function from thres0.01 to speed up convergence. You will need to modify the file and change the cutoff in detlist to 0.0075 with a text editor. Repeat the optimization steps and submit the calculation.

When you are done, use qmca to analyze the results. Compare the energies at these two coefficient cutoffs with the energies obtained with DFT orbitals. Due to the time limitations of this tutorial it is not practical to optimize the wave-functions with a smaller cutoff, since this would require more samples and longer runs due to the larger number of optimizable parameters. Figure 19.5 shows the results of such exercise, the DMC energy as a function of the cutoff in the wave-function. As can be seen, a large improvement in the energy is obtained as the number of configurations is increased.

Figure 19.5: DMC energy as a function of the sum of the square of CI coefficients from CISD.
19.5.3 CISD, CASCI and SOCI

Go to “ex3_multi-slater-jastrow” and inspect folders for the remaining wave-function types: CASCI and SOCI. Follow steps in the previous exercise and obtain the optimized wave-functions for these determinant choices. Notice the SOCI GAMESS output is not included because it is large. Already converted XML inputs can be found in “ex3_multi-slater-jastrow/soci/thres*”.

A CASCI wave-function is produced from a CI calculation that includes all the determinants in a complete active space (CAS) calculation, in this case using the orbitals from a previous CASSCF calculation. In this case we used a CAS(8,8) active space, that includes all determinants generated by distributing 8 electrons in the lowest 8 orbitals. A second-order CI (SOCI) calculation is similar to the CAS-CI calculation, but in addition to the determinants in the CAS it also includes all single and double excitations from all of them, leading to a much larger determinant set. Since we now have considerable experience optimizing wave-functions and calculating DMC energies, we will leave it to the student to complete the remaining tasks on its own. If you need help, refer to previous exercises in the tutorial. Perform optimizations for both wave-functions using cutoffs in the CI expansion of 0.01 and 0.0075. If there is enough time left, try to optimize the wave-functions with a cutoff of 0.005. Analyze the results and plot the energy as a function of cutoff for all three cases, CISD, CAS-CI and SOCI.

Figure 19.5 shows the result of similar calculations using more samples and smaller cutoffs. The results should be similar to those produced in the tutorial. For reference, the exact energy of the water molecule with ECPs is approximately -17.276 Ha. From the results of the tutorial, how does the selection of determinants is related to the expected DMC energy? What about the choice in the set of orbitals?
19.6 Appendix A: GAMESS input

In this section we provide a brief description of the GAMESS input needed to produce trial wave-function for QMC calculations with QMCPACK. We assume basic familiarity with GAMESS input structure, in particular regarding the input of atomic coordinates and the definition of gaussian basis sets. This section will focus on the generation of the output files needed by the converter tool, convert4qmc. For a description of the converter, see B.

Only a subset of the methods available in GAMESS can be used to generate wave-functions for QMCPACK and we restrict our description here to these. For a complete description of all the options and methods available in GAMESS, please refer to the official documentation which could be found in "http://www.msg.ameslab.gov/gamess/documentation.html".

Currently, convert4qmc can process output for the following methods in GAMESS (in SCFTYP): RHF, ROHF, and MCSCF. Both HF as well as DFT calculations (any DFT type) could be used in combination with RHF and ROHF calculations. For MCSCF and CI calculations, ALDET, ORMAS and GUGA drivers can be used (see below for details).

19.6.1 HF input

The following input will perform a restricted HF calculation on a closed-shell singlet (multiplicity=1). This will generate RHF orbitals for any molecular system defined in $DATA ...

```
$CONTROL SCFTYP=RHF RUNTYP=ENERGY MULT=1
ISPHER=1 EXETYP=RUN COORD=UNIQUE MAXIT=200 $END
$SYSTEM MEMORY=150000000 $END
$GUESS GUESS=HUCKEL $END
$SCF DIRSCF=.TRUE. $END
$DATA ...
Atomic Coordinates and basis set ...
$END
```

Main options:

1. SCFTYP: Type of SCF method, options: RHF, ROHF, MCSCF, UHF and NONE.
2. RUNTYP: Type of run. For QMCPACK wave-function generation this should always be ENERGY.
3. MULT: Multiplicity of the molecule.
4. ISPHER: Use spherical harmonics (1) or cartesian basis functions (-1).
5. COORD: Input structure for the atomic coordinates in $DATA.

19.6.2 DFT calculations

The main difference between the input for a RHF/ROHF calculation and a DFT calculation is the definition of the DFTTYP parameter. If this is set in the $CONTROL section, a DFT calculation will be performed with the appropriate functional. Notice that while the default values are usually adequate, DFT calculations have many options involving the integration grids and accuracy settings. Make sure you study the input manual to be aware of these. Refer to the input manual for a list of the implemented exchange-correlation functionals.
19.6.3 Multi-Configuration Self-Consistent Field (MCSCF)

MCSCF calculations are performed by setting SCFTYP=MCSCF in the `CONTROL` section. If this option is set, an `MCSCF` section must be added to the input file with the options for the calculation. An example section for the water molecule used in the tutorial is shown below.

```
$MCSCF CISTEP=GUGA MAXIT=1000 FULLNR=.TRUE. ACURCY=1.0D-5 $END
```

The most important parameter is CISTEP, which defines the CI package used. The only options compatible with QMCPACK are: ALDET, GUGA, and ORMAS. Depending on the package used, additional input sections are needed.

19.6.4 Configuration Interaction (CI)

Configuration interaction (full CI, truncated CI, CAS-CI, etc) calculations are performed by setting SCFTYP=NONE and CITYP=GUGA, ALDET, ORMAS. Each one of this packages requires further input sections, which are typically slightly different to the input sections needed for MCSCF runs.

19.6.5 GUGA: Unitary Group CI package

The GUGA package is the only alternative if one wants CSFs with GAMESS. Below we provide a very brief description of input sections needed to perform MCSCF, CASCI, truncated CI and SOCI with this package. For a complete description of these methods and all the options available, please refer to the GAMESS input manual.

GUGA-MCSCF

The following input section performs a CASCI calculation, with a CAS that includes 8 electrons in 8 orbitals (4 DOC and 4 VAL), e.g. CAS(8,8). NMCC is the number of frozen orbitals (doubly occupied orbitals in all determinants), NDOC is the number of double occupied orbitals in the reference determinant, NVAL is the number of singly occupied orbitals in the reference (for spin polarized cases), and NVAL is the number of orbitals in the active space. Since FORS is set to .TRUE., all configurations in the active space will be included. ISTSYM defines the symmetry of the desired state.

```
$MCSCF CISTEP=GUGA MAXIT=1000 FULLNR=.TRUE. ACURCY=1.0D-5 $END
$DRT GROUP=C2v NMCC=0 NDOC=4 NALP=0 NVAL=4 ISTSYM=1 MXNINT= 500000 FORS=.TRUE. $END
```

GUGA-CASCI

The following input section performs a CASCI calculation, with a CAS that includes 8 electrons in 8 orbitals (4 DOC and 4 VAL), e.g. CAS(8,8). NFZC is the number of frozen orbitals (doubly occupied orbitals in all determinants). All other parameters are identical to those in the MCSCF input section.

```
$CIDRT GROUP=C2v NFZC=0 NDOC=4 NALP=0 NVAL=4 NPRT=2 ISTSYM=1 FORS=.TRUE. MXNINT= 500000 $END
$GUDIA PRTTOL=0.001 CVGTOL=1.0E-5 ITERMX=1000 $END
```
GUGA-Truncated CI

The following input sections will lead to a truncated CI calculation, in this particular case it will perform a CISD calculation since IEXCIT is set to 2. Other values in IEXCIT will lead to different CI truncations, for example IEXCIT=4 will lead to CISDTQ. Notice that only the lowest 30 orbitals will be included in the generation of the excited determinants in this case. For a full CISD calculation, NVAL should be set to the total number of virtual orbitals.

```
$CIDRT GROUP=C2v NFZC=0 NDOC=4 NALP=0 NVAL=30 NPRT=2 ISTSYM=1 IEXCIT=2 MXNINT=500000 $END
$GUGDIA PRTTOL=0.001 CVGTOL=1.0E-5 ITERMX=1000 $END
```

GUGA-SOCI

The following input section performs a SOCI calculation, with a CAS that includes 8 electrons in 8 orbitals (4 DOC and 4 VAL), e.g. CAS(8,8). Since SOCI is set to .TRUE., all single and double determinants from all determinants in the CAS(8,8) will be included.

```
$CIDRT GROUP=C2v NFZC=0 NDOC=4 NALP=0 NVAL=4 NPRT=2 ISTSYM=1 SOCI=.TRUE. NEXT =30 MXNINT=500000 $END
$GUGDIA PRTTOL=0.001 CVGTOL=1.0E-5 ITERMX=1000 $END
```

19.6.6 ECP

To use Effective Core Potentials (ECP) in GAMESS, you must define a {$ECP . . . $END} block. There must be a definition of a potential for every atom in the system, including symmetry equivalent ones. In addition, they must appear in the particular order expected by GAMESS. Below is an example of an ECP input block for a single water molecule using BFD ECPs. To turn on the use of ECPs, the option “ECP=READ” must be added to the CONTROL input block.

```
$ECP
O-QMC GEN 2 1
 3
 6.00000000 1 9.29793903
 55.78763416 3 8.86492204
 -38.81978498 2 8.62925665
 1
 38.41914135 2 8.71924452
H-QMC GEN 0 0
 3
 1.000000000000 1 25.000000000000
 25.000000000000 3 10.821821902641
 -8.228005709676 2 9.368618758833
H-QMC
$END
```
19.7 Appendix B: convert4qmc

To generate the particleset and wavefunction XML blocks required by QMCPACK in calculations with molecular systems, the converter convert4qmc must be used. The converter will read the standard output from the appropriate Quantum Chemistry calculation and will generate all the necessary input for QMCPACK. Below we describe the main options of the converter for GAMESS output. In general, there are 3 ways to use the converter depending on the type of calculation performed. The minimum syntax for each option is found below. For a description of the xml files produced by the converter, see section E.

1. For all single determinant calculations (HF and DFT with any DFTTYP):

   ```
   convert4qmc -gamessAscii single det.out
   ```

   - single det.out is the standard output generated by GAMESS.

2. *(This option is not recommended. Use option below to avoid mistakes.)* For multi-determinant calculations where the orbitals and configurations are read from different files (for example when using orbitals from a MCSCF run and configurations from a subsequent CI run):

   ```
   convert4qmc -gamessAscii orbitals multidet.out -ci cicoeff multidet.out
   ```

   - orbitals_multidet.out is the standard output from the calculation that generates the orbitals. cicoeff multidet.out is the standard output from the calculation that calculates the CI expansion.

3. For multi-determinant calculations where the orbitals and configurations are read from the same file, using PRTMO=.T. in the GUESS input block:

   ```
   convert4qmc -gamessAscii multi det.out -ci multi det.out -readInitialGuess Norb
   ```

   - multi_det.out is the standard output from the calculation that calculates the CI expansion.

Options:

- **-gamessAscii file.out**: Standard output of GAMESS calculation. With the exception of determinant configurations and coefficients in multi-determinant calculations, everything else is read from this file including: atom coordinates, basis sets, single particle orbitals, ECPs, number of electrons, multiplicity, etc.

- **-ci file.out**: In multi-determinant calculations, determinant configurations and coefficients are read from this file. Notice that single particle orbitals are NOT read from this file. Recognized CI packages are: ALDET, GUGA and ORMAS. Output produced with the GUGA package MUST have the option “NPRT=2” in the CIDRT or DRT input blocks.
- **-threshold cutoff**: Cutoff in multi-determinant expansion. Only configurations with coefficients above this value are printed.

- **-zeroCI**: Sets to zero the CI coefficients of all determinants, with the exception of the first one.

- **-readInitialGuess Norb**: Reads Norb initial orbitals (“INITIAL GUESS ORBITALS”) from GAMESS output. These are orbitals generated by the GUESS input block and printed with the option “PRTMO=.T.”. Notice that this is useful only in combination with the option “GUESS=MOREAD” and in cases where the orbitals are not modified in the GAMESS calculation, e.g. CI runs. This is the recommended option in all CI calculations.

- **-NaturalOrbitals Norb**: Read Norb “NATURAL ORBITALS” from GAMESS output. The natural orbitals must exist in the output, otherwise the code aborts.

- **-add3BodyJ**: Adds three-body Jastrow terms (e-e-I) between electron pairs (both same spin and opposite spin terms) and all ion species in the system. The radial function is initialized to zero and the default cutoff is 10.0 bohr. The converter will add a one- and two-body Jastrow to the wavefunction block by default.

Useful notes:

- The type of single particle orbitals read by the converter depends on the type of calculation and on the options used. By default, when neither -readInitialGuess or -NaturalOrbitals are used, the following orbitals are read in each case (notice that -readInitialGuess or -NaturalOrbitals are mutually exclusive):
  - RHF and ROHF: “EIGENVECTORS”
  - MCSCF: “MCSCF OPTIMIZED ORBITALS”
  - GUGA, ALDET, ORMAS: Cannot read orbitals without -readInitialGuess or -NaturalOrbitals options.

- The single particle orbitals and printed CI coefficients in MCSCF calculations are not consistent in GAMESS. The printed CI coefficients correspond to the next-to-last iteration, they are not recalculated with the final orbitals. So in order to get appropriate CI coefficients from MCSCF calculations, a subsequent CI (no SCF) calculation is needed to produce consistent orbitals. In principle, it is possible to read the orbitals from the MCSCF output and the CI coefficients and configurations from the output of the following CI calculations. This could lead to problems in principle, since GAMESS will rotate initial orbitals by default in order to obtain an initial guess consistent with the symmetry of the molecule. This last step is done by default and can change the orbitals reported in the MCSCF calculation before the CI is performed. In order to avoid this problem, it is highly recommended to use option #3 above to read all the information from the output of the CI calculation, this requires the use of “PRTMO=.T.” in the GUESS input block. Since the orbitals are printed after any symmetry rotation, the resulting output will always be consistent.
19.8 Appendix C: Wave-function Optimization XML block

```xml
<loop max="10">
  <$mc method="linear" move="pbyp" checkpoint="-1" gpu="no">
    <parameter name="blocks">10</parameter>
    <parameter name="warmupsteps">25</parameter>
    <parameter name="steps">1</parameter>
    <parameter name="substeps">20</parameter>
    <parameter name="timestep">0.5</parameter>
    <parameter name="samples">10240</parameter>
    <parameter name="energy">0.95</parameter>
    <parameter name="unreweightedvariance">0.0</parameter>
    <parameter name="reweightedvariance">0.05</parameter>
    <parameter name="useDrift">yes</parameter>
    <parameter name="bigchange">10.0</parameter>
    <parameter name="LocalEnergy">hdf5="no"</parameter>
    <parameter name="usebuffer">yes</parameter>
    <parameter name="nonlocalpp">yes</parameter>
    <parameter name="MinMethod">quartic</parameter>
    <parameter name="exp0">-6</parameter>
    <parameter name="alloweddifference">1.0e-5</parameter>
    <parameter name="stepsize">0.15</parameter>
    <parameter name="nstabilizers">1</parameter>
  </mc>
</loop>
```

Figure 19.6: Sample XML optimization block.

Options:

- bigchange: (default 50.0) largest parameter change allowed
- usebuffer: (default no) Save useful information during VMC
- nonlocalpp: (default no) Include non-local energy on 1-D min
- MinMethod: (default quartic) Method to calculate magnitude of parameter change quartic:
  fit quartic polynomial to 4 values of the cost function obtained using reweighting along
  chosen direction linemin: direct line minimization using reweighting rescale: no 1-D minimization.
  Uses Umrigars suggestions.
- stepsize: (default 0.25) step size in either quartic or linemin methods.
- alloweddifference: (default 1e-4) Allowed increased in energy
- exp0: (default -16.0) Initial value for stabilizer (shift to diagonal of H) Actual value of stabilizer
  is 10 exp0
- nstabilizers: (default 3) Number of stabilizers to try
- stabilizerScale: (default 2.0) Increase in value of exp0 between iterations.
- max its: (default 1) number of inner loops with same sample
• minwalkers: (default 0.3) minimum value allowed for the ratio of effective samples to actual number of walkers in a reweighting step. The optimization will stop if the effective number of walkers in any reweighting calculation drops below this value. Last set of acceptable parameters are kept.

• maxWeight: (default 1e6) Maximum weight allowed in reweighting. Any weight above this value will be reset to this value.

Recommendations:

• Set samples to equal to (#threads)*blocks.

• Set steps to 1. Use substeps to control correlation between samples.

• For cases where equilibration is slow, increase both substeps and warmupsteps.

• For hard cases (e.g. simultaneous optimization of long MSD and 3-Body J), set exp0 to 0 and do a single inner iteration (max its=1) per sample of configurations.
19.9 Appendix D: VMC and DMC XML block

Figure 19.7: Sample XML blocks for VMC and DMC calculations.

General Options:

- **move**: (default "walker") Type of electron move. Options: "pbyp" and "walker".
- **checkpoint**: (default ":-1") (If > 0) Generate checkpoint files with given frequency. The calculations can be restarted/continued with the produced checkpoint files.
- **useDrift**: (default "yes") Defines the sampling mode. useDrift = "yes" will use Langevin acceleration to sample the VMC and DMC distributions, while useDrift="no" will use random displacements in a box.
- **warmupSteps**: (default 0) Number of steps warmup steps at the beginning of the calculation. No output is produced for these steps.
- **blocks**: (default 1) Number of blocks (outer loop).
- **steps**: (default 1) Number of steps per blocks (middle loop).
- **sub steps**: (default 1) Number of substeps per step (inner loop). During sub steps, the local energy is not evaluated in VMC calculations, which leads to faster execution. In VMC calculations, set sub steps to the average autocorrelation time of the desired quantity.
- **time step**: (default 0.1) Electronic time step in bohr.
- **samples**: (default 0) Number of walker configurations saved during the current calculation.
• **walkers**: (default #threads) In VMC, sets the number of walkers per node. The total number of walkers in the calculation will be equal to walkers*(# nodes).

Options unique to DMC:

• **targetWalkers**: (default #walkers from previous calculation, e.g. VMC.) Sets the target number of walkers. The actual population of walkers will fluctuate around this value. The walkers will be distributed across all the nodes in the calculation. On a given node, the walkers are split across all the threads in the system.

• **nonlocalmoves**: (default "no") Set to "yes" to turns on the use of Casula’s T-moves.
19.10 Appendix E: Wave-function XML block

In this section we describe the basic format of a QMCPACK wavefunction XML block. Everything listed in this section is generated by the appropriate converter tools. Little to no modification is needed when performing standard QMC calculations. As a result, this section is meant mainly for illustration purposes. Only experts should attempt to modify these files (with very few exceptions like the cutoff of CI coefficients and the cutoff in Jastrow functions) since changes can lead to unexpected results.

A QMCPACK wavefunction XML block is a combination of a determinantset, which contains the anti-symmetric part of the wave-function, and one or more jastrow blocks. The syntax of the anti-symmetric block depends on whether the wave-function is a single determinant or a multi-determinant expansion. Figure 19.8 shows the general structure of the single determinant case. The determinantset block is composed of a basisset block, which defines the atomic orbital basis set, and a slaterdeterminant block, which defines the single particle orbitals and occupation numbers of the Slater determinant. Figure 19.9 shows a section of a basisset block for an oxygen atom. The
structure of this block is rigid and should not be modified. Figure 19.10 shows a (piece of a) sample of a slaterdeterminant block. The slaterdeterminant block consists of 2 determinant blocks, one for each electron spin. The parameter “size” in the determinant block refers to the number of single particle orbitals present while the “size” parameter in the coefficient block refers to the number of atomic basis functions per single particle orbital.

Figure 19.10: Sample XML block for the single slater determinant case.

Figure 19.11 shows the general structure of the multi-determinant case. Similar to the single determinant case, the determinantset must contain a basisset block. This definition is identical to
the one described above. In this case, the definition of the single particle orbitals must be done independently from the definition of the determinant configurations, the latter is done in the sposet block while the former is done on the multideterminant block. Notice that 2 sposet sets must be defined, one for each electron spin. The name of reach sposet set is required in the definition of the multideterminant block. The determinants are defined in terms of occupation numbers based on these orbitals.

```xml
<wavefunction id="psi0" target="e">
  <determinantset name="LCAOSet" type="MolecularOrbital" transform="yes" source="ion0">
    <basisset name="LCAOSet">
      <atomicBasisSet name="Gaussian-62" angular="cartesian" type="Gaussian">
        <elementType "0" normalized="no">
        ...
      </atomicBasisSet>
    </basisset>
    <sposet basisset="LCAOSet" name="sop-up" size="3">
      <occupation mode="ground"/>
      <coefficient size="40" id="updetC">
        ...
      </coefficient>
    </sposet>
    <sposet basisset="LCAOSet" name="sop-dn" size="3">
      <occupation mode="ground"/>
      <coefficient size="40" id="downdetC">
        ...
      </coefficient>
    </sposet>
    <multideterminant optimize="yes" spo_up="sop-up" spo_dn="sop-dn">
      <detlist size="07" type="CSF" nca="9" ncb="6" nca="4" ncb="4" nstates="8" cutoff="0.01">
        <csf id="CSF00 0" exctlvl="0" coeff="0.984378" qchem_coeff="0.984378" occ="22220000">
          <det id="csf_0-0" coeff="1" alpha="11110000" beta="11110000"/>
        </csf>
        ...
      </detlist>
      </multideterminant>
    </determinantset>
  </wavefunction>
```

Figure 19.11: Basic framework for a multi-determinant determinantset XML block.

There are various options in the multideterminant block that users should be aware of.

- **cutoff**: (IMPORTANT!) Only configurations with (absolute value) “qchem coeff” larger than this value will be read by QMCPACK.
- **optimize**: Turn on/off the optimization of linear CI coefficients.
- **coeff**: (in csf) Current coefficient of given configuration. Gets updated during wavefunction optimization.
• qchem coeff: (in csf) Original coefficient of given configuration from GAMESS calculation. This is used when applying a cutoff to the configurations read from the file. The cutoff is applied on this parameter and not on the optimized coefficient.

• nca and nab: number of core orbitals for up/down electrons. A core orbital is an orbital that is doubly occupied in all determinant configurations, not to be confused with core electrons. These are not explicitly listed on the definition of configurations.

• nea and neb: number of up/down active electrons (those being explicitly correlated).

• nstates: number of correlated orbitals

• size (in detlist): contains the number of configurations in the list.

The remaining part of the determinant set block is the definition of jastrow factor. Any number of these can be defined. Figure 19.12 shows a sample jastrow block including one-, two- and three-body terms. This is the standard block produced by convert4qmc with the option -add3BodyJ (this particular example is for a water molecule). Optimization of individual radial functions can be turned on/off using the “optimize” parameter. It can be added to any coefficients block, even though it is currently not present in the J1 and J2 blocks.

```
<jastrow name="J2" type="Two-Body" function="B spline" print="yes">
  <correlation rcut="10" size="10" speciesA="u" speciesB="u">
    <coefficients id="uu" type="Array">0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0</coefficients>
  </correlation>
  <correlation rcut="10" size="10" speciesA="u" speciesB="d">
    <coefficients id="ud" type="Array">0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0</coefficients>
  </correlation>
</jastrow>

<jastrow name="J1" type="One-Body" function="B spline" source="1on0" print="yes">
  <correlation rcut="10" size="10" cusp="0" elementType="O">
    <coefficients id="e0" type="Array">0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0</coefficients>
  </correlation>
  <correlation rcut="10" size="10" cusp="0" elementType="H">
    <coefficients id="eH" type="Array">0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0</coefficients>
  </correlation>
</jastrow>

<jastrow name="J3" type="cube" function="polynomial" source="ion0" print="yes">
  <correlation ispecies="0" especies="u" isize="3" eisize="3" rcut="10">
    <coefficients id="uu0" type="Array" optimize="yes">
      <coefficients>
      </coefficients>
    </correlation>
  <correlation ispecies="0" especies1="u" especies2="d" isize="3" eisize="3" rcut="10">
    <coefficients id="ud0" type="Array" optimize="yes">
      <coefficients>
      </coefficients>
    </correlation>
  <correlation ispecies="H" especies="u" isize="3" eisize="3" rcut="10">
    <coefficients id="uH0" type="Array" optimize="yes">
      <coefficients>
      </coefficients>
    </correlation>
  <correlation ispecies="H" especies1="u" especies2="d" isize="3" eisize="3" rcut="10">
    <coefficients id="udH" type="Array" optimize="yes">
      <coefficients>
      </coefficients>
    </correlation>
</jastrow>
```

Figure 19.12: Sample Jastrow XML block.

This training assumes basic familiarity with the UNIX operating system. In particular, we use simple scripts written in “csh”. In addition, we assume that the student has obtained all the neces-
sary files and executables, and that the location of the training files are located at ${\$\text{TRAINING TOP}}$.

The goal of the training not only to familiarize the student with the execution and options in QMCPACK, but also to introduce him/her to important concepts in quantum Monte Carlo calculations and many-body electronic structure calculations.
Chapter 20

Lab 4: Condensed Matter Calculations

20.1 Topics covered in this Lab

- tiling DFT primitive cells into QMC supercells
- reducing finite size errors via extrapolation
- reducing finite size errors via averaging over twisted boundary conditions
- using the B-spline mesh factor to reduce memory requirements
- using a coarsely resolved vacuum buffer region to reduce memory requirements
- calculating the DMC total energies of representative 2D and 3D extended systems

20.2 Lab directories and files

```
labs/lab4_condensed_matter/
├── Be-2at-setup.py - DFT only for prim to conv cell
├── Be-2at-qmc.py - QMC only for prim to conv cell
├── Be-16at-qmc.py - DFT and QMC for prim to 16 atom cell
├── graphene-setup.py - DFT and OPT for graphene
├── graphene-loop-mesh.py - VMC scan over orbital bspline mesh factors
├── graphene-final.py - DMC for final meshfactor
├── pseudopotentials - pseudopotential directory
│   ├── Be.ncpp - Be PP for Quantum ESPRESSO
│   ├── Be.xml - Be PP for QMCPACK
│   ├── C.BFD.upf - C PP for Quantum ESPRESSO
│   └── C.BFD.xml - C PP for QMCPACK
```

The goal of this lab will be to introduce you to the somewhat specialized problems involved in performing diffusion Monte Carlo calculations on condensed matter as opposed to the atoms and molecules that were the focus of earlier labs. Calculations will be performed on two different systems. Firstly, we will perform a series of calculations on BCC beryllium focusing on the necessary methodology to limit finite size effects. Secondly, we will perform calculations on graphene as an example of a system where qmcpack’s ability to handle cases with mixed periodic and open boundary conditions is useful. This example will also focus on strategies to limit memory usage.
for such systems. All of the calculations performed in this lab will utilize the Nexus workflow
management system that vastly simplifies the process by automating the steps of generating trial
wavefunctions and performing DMC calculations.

20.3 Preliminaries

For any DMC calculation, we must start with a trial wavefunction. As is typical for our calculations
of condensed matter, we will produce this wavefunction using density functional theory. Specifically,
we will use quantum espresso to generate a slater determinant of single particle orbitals. This is
done as a three step process. First, we calculate the converged charge density by performing a
DFT calculation with a fine grid of k-points to fully sample the Brillouin zone. Next, a non-self
consistent calculation is performed at the specific k-points needed for the supercell and twists
needed in the DMC calculation (more on this later). Finally, a wavefunction is converted from
the binary representation used by quantum espresso to the portable hdf5 representation used by
qmcpack.

The choice of k-points necessary to generate the wavefunctions depends on both the super-
cell chosen for the DMC calculation and by the supercell twist vectors needed. Recall that the
wavefunction in a plane wave DFT calculation is written using Bloch’s theorem as:

$$\Psi(\vec{r}) = e^{i\vec{k} \cdot \vec{r}} u(\vec{r})$$  \hspace{1cm} (20.1)

Where \(\vec{k}\) is confined to the first Brillouin zone of the cell chosen and \(u(\vec{r})\) is periodic in this
simulation cell. A plane wave DFT calculation stores the periodic part of the wavefunction as
a linear combination of plane waves for each single particle orbital at all k-points selected. The
symmetry of the system allows us to generate an arbitrary supercell of the primitive cell as follows:
Consider the set of primitive lattice vectors, \(\{a_1^p, a_2^p, a_3^p\}\). We may write these vectors in a matrix,
\(L_p\), whose rows are the primitive lattice vectors. Consider a non-singular matrix of integers, \(S\). A
corresponding set of supercell lattice vectors, \(\{a_1^s, a_2^s, a_3^s\}\), can be constructed by the matrix product

$$a_i^s = S_{ij} a_j^p$$  \hspace{1cm} (20.2)

If the primitive cell contains \(N_p\) atoms, the supercell will then contain \(N_s = |\det(S)| N_p\) atoms.

Now, the wavefunction at any point in this new supercell can be related to the wavefunction
in the primitive cell by finding the linear combination of primitive lattice vectors that maps this
point back to the primitive cell:

$$\vec{r}' = \vec{r} + x a_1^p + y a_2^p + z a_3^p = \vec{r} + T$$  \hspace{1cm} (20.3)

where \(x, y, z\) are integers. Now the wavefunction in the supercell at point \(\vec{r}'\) can be written in terms
of the wavefunction in the primitive cell at \(\vec{r}'\) as:

$$\Psi(\vec{r}) = \Psi(\vec{r}') e^{i\vec{T} \cdot \vec{k}}$$  \hspace{1cm} (20.4)

where \(\vec{k}\) is confined to the first Brillouin zone of the primitive cell. We have also chosen the
supercell twist vector which places a constraint on the form of the wavefunction in the supercell.
The combination of these two constraints allows us to identify family of N k-points in the primitive
cell that satisfy the constraints. Thus for a given supercell tiling matrix and twist angle, we can
write the wavefunction everywhere in the supercell by knowing the wavefunction a N k-points in
the primitive cell. This means that the memory necessary to store the wavefunction in a supercell is
only linear in the size of the supercell rather than the quadratic cost if symmetry were neglected.
20.4 Total energy of BCC beryllium

As was discussed in this morning’s lectures when performing calculations of periodic solids with QMC, it is essential to work with a reasonable size supercell rather than the primitive cells that are common in mean field calculations. Specifically, all of the finite size correction schemes discussed in the morning require that the exchange-correlation hole be considerably smaller than the periodic simulation cell. Additionally, finite size effects are lessened as the distance between the electrons in the cell and their periodic images increases, so it is advantageous to generate supercells that are as spherical as possible so as to maximize this distance. However, there is a competing consideration in that for calculating total energies we often want to be able to extrapolate the energy per particle to the thermodynamic limit by means of the following formula in 3 dimensions:

\[
E_{\text{inf}} = C + E_N/N
\]  

This formula derived assuming the shape of the supercells is consistent (more specifically that the periodic distances scale uniformly with system size), meaning we will need to do a uniform tiling, ie, 2x2x2, 3x3x3 etc. As a 3x3x3 tiling is 27 times larger than the supercell and the practical limit of DMC is on the order of 200 atoms (depending on Z), sometimes it is advantageous to choose a less spherical supercell with fewer atoms rather than a more spherical one that is too expensive to tile.

In the case of a BCC crystal, it is possible to tile the one atom primitive cell to a cubic supercell by only doubling the number of electrons. This is the best possible combination of a small number of atoms that can be tiled and a regular box that maximizes the distance between periodic images. We will need to determine the tiling matrix \( S \) that generates this cubic supercell by solving the following equation for the coefficients of the \( S \) matrix:

\[
\begin{bmatrix}
1 & 0 & 0 \\
0 & 1 & 0 \\
0 & 0 & 1 \\
\end{bmatrix} = \begin{bmatrix}
s_{11} & s_{12} & s_{13} \\
s_{21} & s_{22} & s_{23} \\
s_{31} & s_{32} & s_{33} \\
\end{bmatrix} \cdot \begin{bmatrix}
0.5 & 0.5 & -0.5 \\
-0.5 & 0.5 & 0.5 \\
0.5 & -0.5 & 0.5 \\
\end{bmatrix}
\]  

We will now use Nexus to generate the trial wavefunction for this BCC beryllium.

Fortunately, the Nexus will handle determination of the proper k-vectors given the tiling matrix. All that is needed is to place the tiling matrix in the Be-2at-setup.py file. Now the definition of the physical system is:

```python
cbc_Be = generate_physical_system(
    lattice = 'cubic',
    cell = 'primitive',
    centering = 'I',
    atoms = 'Be',
    constants = 3.490,
    units = 'A',
    net_charge = 0,
    net_spin = 0,
    Be = 2,
    tiling = [[a,b,c], [d,e,f], [g,h,i]],
    kgrid = kgrid,
    kshift = (.5,.5,.5)
)
```

Where the tiling line should be replaced with the row major tiling matrix from above. This script file will now perform a converged DFT calculation to generate the charge density in a directory.
called bcc-beryllium/scf and perform a non self consistent DFT calculation to generate single particle orbitals in the directory bcc-beryllium/nscf. Fortunately, Nexus will calculate the required k-points needed to tile the wavefunction to the supercell, so all that is necessary is the granularity of the supercell twists and whether this grid is shifted from the origin. Once this is finished, it performs the conversion from pwscf’s binary format to the hdf5 format used by qmcpack. Finally, it will optimize the coefficients of one-body and two-body jastrow factors in the supercell defined by the tiling matrix.

Run these calculations by executing the script Be-2at-setup.py. You will notice that such small calculations as are required to generate the wavefunction of Be in a one atom cell are rather inefficient to run on a high performance computer such as vesta in terms of the time spent doing calculations versus time waiting on the scheduler and booting compute nodes. One of the benefits of the portable hdf format that is used by qmcpack is that you can generate data like wavefunctions on a local workstation or other convenient resource and only use high performance clusters for the more expensive QMC calculations.

In this case, the wavefunction is generated in the directory bcc-beryllium/nscf-2at_222/pwscf_output in a file called pwscf.pwscf.h5. It can be useful for debugging purposes to be able to verify the contents of this file are what you expect. For instance, you can use the tool h5ls to check the geometry of the cell where the dft calculations were performed, or number of k-points or electrons in the calculation. This is done with the command: h5ls -d pwscf.pwscf.h5/supercell or h5ls -d pwscf.pwscf.h5/electrons.

In the course of running Be-2at-setup.py, you will get an error when attempting to perform the vmc and wavefunction optimization calculations. This is due to the fact that the wavefunction has been generated supercell twists of the form (+/- 1/4, +/- 1/4, +/- 1/4). In the case that the supercell twist contains only 0 or 1/2, it is possible to operate entirely with real arithmetic. The executable that has been indicated in Be-2at-setup.py has been compiled for this case. Note that where this is possible, the memory usage is a factor of two less than the general case and the calculations are somewhat faster. However, it is often necessary to perform calculations away from these special twist angles in order to reduce finite size effects. To fix this, delete the directory bcc-beryllium/opt-2at, change the line in near the top of Be-2at-setup.py from

```python
qmcpack = '/soft/applications/qmcpack/Binaries/qmcpack'
```

to

```python
qmcpack = '/soft/applications/qmcpack/Binaries/qmcpack_comp'
```

and rerun the script.

When the optimization calculation has finished, check that everything has proceeded correctly by looking at the output in the opt-2at directory. Firstly, you can grep the output file for Delta to see if the cost function has indeed been decreasing during the optimization. You should find something like:

<table>
<thead>
<tr>
<th>OldCost</th>
<th>NewCost</th>
<th>Delta Cost</th>
</tr>
</thead>
<tbody>
<tr>
<td>4.8789147e-02</td>
<td>4.0695360e-02</td>
<td>-8.0937871e-03</td>
</tr>
<tr>
<td>3.8507795e-02</td>
<td>3.8338486e-02</td>
<td>-1.6930674e-04</td>
</tr>
<tr>
<td>4.1079105e-02</td>
<td>4.0898345e-02</td>
<td>-1.8076319e-04</td>
</tr>
<tr>
<td>4.2681333e-02</td>
<td>4.2356598e-02</td>
<td>-3.2473514e-04</td>
</tr>
</tbody>
</table>
OldCost: 3.9168577e-02 NewCost: 3.8552883e-02 Delta Cost:-6.1569350e-04
OldCost: 4.3977361e-02 NewCost: 4.2865751e-02 Delta Cost:-1.1116183e-03

Which shows that the starting wavefunction was fairly good and that most of the optimization occurred in the first step. Confirm this by using qmca to look at how the energy and variance changed over the course of the calculation with the command: qmca -q ev -e 10 *.scalar.dat executed in the opt-2at directory. You should get output like the following:

<table>
<thead>
<tr>
<th>series</th>
<th>LocalEnergy</th>
<th>Variance</th>
<th>ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>opt 0</td>
<td>-2.159139 +/- 0.001897</td>
<td>0.047343 +/- 0.000758</td>
<td>0.0219</td>
</tr>
<tr>
<td>opt 1</td>
<td>-2.163752 +/- 0.001305</td>
<td>0.039389 +/- 0.000666</td>
<td>0.0182</td>
</tr>
<tr>
<td>opt 2</td>
<td>-2.160913 +/- 0.001347</td>
<td>0.040879 +/- 0.000682</td>
<td>0.0189</td>
</tr>
<tr>
<td>opt 3</td>
<td>-2.162043 +/- 0.001223</td>
<td>0.041183 +/- 0.001250</td>
<td>0.0190</td>
</tr>
<tr>
<td>opt 4</td>
<td>-2.162441 +/- 0.000865</td>
<td>0.039597 +/- 0.000342</td>
<td>0.0183</td>
</tr>
<tr>
<td>opt 5</td>
<td>-2.161287 +/- 0.000732</td>
<td>0.039954 +/- 0.000498</td>
<td>0.0185</td>
</tr>
<tr>
<td>opt 6</td>
<td>-2.163458 +/- 0.000973</td>
<td>0.044431 +/- 0.003583</td>
<td>0.0205</td>
</tr>
<tr>
<td>opt 7</td>
<td>-2.163495 +/- 0.001027</td>
<td>0.040783 +/- 0.000413</td>
<td>0.0189</td>
</tr>
</tbody>
</table>

Now that the optimization has completed successfully, we can perform dmc calculations. The first goal of the calculations will be to try to eliminate the one body finite size effects by twist averaging. The script Be-2at-qmc.py has the necessary input. Note on line 42 two twist grids are specified, (2,2,2) and (3,3,3). Change the tiling matrix in this input file as in Be-2at-qmc.py and start the calculations. Note that this workflow takes advantage of qmcpack’s ability to group jobs. If you look in the directory dmc-2at_222 at the job submission script, (dmc.qsub.in) you will note that rather than operating on an xml input file, qmcapp is targeting a text file called dmc.in. This file is a simple text file that contains the names of the 8 xml input files needed for this job, one for each twist. When operated in this mode, qmcapp will use mpi groups to run multiple copies of itself within the same mpi context. This is often useful both in terms of organizing calculations and also for taking advantage of the large job sizes that computer centers often encourage.

The dmc calculations in this case are designed to complete in a few minutes. When they have finished running, first look at the scalar.dat files corresponding to the dmc calculations at the various twists in dmc-2at_222. Using a command like 'qmca -q ev -e 32 *.s001.scalar.dat' (with a suitably chosen number of blocks for the equilibration), you will see that the dmc energy in each calculation is nearly identical within the statistical uncertainty of the calculations. In the case of a large supercell, this is often indicative of a situation where the Brillouin zone is so small that the one body finite size effects are nearly converged without any twist averaging. In this case, however, this is because of the symmetry of the system. For this cubic supercell, all of the twist angles chosen in this shifted 2x2x2 grid are equivalent by symmetry. In the case where substantial resources are required to equilibrate the dmc calculations, it can be beneficial to avoid repeating such twists and instead simply weight them properly. In this case however where the equilibration is inexpensive, there is no benefit to adding such complexity as the calculations can simply be averaged together and the result is equivalent to performing a single longer calculation.

Using the command qmc -a -q ev -e 16 *.s001.scalar.dat, average the dmc energies in dmc-
2at_222 and dmc-2at_333 to see whether the one body finite size effects are converged with a 3x3x3 grid of twists. As beryllium as a metal, the convergence is quite poor (0.025 Ha / Be or 0.7 eV / Be). If this were a production calculation it would be necessary to perform calculations on much larger grids of supercell twists to eliminate the one body finite size effects.

In this case there are several other calculations that would warrent a high priority. A script Be-16at-qmc.py has been provided where you can imput the appropriate tiling matrix for a 16 atom cell and perform calculations to estimate the two body finite size effects which will also be quite large in the 2 atom calculations. This script will take approximately 30 minutes to run to completion, so depending on interest, you can either run it, or also work to modify the scripts to address the other technical issues that would be necessary for a production calculation such as calculating the population bias or the timestep error in the dmc calculations.

Another useful exercise would be to attempt to validate this pseudopotential by calculating the ionization potential and electron affinity of the isolated atom and comparing to the experimental values: IP = 9.3227 eV, EA = 2.4 eV.

20.5 Handling a 2D system: graphene

In this section we will examine a calculation of an isolated sheet of graphene. As graphene is a two dimensional system, we will take advantage of qmcpack's ability to mix periodic and open boundary conditions to eliminate and spurious interaction of the sheet with its images in the z direction. Run the script graphene-setup.py which will generate the wavefunction and optimize one and two body jastrow factors. In the script, notice line 160: bconds = 'ppn' in the generate_qmcpack function which specifies this mix of open and periodic boundary conditions. As a consequence of this, the atoms will need to be kept away from this open boundary in the z direction as the electronic wavefunction will not be defined outside of the simulation box in this direction. For this reason, all of the atom positions in at the beginning of the file have z coordinates 7.5. At this point, run the script graphene-setup.py.

Aside from the change in boundary conditions, the main thing that distinguished this kind of calculation from the beryllium example above is the large amount of vacuum in the cell. While this is a very small calculation designed to run quickly in the tutorial, in general a more converged calculation would quickly become memory limited on an architecture like BG/Q. When the initial wavefunciton optimization has completed to your satisfaction, run the script graphene-loop-mesh.py. This examines within variational Monte Carlo an appraoch to reducing the memory required to store the wavefunction. In graphene-loop-mesh.py, the spacing between the b-spline points is varied uniformly. The mesh spacing is a prefactor to the linear spacing between the spline points, so the memory usage goes as the cube of the meshfactor. When you run the calculations, examine the .s000.scalar.dat files with qmca to determine the lowest possible mesh spacing that preserves both the vmc energy and the variance.

Finally, edit the file graphene-final.py which will perform two DMC calculations. In the first, (qmc1) replace the following lines:

```
    meshfactor  = xxx,
    precision   = '----',
```

using the values you have determined to perform the calculation with as small as possible of wavefunction. Note that we can also use single precision arithmetic to store the wavefunction by specifying precision='single'. When you run the script, compare the output of the two DMC calculations in terms of energy and variance. Also see if you can calculate the fraction of memory that you were able to save by using a meshfactor other than 1 and single precision arithmetic.
20.6 Conclusion

Upon completion of this lab, you should be able to use Nexus to perform DMC calculations on periodic solids when provided with a pseudopotential. You should also be able to reduce the size of the wavefunction in a solid state calculation in cases where memory is a limiting factor.
Chapter 21

Additional Tools

QMCPACK provides a set of lightweight executables that address certain common problems in QMC workflow and analysis. These range from conversion utilities between different file formats and QMCPACK (e.g. ppconvert and convert4qmc), (extract-eshdf-kvectors), to post-processing utilities (trace-density and qmcfinitesize), and to many others. In this chapter, we cover the use cases, syntax, and features of all additional tools provided with QMCPACK.

21.1 Initialization Tools

21.1.1 getSupercell

21.2 Post-Processing

21.2.1 qmca

qmca is a versatile tool to analyze and plot the raw data from QMCPACK *.scalar.dat files. It is a python executable and part of the Nexus suite of tools. It can be found in trunk/nexus/executables. For more detail, see section 12.1.

21.2.2 qfit

qfit is a curve fitting tool to obtain statistical error bars on fitted parameters. It is useful for DMC timestep extrapolation. For more details, see section 12.2.

21.2.3 qmcfinitesize

qmcfinitesize is a utility to compute many-body finite-size corrections to the energy. It is a C++ executable that is built alongside the qmcpack executable. It can be found in trunk/build/bin.

21.3 Converters

21.3.1 convert4qmc

Convert4qmc allows conversion of orbitals and wavefunctions from quantum chemistry output files to QMCPACK XML and HDF5 input files. It is a small C++ executable that is built alongside the QMCPACK executable, and can be found in build/bin.
To date, convert4qmc supports the following codes: GAMESS[33], Pyscf[34], Quantum Package[26] and GAMESS-FMO[35, 33]

**General use**

General usage of convert4qmc can be prompted by running with no options:

```bash
>convert4qmc
```

```bash
class [-gaussian|-casino|-gamesxml|-gamess|-gamessFMO|VSVB|-QP|-pyscf] filename
[-nojastrow -hdf5 -prefix title -addCusp -production]
[-psi_tag psi0 -ion_tag ion0 -gridtype log|log0|linear -first ri -last rf]
[-size npts -ci file.out -threshold cimin -TargetState state_number
-NaturalOrbitals NumToRead -optDetCoeffs]
Defaults: -gridtype log -first 1e-6 -last 100 -size 1001 -ci required
-threshold 0.01 -TargetState 0 -prefix sample
When the input format is missing, the extension of filename is used to determine the format
*.Fchk -> gaussian; *out -> gamess; *data -> casino; *.xml ->
gamesxml
```

As an example, to convert a GAMESS calculation using a single determinant, the following usage is sufficient:

```bash
convert4qmc -gamess MyGamessOutput.out
```

By default, the converter will generate multiple files:

<table>
<thead>
<tr>
<th>Output</th>
<th>File type</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>*.qmc.in-wfs.xml</td>
<td>XML</td>
<td>default</td>
<td>Main input file for QMCPACK</td>
</tr>
<tr>
<td>*.qmc.in-wfnoj.xml</td>
<td>XML</td>
<td>default</td>
<td>Main input file for QMCPACK</td>
</tr>
<tr>
<td>*.structure.xml</td>
<td>XML</td>
<td>default</td>
<td>file containing the structure of the system</td>
</tr>
<tr>
<td>*.wfnj.xml</td>
<td>XML</td>
<td>default</td>
<td>Wavefunction file with 1, 2 and 3 body Jastrows</td>
</tr>
<tr>
<td>*.wfnj.xml</td>
<td>XML</td>
<td>default</td>
<td>Wavefunction file with no Jastrows.</td>
</tr>
<tr>
<td>*.orbs.h5</td>
<td>HDF5</td>
<td>with -hdf5</td>
<td>HDF5 file containing all wavefunction data</td>
</tr>
</tbody>
</table>

If no `-prefix` option is specified, the prefix is taken from the input file name. For instance, if the GAMESS output file is `Mysim.out` the files generated by convert4qmc will use the prefix `Mysim` and output files will be `Mysim.qmc.in-wfs.xml`, `Mysim.structure.xml` and so on.

- Files `*.in-wfs.xml` and `*.in-wfnoj.xml`
  These are the input files for QMCPACK. The geometry and the wavefunction are stored
in external files *.structure.xml and *.wfj.xml (referenced from *.in-wfs.xml) or *.qmc.wfnoj.xml (referenced from *.qmc.in-wfnoj.xml). The Hamiltonian section is included and the presence or not of an ECP is detected during the conversion. If use of an ECP is detected, a default ECP name is added (e.g. H.qmcpp.xml) and it is the responsibility of the user to modify the ECP name to match the one used to generate the wavefunction.

```xml
<?xml version="1.0"?>
<simulation>
    <!--
Example QMCPACK input file produced by convert4qmc

It is recommend to start with only the initial VMC block and adjust parameters based on the measured energies, variance, and statistics.

-->    
    <!--Name and Series number of the project.-->
    <project id="gms" series="0"/>
    <!--Link to the location of the Atomic Coordinates and the location of the Wavefunction.-->
    <include href="gms.structure.xml"/>
    <include href="gms.wfnoj.xml"/>
    <!--Hamiltonian of the system. Default ECP filenames are assumed.-->
    <hamiltonian name="h0" type="generic" target="e">
        <pairpot name="ElecElec" type="coulomb" source="e" target="e">
            physical="true"
        </pairpot>
        <pairpot name="IonIon" type="coulomb" source="ion0" target="ion0"/>
        <pairpot name="PseudoPot" type="pseudo" source="ion0" wavefunction="psi0"/>
    </hamiltonian>

The qmc.in-wfnoj.xml file will have one VMC block with a minimum number of blocks to reproduce the HF/DFT energy used to generate the trial wavefunction.

```xml
<qmc method="vmc" move="pbyp" checkpoint="-1">
    <estimator name="LocalEnergy" hdf5="no"/>
</qmc>
```
If the qmc.in-wfj.xml file is used, Jastrow optimization blocks followed by a VMC and DMC block are included. These blocks contain default values to allow the user to test the accuracy of a system, however, they need to be updated and optimized for each system. The initial values might only be suitable for a small molecule.

Example follow-up VMC optimization using more samples for greater accuracy

-->
Production VMC and DMC

Examine the results of the optimization before running these blocks.

e.g. Choose the best optimized jastrow from all obtained, put in wavefunction file, do not reoptimize.

```xml
<qmc method="vmc" move="pbyp" checkpoint="-1">
  <estimator name="LocalEnergy" hdf5="no"/>
  <parameter name="warmupSteps">100</parameter>
  <parameter name="blocks">200</parameter>
  <parameter name="steps">50</parameter>
  <parameter name="substeps">8</parameter>
  <parameter name="timestep">0.5</parameter>
  <parameter name="usedrift">no</parameter>
  <parameter name="samples">16000</parameter>
</qmc>

<qmc method="dmc" move="pbyp" checkpoint="20">
  <estimator name="LocalEnergy" hdf5="no"/>
  <parameter name="targetwalkers">16000</parameter>
  <parameter name="reconfiguration">no</parameter>
  <parameter name="warmupSteps">100</parameter>
  <parameter name="timestep">0.005</parameter>
  <parameter name="steps">100</parameter>
  <parameter name="blocks">100</parameter>
  <parameter name="nonlocalmoves">yes</parameter>
</qmc>
```

- **File .structure.xml**
  This file will be referenced from the main qmcpack input. It contains the geometry of the system, position of the atoms, number of atoms, atomic types and charges, and number of electrons.

- **Files .wfj.xml and .wfnoj.xml**
  These files contain the basis set detail, orbital coefficients, and the 1, 2, 3 body Jastrow (in the case of .wfj.xml). If the wavefunction is multideterminant, the expansion will be at the end of the file. It is recommended to use the option `-hdf5` when large molecules are studied to store the data more compactly in an HDF5 file.

- **File .orbs.h5**
  This file is only generated if the option `-hdf5` is added as follows:
**convert4qmc command line options**

<table>
<thead>
<tr>
<th>Option name</th>
<th>Value</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>-nojastrow</td>
<td>-</td>
<td>-</td>
<td>Force no jastrow. qmc.in.wfj will not be generated</td>
</tr>
<tr>
<td>-hdf5</td>
<td>-</td>
<td>-</td>
<td>Force the wf to be in HDF5 format</td>
</tr>
<tr>
<td>-prefix</td>
<td>string</td>
<td>-</td>
<td>All created files will have the name of the string</td>
</tr>
<tr>
<td>-addCusp</td>
<td>-</td>
<td>-</td>
<td>Force to add orbital cusp correction (ONLY for all-electron)</td>
</tr>
<tr>
<td>-production</td>
<td>-</td>
<td>-</td>
<td>Generates specific blocks in the input</td>
</tr>
<tr>
<td>-psi_tag</td>
<td>string</td>
<td>psi0</td>
<td>Name of the electrons particles inside QMCPACK</td>
</tr>
<tr>
<td>-ion_tag</td>
<td>string</td>
<td>ion0</td>
<td>Name of the ion particles inside QMCPACK</td>
</tr>
</tbody>
</table>

- **-nojastrow**
  This option generates only an input file *.qmc.in.wfnxml containing no Jastrow optimization blocks and references a wavefunction file *.wfnoj.xml containing no jastrow section.

- **-hdf5**
  This option generates the *.orbs.h5 HDF5 file containing the basis set and the orbital coefficients. If the wavefunction contains a multideterminant expansion from Quantum Package, it will also be stored in this file. This option minimizes the size of the *.wfj.xml, which points to the HDF file, as in the following example:

```xml
<?xml version="1.0"?>
<qmcsystem>
```

In this case, the *.wfj.xml or *.wfnoj.xml files will point to this HDF file. Information about the basis set, orbital coefficients and the multideterminant expansion is put in this file and removed from the wavefunction files, making them smaller.
Jastrow functions will be included if the option “-nojastrow” was not specified. Note that when initially optimizing a wavefunction, temporarily removing/disabling the three body Jastrow is recommended.

- **-prefix**
  Sets the prefix for all output generated by convert4qmc. If not specified, convert4qmc will use the defaults for:

  - **Gamess**
    If the Gamess output file is named “Name.out” or “Name.output”, all files generated by convert4qmc will carry Name as a prefix (i.e Name.qmc.in.xml).

  - **Pyscf**
    If the Pyscf output file is named “Name.H5”, all files generated by convert4qmc will carry Name as a prefix (i.e Name.qmc.in.xml).

  - **Quantum Package**
    If the Quantum Package output file is named “Name.dump”, all files generated by convert4qmc will carry Name as a prefix (i.e Name.qmc.in.xml).

- **-addCusp**
  This option is very important for all-electron (AE) calculations. In this case, orbitals have to be corrected for the electron-nuclear cusp. The cusp correction scheme follows the algorithm described by Ma et. al. [36] When this option is present, the wavefunction file has a new set of tags:
The tag “cuspCorrection” in the wfj.xml (or wnfoj.xml) wavefunction file will force correction of the orbitals at the beginning of the QMCPACK run.

In the “orbitals“ section of the wavefunction file, a new tag “cuspInfo” will be added for orbitals spin-up and orbitals spin-down:

These tags will point to the files updet.cuspInfo.xml and downdet.cuspInfo.xml. By default, the converter assumes that the files are located in the relative path ../CuspCorrection/. If the directory ../CuspCorrection does not exist, or if the files are not present in that directory, QMCPACK will run the cusp correction algorithm to generate both files. If the files exist, then /qmcpack will apply the corrections to the orbitals.

**Important notes:**
- The cusp correction algorithm is limited to the AoS version of the code. SoA implementation is under progress.
- The AoS code for cusp correction is unfortunately serial. Since the correction needs to be applied for every ion and then for every orbital on that ion, this operation can be extremely costly (slow) for large systems. It is recommended to run the correction on a single fast processor and then transfer updet.cuspInfo.xml and downdet.cuspInfo.xml to the HPC cluster where longer runs will be performed.
- In the AoS implementation, the cusp correction scheme generates a temporary file for every orbital and every atom. This can lead to a very large number of temporary files. It is recommended to run cusp correction in a separate directory “CuspCorrection” as suggested by the path in the wavefunction, and to do so on a high performance filesystem.

- **-psi_tag**
  QMCPACK builds the wavefunction as a named object. In the vast majority of cases, one wavefunction is simulated at a time, but there may be situations where we want to distinguish different parts of a wavefunction, or even use multiple wavefunctions. This option can change the name for these cases.
• `-ion_tag`
  Similar to the `-psi_tag` but for the type of ions.

```xml
<particleiset name="ion0" size="2">
```

• `-production`

Without this option, input files with standard optimization, VMC, and DMC blocks are generated. When the “-production” option is specified, an input file containing more complex options that may be more suitable for large runs at HPC centers is generated. This option is for users who are already familiar with QMC and QMCPACK. Feedback on the standard and production sample inputs is encouraged.

The following options are specific to using MCSCF multideterminants from Gamess.

<table>
<thead>
<tr>
<th>Option</th>
<th>Value</th>
<th>Default</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>-ci</code></td>
<td>String</td>
<td>none</td>
<td>Name of the file containing the CI expansion</td>
</tr>
<tr>
<td><code>-threshold</code></td>
<td>double</td>
<td>none</td>
<td>Cutoff of the weight of the determinants</td>
</tr>
<tr>
<td><code>-TargetState</code></td>
<td>int</td>
<td>none</td>
<td>?</td>
</tr>
<tr>
<td><code>-NaturalOrbitals</code></td>
<td>int</td>
<td>none</td>
<td>?</td>
</tr>
<tr>
<td><code>-optDetCoeffs</code></td>
<td>-</td>
<td>-</td>
<td>Enable the optimization of CI coefficients.</td>
</tr>
</tbody>
</table>

• keyword `-ci`
  Path/name of the file containing the CI expansion in a gamess Format.

• keyword `-threshold`
  The CI expansion contains coefficients (weights) for each determinant. This option sets the maximum coefficient to include in the QMC run.

• keyword `-TargetState`
  ?

• keyword `-NaturalOrbitals`
  ?

• keyword `-optDetCoeffs`
  This flag enables the optimization of the CI expansion coefficients. By default, the optimization of the coefficients is disabled during wavefunction optimization runs.

Examples and more thorough descriptions of these options can be found in the Lab section of this manual: Chapter 19.

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Grid options

These parameters control how the basis set is projected on a grid. The default parameters are chosen to be very efficient. Unless you have a very good reason, it is not recommended to modify them.

- **-gridtype**
  Grid type can be logarithmic, logarithmic base 10 or linear

- **-first**
  First value of the grid

- **-last**
  Last value of the grid

- **-size**
  Number of points in the grid between “first” and “last”.

Supported codes

- **Pyscf**

  Pyscf[34] is an all-purpose quantum chemistry code that can run calculations from simple Hartree-Fock to DFT, MCSCF, and CCSD, and for both isolated systems and periodic boundary conditions. Pyscf can be downloaded from [https://github.com/sunqm/pyscf](https://github.com/sunqm/pyscf). Many examples and tutorials can be found on the Pyscf website and all types of single determinants calculations are compatible with QMCPACK, thanks to active support from the authors of Pyscf. A few additional steps are necessary to generate an output readable by convert4qmc.

  This example shows how to run a Hartree-Fock calculation for the LiH dimer molecule from Pyscf and convert the wavefunction for QMCPACK.

  - **Python path**
    Pyscf is a Python based code. A python module named **PyscfToQmcpack** containing the function **savetoqmcpack** is provided by QMCPACK and is located at
qmcpack/src/QMCTools/PyscfToQmcpack.py. To be accessible to the Pyscf script, this path must be added to the PYTHONPATH environment variable. For the bash shell, this can be done as follows:

```
export PYTHONPATH=/PATH_TO_QMCPACK/qmcpack/src/QMCTools:$PYTHONPATH
```

### Pyscf Input File

Copy and paste the following code in a file named LiH.py

```python
#!/usr/bin/env python
from pyscf import gto, scf, df
import numpy

cell = gto.M(
    atom = '''
    Li 0.0 0.0 0.0
    H 0.0 0.0 3.0139239778''',
    basis = 'cc-pv5z',
    unit = 'bohr',
    spin = 0,
    verbose = 5,
    cart = False,
)
mf = scf.ROHF(cell)
mf.kernel()

###SPECIFIC TO QMCPACK###
title = 'LiH'
from PyscfToQmcpack import savetoqmcpack

savetoqmcpack(cell, mf, title)
```

The arguments to the function `savetoqmcpack` are:

* **cell**
  This is the object returned from `gto.M`, containing the type of atoms, geometry, basisset, spin etc..

* **mf**
  This is an object representing the pyscf level of theory; in this example, ROHF. This object contains the orbitals coefficients of the calculations.

* **title**
  The name of the output file generated by pyscf. By default, the name of the generated file will be “default” if nothing is specified.
By adding the three lines below the “SPECIFIC TO QMCPACK” comment in the input file, the script will dump all the necessary data for QMCPACK in an HDF5 file using the value of “title” as an output name. Pyscf is run as follows:

```bash
> python LiH.py
```

The generated HDF5 can be read by convert4qmc to generate the appropriate QMCPACK input files.

### Generating input files

As described in the previous section, generating input files for pyscf is as follows:

```bash
> convert4qmc -pyscf LiH.h5
```

The HDF5 file produced by “savetoqmcpack” contains the wavefunction in a form directly readable by QMCPACK. The wavefunction files from convert4qmc reference this HDF file, as if the “-hdf5” option were specified (converting from Pyscf implies the “-hdf5” option is always present).

An implementation of periodic boundary conditions with Gaussian orbitals from Pyscf is under development.

- **Quantum Package**
  
  Quantum Package[26] (QP) is a quantum chemistry code developed by the LCPQ laboratory in Toulouse, France. It can be downloaded from [https://github.com/LCPQ/quantum-package](https://github.com/LCPQ/quantum-package), and the tutorial within is quite extensive. The tutorial section of QP can guide you on how to install and run the code.

  After a QP calculation, the data needed for convert4qmc can be generated through:

  ```bash
  qp_run save_for_qmcpack Myrun.ezfio &> Myrun.dump
  ```

  Convert4qmc can read this format and generate QMCPACK input files in XML and HDF5 format. For example:

  ```bash
  convert4qmc -QP Myrun.dump
  ```

  The main reason to use Quantum Package is to access the CIPSI algorithm to generate a multideterminant wavefunction. CIPSI is the preferred choice for generating a selected CI trial wavefunction for QMCPACK. An example on how to use QP for Hartree-Fock and selected CI can be found in Chapter 14.1.1 of this manual. The converter code is actively maintained and co-developed by both QMCPACK and QP developers. An HDF5 output file from QP is under development that will mimic the current behavior of the Pyscf output.

- **GAMESS**

  QMCPACK can use the output of GAMESS[33] for any type of single determinant calculation (HF or DFT) or multideterminant (MCSCF) calculation. A description with an example can be found in the Advanced Molecular Calculations Lab (section 19).
21.3.2 pw2qmcpack.x

pw2qmcpack.x is an executable that converts PWSCF wavefunctions to QMCPACK readable HDF5 format. This utility is built alongside the Quantum Espresso post-processing utilities. This utility is written in Fortran90, and is distributed as a patch of the Quantum Espresso source code. The patch, as well as automated QE download and patch scripts, can be found in `trunk/external_codes/quantum_espresso`.

pw2qmcpack used to be used in serial without problems in small systems and becomes a severe bottleneck for a large system. Due to the large energy cutoff in the calculation with pw.x required by the pseudopotentials and the increasing sizes of systems we are interested in, one limitation of QE can be easily reached that `wf_collect=.true.` results in problems of writing and loading correct plane wave coefficients on disks by pw.x because of the 32bit integer issue. Thus, pw2qmcpack.x fails to convert the orbitals for QMCPACK.

Since Quantum ESPRESSO 5.3.0, the new converter has been fully parallelized to overcome that limitation completely. By setting `wf_collect=.false.` (by default `.false., 6.1 and before and .true. since 6.2), pw.x doesn’t collect the whole wave function into individual files for each k point but write one small file for each processor instead. By just running pw2qmcpack.x in the same parallel setup (MPI tasks and k-pools) as the last scf/nscf calculation with pw.x, the orbitals distributed among processors will first be aggregated by the converter into individual temporal HDF5 files for each k-pool and then merged into the final file. In large calculations, users should benefit from a significant reduction of time in writing the wave function by pw.x thanks to avoiding the wavefunction collection.

pw2qmcpack has been included in the test suite of QMCPACK, see instructions about how to activate the tests in Sec. 3.11. There are tests labeled “no-collect” running the pw.x with setting `wf_collect=.false.`. The input files are stored at examples/solids/dft-inputs-polarized-no-collect. The scf, nscf, pw2qmcpack runs are performed on 16, 12, 12 MPI tasks with 16, 2, 2 k-pools respectively.

21.3.3 ppconvert

ppconvert is a utility to convert pseudopotentials between different commonly used formats. It is a stand alone C++ executable that is not built by default but accessible via adding `-DBUILD_PPCONVERT=1` to cmake and then typing `make ppconvert`. Currently it converts CASINO, FHI, UPF (generated by OPIUM), BFD, GAMESS formats to several formats including XML (QMCPACK) and UPF (Quantum ESPRESSO). See all the formats via `ppconvert -h`. For the output formats requiring Kleinman-Bylander projectors, the atom will be solved with DFT if the projectors are not provided in the input formats. This requires providing reference states and sometimes needs extra tuning for heavy elements. To avoid ghost states, the local channel can be changed via the `--local_channel` option. Ghost state considerations are similar to those of DFT calculations, but may be worse if ghost states were not considered during the original pseudopotential construction. To make the self-consistent calculation converge, the density mixing parameter may need to be reduced via the `--density_mix` option.

Note that the reference state should include only the valence electrons. One reference state should be included for each channel in the pseudopotential. For example, for a sodium atom with a neon core, the reference state would be “1s(1)”. `--s_ref` needs to include a 1s state, `--p_ref` needs to include a 2p state, `--d_ref` needs to include a 3d state, etc. If not specified, a corresponding state with zero occupation is added. If the reference state is chosen as the neon core, setting empty reference states “” is technically correct. In practice, reasonable reference states should be
picked with care. For pseudopotentials with semi-core electrons in the valence, the reference state can be long. For example, Ti pseudopotential has 12 valence electrons. When using the neutral atom state, --s_ref, --p_ref, --d_ref are all set as “1s(2)2p(6)2s(2)3d(2)”. When using an ionized state, the three reference states are all set as “1s(2)2p(6)2s(2)” or “1s(2)2p(6)2s(2)3d(0)”. Unfortunately, if the generated UPF file is used in Quantum ESPRESSO, the calculation may be incorrect due to the presence of “ghost” states. Potentially these can be removed by adjusting the local channel, e.g. by setting --local_channel 1 which chooses the p channel as the local channel instead of d. For this reason, validation of UPF pseudopotentials is always required from the third row and strongly encouraged in general. For example, check that the expected ionization potential and electron affinities are obtained for the atom and check that dimer properties are consistent with those obtained by a Quantum Chemistry code or a plane-wave code that does not use the Kleinman-Bylander projectors.

21.4 Obtaining pseudopotentials

21.4.1 Pseudopotentiallibrary.org

An open website collecting community developed and tested pseudopotentials for QMC and other many-body calculations is being developed at https://pseudopotentiallibrary.org. This site includes potentials in QMCPACK format and an increasing range of electronic structure and quantum chemistry codes. We recommend using potentials from this site if available and suitable for your science application.

21.4.2 Opium

Opium is a pseudopotential generation code available from the website http://opium.sourceforge.net/. Opium can generate pseudopotentials with either Hartree-Fock or DFT methods. Once you have a useable pseudopotential param file (for example, Li.param), generate pseudopotentials for use in Quantum ESPRESSO with the upf format as follows:

Listing 21.1: Generate UPF-formatted pseudopotential with Opium

```bash
opium Li.param Li.log all upf
```

This generates a UPF-formatted pseudopotential (Li.upf, in this case) for use in Quantum ESPRESSO. The pseudopotential conversion tool ppconvert can then convert UPF to FSAtom xml format for use in QMCPACK:

Listing 21.2: Convert UPF-formatted pseudopotential to FSAtom xml format

```bash
ppconvert --upf_pot Li.upf --xml Li.xml
```

21.4.3 Burkatzki-Filippi-Dolg

Burkatzki et al. developed a set of energy-consistent pseudopotentials for use in QMC [3, 5], available at http://www.burkatzki.com/pseudos/index.2.html. To convert for use in QMCPACK, select a pseudopotential (choice of basis set is irrelevant to conversion) in GAMESS format and copy the ending (pseudopotential) lines beginning with(element symbol)-QMC GEN:

Listing 21.3: BFD Li pseudopotential in GAMESS format

```
Li-QMC GEN 2 1
```
Save these lines to a file (here, named Li.BFD.gamess; the exact name may be anything as long as it is passed to ppconvert after --gamess_pot). Then, convert using ppconvert with the following:

Listing 21.4: Convert GAMESS-formatted pseudopotential to FSAtom xml format

```
ppconvert --gamess_pot Li.BFD.gamess --s_ref "2s(1)" --p_ref "2p(0)" --xml Li.BFD.xml
```

Listing 21.5: Convert GAMESS-formatted pseudopotential to Quantum ESPRESSO UPF format

```
ppconvert --gamess_pot Li.BFD.gamess --s_ref "2s(1)" --p_ref "2p(0)" --log_grid --upf Li.BFD.upf
```

21.4.4 CASINO

The QMC code CASINO also makes available its pseudopotentials available at the website [https://vallico.net/casinoqmc/pplib/](https://vallico.net/casinoqmc/pplib/). To use one in QMCPACK, select a pseudopotential and download its summary file (summary.txt), its tabulated form (pp.data), and (for ppconvert to construct the projectors to convert to Quantum ESPRESSO’s UPF format) a CASINO atomic wavefunction for each angular momentum channel (awfn.data_*). Then, to convert using ppconvert, issue the following command:

Listing 21.6: Convert CASINO-formatted pseudopotential to Quantum ESPRESSO UPF format

```
ppconvert --casino_pot pp.data --casino_us awfn.data_s1_2S --casino_up awfn.data_p1_2P --casino_ud awfn.data_d1_2D --upf Li.TN-DF.upf
```

QMCPACK can directly read in the CASINO-formated pseudopotential (pp.data), but four parameters found in the pseudopotential summary file must be specified in the pseudo element (l-local, lmax, nrule, cutoff)[see Section 9.2.2 for details]:

Listing 21.7: XML syntax to use CASINO-formatted pseudopotentials in QMCPACK

```
<pairpot type="pseudo" name="PseudoPot" source="ion0" wavefunction="psl0" format="xml">
  <pseudo elementType="Li" href="Li.pp.data" format="casino" l-local="s" lmax="2" nrule="2" cutoff="2.19"/>
  <pseudo elementType="H" href="H.pp.data" format="casino" l-local="s" lmax="2" nrule="2" cutoff="0.5"/>
</pairpot>
```
Chapter 22

External Tools

This chapter provides some information on using QMCPACK with external tools.

22.1 VTune

Intel’s VTune profiler has an API that allows program control over collection (pause/resume) and can add information to the profile data (e.g. delineating tasks).

22.1.1 VTune API

If the variable USE_VTUNE_API is set, QMCPACK will check that the include file (ittnotify.h) and the library (libittnotify.a) can be found. To provide CMake with the VTune paths, add the include path to CMAKE_CXX_FLAGS and the the library path to CMAKE_LIBRARY_PATH.

An example of options to be passed to CMake

```
-DCMAKE_CXX_FLAGS=-I/opt/intel/vtune_amplifier_xe/include \
-DCMAKE_LIBRARY_PATH=/opt/intel/vtune_amplifier_xe/lib64
```

22.2 NVIDIA Tools Extensions (NVTX)

NVIDIA’s Tools Extensions (NVTX) API enables programmers to annotate their source code when used with the NVIDIA profilers.

22.2.1 NVTX API

If the variable USE_NVTX_API is set, QMCPACK will add the library (libnvToolsExt.so) to the qmcpack target. To add NVTX annotations to a function, it is necessary to include the nvToolsExt.h header file and then make the appropriate calls into the NVTX API. For more information about the NVTX API, see [https://docs.nvidia.com/cuda/profiler-users-guide/index.html#nvtx](https://docs.nvidia.com/cuda/profiler-users-guide/index.html#nvtx). Any additional calls to the NVTX API should be guarded by the USE_NVTX_API compiler define.

22.2.2 Timers as Tasks

To aid in connecting the timers in the code to the profile data, the start/stop of timers will be recorded as a task if USE_VTUNE_TASKS is set.
In addition to compiling with USE_VTUNE_TASKS, an option needs to be set at runtime to collect the task API data. In the GUI, select the checkbox labeled "Analyze user tasks" when setting up the analysis type. For the command line, set the enable-user-tasks knob to true. For example,

```
amplxe-cl -collect hotspots -knob enable-user-tasks=true ...
```

Collection with the timers set at "fine" can generate too much task data in the profile. Collection with the timers at "medium" collects a more reasonable amount of task data.
Chapter 23

Contributing to the Manual

This section briefly describes how to contribute to the manual. It is primarily “by developers, for developers”. This section should iterate until a consistent view on style/contents is reached.

Desirable:

- Use the table templates below when describing XML input.
- Place unformatted text targeted at developers in comments. Include generously.
- Encapsulate formatted text aimed at developers (like this entire chapter), in \dev{} . Text encapsulated in this way will be removed from the user version of the manual by editing the definition of \dev in qmcpack_manual.tex . Existing but deprecated or partially functioning features fall in this category.

Missing sections (these are opinions, not decided priorities):

- Description of XML input in general. Discuss XML format, use of attributes and <parameter/>’s in general, case sensitivity (input is generally case sensitive), and behavior of QMCPACK when unrecognized XML elements are encountered (they are generally ignored without notification).
- Overview of the input file in general, broad structure, and at least one full example that works in isolation.

Information currently missing for a complete reference specification:

- Noting how many instances of each child element are allowed. Examples: simulation=1 only, method=1 or more, jastrow=0 or more.

Below are template tables for describing XML elements in reference fashion. A number of examples can be found in e.g. Chapter 9. Preliminary style is (please weigh in with opinions): typewriter text (\texttt{}) for XML element, attribute, and parameter names, normal text for literal information in datatype/values/default columns, bold (\textbf{}) text if an attribute/parameter must take on a particular value (values column), italics (\textit{}) for descriptive (non-literal) information in the values column (e.g. anything, non-zero, etc.), required/optional attributes/parameters noted by some_attr^r/ some_attr^o superscripts. Valid datatypes are text, integer, real, boolean, and arrays of each. Fixed length arrays can be noted, e.g. by “real array(3)”.

Template for a generic XML element:
"Factory" elements are XML elements that share a tag, but whose contents change based on the value of an attribute (or sometimes multiple attributes take). The attribute(s) that determine the allowed contents is referred to below as the “type selector” (e.g. for `<estimator/>` elements, the type selector is usually the `type` attribute). These types of elements are frequently encountered as they correspond (sometimes loosely, sometimes literally) to polymorphic classes in QMCPACK that are built in “factories”. This name is true to the underlying code, but may be obscure to the general user (is there a better name to retain the general meaning?).

The template below should be provided each time a new “factory” type is encountered (like `<estimator/>`). The table lists all types of possible elements (see “type options” below) and any attributes that are common to all possible related elements. Specific “derived” elements are then described one at a time with the template above, noting the type selector in addition to the XML tag (e.g. “estimator_type=density element”).

Template for shared information about “factory” elements.
**generic factory element**

<table>
<thead>
<tr>
<th>parent elements:</th>
<th>parent1 parent2</th>
</tr>
</thead>
<tbody>
<tr>
<td>child elements:</td>
<td>child1 child2 child3 ...</td>
</tr>
<tr>
<td>type selector:</td>
<td>some attribute</td>
</tr>
<tr>
<td>type options:</td>
<td>Selection1</td>
</tr>
<tr>
<td></td>
<td>Selection2</td>
</tr>
<tr>
<td></td>
<td>Selection3</td>
</tr>
<tr>
<td></td>
<td>...</td>
</tr>
</tbody>
</table>

shared attributes:

<table>
<thead>
<tr>
<th>name</th>
<th>datatype</th>
<th>values</th>
<th>default</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>attr1</td>
<td>text</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>attr2</td>
<td>integer</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Chapter 24

Unit Testing

Unit testing is a standard software engineering practice to aid in ensuring a quality product. A good suite of unit tests provides confidence in refactoring and changing code, provides some documentation on how classes and functions are used, and can drive a more decoupled design.

If unit tests do not already exist for a section of code, you are encouraged to add them when modifying that section of code. New code additions should also include unit tests. When possible, fixes for specific bugs should also include a unit test that would have caught the bug.

24.1 Unit testing framework

The Catch framework is used for unit testing. See the project site for a tutorial and documentation: [https://github.com/philsquared/Catch](https://github.com/philsquared/Catch)

Catch consists solely of header files. It is distributed as a single include file about 400KB in size. In QMCPACK, it is stored in `external_codes/catch`.

24.2 Unit test organization

The source for the unit tests is located in the `tests` directory under each directory in `src` (e.g. `src/QMCWavefunctions/tests`). All of the tests in each `tests` directory get compiled into an executable. After building the project, the individual unit test executables can be found in `build/tests/bin`. For example, the tests in `src/QMCWavefunctions/tests` are compiled into `build/tests/bin/test_wavefunction`.

All the unit test executables are collected under `ctest` with the `unit` label. When checking the whole code, it’s useful to run through cmake (`cmake -L unit`). When working on an individual directory, it’s useful to run the individual executable.

Some of the tests reference input files. The unit test CMake setup places those input files in particular locations under the `tests` directory (e.g. `tests/xml_test`). The individual test needs to be run from that directory to find the expected input files.

Command line options are available on the unit test executables. Some of the more useful ones are

`-h` List command line options.

`--list-tests` List all the tests in the executable.
A test name can be given on the command line to execute just that test. This is useful when iterating on a particular test, or when running in the debugger. Test names often contain spaces, so most command line environments require enclosing the test name in single or double quotes.

24.3 Example

The first example is one test from src/Numerics/tests/test_grid_functor.cpp

```
TEST_CASE("double_1d_grid_functor", "[numerics]")
{
    LinearGrid<double> grid;
    OneDimGridFunctor<double> f(&grid);

    grid.set(0.0, 1.0, 3);
    REQUIRE(grid.size() == 3);
    REQUIRE(grid.rmin() == 0.0);
    REQUIRE(grid.rmax() == 1.0);
    REQUIRE(grid.dh() == Approx(0.5));
    REQUIRE(grid.dr(1) == Approx(0.5));
}
```

The test function declaration is TEST_CASE("double_1d_grid_functor", "[numerics]"). The first argument is the test name, and it must be unique in the test suite. The second argument is an optional list of tags. Each tag is a name surrounded by brackets ("[tag1][tag2]"). It can also be the empty string.

The REQUIRE macro accepts expressions with C++ comparison operators and records an error if the value of the expression is false.

Floating point numbers may have small differences due to roundoff, etc. The Approx class adds some tolerance to the comparison. Place it on either side of the comparison (e.g. `Approx(a) == 0.3` or `a = Approx(0.3)`). To adjust the tolerance, use the epsilon and scale methods to `Approx (REQUIRE(Approx(a).epsilon(0.001) = 0.3));`

24.3.1 Expected output

When running the test executables individually, the output of a run with no failures should look like

```
===============================================================================
All tests passed (26 assertions in 4 test cases)
```

A test with failures will look like
test_numerics is a Catch v1.4.0 host application.
Run with -? for options

double_1d_grid_functor

/home/user/qmcpack/src/Numerics/tests/test_grid_functor.cpp:29

/home/user/qmcpack/src/Numerics/tests/test_grid_functor.cpp:39: FAILED:
  REQUIRE( grid.dh() == Approx(0.6) )
with expansion:
  0.5 == Approx( 0.6 )

===============================================================================
test cases:  4  |  3 passed |  1 failed
assertions:  25  |  24 passed |  1 failed

24.4 Adding tests

There are three scenarios covered here: adding a new test in an existing file, adding a new test file, or adding a new test directory.

24.4.1 Adding a test to existing file

Copy an existing test, or from the example shown here. Be sure to change the test name.

24.4.2 Adding a test file

When adding a new test file, create a file in the test directory, or copy from an existing file. Add the file name to the ADD_EXECUTABLE in the CMakeLists.txt file in that directory.

One (and only one) file must define the main function for the test executable by defining CATCH_CONFIG_MAIN before including the Catch header. If more than one file defines this value, there will be linking errors about multiply defined values.

Some of the tests need to shut down MPI properly to avoid extraneous error messages. Those tests include Message/catch_mpi_main.hpp instead of defining CATCH_CONFIG_MAIN.

24.4.3 Adding a test directory

Copy the CMakeLists.txt file from an existing tests directory. Change the SRC_DIR name and the files in the ADD_EXECUTABLES line. The libraries to link in TARGET_LINK_LIBRARIES may need to be updated.
Add the new test directory to src/CMakeLists.txt in the BUILD_UNIT_TESTS section near the end.

24.5 Testing with random numbers

Many algorithms and parts of the code depend on random numbers, which makes validating the results difficult. One solution is to verify that certain properties hold for any random number. This approach is valuable at some levels of testing, but is unsatisfying at the unit test level.

The Utilities directory contains a 'fake' random number generator that can be used for deterministic tests of these parts of the code. Currently it outputs a single, fixed value every time it is called, but it could be expanded to produce more varied, but still deterministic, sequences. See src/QMCDrivers/test_vmc.cpp for an example of using the fake random number generator.
Chapter 25

QMCPACK Design and Feature Documentation

This section contains information on the overall design of QMCPACK. Also included in this section are detailed explanations/derivations of major features and algorithms present in the code.

25.1 QMCPACK Design

TBD.
25.2 Feature: Optimized Long-Ranged Breakup (Ewald)

Consider a group of particles interacting with long-ranged central potentials, $v^{\alpha\beta}(|r_i^\alpha - r_j^\beta|)$, where the Greek superscripts represent the particle species (eg. $\alpha =$ electron, $\beta =$ proton), and Roman subscripts refer to particle number within a species. We can then write the total interaction energy for the system as,

$$V = \sum_\alpha \left\{ \sum_{i<j} v^{\alpha\alpha}(|r_i^\alpha - r_j^\alpha|) + \sum_{\beta<\alpha} \sum_{i,j} v^{\alpha\beta}(|r_i^\alpha - r_j^\beta|) \right\}$$ (25.1)

25.2.1 The Long-Range Problem

Consider such a system in periodic boundary conditions in a cell defined by primitive lattice vectors $a_1, a_2,$ and $a_3$. Let $L \equiv n_1a_1 + n_2a_2 + n_3a_3$ be a direct lattice vector. Then the interaction energy per cell for the periodic system is given by

$$V = \sum_L \sum_\alpha \left\{ \sum_{i<j} v^{\alpha\alpha}(|r_i^\alpha - r_j^\alpha + L|) + \sum_{\beta<\alpha} \sum_{i,j} v^{\alpha\beta}(|r_i^\alpha - r_j^\beta + L|) \right\} + \sum_{L \neq 0} \sum_\alpha N^\alpha v^{\alpha\alpha}(|L|)$$ (25.2)

where $N^\alpha$ is the number particles of species $\alpha$. If the potentials $v^{\alpha\beta}(r)$ are indeed long-range, the summation over direct lattice vectors will not converge in this naive form. A solution to the problem was posited by Ewald. We break the central potentials into two pieces – a short range and a long range part define by

$$v^{\alpha\beta}(r) = v_s^{\alpha\beta}(r) + v_l^{\alpha\beta}(r).$$ (25.3)

We will perform the summation over images for the short-range part in real space, while performing the sum for the long-range part in reciprocal space. For simplicity, we choose $v_s^{\alpha\beta}(r)$ so that it is identically zero at the half the box length. This eliminates the need to sum over images in real space.

25.2.2 Reciprocal-Space Sums

Heterologous terms

We begin with (25.2), starting with the heterologous terms, i.e. the terms involving particles of different species. The short-range terms are trivial, so we neglect them here.

$$\text{heterologous} = \frac{1}{2} \sum_{\alpha \neq \beta} \sum_i \sum_j \sum_L v_l^{\alpha\beta}(r_i^\alpha - r_j^\beta + L)$$ (25.4)
We insert the resolution of unity in real space twice,

\[
\text{heterologous} = \frac{1}{2} \sum_{\alpha \neq \beta} \int_{\text{cell}} \, dr \, dr' \sum_{i,j} \delta(r_i^\alpha - r) \delta(r_j^\beta - r') \sum_{L} v_i^{\alpha \beta} (|r - r' + L|) \quad (25.5)
\]

\[
= \frac{1}{2 \Omega^2} \sum_{\alpha \neq \beta} \int_{\text{cell}} \, dr \, dr' \sum_{k,k',i,j} e^{ik(r_i^\alpha - r)} e^{ik'(r_j^\beta - r')} \sum_{L} v_i^{\alpha \beta} (|r - r' + L|)
\]

\[
= \frac{1}{2 \Omega^2} \sum_{\alpha \neq \beta} \int_{\text{cell}} \, dr \, dr' \sum_{k,k',i,j} e^{ik(r_i^\alpha - r)} e^{ik'(r_j^\beta - r')} e^{ik''(r_i^\alpha - r')} v_i^{\alpha \beta}.
\]

Here, the \(k\) summations are over reciprocal lattice vectors given by \(k = m_1 b_1 + m_2 b_2 + m_3 b_3\), where

\[
b_1 = 2\pi \frac{a_2 \times a_3}{a_1 \cdot (a_2 \times a_3)},
\]

\[
b_2 = 2\pi \frac{a_3 \times a_1}{a_1 \cdot (a_2 \times a_3)},
\]

\[
b_3 = 2\pi \frac{a_1 \times a_2}{a_1 \cdot (a_2 \times a_3)}.
\]

We note that \(k \cdot L = 2\pi(n_1 m_1 + n_2 m_2 + n_3 m_3)\).

\[
v_{k''}^{\alpha \beta} = \frac{1}{\Omega} \int_{\text{cell}} \, dr'' \sum_{L} e^{-i k'' \cdot (|r'' + L|)} v_{k''}^{\alpha \beta} (|r'' + L|), \quad (25.7)
\]

\[
= \frac{1}{\Omega} \int_{\text{all space}} \, d\tilde{r} \, e^{-i k'' \cdot \tilde{r}} v_{k''}^{\alpha \beta} (\tilde{r}), \quad (25.8)
\]

where \(\Omega\) is the volume of the cell. Here we have used the fact that summing over all cells of the integral over the cell is equivalent to integrating over all space.

\[
\text{hetero} = \frac{1}{2 \Omega^2} \sum_{\alpha \neq \beta} \int_{\text{cell}} \, dr \, dr' \sum_{k,k',i,j} e^{i(k \cdot r_i^\alpha + k' \cdot r_j^\beta)} e^{i(k'' \cdot r_i^\alpha - i(k'' + k') \cdot r')} v_{k''}^{\alpha \beta}. \quad (25.9)
\]

We have

\[
\frac{1}{\Omega} \int_{\text{cell}} \, dr \, e^{i(k-k') \cdot r} = \delta_{k,k'}, \quad (25.10)
\]

Then, performing the integrations we have

\[
\text{hetero} = \frac{1}{2} \sum_{\alpha \neq \beta} \sum_{k,k'} \sum_{i,j} e^{i(k \cdot r_i^\alpha + k' \cdot r_j^\beta)} \delta_{k,k'} \delta_{-k',k''} v_{k''}^{\alpha \beta}. \quad (25.11)
\]

We now separate the summations, yielding

\[
\text{hetero} = \frac{1}{2} \sum_{\alpha \neq \beta} \sum_{k,k'} \left[ \sum_i e^{i k \cdot r_i^\alpha} \right] \left[ \sum_j e^{i k' \cdot r_j^\beta} \right] \delta_{k,k'} \delta_{-k',k''} v_{k''}^{\alpha \beta}. \quad (25.12)
\]
Summing over $k$ and $k'$, we have

$$\text{hetero} = \frac{1}{2} \sum_{\alpha \neq \beta} \sum_{k'} \rho_{k'}^\beta \rho_{-k'}^\alpha \nu_{k'}^\alpha \nu_{k'}^\beta.$$  

(25.13)

We can simplify the calculation a bit further by rearranging the sums over species,

$$\text{hetero} = \frac{1}{2} \sum_{\alpha > \beta} \sum_k \left( \rho_k^\alpha \rho_{-k}^\beta + \rho_{-k}^\alpha \rho_k^\beta \right) \nu_k^\alpha \nu_k^\beta$$  

(25.14)

$$= \sum_{\alpha > \beta} \sum_k \Re \left( \rho_k^\alpha \rho_{-k}^\beta \right) \nu_k^\alpha \nu_k^\beta.$$  

(25.15)

**Homologous Terms**

We now consider the terms involving particles of the same species interacting with each other. The algebra is very similar to that above, with the slight difficulty of avoiding the self-interaction term.

$$\text{homologous} = \sum_{\alpha} \sum_L \sum_{i<j} v_L^{\alpha \alpha} (|r_i^\alpha - r_j^\alpha + L|)$$  

(25.16)

$$= \frac{1}{2} \sum_{\alpha} \sum_L \sum_{i \neq j} v_L^{\alpha \alpha} (|r_i^\alpha - r_j^\alpha + L|)$$  

(25.17)

$$\text{homologous} = \frac{1}{2} \sum_{\alpha} \sum_L \left[ -N^\alpha v_L^{\alpha \alpha} (|L|) + \sum_{i,j} v_L^{\alpha \alpha} (|r_i^\alpha - r_j^\alpha + L|) \right]$$  

(25.18)

$$= \frac{1}{2} \sum_{\alpha} \sum_L (|\rho_L^\alpha|^2 - N) v_L^{\alpha \alpha}$$  

(25.19)

**Madelung Terms**

Let us now consider the Madelung term for a single particle of species $\alpha$. This term corresponds to the interaction of a particle with all of its periodic images.

$$v_M^\alpha = \frac{1}{2} \sum_{L \neq 0} v^{\alpha \alpha} (|L|)$$  

(25.20)

$$= \frac{1}{2} \left[ -v_L^{\alpha \alpha} (0) + \sum_L v^{\alpha \alpha} (|L|) \right]$$  

(25.21)

$$= \frac{1}{2} \left[ -v_L^{\alpha \alpha} (0) + \sum_k v_k^{\alpha \alpha} \right]$$  

(25.22)

**k = 0 terms**

Thus far, we have neglected what happens at the special point $k = 0$. For many long-range potentials, such as the coulomb potential, $v_k^{\alpha \alpha}$ diverges for $k = 0$. However, we recognize that for a charge-neutral system, the divergent part of the terms cancel each other. If all the potential in the system were precisely coulomb, the $k = 0$ terms would cancel precisely, yielding zero. For systems
involving pseudopotentials, however, it may be the case the resulting term is finite, but nonzero. Consider the terms from $k = 0$,

$$V_{k=0} = \sum_{\alpha > \beta} N^\alpha N^\beta v_{k=0}^{\alpha\beta} + \frac{1}{2} \sum_\alpha (N^\alpha)^2 v_{k=0}^{\alpha\alpha} \tag{25.23}$$

$$= \frac{1}{2} \sum_{\alpha, \beta} N^\alpha N^\beta v_{k=0}^{\alpha\beta}. \tag{25.24}$$

Next, we must compute $v_{k=0}^{\alpha\beta}$.

$$v_{k=0}^{\alpha\beta} = \frac{4\pi}{\Omega} \int_0^\infty \, dr \, r^2 v^{\alpha\beta}_l(r) \tag{25.25}$$

We recognize that this integral will not converge because of the large-$r$ behavior. However, we recognize that when we do the sum in (25.24), the large-$r$ parts of the integrals will cancel precisely. Therefore, we define

$$\tilde{v}_{k=0}^{\alpha\beta} = \frac{4\pi}{\Omega} \int_0^{r_{\text{end}}} \, dr \, r^2 v^{\alpha\beta}_l(r), \tag{25.26}$$

where $r_{\text{end}}$ is some cutoff value after which the potential tails precisely cancel.

Neutralizing Background Terms

For systems with a net charge, such as the one-component plasma (jellium), we add a uniform background charge which makes the system neutral. When we do this, we must add a term which comes from the interaction of the particle with the neutral background. It is a constant term, independent of the particle positions. In general, we have a compensating background for each species, which largely cancels out for neutral systems.

$$V_{\text{background}} = -\frac{1}{2} \sum_\alpha (N^\alpha)^2 v^{\alpha\alpha}_s - \sum_{\alpha > \beta} N^\alpha N^\beta v^{\alpha\beta}_s, \tag{25.27}$$

where $v^{\alpha\beta}_s$ is given by

$$v^{\alpha\beta}_s = \frac{1}{\Omega} \int_0^{r_c} \, d^3r \, v^{\alpha\beta}_s(r) \tag{25.28}$$

$$= \frac{4\pi}{\Omega} \int_0^{r_c} \, r^2 v_s(r) \, dr$$
25.2.3 Combining Terms

Here, we sum all of the terms we computed in the sections above,

\[ V = \sum_{\alpha > \beta} \left[ \sum_{i,j} v_s(|r^\alpha_i - r^\beta_j|) + \sum_k \mathcal{R} e \left( \rho_k^{\alpha \beta} \right) v_k^{\alpha \beta} - N^\alpha N^\beta v_{s0}^{\alpha \beta} \right] \]

\[ + \sum_{\alpha} \left[ N^\alpha v_M^\alpha + \sum_{i,j} v_s(|r^\alpha_i - r^\alpha_j|) + \frac{1}{2} \sum_k (|\rho_k^\alpha|^2 - N) v_k^{\alpha \alpha} - \frac{1}{2} (N_\alpha)^2 v_{s0}^{\alpha \alpha} \right] \]

\[ = \sum_{\alpha > \beta} \left[ \sum_{i,j} v_s(|r^\alpha_i - r^\beta_j|) + \sum_k \mathcal{R} e \left( \rho_k^{\alpha \beta} \right) v_k^{\alpha \beta} - N^\alpha N^\beta v_{s0}^{\alpha \beta} + \tilde{V}_{k=0} \right] \]

\[ + \sum_{\alpha} \left[ -\frac{N^\alpha v_l^{\alpha \alpha}(0)}{2} + \sum_{i>j} v_s(|r^\alpha_i - r^\alpha_j|) + \frac{1}{2} \sum_k |\rho_k^\alpha|^2 v_k^{\alpha \alpha} - \frac{1}{2} (N_\alpha)^2 v_{s0}^{\alpha \alpha} + \tilde{V}_{k=0} \right] \]

(25.29)

25.2.4 Computing the Reciprocal Potential

Now we return to (25.8). Without loss of generality, we define for convenience \( k = k\hat{z} \).

\[ v_k^{\alpha \beta} = \frac{2\pi}{\Omega} \int_0^\infty dr \int_{-1}^1 d\cos(\theta) \; r^2 e^{-ikr\cos(\theta)} v_l^{\alpha \beta}(r) \]  

(25.30)

We do the angular integral first. By inversion symmetry, the imaginary part of the integral vanishes, yielding

\[ v_k^{\alpha \beta} = \frac{4\pi}{\Omega k} \int_0^\infty dr \; r \sin(kr) v_l^{\alpha \beta}(r). \]  

(25.31)

25.2.5 The Coulomb Potential

For the case of the Coulomb potential, the above integral is not formally convergent if we do the integral naively. We may remedy the situation by including a convergence factor, \( e^{-kor} \). For a potential of the form \( v^{\text{coul}}(r) = q_1 q_2 / r \), this yields

\[ v_k^{\text{screened coul}} = \frac{4\pi q_1 q_2}{\Omega k} \int_0^\infty dr \sin(kr) e^{-kor} \]  

(25.32)

\[ = \frac{4\pi q_1 q_2}{\Omega (k^2 + k_0^2)} \]  

(25.33)

Allowing the convergence factor to tend to zero, we have

\[ v_k^{\text{coul}} = \frac{4\pi q_1 q_2}{\Omega k^2} \]  

(25.34)

For more generalized potentials with a coulomb tail, we cannot evaluate (25.31) numerically but must handle the coulomb part analytically. In this case, we have

\[ v_k^{\alpha \beta} = \frac{4\pi}{\Omega} \left\{ \frac{q_1 q_2}{k^2} + \int_0^\infty dr \sin(kr) \left[ v_l^{\alpha \beta}(r) - \frac{q_1 q_2}{r} \right] \right\} \]  

(25.35)
25.2.6 Efficient calculation methods

Fast computation of $\rho_k$

We wish to quickly calculate the quantity

$$\rho_k^\alpha \equiv \sum_i e^{i k \cdot r_i^\alpha} \quad (25.36)$$

First, we write

$$k = m_1 b_1 + m_2 b_2 + m_3 b_3 \quad (25.37)$$

$$k \cdot r_i^\alpha = m_1 b_1 \cdot r_i^\alpha + m_2 b_2 \cdot r_i^\alpha + m_3 b_3 \cdot r_i^\alpha \quad (25.38)$$

$$e^{i k \cdot r_i^\alpha} = \begin{bmatrix} e^{i b_1 \cdot r_i^\alpha} \\ e^{i b_2 \cdot r_i^\alpha} \\ e^{i b_3 \cdot r_i^\alpha} \end{bmatrix}^{m_3} \quad (25.39)$$

Now, we note that

$$[C_i^\alpha]_{m_1} = C_i^{\alpha} C_i^{\alpha} (m_1 - 1). \quad (25.40)$$

This allows us to recursively build up an array of the $C_i^\alpha$s, and then compute $\rho_k$ for all $k$-vectors by looping over all $k$-vectors, requiring only two complex multiplies per particle per $k$.

**Algorithm 1** Algorithm to quickly calculate $\rho_k^\alpha$.

Create list of $k$-vectors and corresponding $(m_1, m_2, m_3)$ indices.

for all $\alpha \in$ species do

Zero out $\rho_k^\alpha$

for all $i \in$ particles do

for $j \in [1 \cdots 3]$ do

Compute $C_j^{\alpha} \equiv e^{i b_j \cdot r_i^\alpha}$

for $m \in [-m_{\text{max}} \cdots m_{\text{max}}]$ do

Compute $[C_j^{\alpha}]^m$ and store in array

end for

end for

for all $(m_1, m_2, m_3) \in$ index list do

Compute $e^{i k \cdot r_i^\alpha} = [C_1^\alpha]_{m_1} [C_2^\alpha]_{m_2} [C_3^\alpha]_{m_3}$ from array

end for

end for

end for

25.2.7 Gaussian Charge Screening Breakup

This original approach to the short and long-ranged breakup adds an opposite screening charge of gaussian shape around each point charge. It then removes the charge in the long-ranged part of the potential. In this potential,

$$v_{\text{long}}(r) = \frac{q_1 q_2}{r} \operatorname{erf}(\alpha r), \quad (25.41)$$

where $\alpha$ is an adjustable parameter used to control how short-ranged the potential should be. If the box size is $L$, a typical value for $\alpha$ might be $7/(Lq_1 q_2)$. We should note that this form
for the long-ranged potential should also work for any general potential with a coulomb tail, e.g. pseudo-Hamiltonian potentials. For this form of the long-ranged potential, we have in $k$-space

$$v_k = \frac{4\pi q_1 q_2 \exp \left( \frac{-k^2}{4\alpha^2} \right)}{\Omega k^2}.$$ (25.42)

### 25.2.8 Optimized Breakup Method

In this section, we undertake the task of choosing a long-range/short-range partitioning of the potential which is optimal in that it minimizes the error for given real and $k$-space cutoffs $r_c$ and $k_c$. Here, we modify slightly the method introduced Natoli and Ceperley[9]. We choose $r_c = \frac{1}{2} \min \{L_i\}$, so that we require the nearest image in real space summation. $k_c$ is then chosen so as to satisfy our accuracy requirements.

Here we modify our notation slightly to accommodate details not required above. We restrict our discussion to the interaction of two particles species (which may be the same), and drop our species indices. Thus we are looking for short and long-range potentials defined by,

$$v(r) = v^s(r) + v^\ell(r)$$ (25.43)

Define $v^s_k$ and $v^\ell_k$ to be the respective Fourier transforms of the above. The goal is to choose $v^s(r)$ such that its value and first two derivatives vanish at $r_c$, while making $v^\ell(r)$ as smooth as possible so that $k$-space components, $v^\ell_k$, are very small for $k > k_c$. Here, we describe how to do this in an optimal way.

Define the periodic potential, $V_p$, as

$$V_p(r) = \sum_l v(|r + l|),$$ (25.44)

where $r$ is the displacement between the two particles and $l$ is a lattice vector. Let us then define our approximation to this potential, $V_a$, as

$$V_a(r) = v^s(r) + \sum_{|k|<k_c} v^\ell_k e^{ik\cdot r}$$ (25.45)

Now, we seek to minimize the RMS error over the cell,

$$\chi^2 = \frac{1}{\Omega} \int_{\Omega} d^3r \ |V_p(r) - V_a(r)|^2$$ (25.46)

We may write

$$V_p(r) = \sum_k v_k e^{ik\cdot r},$$ (25.47)

where

$$v_k = \frac{1}{\Omega} \int d^3r \ e^{-ik\cdot r} v(r).$$ (25.48)

We now need a basis in which to represent the broken up potential. We may choose to represent either $v^s(r)$ or $v^\ell(r)$ in a real-space basis. Natoli and Ceperley chose the prior in their paper. We choose the latter for a number of reasons. First, singular potentials are difficult to represent in a linear basis unless the singularity is explicitly included. This requires a separate basis for each type of singularity. The short-range potential may have an arbitrary number of features for $r < r_c$ and
still be a valid potential. By construction, however, we desire that $v^\ell (r)$ be smooth in real-space so that its Fourier transform falls off quickly with increasing $k$. We therefore expect that, in general, $v^\ell (r)$ should be well-represented by fewer basis functions than $v^s (r)$. Therefore, we define,

$$v^\ell (r) \equiv \begin{cases} \sum_{n=0}^{J-1} t_n h_n (r) & \text{for } r \leq r_c \\ v(r) & \text{for } r > r_c. \end{cases}$$  \hspace{1cm} (25.49)$$

where the $h_n (r)$ are a set of $J$ basis functions. We require that the two cases agree on the value and first two derivatives at $r_c$. We may then define

$$c_{nk} \equiv \frac{1}{\Omega} \int_0^{r_c} d^3 r \ e^{-i k r} h_n (r).$$  \hspace{1cm} (25.50)$$

Similarly, we define

$$x_k \equiv -\frac{1}{\Omega} \int_{r_c}^{\infty} d^3 r \ e^{-i k r} v(r).$$  \hspace{1cm} (25.51)$$

Therefore,

$$v^\ell_k = -x_k + \sum_{n=0}^{J-1} t_n c_{nk}$$  \hspace{1cm} (25.52)$$

Because $v^s (r)$ goes identically to zero at the box edge, inside the cell we may write

$$v^s (r) = \sum_k v^s_k e^{i k r}$$  \hspace{1cm} (25.53)$$

We then write

$$\chi^2 = \frac{1}{\Omega} \int_{\Omega} d^3 r \ \left| \sum_k e^{i k r} (v_k - v^s_k) - \sum_{|k| \leq k_c} v^\ell_k \right|^2$$  \hspace{1cm} (25.54)$$

We see that if we define

$$v^s (r) \equiv v(r) - v^\ell (r)$$  \hspace{1cm} (25.55)$$

Then

$$v^\ell_k + v^s_k = v_k,$$  \hspace{1cm} (25.56)$$

which then cancels out all terms for $|k| < k_c$. Then we have

$$\chi^2 = \frac{1}{\Omega} \int_{\Omega} d^3 r \ \left| \sum_{|k| > k_c} e^{i k r} (v_k - v^s_k) \right|^2$$  \hspace{1cm} (25.57)$$

$$= \frac{1}{\Omega} \int_{\Omega} d^3 r \ \left| \sum_{|k| > k_c} e^{i k r} v^\ell_k \right|^2$$  \hspace{1cm} (25.58)$$

$$= \frac{1}{\Omega} \int_{\Omega} d^3 r \ \left| \sum_{|k| > k_c} e^{i k r} \left( -x_k + \sum_{n=0}^{J-1} t_n c_{nk} \right) \right|^2$$  \hspace{1cm} (25.59)$$

We expand the summation,

$$\chi^2 = \frac{1}{\Omega} \int_{\Omega} d^3 r \ \sum_{|k|,|k'| > k_c} e^{i (k-k') r} \left( x_k - \sum_{n=0}^{J-1} t_n c_{nk} \right) \left( x_{k'} - \sum_{m=0}^{J-1} t_m c_{mk'} \right)$$  \hspace{1cm} (25.60)$$

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We take the derivative w.r.t. $t_m$, 
\[
\frac{\partial \chi^2}{\partial t_m} = \frac{2}{\Omega} \int_{\Omega} d^3r \sum_{\{k,k'\} > k_c} e^{i(k-k') \cdot r} \left( x_k - \sum_{n=0}^{J-1} t_n c_{nk} \right) c_{mk'}
\]  
(25.61)

We integrate w.r.t. $r$, yielding a Kronecker $\delta$.
\[
\frac{\partial \chi^2}{\partial t_m} = 2 \sum_{\{k,k'\} > k_c} \delta_{k,k'} \left( x_k - \sum_{n=0}^{J-1} t_n c_{nk} \right) c_{mk'}
\]  
(25.62)

Summing over $k'$ and equating the derivative to zero, we find the minimum of our error function is given by
\[
\sum_{n=0}^{J-1} \sum_{\{k\} > k_c} c_{mk} c_{nk} t_n = \sum_{\{k\} > k_c} x_k c_{mk},
\]  
(25.63)

which is equivalent in form to equation (19) in [9], where we have $x_k$, instead of $V_k$. Thus, we see that we may optimize the short-range or long-range potential in simply by choosing to use $V_k$ or $x_k$ in the above equation. We now define
\[
A_{mn} = \sum_{\{k\} > k_c} c_{mk} c_{nk}
\]  
(25.64)
\[
b_m = \sum_{\{k\} > k_c} x_k c_{mk}
\]  
(25.65)

Thus, it becomes clear that our minimization equations can be cast in the canonical linear form,
\[
At = b.
\]  
(25.66)

**Solution by SVD**

In practice, we note that the matrix $A$ frequently becomes singular in practice. For this reason, we use the singular value decomposition to solve for $t_n$. This factorization decomposes $A$ as
\[
A = U S V^T,
\]  
(25.67)

where $U^T U = V^T V = 1$ and $S$ is diagonal. In this form, we have
\[
t = \sum_{i=0}^{J-1} \left( \frac{U_{(i)} \cdot b}{S_{ii}} \right) V_{(i)},
\]  
(25.68)

where the parenthesized subscripts refer to columns. The advantage of this form is that if $S_{ii}$ is zero or very near zero, the contribution of the $i$th of $V$, may be neglected, since it represents a numerical instability and has little physical meaning. It represents the fact that the system cannot distinguish between two linear combinations of the basis functions. Using the SVD in this manner is guaranteed to be stable. This decomposition is available in LAPACK in the DGESVD subroutine.
Constraining Values

Often, we wish to constrain the value of \( t_n \) to have a fixed value to enforce a boundary condition, for example. To do this, we define
\[
b' = b - t_n A_{(n)}.
\]

We then define \( A^* \) as \( A \) with the \( n \)th row and column removed, and \( b^* \) as \( b' \) with the \( n \)th element removed. Then we solve the reduced equation \( A^* t^* = b^* \), and finally insert \( t_n \) back into the appropriate place in \( t^* \) to recover the complete, constrained vector \( t \). This may be trivially generalized to an arbitrary number of constraints.

The LPQHI basis

The above discussion was general and independent of the basis used to represent \( v^\ell(r) \). In this section, we introduce a convenient basis of localized interpolant functions, similar to those used for splines, which have a number of properties which are convenient for our purposes.

First, we divide the region from 0 to \( r_c \) into \( M - 1 \) subregions, bounded above and below by points we term knots, defined by \( r_j \equiv j\Delta \), where \( \Delta \equiv r_c/(M - 1) \). We then define compact basis elements, \( h_{j\alpha} \), which span the region \([r_{j-1}, r_{j+1}]\), except for \( j = 0 \) and \( j = M \). For \( j = 0 \), only the region \([r_0, r_1]\), while for \( j = M \), only \([r_{M-1}, r_M]\). Thus the index \( j \) identify the knot the element is centered on, while \( \alpha \) is an integer from 0 to 2 indicating one of three function shapes. The dual index can be mapped to the single index above by the relation, \( n = 3j + \alpha \). The basis functions are then defined as
\[
h_{j\alpha}(r) = \begin{cases} 
\Delta^\alpha \sum_{n=0}^{5} S_{\alpha n} \left( \frac{r-r_j}{\Delta} \right)^n, & r_j < r \leq r_{j+1} \\
(-\Delta)^\alpha \sum_{n=0}^{5} S_{\alpha n} \left( \frac{r-r_j}{\Delta} \right)^n, & r_{j-1} < r \leq r_j \\
0, & \text{otherwise},
\end{cases}
\]

where the matrix \( S_{\alpha n} \) is given by
\[
S = \begin{bmatrix} 
1 & 0 & 0 & -10 & 15 & -6 \\
0 & 1 & 0 & -6 & 8 & -3 \\
0 & 0 & \frac{1}{2} & -\frac{3}{2} & -\frac{3}{2} & -\frac{1}{2}
\end{bmatrix}.
\]

Figure 25.1 shows plots of these function shapes.

The basis functions have the property that at the left and right extremes, i.e. \( r_{j-1} \) and \( r_{j+1} \), their values and first two derivatives are zero. At the center, \( r_j \), we have the properties,
\[
\begin{align*}
h_{j0}(r_j) &= 1, & h_{j0}'(r_j) &= 0, & h_{j0}''(r_j) &= 0 \\
h_{j1}(r_j) &= 0, & h_{j1}'(r_j) &= 1, & h_{j1}''(r_j) &= 0 \\
h_{j2}(r_j) &= 0, & h_{j2}'(r_j) &= 0, & h_{j2}''(r_j) &= 1
\end{align*}
\]

These properties allow the control of the value and first two derivatives of the represented function at any knot value simply by setting the coefficients of the basis functions centered around that knot. Used in combination with the method described in section 25.2.8 above, boundary conditions can easily be enforced. In our case, we wish require that
\[
h_{M0} = v(r_c), \quad h_{M1} = v'(r_c), \quad \text{and} \quad h_{M2} = v''(r_c).
\]

This ensures that \( v^8 \) and its first two derivatives vanish at \( r_c \).
Figure 25.1: Basis functions $h_{j0}$, $h_{j1}$, and $h_{j2}$ are shown. We note at the left and right extremes, the values and first two derivatives of the functions are zero, while at the center, $h_{j0}$ has a value of 1, $h_{j1}$ has a first derivative of 1, and $h_{j2}$ has a second derivative of 1.

**Fourier coefficients**

We wish now to calculate the Fourier transforms of the basis functions, defined as

$$c_{jak} = \frac{1}{\Omega} \int_0^r d^3r e^{-ikr} h_{ja}(r)$$

We then may write,

$$c_{jak} = \begin{cases} 
\Delta^a \sum_{n=0}^5 S_{an} D_{jkn}^+ & j = 0 \\
\Delta^a \sum_{n=0}^5 S_{an} (-1)^{a+n} D_{Mkn}^- & j = M \\
\Delta^a \sum_{n=0}^5 S_{an} \left[ D_{jkn}^+ + (-1)^{a+n} D_{jkn}^- \right] & \text{otherwise},
\end{cases}$$

(25.77)

where

$$D_{jkn}^\pm = \frac{1}{\Omega} \int_{r_j}^{r_j \pm 1} d^3r \ e^{-ikr} \left( \frac{r - r_j}{\Delta} \right)^n.$$  

(25.78)

We then further make the definition that

$$D_{jkn}^\pm = \pm \frac{4\pi}{k\Omega} \left[ \Delta \text{Im} \left( E_{jkn}^\pm \left( E_{j(k+1)n}^\pm \right) + r_j \text{Im} \left( E_{jkn}^\pm \right) \right) \right]$$

(25.79)

It can then be shown that

$$E_{jkn}^\pm = \begin{cases} 
-\frac{i}{k} e^{ikr_j} \left( e^{ik \Delta} - 1 \right) & \text{if } n = 0, \\
-\frac{i}{k} \left[ (\pm 1)^n e^{ik(r_j \pm \Delta)} - \frac{n}{2} E_{jkn}^\pm \right] & \text{otherwise}.
\end{cases}$$

(25.80)

Note that these equations correct typographical errors present in [9].
Enumerating \( k \)-points

We note that the summations over \( k \) which have been ubiquitous in this paper requires enumeration of the \( k \)-vectors. In particular, we should sum over all \(|k| > k_c\). In practice, we must limit our summation to some finite cutoff value \( k_c < |k| < k_{\text{max}} \), where \( k_{\text{max}} \) should be of order \( 3000/L \), where \( L \) is the minimum box dimension. Enumerating these vectors in a naive fashion even for this finite cutoff would prove quite prohibitive, as it requires \( \sim 10^9 \) vectors.

Our first optimization come in realizing that all quantities in this calculation require only \( |k| \), and not \( k \) itself. Thus, we may take advantage of the great degeneracy of \(|k|\). We create a list of \((k,N)\) pairs, where \( N \) is the number of vectors with magnitude \( k \). We make nested loops over \( n_1, n_2, \) and \( n_3 \), yielding \( k = n_1b_1 + n_2b_2 + n_3b_3 \). If \(|k|\) is in the required range, we check to see if there is already an entry with that magnitude on our list, incrementing the corresponding \( N \) if there is, or creating a new entry if not. Doing so typically saves a factor of \( \sim 200 \) in storage and computation.

This reduction is still not sufficient for large \( k_{\text{max}} \), since it requires that we still look over \( 10^9 \) entries. To further reduce cost, we may pick an intermediate cutoff, \( k_{\text{cont}} \), above which we will approximate the degeneracy assuming a continuum of \( k \)-points. We stop our exact enumeration at \( k_{\text{cont}} \), and then add \( \sim 1000 \) points, \( k_i \), uniformly spaced between \( k_{\text{cont}} \) and \( k_{\text{max}} \). We then approximate the degeneracy by

\[
N_i = \frac{4\pi}{3} \left( \frac{k_b^3 - k_a^3}{(2\pi)^3/\Omega} \right),
\]

where \( k_b = (k_i + k_{i+1})/2 \) and \( k_a = (k_i + k_{i-1}) \). In doing so, we typically reduce our total number of \( k \)-points to sum over \( \sim 2500 \) from the \( 10^9 \) we had to start.

Calculating \( x_k \)’s

**The coulomb potential**

For \( v(r) = \frac{1}{r} \), \( x_k \) is given by

\[
x_k^{\text{coulomb}} = -\frac{4\pi}{\Omega k^2} \cos(kr_c)
\]

**The \( 1/r^2 \) potential**

For \( v(r) = \frac{1}{r^2} \), \( x_k \) is given by

\[
x_k^{1/r^2} = \frac{4\pi}{\omega k} \left[ \text{Si}(kr_c) - \frac{\pi}{2} \right],
\]

where the \textit{sin integral}, \( \text{Si}(z) \), is given by

\[
\text{Si}(z) \equiv \int_0^z \frac{\sin t}{t} dt.
\]

**The \( 1/r^3 \) potential**

For \( v(r) = \frac{1}{r^3} \), \( x_k \) is given by

\[
x_k^{1/r^3} = \frac{4\pi}{\Omega k} \left[ k\text{Ci}(kr_c) - \frac{\sin(kr_c)}{r_c} \right],
\]

where the \textit{cosine integral}, \( \text{Ci}(z) \), is given by

\[
\text{Ci}(z) \equiv -\int_z^\infty \frac{\cos t}{t} dt.
\]
The $1/r^4$ potential

For $v(r) = \frac{1}{r^4}$, $x_k$ is given by

$$x_k^{1/r^4} = -\frac{4\pi}{\Omega k} \left\{ \frac{k \cos(kr_c)}{2r_c} + \frac{\sin(kr_c)}{2r_c^2} + \frac{k^2}{2} \left[ \text{Si}(kr_c) - \frac{\pi}{2} \right] \right\}$$

(25.87)
25.3 Feature: Optimized Long-Ranged Breakup (Ewald) 2

Given a lattice of vectors $\mathbf{L}$, its associated reciprocal lattice of vectors $\mathbf{k}$ and a function $\psi(\mathbf{r})$ periodic on the lattice we define its Fourier transform $\tilde{\psi}(\mathbf{k})$ as

$$
\tilde{\psi}(\mathbf{k}) = \frac{1}{\Omega} \int_{\Omega} d\mathbf{r} \psi(\mathbf{r}) e^{-i\mathbf{k}\mathbf{r}}
$$

(25.88)

where we indicated both the cell domain and the cell volume by $\Omega$. $\psi(\mathbf{r})$ can then be expressed as

$$
\psi(\mathbf{r}) = \sum_k \tilde{\psi}(\mathbf{k}) e^{i\mathbf{k}\mathbf{r}}
$$

(25.89)

The potential generated by charges sitting on the lattice positions at a particular point $\mathbf{r}$ inside the cell is given by

$$
V(\mathbf{r}) = \sum_{\mathbf{L}} v(|\mathbf{r} + \mathbf{L}|)
$$

(25.90)

and its Fourier transform can be explicitly written as a function of $V$ or $v$

$$
\tilde{V}(\mathbf{k}) = \frac{1}{\Omega} \int_{\Omega} d\mathbf{r} V(\mathbf{r}) e^{-i\mathbf{k}\mathbf{r}} = \frac{1}{\Omega} \int_{\mathbb{R}^3} d\mathbf{r} v(\mathbf{r}) e^{-i\mathbf{k}\mathbf{r}}
$$

(25.91)

where $\mathbb{R}^3$ denotes the whole 3-dimensional space. We now want to find the best (“best” to be defined later) approximate potential of the form

$$
V_a(\mathbf{r}) = \sum_{k \leq k_c} \tilde{Y}(\mathbf{k}) e^{i\mathbf{k}\mathbf{r}} + W(\mathbf{r})
$$

(25.92)

where $W(\mathbf{r})$ has been chosen to go to 0 smoothly when $r = r_c$, being $r_c$ lower or equal to the Wigner-Seitz radius of the cell. Note also the cutoff $k_c$ on the momentum summation.

The best form of $\tilde{Y}(\mathbf{k})$ and $W(\mathbf{r})$ is given by minimizing

$$
\chi^2 = \frac{1}{\Omega} \int d\mathbf{r} \left( V(\mathbf{r}) - \tilde{W}(\mathbf{r}) - \sum_{k \leq k_c} \tilde{Y}(\mathbf{k}) e^{i\mathbf{k}\mathbf{r}} \right)^2
$$

(25.93)

or the reciprocal space equivalent

$$
\chi^2 = \sum_{k \leq k_c} (\tilde{V}(\mathbf{k}) - \tilde{W}(\mathbf{k}) - \tilde{Y}(\mathbf{k}))^2 + \sum_{k > k_c} (\tilde{V}(\mathbf{k}) - \tilde{W}(\mathbf{k}))^2
$$

(25.94)

Eq.25.94 follows from Eq.25.93 and the unitarity (norm conservation) of the Fourier transform. This last condition is minimized by

$$
\tilde{Y}(\mathbf{k}) = \tilde{V}(\mathbf{k}) - \tilde{W}(\mathbf{k})
$$

$$
\min_{\tilde{W}(\mathbf{k})} \sum_{k > k_c} (\tilde{V}(\mathbf{k}) - \tilde{W}(\mathbf{k}))^2
$$

(25.95)

We now use a set of basis function $c_i(\mathbf{r})$ vanishing smoothly at $r = r_c$ to expand $W(\mathbf{r})$ i.e.

$$
W(\mathbf{r}) = \sum_i t_i c_i(\mathbf{r}) \quad \text{or} \quad \tilde{W}(\mathbf{k}) = \sum_i t_i \tilde{c}_i(\mathbf{k})
$$

(25.96)

Inserting the reciprocal space expansion of $\tilde{W}$ in the second condition of Eq.25.93 and minimizing with respect to $t_i$ leads immediately to the linear system $\mathbf{At} = \mathbf{b}$ where

$$
A_{ij} = \sum_{k > k_c} \tilde{c}_i(k) \tilde{c}_j(k) \quad b_j = \sum_{k > k_c} V(k) \tilde{c}_j(k)
$$

(25.97)

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25.3.1 Basis functions

The basis functions are splines. We define a uniform grid with \( N \) uniformly spaced knots at position \( r_i = \frac{r}{N} \) where \( i \in [0, N-1] \). On each knot we center \( m+1 \) piecewise polynomials \( c_{i\alpha}(r) \) with \( \alpha \in [0, m] \), defined as

\[
c_{i\alpha}(r) = \begin{cases} 
\Delta^\alpha \sum_{n=0}^{N} S_{\alpha n} \left( \frac{r-r_i}{\Delta} \right)^n & r_i < r \leq r_{i+1} \\
\Delta^{-\alpha} \sum_{n=0}^{N} S_{\alpha n} \left( \frac{r-r_i}{\Delta} \right)^n & r_{i-1} < r \leq r_i \\
0 & |r-r_i| > \Delta
\end{cases}
\] (25.98)

These functions and their derivatives are, by construction, continuous and odd (even) (with respect to \( r - r_i \)). We further ask them to satisfy

\[
\frac{d^\beta}{dr^\beta} c_{i\alpha}(r) \bigg|_{r=r_i} = \delta_{\alpha\beta} \quad \beta \in [0, m] \\
\frac{d^\beta}{dr^\beta} c_{i\alpha}(r) \bigg|_{r=r_{i+1}} = 0 \quad \beta \in [0, m]
\] (25.99, 25.100)

(The parity of the functions guarantees that the second constraint is satisfied at \( r_{i-1} \) as well). These constraints have a simple interpretation: the basis functions and their first \( m \) derivatives are 0 on the boundary of the subinterval where they are defined; the only function to have a non zero \( \beta \)-th derivative in \( r_i \) is \( c_{i\alpha} \). These \( 2(m+1) \) constraints therefore impose \( N = 2m+1 \). Inserting the definitions of Eq. (25.98) in the constraints of Eq. (25.100) leads to the set of \( 2(m+1) \) linear equations that fixes the value of \( S_{\alpha n} \):

\[
\Delta^{\alpha-\beta} S_{\alpha \beta}! = \delta_{\alpha\beta}
\] (25.101)

\[
\Delta^{\alpha-\beta} \sum_{n=\beta}^{2m+1} S_{\alpha n} \frac{n!}{(n-\beta)!} = 0
\] (25.102)

One can further simplify inserting the first of these equations into the second and write the linear system as

\[
\sum_{n=m+1}^{2m+1} S_{\alpha n} \frac{n!}{(n-\beta)!} = \begin{cases} 
\frac{-1}{(\alpha-\beta)!} & \alpha \geq \beta \\
0 & \alpha < \beta
\end{cases}
\] (25.103)

25.3.2 Fourier components of the basis functions in 3D

\( k \neq 0 \), non coulomb case.

We now need to evaluate the Fourier transform \( \widetilde{c}_{i\alpha}(k) \). Let us start by writing the definition

\[
\widetilde{c}_{i\alpha}(k) = \frac{1}{\omega} \int_{\Omega} dr e^{-i k r} c_{i\alpha}(r)
\] (25.104)

Because \( c_{i\alpha} \) is different from zero only inside the spherical crown defined by \( r_{i-1} < r < r_i \) one can conveniently compute the integral in spherical coordinates as
\[
\tilde{c}_{i\alpha}(k) = \Delta^\alpha \sum_{n=0}^{N} S_{\alpha n} [D^+_{in}(k) + w_{\text{knot}}(-1)^{\alpha+n} D^-_{in}(k)]
\] (25.105)

where we used the definition \( w_{\text{knot}} = 1 - \delta_{i0} \) and

\[
D^\pm_{in}(k) = \pm \frac{4\pi}{k\Omega} \text{Im} \left[ \int_{r_i}^{r_i+\Delta} dr \left( \frac{r - r_i}{\Delta} \right)^n re^{ikr} \right]
\] (25.106)

obtained by integrating the angular part of the Fourier transform. Using the identity

\[
\left( \frac{r - r_i}{\Delta} \right)^n r = \Delta \left( \frac{r - r_i}{\Delta} \right)^{n+1} + \left( \frac{r - r_i}{\Delta} \right)^n r_i
\] (25.107)

and the definition

\[
E^\pm_{in}(k) = \int_{r_i}^{r_i+\Delta} dr \left( \frac{r - r_i}{\Delta} \right)^n e^{ikr}
\] (25.108)

we rewrite Eq.25.106 as

\[
D^\pm_{in}(k) = \pm \frac{4\pi}{k\Omega} \text{Im} \left[ \Delta E^\pm_{i(n+1)}(k) + r_i E^\pm_{in}(k) \right]
\] (25.109)

Finally, using integration by part, one can define \( E^\pm_{in} \) recursively

\[
E^\pm_{in}(k) = \frac{1}{ik} \left[ (\pm)^n e^{ik(r_i+\Delta)} - \frac{n}{\Delta} E^\pm_{i(n-1)}(k) \right]
\] (25.110)

starting from the \( n = 0 \) term

\[
E^\pm_{i0}(k) = \frac{1}{ik} e^{ikr_i} \left( e^{ik\Delta} - 1 \right)
\] (25.111)

\( k \neq 0, \) coulomb case.

To efficiently treat the coulomb divergence at the origin it is convenient to use a basis set \( c^\text{coul}_{i\alpha} \) of the form

\[
c^\text{coul}_{i\alpha} = \frac{c_{i\alpha}}{r}
\] (25.112)

An equation identical to Eq.25.106 holds but with the modified definition

\[
D^\pm_{in}(k) = \pm \frac{4\pi}{k\Omega} \text{Im} \left[ \int_{r_i}^{r_i+\Delta} dr \left( \frac{r - r_i}{\Delta} \right)^n e^{ikr} \right]
\] (25.113)

which can be simply expressed using \( E^\pm_{in}(k) \) as

\[
D^\pm_{in}(k) = \pm \frac{4\pi}{k\Omega} \text{Im} \left[ E^\pm_{in}(k) \right]
\] (25.114)
\( k = 0 \) **coulomb and non coulomb case.**

The definitions of \( D_{in}(k) \) given so far are clearly incompatible with the choice \( k = 0 \) (they involve division by \( k \)). For the non-coulomb case the starting definition is

\[
D_{in}^\pm(0) = \pm \frac{4\pi}{\Omega} \int_{r_i}^{r_i+\Delta} r^2 \left( \frac{r - r_i}{\Delta} \right)^n dr \quad (25.115)
\]

Using the definition \( I_n^\pm = (\pm)^{n+1} \Delta/(n + 1) \) we can express this as

\[
D_{in}^\pm(0) = \pm \frac{4\pi}{\Omega} \left[ \Delta I_{n+2}^\pm + 2r_i \Delta I_{n+1}^\pm + 2r_i^2 I_n^\pm \right] \quad (25.116)
\]

For the coulomb case one get

\[
D_{in}^\pm(0) = \pm \frac{4\pi}{\Omega} \left( \Delta I_{n+1}^\pm + r_i I_n^\pm \right) \quad (25.117)
\]

### 25.3.3 Fourier components of the basis functions in 2D

Eq. 25.105 still holds provided we define

\[
D_{in}^\pm(k) = \pm \frac{2\pi}{\Omega \Delta^n} \sum_{j=0}^{n} \binom{n}{j} (-r_i)^{n-j} \int_{r_i}^{r_i+\Delta} drr_j^{1-C} J_0(kr) \quad (25.118)
\]

where \( C = 1(= 0) \) for the coulomb(non coulomb) case. Eq. 25.118 is obtained using the integral definition of the zero order Bessel function of the first kind

\[
J_0(z) = \frac{1}{\pi} \int_0^\pi e^{iz \cos \theta} d\theta \quad (25.119)
\]

and the binomial expansion for \( (r - r_i)^n \). The integrals can be computed recursively using the following identities

\[
\int dzJ_0(z) = \frac{z}{2} [\pi J_1(z)H_0(z) + J_0(z)(2 - \pi H_1(z))] \quad (25.120)
\]

\[
\int dzzJ_0(z) = zJ_1(z) \quad (25.121)
\]

\[
\int dzz^nJ_0(z) = z^n J_1(z) + (n - 1)x^{n-1}J_0(z) - (n - 1)^2 \int dzz^{n-2}J_0(z) \quad (25.122)
\]

Eq. 25.122 is obtained using Eq. 25.121, integration by part and the identity \( \int J_1(z)dz = -J_0(z) \). In Eq. 25.120 \( H_0 \) and \( H_1 \) are Struve functions.
25.3.4 Construction of the matrix elements

Using the above equations one can construct the matrix elements in Eq. 25.97 and proceed solving for the $t_i$. It is sometimes desirable to put some constraints on the value of $t_i$. For example, when the coulomb potential is concerned one may want to set $t_0 = 1$. If the first $g$ variable are constrained by $t_m = \gamma_m$ with $m = [1, g]$ one can simply redefine Eq. 25.97 as

$$A_{ij} = \sum_{k \geq k_e} \bar{c}_i(k) \bar{c}_j(k) \quad i, j \notin [1, g]$$

$$b_j = \sum_{k > k_e} \left( \bar{V}(k) - \sum_{m=1}^{g} \gamma_m \bar{c}_m(k) \right) \bar{c}_j(k) \quad j \notin [1, g]$$

(25.123)
25.4 Feature: Cubic Spline Interpolation

We present the basic equations and algorithms necessary to construct and evaluate cubic interpolating splines in one, two, and three dimensions. Equations are provided for both natural and periodic boundary conditions.

25.4.1 One Dimension

Let us consider the problem in which we have a function \( y(x) \) specified at a discrete set of points \( x_i \), such that \( y(x_i) = y_i \). We wish to construct a piece-wise cubic polynomial interpolating function, \( f(x) \), which satisfies the following conditions:

- \( f(x_i) = y_i \)
- \( f'(x_i^-) = f'(x_i^+) \)
- \( f''(x_i^-) = f''(x_i^+) \)

**Hermite Interpolants**

In our piecewise representation, we wish to store only the values, \( y_i \), and first derivatives, \( y'_i \), of our function at each point \( x_i \), which we call knots. Given this data, we wish to construct the piecewise cubic function to use between \( x_i \) and \( x_{i+1} \) which satisfies the above conditions. In particular, we wish to find the unique cubic polynomial, \( P(x) \) satisfying

\[
\begin{align*}
P(x_i) &= y_i, \\
P(x_{i+1}) &= y_{i+1} \quad (25.124) \\
P'(x_i) &= y'_i \quad (25.125) \\
P'(x_{i+1}) &= y'_{i+1} \quad (25.126) \\
n_i &\equiv x_{i+1} - x_i \quad (25.128) \\
t &\equiv \frac{x - x_i}{n_i}. \quad (25.129)
\end{align*}
\]

We then define the basis functions,

\[
\begin{align*}
p_1(t) &= (1 + 2t)(t - 1)^2 \quad (25.130) \\
q_1(t) &= t(t - 1)^2 \quad (25.131) \\
p_2(t) &= t^2(3 - 2t) \quad (25.132) \\
q_2(t) &= t^2(t - 1) \quad (25.133)
\end{align*}
\]

On the interval, \((x_i, x_{i+1})\), we define the interpolating function,

\[
P(x) = y_ip_1(t) + y_{i+1}p_2(t) + n \left[ y'_iq_1(t) + y'_{i+1}q_2(t) \right] \quad (25.134)
\]

It can be easily verified that \( P(x) \) satisfies conditions (25.124) through (25.127). It is now left to determine the proper values for the \( y'_i \)'s such that the continuity conditions given above are satisfied.

By construction, the value of the function and derivative will match at the knots, i.e.

\[
P(x_i^-) = P(x_i^+), \quad P'(x_i^-) = P'(x_i^+). \quad (25.135)
\]
Then we must now enforce only the second derivative continuity:

\[ P''(x^-_i) = P''(x^+_i) \]  
\[ \frac{1}{h_i^{-1}} [6y_i - 6y_i + h_{i-1}(2y'_{i-1} + 4y'_i)] = \frac{1}{h_i^2} [-6y_i + 6y_{i+1} + h_i(-4y'_i - 2y'_{i+1})] \]

Let us define

\[ \lambda_i \equiv \frac{h_i}{2(h_i + h_{i-1})} \]  
\[ \mu_i \equiv \frac{h_{i-1}}{2(h_i + h_{i-1})} = \frac{1}{2} - \lambda_i. \]

Then we may rearrange,

\[ \lambda_i y_{i-1}' + y_i' + \mu_i y_{i+1}' = 3 \left[ \lambda_i \frac{y_i - y_{i-1}}{h_{i-1}} + \mu_i \frac{y_{i+1} - y_i}{h_i} \right] \]

This equation holds for all \( 0 < i < (N-1) \), so we have a tridiagonal set of equations. The equations for \( i = 0 \) and \( i = N-1 \) depend on the boundary conditions we are using.

**Periodic boundary conditions**

For periodic boundary conditions, we have

\[ y'_0 + \mu_0 y'_1 + \lambda_0 y'_0 = d_0 \]
\[ \lambda_1 y'_0 + y'_1 + \mu_1 y'_2 + \lambda_1 y'_0 = d_1 \]
\[ \lambda_2 y'_1 + y'_2 + \mu_2 y'_3 + \lambda_2 y'_1 = d_2 \]
\[ \vdots \]
\[ \lambda_{N-1} y'_{N-2} + \mu_{N-1} y'_{N-1} = d_3 \]

Or, in matrix form, we have,

\[
\begin{pmatrix}
1 & \mu_0 & 0 & 0 & \cdots & 0 & \lambda_0 \\
\lambda_1 & 1 & \mu_1 & 0 & \cdots & 0 & 0 \\
0 & \lambda_2 & 1 & \mu_2 & \cdots & 0 & 0 \\
\vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\
0 & 0 & 0 & \lambda_{N-3} & 1 & \mu_{N-3} & 0 \\
0 & 0 & 0 & 0 & \lambda_{N-2} & 1 & \mu_{N-2} \\
\mu_{N-1} & 0 & 0 & 0 & 0 & \lambda_{N-1} & 1
\end{pmatrix}
\begin{pmatrix}
y'_0 \\
y'_1 \\
y'_2 \\
\vdots \\
y'_{N-3} \\
y'_{N-2} \\
y'_{N-1}
\end{pmatrix} =
\begin{pmatrix}
d_0 \\
d_1 \\
d_2 \\
\vdots \\
d_{N-3} \\
d_{N-2} \\
d_{N-1}
\end{pmatrix}.
\]

The system is tridiagonal except for the two elements in the upper right and lower left corners. These terms complicate the solution a bit, although it can still be done in \( O(N) \) time. We first proceed down the rows, eliminating the first non-zero term in each row by subtracting the appropriate multiple of the previous row. At the same time, we also eliminate the first element in the last row, shifting the position of the first non-zero element to the right with each iteration. When we get to the final row, we will have the value for \( y'_{N-1} \). We can then proceed back upward, backsubstituting values from the rows below to calculate all the derivatives.
Complete boundary conditions

If we specify the first derivatives of our function at the end points, we have what is known as complete boundary conditions. The equations in that case are trivial to solve:

\[
\begin{pmatrix}
1 & 0 & 0 & 0 & \cdots & 0 & 0 \\
\lambda_1 & 1 & \mu_1 & 0 & \cdots & 0 & 0 \\
0 & \lambda_2 & 1 & \mu_2 & \cdots & 0 & 0 \\
\vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\
0 & 0 & 0 & \lambda_{N-3} & 1 & \mu_{N-3} & 0 \\
0 & 0 & 0 & 0 & \lambda_{N-2} & 1 & \mu_{N-2} \\
0 & 0 & 0 & 0 & 0 & 0 & 1 \\
\end{pmatrix}
\begin{pmatrix}
y' \left( x_0 \right) \\
y' \left( x_1 \right) \\
y' \left( x_2 \right) \\
\vdots \\
y' \left( x_{N-3} \right) \\
y' \left( x_{N-2} \right) \\
y' \left( x_{N-1} \right) \\
\end{pmatrix}
= \begin{pmatrix}
d_0 \\
d_1 \\
d_2 \\
\vdots \\
d_{N-3} \\
d_{N-2} \\
d_{N-1} \\
\end{pmatrix},
\]

This system is completely tridiagonal and we may solve trivially by performing row eliminations downward, then proceeding upward as before.

Natural boundary conditions

If we do not have information about the derivatives at the boundary conditions, we may construct a natural spline, which assumes the second derivatives are zero at the end points of our spline. In this case our system of equations is the following:

\[
\begin{pmatrix}
1 & \frac{1}{2} & 0 & 0 & \cdots & 0 & 0 \\
\lambda_1 & 1 & \mu_1 & 0 & \cdots & 0 & 0 \\
0 & \lambda_2 & 1 & \mu_2 & \cdots & 0 & 0 \\
\vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\
0 & 0 & 0 & \lambda_{N-3} & 1 & \mu_{N-3} & 0 \\
0 & 0 & 0 & 0 & \lambda_{N-2} & 1 & \mu_{N-2} \\
0 & 0 & 0 & 0 & 0 & 0 & 1 \\
\end{pmatrix}
\begin{pmatrix}
y' \left( x_0 \right) \\
y' \left( x_1 \right) \\
y' \left( x_2 \right) \\
\vdots \\
y' \left( x_{N-3} \right) \\
y' \left( x_{N-2} \right) \\
y' \left( x_{N-1} \right) \\
\end{pmatrix}
= \begin{pmatrix}
d_0 \\
d_1 \\
d_2 \\
\vdots \\
d_{N-3} \\
d_{N-2} \\
d_{N-1} \\
\end{pmatrix},
\]

with

\[
d_0 = \frac{3}{2} \frac{y_1 - y_0}{h_0}, \quad d_{N-1} = \frac{3}{2} \frac{y_{N-1} - y_{N-2}}{h_{N-1}}.
\]

25.4.2 Bicubic Splines

It is possible to extend the cubic spline interpolation method to functions of two variables, i.e. \( F(x, y) \). In this case, we have a rectangular mesh of points given by \( F_{ij} \equiv F(x_i, y_j) \). In the case of 1D splines, we needed to store the value of the first derivative of the function at each point, in addition to the value. In the case of bicubic splines, we need to store four quantities for each mesh point:

\[
F_{ij} \equiv F(x_i, y_i) \quad \text{(25.145)}
\]
\[
F^x_{ij} \equiv \partial_x F(x_i, y_i) \quad \text{(25.146)}
\]
\[
F^y_{ij} \equiv \partial_y F(x_i, y_i) \quad \text{(25.147)}
\]
\[
F^{xy}_{ij} \equiv \partial_x \partial_y F(x_i, y_i) \quad \text{(25.148)}
\]

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Consider the point \((x, y)\) at which we wish to interpolate \(F\). We locate the rectangle which contains this point, such that \(x_i \leq x < x_{i+1}\) and \(y_i \leq y < y_{i+1}\). Let

\[
\begin{align*}
    h &\equiv x_{i+1} - x_i \\
    l &\equiv y_{i+1} - y_i \\
    u &\equiv \frac{x - x_i}{h} \\
    v &\equiv \frac{y - y_i}{l}
\end{align*}
\]

Then, we calculate the interpolated value as

\[
F(x, y) = \left( \begin{array}{c} p_1(u) \\ p_2(u) \\ hq_1(u) \\ hq_2(u) \end{array} \right)^T \left( \begin{array}{cccc}
    F_{i,j} & F_{i+1,j} & F_{i,j}^y & F_{i,j}^{y+1} \\
    F_{i+1,j} & F_{i+1,j+1} & F_{i+1,j}^y & F_{i+1,j+1}^{y+1} \\
    F_{i,j}^x & F_{i+1,j}^x & F_{i,j}^{xy} & F_{i,j}^{xy+1} \\
    F_{i+1,j}^x & F_{i+1,j+1}^x & F_{i+1,j}^{xy} & F_{i+1,j+1}^{xy+1} \end{array} \right) \left( \begin{array}{c} p_1(v) \\ p_2(v) \\ kq_1(v) \\ kq_2(v) \end{array} \right) \tag{25.153}
\]

**Construction bicubic splines**

We now address the issue of how to compute the derivatives that are needed for the interpolation. The algorithm is quite simple. For every \(x_i\), we perform the tridiagonal solution as we did in the 1D splines to compute \(F_{ij}^y\). Similarly, we perform a tridiagonal solve for every value of \(F_{ij}^x\). Finally, in order to compute the cross-derivative we may *either* to the tridiagonal solve in the \(y\) direction of \(F_{ij}^x\), or solve in the \(x\) direction for \(F_{ij}^x\) to obtain the cross-derivatives, \(F_{ij}^{xy}\). Hence, only minor modifications to the 1D interpolations are necessary.

### 25.4.3 Tricubic Splines

Bicubic interpolation required two four-component vectors and a 4x4 matrix. By extension, tricubic interpolation requires three 4-component vectors and a 4x4x4 tensor. We summarize the forms of these vectors below.

\[
\begin{align*}
    h &\equiv x_{i+1} - x_i \\
    l &\equiv y_{i+1} - y_i \\
    m &\equiv z_{i+1} - z_i \\
    u &\equiv \frac{x - x_i}{h} \\
    v &\equiv \frac{y - y_i}{l} \\
    w &\equiv \frac{z - z_i}{m}
\end{align*}
\]

\[
\begin{align*}
    \vec{a} &= \left( \begin{array}{cccc}
    p_1(u) & p_2(u) & hq_1(u) & hq_2(u) \end{array} \right)^T \\
    \vec{b} &= \left( \begin{array}{cccc}
    p_1(v) & p_2(v) & kq_1(v) & kq_2(v) \end{array} \right)^T \\
    \vec{c} &= \left( \begin{array}{cccc}
    p_1(w) & p_2(w) & lq_1(w) & lq_2(w) \end{array} \right)^T
\end{align*}
\]
\[
\begin{pmatrix}
A_{000} = F_{i,j,k} & A_{001} = F_{i,j,k+1} & A_{002} = F_{i,j,k}^z & A_{003} = F_{i,j,k+1}^z \\
A_{010} = F_{i,j+1,k} & A_{011} = F_{i,j+1,k+1} & A_{012} = F_{i,j+1,k}^z & A_{013} = F_{i,j+1,k+1}^z \\
A_{020} = F_{i+1,j,k} & A_{021} = F_{i+1,j,k+1} & A_{022} = F_{i+1,j,k}^y & A_{023} = F_{i+1,j,k+1}^y \\
A_{030} = F_{i+1,j+1,k} & A_{031} = F_{i+1,j+1,k+1} & A_{032} = F_{i+1,j+1,k}^y & A_{033} = F_{i+1,j+1,k+1}^y \\
A_{100} = F_{i+1,j,k} & A_{101} = F_{i+1,j,k+1} & A_{102} = F_{i+1,j,k}^z & A_{103} = F_{i+1,j,k+1}^z \\
A_{110} = F_{i+1,j+1,k} & A_{111} = F_{i+1,j+1,k+1} & A_{112} = F_{i+1,j+1,k}^z & A_{113} = F_{i+1,j+1,k+1}^z \\
A_{120} = F_{i+1,j+1,k} & A_{121} = F_{i+1,j+1,k+1} & A_{122} = F_{i+1,j+1,k}^y & A_{123} = F_{i+1,j+1,k+1}^y \\
A_{130} = F_{i+1,j+1,k} & A_{131} = F_{i+1,j+1,k+1} & A_{132} = F_{i+1,j+1,k}^y & A_{133} = F_{i+1,j+1,k+1}^y \\
A_{200} = F_{i,j,k}^x & A_{201} = F_{i,j,k+1}^x & A_{202} = F_{i,j,k}^{xz} & A_{203} = F_{i,j,k+1}^{xz} \\
A_{210} = F_{i,j+1,k}^x & A_{211} = F_{i,j+1,k+1}^x & A_{212} = F_{i,j+1,k}^{xy} & A_{213} = F_{i,j+1,k+1}^{xy} \\
A_{220} = F_{i+1,j,k}^{xy} & A_{221} = F_{i+1,j,k+1}^{xy} & A_{222} = F_{i+1,j,k}^{xyz} & A_{223} = F_{i+1,j,k+1}^{xyz} \\
A_{230} = F_{i+1,j+1,k}^{xyz} & A_{231} = F_{i+1,j+1,k+1}^{xyz} & A_{232} = F_{i+1,j+1,k}^{xyz} & A_{233} = F_{i+1,j+1,k+1}^{xyz} \\
A_{300} = F_{i+1,j,k}^x & A_{301} = F_{i+1,j,k+1}^x & A_{302} = F_{i+1,j,k}^{xz} & A_{303} = F_{i+1,j,k+1}^{xz} \\
A_{310} = F_{i+1,j+1,k}^x & A_{311} = F_{i+1,j+1,k+1}^x & A_{312} = F_{i+1,j+1,k}^{xy} & A_{313} = F_{i+1,j+1,k+1}^{xy} \\
A_{320} = F_{i+1,j+1,k}^{xy} & A_{321} = F_{i+1,j+1,k+1}^{xy} & A_{322} = F_{i+1,j+1,k}^{xyz} & A_{323} = F_{i+1,j+1,k+1}^{xyz} \\
A_{330} = F_{i+1,j+1,k}^{xyz} & A_{331} = F_{i+1,j+1,k+1}^{xyz} & A_{332} = F_{i+1,j+1,k}^{xyz} & A_{333} = F_{i+1,j+1,k+1}^{xyz}
\end{pmatrix}
\]

(25.163)

Now, we can write

\[F(x, y, z) = \sum_{i=0}^{3} a_i \sum_{j=0}^{3} b_j \sum_{k=0}^{3} c_k A_{i,j,k}\]

(25.164)

The appropriate derivatives of \( F \) may be computed by a generalization of the method used for bicubic splines above.
25.5 Feature: B-spline Orbital Tiling (Band Unfolding)

In continuum quantum Monte Carlo simulations, it is necessary to evaluate the electronic orbitals of a system at real-space positions hundreds of millions of times. It has been found that if these orbitals are represented in a localized, B-spline basis, each evaluation takes a small, constant time which is independent of system size.

Unfortunately, the memory required for storing the B-spline grows with the second power of the system size. If we are studying perfect crystals, however, this can be reduced to linear scaling if we tile the primitive cell. In this approach, a supercell is constructed by tiling the primitive cell \( N_1 \times N_2 \times N_3 \) in the three lattice directions. The orbitals are then represented in real space only in the primitive cell, and an \( N_1 \times N_2 \times N_3 \) k-point mesh. To evaluate an orbital at any point in the supercell, it is only necessary to wrap that point back into the primitive cell, evaluate the spline, and then multiply the phase factor, \( e^{-i\mathbf{k}\cdot\mathbf{r}} \).

Here, we show that this approach can be generalized to a tiling constructed with a \( 3 \times 3 \) nonsingular matrix of integers, of which the above approach is a special case. This generalization brings with it a number of advantages. The primary reason for performing supercell calculations in QMC is to reduce finite-size errors. These errors result from three sources: 1) the quantization of the crystal momentum; 2) the unphysical periodicity of the exchange-correlation hole of the electron; and 3) the kinetic-energy contribution from the periodicity of the long-range jastrow correlation functions. The first source of error can be largely eliminated by twist averaging. If the simulation cell is large enough that XC hole does not “leak” out of the simulation cell, the second source can be eliminated either through use of the MPC interaction or the \textit{a posteriori} correction of Chiesa et. al.

The satisfaction of the leakage requirement is controlled by whether the minimum distance, \( L_{\text{min}} \) from one supercell image to the next is greater than the width of the XC hole. Therefore, given a choice, it is best to use a cell which is as nearly cubic as possible, since this choice maximizes \( L_{\text{min}} \) for a given number of atoms. Most often, however, the primitive cell is not cubic. In these cases, if we wish to choose the optimal supercell to reduce finite size effects, we cannot utilize the simple primitive tiling scheme. In the generalized scheme we present, it is possible to choose far better supercells (from the standpoint of finite-size errors), while retaining the storage efficiency of the original tiling scheme.

25.5.1 The mathematics

Consider the set of primitive lattice vectors, \( \{ \mathbf{a}_1^p, \mathbf{a}_2^p, \mathbf{a}_3^p \} \). We may write these vectors in a matrix, \( \mathbf{L}_p \), whose rows are the primitive lattice vectors. Consider a non-singular matrix of integers, \( \mathbf{S} \). A corresponding set of supercell lattice vectors, \( \{ \mathbf{a}_1^s, \mathbf{a}_2^s, \mathbf{a}_3^s \} \), can be constructed by the matrix product

\[
\mathbf{a}_i^s = S_{ij} \mathbf{a}_j^p
\]

If the primitive cell contains \( N_p \) atoms, the supercell will then contain \( N_s = |\det(\mathbf{S})|N_p \) atoms.
25.5.2 Example: FeO

As an example, consider the primitive cell for antiferromagnetic FeO (wustite) in the rocksalt structure. The primitive vectors, given in units of the lattice constant, are given by

\[
\begin{align*}
a_1^s & = \frac{1}{2} \hat{x} + \frac{1}{2} \hat{y} + \hat{z} \\
a_2^s & = \frac{1}{2} \hat{x} + \hat{y} + \frac{1}{2} \hat{z} \\
a_3^s & = \hat{x} + \frac{1}{2} \hat{y} + \frac{1}{2} \hat{z}
\end{align*}
\]

(25.166) (25.167) (25.168)

This primitive cell contains two iron atoms and two oxygen atoms. It is a very elongated cell with acute angles, and thus has a short minimum distance between adjacent images.

The smallest cubic cell consistent with the AFM ordering can be constructed with the matrix

\[
S = \begin{bmatrix}
-1 & -1 & 3 \\
-1 & 3 & -1 \\
3 & -1 & -1
\end{bmatrix}
\]

(25.169)

This cell has \(2 \det(S) = 32\) iron atoms and 32 oxygen atoms. In this example, we may perform the simulation in the 32-iron supercell, while storing the orbitals only in the 2-iron primitive cell, for a savings of a factor of 16.

The k-point mesh

In order to be able to use the generalized tiling scheme, we need to have the appropriate number of bands to occupy in the supercell. This may be achieved by appropriately choosing the k-point mesh. In this section, we explain how these points are chosen.

For simplicity, let us assume that the supercell calculation will be performed at the \(\Gamma\)-point. We may lift this restriction very easily later. The fact that supercell calculation is performed at \(\Gamma\) implies that the k-points used in the primitive-cell calculation must be \(G\)-vectors of the superlattice. This still leaves us with an infinite set of vectors. We may reduce this set to a finite number by considering that the orbitals must form an linearly independent set. Orbitals with k-vectors \(k_1^p\) and \(k_2^p\) will differ by at most a constant factor if \(k_1^p - k_2^p = G^p\), where \(G^p\) is a reciprocal lattice vector of the primitive cell.

Combining these two considerations gives us a prescription for generating our k-point mesh. The mesh may be taken to be the set of k-point which are \(G\)-vectors of the superlattice, reside within the first Brillouin zone (FBZ) of the primitive lattice, whose members do not differ a \(G\)-vector of the primitive lattice. Upon constructing such a set, we find that the number of included k-points is equal to \(|\det(S)|\), precisely the number we need. This can by considering the fact that the supercell has a volume \(|\det(S)|\) times that of the primitive cell. This implies that the volume of the supercell’s FBZ is \(|\det(S)|^{-1}\) times that of the primitive cell. Hence, \(|\det(S)|\) \(G\)-vectors of the supercell will fit in the FBZ of the primitive cell. Removing duplicate k-vectors, which differ from another by a reciprocal lattice vector, avoids double-counting vectors which lie on zone faces.

Formulae

Let \(A\) be the matrix whose rows are the direct lattice vectors, \(\{a_i\}\). The, let the matrix \(B\) be defined as \(2\pi(A^{-1})^\dagger\). Its rows are the primitive reciprocal lattice vectors. Let \(A_p\) and \(A_s\) represent
the primitive and superlattice matrices, respectively, and similarly for their reciprocals. Then we have

\[
\begin{align*}
A_s &= SA_p & \quad (25.170) \\
B_s &= 2\pi [(SA_p)^{-1}]^\dagger & \quad (25.171) \\
      &= 2\pi [A_p^{-1}S^{-1}]^\dagger & \quad (25.172) \\
      &= 2\pi (S^{-1})^\dagger (A_p^{-1})^\dagger & \quad (25.173) \\
      &= (S^{-1})^\dagger B_p & \quad (25.174)
\end{align*}
\]

Consider a k-vector, \(k\). It may be alternatively be written in basis of reciprocal lattice vectors as \(t\).

\[
\begin{align*}
k &= (t^\dagger B)^\dagger & \quad (25.175) \\
    &= B^\dagger t & \quad (25.176) \\
t &= (B^\dagger)^{-1}k & \quad (25.177) \\
    &= (B^{-1})^\dagger k & \quad (25.178) \\
    &= \frac{Ak}{2\pi} & \quad (25.179)
\end{align*}
\]

We may then express a twist vector of the primitive lattice, \(t_p\) in terms of the superlattice.

\[
\begin{align*}
t_s &= \frac{A_s k}{2\pi} & \quad (25.180) \\
    &= \frac{A_s B_p^\dagger t_p}{2\pi} & \quad (25.181) \\
    &= \frac{SA_p B_p^\dagger t_p}{2\pi} & \quad (25.182) \\
    &= \frac{2\pi SA_p A_p^{-1} t_p}{2\pi} & \quad (25.183) \\
    &= St_p & \quad (25.184)
\end{align*}
\]

This gives the simple result that twist-vectors transform in precisely the same way as direct lattice vectors.
25.6 Feature: Hybrid orbital representation

\[
\phi(r) = \sum_{\ell=0}^{\ell_{\text{max}}} \sum_{m=-\ell}^{\ell} Y_{\ell m}(\hat{\Omega}) u_{\ell m}(r),
\]

(25.185)

where \( u_{\ell m}(r) \) are complex radial functions represented in some radial basis (e.g. splines).

25.6.1 Real Spherical Harmonics

If \( \phi(r) \) can be written as purely real, we can change the representation so that

\[
\phi(r) = \sum_{\ell=0}^{\ell_{\text{max}}} \sum_{m=-\ell}^{\ell} Y_{\ell m}(\hat{\Omega})^{R} u_{\ell m}(r),
\]

(25.186)

where \( Y_{\ell m}^{R} \) are the real spherical harmonics defined by

\[
Y_{\ell m} = \begin{cases} 
Y_{\ell 0} & \text{if } m = 0 \\
\frac{1}{2} (Y_{\ell m}^{+} + (-1)^m Y_{\ell m}^{-}) & \text{if } m > 0 \\
\frac{1}{2} (Y_{\ell m}^{-} - (-1)^m Y_{\ell m}^{+}) & \text{if } m < 0.
\end{cases}
\]

(25.187)

We need then to relate \( u_{\ell m} \) to \( u_{\ell m}^{R} \). We wish to express,

\[
\text{Re} \left[ \phi(r) \right] = \sum_{\ell=0}^{\ell_{\text{max}}} \sum_{m=-\ell}^{\ell} \text{Re} \left[ Y_{\ell m}^{R} u_{\ell m}(r) \right]
\]

(25.188)

in terms of \( u_{\ell m}^{R} \) and \( Y_{\ell m} \).

\[
\text{Re} \left[ Y_{\ell m}^{R} u_{\ell m} \right] = \text{Re} \left[ Y_{\ell m}^{R} \right] \text{Re} \left[ u_{\ell m} \right] - \text{Im} \left[ Y_{\ell m}^{R} \right] \text{Im} \left[ u_{\ell m} \right]
\]

(25.189)

For \( m > 0 \),

\[
\text{Re} \left[ Y_{\ell m}^{R} \right] = Y_{\ell m} \quad \text{and} \quad \text{Im} \left[ Y_{\ell m}^{R} \right] = Y_{\ell -m}.
\]

(25.190)

For \( m < 0 \),

\[
\text{Re} \left[ Y_{\ell m}^{R} \right] = (-1)^m Y_{\ell -m} \quad \text{and} \quad \text{Im} \left[ Y_{\ell m}^{R} \right] = -(-1)^m Y_{\ell m}.
\]

(25.191)

Then for \( m > 0 \),

\[
\begin{align*}
\bar{u}_{\ell m} &= \text{Re} \left[ u_{\ell m} \right] + (-1)^m \text{Re} \left[ u_{\ell -m} \right] \\
\bar{u}_{\ell -m} &= -\text{Im} \left[ u_{\ell m} \right] + (-1)^m \text{Im} \left[ u_{\ell -m} \right].
\end{align*}
\]

(25.192)

(25.193)

25.6.2 Projecting to atomic orbitals

Inside a muffin tin, orbitals are represented as product of spherical harmonics and 1D radial functions, primarily represented by splines. For a muffin tin centered at \( \mathbf{I} \),

\[
\phi_{n}(r) = \sum_{\ell,m} Y_{\ell m}(r - \mathbf{I}) u_{\ell m}(|r - \mathbf{I}|)
\]

(25.194)

Let use consider the case that our original representation for \( \phi(r) \) is of the form

\[
\phi_{n,k}(r) = \sum_{G} c_{G+k}^{n} e^{i(G+k)\cdot r}
\]

(25.195)
Recall that
\[ e^{\mathbf{i} \mathbf{r} \cdot \mathbf{k}} = 4\pi \sum_{\ell, m} i^\ell j_\ell(|\mathbf{r}|) Y_{\ell m}(\hat{\mathbf{k}}) Y_{\ell m}^*(\hat{\mathbf{r}}). \]  
(25.196)

Conjugating,
\[ e^{-\mathbf{i} \mathbf{r} \cdot \mathbf{k}} = 4\pi \sum_{\ell, m} (-i)^\ell j_\ell(|\mathbf{r}|) \left[ Y_{\ell m}(\hat{\mathbf{k}}) \right]^* Y_{\ell m}(\hat{\mathbf{r}}). \]  
(25.197)

Setting \( \mathbf{k} \to -\mathbf{k} \),
\[ e^{\mathbf{i} \mathbf{r} \cdot \mathbf{k}} = 4\pi \sum_{\ell, m} i^\ell j_\ell(|\mathbf{r}|) \left[ Y_{\ell m}(\hat{\mathbf{k}}) \right]^* Y_{\ell m}(\hat{\mathbf{r}}). \]  
(25.198)

Then,
\[ e^{\mathbf{i} \mathbf{k} \cdot (\mathbf{r} - \mathbf{I})} = 4\pi \sum_{\ell, m} i^\ell j_\ell(|\mathbf{r} - \mathbf{I}|) \left[ Y_{\ell m}(\hat{\mathbf{k}}) \right]^* Y_{\ell m}(\mathbf{r} - \mathbf{I}). \]  
(25.199)

Then
\[ e^{\mathbf{i} \mathbf{r} \cdot \mathbf{k}} = 4\pi e^{\mathbf{i} \mathbf{k} \cdot \mathbf{I}} \sum_{\ell, m} i^\ell j_\ell(|\mathbf{r} - \mathbf{I}|) \left[ Y_{\ell m}(\hat{\mathbf{k}}) \right]^* Y_{\ell m}(\mathbf{r} - \mathbf{I}). \]  
(25.200)

Then
\[ \phi_{n, \mathbf{k}}(\mathbf{r}) = \sum_{\mathbf{G}} 4\pi c_n^G e^{\mathbf{i}(\mathbf{G} + \mathbf{k} \cdot \mathbf{I})} \sum_{\ell, m} i^\ell j_\ell(|\mathbf{G} + \mathbf{k}|) \left[ Y_{\ell m}(\mathbf{G} + \mathbf{k}) \right]^* Y_{\ell m}(\mathbf{r} - \mathbf{I}). \]  
(25.201)

Comparing to (25.194),
\[ \tilde{u}_{\ell m}(\mathbf{r}) = 4\pi i^\ell \sum_{\mathbf{G}} c_{\mathbf{G} + \mathbf{k}}^n e^{\mathbf{i}(\mathbf{G} + \mathbf{k} \cdot \mathbf{I})} j_\ell(|\mathbf{G} + \mathbf{k}||\mathbf{r}|) \left[ Y_{\ell m}(\mathbf{G} + \mathbf{k}) \right]^*. \]  
(25.202)

If we had adopted the opposite sign convention for Fourier transforms (as is unfortunately the case in wconvert), we would have
\[ u_{\ell m}(\mathbf{r}) = 4\pi (-i)^\ell \sum_{\mathbf{G}} c_{\mathbf{G} + \mathbf{k}}^n e^{-\mathbf{i}(\mathbf{G} + \mathbf{k} \cdot \mathbf{I})} j_\ell(|\mathbf{G} + \mathbf{k}||\mathbf{r}|) \left[ Y_{\ell m}(\mathbf{G} + \mathbf{k}) \right]^*. \]  
(25.203)
25.7 Feature: Electron-electron-ion Jastrow factor

The general form of the 3-body Jastrow we describe here depends on the three inter-particle distances, \((r_{ij}, r_{il}, r_{jl})\).

\[ J_3 = \sum_{I \in \text{ions}} \sum_{j \neq i} U(r_{ij}, r_{il}, r_{jl}) \tag{25.204} \]

Note that we constrain the form of \(U\) such that \(U(r_{ij}, r_{il}, r_{jl}) = U(r_{ij}, r_{jl}, r_{il})\), so as to preserve the particle symmetry of the wave function. We then compute the gradient as

\[
\nabla_i J_3 = \sum_{I \in \text{ions}} \sum_{j \neq i} \left[ \frac{\partial U(r_{ij}, r_{il}, r_{jl})}{\partial r_{ij}} \frac{\mathbf{r}_i - \mathbf{r}_j}{|\mathbf{r}_i - \mathbf{r}_j|} + \frac{\partial U(r_{ij}, r_{il}, r_{jl})}{\partial r_{il}} \frac{\mathbf{r}_i - \mathbf{I}}{|\mathbf{r}_i - \mathbf{I}|} \right] \tag{25.205} \]

To compute the laplacian, we take

\[
\nabla_i^2 J_3 = \nabla_i \cdot (\nabla_i J_3) \tag{25.206} \]

\[
= \sum_{I \in \text{ions}} \sum_{j \neq i} \left[ \frac{\partial^2 U}{\partial r_{ij}^2} + \frac{2 \partial U}{r_{ij}^2} \frac{\mathbf{r}_{ij}}{r_{ij}} + 2 \frac{\partial^2 U}{\partial r_{ij} \partial r_{il}} \frac{\mathbf{r}_{ij} \cdot \mathbf{r}_{il}}{r_{ij} r_{il}} + \frac{\partial^2 U}{\partial r_{il}^2} + \frac{2 \partial U}{r_{il}^2} \frac{1}{r_{il}} \right] \]

We now wish to compute the gradient of these terms w.r.t. the ion position, \(I\).

\[
\nabla_I J_3 = -\sum_{j \neq i} \left[ \frac{\partial U(r_{ij}, r_{il}, r_{jl})}{\partial r_{il}} \frac{\mathbf{r}_i - \mathbf{I}}{|\mathbf{r}_i - \mathbf{I}|} + \frac{\partial U(r_{ij}, r_{il}, r_{jl})}{\partial r_{jl}} \frac{\mathbf{r}_j - \mathbf{I}}{|\mathbf{r}_j - \mathbf{I}|} \right] \tag{25.207} \]

For the gradient w.r.t. \(i\) of the gradient w.r.t. \(I\), the result is a tensor,

\[
\nabla_I \nabla_i J_3 = \nabla_i \sum_{j \neq i} \left[ \frac{\partial U(r_{ij}, r_{il}, r_{jl})}{\partial r_{ij}} \frac{\mathbf{r}_i - \mathbf{r}_j}{|\mathbf{r}_i - \mathbf{r}_j|} + \frac{\partial U(r_{ij}, r_{il}, r_{jl})}{\partial r_{il}} \frac{\mathbf{r}_i - \mathbf{I}}{|\mathbf{r}_i - \mathbf{I}|} \right] \tag{25.208} \]

\[
= -\sum_{j \neq i} \left[ \frac{\partial^2 U}{\partial r_{ij} \partial r_{il}} \hat{r}_{ij} \otimes \hat{r}_{il} + \left( \frac{\partial^2 U}{\partial r_{ij}^2} - \frac{\partial U}{r_{il}^2} \right) \frac{\mathbf{r}_{il} \otimes \mathbf{r}_{il}}{r_{il}^2} + \frac{\partial U}{r_{il}^2} \frac{1}{r_{il}} \right] \]

\[
\nabla_I \nabla_i J_3 = \nabla_i \sum_{j \neq i} \left[ \frac{\partial U(r_{ij}, r_{il}, r_{jl})}{\partial r_{ij}} \frac{\mathbf{r}_i - \mathbf{r}_j}{|\mathbf{r}_i - \mathbf{r}_j|} + \frac{\partial U(r_{ij}, r_{il}, r_{jl})}{\partial r_{il}} \frac{\mathbf{r}_i - \mathbf{I}}{|\mathbf{r}_i - \mathbf{I}|} \right] \tag{25.209} \]

\[
= \sum_{j \neq i} \left[ -\frac{\partial^2 U}{\partial r_{ij} \partial r_{il}} \hat{r}_{ij} \otimes \hat{r}_{il} + \left( -\frac{\partial^2 U}{\partial r_{il}^2} + \frac{\partial U}{r_{il}^2} \right) \frac{\mathbf{r}_{il} \otimes \mathbf{r}_{il}}{r_{il}^2} - \frac{\partial U}{r_{il}^2} \frac{1}{r_{il}} \right] \]
For the laplacian,

$$\nabla_I \nabla^2_J = \nabla_I [\nabla_i \cdot (\nabla_i J_3)]$$

$$= \nabla_I \sum_{j \neq i} \left[ \frac{\partial^2 U}{\partial r_{ij}^2} + \frac{2}{r_{ij}} \frac{\partial U}{\partial r_{ij}} + \frac{\partial^2 U}{\partial r_{ij} \partial r_{il}} \frac{\mathbf{r}_{il} \cdot \mathbf{r}_{il}}{r_{ij}^2 r_{il}^2} + \frac{\partial^2 U}{\partial r_{il}^2} + \frac{2}{r_{il}^2} \frac{\partial U}{\partial r_{il}} \right]$$

$$= \sum_{j \neq i} \left[ \frac{\partial^3 U}{\partial r_{il} \partial r_{ij}^2} + \frac{2}{r_{ij}} \frac{\partial^2 U}{\partial r_{il} \partial r_{ij}} + 2 \left( \frac{\partial^3 U}{\partial r_{ij} \partial r_{il}^2} - \frac{1}{r_{il}^2} \frac{\partial^2 U}{\partial r_{ij} \partial r_{il}} \right) \frac{\mathbf{r}_{il} \cdot \mathbf{r}_{il}}{r_{ij} r_{il}^2} + \frac{\partial^3 U}{\partial r_{il}^3} - \frac{2}{r_{il}^3} \frac{\partial U}{\partial r_{il}} + \frac{2}{r_{il}^2} \frac{\partial^2 U}{\partial r_{il}^2} \right]$$

$$+ \sum_{j \neq i} \left[ \frac{\partial^3 U}{\partial r_{ij}^2 \partial r_{jI}} + \frac{2}{r_{ij}} \frac{\partial^2 U}{\partial r_{ij} \partial r_{jI}} + \frac{\partial^3 U}{\partial r_{ij} \partial r_{ij} \partial r_{jI}} \frac{\mathbf{r}_{il} \cdot \mathbf{r}_{il}}{r_{ij}^2 r_{ij}^2} + \frac{\partial^3 U}{\partial r_{il}^3} + \frac{2}{r_{il}^3} \frac{\partial^2 U}{\partial r_{il}^2} \right] \frac{1 - \mathbf{r}_j}{|\mathbf{r}_j - \mathbf{I}|}$$

$$+ \sum_{j \neq i} \left[ -\frac{2}{r_{il}^2} \frac{\partial^2 U}{\partial r_{ij} \partial r_{il}} \right] \frac{\mathbf{r}_{ij}}{r_{ij}}$$
25.8 Feature: Reciprocal-Space Jastrow Factors

25.8.1 Two-body Jastrow

\[ J_2 = \sum_{\mathbf{G} \neq 0} \sum_{i \neq j} a_{\mathbf{G}} e^{i \mathbf{G} \cdot (\mathbf{r}_i - \mathbf{r}_j)} \]  

(25.211)

This may be rewritten as

\[
J_2 = \sum_{\mathbf{G} \neq 0} \sum_{i \neq j} a_{\mathbf{G}} e^{i \mathbf{G} \cdot \mathbf{r}_i} e^{-i \mathbf{G} \cdot \mathbf{r}_j} 
\]

\[
= \sum_{\mathbf{G} \neq 0} a_{\mathbf{G}} \left\{ \sum_{\rho_{\mathbf{G}}} e^{i \mathbf{G} \cdot \mathbf{r}_i} \left( \sum_{\rho_{-\mathbf{G}}} e^{-i \mathbf{G} \cdot \mathbf{r}_j} \right) - 1 \right\} 
\]

(25.213)

The \(-1\) is just a constant term and may be subsumed into the \(a_{\mathbf{G}}\) coefficient by a simple redefinition. This leaves a simple, but general, form:

\[ J_2 = \sum_{\mathbf{G} \neq 0} a_{\mathbf{G}} \rho_{\mathbf{G}} \rho_{-\mathbf{G}} \]  

(25.214)

We may now further constrain this on physical grounds. First, we recognize that \(J_2\) should be real. Since \(\rho_{-\mathbf{G}} = \rho_{\mathbf{G}}^{*}\), it follows that \(\rho_{\mathbf{G}} \rho_{-\mathbf{G}} = |\rho_{\mathbf{G}}|^2\) is real, so that \(a_{\mathbf{G}}\) must be real. Furthermore, we group the \(\mathbf{G}'s\) into \((+ \mathbf{G}, - \mathbf{G})\) pairs, and sum over only the positive vectors to save time.

25.8.2 One-body Jastrow

The one-body Jastrow has a similar form, but depends on the displacement from the electrons to the ions in the system.

\[ J_1 = \sum_{\mathbf{G} \neq 0} \sum_{\alpha} \sum_{i \in \mathbf{I}^\alpha_{\text{elec}}} \sum_{j \in \mathbf{I}^\alpha_{\text{elec}}} b_{\mathbf{G}}^{\alpha} e^{i \mathbf{G} \cdot (\mathbf{I}^\alpha_{j} - \mathbf{r}_i)} \]  

(25.215)

where \(\alpha\) denotes the different ionic species. We may rewrite this in terms of \(\rho_{\mathbf{G}}^{\alpha}\),

\[ J_1 = \sum_{\mathbf{G} \neq 0} \left[ \sum_{\alpha} b_{\mathbf{G}}^{\alpha} \rho_{\mathbf{G}}^{\alpha} \right] \rho_{-\mathbf{G}} \]  

(25.216)

where

\[ \rho_{\mathbf{G}}^{\alpha} = \sum_{i \in \mathbf{I}^\alpha} e^{i \mathbf{G} \cdot \mathbf{I}^\alpha_{i}}. \]  

(25.217)

We note that in the above equation, for a single configuration of the ions, the sum in brackets can be rewritten as a single constant. This implies that the per-species one-body coefficients, \(b_{\mathbf{G}}^{\alpha}\), are underdetermined for single configuration of the ions. In general, if we have \(N\) species, we need \(N\) linearly independent ion configurations to uniquely determine \(b_{\mathbf{G}}^{\alpha}\). For this reason, we will drop the \(\alpha\) superscript of \(b_{\mathbf{G}}\) for now.

If we do desire to find a reciprocal space one-body Jastrow that is transferable to systems with different ion positions and \(N\) ionic species, we must perform compute \(b_{\mathbf{G}}\) for \(N\) different ion configurations. We may then construct \(N\) equations at each value of \(\mathbf{G}\) to solve for the \(N\) unknown values, \(b_{\mathbf{G}}^{\alpha}\).
In the two-body case, \( a_G \) was constrained to be real by the fact that \( \rho_G \rho_{-G} \) was real. However, in the one-body case, there is no such guarantee about \( \rho^\alpha_G \rho^\beta_{-G} \). Therefore, in general, \( b_G \) may be complex.

### 25.8.3 Symmetry considerations

For a crystal, many of the \( G \)-vectors will be equivalent by symmetry. It is useful then, to divide the \( G \)-vectors into symmetry-related groups and then to require that they share a common coefficient. Two vectors, \( G \) and \( G' \), may be considered symmetry related if, for all \( \alpha \) and \( \beta \),

\[
\rho^\alpha_G \rho^\beta_G = \rho^\alpha_{G'} \rho^\beta_{-G'}.
\]  

(25.218)

For the one-body term, we may also omit from our list of \( G \)-vectors those for which all species structure factors are zero. This is equivalent to saying that, if we are tiling a primitive cell, we should include only the \( G \)-vectors of the primitive cell, and not the supercell. Note that this is not the case for the two-body term, since the exchange-correlation hole should not have the periodicity of the primitive cell.

### 25.8.4 Gradients and Laplacians

\[
\nabla r_i J^2 = \sum_{G \neq 0} a_G \left[ (\nabla r_i \rho_G) \rho_{-G} + \text{c.c.} \right] \]  

(25.219)

\[
= \sum_{G \neq 0} 2G a_G \text{Re} \left( i e^{i G r_i} \rho_{-G} \right) \]  

(25.220)

\[
= \sum_{G \neq 0} -2G a_G \text{Im} \left( e^{i G r_i} \rho_{-G} \right) \]  

(25.221)

The Laplacian is then given by

\[
\nabla^2 J^2 = \sum_{G \neq 0} a_G \left[ (\nabla^2 \rho_G) \rho_{-G} + \text{c.c.} + 2 (\nabla \rho_G) \cdot (\nabla \rho_{-G}) \right] \]  

(25.222)

\[
= \sum_{G \neq 0} a_G \left[ -2G^2 \text{Re}\left( e^{i G r_i} \rho_{-G} \right) + 2 \left( i Ge^{i G r_i} \right) \cdot \left( -iGe^{-i G r_i} \right) \right] \]  

(25.223)

\[
= 2 \sum_{G \neq 0} G^2 a_G \left[ -\text{Re} \left( e^{i G r_i} \rho_{-G} \right) + 1 \right] \]  

(25.224)
Chapter 26

Development Guide

The section gives guidance on how to extend the functionality of QMCPACK. Future examples will likely include topics such as the addition of a jastrow function or add a new QMC method.

26.1 Scalar Estimator Implementation

26.1.1 Introduction: Life of a Specialized QMCHamiltonianBase

Almost all observables in QMCPACK are implemented as specialized derived classes of the QMCHamiltonianBase base class. Each observable is instantiated in HamiltonianFactory and added to QMCHamiltonian for tracking. QMCHamiltonian tracks two types of observables: main and auxiliary. Main observables contribute to the local energy. These observables are elements of the simulated Hamiltonian such as kinetic or potential energy. auxiliary observables are expectation values of matrix elements that do not contribute to the local energy. These Hamiltonians do not affect the dynamics of the simulation. In the code, the main observables are labeled by “physical” flag, the auxiliary observables have “physical” set to false.

Initialization

When an `<estimator type="est_type" name="est_name" other_stuff="value"/>` tag is present in the `<hamiltonian/>` section, it is first read by HamiltonianFactory. In general, the type of the estimator will determine which specialization of QMCHamiltonianBase to be instantiated, and a derived class with `myName="est_name"` will be constructed. Then, the put() method of this specific class will be called to read any other parameters in the `<estimator/>` xml node. Sometimes these parameters will be read by HamiltonianFactory instead, because it can access more objects than QMCHamiltonianBase.

Cloning

When OpenMP threads are spawned, the estimator will be cloned by the CloneManager, which is a parent class of many QMC drivers.

```cpp
// In CloneManager.cpp
#pragma omp parallel for shared(w,psi,ham)
for(int ip=1; ip<NumThreads; ++ip)
{
    wClones[ip]=new MCWalkerConfiguration(w);
    psiClones[ip]=psi.makeClone(*wClones[ip]);
}
```
In the above snippet, `ham` is the reference to the estimator on the master thread. If the implemented estimator does not allocate memory for any array, then the default constructor should suffice for the `makeClone` method.

```cpp
// In SpeciesKineticEnergy.cpp
QMCHamiltonianBase* SpeciesKineticEnergy::makeClone(ParticleSet& qp, 
    TrialWaveFunction& psi)
{
    return new SpeciesKineticEnergy(*this);
}
```

If memory is allocated during estimator construction (usually when parsing the xml node in the `put` method), then the `makeClone` method should perform the same initialization on each thread.

```cpp
QMCHamiltonianBase* LatticeDeviationEstimator::makeClone(ParticleSet& qp, 
    TrialWaveFunction& psi)
{
    LatticeDeviationEstimator* myclone = new LatticeDeviationEstimator(qp,spset, 
        tgroup,sgroup);
    myclone->put(input_xml);
    return myclone;
}
```

Evaluate

After the observable class (derived class of QMCHamiltonianBase) is constructed and prepared (by the `put()` method), it is ready to be used in a QMCDriver. A QMCDriver will call `H.auxHevaluate(W,thisWalker)` after every accepted move, where `H` is the QMCHamiltonian that holds all main and auxiliary Hamiltonian elements, `W` is a MCWalkerConfiguration and `thisWalker` is a pointer to the current walker being worked on. As shown below, this function goes through each auxiliary Hamiltonian element and evaluate it using the current walker configuration. Under the hood, observables are calculated and dumped to the main particle set’s property list for later collection.

```cpp
// In QMCHamiltonian.cpp
// This is more efficient.
// Only calculate auxH elements if moves are accepted.
void QMCHamiltonian::auxHevaluate(ParticleSet& P, Walker_t& ThisWalker)
{
    #if !defined(REMOVE_TRACEMANAGER)
        collect_walker_traces(ThisWalker,P.current_step);
    #endif
    for(int i=0; i<auxH.size(); ++i)
    {
        auxH[i]->setHistories(ThisWalker);
        RealType sink = auxH[i]->evaluate(P);
        auxH[i]->setObservables(Observables);
        #if !defined(REMOVE_TRACEMANAGER)
            auxH[i]->collect_scalar_traces();
        #endif
        auxH[i]->setParticlePropertyList(P.PropertyList,myIndex);
    }
}
```
For estimators that contribute to the local energy (main observables), the return value of evaluate() is used in accumulating the local energy. For auxiliary estimators, the return value is not used (the local variable above), only the value of Value is recorded property lists by the setObservables() method as shown in the above code snippet. By default, the setObservables() method will transfer auxH[i]->Value to P.PropertyList[auxH[i]->myIndex]. The same property list is also kept by the particle set being moved by QMCDriver. This list is updated by auxH[i]->setPropertyList(P.PropertyList,myIndex), where myIndex is the starting index of space allocated to this specific auxiliary Hamiltonian in the property list kept by the target particle set P.

Collection

The actual statistics are collected within the QMCDriver, which owns an EstimatorManager object. This object (or a clone in the case of multithreading) will be registered with each mover it owns. For each mover (such as VMCUpdatePbyP derived from QMCUpdateBase), an accumulate() call is made, which by default, makes an accumulate(walkerSet) call to the EstimatorManager it owns. Since each walker has a property set, EstimatorManager uses that local copy to calculate statistics. The EstimatorManager performs block averaging and file I/O.

26.1.2 Single Scalar Estimator Implementation Guide

Almost all of the defaults can be utilized for a single scalar observable. With any luck, only the put() and evaluate() methods need to be implemented. As an example, this section will present a step-by-step guide to implement a SpeciesKineticEnergy estimator that calculates the kinetic energy of a specific species instead of the entire particle set. For example, a possible input to this estimator can be:

```xml
<estimator type="specieskinetic" name="ukinetic" group="u"/>
<estimator type="specieskinetic" name="dkinetic" group="d"/>
```

This should create two extra columns in the scalar.dat file that contains the kinetic energy of the up and down electrons in two separate columns. If the estimator is properly implemented, then the sum of these two columns should be equal to the default Kinetic column.

Barebone

The first step is to create a barebone class structure for this simple scalar estimator. The goal is to be able to instantiate this scalar estimator with an xml node and have it print out a column of zeros in the scalar.dat file.

To achieve this, first create a header file “SpeciesKineticEnergy.h” in QMCHamiltonians folder, with only the required functions declared as follows:

```c++
// In SpeciesKineticEnergy.h
#ifndef QMCPLUSPLUS_SPECIESKINETICENERGY_H
#define QMCPLUSPLUS_SPECIESKINETICENERGY_H

#include <Particle/WalkerSetRef.h>
#include <QMCHamiltonians/QMCHamiltonianBase.h>

namespace qmcplusplus
```

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Notice a local reference `tpset` to the target particle set `P` is saved in the constructor. The target particle set carries much information useful for calculating observables. Next, make "SpeciesKineticEnergy.cpp" and make vacuous definitions.

```cpp
// In SpeciesKineticEnergy.cpp
#include <QMCHamiltonians/SpeciesKineticEnergy.h>
namespace qmcplusplus {

bool SpeciesKineticEnergy::put(xmlNodePtr cur) {
    return true;
}

bool SpeciesKineticEnergy::get(std::ostream& os) const {
    return true;
}

SpeciesKineticEnergy::Return_t SpeciesKineticEnergy::evaluate(ParticleSet& P) {
    Value = 0.0;
    return Value;
}
}
```
QMCHamiltonianBase* SpeciesKineticEnergy::makeClone(ParticleSet& qp,
TrialsWaveFunction& psi)
{
    // no local array allocated, default constructor should be enough
    return new SpeciesKineticEnergy(*this);
}

} // namespace qmcplusplus

Now, head over to Hamiltonian Factory and instantiate this observable if an xml node is found requesting it. Look for “gofr” in HamiltonianFactory.cpp, for example, and follow the if block

// In HamiltonianFactory.cpp
#include <QMCHamiltonians/SpeciesKineticEnergy.h>
else if(potType == "specieskinetic")
{
    SpeciesKineticEnergy* apot = new SpeciesKineticEnergy(*target_particle_set);
    apot->put(cur);
    targetH->addOperator(apot,potName,false);
}

The last argument of addOperator(), i.e. the false flag, is crucial. This tells QMCPACK that the observable we implemented is not a physical Hamiltonian, thus it will not contribute to the local energy. Changes to the local energy will alter the dynamics of the simulation. Finally, add “SpeciesKineticEnergy.cpp” to HAMSRCs in “CMakeLists.txt” located in the QMCHamiltonians folder. Now, recompile QMCPACK and run it on an input that requests <estimator type="specieskinetic" name="ukinetic"/> in the hamiltonian block. A columns of zeros should appear in the scalar.dat file under the name “ukinetic”.

Evaluate

The evaluate() method is where we perform the calculation of the desired observable. In a first iteration, we will simply hard-code the name and mass of the particles

// In SpeciesKineticEnergy.cpp
#include <QMCHamiltonians/BareKineticEnergy.h> // laplacian() defined here
SpeciesKineticEnergy::Return_t SpeciesKineticEnergy::evaluate(ParticleSet& P)
{
    std::string group="u";
    RealType minus_over_2m = -0.5;

    SpeciesSet& tspecies(P.getSpeciesSet());

    Value = 0.0;
    for (int iat=0; iat<P.getTotalNum(); iat++)
    {
        if (tspecies.speciesName[ P.GroupID(iat) ] == group)
        {
            Value += minus_over_2m*laplacian(P.G[iat],P.L[iat]);
        }
    }
    return Value;
Voilà, you should now be able to compile QMCPACK, rerun, and see that the values in the “ukinetic” column are no longer zero. Now, the only task left to make this basic observable complete is to read in the extra parameters instead of hard-coding them.

Parse Extra Input

The preferred method to parse extra input parameters in the xml node is to implement the put() function of our specific observable. Suppose we wish to read in a single string that tells us whether to record the kinetic energy of the up electron (group=“u”) or the down electron (group=“d”). This is easily achievable using the OhmmsAttributeSet class

```cpp
// In SpeciesKineticEnergy.cpp
#include <OhmmsData/AttributeSet.h>
bool SpeciesKineticEnergy::put(xmlNodePtr cur)
{
    // read in extra parameter "group"
    OhmmsAttributeSet attrib;
    attrib.add(group,"group");
    attrib.put(cur);

    // save mass of specified group of particles
    SpeciesSet& tspecies(tpset.getSpeciesSet());
    int group_id  = tspecies.findSpecies(group);
    int massind   = tspecies.getAttribute("mass");
    minus_over_2m = -1./(2.*tspecies(massind,group_id));

    return true;
}
```

where we may keep “group” and “minus_over_2m” as local variables to our specific class.

```cpp
// In SpeciesKineticEnergy.h
private:
    ParticleSet& tpset;
    std::string  group;
    RealType     minus_over_2m;
```

Notice, the above operations are made possible by the saved reference to the target particle set. Last but not least, compile and run a full example (i.e. a short DMC calculation) with the following xml nodes in your input

```xml
<estimator type="specieskinetic" name="ukinetic" group="u"/>
<estimator type="specieskinetic" name="dkinetic" group="d"/>
```

Make sure the sum of the "ukinetic" and "dkinetic" columns is exactly the same as the Kinetic columns at every block.

For easy reference, the complete list of changes is summarized bellow

```cpp
// In HamiltonianFactory.cpp
#include "QMCHamiltonians/SpeciesKineticEnergy.h"
else if(potType == "specieskinetic")
```
SpeciesKineticEnergy* apot = new SpeciesKineticEnergy(*targetPtcl);
apot->put(cur);
targetH->addOperator(apot,potName,false);

// In SpeciesKineticEnergy.h
#include <Particle/WalkerSetRef.h>
#include <QMCHamiltonians/QMCHamiltonianBase.h>
namespace qmcplusplus
{
    class SpeciesKineticEnergy: public QMCHamiltonianBase
    {
        public:
            SpeciesKineticEnergy(ParticleSet& P):tpset(P){
            }
            // xml node is read by HamiltonianFactory, eg. the sum of following should be equivalent to Kinetic
            // <estimator name="ukinetic" type="specieskinetic" target="e" group="u"/>
            // <estimator name="dkinetic" type="specieskinetic" target="e" group="d"/>
            bool put(xmlNodePtr cur); // read input xml node, required
            bool get(std::ostream& os) const; // class description, required

            Return_t evaluate(ParticleSet& P);
            inline Return_t evaluate(ParticleSet& P, std::vector<NonLocalData>& Txy)
            {
                // delegate responisbility inline for speed
                return evaluate(P);
            }
            // pure virtual functions require overrider
            void resetTargetParticleSet(ParticleSet& P) { } // required
            QMCHamiltonianBase* makeClone(ParticleSet& qp, TrialWaveFunction& psi); // required

        private:
            ParticleSet& tpset; // reference to target particle set
            std::string group; // name of species to track
            RealType minus_over_2m; // mass of the species !! assume same mass
            // for multiple species, simply initialize multiple estimators
        }
    } // namespace qmcplusplus
} // namespace qmcplusplus

// In SpeciesKineticEnergy.cpp
#include <QMCHamiltonians/QMCHamiltonianBase.h>
#include <QMCHamiltonians/BareKineticEnergy.h> // laplaician() defined here
#include <OhmmsData/AttributeSet.h>
namespace qmcplusplus
{

    bool SpeciesKineticEnergy::put(xmlNodePtr cur)
    {
        // read in extra parameter "group"
        OhmmsAttributeSet attrib;
        attrib.add("group");
        attrib.put(cur);

        // save mass of specified group of particles
        int group_id = tspecies.findSpecies(group);
        int massind = tspecies.getAttribute("mass");
        minus_over_2m = -1./(2.*tspecies(massind,group_id));

        return true;
    }

    bool SpeciesKineticEnergy::get(std::ostream& os) const
    { // class description
        os << "SpeciesKineticEnergy: " << myName << " for species " << group;
        return true;
    }

    SpeciesKineticEnergy::Return_t SpeciesKineticEnergy::evaluate(ParticleSet& P)
    {
        Value = 0.0;
        for (int iat=0; iat<P.getTotalNum(); iat++)
        {
            if (tspecies.speciesName[ P.GroupID(iat) ] == group)
            {
                Value += minus_over_2m*laplacian(P.G[iat],P.L[iat]);
            }
        }
        return Value;
    }

    QMCHamiltonianBase* SpeciesKineticEnergy::makeClone(ParticleSet& qp,
        TrialWaveFunction& psi)
    { // default constructor
        return new SpeciesKineticEnergy(*this);
    }
}

// namespace qmcplusplus

26.1.3 Multiple Scalars

It is fairly straight-forward to created more than one column in the scalar.dat file with a single observable class. For example, if we want a single SpeciesKineticEnergy estimator to record the kinetic energies of all species in the target particle set simultaneously, we only have to write two new methods: addObservables() and setObservables(), then tweak the behavior of evaluate(). Firstly, we will have to override the default behavior of addObservables() to make room for more than one
column in the scalar.dat file as follows

```cpp
// In SpeciesKineticEnergy.cpp
void SpeciesKineticEnergy::addObservables(PropertySetType& plist, BufferType& collectables)
{
    myIndex = plist.size();
    for (int ispec=0; ispec<num_species; ispec++)
    { // make columns named "$myName_u", "$myName_d" etc.
        plist.add(myName + "_" + species_names[ispec]);
    }
}
```

where “num_species” and “species_name” can be local variables initialized in the constructor. We should also initialize some local arrays to hold temporary data

```cpp
// In SpeciesKineticEnergy.h
private:
    int num_species;
    std::vector<std::string> species_names;
    std::vector<RealType> species_kinetic, vec_minus_over_2m;

// In SpeciesKineticEnergy.cpp
SpeciesKineticEnergy::SpeciesKineticEnergy(ParticleSet& P): tpset(P)
{
    SpeciesSet& tspecies(P.getSpeciesSet());
    int massind = tspecies.getAttribute("mass");

    num_species = tspecies.size();
    species_kinetic.resize(num_species);
    vec_minus_over_2m.resize(num_species);
    species_names.resize(num_species);
    for (int ispec=0; ispec<num_species; ispec++)
    {
        species_names[ispec] = tspecies.speciesName[ispec];
        vec_minus_over_2m[ispec] = -1./(2.*tspecies(massind, ispec));
    }
}
```

Next, we need to override the default behavior of setObservables() to transfer multiple values to the property list kept by the main particle set, which eventually go into the scalar.dat file

```cpp
// In SpeciesKineticEnergy.cpp
void SpeciesKineticEnergy::setObservables(PropertySetType& plist)
{
    // slots in plist must be allocated by addObservables() first
    copy(species_kinetic.begin(), species_kinetic.end(), plist.begin()+myIndex);
}
```

Finally, we need to change the behavior of evaluate() to fill the local vector “species_kinetic” with appropriate observable values

```cpp
SpeciesKineticEnergy::Return_t SpeciesKineticEnergy::evaluate(ParticleSet& P)
{
    std::fill(species_kinetic.begin(), species_kinetic.end(), 0.0);
    for (int iat=0; iat<P.getTotalNum(); iat++)
    
```
{  
  int ispec = P.GroupID(iat);
  species_kinetic[ispec] += vec_minus_over_2m[ispec]*laplacian(P.G[iat],P.L[iat]);
}

Value = 0.0; // Value is no longer used
return Value;

That’s it! SpeciesKineticEnergy estimator no longer needs the “group” input and will automatically output the kinetic energy of every species in the target particle set in multiple columns. You should now be able to run with <estimator type="specieskinetic" name="skinetic"/> and check that the sum of all columns that starts with “skinetic” is equal to the default “Kinetic” column.

26.1.4 HDF5 Output

If we desire an observable that will output hundreds of scalars per simulation step (eg. SkEstimator), then it is preferred to output to the stat.h5 file instead of the scalar.dat file for better organization. A large chunk of data to be registered in the stat.h5 file is called a “Collectable” in QMCPACK. In particular, if a QMCHamiltonianBase object is initialized with UpdateMode.set(COLLECTABLE,1) then the “Collectables” object carried by the main particle set will be processed and written to the stat.h5 file, where “UpdateMode” is a bit set (i.e. a collection of flags) with the following enumeration

```cpp
// In QMCHamiltonianBase.h
/// enum for UpdateMode
enum {PRIMARY=0,
      OPTIMIZABLE=1,
      RATIOUPDATE=2,
      PHYSICAL=3,
      COLLECTABLE=4,
      NONLOCAL=5,
      VIRTUALMOVES=6
};
```

As a simple example, to put the two columns we produced in the previous section into the stat.h5 file, we will first need to declare that our observable uses “Collectables”

```cpp
// In constructor add:
hdf5_out = true;
UpdateMode.set(COLLECTABLE,1);
```

Then make some room in the “Collectables” object carried by the target particle set.

```cpp
// In addObservables(PropertySetType& plist, BufferType& collectables) add:
if (hdf5_out)
{
  h5_index = collectables.size();
  std::vector<RealType> tmp(num_species);
  collectables.add(tmp.begin(),tmp.end());
}
```

Next make some room in the stat.h5 file by overriding the registerCollectables() method.
Finally, edit evaluate() to use the space in the “Collectables” object.

```cpp
// In SpeciesKineticEnergy.cpp
SpeciesKineticEnergy::Return_t SpeciesKineticEnergy::evaluate(ParticleSet& P)
{
    RealType wgt = tWalker->Weight; // MUST explicitly use DMC weights in Collectables!
    std::fill(species_kinetic.begin(),species_kinetic.end(),0.0);
    for (int iat=0; iat<P.getTotalNum(); iat++)
    {
        int ispec = P.GroupID(iat);
        species_kinetic[ispec] += vec_minus_over_2m[ispec]*laplacian(P.G[iat],P.L[iat]);
        P.Collectables[h5_index + ispec] += vec_minus_over_2m[ispec]*laplacian(P.G[iat],P.L[iat])*wgt;
    }
    Value = 0.0; // Value is no longer used
    return Value;
}
```

That should be it. There should now be a new entry in the stat.h5 file containing the same columns of data as the scalar.dat file. After this check, we should clean up the code by

1. make “hdf5_out” and input flag by editing the put() method
2. disable output to scalar.dat when “hdf5_out” flag is on

### 26.2 Slater-Backflow Wavefunction Implementation Details

For simplicity, consider \( N \) identical fermions of the same spin (e.g. up electrons) at spatial locations \( \{r_1, r_2, \ldots, r_N\} \). Then the Slater determinant can be written as

\[
S = \det M,
\]

where each entry in the determinant is a single-particle orbital evaluated at a particle position

\[
M_{ij} = \phi_i(r_j).
\]
When backflow transformation is applied to the Determinant, the particle coordinates \( r_i \) that go into the single-particle orbitals are replaced by quasi-particle coordinates \( x_i \)

\[
M_{ij} = \phi_i(x_j), \tag{26.3}
\]

where

\[
x_i = r_i + \sum_{j=1,j\neq i}^{N} \eta(r_{ij})(r_i - r_j). \tag{26.4}
\]

\( r_{ij} = |r_i - r_j| \). The integers \( i,j \) label the particle/quasi-particle. There is a one-to-one correspondence between the particles and the quasi-particles, which is simplest when \( \eta = 0 \).

### 26.2.1 Value

The evaluation of the Slater-Backflow wavefunction is almost identical to that of a Slater wavefunction. The only difference is that the quasi-particles coordinates are used to evaluate the single-particle orbitals. The actual value of the determinant is stored during the inversion of the matrix \( M \). Suppose \( M = LU \), then \( S = \prod_{i=1}^{N} L_i U_i \).

```c
// In DiracDeterminantWithBackflow::evaluateLog(P,G,L)
Phi->evaluate(BFTrans->QP, FirstIndex, LastIndex, psiM,dpsiM,grad_grad_psiM);
psiMinv = psiM;
LogValue=InvertWithLog(psiMinv.data(),NumPtcls,NumOrbitals,WorkSpace.data(),Pivot.data(),PhaseValue);
```

QMCPACK represents the complex value of the wavefunction in polar coordinates \( S = e^U e^{i\theta} \). Specifically, \( \text{LogValue} U \) and \( \text{PhaseValue} \theta \) are handled separately. In the following, I will consider derivatives of the log value only.

### 26.2.2 Gradient

To evaluate particle gradient of the log value of the Slater-Backflow wavefunction, we can use the logdet identity in eq. \((26.5)\). This identity maps the derivative of logdet \( M \) with respect to a real variable \( p \) to a trace over \( M^{-1} dM \)

\[
\frac{\partial}{\partial p} \log \det M = \text{tr} \left(M^{-1} \frac{\partial M}{\partial p}\right). \tag{26.5}
\]

Following Kwon, Ceperley, and Martin \[17\], the particle gradient

\[
G_i^\alpha \equiv \frac{\partial}{\partial r_i^\alpha} \log \det M = \sum_{j=1}^{N} \sum_{\beta=1}^{3} F_{jj}^{\beta} A_{jj}^{\alpha\beta}, \tag{26.6}
\]

where the quasi-particle gradient matrix

\[
A_{ij}^{\alpha\beta} \equiv \frac{\partial x_j^{\beta}}{\partial r_i^\alpha}, \tag{26.7}
\]
and the intermediate matrix

\[ F_{ij}^\alpha \equiv \sum_k M_{ik}^{-1} dM_{kj}^\alpha, \]  

(26.8)

with the single-particle orbital derivatives (w.r. to quasi-particle coordinates)

\[ dM_{ij}^\alpha \equiv \frac{\partial M_{ij}}{\partial x_j^\alpha}. \]  

(26.9)

Notice, I have made the name change of \( \phi \to M \) from the notations of ref. [17]. This name change is intended to help the reader associate \( M \) with the QMCPACK variable \( \psi_M \).

```
// In DiracDeterminantWithBackflow::evaluateLog(P,G,L)
for(int i=0; i<num; i++) // k in above formula
{
  for(int j=0; j<NumPtcls; j++)
  {
    for(int k=0; k<OHMMS_DIM; k++) // alpha in above formula
    {
      myG(i) += dot(BFTrans->Amat(i,FirstIndex+j),Fmat(j,j));
    }
  }
}
```

Eq. (26.6) is still relatively simple to understand. The \( A \) matrix maps changes in particle coordinates \( dr \) to changes in quasi-particle coordinates \( dx \). Dotting \( A \) into \( F \) propagates \( dx \) to \( dM \). Thus \( F \cdot A \) is the term inside the trace operator of eq. (26.5). Finally, performing the trace completes the evaluation of the derivative.

### 26.2.3 Laplacian

The particle laplacian is given in ref. [17] as

\[ L_i \equiv \sum_{\alpha} \frac{\partial^2}{\partial (r_i^\alpha)^2} \log \det M = \sum_{jk} B_{ij}^\alpha F_{jj}^\gamma - \sum_{jk} A_{ij}^\alpha A_{ik}^\gamma \times \left( F_{kj}^\alpha F_{jk}^\gamma - \delta_{jk} \sum_m M_{jm}^{-1} d2M_{mj}^\beta \right), \]  

(26.10)

where the quasi-particle laplacian matrix

\[ B_{ij}^\alpha \equiv \sum_{\beta} \frac{\partial^2 x_j^\alpha}{\partial (r_i^\beta)^2}, \]  

(26.11)

with the second derivatives of the single-particles orbitals being

\[ d2M_{ij}^\alpha \equiv \frac{\partial^2 M_{ij}}{\partial x_j^\alpha \partial x_j^\beta}. \]  

(26.12)

Schematically, \( L_i \) has contributions from 3 terms of the form \( BF, AAFF, \text{tr}(AA,Md2M) \), respectively. \( A, B, M, d2M, \) and \( F \) can be calculated and stored before the calculations of \( L_i \). The first \( BF \) term can be directly calculated in a loop over quasi-particle coordinates \( j \alpha \).
Notice $B_{ij}^\alpha$ is stored in Bmat_full, NOT Bmat.

The remaining two terms both involve $AA$. Thus, it is best to define a temporary tensor $AA$

$$iAA_{jk}^{\alpha\gamma} \equiv \sum_\alpha A_{ij}^\alpha A_{jk}^{\alpha\gamma};$$

which we will overwrite for each particle $i$. Similarly, define $FF$

$$FF_{jk}^{\alpha\gamma} \equiv F_{kj}^\alpha F_{jk}^{\alpha\gamma},$$

which is simply the outer product of $F \otimes F$. Then the $AAFF$ term can be calculated by fully contracting $AA$ with $FF$.

Finally, define the single-particle orbital derivative term

$$Md^2M_j^{\beta\gamma} = \sum_m M_{jm}^{-1}d^2M_{mj}^{\beta\gamma};$$

then the last term is given by the contraction of $Md^2M$ ($q_j$) with the diagonal of $AA$. 

```cpp
// In DiracDeterminantWithBackflow::evaluateLog(P,G,L)
for(int j=0; j<NumPtcls; j++)
    for(int k=0; k<NumPtcls; k++)
        for(int i=0; i<num; i++)
        {
            HessType q_j;
            q_j=0.0;
            for(int k=0; k<NumPtcls; k++)
                q_j += psiMinv(j,k)*grad_grad_psiM(j,k);
            for(int i=0; i<num; i++)
            {
                Tensor<RealType,OHMMS_DIM> AA = dot(transpose(BFTrans->Amat(i,FirstIndex+j)),BFTrans->Amat(i,FirstIndex+j));
                HessType FF = outerProduct(Fmat(k,j),Fmat(j,k));
                myL(i) -= traceAtB(AA,FF);
            }
        }
```
26.2.4 Wavefunction Parameter Derivative

In order to use the robust linear optimization method of ref. [18], the trial wavefunction needs to know its contributions to the overlap and hamiltonian matrices. In particular, we need derivatives of these matrices with respect to wavefunction parameters. As a consequence, the wavefunction $\psi$ needs to be able to evaluate $\frac{\partial}{\partial p} \ln \psi$ and $\frac{\partial}{\partial p} H\psi$, where $p$ is a parameter.

When two-body backflow is considered, a wavefunction parameter $p$ enters the $\eta$ function only (eq. (26.4)). $r$, $\phi$, and $M$ are do not explicitly dependent on $p$. Derivative of the log value is almost identical to particle gradient. Namely, eq. (26.6) applies upon the substitution $r_i^\alpha \to p$

$$\frac{\partial}{\partial p} \ln M = \sum_{j=1}^{N} \sum_{\beta=1}^{3} F_{ij}^\beta \left( pC_j^{\beta} \right),$$  

(26.16)

where the quasi-particle derivatives are stored in $C_{\text{mat}}$

$$pC_i^\alpha \equiv \frac{\partial}{\partial p} x_i^\alpha.$$  

(26.17)

The change in local kinetic energy is a lot more difficult to calculate

$$\frac{\partial T_{\text{local}}}{\partial p} = \frac{\partial}{\partial p} \left\{ \left( \sum_{i=1}^{N} \frac{1}{2m_i} \nabla_i^2 \right) \ln \det M \right\} = \sum_{i=1}^{N} \frac{1}{2m_i} \frac{\partial}{\partial p} L_i,$$

(26.18)

where $L_i$ is the particle laplacian defined in eq. (26.10). In order to evaluate eq. (26.18), we need to calculate parameter derivatives of all three terms defined in the laplacian evaluation. Namely $(B)(F)$, $(AA)(FF)$, and $\text{tr}(AA, Md2M)$, where I have put parentheses around previously identified data structures. After $\frac{\partial}{\partial p}$ hits, each of the 3 terms will split into two terms by the product rule. Each smaller term will contain a contraction of two data structures. Therefore, we will need to calculate the parameter derivatives of each data structure defined in the laplacian evaluation

$$pX_{ij}^{\alpha\beta} \equiv \frac{\partial}{\partial p} A_{ij}^{\alpha\beta}$$  

(26.19)

$$pY_{ij}^{\alpha} \equiv \frac{\partial}{\partial p} B_{ij}^{\alpha}$$  

(26.20)

$$pdF_{ij}^{\alpha} \equiv \frac{\partial}{\partial p} F_{ij}^{\alpha}$$  

(26.21)

$$pAA_{jk}^{\beta\gamma} \equiv \frac{\partial}{\partial p} iAA_{jk}^{\beta\gamma}$$  

(26.22)

$$pFF_{jk}^{\alpha\gamma} \equiv \frac{\partial}{\partial p} FF_{jk}^{\alpha\gamma}$$  

(26.23)

$$pM2M_{j}^{\beta\gamma} \equiv \frac{\partial}{\partial p} M2M_{j}^{\beta\gamma}$$  

(26.24)

$X$ and $Y$ are stored as $X_{\text{mat}}$, and $Y_{\text{mat}}$ (NOT $Y_{\text{mat}}$) in the code. $dF$ is $dFa$. $AA'$ is not fully store, intermediate values are stored in $A_{ij}^{\text{sum}}$ and $a_{j}^{\text{sum}}$. $FF'$ is calculated on-the-fly as $dF \otimes F + F \otimes dF$. $Md2M'$ is not stored, intermediate values are stored in $q_{j}^{\text{prime}}$. 

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References


Appendix A

Derivation of twist averaging efficiency

In this appendix we derive the relative statistical efficiency of twist averaging with an irreducible (weighted) set of k-points versus using uniform weights over an unreduced set of k-points (e.g. a full Monkhorst-Pack mesh).

Consider the weighted average of a set of statistical variables \(x_m\) with weights \(w_m\):

\[
 x_{TA} = \frac{\sum_m w_m x_m}{\sum_m w_m} \quad \text{(A.1)}
\]

If produced by a finite quantum Monte Carlo run at a set of twist angles/k-points \(\{k_m\}\), each variable mean \(\langle x_m \rangle\) has a statistical error bar \(\sigma_m\) and we can also obtain the statistical error bar of the mean of the twist averaged quantity \(\langle x_{TA} \rangle\):

\[
 \sigma_{TA} = \left( \frac{\sum_m w_m^2 \sigma_m^2}{\sum_m w_m} \right)^{1/2} \quad \text{(A.2)}
\]

The error bar of each individual twist \(\sigma_m\), is related to the autocorrelation time \(\kappa_m\), intrinsic variance \(v_m\), and number of post-equilibration Monte Carlo steps \(N_{\text{step}}\) in the following way:

\[
 \sigma_m^2 = \frac{\kappa_m v_m}{N_{\text{step}}} \quad \text{(A.3)}
\]

In the setting of twist averaging, the autocorrelation time and variance for different twist angles are often very similar across twists and we have

\[
 \sigma_m^2 = \sigma^2 = \frac{\kappa v}{N_{\text{step}}} \quad \text{(A.4)}
\]

If we define the total weight as \(W\), i.e. \(W = \sum_{m=1}^{M} w_m\), for the weighted case with \(M\) irreducible twists the error bar is

\[
 \sigma_{TA}^{\text{weighted}} = \left( \frac{\sum_{m=1}^{M} w_m^2}{W} \right)^{1/2} \sigma \quad \text{(A.5)}
\]

For uniform weighting with \(w_m = 1\) the number of twists is \(W\) and we have

\[
 \sigma_{TA}^{\text{uniform}} = \frac{1}{\sqrt{W}} \sigma \quad \text{(A.6)}
\]
We are interested in comparing the efficiency of choosing weights uniformly or based on the irreducible multiplicity of each twist angle for a given target error bar $\sigma_{\text{target}}$. The number of Monte Carlo steps required to reach this target for uniform weighting is

$$N_{\text{step}}^{\text{uniform}} = \frac{1}{W} \frac{\kappa v}{\sigma_{\text{target}}^2}$$

(A.7)

while for non-uniform weighting we have

$$N_{\text{step}}^{\text{weighted}} = \sum_{m=1}^{M} \frac{w_m^2}{W^2} \frac{\kappa v}{\sigma_{\text{target}}^2}$$

$$= \sum_{m=1}^{M} \frac{w_m^2}{W} N_{\text{step}}^{\text{uniform}}$$

(A.8)

The Monte Carlo efficiency is defined as

$$\xi = \frac{1}{\sigma^2 t}$$

(A.9)

where $\sigma$ is the error bar and $t$ is the total cpu time required for the Monte Carlo run.

The main advantage made possible by irreducible twist weighting is to reduce the equilibration time overhead by having fewer twists, and hence fewer Monte Carlo runs to equilibrate. In the context of twist averaging, the total cpu time for a run can be considered to be

$$t = N_{\text{twist}} (N_{\text{eq}} + N_{\text{step}}) t_{\text{step}}$$

(A.10)

where $N_{\text{twist}}$ is the number of twists, $N_{\text{eq}}$ is the number of Monte Carlo steps required to reach equilibrium, $N_{\text{step}}$ is the number of Monte Carlo steps included in the statistical averaging as before, and $t_{\text{step}}$ is the wall clock time required to complete a single Monte Carlo step. For uniform weighting $N_{\text{twist}} = W$ while for irreducible weighting $N_{\text{twist}} = M$.

We can now calculate the relative efficiency ($\eta$) of irreducible vs. uniform twist weighting with the aim of obtaining a target error bar $\sigma_{\text{target}}$:

$$\eta = \frac{\xi_{\text{weighted}}}{\xi_{\text{uniform}}}$$

$$= \frac{\sigma_{\text{target}}^2 \xi_{\text{uniform}}^{\text{TA}}}{\sigma_{\text{target}}^2 \xi_{\text{weighted}}^{\text{TA}}}$$

$$= \frac{W (N_{\text{eq}} + N_{\text{step}}^{\text{uniform}})}{M (N_{\text{eq}} + N_{\text{step}}^{\text{weighted}})}$$

$$= \frac{W (N_{\text{eq}} + N_{\text{step}}^{\text{uniform}})}{M (N_{\text{eq}} + \sum_{m=1}^{M} \frac{w_m^2}{W} N_{\text{step}}^{\text{uniform}})}$$

$$= \frac{W}{M} \frac{1 + f}{1 + \sum_{m=1}^{M} \frac{w_m^2}{W} f}$$

(A.11)

In this last expression, $f$ is the ratio of the number of usable Monte Carlo steps to the number that must be discarded during equilibration ($f = N_{\text{step}}^{\text{uniform}} / N_{\text{eq}}$) and as before $W = \sum_m w_m$, which is the number of twist angles in the uniform weighting case. It is important to recall that $N_{\text{step}}^{\text{uniform}}$ in
$f$ is defined relative to uniform weighting; it is the number of Monte Carlo steps required to reach a target accuracy in the case of uniform twist weights.

The formula for $\eta$ above can be easily changed with the help of Eq. A.8 to reflect the number of Monte Carlo steps obtained in an irreducibly weighted run instead. A good exercise is to consider runs one has already completed with either uniform or irreducible weighting and calculate the expected efficiency change had the opposite type of weighting been used.

The break even point ($\eta = 1$) can be found at a usable step fraction of

$$f = \frac{W - M}{M \sum_{m=1}^{M} w_m^2 - W} \quad (A.12)$$

The relative efficiency ($\eta$) above is useful to consider in view of certain scenarios. An important case is where the number of required sampling steps is no larger than the number of equilibration steps, i.e. $f \approx 1$. For a very simple case with 8 uniform twists with irreducible multiplicities of $w_m \in \{1, 3, 3, 1\}$ ($W = 8$, $M = 4$), the relative efficiency of irreducible vs. uniform weighting is $\eta = \frac{8 \cdot 2}{11 + 20/8} \approx 1.14$. In this case, irreducible weighting is about 14% more efficient than uniform weighting.

Another interesting case is where the number of sampling steps you can reach with uniform twists before wall clock time runs out is small relative to the number of equilibration steps ($f \to 0$). In this limit $\eta \approx W/M$. For our 8 uniform twist example, this would result in a relative efficiency of $\eta = 8/4 = 2$ making irreducible weighting twice as efficient.

A final case of interest is where the equilibration time is short relative to the available sampling time ($f \to \infty$), giving $\eta \approx W^2/(M \sum_{m=1}^{M} w_m^2)$. Again for our simple example we find $\eta = 8^2/(4 \times 20) \approx 0.8$, with uniform weighting being 25% more efficient than irreducible.

For this simple example, the crossover point for irreducible weighting being more efficient than uniform weighting is $f < 2$, i.e. when the available sampling period is less than twice the length of the equilibration period. The expected efficiency ratio and crossover point should be checked for the particular case under consideration to inform the choice between twist averaging methods.
Appendix B

QMCPACK papers

The following is a list of all papers, theses, and book chapters known to use QMCPACK. Please let the developers know if your paper is missing, if you know of other works, or an entry is incorrect. We list papers whether they cite QMCPACK directly or not. This list will be placed on the http://www.qmcpack.org website.


