

# **SPPARKS Users Manual**

Stochastic Parallel PArTicle Kinetic Simulator

<http://www.sandia.gov/~sjplimp/spparks.html> - Sandia National Laboratories

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# SPPARKS Documentation

## Version info:

The SPPARKS "version" is the date when it was released, such as 1 May 2010. SPPARKS is updated continuously. Whenever we fix a bug or add a feature, we release it immediately, and post a notice on [this page of the WWW site](#). Each dated copy of SPPARKS contains all the features and bug-fixes up to and including that version date. The version date is printed to the screen and logfile every time you run SPPARKS. It is also in the file `src/version.h` and in the SPPARKS directory name created when you unpack a tarball.

- If you browse the HTML or PDF doc pages on the SPPARKS WWW site, they always describe the most current version of SPPARKS.
- If you browse the HTML or PDF doc pages included in your tarball, they describe the version you have.

SPPARKS stands for Stochastic Parallel PARticle Kinetic Simulator.

SPPARKS is a kinetic Monte Carlo (KMC) code designed to run efficiently on parallel computers using both KMC and Metropolis Monte Carlo algorithms. It was developed at Sandia National Laboratories, a US Department of Energy facility, with funding from the DOE. It is an open-source code, distributed freely under the terms of the GNU Public License (GPL).

The developers of SPPARKS are [Steve Plimpton](#), Aidan Thompson, and Alex Slepoy. They can be contacted at [sjplimp@sandia.gov](mailto:sjplimp@sandia.gov), [athomps@sandia.gov](mailto:athomps@sandia.gov), and [alexander.slepoy@nnsa.doe.gov](mailto:alexander.slepoy@nnsa.doe.gov). The [SPPARKS WWW Site](#) at <http://www.cs.sandia.gov/~sjplimp/spparks.html> has more information about the code and its uses.

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The SPPARKS documentation is organized into the following sections. If you find errors or omissions in this manual or have suggestions for useful information to add, please send an email to the developers so we can improve the SPPARKS documentation.

Once you are familiar with SPPARKS, you may want to bookmark [this page](#) at `Section_commands.html#comm` since it gives quick access to documentation for all SPPARKS commands.

[PDF file](#) of the entire manual, generated by [htmldoc](#)

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## 1. Introduction

These sections provide an overview of what SPPARKS can do, describe what it means for SPPARKS to be an open-source code, and acknowledge the funding and people who have contributed to SPPARKS.

- 1.1 [What is SPPARKS](#)
  - 1.2 [SPPARKS features](#)
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  - 1.4 [Acknowledgments and citations](#)
- 

### 1.1 What is SPPARKS

SPPARKS is a Monte Carlo code that has algorithms for kinetic Monte Carlo (KMC), rejection KMC (rKMC), and Metropolis Monte Carlo (MMC). On-lattice and off-lattice applications with spatial sites on which "events" occur can be simulated in parallel.

KMC is also called true KMC or rejection-free KMC. rKMC is also called null-event MC. In a generic sense the code's KMC and rKMC solvers catalog a list of events, each with an associated probability, choose a single event to perform, and advance time by the correct amount. Events may be chosen individually at random, or a sweep of enumerated sites can be performed to select possible events in a more ordered fashion.

Note that rKMC is different from Metropolis MC, which is sometimes called thermodynamic-equilibrium MC or barrier-free MC, in that rKMC still uses rates to define events, often associated with the rate for the system to cross some energy barrier. Thus both KMC and rKMC track the dynamic evolution of a system in a time-accurate manner as events are performed. Metropolis MC is typically used to sample states from a system in equilibrium or to drive a system to equilibrium (energy minimization). It does this by performing (possibly) non-physical events. As such it has no requirement to sample events with the correct relative probabilities or to limit itself to physical events (e.g. it can change an atom to a new species). Because of this it also does not evolve the system in a time-accurate manner; in general there is no "time" associated with Metropolis MC events.

Applications are implemented in SPPARKS which define events and their probabilities and acceptance/rejection criteria. They are coupled to solvers or sweepers to perform KMC or rKMC simulations. The KMC or rKMC options for an application in SPPARKS can be written to define rates based on energy differences between the initial and final state of an event and a Metropolis-style accept/reject criterion based on the Boltzmann factor. SPPARKS will then perform a Metropolis-style Monte Carlo simulation.

In parallel, a geometric partitioning of the simulation domain is performed. Sub-partitioning of processor domains into colors or quadrants (2d) and octants (3d) is done to enable multiple events to be performed on multiple processors simultaneously. Communication of boundary information is performed as needed.

Parallelism can also be invoked to perform multiple runs on a collection of processors, for statistical purposes.

SPPARKS is designed to be easy to modify and extend. For example, new solvers and sweeping rules can be added, as can new applications. Applications can define new commands which are read from the input script.

SPPARKS is written in C++. It runs on single-processor desktop or laptop machines, but for some applications, can also run on parallel computers. SPPARKS will run on any parallel machine that compiles C++ and supports the [MPI](#) message-passing library. This includes distributed- or shared-memory machines.

SPPARKS is a freely-available open-source code. See the [SPPARKS WWW Site](#) for download information. It is distributed under the terms of the [GNU Public License](#), which means you can use or modify the code however you wish. The only restrictions imposed by the GPL are on how you distribute the code further. See [this section](#) for a brief discussion of the open-source philosophy.

---

## 1.2 SPPARKS features

These are three kinds of applications in SPPARKS:

- on-lattice
- off-lattice
- general

On-lattice applications define static event sites with a fixed neighbor connectivity. Off-lattice applications define mobile event sites such as particles. A particle's neighbors are typically specified by a cutoff distance. General applications have no spatial component.

The set of on-lattice applications currently in SPPARKS are:

- diffusion model
- Ising model
- Potts model
- membrane model

The set of off-lattice applications currently in SPPARKS are:

- Metropolis atomic relaxation model

The set of general applications currently in SPPARKS are:

- biochemical reaction network model
- test driver for solvers using a synthetic biochemical network

These are the KMC solvers currently available in SPPARKS and their scaling properties:

- linear search,  $O(N)$
- tree search,  $O(\log N)$
- composition-rejection search,  $O(1)$

### Pre- and post-processing:

Our group has written and released a separate toolkit called [Pizza.py](#) which provides tools which can be used to setup, analyze, plot, and visualize data for SPPARKS simulations. Pizza.py is written in [Python](#) and is available for download from [the Pizza.py WWW site](#).

---

## 1.4 Open source distribution

SPPARKS comes with no warranty of any kind. As each source file states in its header, it is a copyrighted code that is distributed free-of-charge, under the terms of the [GNU Public License](#) (GPL). This is often referred to as open-source distribution - see [www.gnu.org](http://www.gnu.org) or [www.opensource.org](http://www.opensource.org) for more details. The legal text of the GPL is



in the LICENSE file that is included in the SPPARKS distribution.

Here is a summary of what the GPL means for SPPARKS users:

- (1) Anyone is free to use, modify, or extend SPPARKS in any way they choose, including for commercial purposes.
- (2) If you distribute a modified version of SPPARKS, it must remain open-source, meaning you distribute source code under the terms of the GPL. You should clearly annotate such a code as a derivative version of SPPARKS.
- (3) If you distribute any code that used SPPARKS source code, including calling it as a library, then that must also be open-source, meaning you distribute its source code under the terms of the GPL.
- (4) If you give SPPARKS files to someone else, the GPL LICENSE file and source file headers (including the copyright and GPL notices) should remain part of the code.

In the spirit of an open-source code, if you use SPPARKS for something useful or if you fix a bug or add a new feature or application to the code, let us know. We would like to include your contribution in the released version of the code and/or advertise your success on our WWW page.

---

## 1.4 Acknowledgments and citations

SPPARKS is distributed by [Sandia National Laboratories](#). SPPARKS development has been funded by the [US Department of Energy](#) (DOE), through its LDRD and ASC programs.

The primary authors of SPPARKS are Steve Plimpton, Aidan Thompson, and Alex Slepoy. They can be contacted via email: [sjplimp@sandia.gov](mailto:sjplimp@sandia.gov), [athomps@sandia.gov](mailto:athomps@sandia.gov), [alexander.slepoy@nnsa.doe.gov](mailto:alexander.slepoy@nnsa.doe.gov).

The following Sandians have also contributed to the design and ideas in SPPARKS:

- Corbett Battaile
- Liz Holm
- Ed Webb

## 2. Getting Started

This section describes how to unpack, make, and run SPPARKS.

- [2.1 What's in the SPPARKS distribution](#)
  - [2.2 Making SPPARKS](#)
  - [2.3 Making SPPARKS with optional packages](#)
  - [2.4 Building SPPARKS as a library](#)
  - [2.5 Running SPPARKS](#)
  - [2.6 Command-line options](#)
- 

### 2.1 What's in the SPPARKS distribution

When you download SPPARKS you will need to unzip and untar the downloaded file with the following commands, after placing the tarball in an appropriate directory.

```
gunzip spparks*.tar.gz
tar xvf spparks*.tar
```

This will create a spparks directory containing two files and several sub-directories:

README	text file
LICENSE	the GNU General Public License (GPL)
doc	documentation
examples	test problems
src	source files

---

### 2.2 Making SPPARKS

This section has the following sub-sections:

- [Read this first](#)
  - [Building a SPPARKS executable](#)
  - [Common errors that can occur when making SPPARKS](#)
  - [Editing a new low-level Makefile](#)
  - [Additional build tips](#)
  - [Building for a Mac](#)
  - [Building for Windows](#)
- 

#### *Read this first:*

Building SPPARKS can be non-trivial. You will likely need to edit a makefile, there are compiler options, additional libraries can be used (MPI, JPEG), etc. Please read this section carefully. If you are not comfortable with makefiles, or building codes on a Unix platform, or running an MPI job on your machine, please find a local expert to help you.

---

#### *Building a SPPARKS executable:*

The src directory contains the C++ source and header files for SPPARKS. It also contains a top-level Makefile and a MAKE sub-directory with low-level Makefile.\* files for several machines. From within the src directory, type "make" or "gmake". You should see a list of available choices. If one of those is the machine and options you want, you can type a command like:

```
make linux
gmake mac
```

Note that on a multi-processor or multi-core platform you can launch a parallel make, by using the "-j" switch with the make command, which will typically build SPPARKS more quickly.

If you get no errors and an executable like spk\_linux or spk\_mac is produced, you're done; it's your lucky day.

---

### ***Common errors that can occur when making SPPARKS:***

(1) If the make command breaks immediately with errors that indicate it can't find files with a "\*" in their names, this can be because your machine's make doesn't support wildcard expansion in a makefile. Try gmake instead of make. If that doesn't work, try using a -f switch with your make command to use Makefile.list which explicitly lists all the needed files, e.g.

```
make makelist
make -f Makefile.list linux
gmake -f Makefile.list mac
```

The first "make" command will create a current Makefile.list with all the file names in your src dir. The 2nd "make" command (make or gmake) will use it to build SPPARKS.

(2) Other errors typically occur because the low-level Makefile isn't setup correctly for your machine. If your platform is named "foo", you need to create a Makefile.foo in the MAKE sub-directory. Use whatever existing file is closest to your platform as a starting point. See the next section for more instructions.

---

### ***Editing a new low-level Makefile.foo:***

These are the issues you need to address when editing a low-level Makefile for your machine. With a couple exceptions, the only portion of the file you should need to edit is the "System-specific Settings" section.

(1) Change the first line of Makefile.foo to include the word "foo" and whatever other options you set. This is the line you will see if you just type "make".

(2) The "compiler/linker settings" section lists compiler and linker settings for your C++ compiler, including optimization flags. You can use g++, the open-source GNU compiler, which is available on all Unix systems. You can also use mpicc which will typically be available if MPI is installed on your system, though you should check which actual compiler it wraps. Vendor compilers often produce faster code. On boxes with Intel CPUs, we suggest using the commercial Intel icc compiler, which can be downloaded from [Intel's compiler site](#).

If building a C++ code on your machine requires additional libraries, then you should list them as part of the LIB variable.

The DEPFLAGS setting is what triggers the C++ compiler to create a dependency list for a source file. This speeds re-compilation when source (\*.cpp) or header (\*.h) files are edited. Some compilers do not support dependency file creation, or may use a different switch than -D. GNU g++ works with -D. If your compiler can't create dependency files (a long list of errors involving \*.d files), then you'll need to create a Makefile.foo patterned after Makefile.storm, which uses different rules that do not involve dependency files.

(3) The "system-specific settings" section has 3 parts.

(3.a) The SPK\_INC variable is used to include options that turn on system-dependent ifdefs within the SPPARKS code. The settings that are currently recognized are:

- -DSPPARKS\_GZIP
- -DSPPARKS\_JPEG

The read\_sites and dump commands will read/write gzipped files if you compile with -DSPPARKS\_GZIP. It requires that your Unix support the "popen" command.

If you use -DSPPARKS\_JPEG, the [dump image](#) command will be able to write out JPEG image files. If not, it will only be able to write out text-based PPM image files. For JPEG files, you must also link SPPARKS with a JPEG library. See section (3.c) below for more details on this.

(3.b) The 3 MPI variables are used to specify an MPI library to build SPPARKS with.

If you want SPPARKS to run in parallel, you must have an MPI library installed on your platform. If you use an MPI-wrapped compiler, such as "mpicc" to build SPPARKS, you can probably leave these 3 variables blank. If you do not use "mpicc" as your compiler/linker, then you need to specify where the mpi.h file (MPI\_INC) and the MPI library (MPI\_PATH) is found and its name (MPI\_LIB).

If you are installing MPI yourself, we recommend Argonne's MPICH 1.2 or 2.0 or OpenMPI. MPICH can be downloaded from the [Argonne MPI site](#). OpenMPI can be downloaded the [OpenMPI site](#). LAM MPI should also work. If you are running on a big parallel platform, your system people or the vendor should have already installed a version of MPI, which will be faster than MPICH or OpenMPI or LAM, so find out how to build and link with it. If you use MPICH or OpenMPI or LAM, you will have to configure and build it for your platform. The MPI configure script should have compiler options to enable you to use the same compiler you are using for the SPPARKS build, which can avoid problems that can arise when linking SPPARKS to the MPI library.

If you just want SPPARKS to run on a single processor, you can use the STUBS library in place of MPI, since you don't need a true MPI library installed on your system. See the Makefile.serial file for how to specify the 3 MPI variables. You will also need to build the STUBS library for your platform before making SPPARKS itself. From the STUBS dir, type "make" and it will hopefully create a libmpi.a suitable for linking to SPPARKS. If this build fails, you will need to edit the STUBS/Makefile for your platform.

The file STUBS/mpi.cpp has a CPU timer function MPI\_Wtime() that calls gettimeofday() . If your system doesn't support gettimeofday() , you'll need to insert code to call another timer. Note that the ANSI-standard function clock() rolls over after an hour or so, and is therefore insufficient for timing long SPPARKS simulations.

(3.c) The 3 JPG variables are used to specify a JPEG library which SPPARKS uses when writing a JPEG file via the [dump image](#) command. These can be left blank if you are not using the -DSPPARKS\_JPEG switch discussed above in section (3.a).

A standard JPEG library usually goes by the name libjpeg.a and has an associated header file jpeglib.h. Whichever JPEG library you have on your platform, you'll need to set the appropriate JPG\_INC, JPG\_PATH, and JPG\_LIB variables in Makefile.foo so that the compiler and linker can find it.

That's it. Once you have a correct Makefile.foo and you have pre-built any other libraries it will use (e.g. MPI, JPEG), all you need to do from the src directory is type one of these 2 commands:

That's it. Once you have a correct Makefile.foo and you have pre-built the MPI library it uses, all you need to do

from the src directory is type one of these 2 commands:

```
make foo
gmake foo
```

You should get the executable spk\_foo when the build is complete.

---

### ***Additional build tips:***

#### (1) Building SPPARKS for multiple platforms.

You can make SPPARKS for multiple platforms from the same src directory. Each target creates its own object sub-directory called Obj\_name where it stores the system-specific \*.o files.

#### (2) Cleaning up.

Typing "make clean" will delete all \*.o object files created when SPPARKS is built.

#### (3) Changing the size limits in src/spktype.h

If you get an error that refers to size limits set in src/spktype.h then you may need to change one or more settings in that file and re-compile SPPARKS.

By default the file is setup to allow models to be run with more than 2 billions sites, limited only by available physical memory on your machine. This requires the use of 64-bit integers for site IDs and tallying system statistics (e.g. number of accepted events). If your system or MPI implementation does not support 64-bit integers, or you wish to save memory by using 32-bit integers for these quantities, then you can change the settings by editing the file. If you use 32-bit integers, then you will be limited to model with around 2 billions sites.

As the documentation in that file explains, you have basically two choices to make:

- set the data type size of integer site IDs to 4 or 8 bytes
- set the data type size of integers that store tallies to 4 or 8 bytes

Note that in src/spktype.h there are also settings for the MPI data types associated with the site IDs and system tally sizes, which need to be set consistent with the associated C data types.

In all cases, the size of problem that can be run on a per-processor basis is limited by 4-byte integer storage to about 2 billion sites per processor ( $2^{31}$ ), which should not normally be a restriction since such a problem would have a huge per-processor memory footprint due to neighbor lists and would run very slowly in terms of CPU time.

### ***Building for a Mac:***

OS X is BSD Unix, so it already works. See the Makefile.mac file.

---

### ***Building for Windows:***

SPPARKS is just C++ with MPI calls, so it should be possible to build it for a Windows box, either using a Linux installation such as cygwin (see src/MAKE/Makefile.cygwin), or importing the source files into Visual Studio C++ and building it there. For the latter you are on your own. The SPPARKS developers do not use Windows.

But if you figure out how to do it, or create a Visual Studio project that works, please let us know, and we can release the instructions/files for how to do this as part of SPPARKS.

---

## 2.3 Making SPPARKS with optional packages

NOTE: this sub-section is currently a placeholder. There are no packages distributed with the current version of SPPARKS.

The source code for SPPARKS is structured as a large set of core files which are always used, plus optional packages, which are groups of files that enable a specific set of features. You can see the list of both standard and user-contributed packages by typing "make package".

Any or all packages can be included or excluded when SPPARKS is built. You may wish to exclude certain packages if you will never run certain kinds of simulations.

By default, SPPARKS includes no packages.

Packages are included or excluded by typing "make yes-name" or "make no-name", where "name" is the name of the package. You can also type "make yes-all" or "make no-all" to include/exclude all packages. These commands work by simply moving files back and forth between the main src directory and sub-directories with the package name, so that the files are seen or not seen when SPPARKS is built. After you have included or excluded a package, you must re-build SPPARKS.

Additional make options exist to help manage SPPARKS files that exist in both the src directory and in package sub-directories. You do not normally need to use these commands unless you are editing SPPARKS files or have downloaded a patch from the SPPARKS WWW site. Typing "make package-update" will overwrite src files with files from the package directories if the package has been included. It should be used after a patch is installed, since patches only update the master package version of a file. Typing "make package-overwrite" will overwrite files in the package directories with src files. Typing "make package-check" will list differences between src and package versions of the same files.

---

## 2.4 Building SPPARKS as a library

SPPARKS can be built as a library, which can then be called from another application or a scripting language. Building SPPARKS as a library is done by typing

```
make makelib  
make -f Makefile.lib foo
```

where foo is the machine name. The first "make" command will create a current Makefile.lib with all the file names in your src dir. The 2nd "make" command will use it to build SPPARKS as a library. This requires that Makefile.foo have a library target (lib) and system-specific settings for ARCHIVE and ARFLAGS. See Makefile.linux for an example. The build will create the file libspk\_foo.a which another application can link to.

When used from a C++ program, the library allows one or more SPPARKS objects to be instantiated. All of SPPARKS is wrapped in a SPPARKS\_NS namespace; you can safely use any of its classes and methods from within your application code, as needed.

When used from a C or Fortran program or a scripting language, the library has a simple function-style interface, provided in library.cpp and library.h.

You can add as many functions as you wish to library.cpp and library.h. In a general sense, those functions can

access SPPARKS data and return it to the caller or set SPPARKS data values as specified by the caller. These 4 functions are currently included in library.cpp:

```
void spparks_open(int, char **, MPI_Comm, void **ptr);
void spparks_close(void *ptr);
int spparks_file(void *ptr, char *);
int spparks_command(void *ptr, char *);
```

The SPPARKS\_open() function is used to initialize SPPARKS, passing in a list of strings as if they were [command-line arguments](#) when SPPARKS is run from the command line and a MPI communicator for SPPARKS to run under. It returns a ptr to the SPPARKS object that is created, and which should be used in subsequent library calls. Note that SPPARKS\_open() can be called multiple times to create multiple SPPARKS objects.

The SPPARKS\_close() function is used to shut down SPPARKS and free all its memory. The SPPARKS\_file() and SPPARKS\_command() functions are used to pass a file or string to SPPARKS as if it were an input file or single command read from an input script.

---

## 2.5 Running SPPARKS

By default, SPPARKS runs by reading commands from stdin; e.g. spk\_linux < in.file. This means you first create an input script (e.g. in.file) containing the desired commands. [This section](#) describes how input scripts are structured and what commands they contain.

You can test SPPARKS on any of the sample inputs provided in the examples directory. Input scripts are named in.\* and sample outputs are named log.\*.name.P where name is a machine and P is the number of processors it was run on.

Here is how you might run the Potts model tests on a Linux box, using mpirun to launch a parallel job:

```
cd src
make linux
cp spk_linux ../examples/lj
cd ../examples/potts
mpirun -np 4 spk_linux <in.potts
```

The screen output from SPPARKS is described in the next section. As it runs, SPPARKS also writes a log.spparks file with the same information.

Note that this sequence of commands copies the SPPARKS executable (spk\_linux) to the directory with the input files. This may not be necessary, but some versions of MPI reset the working directory to where the executable is, rather than leave it as the directory where you launch mpirun from (if you launch spk\_linux on its own and not under mpirun). If that happens, SPPARKS will look for additional input files and write its output files to the executable directory, rather than your working directory, which is probably not what you want.

If SPPARKS encounters errors in the input script or while running a simulation it will print an ERROR message and stop or a WARNING message and continue. See [this section](#) for a discussion of the various kinds of errors SPPARKS can or can't detect, a list of all ERROR and WARNING messages, and what to do about them.

SPPARKS can run a problem on any number of processors, including a single processor. SPPARKS can run as large a problem as will fit in the physical memory of one or more processors. If you run out of memory, you must run on more processors or setup a smaller problem.

---

## 2.6 Command-line options

At run time, SPPARKS recognizes several optional command-line switches which may be used in any order. For example, `spk_ibm` might be launched as follows:

```
mpirun -np 16 spk_ibm -var f tmp.out -log my.log -screen none <in.alloy
```

These are the command-line options:

```
-echo style
```

Set the style of command echoing. The style can be *none* or *screen* or *log* or *both*. Depending on the style, each command read from the input script will be echoed to the screen and/or logfile. This can be useful to figure out which line of your script is causing an input error. The default value is *log*. The echo style can also be set by using the [echo](#) command in the input script itself.

```
-partition 8x2 4 5 ...
```

Invoke SPPARKS in multi-partition mode. When SPPARKS is run on *P* processors and this switch is not used, SPPARKS runs in one partition, i.e. all *P* processors run a single simulation. If this switch is used, the *P* processors are split into separate partitions and each partition runs its own simulation. The arguments to the switch specify the number of processors in each partition. Arguments of the form *M*x*N* mean *M* partitions, each with *N* processors. Arguments of the form *N* mean a single partition with *N* processors. The sum of processors in all partitions must equal *P*. Thus the command "-partition 8x2 4 5" has 10 partitions and runs on a total of 25 processors.

The input script specifies what simulation is run on which partition; see the [variable](#) and [next](#) commands. This [howto section](#) gives examples of how to use these commands in this way. Simulations running on different partitions can also communicate with each other; see the [temper](#) command.

```
-in file
```

Specify a file to use as an input script. This is an optional switch when running SPPARKS in one-partition mode. If it is not specified, SPPARKS reads its input script from stdin - e.g. `spk_linux < in.run`. This is a required switch when running SPPARKS in multi-partition mode, since multiple processors cannot all read from stdin.

```
-log file
```

Specify a log file for SPPARKS to write status information to. In one-partition mode, if the switch is not used, SPPARKS writes to the file `log.spparks`. If this switch is used, SPPARKS writes to the specified file. In multi-partition mode, if the switch is not used, a `log.SPPARKS` file is created with hi-level status information. Each partition also writes to a `log.SPPARKS.N` file where *N* is the partition ID. If the switch is specified in multi-partition mode, the hi-level logfile is named "file" and each partition also logs information to a `file.N`. For both one-partition and multi-partition mode, if the specified file is "none", then no log files are created. Using a [log](#) command in the input script will override this setting.

```
-screen file
```

Specify a file for SPPARKS to write its screen information to. In one-partition mode, if the switch is not used, SPPARKS writes to the screen. If this switch is used, SPPARKS writes to the specified file instead and you will see no screen output. In multi-partition mode, if the switch is not used, hi-level status information is written to the screen. Each partition also writes to a `screen.N` file where *N* is the partition ID. If the switch is specified in multi-partition mode, the hi-level screen dump is named "file" and each partition also writes screen information to



a file.N. For both one-partition and multi-partition mode, if the specified file is "none", then no screen output is performed.

`-var name value`

Specify a variable that will be defined for substitution purposes when the input script is read. "Name" is the variable name which can be a single character (referenced as \$x in the input script) or a full string (referenced as \${abc}). The value can be any string. Using this command-line option is equivalent to putting the line "variable name index value" at the beginning of the input script. Defining a variable as a command-line argument overrides any setting for the same variable in the input script, since variables cannot be re-defined. See the [variable](#) command for more info on defining variables and [this section](#) for more info on using variables in input scripts.

## 3. Commands

This section describes how a SPPARKS input script is formatted and what commands are used to define a simulation.

- [3.1 SPPARKS input script](#)
  - [3.2 Parsing rules](#)
  - [3.3 Input script structure](#)
  - [3.4 Commands listed by category](#)
  - [3.5 Commands listed alphabetically](#)
- 

### 3.1 SPPARKS input script

SPPARKS executes by reading commands from an input script (text file), one line at a time. When the input script ends, SPPARKS exits. Each command causes SPPARKS to take some action. It may set an internal variable, read in a file, or run a simulation. Most commands have default settings, which means you only need to use the command if you wish to change the default.

In many cases, the ordering of commands in an input script is not important. However the following rules apply:

(1) SPPARKS does not read your entire input script and then perform a simulation with all the settings. Rather, the input script is read one line at a time and each command takes effect when it is read. Thus this sequence of commands:

```
count    ligand 10000
run      100
run      100
```

does something different than this sequence:

```
run      100
count    ligand 10000
run      100
```

In the first case, the count of ligand molecules is set to 10000 before the first simulation and whatever the count becomes will be used as input for the second simulation. In the 2nd case, the default count of 0 is used for the 1st simulation and then the count is set to 10000 molecules before the second simulation.

(2) Some commands are only valid when they follow other commands. For example you cannot set the count of a molecular species until the `add_species` command has been used to define that species.

(3) Sometimes command B will use values that can be set by command A. This means command A must precede command B in the input script if it is to have the desired effect.

(4) Some commands are only used by a specific application(s).

Many input script errors are detected by SPPARKS and an ERROR or WARNING message is printed. [This section](#) gives more information on what errors mean. The documentation for each command lists restrictions on how the command can be used.

---

## 3.2 Parsing rules

Each non-blank line in the input script is treated as a command. SPPARKS commands are case sensitive. Command names are lower-case, as are specified command arguments. Upper case letters may be used in file names or user-chosen ID strings.

Here is how each line in the input script is parsed by SPPARKS:

- (1) If the line ends with a "&" character (with no trailing whitespace), the command is assumed to continue on the next line. The next line is concatenated to the previous line by removing the "&" character and newline. This allows long commands to be continued across two or more lines.
  - (2) All characters from the first "#" character onward are treated as comment and discarded.
  - (3) The line is searched repeatedly for \$ characters which indicate variables that are replaced with a text string. If the \$ is followed by curly brackets, then the variable name is the text inside the curly brackets. If no curly brackets follow the \$, then the variable name is the character immediately following the \$. Thus \${myTemp} and \$x refer to variable names "myTemp" and "x". See the [variable](#) command for details of how strings are assigned to variables and how they are substituted for in input scripts.
  - (4) The line is broken into "words" separated by whitespace (tabs, spaces). Note that words can thus contain letters, digits, underscores, or punctuation characters.
  - (5) The first word is the command name. All successive words in the line are arguments.
  - (6) Text with spaces can be enclosed in double quotes so it will be treated as a single argument. See the [dump](#) [modify](#) or [fix print](#) commands for examples. A '#' or '\$' character that in text between double quotes will not be treated as a comment or substituted for as a variable.
- 

## 3.3 Input script structure

This section describes the structure of a typical SPPARKS input script. The "examples" directory in the SPPARKS distribution contains sample input scripts; the corresponding problems are discussed in [this section](#), and some are animated on the [SPPARKS WWW Site](#).

A SPPARKS input script typically has 3 parts:

- choice of application, solver, sweeper
- settings
- run a simulation

The last 2 parts can be repeated as many times as desired. I.e. run a simulation, change some settings, run some more, etc. Each of the 3 parts is now described in more detail. Remember that almost all the commands need only be used if a non-default value is desired.

### (1) Choice of application, solver, sweep method

Use the [app\\_style](#), [solve\\_style](#), and [sweep](#) commands to setup the kind of simulation you wish to run. Note that sweeping is only relevant to applications that define a geometric lattice of event sites and only if you wish to perform rejection kinetic Monte Carlo updates.

### (2) Settings

Parameters for a simulation can be defined by application-specific commands or by generic commands that are common to many kinds of applications. See the doc pages for individual applications for information on the former. Examples of the latter are the [stats](#) and [temperature](#) commands.

The [diag\\_style](#) command can also be used to setup various diagnostic computations to perform during a simulation.

### (3) Run a simulation

A kinetic or Metropolis Monte Carlo simulation is performed using the [run](#) command.

---

## 3.4 Commands listed by category

This section lists all SPPARKS commands, grouped by category. The [next section](#) lists the same commands alphabetically. Note that some commands are only usable with certain applications. Also, some style options for some commands are part of specific SPPARKS packages, which means they cannot be used unless the package was included when SPPARKS was built. Not all packages are included in a default SPPARKS build. These dependencies are listed as Restrictions in the command's documentation.

Initialization commands:

[app\\_style](#), [create\\_box](#), [create\\_sites](#), [processors](#), [read\\_sites](#), [region](#), [solve\\_style](#)

Setting commands:

[dimension](#), [boundary](#), [lattice](#), [pair\\_coeff](#), [pair\\_style](#), [reset\\_time](#), [sector](#), [seed](#), [sweep](#), [set](#)

Application-specific commands:

[add\\_reaction](#), [add\\_species](#), [barrier](#), [count](#), [deposition](#), [ecoord](#), [inclusion](#), [pin](#), [temperature](#), [volume](#)

Output commands:

[diag\\_style](#), [dump](#), [dump image](#), [dump\\_modify](#), [dump\\_one](#), [stats](#), [undump](#)

Actions:

[run](#),

Miscellaneous:

[clear](#), [echo](#), [if](#), [include](#), [jump](#), [label](#), [log](#), [next](#), [print](#), [shell](#), [variable](#)

---

## 3.5 Individual commands

This section lists all SPPARKS commands alphabetically, with a separate listing below of styles within certain commands. The [previous section](#) lists the same commands, grouped by category. Note that some commands are only usable with certain applications. Also, some style options for some commands are part of specific SPPARKS packages, which means they cannot be used unless the package was included when SPPARKS was built. Not all packages are included in a default SPPARKS build. These dependencies are listed as Restrictions in the command's documentation.

<a href="#">add_reaction</a>	<a href="#">add_species</a>	<a href="#">app_style</a>	<a href="#">barrier</a>	<a href="#">boundary</a>	<a href="#">clear</a>
<a href="#">count</a>	<a href="#">create_box</a>	<a href="#">create_sites</a>	<a href="#">deposition</a>	<a href="#">diag_style</a>	<a href="#">dimension</a>
<a href="#">dump</a>	<a href="#">dump image</a>	<a href="#">dump_modify</a>	<a href="#">dump_one</a>	<a href="#">echo</a>	<a href="#">ecoord</a>
<a href="#">event</a>	<a href="#">if</a>	<a href="#">include</a>	<a href="#">inclusion</a>	<a href="#">jump</a>	<a href="#">label</a>
<a href="#">lattice</a>	<a href="#">log</a>	<a href="#">next</a>	<a href="#">pair_coeff</a>	<a href="#">pair_style</a>	<a href="#">pin</a>
<a href="#">print</a>	<a href="#">processors</a>	<a href="#">read_sites</a>	<a href="#">region</a>	<a href="#">reset_time</a>	<a href="#">run</a>
<a href="#">sector</a>	<a href="#">seed</a>	<a href="#">set</a>	<a href="#">shell</a>	<a href="#">solve_style</a>	<a href="#">stats</a>
<a href="#">sweep</a>	<a href="#">temperature</a>	<a href="#">undump</a>	<a href="#">variable</a>	<a href="#">volume</a>	

---

Application styles. See the [app\\_style](#) command for one-line descriptions of each style or click on the style itself for a full description:

<a href="#">chemistry</a>	<a href="#">diffusion</a>	<a href="#">erbium</a>	<a href="#">ising</a>	<a href="#">ising/single</a>	<a href="#">membrane</a>	<a href="#">potts</a>	<a href="#">potts/neigh</a>
<a href="#">potts/neighonly</a>	<a href="#">potts/pin</a>	<a href="#">relax</a>	<a href="#">sos</a>	<a href="#">test/group</a>			

---

Solve styles. See the [solve\\_style](#) command for one-line descriptions of each style or click on the style itself for a full description:

<a href="#">group</a>	<a href="#">linear</a>	<a href="#">tree</a>
-----------------------	------------------------	----------------------

---

Pair styles. See the [pair\\_style](#) command for one-line descriptions of each style or click on the style itself for a full description:

<a href="#">lj/cut</a>
------------------------

---

Diagnostic styles. See the [diag\\_style](#) command for one-line descriptions of each style or click on the style itself for a full description:

<a href="#">cluster</a>	<a href="#">diffusion</a>	<a href="#">erbium</a>	<a href="#">energy</a>	<a href="#">propensity</a>
-------------------------	---------------------------	------------------------	------------------------	----------------------------

## 4. How-to discussions

The following sections describe how to perform various operations in SPPARKS.

### 4.1 [Running multiple simulations from one input script](#)

### 4.2 [Coupling SPPARKS to other codes](#)

The example input scripts included in the SPPARKS distribution and highlighted in [this section](#) also show how to setup and run various kinds of problems.

---

### 4.1 Running multiple simulations from one input script

This can be done in several ways. See the documentation for individual commands for more details on how these examples work.

If "multiple simulations" means continue a previous simulation for more timesteps, then you simply use the [run](#) command multiple times. For example, this script

```
app_style ising/2d/4n 100 100 12345
...
run 1.0
run 1.0
run 1.0
run 1.0
run 1.0
```

would run 5 successive simulations of the same system for a total of 5.0 seconds of elapsed time.

If you wish to run totally different simulations, one after the other, the [clear](#) command can be used in between them to re-initialize SPPARKS. For example, this script

```
app_style ising/2d/4n 100 100 12345
...
run 1.0
clear
app_style ising/2d/4n 200 200 12345
...
run 1.0
```

would run 2 independent simulations, one after the other.

For large numbers of independent simulations, you can use [variables](#) and the [next](#) and [jump](#) commands to loop over the same input script multiple times with different settings. For example, this script, named in.runs

```
variable d index run1 run2 run3 run4 run5 run6 run7 run8
shell cd $d
app_style ising/2d/4n 100 100 12345
include temperature.txt
run 1.0
shell cd ..
clear
next d
jump in.runs
```

would run 8 simulations in different directories, using a temperature.txt file in each directory with an input command to set the temperature. The same concept could be used to run the same system at 8 different sizes, using a size variable and storing the output in different log files, for example

```
variable a loop 8
variable size index 100 200 400 800 1600 3200 6400 10000
log log.${size}
app_style ising/2d/4n ${size} ${size} 12345
run 1.0
next size
next a
jump in.runs
```

All of the above examples work whether you are running on 1 or multiple processors, but assumed you are running SPPARKS on a single partition of processors. SPPARKS can be run on multiple partitions via the "-partition" command-line switch as described in [this section](#) of the manual.

In the last 2 examples, if SPPARKS were run on 3 partitions, the same scripts could be used if the "index" and "loop" variables were replaced with *universe*-style variables, as described in the [variable](#) command. Also, the "next size" and "next a" commands would need to be replaced with a single "next a size" command. With these modifications, the 8 simulations of each script would run on the 3 partitions one after the other until all were finished. Initially, 3 simulations would be started simultaneously, one on each partition. When one finished, that partition would then start the 4th simulation, and so forth, until all 8 were completed.

---

## 4.2 Coupling SPPARKS to other codes

SPPARKS is designed to allow it to be coupled to other codes. For example, an atomistic code might relax atom positions and pass those positions to SPPARKS. Or a continuum finite element (FE) simulation might use a Monte Carlo relaxation to formulate a boundary condition on FE nodal points, compute a FE solution, and return the results to the MC calculation.

SPPARKS can be coupled to other codes in at least 3 ways. Each has advantages and disadvantages, which you'll have to think about in the context of your application.

(1) Define a new [diag\\_style](#) command that calls the other code. In this scenario, SPPARKS is the driver code. During its timestepping, the diagnostic is invoked, and can make library calls to the other code, which has been linked to SPPARKS as a library. See [this section](#) of the documentation for info on how to add a new diagnostic to SPPARKS.

(2) Define a new SPPARKS command that calls the other code. This is conceptually similar to method (1), but in this case SPPARKS and the other code are on a more equal footing. Note that now the other code is not called during the even loop of a SPPARKS run, but between runs. The SPPARKS input script can be used to alternate SPPARKS runs with calls to the other code, invoked via the new command.

In this scenario, the other code can be called as a library, as in (1), or it could be a stand-alone code, invoked by a system() call made by the command (assuming your parallel machine allows one or more processors to start up another program). In the latter case the stand-alone code could communicate with SPPARKS thru files that the command writes and reads.

See [this section](#) of the documentation for how to add a new command to SPPARKS.

(3) Use SPPARKS as a library called by another code. In this case the other code is the driver and calls SPPARKS as needed. Or a wrapper code could link and call both SPPARKS and another code as libraries.

[This section](#) of the documentation describes how to build SPPARKS as a library. Once this is done, you can interface with SPPARKS either via C++, C, or Fortran (or any other language that supports a vanilla C-like interface, e.g. a scripting language). For example, from C++ you could create one (or more) "instances" of SPPARKS, pass it an input script to process, or execute individual commands, all by invoking the correct class methods in SPPARKS. From C or Fortran you can make function calls to do the same things. Library.cpp and library.h contain such a C interface with the functions:

```
void spparks_open(int, char **, MPI_Comm, void **);
void spparks_close(void *);
void spparks_file(void *, char *);
char *spparks_command(void *, char *);
```

The functions contain C++ code you could write in a C++ application that was invoking SPPARKS directly. Note that SPPARKS classes are defined within a SPPARKS namespace (SPPARKS\_NS) if you use them from another C++ application.

Two of the routines in library.cpp are of particular note. The SPPARKS\_open() function initiates SPPARKS and takes an MPI communicator as an argument. It returns a pointer to a SPPARKS "object". As with C++, the SPPARKS\_open() function can be called multiple times, to create multiple instances of SPPARKS.

SPPARKS will run on the set of processors in the communicator. This means the calling code can run SPPARKS on all or a subset of processors. For example, a wrapper script might decide to alternate between SPPARKS and another code, allowing them both to run on all the processors. Or it might allocate half the processors to SPPARKS and half to the other code and run both codes simultaneously before syncing them up periodically.

Library.cpp contains a SPPARKS\_command() function to which the caller passes a single SPPARKS command (a string). Thus the calling code can read or generate a series of SPPARKS commands (e.g. an input script) one line at a time and pass it thru the library interface to setup a problem and then run it.

A few other sample functions are included in library.cpp, but the key idea is that you can write any functions you wish to define an interface for how your code talks to SPPARKS and add them to library.cpp and library.h. The routines you add can access any SPPARKS data. The examples/couple directory has example C++ and C codes which show how a stand-alone code can link SPPARKS as a library, run SPPARKS on a subset of processors, grab data from SPPARKS, change it, and put it back into SPPARKS.



## 5. Example problems

The SPPARKS distribution includes an examples sub-directory with several sample problems. Each problem is in a sub-directory of its own. Most are small models that can be run quickly, requiring at most a couple of minutes to run on a desktop machine. Each problem has an input script (in.\*) and produces a log file (log.\*) and dump file (dump.\*) when it runs. A few sample log file outputs on different machines and different numbers of processors are included in the directories to compare your answers to. E.g. a log file like log.potts.foo.P means it ran on P processors of machine "foo".

In some cases, the dump files produced by the example runs can be animated using the various visualization tools, such as the Pizza.py toolkit referenced in the [Additional Tools](#) section of the SPPARKS documentation. Animations of some of these examples can be viewed on the Movies section of the [SPPARKS WWW Site](#).

These are the sample problems in the examples sub-directories:

groups	test of group-based KMC solver
ising	standard Ising model
membrane	membrane model of pore formation around protein inclusions
potts	multi-state Potts model for grain growth

Here is how you might run and visualize one of the sample problems:

```
cd examples/potts
cp ../../src/spk_linux .           # copy SPPARKS executable to this dir
spk_linux <in.potts                # run the problem
```

Running the simulation produces the files *dump.potts* and *log.spparks*.

## 6. Performance & scalability

Eventually this section will highlight SPPARKS performance in serial and parallel on interesting Monte Carlo benchmarks.

## 7. Additional tools

SPPARKS is designed to be a Monte Carlo (MC) kernel for performing kinetic MC or Metropolis MC computations. Additional pre- and post-processing steps are often necessary to setup and analyze a simulation. This section describes additional tools that may be useful.

Users can extend SPPARKS by writing diagnostic classes that perform desired analysis or computations. See [this section](#) for more info.

Our group has written and released a separate toolkit called [Pizza.py](#) which provides tools which may be useful for setup, analysis, plotting, and visualization of SPPARKS simulations. Pizza.py is written in [Python](#) and is available for download from [the Pizza.py WWW site](#).

## 8. Modifying & extending SPPARKS

SPPARKS is designed in a modular fashion so as to be easy to modify and extend with new functionality.

In this section, changes and additions users can make are listed along with minimal instructions. If you add a new feature to SPPARKS and think it will be of interest to general users, we encourage you to submit it to the developers for inclusion in the released version of SPPARKS.

The best way to add a new feature is to find a similar feature in SPPARKS and look at the corresponding source and header files to figure out what it does. You will need some knowledge of C++ to be able to understand the hi-level structure of SPPARKS and its class organization, but functions (class methods) that do actual computations are written in vanilla C-style code and operate on simple C-style data structures (vectors and arrays).

Most of the new features described in this section require you to write a new C++ derived class. Creating a new class requires 2 files, a source code file (\*.cpp) and a header file (\*.h). The derived class must provide certain methods to work as a new option. Depending on how different your new feature is compared to existing features, you can either derive from the base class itself, or from a derived class that already exists. Enabling SPPARKS to invoke the new class is as simple as adding two lines to the style\_user.h file, in the same syntax as other SPPARKS classes are specified in the style.h file.

The advantage of C++ and its object-orientation is that all the code and variables needed to define the new feature are in the 2 files you write, and thus shouldn't make the rest of SPPARKS more complex or cause side-effect bugs.

Here is a concrete example. Suppose you write 2 files app\_foo.cpp and app\_foo.h that define a new class AppFoo that implements a Monte Carlo model described in the classic 1997 [paper](#) by Foo, et al. If you wish to invoke that application in a SPPARKS input script with a command like

```
app_style foo 0.1 3.5
```

you put your 2 files in the SPPARKS src directory and re-make the code. The app\_foo.h file should have these lines at the top

```
#ifdef APP_CLASS
AppStyle(foo, AppFoo)
#else
```

where "foo" is the style keyword to be used in the app\_style command, and AppFoo is the class name in your C++ files.

When you re-make SPPARKS, your new application becomes part of the executable and can be invoked with a app\_style command like the example above. Arguments like 0.1 and 3.5 can be defined and processed by your new class.

Here is a list of the new features that can be added in this way.

- [Application styles](#)
- [Diagnostic styles](#)
- [Input script commands](#)
- [Solve styles](#)

As illustrated by the application example, these options are referred to in the SPPARKS documentation as the "style" of a particular command.

The instructions below give the header file for the base class that these styles are derived from. Public variables in that file are ones used and set by the derived classes which are also used by the base class. Sometimes they are also used by the rest of SPPARKS. Virtual functions in the base class header file which are set = 0 are ones you must define in your new derived class to give it the functionality SPPARKS expects. Virtual functions that are not set to 0 are functions you can optionally define.

---

## Application styles

In SPPARKS, applications are what define the simulation model that is evolved via Monte Carlo algorithms. A new model typically requires adding a new application to the code. Read the doc page for the [app\\_style](#) command to understand the distinction between on-lattice and off-lattice applications. A new off-lattice application can be anything you wish. On-lattice applications are derive from the AppLattice class.

For on-lattice and off-lattice applications, here is a brief description of methods you define in your new derived class. Some of them are required; some are optional. See app.h for details.

input_app	additional commands the application defines
grow_app	set pointers to per-site arrays used by the application
init_app	initialize the application before a run
site_energy	compute energy of a site
site_event_rejection	perform an event with null-bin rejection (for rKMC)
site_propensity	compute propensity of all events on a site (for KMC)
site_event	perform an event (for KMC)

Note that two of the methods are required if you want your application to perform kinetic Monte Carlo (KMC) with a [solver](#). One of the methods is required if you want your application to perform rejection KMC (rKMC) with a [sweep method](#).

The constructor for your application class also needs to define, to insure proper operation with the "KMC solvers'\_solve.html and rejection KMC [sweep methods](#). These are the flags, all of which have default values set in app\_lattice.cpp:

ninteger	how many integer values are defined per site
ndouble	how many floating point values are defined per site
delp propensity	how many neighbors away values are needed to compute propensity
delevent	how many neighbors away may the value can be changed by an event
allow_kmc	1 if methods are provided for KMC
allow_rejection	1 if methods are provided for rejection KMC
allow_masking	1 if rKMC method supports masking
numrandom	# of random numbers used by the site_event_rejection method

## Diagnostic styles

Diagnostic classes compute some form of analysis periodically during a simulation. See the [diag\\_style](#) command for details.

To add a new diagnostic, here is a brief description of methods you define in your new derived class. Some of them are required; some are optional. See `diag.h` for details.

init	setup the computation
compute	perform the analysis computation
stats_header	what to add to statistics header for this diagnostic
stats	fields added to statistics by this diagnostic

---

## Input script commands

New commands can be added to SPPARKS input scripts by adding new classes that have a "command" method and are listed in the Command sections of `style_user.h` (or `style.h`). For example, the shell commands (`cd`, `mkdir`, `rm`, etc) are implemented in this fashion. When such a command is encountered in the SPPARKS input script, SPPARKS simply creates a class with the corresponding name, invokes the "command" method of the class, and passes it the arguments from the input script. The command method can perform whatever operations it wishes on SPPARKS data structures.

The single method your new class must define is as follows:

command	operations performed by the new command
---------	---

Of course, the new class can define other methods and variables as needed.

---

## Solve styles

In SPPARKS, a solver performs the kinetic Monte Carlo (KMC) operation of selecting an event from a list of events and associated probabilities. See the [solve\\_style](#) command for details.

To add a new KMC solver, here is a brief description of methods you define in your new derived class. Some of them are required; some are optional. See `diag.h` for details.

Here is a brief description of methods you define in your new derived class. All of them are required. See `solve.h` for details.

clone	make a copy of the solver for use within a sector of the domain
init	initialize the solver
update	update one or more event probabilities
resize	change the number of events in the list
event	select an event and associated timestep

---

---

(Foo) Foo, Morefoo, and Maxfoo, J of Classic Monte Carlo Applications, 75, 345 (1997).

## 9. Errors

This section describes the various kinds of errors you can encounter when using SPPARKS.

[9.1 Common problems](#)

[9.2 Reporting bugs](#)

[9.3 Error & warning messages](#)

---

### 9.1 Common problems

A SPPARKS simulation typically has two stages, setup and run. Many SPPARKS errors are detected at setup time; others may not occur until the middle of a run.

SPPARKS tries to flag errors and print informative error messages so you can fix the problem. Of course SPPARKS cannot figure out your physics mistakes, like choosing too big a timestep or setting up an invalid lattice. If you find errors that SPPARKS doesn't catch that you think it should flag, please send an email to the developers.

If you get an error message about an invalid command in your input script, you can determine what command is causing the problem by looking in the log.spparks file or using the [echo command](#) to see it on the screen. For example you can run your script as

```
spk_linux -echo screen <in.script
```

For a given command, SPPARKS expects certain arguments in a specified order. If you mess this up, SPPARKS will often flag the error, but it may read a bogus argument and assign a value that is not what you wanted. E.g. if the input parser reads the string "abc" when expecting an integer value, it will assign the value of 0 to a variable.

Generally, SPPARKS will print a message to the screen and exit gracefully when it encounters a fatal error. Sometimes it will print a WARNING and continue on; you can decide if the WARNING is important or not. If SPPARKS crashes or hangs without spitting out an error message first then it could be a bug (see [this section](#)) or one of the following cases:

SPPARKS runs in the available memory each processor can allocate. All large memory allocations in the code are done via C-style malloc's which will generate an error message if you run out of memory. Smaller chunks of memory are allocated via C++ "new" statements. If you are unlucky you could run out of memory when one of these small requests is made, in which case the code will crash, since SPPARKS doesn't trap on those errors.

Illegal arithmetic can cause SPPARKS to run slow or crash. This is typically due to invalid physics and numerics that your simulation is computing. If you see wild energy values or NaN values in your SPPARKS output, something is wrong with your simulation.

In parallel, one way SPPARKS can hang is due to how different MPI implementations handle buffering of messages. If the code hangs without an error message, it may be that you need to specify an MPI setting or two (usually via an environment variable) to enable buffering or boost the sizes of messages that can be buffered.

---

## 9.2 Reporting bugs

If you are confident that you have found a bug in SPPARKS, please send an email to the developers.

First, check the "New features and bug fixes" section of the [SPPARKS WWW site](#) to see if the bug has already been reported or fixed.

If not, the most useful thing you can do for us is to isolate the problem. Run it on the smallest problem and fewest number of processors and with the simplest input script that reproduces the bug.

In your email, describe the problem and any ideas you have as to what is causing it or where in the code the problem might be. We'll request your input script and data files if necessary.

---

## 9.3 Error & warning messages

These are two alphabetic lists of the [ERROR](#) and [WARNING](#) messages SPPARKS prints out and the reason why. If the explanation here is not sufficient, the documentation for the offending command may help. Grepping the source files for the text of the error message and staring at the source code and comments is also not a bad idea! Note that sometimes the same message can be printed from multiple places in the code.

### Errors:

*Adding site to bin it is not in*

Internal SPPARKS error.

*Adding site to illegal bin*

Internal SPPARKS error.

*All pair coeffs are not set*

Self-explanatory.

*All universe/uloop variables must have same # of values*

Self-explanatory.

*All variables in next command must be same style*

Self-explanatory.

*Another input script is already being processed*

Cannot attempt to open a 2nd input script, when the original file is still being processed.

*App cannot use both a KMC and rejection KMC solver*

You cannot define both a solver and sweep option.

*App did not set dt\_sweep*

Internal SPPARKS error.

*App needs a KMC or rejection KMC solver*

You must define either a solver or sweep option.

*App relax requires a pair potential*

Self-explanatory.

*App style proc count is not valid for 1d simulation*

There can only be 1 proc in y and z dimensions for 1d models.

*App style proc count is not valid for 2d simulation*

There can only be 1 proc in the z dimension for 2d models.

*App\_style command after simulation box is defined*

Self-explanatory.

*App\_style specific command before app\_style set*

Self-explanatory.

*Application cutoff is too big for processor sub-domain*

There must be at least 2 bins per processor in each dimension where sectoring occurs.



*Arccos of invalid value in variable formula*

Argument of arccos() must be between -1 and 1.

*Arcsin of invalid value in variable formula*

Argument of arcsin() must be between -1 and 1.

*Bad connectivity result*

Internal SPPARKS error. Should not occur.

*Box bounds are invalid*

Lo bound >= hi bound.

*Can only read neighbors for on-lattice applications*

Self-explanatory.

*Can only use ecoord command with app\_style diffusion nonlinear*

Self-explanatory.

*Cannot color this combination of lattice and app*

Coloring is not supported on this lattice for the neighbor dependencies of this application.

*Cannot color without a lattice definition of sites*

Self-explanatory.

*Cannot create box after simulation box is defined*

Self-explanatory.

*Cannot create box with this application style*

This application does not support spatial domains.

*Cannot create sites after sites already exist*

Self-explanatory.

*Cannot create sites with undefined lattice*

Must use lattice commands first to define a lattice.

*Cannot define Schwoebel barrier without Schwoebel model*

Self-explanatory.

*Cannot open diag style cluster dump file*

Self-explanatory.

*Cannot open diag\_style cluster dump file*

Self-explanatory.

*Cannot open diag\_style cluster output file*

Self-explanatory.

*Cannot open dump file*

Self-explanatory.

*Cannot open file %s*

Self-explanatory.

*Cannot open gzipped file*

Self-explanatory.

*Cannot open input script %s*

Self-explanatory.

*Cannot open log.spparks*

Self-explanatory.

*Cannot open logfile %s*

Self-explanatory.

*Cannot open logfile*

Self-explanatory.

*Cannot open screen file*

The screen file specified as a command-line argument cannot be opened. Check that the directory you are running in allows for files to be created.

*Cannot open universe log file*

For a multi-partition run, the master log file cannot be opened. Check that the directory you are running in allows for files to be created.

*Cannot open universe screen file*

For a multi-partition run, the master screen file cannot be opened. Check that the directory you are running in allows for files to be created.

*Cannot read neighbors unless max neighbors is set*

This is a setting in the header of the sites file.

*Cannot read sites after sites already exist*

Self-explanatory.

*Cannot redefine variable as a different style*

An equal-style variable can be re-defined but only if it was originally an equal-style variable.

*Cannot run application until simulation box is defined*

Self-explanatory.

*Cannot use %s command until sites exist*

This command requires sites exist before using it in an input script.

*Cannot use KMC solver in parallel with no sectors*

Self-explanatory.

*Cannot use color/strict rejection KMC with sectors*

Self-explanatory.

*Cannot use create\_sites basis with random lattice*

Self-explanatory.

*Cannot use diag\_style cluster without a lattice defined*

This diagnostic uses the lattice style to dump OpenDx files.

*Cannot use dump\_one for first snapshot in dump file*

Self-explanatory.

*Cannot use random rejection KMC in parallel with no sectors*

Self-explanatory.

*Cannot use raster rejection KMC in parallel with no sectors*

Self-explanatory.

*Cannot use region INF or EDGE when box does not exist*

Can only define a region with these parameters after a simulation box has been defined.

*Choice of sector stop led to no rKMC events*

Self-explanatory.

*Color stencil is incommensurate with lattice size*

Since coloring induces a pattern of colors, this pattern must fit an integer number of times into a periodic lattice.

*Could not find dump ID in dump\_modify command*

Self-explanatory.

*Could not find dump ID in dump\_one command*

Self-explanatory.

*Could not find dump ID in undump command*

Self-explanatory.

*Create\_box command before app\_style set*

Self-explanatory.

*Create\_box region ID does not exist*

Self-explanatory.

*Create\_box region must be of type inside*

Self-explanatory.

*Create\_sites command before app\_style set*

Self-explanatory.

*Create\_sites command before simulation box is defined*

Self-explanatory.

*Create\_sites region ID does not exist*

Self-explanatory.

*Creating a quantity application does not support*

The application defines what variables it supports. You cannot set a variable with the `create_sites` command for a variable that isn't supported.

*Diag dump\_style does not work if ncluster > 2^31*

Self-explanatory.

*Diag dump\_style incompatible with lattice style*

Not all lattice styles can be output as OpenDx files.

*Diag propensity requires KMC solve be performed*

Only KMC solvers compute a propensity for sites and the system.

*Diag style cluster dump file name too long*

Self-explanatory.

*Diag style incompatible with app style*

The lattice styles of the diagnostic and the on-lattice application must match.

*Diag cluster dvalue in neighboring clusters do not match*

Internal SPPARKS error.

*Diag cluster ivalue in neighboring clusters do not match*

Internal SPPARKS error.

*Diag\_style command before app\_style set*

Self-explanatory.

*Diag\_style diffusion requires app\_style diffusion*

Self-explanatory.

*Did not assign all sites correctly*

One or more sites in the `read_sites` file were not assigned to a processor correctly.

*Did not create correct number of sites*

One or more created sites were not assigned to a processor correctly.

*Dimension command after lattice is defined*

Self-explanatory.

*Dimension command after simulation box is defined*

Self-explanatory.

*Divide by 0 in variable formula*

Self-explanatory.

*Dump ID already exists*

Self-explanatory.

*Dump command before app\_style set*

Self-explanatory.

*Dump command can only be used for spatial applications*

Self-explanatory.

*Dump requires propensity but no KMC solve performed*

Only KMC solvers compute propensity for sites.

*Dump\_modify command before app\_style set*

Self-explanatory.

*Dump\_one command before app\_style set*

Self-explanatory.

*Dumping a quantity application does not support*

The application defines what variables it supports. You cannot output a variable in a dump that isn't supported.

*Failed to allocate %ld bytes for array %s*

Your SPPARKS simulation has run out of memory. You need to run a smaller simulation or on more processors.

*Failed to reallocate %ld bytes for array %s*

Your SPPARKS simulation has run out of memory. You need to run a smaller simulation or on more processors.

*Ghost connection was not found*  
Internal SPPARKS error. Should not occur.

*Ghost site was not found*  
Internal SPPARKS error. Should not occur.

*Illegal ... command*  
Self-explanatory. Check the input script syntax and compare to the documentation for the command. You can use -echo screen as a command-line option when running SPPARKS to see the offending line.

*Incorrect args for pair coefficients*  
Self-explanatory.

*Incorrect lattice neighbor count*  
Internal SPPARKS error.

*Incorrect site format in data file*  
Self-explanatory.

*Incorrect value format in data file*  
Self-explanatory.

*Input line too long after variable substitution*  
This is a hard (very large) limit defined in the input.cpp file.

*Input line too long: %s*  
This is a hard (very large) limit defined in the input.cpp file.

*Invalid command-line argument*  
One or more command-line arguments is invalid. Check the syntax of the command you are using to launch SPPARKS.

*Invalid dump\_modify threshold operator*  
Self-explanatory.

*Invalid event count for app\_style test/group*  
Number of events must be > 0.

*Invalid keyword in dump command*  
Self-explanatory.

*Invalid math function in variable formula*  
The math function is not recognized.

*Invalid number of sectors*  
Self-explanatory.

*Invalid pair style*  
Self-explanatory.

*Invalid probability bounds for app\_style test/group*  
Self-explanatory.

*Invalid probability bounds for solve\_style group*  
Self-explanatory.

*Invalid probability delta for app\_style test/group*  
Self-explanatory.

*Invalid region style*  
Self-explanatory.

*Invalid site ID in Sites section of data file*  
Self-explanatory.

*Invalid syntax in variable formula*  
Self-explanatory.

*Invalid variable evaluation in variable formula*  
A variable used in a formula could not be evaluated.

*Invalid variable in next command*  
Self-explanatory.

*Invalid variable name in variable formula*  
Variable name is not recognized.

*Invalid variable name*

Variable name used in an input script line is invalid.

*Invalid variable style with next command*

Variable styles *equal* and *world* cannot be used in a next command.

*Invalid volume setting*

Volume must be set to value  $> 0$ .

*KMC events are not implemented in app*

Not every application supports KMC solvers.

*Label wasn't found in input script*

Self-explanatory.

*Lattice command before app\_style set*

Self-explanatory.

*Lattice style does not match dimension*

Self-explanatory.

*Log of zero/negative in variable formula*

Self-explanatory.

*Mask logic not implemented in app*

Not every application supports masking.

*Mismatch in counting for dbufclust*

Self-explanatory.

*Must read Sites before Neighbors*

Self-explanatory.

*Must read Sites before Values*

Self-explanatory.

*Must use -in switch with multiple partitions*

A multi-partition simulation cannot read the input script from stdin. The `-in` command-line option must be used to specify a file.

*Must use create\_sites box for on-lattice applications*

Self-explanatory.

*Must use value option before basis option in create\_sites command*

Self-explanatory.

*No reactions defined for chemistry app*

Use the `add_reaction` command to specify one or more reactions.

*No solver class defined*

Self-explanatory.

*Number of sites does not match existing sites*

File being read by `read_sites` command is not consistent with sites already defined.

*One or more sites have invalid values*

The application only allows sites to be initialized with specific values.

*PBC remap of site failed*

Internal SPPARKS error.

*Pair\_coeff command before app\_style set*

Self-explanatory.

*Pair\_coeff command before pair\_style is defined*

Self-explanatory.

*Pair\_style command before app\_style set*

Self-explanatory.

*Power by 0 in variable formula*

Self-explanatory.

*Processor partitions are inconsistent*

The total number of processors in all partitions must match the number of processors LAMMPS is running on.

*Processors command after simulation box is defined*

Self-explanatory.

*Random lattice has no connectivity*

The cutoff distance is likely too short.

*Reaction ID %s already exists*

Cannot re-define a reaction.

*Reaction cannot have more than MAX\_PRODUCT products*

Self-explanatory.

*Reaction has no numeric rate*

Self-explanatory.

*Reaction must have 0,1,2 reactants*

Self-explanatory.

*Read\_sites command before app\_style set*

Self-explanatory.

*Read\_sites simulation box different than current box*

Self-explanatory.

*Region command before app\_style set*

Self-explanatory.

*Region intersect region ID does not exist*

Self-explanatory.

*Region union region ID does not exist*

Self-explanatory.

*Rejection events are not implemented in app*

Self-explanatory.

*Reset\_time command before app\_style set*

Self-explanatory.

*Reuse of region ID*

Self-explanatory.

*Run command before app\_style set*

Self-explanatory.

*Run upto value is before current time*

Self-explanatory.

*Seed command has not been used*

The seed command must be used if another command requires random numbers.

*Set command before sites exist*

Self-explanatory.

*Set command region ID does not exist*

Self-explanatory.

*Set if test on quantity application does not support*

The application defines what variables it supports. You cannot do an if test with the set command on a variable that isn't supported.

*Setting a quantity application does not support*

The application defines what variables it supports. You cannot set a variable with the set command on a variable that isn't supported.

*Simulation box is not multiple of current lattice settings*

This likely occurred because the lattice was re-defined after the simulation box was created.

*Site not in my bin domain*

Internal SPPARKS error.

*Site-site interaction was not found*

Internal SPPARKS error.

*Solve\_style command before app\_style set*

Self-explanatory.

*Species ID %s already exists*

Self-explanatory.

*Species ID %s does not exist*

Self-explanatory.

*Sqrt of negative in variable formula*

Self-explanatory.

*Stats command before app\_style set*

Self-explanatory.

*Substitution for illegal variable*

Self-explanatory.

*Threshold for a quantity application does not support*

The application defines what variables it supports. You cannot do a threshold test with the dump command on a variable that isn't supported.

*Too many neighbors per site*

Internal SPPARKS error.

*Unbalanced quotes in input line*

No matching end double quote was found following a leading double quote.

*Undump command before app\_style set*

Self-explanatory.

*Unexpected end of data file*

Self-explanatory.

*Universe/uloop variable count < # of partitions*

A universe or uloop style variable must specify a number of values  $\geq$  to the number of processor partitions.

*Unknown command: %s*

The command is not known to SPPARKS. Check the input script.

*Unknown identifier in data file: %s*

Self-explanatory.

*Unknown species in reaction command*

Self-explanatory.

*Unrecognized command*

The command is assumed to be application specific, but is not known to SPPARKS. Check the input script.

*Use of region with undefined lattice*

The lattice command must be used before defining a geometric region.

*Variable name must be alphanumeric or underscore characters*

Self-explanatory.

*World variable count doesn't match # of partitions*

A world-style variable must specify a number of values equal to the number of processor partitions.

## **Warnings:**

## add\_reaction command

### Syntax:

```
add_reaction reactant1 reactant2 rate product1 product2 ...
```

- reactant1, reactant2 = 0, 1, or 2 reactant species
- rate = reaction rate (see units below)
- product1, product2 = 0, 1, or more product species

### Examples:

```
add_reaction A B 1.0e10 C
add_reaction 1.0 d
add_reaction b2 1.0e-10 c3 d4 e3
```

### Description:

This command defines a chemical reaction for use in the [app\\_style chemistry](#) application.

Each reaction has 0, 1, or 2 reactants. It also has 0, 1, or more products. The reactants and products are specified by species ID strings, as defined by the [add\\_species](#) command.

The units of the specified rate constant depend on how many reactants participate in the reaction:

- 0 reactants = rate is molarity/sec
- 1 reactant = rate is 1/sec
- 2 reactants = rate is 1/molarity-sec

Thus the first reaction listed above represents an A and B molecule binding to form a complex C at a rate of 1.0e10 per molarity per second. I.e.  $A + B \rightarrow C$ .

### Restrictions:

This command can only be used as part of the [app\\_style chemistry](#) application.

### Related commands:

[app\\_style chemistry](#), [add\\_species](#)

**Default:** none



## add\_species command

### Syntax:

```
add_species name1 name2 ...
```

- name1,name2 = ID strings for different species

### Examples:

```
add_species kinase  
add_species NFkB kinase2 NFkB-IKK
```

### Description:

This command defines the names of one or more chemical species for use in the [app\\_style chemistry](#) application.

Each ID string can be any sequence of non-whitespace characters (alphanumeric, dash, underscore, etc).

### Restrictions:

This command can only be used as part of the [app\\_style chemistry](#) application.

### Related commands:

[app\\_style chemistry](#), [add\\_reaction](#), [count](#)

**Default:** none

## app\_style chemistry command

### Syntax:

```
app_style chemistry
```

- chemistry = application style name

### Examples:

```
app_style chemistry
```

### Description:

This is a general application which evolves a set of coupled chemical reactions stochastically, producing a time trace of species concentrations. Chemical species are treated as counts of individual molecules reacting within a reaction volume in a well-mixed fashion. Individual reactions are chosen via the direct method variant of the Stochastic Simulation Algorithm (SSA) of [\(Gillespie\)](#).

A prototypical example is to use this model to simulate the execution of a protein signaling network in a biological cell.

This application can only be evolved using a kinetic Monte Carlo (KMC) algorithm. You must thus define a KMC solver to be used with the application via the [solve\\_style](#) command

---

The following additional commands are defined by this application:

<a href="#">add_reaction</a>	define a chemical reaction
<a href="#">add_species</a>	define a chemical species
<a href="#">count</a>	specify molecular count of a species
<a href="#">volume</a>	specify volume of the chemical reactor

---

**Restrictions:** none

**Related commands:** none

**Default:** none

---

(Gillepsie) Gillespie, J Chem Phys, 22, 403-434 (1976); Gillespie, J Phys Chem, 81, 2340-2361 (1977).

## app\_style diffusion command

### Syntax:

```
app_style diffusion estyle dstyle args
```

- diffusion = application style name
- estyle = *off* or *linear* or *nonlinear*
- dstyle = *hop* or *schwoebel*

```
hop args = none
schwoebel args = Nmax Nmin
Nmax = max # of neighbors the initial Schwoebel site can have
Nmin = min # of neighbors the final Schwoebel site can have
```

### Examples:

```
app_style diffusion linear hop
app_style diffusion nonlinear schwoebel 5 2
```

### Description:

This is an on-lattice application which performs diffusive hops on a lattice whose sites are partially occupied and partially unoccupied (vacancies). It can be used to model surface diffusion or bulk diffusion on 2d or 3d lattices. It is equivalent to a 2-state Ising model performing Kawasaki dynamics where neighboring sites exchange their spins as the model evolves. Each lattice site stores a value which is 1 for vacant or 2 for occupied or 3 for vacant and a non-deposition site. See the [deposition](#) command for more details on the value = 3 sites.

The *estyle* setting determines how energy is used in computing the probability of hop events, which is related to the Hamiltonian for the system.

The Hamiltonian representing the energy of an occupied site I for the *off* style is 0, which simply means energy is not used in determining the hop probabilities. Instead, see the [barrier](#) command.

The Hamiltonian representing the energy of an occupied site I for the *linear* style is as follows:

$$H_i = \sum_j \delta_{ij}$$

where  $\sum_j$  is a sum over all the neighbor sites of site I and  $\delta_{ij}$  is 0 if site J is occupied and 1 if site J is vacant. The  $H_i$  for a vacant site is 0.

The Hamiltonian representing the energy of an occupied site I for the *nonlinear* style is as follows:

$$H_i = \text{Eng}(\sum_j \delta_{ij})$$

where  $\sum_j$  is the sum over all its neighbor sites and  $\delta_{ij}$  now 1 if site J is occupied and 0 otherwise. Thus the summation computes the coordination number of site I. Note that this definition of  $\delta_{ij}$  is the opposite of how it is defined for estyle *linear*. The function Eng() is a tabulated function with values specified via the [ecoord](#) command. This effectively allows the energy to be a non-linear function of coordination number. As before the  $H_i$  for a vacant site is 0.

For all these *estyle* settings, the energy of the entire system is the sum of  $H_i$  over all sites.

The *dstyle* setting determines what kind of diffusive hops are modeled. For *hop*, only simple nearest-neighbor hops occur where an atom hops to a neighboring vacant site. For *schwoebel*, Schwoebel hops can also occur, which are defined in the following way. An atom I can hop to a 2nd neighbor vacant site K if there are two intermediate 1st neighbor sites J1 and J2, where J1 is vacant and J2 is occupied, and J1 and J2 are neighbors of each other. Additionally the initial site I can have no more than  $N_{max}$  occupied neighbors (its coordination number), and the destination site K can have no fewer than  $N_{min}$  neighbors.

---

The [deposition](#) command can be used with this application to add atoms to the system in competition with hop events.

**IMPORTANT NOTE:** If you have a free surface you are depositing onto, it may also be possible for atoms to diffuse away from this surface, i.e. desorb into a vacuum. This application does not do anything special with those atoms (e.g. remove them), so they may clump together or induce deposition to take place onto the clumps above the surface. If you wish to prevent this you should insure that desorption is an energetically unfavorable event.

The [barrier](#) command can be used with this application to add an energy barrier to the model for nearest-neighbor hop and Schwoebel hop events, as discussed below.

The [ecoord](#) command can be used with the *nonlinear* version of this application to set tabulated values for the Hamiltonian `Eng()` function as described above.

Note that *estyle nonlinear* should give the same answer as *estyle linear* if the tabulated function specified by the [ecoord](#) command is specified as  $E_0 = N$ ,  $E_1 = N-1$ , ...  $E_{N-1} = 1$ ,  $E_N = 0$ , where  $N$  = the number of neighbors of each lattice site, i.e. the maximum coordination number. In this scenario, the energy is effectively a linear function of coordination number.

---

This application performs Kawasaki dynamics, in that the "spins" on two neighboring sites are swapped, where spin can be thought of as a flag representing occupied or vacant. Equivalently, an atom hops from an occupied site to a vacancy site.

As explained on [this page](#), this application can be evolved by either a kinetic Monte Carlo (KMC) or rejection KMC (rKMC) algorithm. You must thus define a KMC solver or sweeping method to be used with the application via the [solve\\_style](#) or [sweep](#) commands. The *linear* *estyle* supports both KMC and rKMC options. The other *estyles* only support KMC options. If the [deposition](#) command is used, then only KMC options are supported.

For solution by a KMC algorithm, the possible events an occupied site can perform are swaps with vacant neighbor sites. The probability of each such event depends on several variables: the *estyle* setting, whether the [barrier](#) command is used, whether the hop is downhill or uphill in energy, and whether the [temperature](#) is 0.0 or finite. The following table gives the hop probability for each possible combination of these variables.

Energy	Barrier	Direction	Temperature	Probability
no	no	N/A	either	1
no	yes	N/A	0.0	0
no	yes	N/A	finite	$\exp(-Q/kT)$
yes	no	down	either	1
yes	no	up	0.0	0
yes	no	up	finite	$\exp(-dE/kT)$
yes	yes	down	0.0	0
yes	yes	down	finite	$\exp(-Q/kT)$
yes	yes	up	0.0	0

yes	yes	up	finite	$\exp((-dE-Q)/kT)$
-----	-----	----	--------	--------------------

If *estyle* is set to *off*, then energy is "no" in the table. Any other *estyle* setting is energy = "yes". Barrier is "no" in the table if the "barrier" command is not used, else it is "yes" in the table. The direction of energy change (downhill versus uphill) is only relevant if energy is "yes", else it is N/A. The "either" entry for temperature means 0.0 or finite.

The value  $dE = E_{\text{final}} - E_{\text{initial}}$  refers to the energy change in the system due to the hop. For *estyle linear* this can be computed from just the sites I,J. For *estyle nonlinear* the energy of the neighbors of both sites I,J must also be computed.

For solution by a Metropolis algorithm, the hop event is performed or not if the probability in the table is 1 or 0. For intermediate values, a uniform random number R between 0 and 1 is generated and the hop event is accepted if  $R < \text{probability}$  in the table.

---

The following additional commands are defined by this application. The *ecoord* command can only be used with the *nonlinear* energy style.

<a href="#">barrier</a>	define energy barriers for hop events
<a href="#">deposition</a>	define deposition events
<a href="#">ecoord</a>	specify site energy as a function of coordination number
<a href="#">temperature</a>	set Monte Carlo temperature

---

**Restrictions:** none

**Related commands:**

[app\\_style ising](#)

**Default:** none

## app\_style erbium command

### Syntax:

```
app_style erbium
```

- erbium = style name of this application

### Examples:

```
app_style erbium
```

### Description:

This application simulates a model of reaction and diffusion on a specialized Erbium lattice, which consists of an fcc lattice for the Erbium and additional tetrahedral and octahedral interstitial sites.

This application stores 2 integers per lattice site. The first integer (i1) is the "type" of the site:

- type = 1 = fcc
- type = 2 = octahedral
- type = 3 = tetrahedral

The second integer (i2) is the element on the site:

- element = 1 = erbium
- element = 2 = hydrogen
- element = 3 = helium
- element = 4 = vacancy

The 3-fold lattice should be created using the [lattice fcc/octa/tetra](#) command, which gives details of its geometry and neighbor connectivity.

The 3-fold lattice should normally be initialized in the following way, using the [set](#) command. All fcc sites are for erbium atoms and are fully occupied. All octahedral sites are initially vacant. A fraction of the tetrahedral sites is initialized with hydrogen atoms; the remainder are vacant.

The [event](#) command is used to define what kinds of diffusive hops and reaction events occur in the model. These can include correlated hops where a central site coordinates a change at two of its neighbor sites. Reaction events that transmute a Hydrogen atom to a Helium are also possible.

As explained on [this page](#), this application can be evolved only by a kinetic Monte Carlo (KMC). You must thus define a KMC solver to be used with the application via the [solve\\_style](#) command.

For solution by a KMC algorithm, the list of events that can occur at each site is determined by its current neighbors and by the events specified via the [event](#) command. The relative probability of each event occurring is computed as a function of the rate or energy value specified in the [event](#) command and the temperature specified via the [temperature](#) command. The details are explained in the doc page for the [event](#) command.

---

The following additional commands are defined by this application.

<a href="#">event</a>	definition of an event on the 3-fold lattice
<a href="#">temperature</a>	set Monte Carlo temperature

---

**Restrictions:** none

**Related commands:**

[diag\\_style erbium](#)

**Default:** none

## app\_style ising command

### app\_style ising/single command

#### Syntax:

```
app_style style
```

- style = *ising* or *ising/single*

#### Examples:

```
app_style ising
app_style ising/single
```

#### Description:

These are on-lattice applications which evolve a 2-state Ising model, where each lattice site has a spin of 1 or 2. Sites flip their spin as the model evolves.

The Hamiltonian representing the energy of site I is as follows:

$$H_i = \sum_j \delta_{ij}$$

where  $\sum_j$  is a sum over all the neighbor sites of site I and  $\delta_{ij}$  is 0 if the spin of sites I and J are the same and 1 if they are different. The energy of the entire system is the sum of  $H_i$  over all sites.

This application performs Glauber dynamics, meaning the spin is flipped on a single site. See [app\\_style diffusion](#) for an Ising model which performs Kawasaki dynamics, meaning the spins on two neighboring sites are swapped.

As explained on [this page](#), this application can be evolved by either a kinetic Monte Carlo (KMC) or rejection KMC (rKMC) algorithm. You must thus define a KMC solver or sweeping method to be used with the application via the [solve\\_style](#) or [sweep](#) commands.

For solution by a KMC algorithm, a site event is a spin flip and its probability is  $\min[1, \exp(-dE/kT)]$ , where  $dE = E_{\text{final}} - E_{\text{initial}}$  using the Hamiltonian defined above for the energy of the site, and T is the temperature of the system defined by the [temperature](#) command (which includes the Boltzmann constant k implicitly).

For solution by a rKMC algorithm, the *ising* and *ising/single* styles use a different rejection-based algorithm. For the *ising* style, the spin is set randomly to 1 or 2. For the *ising/single* style, the spin is flipped to its opposite value. In either case,  $dE = E_{\text{final}} - E_{\text{initial}}$  is calculated, as is a uniform random number R between 0 and 1. The new state is accepted if  $R < \min[1, \exp(-dE/kT)]$ .

---

The following additional commands are defined by this application:

<a href="#">temperature</a>	set Monte Carlo temperature
-----------------------------	-----------------------------

---

**Restrictions:** none

**Related commands:**



app\_style potts

**Default:** none

## app\_style membrane command

### Syntax:

```
app_style membrane w01 w11 mu
```

- membrane = style name of this application
- w01 = sovent-protein interaction energy (typically 1.25)
- w11 = sovent-solvent interaction energy (typically 1.0)
- mu = chemical potential to insert a solvent (typically -2.0)

### Examples:

```
app_style membrane 1.25 1.0 -3.0
```

### Description:

This is an on-lattice application which evolves a membrane model, where each lattice site is in one of 3 states: lipid, water, or protein. Sites flip their state as the model evolves. See the paper of ([Sarkisov](#)) for a description of the model and its applications to porous media. Here it is used to model the state of a lipid membrane around embedded proteins, such as one enclosing a biological cell.

In the model, protein sites are defined by the [inclusion](#) command and never change. The remaining sites are initially lipid and can flip between solvent and lipid as the model evolves. Typically, water will coat the surface of the proteins and create a pore in between multiple proteins if they are close enough together.

The Hamiltonian represeting the energy of site I is as follows:

$$H = - \mu x_i - \text{Sum}_j (w11 a_{ij} + w01 b_{ij})$$

where  $\text{Sum}_j$  is a sum over all the neighbor sites of site I,  $x_i = 1$  if site I is solvent and 0 otherwise,  $a_{ij} = 1$  if both the I,J sites are solvent and 0 otherwise,  $b_{ij} = 1$  if one of the I,J sites is solvent and the other is protein and 0 otherwise. Mu and w11 and w01 are user inputs. As discussed in the paper, this is essentially a lattice gas grand-canonical Monte Carlo model, which is isomorphic to an Ising model. The mu term is a penalty for inserting solvent which prevents the system from becoming all solvent, which the 2nd term would prefer.

As explained on [this page](#), this application can be evolved by either a kinetic Monte Carlo (KMC) or rejection KMC (rKMC) algorithm. You must thus define a KMC solver or sweeping method to be used with the application via the [solve\\_style](#) or [sweep](#) commands.

For solution by a KMC algorithm, a site event is a spin flip from a lipid to fluid state or vice versa. The probability of the event is  $\min[1, \exp(-dE/kT)]$ , where  $dE = E_{\text{final}} - E_{\text{initial}}$  using the Hamiltonian defined above for the energy of the site, and T is the temperature of the system defined by the [temperature](#) command (which includes the Boltzmann constant k implicitly).

For solution by a Metropolis algorithm, the site is set randomly to fluid or lipid, unless it is a protein site in which case it is skipped altogether. The energy change  $dE = E_{\text{final}} - E_{\text{initial}}$  is calculated, as is a uniform random number R between 0 and 1. The new state is accepted if  $R < \min[1, \exp(-dE/kT)]$ , else it is rejected.

---

The following additional commands are defined by these applications:

<a href="#">inclusion</a>	specify which sites are proteins
<a href="#">temperature</a>	set Monte Carlo temperature

---

**Restrictions:** none

**Related commands:** none

**Default:** none

---

**(Sarkisov)** Sarkisov and Monson, Phys Rev E, 65, 011202 (2001).

## app\_style potts command

## app\_style potts/neigh command

## app\_style potts/neighborly command

### Syntax:

```
app_style style Q
```

- style = *potts* or *potts/neigh* or *potts/neighborly*
- Q = number of spin states

### Examples:

```
app_style potts 100
app_style potts/neigh 20
```

### Description:

These are on-lattice applications which evolve a Q-state Ising model or Potts model, where each lattice site has a spin value from 1 to Q. Sites flip their spin as the model evolves.

The Hamiltonian representing the energy of site I is as follows:

$$H_i = \sum_j \delta_{ij}$$

where  $\sum_j$  is a sum over all the neighbor sites of site I and  $\delta_{ij}$  is 0 if the spin of sites I and J are the same and 1 if they are different. The energy of the entire system is the sum of  $H_i$  over all sites.

These applications perform Glauber dynamics, meaning the spin is flipped on a single site. See [app\\_style diffusion](#) for an Ising model which performs Kawasaki dynamics, meaning the spins on two neighboring sites are swapped.

As explained on [this page](#), these applications can be evolved by either a kinetic Monte Carlo (KMC) or rejection KMC (rKMC) algorithm. You must thus define a KMC solver or sweeping method to be used with the application via the [solve\\_style](#) or [sweep](#) commands.

For solution by a KMC algorithm, a site event is a spin flip and its probability is  $\min[1, \exp(-dE/kT)]$ , where  $dE = E_{\text{final}} - E_{\text{initial}}$  using the Hamiltonian defined above for the energy of the site, and T is the temperature of the system defined by the [temperature](#) command (which includes the Boltzmann constant k implicitly). The KMC algorithm does not allow spin flips known as "wild" flips, even at finite temperature. These are flips to values that are not equal to any neighbor site value.

For solution by a rKMC algorithm, the various styles use different rejection-based algorithms. For the *potts* style, a random spin from 1 to Q is chosen. For the *potts/neigh* style, a spin is chosen randomly from the values held by neighbor sites and a null-bin of a size which extends the possible events up to the maximum number of neighbors. For example, imagine a site has 12 neighbors and the 12 sites have 4 different spin values. Then each of the 4 neighbor spin values will be chosen with 1/12 probability and the null bin will be chosen with 8/12 probability. For the *potts/neighborly* style, the null bin is discarded, so in this case each of the 4 spin values will be chosen with

1/4 probability. In all the cases,  $dE = E_{\text{final}} - E_{\text{initial}}$  is calculated, as is a uniform random number  $R$  between 0 and 1. The new state is accepted if  $R < \min[1, \exp(-dE/kT)]$ , else it is rejected.

The rKMC algorithm for the *potts* style does allow spin flips known as "wild" flips. These are flips to values that are not equal to any neighbor site value. At temperature 0.0 these are effectively disallowed, since they will increase the energy of the system (except in the uninteresting case when the site already has a spin value not equal to any neighbor values), but at finite temperature they will have a non-zero probability of occurring.

---

The following additional commands are defined by these applications:

<a href="#">temperature</a>	set Monte Carlo temperature
-----------------------------	-----------------------------

---

**Restrictions:** none

**Related commands:**

[app\\_style ising](#)

**Default:** none

## app\_style potts/pin command

### Syntax:

```
app_style potts/pin Q
```

- potts/pin = application style name
- Q = number of spin states

### Examples:

```
app_style potts/pin 100
```

### Description:

This is an on-lattice application which evolves a Q-state Potts model in the presence of pinning sites, which are sites tagged with a spin value of Q+1 which do not change. Their effect is typically to pin or inhibit grain growth in various ways.

The Hamiltonian representing the energy of site I is as follows:

$$H_i = \sum_j \delta_{ij}$$

where  $\sum_j$  is a sum over all the neighbor sites of site I and  $\delta_{ij}$  is 0 if the spin of sites I and J are the same and 1 if they are different. The energy of the entire system is the sum of  $H_i$  over all sites.

This application performs Glauber dynamics, meaning the spin is flipped on a single site. See [app\\_style diffusion](#) for an Ising model which performs Kawasaki dynamics, meaning the spins on two neighboring sites are swapped.

As explained on [this page](#), this application can be evolved by either a kinetic Monte Carlo (KMC) or rejection KMC (rKMC) algorithm. You must thus define a KMC solver or sweeping method to be used with the application via the [solve\\_style](#) or [sweep](#) commands.

For solution by a KMC algorithm, a site event is a spin flip and its probability is  $\min[1, \exp(-dE/kT)]$ , where  $dE = E_{\text{final}} - E_{\text{initial}}$  using the Hamiltonian defined above for the energy of the site, and T is the temperature of the system defined by the [temperature](#) command (which includes the Boltzmann constant k implicitly). The KMC algorithm does not allow spin flips known as "wild" flips, even at finite temperature. These are flips to values that are not equal to any neighbor site value. The KMC algorithm also does not allow spin flips to a pinned site value.

For solution by a rKMC algorithm, a random spin from 1 to Q is chosen. Note that this does not allow a spin flip to a pinned site value, since those sites are set to Q+1. When the flip is attempted  $dE = E_{\text{final}} - E_{\text{initial}}$  is calculated, as is a uniform random number R between 0 and 1. The new state is accepted if  $R < \min[1, \exp(-dE/kT)]$ , else it is rejected.

---

The following additional commands are defined by this application:

<a href="#">pin</a>	create a set of pinned sites
<a href="#">temperature</a>	set Monte Carlo temperature

---

**Restrictions:** none

**Related commands:**

[app\\_style](#) [potts](#)

**Default:** none

## app\_style potts/strain command

### Syntax:

```
app_style potts/strain Q
```

- potts/strain = application style name
- Q = number of spin states

### Examples:

```
app_style potts/strain 100
```

### Description:

This is an on-lattice application which evolve a Q-state Potts model with a per-site strain, where each lattice site has a spin value from 1 to Q. Sites flip their spin as the model evolves. The strain energy can influence the grain growth.

The Hamiltonian representing the energy of site I is the same as for the Potts model:

$$H_i = \sum_j \delta_{ij}$$

where  $\sum_j$  is a sum over all the neighbor sites of site I and  $\delta_{ij}$  is 0 if the spin of sites I and J are the same and 1 if they are different. The energy of the entire system is the sum of  $H_i$  over all sites.

The per-site strain influences spin flips through altering the effective temperature as discussed below.

This applications perform Glauber dynamics, meaning the spin is flipped on a single site. See [app\\_style diffusion](#) for an Ising model which performs Kawasaki dynamics, meaning the spins on two neighboring sites are swapped.

As explained on [this page](#), this application is evolved by a kinetic Monte Carlo (KMC) algorithm. You must thus define a KMC solver to be used with the application via the [solve\\_style](#) command.

For solution by a KMC algorithm, a site event is a spin flip and its probability is  $1/(1+\text{strain})$  when  $dE \leq 0$  and  $\exp(-dE/kT^*)$  when  $dE > 0$  and the temperature T is finite, where  $dE = E_{\text{final}} - E_{\text{initial}}$  using the Hamiltonian defined above for the energy of the site, T is the temperature of the system defined by the [temperature](#) command (which includes the Boltzmann constant k implicitly), and  $T^* = T (1 + \text{strain})$ . Thus the effect of the strain, defined for each site, is to rescale the temperature.

The KMC algorithm does not allow spin flips known as "wild" flips, even at finite temperature. These are flips to values that are not equal to any neighbor site value.

Strain values are stored for each site as a "double" value. This means they can be assigned to each site using the "d1" keyword with the [set](#) command, or read in via the [read\\_sites](#) command.

The application does not change the strain assigned to each site as the simulation progresses. But if SPPARKS is built and used as a library, as discussed in [this section](#) of the manual, the driver program can alter the per-site settings. The "couple" directory of the [LAMMPS molecular dynamics package](#) includes a sample coupled LAMMPS/SPPARKS application which uses LAMMPS to compute strain values at each site of a snapshot of



grain structure produced by this application running in SPPARKS. The strains are passed back to SPPARKS periodically by the driver application so that more Monte Carlo dynamics can be performed.

---

The following additional command is defined by this application:

<a href="#">temperature</a>	set Monte Carlo temperature
-----------------------------	-----------------------------

---

**Restrictions:** none

**Related commands:**

[app\\_style](#) potts

**Default:** none

## app\_style relax command

### Syntax:

```
app_style relax delta
```

- relax = style name of this application
- delta = maximum displacement distance of a particle (distance units)

### Examples:

```
app_style relax 0.5
```

### Description:

This is an off-lattice application which treats sites as particles which interact through a pair potential and whose collective energy is relaxed via Metropolis Monte Carlo translational moves.

The energy of a particle I is as follows:

$$E_i = \sum_j \phi(R_{ij})$$

where  $\sum_j$  is a sum over all the neighbor of particle I within some cutoff distance,  $\phi()$  is the potential energy function defined by the [pair\\_style](#) command, and  $R_{ij}$  is the distance between particles I and J. The energy of the entire system is the sum of  $E_i$  over all particles. The [pair\\_style](#) command also defines the cutoff distance.

As explained on [this page](#), this application is evolved by a Metropolis Monte Carlo (MMC) algorithm. You must thus define a sweeping method to be used with the application via the [sweep](#) command.

For solution by the MMC algorithm, once a particle is chosen, a translational move of the particle is made, by choosing a random location within a sphere of radius *delta* surrounding the particle. The energy of the particle before and after the move is calculated, to give  $dE = E_{\text{final}} - E_{\text{initial}}$ . The move is accepted if  $R < \min[1, \exp(-dE/kT)]$ , else it is rejected, where R is a uniform random number R between 0 and 1.

---

The following additional commands are defined by this application:

<a href="#">temperature</a>	set Monte Carlo temperature
-----------------------------	-----------------------------

---

**Restrictions:** none

**Related commands:**

**Default:** none

## app\_style sos command

### Syntax:

```
app_style sos bond_energy keyword args
```

- sos = application style name
- bond\_energy = lateral bond energy between columns
- zero or more keyword/value pairs may be appended
- keyword = *xsin*

```
xsin args = amp Lx Lz
  amp = amplitude of initial sine wave
  Lx  = wavelength of initial sine wave in x direction
  Lz  = wavelength pf initial sine wave in z direction (ignored if > 1.0e10)
```

### Examples:

```
app_style sos 1.0 xsin 5.5 20.0 1.0e+20
app_style sos 2.0 none
```

### Description:

The SOS (Solid-on-Solid) model is an on-lattice application that models a solid surface as a 1D or 2D lattice of sites. At each site an integer value represents the height of the surface at that site, so that collectively the heights of all the sites represent a surface profile with no overhangs or vacancies.

The Hamiltonian representing the energy of a site *I* is:

$$H_i = 1/2 \sum_j |h_i - h_j|$$

where *J* is the bond energy, specified through the *bond\_energy* parameter, and *h<sub>i</sub>* and *h<sub>j</sub>* are the heights at sites *I* and *J*.  $\sum_j$  represents a sum over the nearest neighbors of *i*, e.g. the neighbors to the immediate left and right for a 1D lattice.

If the *xsin* keyword is used, an initial height profile is assigned by a sine function. If the *z* dependence is inactive (*Lz* > 1.0e10), this is

$$h_i = \text{round}(\text{amp} \cdot \sin(2\pi x / L_x))$$

If the *z* dependence is active, this is instead:

$$h_i = \text{round}(\text{amp} * \min(\sin(2\pi x / L_x), \sin(2\pi z / L_z)))$$

---

This application performs Kawasaki dynamics, in which each event involves an "atom" hopping from one site to a neighboring site. That is, an event consists of site *I* losing one unit of height, and either site *I*+1 or *I*-1 simultaneously gaining one unit of height.

This application does not allow for use of a rejection KMC (rKMC) algorithm; only KMC options are supported. See [this page](#) for more information. For solution by a KMC algorithm, the probability of each "atom hop" event is  $\min[P_0, P_0 \cdot \exp(-dE/kT)]$ , where *P*<sub>0</sub> is a scaling factor, *dE* = *E*<sub>final</sub> - *E*<sub>initial</sub> using the Hamiltonian defined above for the energy of the site, and *T* is the temperature of the system defined by the [temperature](#) command (which

includes the Boltzmann constant  $k$  implicitly). The scaling factor  $P_0$  is given by  $1/nn$  where  $nn$  is the number of nearest neighbors for each site.

---

The following additional commands are defined by this application:

<a href="#">temperature</a>	set Monte Carlo temperature
-----------------------------	-----------------------------

---

**Restrictions:** none

**Related commands:**

[app\\_style diffusion](#)

## app\_style command

### Syntax:

```
app_style style args
```

- `style` = one of a list of possible style names (see below)
- `args` = arguments specific to an application, see application doc page for details

### Examples:

```
app_style diffusion ...
app_style ising ...
app_style potts ...
app_style relax ...
app_style chemistry ...
app_style test/group ...
```

### Description:

This command defines what model or application SPPARKS will run. There are 3 kinds of applications: on-lattice, off-lattice, and general.

On-lattice applications define a set of static sites in space on which events occur. The sites can represent a crystalline lattice, or be more disordered. The key point is that they are immobile and that each site's neighborhood of nearby sites can be specified. Here is the list of on-lattice applications SPPARKS currently includes:

- [diffusion](#) = vacancy exchange diffusion model
- [erbium](#) = H/He diffusion/reaction on an Erbium lattice
- [ising](#) = Ising model
- [ising/single](#) = variant Ising model
- [membrane](#) = membrane model of lipid, water, protein
- [potts](#) = Potts model for grain growth
- [potts/neighbor](#) = variant Potts model
- [potts/neighboronly](#) = variant Potts model
- [potts/pin](#) = Potts model with pinning sites
- [potts/strain](#) = Potts model with per-site strain

Off-lattice applications define a set of mobile sites in space on which events occur. The sites typically represent particles. Each site's neighborhood of nearby sites is defined by a cutoff distance. Here is the list of off-lattice applications SPPARKS currently includes.

- [relax](#) = Metropolis Monte Carlo relaxation

General applications require no spatial information. Events are defined by the application, as well as the influence of each event on others. Here is the list of general applications SPPARKS currently includes.

- [chemistry](#) = biochemical reaction networks
- [test/group](#) = artificial chemical networks that test [solve\\_style](#)

The general applications in SPPARKS can only be evolved via a kinetic Monte Carlo (KMC) solver, specified by the `solve_style` command. On-lattice and off-lattice applications can be evolved by either a KMC solver or a rejection kinetic Monte Carlo (rKMC) method or a Metropolis (MMC) method. The rKMC and MMC methods are specified by the `sweep` command. Not all on- and off-lattice applications support each option.

KMC models are sometimes called rejection-free KMC or the N-fold way or the Gillespie algorithm in the MC literature. The application defines a list of "events" and associated rates for each event. The solver chooses the next event, and the application updates the system accordingly. This includes updating of the time, which is done accurately since rates are defined for each event. For general applications the definition of an "event" is arbitrary. For on-lattice application zero or more possible events are typically defined for each site.

rKMC models are sometimes called null-event KMC or null-event MC. Sites are chosen via some method (see the `sweep` command), and an event on that site is then selected which is accepted or rejected. Again, the application defines the "events" for each site and associated rates which influence the acceptance or rejection. It also defines the null event which is essentially part of the rejection probability.

For KMC and rKMC models, a time is associated with each event (including the null event) by rates that the user defines. Thus event selection induces a time-accurate simulation. The MMC method is similar to the rKMC method, except that it is not time-accurate. It selects an event to perform and accepts or rejects it, typically based on an energy change in the system. There is no rate associated with the event, and no requirement that events be chosen with relative probabilities corresponding to their rates. The Metropolis method tends to evolve the system towards a low energy state. As with the rKMC method, the `sweep` command is used to determine how sites are selected.

For all three methods (KMC, rKMC, MMC) the rules for how events are defined and are accepted or rejected are discussed in the doc pages for the individual applications.

This table lists the different kinds of solvers and sweeping options that can be used for on- and off-lattice applications in SPPARKS. Serial and parallel refer to running on one or many processors. Sector vs no-sector is what is set by the `sector` command. The rKMC options are set by the `sweep` command. The MMC options are the same as for rKMC.

method	serial/no-sectors	serial/sectors	parallel/no-sectors	parallel/sectors
exact KMC	yes	yes	no	yes
rKMC random	yes	yes	no	yes
rKMC raster	yes	yes	no	yes
rKMC color	yes	yes	yes	yes
rKMC color/strict	yes	no	yes	no

Note that masking can also be turned on for rKMC algorithms via the `sweep` command if the application supports it. Off-lattice applications do not support the *color* or *masking* options.

**Restrictions:** none

**Related commands:** none

**Default:** none

## app\_style test/group command

### Syntax:

```
app_style test/group N Nmax pmax pmin delta keyword value
```

- test/group = application style name
- N = # of events to choose from
- Mmax = max number of dependencies for each event
- pmax = max probability
- pmin = min probability
- delta = percentage adjustment factor for dependent probabilities
- zero or more keyword/value pairs may be appended
- keyword = *lomem*

*lomem* value = *yes* or *no*

### Examples:

```
app_style test/group 10000 30 1.0 1.0e-6 5
app_style test/group 10000 30 1.0 1.0e-9 10 lomem yes
```

### Description:

This is a general application which creates and evolves an artificial network of coupled events to test the performance and scalability of various kinetic Monte Carlo [solvers](#). See the paper by [\(Slepoy\)](#) for additional details on how it has been used.

The set of coupled events can be thought of as a reaction network with N different chemical rate equations or events to choose from. Each equation is coupled to M randomly chosen other equations, where M is a uniform random number from 1 to Mmax. In a chemical reaction sense it is as if an executed reaction creates M product molecules, each of which is a reactant in another reaction, affecting its probability of occurrence.

Initially, the maximum and minimum probability for each event is an exponentially distributed random value between *pmax* and *pmin*. If [solve\\_style group](#) is used, these values should be the same as the *pmax* and *pmin* used as parameters in that command. Pmin must be greater than 0.0.

As events are executed, the artificial network updates the probabilities of dependent reactions directly by adjusting their probability by a uniform random number between -delta and +delta. Since delta is specified as a percentatge, this means  $pold * (1 - \delta/100) \leq pnew \leq pold * (1 + \delta/100)$ . Delta must be less than 100.

If the *lomem* keyword is set to *no*, then the random connectivity of the network is generated beforehand and stored. This is faster when events are executed but limits the size of problem that will fit in memory. If *lomem* is set to *yes*, then the connectivity is generated on the fly, as each event is executed.

This application can only be evolved using a kinetic Monte Carlo (KMC) algorithm. You must thus define a KMC solver to be used with the application via the [solve\\_style](#) command

When the [run](#) command is used with this application it sets the number of events to perform, not the time for the run. E.g.

run 10000

means to perform 10000 events, not to run for 10000 seconds.

---

No additional commands are defined by this application.

---

**Restrictions:** none

**Related commands:**

[solve\\_style group](#)

**Default:**

The default value is lomem = no.

---

**(Slepoy)** Slepoy, Thompson, Plimpton, J Chem Phys, 128, 205101 (2008).



## barrier command

### Syntax:

```
barrier dstyle Q
barrier dstyle delta Q
barrier dstyle I J Q
```

- *dstyle* = *hop* or *schwoebel*
- *Q* = barrier height (energy units)
- *delta* = difference in coordination number of 2 participating sites
- *I,J* = coordination numbers of 2 participating sites

### Examples:

```
barrier hop 0.25
barrier schwoebel 1 0.3
barrier hop -1 0.35
barrier hop 3 4 0.2
barrier schwoebel * * 0.1
barrier hop 2*5 3* 0.1
```

### Description:

This command sets the energy barrier for a diffusive hop of an atom from an occupied site to a nearby vacant site. See the [app\\_style diffusion](#) command for how the barrier is used in conjunction with the energy change of the system due to the hop to calculate a probability for the hop to occur.

Barriers can be assigned to two kinds of diffusive hops. The first is a hop to a nearest-neighbor vacancy, which is specified by setting *dstyle* to *hop*. The second is a Schwoebel hop to a 2nd nearest-neighbor vacancy, which is specified by setting *dstyle* to *schwoebel*. The latter is only allowed if the [app\\_style diffusion](#) command also used *schwoebel* for its *dstyle* setting.

Barriers are assigned based on two coordination numbers, for the initial site of the hopping atom and its final site. In both cases the coordination count does not include the hopping atom itself. Thus typically  $(N_{\max}+1)*(N_{\max}+1)$  values should be specified by using this command one or more times, which can be thought of as an (I,J) matrix entries where both I and J vary from 0 to  $N_{\max}$  inclusive, when  $N_{\max}$  is the number of neighbor sites for each lattice site. There is one such matrix for nearest-neighbor diffusive hops and one for Schwoebel hops. Also note that it is permissible to have  $Q_{ij} \neq Q_{ji}$  to set forward/reverse rates, particularly if the model does not use energies, but only barriers.

If only one argument *Q* is specified, then all matrix values are set to *Q*. If the *Q* value = 0.0, this effectively turns off barriers in the model.

If two arguments *delta* and *Q* are specified, then all matrix elements where  $\delta = J - I$  are set to *Q*.

If three arguments *I* and *J* and *Q* are specified, then the (I,J) element is set to *Q*. In this case, the I,J indices can each be specified in one of two ways. An explicit numeric value can be used, as in the 4th example above. Or a wild-card asterisk can be used to set the energy value for multiple coordination numbers. This takes the form "\*" or "\*n" or "n\*" or "m\*n". If  $N_{\max}$  = the number of neighbor sites, then an asterisk with no numeric values means all coordination numbers from 0 to  $N_{\max}$ . A leading asterisk means all coordination numbers from 0 to *n* (inclusive). A trailing asterisk means all coordination numbers from *n* to  $N_{\max}$  (inclusive). A middle asterisk

means all coordination numbers from  $m$  to  $n$  (inclusive).

The  $Q$  value should be in the energy units defined by the application's Hamiltonian and should be consistent with the units used in any [temperature](#) command.

**Restrictions:**

This command can only be used as part of the [app\\_style diffusion](#) application.

**Related commands:**

[deposition](#), [ecoord](#)

**Default:**

Energy barriers for all hop events are set to 0, which is effectively no barriers.

## boundary command

### Syntax:

```
dimension x y z
```

- $x, y, z = p$  or  $n$  in each dimension

$p$  is periodic  
 $n$  is non-periodic

### Examples:

```
boundary p p n
```

### Description:

Set the style of boundaries for the global simulation box in each dimension. The size of the simulation box is set by the [create\\_box](#) or [read\\_sites](#) commands.

The style  $p$  means the box is periodic in that dimension, so that sites can interact across the boundary.

The styles  $n$  means the box is non-periodic in that dimension, so that sites do not interact across the boundary.

Note that the interaction of a pair of neighboring sites is really controlled by each of their neighbor lists which are setup by either the [create\\_sites](#) or [read sites](#) commands. It is possible to have a periodic system with sites that do not interact across the periodic boundary, because of the way the neighbor lists of sites near the boundary are setup. See the [create\\_sites](#) or [read sites](#) for details.

IMPORTANT NOTE: The boundary command does not yet work with off-lattice applications.

### Restrictions:

This command must be used before the simulation box is defined by a [read\\_sites](#) or [create\\_box](#) command.

A 2d simulation must be periodic in the  $z$  dimension. A 1d simulation must be periodic in the  $y$  and  $z$  dimensions.

### Related commands:

[dimension](#)

### Default:

```
boundary p p p
```

## clear command

### Syntax:

```
clear
```

### Examples:

```
(commands for 1st simulation)
clear
(commands for 2nd simulation)
```

### Description:

This command deletes all data, restores all settings to their default values, and frees all memory allocated by SPPARKS. Once a clear command has been executed, it is as if SPPARKS were starting over, with only the exceptions noted below. This command enables multiple jobs to be run sequentially from one input script.

These settings are not affected by a clear command: the working directory ([shell](#) command), log file status ([log](#) command), echo status ([echo](#) command), and input script variables ([variable](#) command).

**Restrictions:** none

**Related commands:** none

**Default:** none

## count command

### Syntax:

```
count species N
```

- species = ID of chemical species
- N = count of molecules of this species

### Examples:

```
count kinase 10000  
count NFkB-IKK 300
```

### Description:

This command sets the molecular count of a chemical species for use in the [app\\_style chemistry](#) application.

The species ID can be any string defined by the [add\\_species](#) command.

### Restrictions:

This command can only be used as part of the [app\\_style chemistry](#) application.

### Related commands:

[app\\_style chemistry](#), [add\\_species](#), [add\\_reaction](#)

### Default:

The count of a defined species is 0 unless set via this command.

## create\_box command

### Syntax:

```
create_box region-ID
```

- region-ID = ID of region to use as simulation domain

### Examples:

```
create_box mybox
```

### Description:

This command creates a simulation box based on the specified region for on-lattice and off-lattice spatial simulations. Thus a [region](#) command must first be used to define a geometric domain. SPPARKS encloses the region (block, sphere, etc) with an axis-aligned (orthogonal) box which becomes the simulation domain.

The [read\\_sites](#) command can also be used to define a simulation box.

### Restrictions:

The [app\\_style](#) command must be used to define an application before using the `create_box` command.

### Related commands:

[create\\_sites](#), [region](#), [read\\_sites](#)

**Default:** none

## create\_sites command

### Syntax:

```
create_sites style arg keyword values ...
```

- style = *box* or *region*

```
box arg = none
region arg = region-ID
region-ID = sites will only be created if contained in the region
```

- zero or more keyword/value pairs may be appended
- keyword = *value* or *basis*

```
value values = label nvalue
label = site or iN or dN
nvalue = specific value to set all created sites to
basis values = M nvalue
M = which basis site (see asterisk form below)
nvalue = specific value to set all created basis sites to
```

### Examples:

```
create_sites box
create_sites region surf value site 1
create_sites box value i2 0 basis 1 1 basis 2* 2
```

### Description:

This command creates "sites" on a lattice for on-lattice and off-lattice applications. For on-lattice applications it also defines a connectivity between sites that is stored as a neighbor list of nearby sites that each site interacts with.

This command is an alternative to reading in site coordinates and neighbor connectivity via the [read\\_sites](#) command.

To use this command, a simulation box must already exist, created via the [create\\_box](#) command. Likewise a lattice must also be defined using the [lattice](#) command.

In SPPARKS, a "site" is a point in space at which an application, as defined by the [app\\_style](#) command, can perform events. For on-lattice applications, the site is static and has a static set of neighboring sites with which it interacts. For off-lattice applications, a site is like a particle. It moves and has a dynamic neighborhood of nearby particles with which it interacts.

This command generates the set of lattice points that fall within the simulation box. For any periodic dimension, as specified by the [boundary](#) command, the simulation box size must be an integer multiple of the lattice constant, to insure consistent placement of sites near periodic boundaries. SPPARKS is careful to put exactly one site at a periodic boundary (on either side of the box), not zero or two. For non-periodic dimensions, no checking near boundaries is done; if the point is inside or on the boundary, it is a site. The one exception is that points that lie exactly on the upper boundary (in a non-periodic dimension) are considered to be outside the box. Thus in non-periodic dimensions you may need to tweak the simulation box size to get precisely the sites you want.

For the *box* style, all lattice points that fall inside the simulation box are stored as sites, as described in the preceding paragraph. For the *region* style, a lattice point must additionally be consistent with the region volume to be stored as a site. Note that a region can be specified so that its volume is either inside or outside a geometric boundary.

For on-lattice applications, after sites have been created, a neighbor list is also generated for each site, as defined by each [lattice style](#). Think of this as the set of lattice points near a central site, with which it interacts in the sense defined by an application. If the simulation box is periodic in a dimension, the neighbors of a central site may include sites on the other side of the box. This will not be the case for a non-periodic dimension. If some sites do not exist, e.g. when using the *region* style, then some sites will not have a complete set of neighbors.

---

SPPARKS attempts to create sites with consecutive IDs from 1 to N, where N is the total number of sites that fill the simulation box. The numbering is the same, independent of the number of processors. Note that if the simulation box is non-periodic or the *region* style is used, some sites may not exist, so the site IDs will not typically be contiguous. I.e. the largest ID will be greater than the number of created sites.

Depending on the [application](#), each site stores zero or more integer and floating-point values. By default these are set to zero when a site is created by this command. The *value* and *basis* keywords can override the default.

The *value* keyword specifies a per-site value that will be assigned to every site as it is created. The *label* determines which per-site quantity is set. *iN* and *dN* mean the Nth integer or floating-point quantity, with  $1 \leq N \leq N_{\text{max}}$ .  $N_{\text{max}}$  is defined by the application. If *label* is specified as *site* it is the same as *il*. The quantity is set to the specified *nvalue*, which should be either an integer or floating-point numeric value, depending on what kind of per-site quantity is being set.

The *basis* keyword can be used to override the *value* keyword setting for individual basis sites as each unit cell is created. The per-site quantity (e.g. *i2*) specified by the *value* keyword is set for basis sites *M*. The quantity is set to the specified *nvalue* for the *basis* keyword, instead of the *nvalue* from the *value* keyword. See the [lattice](#) command for specifics on how basis atoms and unit cells are defined for each lattice style.

*M* can be specified in one of two ways. An explicit numeric value can be used, such as 2. A wild-card asterisk can also be used in place of or in conjunction with the *M* argument to specify multiple basis sites together. This takes the form "\*" or "\*n" or "n\*" or "m\*n". If *N* = the total number of basis sites, then an asterisk with no numeric values means all sites from 1 to *N*. A leading asterisk means all sites from 1 to *n* (inclusive). A trailing asterisk means all sites from *n* to *N* (inclusive). A middle asterisk means all sites from *m* to *n* (inclusive).

### Restrictions:

The [app\\_style](#) command must be used to define an application before using the `create_sites` command. The [create\\_box](#) command must be used to define the simulation box before using the `create_sites` command.

### Related commands:

[lattice](#), [region](#), [create\\_box](#), [read\\_sites](#)

**Default:** none



## deposition command

### Syntax:

```
deposition rate dirx diry dirz d0 lo hi
```

- rate = rate of atom deposition (atom/sec units)
- dirx,diry,dirz = vector in direction of incidence
- d0 = capture distance (distance units)
- lo,hi = min/max coordination number of deposition site

### Examples:

```
deposition      1.0 0 -1 0 1.0 1 4
deposition      1.0 1 1 -1 1.0 3 10
```

### Description:

This command invokes deposition events in an on-lattice diffusion model, specified by the [app\\_style diffusion](#) command.

Deposition events will compete with diffusive hop events in the diffusion model. Each time a deposition event is selected, a random starting point at the top of the simulation box is selected (top y surface in 2d, top z surface in 3d). The atom trajectory is traced along its incident direction which is specified by (dirx,diry,dirz) and need not be a unit vector. However, diry < 0 and dirz = 0 is required for 2d models. Similarly, dirz < 0 is required for 3d models.

Candidate deposition sites are vacant sites within a perpendicular distance  $d0$  from the incident trajectory which also have a current coordination number  $C$  such that  $lo \leq C \leq hi$ . Note that  $d0$  is specified in distance units which will depend on how you setup your lattice via the [app\\_style](#) command. For example, if you specified your lattice constant or box size in Angstroms, then the distance units for this command are Angstroms as well.

If the incident angle is not vertical, then periodic images of the starting point with associated incident trajectories are considered and the  $d0$  capture distance is applied to whichever trajectory the candidate site is closest to, in a perpendicular sense. This means x-periodicity in 2d and x- and y-periodicity in 3d.

For the set of candidate sites, the selected deposition site is the one closest to the starting point, measuring a projected distance along the incident direction.

**IMPORTANT NOTE:** [App\\_style diffusion](#) defines valid sites as vacant (site value = 1) or occupied (value = 2). When performing deposition, a row (2d) or plane (3d) of sites at the top of the system (where the deposited atoms are incident from) should be set to a value of 3. This prevents those sites from being considered as candidate deposition sites, due to them being neighbors of occupied sites at the bottom of the system in a periodic sense.

### Restrictions:

This command can only be used as part of the [app\\_style diffusion](#) application.

Deposition can currently only be done in serial simulations, not parallel. In serial, it can not be used with multiple [sectors](#), only one sector.

**Related commands:**

[ecoord](#), [barrier](#)

**Default:** none

## diag\_style array command

### Syntax:

```
diag_style array value mode value mode ...
```

- array = style name of this diagnostic
- value =  $iN$  or  $dN$
- mode = *min* or *max* or *mean* or *sum*

### Examples:

```
diag_style array i2 mean
diag_style array d1 sum d1 min d1 max
```

### Description:

The array diagnostic computes the mean, sum, min, or max for a per-site lattice value in the system. The diagnostic can operate on one or more values in one or more modes (min, max, mean, sum). The results are printed as stats output via the [stats](#) command.

### Restrictions:

This diagnostic can only be used for on-lattice applications.

### Related commands:

[diag\\_style](#), [stats](#)

**Default:** none

## diag\_style cluster command

### Syntax:

```
diag_style cluster keyword value keyword value ...
```

- cluster = style name of this diagnostic
- zero or more keyword/value pairs may be appended
- see the [diag\\_style](#) command for additional keyword/value pairs that can be appended to a diagnostic command and which must appear before these keywords
- keyword = *filename* or *dump*

```
filename value = name
    name = name of file to write clustering results to
dump value = style filename
    style = standard or opendx
    filename = file to write viz data to
```

### Examples:

```
diag_style cluster
diag_style cluster stats no delt 1.0 filename cluster3d.a.0.1.dat dump opendx cluster3d.a.0.1.dump
```

### Description:

The cluster diagnostic computes a clustering analysis on all lattice sites in the system, identifying geometric groupings of identical spin values, e.g. a grain in a grain growth model. The total number of clusters is printed as stats output via the [stats](#) command.

Clustering uses a connectivity definition provided by the application (e.g. sites are adjacent and have same spin value) to identify the set of connected clusters.

The variants cluster, cluster2d, and cluster3d are used with applications based on lattice, lattice2d, and lattice3d, respectively.

The *filename* keyword allows an output file to be specified. Every time the cluster analysis is performed, the key properties of each cluster are appended to this file. The output format is:

- Clustering Analysis for Lattice (diag\_style cluster)
- nglobal = *total number of sites*
- nprocs = *number of processors*
- Time = *time*
- ncluster = *total number of cluster*
- id ivalue dvalue size
- *cluster id ivalue dvalue size*

cluster\_id is an arbitrary integer assigned uniquely to each cluster. It will be different for different numbers of processors.

ivalue is an application-specific integer associated with each cluster. For lattice applications, it is the spin value of

all sites in the cluster dvalue is an application-specific double associated with each cluster. size is the numbers of sites in the cluster.

The *dump* keyword causes the cluster ID for each site to be printed out in snapshot format which can be used for visualization purposes. The cluster IDs are arbitrary integers such that two sites have the same ID if and only if they belong to the same cluster. The *standard* setting generates LAMMPS-style. For *cluster2d* and *cluster3d* styles only two values are printed for each site: site index and cluster ID. For the *cluster* style, three additional values are printed: the x, y, and z coordinate of the site (for 2d lattices, z=0). These files can be visualized with various tools in the [LAMMPS package](#) and the [Pizza.py package](#).

The *opendx* keyword generates a set of files that can be read by the OpenDX script called aniso0.net to visualize the clusters in 3D. The filenames are composed of the input filename, followed by a sequential number, followed by '.dx'. Because the OpenDX format assumes a particular ordering of the sites, the *opendx* style can only be used with square and simple cubic lattices.

### **Restrictions:**

This diagnostic can only be used for on-lattice applications.

Applications need to provide `push_connected_neighbors()` and `connected_ghosts()` functions which are called by this diagnostic. If they are not defined, SPPARKS will print an error message.

### **Related commands:**

[diag\\_style](#), [stats](#)

**Default:** none

## diag\_style diffusion command

### Syntax:

```
diag_style diffusion keyword value keyword value ...
```

- diffusion = style name of this diagnostic zero or more keyword/value pairs may be appended
  - see the [diag\\_style](#) command for keyword/value pairs that can be appended to a diagnostic command

### Examples:

```
diag_style diffusion
```

### Description:

The diffusion diagnostic calculates outputs various statistics about the different events that have occurred in a cumulative sense since the simulation began. These values are printed as stats output via the [stats](#) command.

There are 4 kinds of events tallied, not all of which may occur depending on the parameters used in defining the [app\\_style diffusion](#) model.

- successful deposition event
- failed deposition event
- 1st neighbor hop
- 2nd neighbor hop

A successful deposition event is one that resulted in an atom added to the lattice. A failed deposition event is one that was attempted, but no suitable site could be found and thus no atom was added. A 1st neighbor hop is a diffusion hop from a lattice site to a nearest-neighbor vacancy. A 2nd neighbor hop is a Schwoebel hop from a lattice site to a 2nd nearest-neighbor vacancy. See the [app\\_style diffusion](#) command for more info on how Schwoebel hops occur.

### Restrictions:

This diagnostic can only be used with the [app\\_style diffusion](#) application.

### Related commands:

[diag\\_style](#), [stats](#)

**Default:** none

## diag\_style energy command

### Syntax:

```
diag_style energy keyword value keyword value ...
```

- energy = style name of this diagnostic
- see the [diag\\_style](#) command for additional keywords that can be appended to a diagnostic command

### Examples:

```
diag_style energy
```

### Description:

The energy diagnostic computes the total energy of all lattice sites in the system. The energy is printed as stats output via the [stats](#) command.

### Restrictions:

This diagnostic can only be used for on-lattice applications.

### Related commands:

[diag\\_style](#), [stats](#)

**Default:** none

## diag\_style erbium command

### Syntax:

```
diag_style erbium keyword value keyword value ...
```

- `erbium` = style name of this diagnostic
- zero or more keyword/value pairs may be appended
- see the [diag\\_style](#) command for additional keyword/value pairs that can be appended to a diagnostic command and which must appear before these keywords
- keyword = *list*

```
list values = er or h or he or vac or events or sN or dN or tN
er, h, he, vac = counts of how many lattice sites of this type exist
events = total # of events for all sites
sN, dN, tN = cumulative # of events for this reaction that have occurred
```

### Examples:

```
diag_style erbium stats yes list h he vac events s1 d1 t2
```

### Description:

The erbium diagnostic prints out statistics about the system being modeled by [app\\_style erbium](#). The values will be printed as part of [stats](#) output.

Following the *list* keyword you can list one or more of the listed values, in any order.

The *er*, *h*, *he*, and *vac* values will print counts of the number of current sites of each type. The *events* value will print the total # of possible events that can occur as defined by the [event](#) command, given the current state of the lattice, summed over all sites.

The *sN*, *dN*, and *tN* values refer to a tally of events that have actually occurred, as defined by the [event](#) command. The letter "s" means reactions involving a single site, "d" means double reactions involving 2 sites, and "t" means triple reactions involving 3 sites. The N refers to which reaction (from 1 to the number of that type of reaction). I.e. "t2" means the 2nd 3-site reaction defined in your input script. Note that the values printed for *sN*, *dN*, and *tN* are cumulative counts of events from the beginning of the simulation run.

### Restrictions:

This command can only be used as part of the [app\\_style erbium](#) application.

### Related commands:

[diag\\_style](#), [stats](#)

**Default:** none



## diag\_style propensity command

### Syntax:

```
diag_style propensity keyword value keyword value ...
```

- propensity = style name of this diagnostic zero or more keyword/value pairs may be appended
  - see the [diag\\_style](#) command for keyword/value pairs that can be appended to a diagnostic command

### Examples:

```
diag_style propensity
```

### Description:

The propensity diagnostic computes the total propensity of all lattice sites in the system. The propensity is printed as stats output via the [stats](#) command.

The propensity can be thought of as the relative probability of a site site to perform a KMC event. Note that if you are doing Metropolis MC and not kinetic MC, no propensity is defined.

### Restrictions:

This diagnostic can only be used for on-lattice applications.

This diagnostic can only be used for KMC simulations where a [solver](#) is defined.

### Related commands:

[diag\\_style](#), [stats](#)

**Default:** none

## diag\_style command

### Syntax:

```
diag_style style keyword value keyword value ...
```

- *style* = *cluster* or *diffusion* or *energy* or *propensity*
- zero or more keyword/value pairs may be appended
- *keyword* = *stats* or *delay* or *delt* or *logfreq* or *loglinfreq*

```
stats values = yes or no
    yes/no = provide output to stats line
delay values = tdelay
    tdelay = delay evaluating diagnostic until at least this time
delt values = delta
    delta = time increment between evaluations of the diagnostic (seconds)
logfreq or loglinfreq values = N factor
    N = number of repetitions per interval
    factor = scale factor between intervals
```

- see doc pages for individual diagnostic commands for additional keywords - diagnostic-specific keywords must come after any other standard keywords

### Examples:

```
diag_style cluster stats no delt 1.0
diag_style energy
```

### Description:

This command invokes a diagnostic calculation. Currently, diagnostics can only be defined for on-lattice applications. See the [app\\_style](#) command for an overview of such applications.

The diagnostics currently available are:

- [array](#) = statistics of lattice values
- [cluster](#) = grain size statistics for general lattices
- [diffusion](#) = statistics on diffusion events
- [energy](#) = energy of entire system for general lattices
- [propensity](#) = propensity of entire system for general lattices

---

Diagnostics may provide one or more values that are appended to other statistical output and printed to the screen and log file via the [stats](#) command. This is stats output. In addition, the diagnostic may write more extensive output to its own files if requested by diagnostic-specific keywords.

The *stats* keyword controls whether or not the diagnostic appends values to the statistical output. If *stats* is set to *yes*, then none of the other keywords can be used, since the frequency of the [stats](#) output will determine when the diagnostic is called.

If *stats* is set to *no*, then the other keywords can be used, since presumably the diagnostic will create its own output files. The *delt* keyword specifies *Delta* = the interval of time between each diagnostic calculation.

Similarly, the *logfreq* and *loglinfreq* keywords will cause the diagnostic to run at progressively larger intervals during the course of a simulation. There will be  $N$  outputs per interval where the size of each interval scales up by *factor* each time. *Delta* is the time between outputs in the first (smallest) interval. See the [stats](#) command for more information on how the output times are specified. See the [stats](#) command for more information on how the intervals are specified.

If  $N$  is specified as 0, then this will turn off logarithmic intervals, and revert to regular intervals of *delta*.

The *delay* keyword specifies the shortest time at which the diagnostic can be evaluated. This is useful if it is inconvenient to evaluate the diagnostic at time  $t=0$ .

---

**Restrictions:** none

**Related commands:**

[stats](#)

**Default:**

The stats setting is yes.

## dimension command

### Syntax:

```
dimension N
```

- $N = 1$  or  $2$  or  $3$

### Examples:

```
dimension 2
```

### Description:

Set the dimensionality of the simulation for spatial on-lattice or off-lattice models. By default SPPARKS runs 3d simulations. To run a 1d or 2d simulation, this command should be used prior to setting up a simulation box via the [create\\_box](#) or [read\\_sites](#) commands.

### Restrictions:

This command must be used before the simulation box is defined by a [read\\_sites](#) or [create\\_box](#) command.

**Related commands:** none

### Default:

```
dimension 3
```

## dump command

### dump image command

#### Syntax:

```
dump dump-ID style delta filename field1 field2 ...
```

- dump-ID = user-assigned name for the dump
- style = *text* or *image*
- delta = time increment between dumps (seconds)
- filename = name of file to dump snapshots to
- fields = list of arguments for a particular style

```
image fields = discussed on dump image doc page
text fields = id or site or x or y or z or
              energy or propensity or iN or dN
```

#### Examples:

```
dump 1 text 0.25 tmp.dump
dump 1 text 1.0 my.dump id site x y z
dump mydump text 5.0 snap.ising id site energy il
```

#### Description:

The *text* style dumps a snapshot of site values to one or more files at time intervals of *delta* during a simulation. The *image* style creates a JPG or PPM image file of the site configuration every at time intervals of *delta*, as discussed on the [dump image](#) doc page. The remainder of this page refers to the *text* style.

As described below, the filename determines the kind of output (text or binary or gzipped, one big file or one per timestep, one big file or one per processor). The quantities printed are obtained from the application. Only [on-lattice and off-lattice applications](#) support dumps since they are spatial in nature. More than one dump command and file can be used during a simulation by giving each a unique dump-ID. Note that if written in appropriate format, a snapshot from a dump file can easily be converted into a data file suitable for input via the [read\\_sites](#) command to restart a simulation.

IMPORTANT NOTE: When running in parallel, the order of sites as printed to the dump file will be in chunks by processor, not ordered by ID. The order will be the same in every snapshot.

The [dump\\_modify](#) command can be used to alter the times at which snapshots are written out as well as defined a subset of sites to write out.

The text-based dump file is in the format of a [LAMMPS dump file](#) which can thus be read-in by the [Pizza.py toolkit](#), converted to other formats, or used for visualization. An important modification to the LAMMPS-style header for each snapshot is the addition of real time to the line containing the snapshot number, i.e.

```
ITEM: TIMESTEP TIME
100      3.23945
```

The entry for "NUMBER OF ATOMS" is really number of sites, and will reflect any reduction in site count due to the [dump\\_modify](#) command, i.e.

```
ITEM: NUMBER OF ATOMS
314159
```

If fields are listed, then only those quantities will be printed for each site. If no fields are listed, then a default set of fields are output, namely "id site x y z". These are the possible field values which may be specified.

The *id* is a unique integer ID for each site.

The *site*, *iN*, and *dN* fields specify a per-site value. *Site* is the same as *iI*. *iN* fields are integer values; *dN* fields are floating-point value. The application defines how many integer and floating-point values are stored for each site.

The *x*, *y*, *z* values are the coordinates of the site.

The *energy* value is what is computed by the `energy()` function in the application. Likewise for the *propensity* value which can be thought of as the relative probability for that site to perform a KMC event. Note that if the application only performs rejection KMC or Metropolis MC, then no propensity is defined.

---

The specified filename determines how the dump file(s) is written. The default is to write one large text file, which is opened when the dump command is invoked and closed when an [undump](#) command is used or when SPPARKS exits.

Dump filenames can contain two wild-card characters. If a "\*" character appears in the filename, then one file per snapshot is written and the "\*" character is replaced with the timestep value. For example, `tmp.dump.*` becomes `tmp.dump.0`, `tmp.dump.10000`, `tmp.dump.20000`, etc.

If a "%" character appears in the filename, then one file is written for each processor and the "%" character is replaced with the processor ID from 0 to P-1. For example, `tmp.dump.%` becomes `tmp.dump.0`, `tmp.dump.1`, ... `tmp.dump.P-1`, etc. This creates smaller files and can be a fast mode of output on parallel machines that support parallel I/O for output.

Note that the "\*" and "%" characters can be used together to produce a large number of small dump files!

If the filename ends with ".bin", the dump file (or files, if "\*" or "%" is also used) is written in binary format. A binary dump file will be about the same size as a text version, but will typically write out much faster. Of course, when post-processing, you will need to convert it back to text format, using your own code to read the binary file. The format of the binary file can be understood by looking at the `src/dump.cpp` file.

If the filename ends with ".gz", the dump file (or files, if "\*" or "%" is also used) is written in gzipped format. A gzipped dump file will be about 3x smaller than the text version, but will also take longer to write.

---

### Restrictions:

This command can only be used as part of on-lattice or off-lattice applications. See the [app\\_style](#) command for further details.

To write gzipped dump files, you must compile SPPARKS with the `-DSPPARKS_GZIP` option - see the [Making SPPARKS](#) section of the documentation.

### Related commands:

`dump_one`, `dump_modify`, `undump`, `stats`

**Default:** none

## dump image command

### Syntax:

dump dump-ID image delta filename color diameter keyword value ...

- ID = user-assigned name for the dump
- image = style of dump command (other style *text* is discussed on the [dump](#) doc page)
- delta = time increment between dumps (seconds)
- filename = name of file to write image to
- color = attribute that determines color of each site
- diameter = attribute that determines size of each site
- zero or more keyword/value pairs may be appended
- keyword = *shape* or *sdiam* or *bdiam* or *crange* or *drange* or *size* or *view* or *center* or *up* or *zoom* or *persp* or *box* or *axes* or *shiny* or *ssao*

*shape* value = *sphere* or *cube*  
*sdiam* value = number = numeric value for site diameter (distance units)  
*boundary* values = attribute width  
 attribute = attribute to use for drawing boundaries between sites  
 width = width of boundary cylinders  
*crange* values = lo hi  
 lo,hi = lower and upper bound (inclusive) of integer color attribute  
*drange* values = lo hi  
 lo,hi = lower and upper bound (inclusive) of integer diameter attribute  
*size* values = width height = size of images  
 width = width of image in # of pixels  
 height = height of image in # of pixels  
*view* values = theta phi = view of simulation box  
 theta = view angle from +z axis (degrees)  
 phi = azimuthal view angle (degrees)  
 theta or phi can be a variable (see below)  
*center* values = flag Cx Cy Cz = center point of image  
 flag = "s" for static, "d" for dynamic  
 Cx,Cy,Cz = center point of image as fraction of box dimension (0.5 = center of box)  
 Cx,Cy,Cz can be variables (see below)  
*up* values = Ux Uy Uz = direction that is "up" in image  
 Ux,Uy,Uz = components of up vector  
 Ux,Uy,Uz can be variables (see below)  
*zoom* value = zfactor = size that simulation box appears in image  
 zfactor = scale image size by factor > 1 to enlarge, factor <1 to shrink  
 zfactor can be a variable (see below)  
*persp* value = pfactor = amount of "perspective" in image  
 pfactor = amount of perspective (0 = none, <1 = some, > 1 = highly skewed)  
 pfactor can be a variable (see below)  
*box* values = yes/no diam = draw outline of simulation box  
 yes/no = do or do not draw simulation box lines  
 diam = diameter of box lines as fraction of shortest box length  
*axes* values = yes/no length diam = draw xyz axes  
 yes/no = do or do not draw xyz axes lines next to simulation box  
 length = length of axes lines as fraction of respective box lengths  
 diam = diameter of axes lines as fraction of shortest box length  
*shiny* value = sfactor = shininess of spheres and cylinders  
 sfactor = shininess of spheres and cylinders from 0.0 to 1.0  
*ssao* value = yes/no seed dfactor = SSAO depth shading  
 yes/no = turn depth shading on/off  
 seed = random # seed (positive integer)  
 dfactor = strength of shading from 0.0 to 1.0



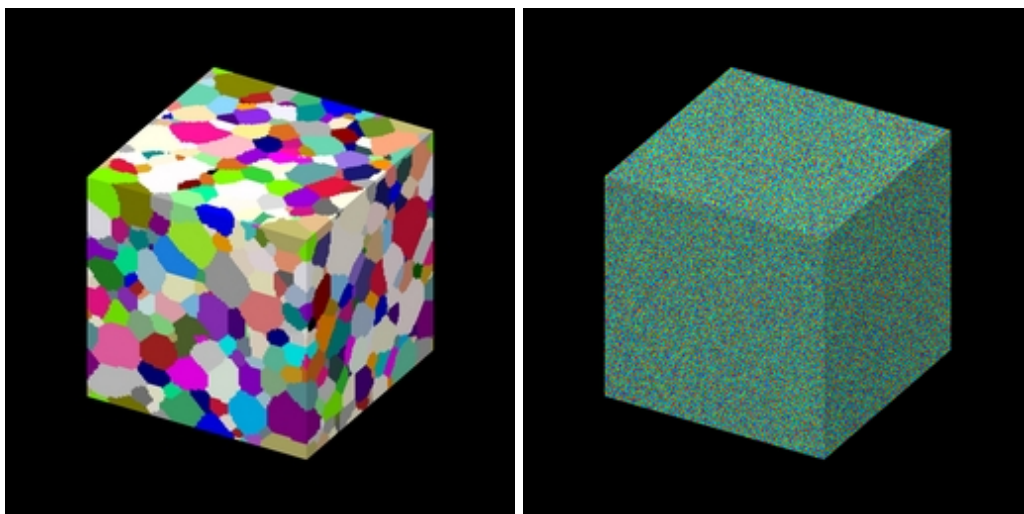
## Examples:

```
dump myDump image 100 dump.*.jpg site site
dump myDump image 100 dump.*.jpg energy i2
```

## Description:

Dump a high-quality ray-traced image of the sites at time intervals of *delta* during a simulation as either a JPG or PPM file. A series of such images can easily be converted into an animated movie of your simulation; see further details below. The *text* dump style writes snapshots of numerical data associated with sites, as discussed on the [dump](#) doc page.

Here are two sample images, rendered as 1024x1024 JPG files. The left image is a million-site lattice; the right image is half a billion sites. Click to see the full-size images:



The [dump\\_modify](#) command can be used to alter the times at which images are written out as well as alter what sites are included in the image.

The filename suffix determines whether a JPG or PPM file is created. If the suffix is ".jpg" or ".jpeg", then a JPG file is created, else a PPM file is created, which is a text-based format. To write out JPG files, you must build SPPARKS with a JPEG library. See [this section](#) of the manual for instructions on how to do this.

---

Dump image filenames must contain a wildcard character "\*", so that one image file per snapshot is written. The "\*" character is replaced with the timestep value. For example, tmp.dump.\*.jpg becomes tmp.dump.0.jpg, tmp.dump.10000.jpg, tmp.dump.20000.jpg, etc. Note that the [dump\\_modify pad](#) command can be used to insure all timestep numbers are the same length (e.g. 00010), which can make it easier to convert a series of images into a movie in the correct ordering.

---

The *color* and *diameter* settings determine the color and size of sites rendered in the image. They can be any attribute defined for the [dump text](#) command, including *site*. Note that the *diameter* setting can be overridden with a numeric value by the optional *sdiam* keyword, in which case you can specify the *diameter* setting with any valid atom attribute.

If an integer attribute such as *site* or *i2* is specified for the *color* setting, then you must use the optional *crange* keyword to specify the range of integer values that are allowed, from *lo* to *hi*. The color of each site is determined by the integer value. By default the mapping of values to colors is done by looping over the set of pre-defined colors listed with the [dump\\_modify](#) command, and assigning the first one to value *lo*, the next to value *lo*+1, and so on, repeating the assignment in a loop if the number of values exceeds the number of pre-defined colors. This

mapping can be changed by the [dump\\_modify scolor](#) command.

If a floating point attribute such as *energy* or *d1* is specified for the *color* setting, then the site's attribute will be associated with a specific color via a "color map", which can be specified via the [dump\\_modify](#) command. The basic idea is that the attribute will be within a range of values, and every value within the range is mapped to a specific color. Depending on how the color map is defined, that mapping can take place via interpolation so that a value of -3.2 is halfway between "red" and "blue", or discretely so that the value of -3.2 is "orange".

If an integer attribute such as *site* or *i2* is specified for the *diameter* setting, then you must use the optional *drange* keyword to specify the range of integer values that are allowed. The size of each site is determined by the integer value. By default all values has diameter 1.0. This mapping can be changed by the [dump\\_modify sdiam](#) command.

If a floating point attribute such as *energy* or *d1* is specified for the *diameter* setting, then the site will be rendered using the site's attribute as the diameter. If the per-site value  $\leq 0.0$ , then the site will not be drawn.

---

The various keywords listed above control how the image is rendered. As listed below, all of the keywords have defaults, most of which you will likely not need to change. The [dump modify](#) also has options specific to the dump image style, particularly for assigning colors to atoms, bonds, and other image features.

---

The *shape* keyword can be specified with a value of *sphere* or *cube*, to draw either a sphere or cube at each site. Cubes typically only make sense for simple square or cubic lattices with regular spacing, so that the cubes will tile the 2d or 3d space without overlapping. The diameter specified for each site will be the diameter of the sphere or the edge length of the cube.

---

The *sdiam* keyword allows you to override the *diameter* setting with a specified numeric value. All sites will be drawn with that diameter.

---

The *boundary* keyword enables drawing of boundaries between neighboring sites that have a different value of the specified attribute. This is a way to visualize the boundary between two contiguous groups of sites based on an attribute that is different for the two groups, even if the sites themselves in the 2 groups are rendered with the same color (due to the value of their *color* setting).

The specified *attribute* can be any attribute defined for the [dump text](#) command, including *site*. A boundary is only drawn between site pairs (I,J), where site I is rendered by the dump image command, site J is one of its nearest neighbors, and the value of the specified *attribute* is different for the 2 sites.

The boundary itself is drawn as 4 cylinders which outline a square. If the 2 adjacent sites are rendered as cubes (via the *shape* setting), then the square is the face common to the 2 adjacent cubes. The diameter of the cylinders is set via the *bdiam* keyword. The color of the cylinders can be set via the [dump\\_modify boundcolor](#) command.

---

The *crange* keyword must be used if the specified *color* setting is an integer attribute such as *site* or *i2*. The *lo* and *hi* values are the range of values that the attribute can have. For example, if spins in a Potts model will range from 1 to 100 (inclusive), then *lo* and *hi* should be specified as 1 and 100.

---

The *drange* keyword must be used if the specified *diameter* setting is an integer attribute such as *site* or *i2*, unless the *sdiam* keyword is used, in which case the *diameter* setting is ignored. The *lo* and *hi* values are the range of values that the attribute can have. For example, if the *i2* attribute will take on the values -1, 0, or 1, then *lo* and *hi* should be specified as -1 and 1

---

The *size* keyword sets the width and height of the created images, i.e. the number of pixels in each direction.

---

The *view*, *center*, *up*, *zoom*, and *persp* values determine how 3d simulation space is mapped to the 2d plane of the image. Basically they control how the simulation box appears in the image.

All of the *view*, *center*, *up*, *zoom*, and *persp* values can be specified as numeric quantities, whose meaning is explained below. Any of them can also be specified as an [equal-style variable](#), by using *v\_name* as the value, where "name" is the variable name. In this case the variable will be evaluated on the timestep each image is created to create a new value. If the equal-style variable is time-dependent, this is a means of changing the way the simulation box appears from image to image, effectively doing a pan or fly-by view of your simulation.

The *view* keyword determines the viewpoint from which the simulation box is viewed, looking towards the *center* point. The *theta* value is the vertical angle from the +z axis, and must be an angle from 0 to 180 degrees. The *phi* value is an azimuthal angle around the z axis and can be positive or negative. A value of 0.0 is a view along the +x axis, towards the *center* point. If *theta* or *phi* are specified via variables, then the variable values should be in degrees.

The *center* keyword determines the point in simulation space that will be at the center of the image. *Cx*, *Cy*, and *Cz* are specified as fractions of the box dimensions, so that (0.5,0.5,0.5) is the center of the simulation box. These values do not have to be between 0.0 and 1.0, if you want the simulation box to be offset from the center of the image. Note, however, that if you choose strange values for *Cx*, *Cy*, or *Cz* you may get a blank image. Internally, *Cx*, *Cy*, and *Cz* are converted into a point in simulation space. If *flag* is set to "s" for static, then this conversion is done once, at the time the dump command is issued. If *flag* is set to "d" for dynamic then the conversion is performed every time a new image is created. If the box size or shape is changing, this will adjust the center point in simulation space.

The *up* keyword determines what direction in simulation space will be "up" in the image. Internally it is stored as a vector that is in the plane perpendicular to the view vector implied by the *theta* and *phi* values, and which is also in the plane defined by the view vector and user-specified up vector. Thus this internal vector is computed from the user-specified *up* vector as

```
up_internal = view cross (up cross view)
```

This means the only restriction on the specified *up* vector is that it cannot be parallel to the *view* vector, implied by the *theta* and *phi* values.

The *zoom* keyword scales the size of the simulation box as it appears in the image. The default *zfactor* value of 1 should display an image mostly filled by the atoms in the simulation box. A *zfactor* > 1 will make the simulation box larger; a *zfactor* < 1 will make it smaller. *Zfactor* must be a value > 0.0.

The *persp* keyword determines how much depth perspective is present in the image. Depth perspective makes lines that are parallel in simulation space appear non-parallel in the image. A *pfactor* value of 0.0 means that parallel lines will meet at infinity (1.0/pfactor), which is an orthographic rendering with no perspective. A *pfactor* value between 0.0 and 1.0 will introduce more perspective. A *pfactor* value > 1 will create a highly skewed image with a large amount of perspective.

**IMPORTANT NOTE:** The *persp* keyword is not yet supported as an option.

---

The *box* keyword determines how the simulation box boundaries are rendered as thin cylinders in the image. If *no* is set, then the box boundaries are not drawn and the *diam* setting is ignored. If *yes* is set, the 12 edges of the box are drawn, with a diameter that is a fraction of the shortest box length in x,y,z (for 3d) or x,y (for 2d). The color of the box boundaries can be set with the [dump\\_modify boxcolor](#) command.

The *axes* keyword determines how the coordinate axes are rendered as thin cylinders in the image. If *no* is set, then the axes are not drawn and the *length* and *diam* settings are ignored. If *yes* is set, 3 thin cylinders are drawn to represent the x,y,z axes in colors red,green,blue. The origin of these cylinders will be offset from the lower left corner of the box by 10%. The *length* setting determines how long the cylinders will be as a fraction of the respective box lengths. The *diam* setting determines their thickness as a fraction of the shortest box length in x,y,z (for 3d) or x,y (for 2d).

---

The *shiny* keyword determines how shiny the objects rendered in the image will appear. The *sfactor* value must be a value  $0.0 \leq sfactor \leq 1.0$ , where *sfactor* = 1 is a highly reflective surface and *sfactor* = 0 is a rough non-shiny surface.

The *ssao* keyword turns on/off a screen space ambient occlusion (SSAO) model for depth shading. If *yes* is set, then atoms further away from the viewer are darkened via a randomized process, which is perceived as depth. The calculation of this effect can increase the cost of computing the image by roughly 2x. The strength of the effect can be scaled by the *dfactor* parameter. If *no* is set, no depth shading is performed.

---

A series of JPG or PPM images can be converted into a movie file and then played as a movie using commonly available tools.

Convert JPG or PPM files into an animated GIF or MPEG or other movie file:

- a) Use the ImageMagick convert program.

```
% convert *.jpg foo.gif
% convert *.ppm foo.mpg
```

- b) Use QuickTime.

Select "Open Image Sequence" under the File menu Load the images into QuickTime to animate them  
Select "Export" under the File menu Save the movie as a QuickTime movie (\*.mov) or in another format

- c) Windows-based tool.

If someone tells us how to do this via a common Windows-based tool, we'll post the instructions here.

Play the movie:

- a) Use your browser to view an animated GIF movie.

Select "Open File" under the File menu Load the animated GIF file

- b) Use the freely available mplayer tool to view an MPEG movie.

```
% mplayer foo.mpg
```

- c) Use the [Pizza.py animate tool](#), which works directly on a series of image files.

```
a = animate("foo*.jpg")
```

- d) QuickTime and other Windows-based media players can obviously play movie files directly.
- 

## Restrictions:

To write JPG images, you must use a -DSPPARKS\_JPEG switch when building SPPARKS and link with a JPEG library. See the [Making LAMMPS](#) section of the documentation for details.

## Related commands:

`dump`, `dump_modify`, `undump`

**Default:**

The defaults for the keywords are as follows:

- `shape = sphere`
- `sdiam = not specified (use diameter setting)`
- `boundary = no default`
- `crange = no default`
- `drange = no default`
- `size = 512 512`
- `view = 60 30 (for 3d)`
- `view = 0 0 (for 2d)`
- `center = s 0.5 0.5 0.5`
- `up = 0 0 1 (for 3d)`
- `up = 0 1 0 (for 2d)`
- `zoom = 1.0`
- `persp = 0.0`
- `box = yes 0.02`
- `axes = no 0.0 0.0`
- `shiny = 1.0`
- `ssao = no`

## dump\_modify command

### Syntax:

dump\_modify dump-ID keyword values ...

- dump-ID = ID of dump to modify
- one or more keyword/value pairs may be appended
- keyword = *backcolor* or *boundcolor* or *boxcolor* or *color* or *delay* or *delta* or *flush* or *logfreq* or *loglinfreq* or *pad* or *region* or *scolor* or *sdiam* or *smap* or *thresh*

```

backcolor arg = color
    color = name of color for background
boundcolor arg = color
    color = name of color for boundaries between sites
boxcolor arg = color
    color = name of color for box lines
color args = name R G B
    name = name of color
    R,G,B = red/green/blue numeric values from 0.0 to 1.0
delay value = tdelay
    tdelay = delay dump until at least this time (seconds)
delta arg = dt
    dt = time increment between dumps (seconds)
flush arg = yes or no
logfreq or loglinfreq values = N factor
    N = number of repetitions per interval
    factor = scale factor between intervals
pad arg = Nchar = # of characters to convert timestep to
region arg = region-ID or "none"
scolor args = I color
    I = integer value or range of values (see below)
    color = name of color or color1/color2/... or random
sdiam args = I diam
    I = integer value or range of values (see below)
    diam = diameter of sites of that value
smap args = lo hi style delta N entry1 entry2 ... entryN
    lo = number or min = lower bound of range of color map
    hi = number or max = upper bound of range of color map
    style = 2 letters = "c" or "d" or "s" plus "a" or "f"
        "c" for continuous
        "d" for discrete
        "s" for sequential
        "a" for absolute
        "f" for fractional
    delta = binsize (only used for style "s", otherwise ignored)
        binsize = range is divided into bins of this width
    N = # of subsequent entries
    entry = value color (for continuous style)
        value = number or min or max = single value within range
        color = name of color used for that value
    entry = lo hi color (for discrete style)
        lo/hi = number or min or max = lower/upper bound of subset of range
        color = name of color used for that subset of values
    entry = color (for sequential style)
        color = name of color used for a bin of values
thresh args = attribute operation value
    attribute = same fields (id,lattice,x,etc) used by dump command
    operation = "" or ">=" or "==" or "!="

```

```
value = numeric value to compare to
these 3 args can be replaced by the word "none" to turn off thresholding
```

## Examples:

```
dump_modify 1 delay 30.0
dump_modify 1 loglinfreq 7 10.0 delay 100.0 flush yes
dump_modify mine thresh energy > 0.0 thresh id <= 1000
```

## Description:

Modify the parameters of a previously defined dump command. Not all parameters are relevant to both the *text* and *image* dump styles.

---

The *backcolor* keyword applies only to the dump *image* style. It sets the background color of the images. The color name can be any of the 140 pre-defined colors (see below) or a color name defined by the dump\_modify color option.

---

The *boundcolor* keyword applies only to the dump *image* style. It sets the color used to draw boundaries between sites, each of which is a set of 4 cylinders, as described in the [dump image](#) doc page. The color name can be any of the 140 pre-defined colors (see below) or a color name defined by the dump\_modify color option.

---

The drawing of boundaries between neighboring sites is enabled by the *boundary* keyword of the [dump image](#) command.

---

The *boxcolor* keyword applies only to the dump *image* style. It sets the color of the simulation box drawn around the sites in each image. See the "dump image box" command for how to specify that a box be drawn. The color name can be any of the 140 pre-defined colors (see below) or a color name defined by the dump\_modify color option.

---

The *color* keyword applies only to the dump *image* style. It allows definition of a new color name, in addition to the 140-predefined colors (see below), and associates 3 red/green/blue RGB values with that color name. The color name can then be used with any other dump\_modify keyword that takes a color name as a value. The RGB values should each be floating point values between 0.0 and 1.0 inclusive.

When a color name is converted to RGB values, the user-defined color names are searched first, then the 140 pre-defined color names. This means you can also use the *color* keyword to overwrite one of the pre-defined color names with new RGB values.

---

The *delay* keyword will suppress output until *tdelay* time has elapsed.

---

The *delta* keyword will suppress output until *tdelay* time has elapsed.

---

The *flush* option determines whether a flush operation is invoked after a dump snapshot is written to the dump file. A flush insures the output in that file is current (no buffering by the OS), even if SPPARKS halts before the simulation completes. The *flush* option is only relevant to the [dump text](#) style.

---

The *logfreq* and *loglinfreq* keywords will produce output at progressively larger intervals during the course of a simulation. There will be *N* outputs per interval where the size of each interval is initially *delta* and then scales up by *factor* each time. See the [stats](#) command for more information on how the output times are specified.

If *N* is specified as 0, then this will turn off logarithmic output, and revert to regular output every *delta* seconds.



---

The *pad* keyword only applies when the dump filename is specified with a wildcard "\*" character which becomes the timestep. If *pad* is 0, which is the default, the timestep is converted into a string of unpadded length, e.g. 100 or 12000 or 2000000. When *pad* is specified with *Nchar* > 0, the string is padded with leading zeroes so they are all the same length = *Nchar*. For example, pad 7 would yield 0000100, 0012000, 2000000. This can be useful so that post-processing programs can easily read the files in ascending timestep order.

---

The *region* keyword allows sub-selection of lattice sites to output. If specified, only sites in the region will be written to the dump file or included in the image. Only one region can be applied as a filter (the last one specified). See the [region](#) command for more details. Note that a region can be defined as the "inside" or "outside" of a geometric shape, and it can be the "union" or "intersection" of a series of simpler regions.

---

The *scolor* keyword applies only to the dump *image* style. It can be used with the [dump image](#) command, when its site color setting is an integer attribute, and a *crange* setting from *lo* to *hi* has been specified to set the color associated with each integer value.

The specified *I* value should be an integer from *lo* to *hi* inclusive. A wildcard asterisk can be used in place of or in conjunction with the *type* argument to specify a range of values. This takes the form "\*" or "\*n" or "n\*" or "m\*n". An asterisk with no numeric values means all values from *lo* to *hi*. A leading asterisk means all values from *lo* to n (inclusive). A trailing asterisk means all values from n to *hi* (inclusive). A middle asterisk means all values from m to n (inclusive).

The specified *color* can be a single color which is any of the 140 pre-defined colors (see below) or a color name defined by the dump\_modify color option. Or it can be two or more colors separated by a "/" character, e.g. red/green/blue. In the former case, that color is assigned to all the specified integer values. In the latter case, the list of colors are assigned in a round-robin fashion to each of the specified integer values.

The specified *color* can also be the word *random*. In this case, random red/blue/green color values, each from 0.0 to 1.0, are generated for each *I* value. This is a convenient way to assign a large number of random colors, without having to list them explicitly by name.

---

The *sdiam* keyword applies only to the dump *image* style. It can be used with the [dump image](#) command, when its site diameter setting is an integer attribute, and a *drange* setting from *lo* to *hi* has been specified to set the diameter associated with each integer value. The specified *I* value should be an integer from *lo* to *hi*. As with the *scolor* keyword, a wildcard asterisk can be used as part of the *I* argument to specify a range of values.

---

The *smap* keyword applies only to the dump *image* style. It can be used with the [dump image](#) command, when its site color setting is a floating point attribute, to setup a color map. The color map is used to assign a specific RGB (red/green/blue) color value to an individual site when it is drawn, based on the atom's attribute, which is a numeric value, e.g. its x coordinate, if the attribute "x" was specified.

The basic idea of a color map is that the site-attribute will be within a range of values, and that range is associated with a series of colors (e.g. red, blue, green). An sites's specific value ( $x = -3.2$ ) can then mapped to the series of colors (e.g. halfway between red and blue), and a specific color is determined via an interpolation procedure.

There are many possible options for the color map, enabled by the *smap* keyword. Here are the details.

The *lo* and *hi* settings determine the range of values allowed for the site attribute. If numeric values are used for *lo* and/or *hi*, then values that are lower/higher than *lo*/*hi* are set to either *lo* or *hi*. I.e. the range is static. If *lo* is specified as *min* or *hi* as *max* then the range is dynamic, and the lower and/or upper bound will be calculated each time an image is drawn, based on the set of sites being visualized.



The *style* setting is two letters, such as "ca". The first letter is either "c" for continuous, "d" for discrete, or "s" for sequential. The second letter is either "a" for absolute, or "f" for fractional.

A continuous color map is one in which the color changes continuously from value to value within the range. A discrete color map is one in which discrete colors are assigned to sub-ranges of values within the range. A sequential color map is one in which discrete colors are assigned to a sequence of sub-ranges of values covering the entire range.

An absolute color map is one in which the values to which colors are assigned are specified explicitly as values within the range. A fractional color map is one in which the values to which colors are assigned are specified as a fractional portion of the range. For example if the range is from -10.0 to 10.0, and the color red is to be assigned to atoms with a value of 5.0, then for an absolute color map the number 5.0 would be used. But for a fractional map, the number 0.75 would be used since 5.0 is 3/4 of the way from -10.0 to 10.0.

The *delta* setting is only specified if the style is sequential. It specifies the bin size to use within the range for assigning consecutive colors to. For example, if the range is from -10.0 to 10.0 and a *delta* of 1.0 is used, then 20 colors will be assigned to the range. The first will be from  $-10.0 \leq \text{color1} < -9.0$ , then 2nd from  $-9.0 \leq \text{color2} < -8.0$ , etc.

The *N* setting is how many entries follow. The format of the entries depends on whether the color map style is continuous, discrete or sequential. In all cases the *color* setting can be any of the 140 pre-defined colors (see below) or a color name defined by the *dump\_modify color* option.

For continuous color maps, each entry has a *value* and a *color*. The *value* is either a number within the range of values or *min* or *max*. The *value* of the first entry must be *min* and the *value* of the last entry must be *max*. Any entries in between must have increasing values. Note that numeric values can be specified either as absolute numbers or as fractions (0.0 to 1.0) of the range, depending on the "a" or "f" in the style setting for the color map.

Here is how the entries are used to determine the color of an individual site, given the value X of its site attribute. X will fall between 2 of the entry values. The color of the site is linearly interpolated (in each of the RGB values) between the 2 colors associated with those entries. For example, if  $X = -5.0$  and the 2 surrounding entries are "red" at -10.0 and "blue" at 0.0, then the site's color will be halfway between "red" and "blue", which happens to be "purple".

For discrete color maps, each entry has a *lo* and *hi* value and a *color*. The *lo* and *hi* settings are either numbers within the range of values or *lo* can be *min* or *hi* can be *max*. The *lo* and *hi* settings of the last entry must be *min* and *max*. Other entries can have any *lo* and *hi* values and the sub-ranges of different values can overlap. Note that numeric *lo* and *hi* values can be specified either as absolute numbers or as fractions (0.0 to 1.0) of the range, depending on the "a" or "f" in the style setting for the color map.

Here is how the entries are used to determine the color of an individual site, given the value X of its site attribute. The entries are scanned from first to last. The first time that  $lo \leq X \leq hi$ , X is assigned the color associated with that entry. You can think of the last entry as assigning a default color (since it will always be matched by X), and the earlier entries as colors that override the default. Also note that no interpolation of a color RGB is done. All sites will be drawn with one of the colors in the list of entries.

For sequential color maps, each entry has only a *color*. Here is how the entries are used to determine the color of an individual site, given the value X of its site attribute. The range is partitioned into N bins of width *binsize*. Thus X will fall in a specific bin from 1 to N, say the Mth bin. If it falls on a boundary between 2 bins, it is considered to be in the higher of the 2 bins. Each bin is assigned a color from the E entries. If  $E < N$ , then the colors are repeated. For example if 2 entries with colors red and green are specified, then the odd numbered bins will be red and the even bins green. The color of the site is the color of its bin. Note that the sequential color map

is really a shorthand way of defining a discrete color map without having to specify where all the bin boundaries are.

---

The *thresh* keyword allows sub-selection of lattice sites to output. Multiple thresholds can be specified. Specifying "none" turns off all threshold criteria. If thresholds are specified, only sites whose attributes meet all the threshold criteria are written to the dump file or included in the image. The possible attributes that can be tested for are the same as the fields that can be specified in the [dump](#) command. Note that different attributes can be output by the dump command than are used as threshold criteria by the dump\_modify command. E.g. you can output the coordinates and propensity of sites whose energy is above some threshold.

### Restrictions:

This command can only be used as part of the lattice-based applications. See the [app\\_style](#) command for further details.

### Related commands:

[dump](#), [dump image](#)

### Default:

The option defaults are

- bgcolor = black
- boundcolor = white
- boxcolor = yellow
- color = 140 color names are pre-defined as listed below
- delay = 0.0
- delta = value used in the [dump](#) command
- flush = yes
- logfreq = off
- loglinfreq = off
- pad = 0
- region = none
- scolor = \* red/green/blue/yellow/aqua/cyan
- sdiam = \* 1.0
- smap = min max cf 2 min blue max red
- thresh = none

---

These are the 140 colors that SPPARKS pre-defines for use with the [dump image](#) and dump\_modify commands. Additional colors can be defined with the dump\_modify color command. The 3 numbers listed for each name are the RGB (red/green/blue) values. Divide each value by 255 to get the equivalent 0.0 to 1.0 value.

aliceblue = 240, 248, 255	antiquewhite = 250, 235, 215	aqua = 0, 255, 255	aquamarine = 127, 255, 212	azure = 240, 255, 255
beige = 245, 245, 220	bisque = 255, 228, 196	black = 0, 0, 0	blanchedalmond = 255, 255, 205	blue = 0, 0, 255
blueviolet = 138, 43, 226	brown = 165, 42, 42	burlywood = 222, 184, 135	cadetblue = 95, 158, 160	chartreuse = 127, 255, 0
chocolate = 210, 105, 30	coral = 255, 127, 80	cornflowerblue = 100, 149, 237	cornsilk = 255, 248, 220	crimson = 220, 20, 60

cyan = 0, 255, 255	darkblue = 0, 0, 139	darkcyan = 0, 139, 139	darkgoldenrod = 184, 134, 11	darkgray = 169, 169, 169
darkgreen = 0, 100, 0	darkkhaki = 189, 183, 107	darkmagenta = 139, 0, 139	darkolivegreen = 85, 107, 47	darkorange = 255, 140, 0
darkorchid = 153, 50, 204	darkred = 139, 0, 0	darksalmon = 233, 150, 122	darkseagreen = 143, 188, 143	darkslateblue = 72, 61, 139
darkslategray = 47, 79, 79	darkturquoise = 0, 206, 209	darkviolet = 148, 0, 211	deeppink = 255, 20, 147	deepskyblue = 0, 191, 255
dimgray = 105, 105, 105	dodgerblue = 30, 144, 255	firebrick = 178, 34, 34	floralwhite = 255, 250, 240	forestgreen = 34, 139, 34
fuchsia = 255, 0, 255	gainsboro = 220, 220, 220	ghostwhite = 248, 248, 255	gold = 255, 215, 0	goldenrod = 218, 165, 32
gray = 128, 128, 128	green = 0, 128, 0	greenyellow = 173, 255, 47	honeydew = 240, 255, 240	hotpink = 255, 105, 180
indianred = 205, 92, 92	indigo = 75, 0, 130	ivory = 255, 240, 240	khaki = 240, 230, 140	lavender = 230, 230, 250
lavenderblush = 255, 240, 245	lawngreen = 124, 252, 0	lemonchiffon = 255, 250, 205	lightblue = 173, 216, 230	lightcoral = 240, 128, 128
lightcyan = 224, 255, 255	lightgoldenrodyellow = 250, 250, 210	lightgreen = 144, 238, 144	lightgrey = 211, 211, 211	lightpink = 255, 182, 193
lightsalmon = 255, 160, 122	lightseagreen = 32, 178, 170	lightskyblue = 135, 206, 250	lightslategray = 119, 136, 153	lightsteelblue = 176, 196, 222
lightyellow = 255, 255, 224	lime = 0, 255, 0	limegreen = 50, 205, 50	linen = 250, 240, 230	magenta = 255, 0, 255
maroon = 128, 0, 0	mediumaquamarine = 102, 205, 170	mediumblue = 0, 0, 205	mediumorchid = 186, 85, 211	mediumpurple = 147, 112, 219
mediumseagreen = 60, 179, 113	mediumslateblue = 123, 104, 238	mediumspringgreen = 0, 250, 154	mediumturquoise = 72, 209, 204	mediumvioletred = 199, 21, 133
midnightblue = 25, 25, 112	mintcream = 245, 255, 250	mistyrose = 255, 228, 225	moccasin = 255, 228, 181	navajowhite = 255, 222, 173
navy = 0, 0, 128	oldlace = 253, 245, 230	olive = 128, 128, 0	olivedrab = 107, 142, 35	orange = 255, 165, 0
orangered = 255, 69, 0	orchid = 218, 112, 214	palegoldenrod = 238, 232, 170	palegreen = 152, 251, 152	paleturquoise = 175, 238, 238
palevioletred = 219, 112, 147	papayawhip = 255, 239, 213	peachpuff = 255, 239, 213	peru = 205, 133, 63	pink = 255, 192, 203
plum = 221, 160, 221	powderblue = 176, 224, 230	purple = 128, 0, 128	red = 255, 0, 0	rosybrown = 188, 143, 143
royalblue = 65, 105, 225	saddlebrown = 139, 69, 19	salmon = 250, 128, 114	sandybrown = 244, 164, 96	seagreen = 46, 139, 87
seashell = 255, 245, 238	sienna = 160, 82, 45	silver = 192, 192, 192	skyblue = 135, 206, 235	slateblue = 106, 90, 205
slategray = 112, 128, 144	snow = 255, 250, 250	springgreen = 0, 255, 127	steelblue = 70, 130, 180	tan = 210, 180, 140
teal = 0, 128, 128	thistle = 216, 191, 216	tomato = 253, 99, 71	turquoise = 64, 224, 208	violet = 238, 130, 238
	white = 255, 255, 255		yellow = 255, 255, 0	

wheat = 245, 222, 179		whitesmoke = 245, 245, 245		yellowgreen = 154, 205, 50
--------------------------	--	-------------------------------	--	-------------------------------

## dump\_one command

### Syntax:

```
dump_one dump-ID
```

- dump-ID = ID of previously defined dump

### Examples:

```
dump_one mine  
dump_one 2
```

### Description:

Dump the current state of the lattice to the dump file defined by the [dump](#) command with this *dump-ID*. This can be useful before or after a run, if the [dump](#) command itself did not produce a snapshot at the desired time or state.

The information dumped is determined by the [dump](#) command which must have been previously specified to use the `dump_one` command.

### Restrictions:

This command cannot be used to trigger the very first snapshot written to the file specified with the [dump](#) command.

### Related commands:

[dump](#)

**Default:** none

## echo command

### Syntax:

```
echo style
```

- style = *none* or *screen* or *log* or *both*

### Examples:

```
echo both  
echo log
```

### Description:

This command determines whether SPPARKS echoes each input script command to the screen and/or log file as it is read and processed. If an input script has errors, it can be useful to look at echoed output to see the last command processed.

**Restrictions:** none

**Related commands:** none

### Default:

```
echo log
```

## ecoord command

### Syntax:

```
ecoord N eng
```

- N = coordination number (see asterisk form below)
- eng = energy of site with this coordination number (energy units)

### Examples:

```
ecoord 8 5.6  
ecoord 0 1.0e20  
ecoord * 1.0  
ecoord 8*12 10.0
```

### Description:

This command sets the energy of an occupied site in a lattice as a function of coordination number, where coordination = the number of occupied neighbor sites. See the [app\\_style diffusion nonlinear](#) command for how the energy change of the system due to a diffusive hop is used to calculate a probability for the hop to occur.

Typically, Nmax+1 values should be specified by using this command one or more times, with N varying from 0 to Nmax, when Nmax is the number of neighbor sites for each lattice site.

The N index can be specified in one of two ways. An explicit numeric value can be used, as in the 1st example above. Or a wild-card asterisk can be used to set the energy value for multiple coordination numbers. This takes the form "\*" or "\*n" or "n\*" or "m\*n". If Nmax = the number of neighbor sites, then an asterisk with no numeric values means all coordination numbers from 0 to Nmax. A leading asterisk means all coordination numbers from 0 to n (inclusive). A trailing asterisk means all coordination numbers from n to Nmax (inclusive). A middle asterisk means all coordination numbers from m to n (inclusive).

Note that if the third example is specified first, followed by the first example, then the effect would be to set the energy value for all coordination numbers to 1.0, then overwrite the energy value for coordination number 8 to 5.6.

The *eng* value should be in the energy units defined by the application's Hamiltonian and should be consistent with the units used in any [temperature](#) command.

### Restrictions:

This command can only be used as part of the [app\\_style diffusion nonlinear](#) application.

### Related commands:

[deposition](#), [barrier](#)

### Default:

Energy values for all coordination numbers are set to 0.

## event command

### Syntax:

```
event Nsite site1 site2 site3 old1 old2 old3 rate new1 new2 new3
```

- Nsite = number of lattice sites involved in the event = 1,2,3
- site1,site2,site3 = *fcc* or *tet* or *oct*
- old1,old2,old3 = *er* or *h* or *he* or *vac*
- rate = rate constant for the event (inverse seconds or energy units)
- new1,new2,new3 = *er* or *h* or *he* or *vac*

### Examples:

```
event      1 tet h 1.78279E-9 he
event      1 oct h 1.78279E-9 he

event      2 tet tet h vac 0.98 vac h
event      2 tet oct h vac 1.89 vac h
event      2 tet oct vac h 0.68 h vac
event      2 tet tet he vac 0.49 vac he
event      2 oct oct he vac 1.49 vac he

event      3 tet oct oct h vac h 0.62 h h vac
event      3 tet oct tet h vac he 1.31 he h vac
event      3 tet oct tet he h vac 0.16 h vac he
event      3 tet oct oct h vac he 0.88 he h vac
event      3 tet oct oct he h vac 0.16 h vac he
```

### Description:

This command defines an event for the "app\_style erbium" application. It can be an event involving one, two, or three lattice sites, as specified by *Nsite*. The first site is the central site which owns the event. The other 2 sites (if specified) are neighbors of the central site.

[App\\_style erbium](#) operates on a 3-fold lattice which contains fcc, tetrahedral, and octahedral sites. The *site1*, *site2*, and *site3* settings specify which kinds of sites are involved in the event: *fcc* or *tet* or *oct*. If *Nsite* = 1, then only *site1* is specified. If *Nsite* = 2, then only *site1* and *site2* are specified.

The *old1*, *old2*, and *old3* settings specify what atoms must be on those sites in order for the event to potentially take place. The possible atoms are *er* for erbium, *h* for hydrogen, *he* for helium, and *vac* for a vacant site. E.g. in the first example above, a Hydrogen atom must be on a tetrahedral site for the event to be possible.

The *rate* setting determines the relative rate at which the event will occur. For *Nsite*=1 events, the units are inverse seconds. For *Nsite*=2 or *Nsite*=3 events, the units are energy, which is converted into a rate via the formula:

$$\text{rate} = \exp(-\text{energy}/kT)$$

where T is the [temperature](#) you have specified.

In this case the *rate* setting should be in the energy units defined by the application's Hamiltonian and should be



consistent with the units used in the [temperature](#) command.

The *new1*, *new2*, and *new3* settings specify what atoms will be on which sites if the event takes place. As with the *old* settings, the possible atoms are *er* for erbium, *h* for hydrogen, *he* for helium, and *vac* for a vacant site. E.g. in the first example above, a Hydrogen atom on a tetrahedral site transmutes into a Helium atom if the event takes place.

Note that the set of Nsite=1,2,3 events listed above are a reasonably full description of a reaction/diffusion model for hydrogen interstitials in an erbium lattice.

**Restrictions:** none

This command can only be used as part of the [app\\_style erbium](#) application.

**Related commands:**

[app\\_style erbium](#)

**Default:** none

## if command

### Syntax:

```
if value1 operator value2 then command1 else command2
```

- value1 = 1st value
- operator = "" or ">=" or "==" or "!="
- value2 = 2nd value
- then = required word
- command1 = command to execute if condition is met
- else = optional word
- command2 = command to execute if condition is not met (optional argument)

### Examples:

```
if ${steps} > 1000 then exit
if $x <= $y then "print X is smaller = $x" else "print Y is smaller = $y"
if ${eng} > 0.0 then "timestep 0.005"
if ${eng} > ${eng_previous} then "jump file1" else "jump file2"
```

### Description:

This command provides an in-then-else test capability within an input script. Two values are numerically compared to each other and the result is TRUE or FALSE. Note that as in the examples above, either of the values can be variables, as defined by the [variable](#) command, so that when they are evaluated when substituted for in the if command, a user-defined computation will be performed which can depend on the current state of the simulation.

If the result of the if test is TRUE, then command1 is executed. This can be any valid SPPARKS input script command. If the command is more than 1 word, it should be enclosed in double quotes, so that it will be treated as a single argument, as in the examples above.

The if command can contain an optional "else" clause. If it does and the result of the if test is FALSE, then command2 is executed.

Note that if either command1 or command2 is a bogus SPPARKS command, such as "exit" in the first example, then executing the command will cause SPPARKS to halt.

**Restrictions:** none

**Related commands:**

[variable](#)

**Default:** none

## include command

### Syntax:

```
include file
```

- file = filename of new input script to switch to

### Examples:

```
include newfile  
include in.run2
```

### Description:

This command opens a new input script file and begins reading SPPARKS commands from that file. When the new file is finished, the original file is returned to. Include files can be nested as deeply as desired. If input script A includes script B, and B includes A, then SPPARKS could run for a long time.

If the filename is a variable (see the [variable](#) command), different processor partitions can run different input scripts.

**Restrictions:** none

**Related commands:**

[variable](#), [jump](#)

**Default:** none

## inclusion command

### Syntax:

```
inclusion x y z r
```

- $x,y,z$  = position of center of protein inclusion
- $r$  = radius of the protein

### Examples:

```
inclusion 10 12 0.0 2.0  
inclusion 10 12 5.4 5.0
```

### Description:

This command defines protein sites on a lattice and can only be used by [app\\_style membrane](#) applications.

Think of the protein as a sphere (or circle) centered at  $x,y,z$  and with a radius of  $r$ . All lattice sites within the sphere (or circle) will be flagged as protein (as opposed to lipid or solvent). For lattices with a 2d geometry, the  $z$  value should be specified as 0.0.

**Restrictions:** none

This command can only be used as part of the [app\\_style pore](#) applications.

### Related commands:

[app\\_style membrane](#)

**Default:** none

## jump command

### Syntax:

```
jump file label
```

- file = filename of new input script to switch to
- label = optional label within file to jump to

### Examples:

```
jump newfile
jump in.run2 runloop
```

### Description:

This command closes the current input script file, opens the file with the specified name, and begins reading SPPARKS commands from that file. The original file is not returned to, although by using multiple jump commands it is possible to chain from file to file or back to the original file.

Optionally, if a 2nd argument is used, it is treated as a label and the new file is scanned (without executing commands) until the label is found, and commands are executed from that point forward. This can be used to loop over a portion of the input script, as in this example. These commands perform 10 runs, each of 10000 steps, and create 10 dump files named file.1, file.2, etc. The [next](#) command is used to exit the loop after 10 iterations. When the "a" variable has been incremented for the tenth time, it will cause the next jump command to be skipped.

```
variable a loop 10
label loop
run 5.0
next a
jump in.1j loop
```

If the jump *file* argument is a variable, the jump command can be used to cause different processor partitions to run different input scripts. In this example, SPPARKS is run on 40 processors, with 4 partitions of 10 procs each. An in.file containing the example variable and jump command will cause each partition to run a different simulation.

```
mpirun -np 40 lmp_ibm -partition 4x10 -in in.file

variable f world script.1 script.2 script.3 script.4
jump $f
```

### Restrictions:

If you jump to a file and it does not contain the specified label, SPPARKS will come to the end of the file and exit.

### Related commands:

[variable](#), [include](#), [label](#), [next](#)

**Default:** none

## label command

### Syntax:

```
label ID
```

- ID = string used as label name

### Examples:

```
label xyz  
label loop
```

### Description:

Label this line of the input script with the chosen ID. Unless a jump command was used previously, this does nothing. But if a [jump](#) command was used with a label argument to begin invoking this script file, then all command lines in the script prior to this line will be ignored. I.e. execution of the script will begin at this line. This is useful for looping over a section of the input script as discussed in the [jump](#) command.

**Restrictions:** none

**Related commands:** none

**Default:** none

## lattice command

### Syntax:

```
lattice style args
```

- style = *none* or *line/2n* or *sq/4n* or *sq/8n* or *tri* or *sc/6n* or *sc/26n* or *bcc* or *fcc* or *diamond* or *fcc/octa/tetra* or *random/1d* or *random/2d* or *random/3d*

```
none args: none
    all other styles except random = scale
    scale = lattice constant (distance units)

random/1d args = Nrandom cutoff
random/2d args = Nrandom cutoff
random/3d args = Nrandom cutoff
    Nrandom = # of random sites
    cutoff = distance within which sites are connected (distance units)
```

### Examples:

```
lattice sq/4n 1.0
lattice fcc 3.52
lattice random/3d 10000 2.0
lattice none
```

### Description:

Define a lattice for use by other commands. In SPPARKS, a lattice is simply a set of points in space, determined by a unit cell with basis atoms, that is replicated infinitely in all dimensions. The arguments of the lattice command can be used to define a wide variety of crystallographic lattices.

A lattice is used by SPPARKS in two ways. First, the [create\\_sites](#) command creates "sites" on the lattice points inside the simulation box. Sites are used by an on-lattice or off-lattice application, specified by the [app\\_style](#) command, which define events that change the values associated with sites (e.g. a spin flip) or the coordinates of the site itself (for off-lattice applications).

Second, the lattice spacing in the x,y,z dimensions is used by other commands such as the [region](#) command to define distance units and define geometric extents, for example in specifying the size of the simulation box via the [create\\_box](#) command.

The lattice style must be consistent with the dimension of the simulation - see the [dimension](#) command and descriptions of each style below.

A lattice consists of a unit cell, a set of basis sites within that cell. The vectors  $a_1, a_2, a_3$  are the edge vectors of the unit cell. This is the nomenclature for "primitive" vectors in solid-state crystallography, but in SPPARKS the unit cell they determine does not have to be a "primitive cell" of minimum volume.

For on-lattice applications (see the [app\\_style](#) command), the lattice definition also infers a connectivity between lattice sites, which is used to generate the list of neighbors of each site. This information is ignored for off-lattice applications. This means that for a 2d off-lattice application, it makes no difference whether a *sq/4n* or *sq/8n* lattice is used; they both simply generate a square lattice of points.

---

In the style descriptions that follow,  $a$  = the lattice constant defined by the lattice command. Sites within a unit cell are defined as  $(x,y,z)$  where  $0.0 \leq x,y,z < 1.0$ .

A lattice of style *line/2n* is a 1d lattice with  $a_1 = a$  0 0 and one basis site per unit cell at (0,0,0). Each lattice point has 2 neighbors.

Lattices of style *sq/4n* and *sq/8n* are 2d lattices with  $a_1 = a$  0 0 and  $a_2 = 0$  a 0, and one basis site per unit cell at (0,0,0). The *sq/4n* style has 4 neighbors per site (east/west/north/south); the *sq/8n* style has 8 neighbors per site (same 4 as *sq/4n* plus 4 corner points).

A lattice of style *tri* is a 2d lattice with  $a_1 = a$  0 0 and  $a_2 = 0$  sqrt(3)\*a 0, and two basis sites per unit cell at (0,0,0) and (0.5,0.5,0). Each lattice points has 6 neighbors.

Lattices of style *sc/6n* and *sc/26n* are 3d lattices with  $a_1 = a$  0 0 and  $a_2 = 0$  a 0 and  $a_3 = 0$  0 a, and one basis site per unit cell at (0,0,0). The *sc/6n* style has 6 neighbors per site (east/west/north/south/up/down); the *sc/26n* style has 26 neighbors per site (surrounding cube including edge and corner points).

Lattices of style *bcc* and *fcc* and *diamond* are 3d lattice with  $a_1 = a$  0 0 and  $a_2 = 0$  a 0 and  $a_3 = 0$  0 a. There are two basis sites per unit cell for *bcc*, 4 basis sites for *fcc*, and 8 sites for *diamond*. The location of the basis sites are defined in any solid-state physics or crystallography text. The *bcc* style has 8 neighbors per site, the *fcc* has 12, and the *diamond* has 4.

A lattice of style *fcc/octa/tetra* is a 3d lattice with  $a_1 = a$  0 0 and  $a_2 = 0$  a 0 and  $a_3 = 0$  0 a. There are 16 basis sites per unit cell, which consist of 4 fcc sites plus 4 octahedral and 8 tetrahedral interstitial sites. Again, these are defined in solid-state physics texts. There are 26 neighbors per fcc and octahedral site, and 14 neighbors per tetrahedral site. More specifically, the neighbors are as follows:

- neighbors of each fcc site: 12 fcc, 6 octa, 8 tetra
- neighbors of each octa site: 6 fcc, 12 octa, 8 tetra
- neighbors of each tetra site: 4 fcc, 4 octa, 6 tetra

The *random* lattice styles are 1d, 2d, and 3d lattices with  $a_1 = 1$  0 0 and  $a_2 = 0$  1 0 and  $a_3 = 0$  0 1. Note that no *scale* parameter is defined and the unit cell is a unit cube, not a cube with side length  $a$ . Thus a [region](#) command using one of these lattices will define its geometric region directly, not as multiples of the *scale* parameter. When the [create\\_sites](#) command is used, it will generate a collection of Nrandom points within the corresponding 1d, 2d, or 3d region or simulation box. The number of neighbors per site is defined by the specified *cutoff* parameter. Two sites I,J will be neighbors of each other if they are closer than the *cutoff* distance apart.

---

The command "lattice none" can be used to turn off a previous lattice definition. Any command that attempts to use the lattice directly will then generate an error. No additional arguments need be used with "lattice none".

---

**Restrictions:** none

**Related commands:**

[dimension](#), [create\\_sites](#), [region](#)

**Default:** none



## log command

### Syntax:

```
log file
```

- file = name of new logfile

### Examples:

```
log log.equil
```

### Description:

This command closes the current SPPARKS log file, opens a new file with the specified name, and begins logging information to it. If the specified file name is *none*, then no new log file is opened.

If multiple processor partitions are being used, the file name should be a variable, so that different processors do not attempt to write to the same log file.

The file "log.spk" is the default log file for a SPPARKS run. The name of the initial log file can also be set by the command-line switch -log. See [this section](#) for details.

**Restrictions:** none

**Related commands:** none

### Default:

The default SPPARKS log file is named log.spk

## next command

### Syntax:

```
next variables
```

- variables = one or more variable names

### Examples:

```
next x
next a t x myTemp
```

### Description:

This command is used with variables defined by the [variable](#) command. It assigns the next value to the variable from the list of values defined for that variable by the [variable](#) command. Thus when that variable is subsequently substituted for in an input script command, the new value is used.

See the [variable](#) command for info on how to define and use different kinds of variables in SPPARKS input scripts. If a variable name is a single lower-case character from "a" to "z", it can be used in an input script command as \$a or \$z. If it is multiple letters, it can be used as \${myTemp}.

If multiple variables are used as arguments to the *next* command, then all must be of the same variable style: *index*, *loop*, *universe*, or *uloop*. An exception is that *universe*- and *uloop*-style variables can be mixed in the same *next* command. *Equal*- or *world*-style variables cannot be incremented by a next command. All the variables specified are incremented by one value from their respective lists.

When any of the variables in the next command has no more values, a flag is set that causes the input script to skip the next [jump](#) command encountered. This enables a loop containing a next command to exit.

When the next command is used with *index*- or *loop*-style variables, the next value is assigned to the variable for all processors. When the next command is used with *universe*- or *uloop*-style variables, the next value is assigned to whichever processor partition executes the command first. All processors in the partition are assigned the same value. Running SPPARKS on multiple partitions of processors via the "-partition" command-line switch is described in [this section](#) of the manual. *Universe*- and *uloop*-style variables are incremented using the files "tmp.spparks.variable" and "tmp.spparks.variable.lock" which you will see in your directory during such a SPPARKS run.

Here is an example of running a series of simulations using the next command with an *index*-style variable. If this input script is named in.polymer, 8 simulations would be run using data files from directories run1 thru run8.

```
variable d index run1 run2 run3 run4 run5 run6 run7 run8
shell cd $d
read_data data.polymer
run 10000
shell cd ..
clear
next d
jump in.polymer
```

If the variable "d" were of style *universe*, and the same in.polymer input script were run on 3 partitions of processors, then the first 3 simulations would begin, one on each set of processors. Whichever partition finished first, it would assign variable "d" the 4th value and run another simulation, and so forth until all 8 simulations were finished.

Jump and next commands can also be nested to enable multi-level loops. For example, this script will run 15 simulations in a double loop.

```
variable i loop 3
variable j loop 5
clear
...
read_data data.polymer.$i$j
print Running simulation $i.$j
run 10000
next j
jump in.script
next i
jump in.script
```

**Restrictions:** none

**Related commands:**

[jump](#), [include](#), [shell](#), [variable](#),

**Default:** none

## pair\_coeff command

### Syntax:

```
pair_coeff I J args ...
```

- I,J = atom types (see asterisk form below)
- args = coefficients for one or more pairs of atom types

### Examples:

#### Examples:

```
pair_coeff 1 2 1.0 1.0 2.5  
pair_coeff 2 * 1.0 1.0
```

### Description:

Specify the pairwise force field coefficients for one or more pairs of atom types. The number and meaning of the coefficients depends on the pair style.

I and J can be specified in one of two ways. Explicit numeric values can be used for each, as in the 1st example above.  $I \leq J$  is required. SPPARKS sets the coefficients for the symmetric J,I interaction to the same values.

A wild-card asterisk can be used in place of or in conjunction with the I,J arguments to set the coefficients for multiple pairs of atom types. This takes the form "\*" or "\*n" or "n\*" or "m\*n". If N = the number of atom types, then an asterisk with no numeric values means all types from 1 to N. A leading asterisk means all types from 1 to n (inclusive). A trailing asterisk means all types from n to N (inclusive). A middle asterisk means all types from m to n (inclusive). Note that only type pairs with  $I \leq J$  are considered; if asterisks imply type pairs where  $J < I$ , they are ignored.

Note that a pair\_coeff command can override a previous setting for the same I,J pair. For example, these commands set the coeffs for all I,J pairs, then overwrite the coeffs for just the I,J = 2,3 pair:

```
pair_coeff * * 1.0 1.0 2.5  
pair_coeff 2 3 2.0 1.0 1.12
```

For many potentials, if coefficients for type pairs with  $I \neq J$  are not set explicitly by a pair\_coeff command, the values are inferred from the I,I and J,J settings by mixing rules. Details on the mixing as it pertains to individual potentials are described on the doc page for the potential.

Here is the list of pair styles defined in SPPARKS. More will be added as new applications are developed. Click on the style to display the formula it computes, arguments specified in the pair\_style command, and coefficients specified by the associated [pair\\_coeff](#) command:

- [pair\\_style lj/cut](#) - cutoff Lennard-Jones potential

**Restrictions:** none

**Related commands:**

pair\_style

**Default:** none

## pair\_style lj command

### Syntax:

```
pair_style lj Ntypes cutoff
```

- lj = style name of this pair style
- Ntypes = # of particle types
- cutoff = global cutoff for pairwise interactions (distance units)

### Examples:

```
pair_style lj 1 2.5  
pair_style lj 3 3.0
```

### Description:

The *lj/cut* style computes the standard 12/6 Lennard-Jones potential, given by

$$E = 4\epsilon \left[ \left( \frac{\sigma}{r} \right)^{12} - \left( \frac{\sigma}{r} \right)^6 \right] \quad r < r_c$$

Rc is the cutoff.

The following coefficients must be defined for each pair of particle types via the [pair\\_coeff](#) command, or by mixing as described below:

- epsilon (energy units)
- sigma (distance units)
- cutoff (distance units)

Note that sigma is defined in the LJ formula as the zero-crossing distance for the potential, not as the energy minimum at  $2^{1/6}$  sigma.

The last coefficients is optional. If not specified, the global LJ cutoff specified in the pair\_style command is used.

---

### Mixing info:

For atom type pairs I,J and I != J, the epsilon and sigma coefficients and cutoff distance for all of the lj/cut pair styles can be mixed. The style of mixing is *geometric*, which means that

```
epsilon_ij = sqrt(epsilon_i * epsilon_j)  
sigma_ij = sqrt(sigma_i * sigma_j)
```

---

**Restrictions:** none

**Related commands:** none

**Default:** none

## pair\_style command

### Syntax:

```
pair_style style args ...
```

- style = one of the styles from the list below
- args = arguments used by a particular style

### Examples:

```
pair_style lj 1 1 2.5
```

### Description:

Set the formula(s) SPPARKS uses to compute pairwise energy of interaction between sites or particles in an off-lattice application.

The coefficients associated with a pair style are typically set for each pair of particle types, and are specified by the [pair\\_coeff](#) command.

Here is the list of pair styles defined in SPPARKS. More will be added as new applications are developed. Click on the style to display the formula it computes, arguments specified in the pair\_style command, and coefficients specified by the associated [pair\\_coeff](#) command:

- [pair\\_style lj/cut](#) - cutoff Lennard-Jones potential

**Restrictions:** none

**Related commands:**

[pair\\_style](#)

**Default:** none



## pin command

### Syntax:

```
pin fraction multiflag nthresh
```

- fraction = fraction of sites (0 to 1) to convert to pinned sites
- multiflag = 0 for single sites, 1 for sites+neighbors
- nthresh = # of neighbor sites which must have different spins

### Examples:

```
pin 0.1 0 2
```

### Description:

This command converts sites on a lattice to pinned sites by setting their spin value to  $Q+1$ , where  $Q$  is defined by a Potts model. This command can only be used by the [app\\_style potts/pin](#) application. The size of the inclusions and their location (anywhere or preferentially near grain boundaries) can be controlled by the *multiflag* and *nthresh* parameters.

The way pinned sites are selected is as follows. A pinned site is chosen randomly. If the site is already a pinned site, then another site is selected. If *multiflag* is set to 1, then if any of the site's neighbors are already a pinned site, then another site is selected. If *nthresh* is a non-zero value, then the # of neighbor sites with spin values different than the chosen site are counted. If the count is less than *nthresh*, then another site is selected.

Once the site is selected, just that site is converted to a pinned site if *multiflag* is 0. If *multiflag* is 1, then the site plus all its neighbors are converted to pinned sites.

This process continues until the desired fraction of changed sites is achieved. The entire process is done in a way that should be independent of the number of processors used to run a particular simulation.

Note that if you pick a large volume fraction and/or a high value for *nthresh* it is possible that SPPARKS will never find enough valid sites to convert to pinned sites. It will then loop endlessly.

**Restrictions:** none

This command can only be used as part of the [app\\_style potts/pin](#) applications.

### Related commands:

[app\\_style potts/pin](#)

**Default:** none

## print command

### Syntax:

```
print string
```

- string = text string to print. may contain variables

### Examples:

```
print "Done with equilibration"  
print "The system temperature is now $t"
```

### Description:

Print a text string to the screen and logfile. The text string must be a single argument, so it should be enclosed in double quotes if it is more than one word. If variables are included in the string, they will be evaluated and their current values printed.

If you want the print command to be executed multiple times (with changing variable values) then the print command could appear in a section of the input script that is looped over (see the [jump](#) and [next](#) commands).

See the [variable](#) command for a description of *equal* style variables which are typically the most useful ones to use with the print command. Equal-style variables can calculate formulas involving mathematical operations, or references to other [variables](#).

**Restrictions:** none

**Related commands:**

[variable](#)

**Default:** none

## processors command

### Syntax:

```
processors Px Py Pz
```

- Px,Py,Pz = # of processors in each dimension of a 3d grid

### Examples:

```
processors 2 4 4
```

### Description:

Specify how processors are mapped as a 3d logical grid to the global simulation box for spatial on-lattice or off-lattice models.

When this command has not been specified, SPPARKS will choose Px, Py, Pz based on the dimensions of the global simulation box so as to minimize the surface/volume ratio of each processor's sub-domain.

Since SPPARKS does not load-balance by changing the grid of 3d processors on-the-fly, this command should be used to override the SPPARKS default if it is known to be sub-optimal for a particular problem.

The product of Px, Py, Pz must equal P, the total # of processors SPPARKS is running on. If multiple partitions are being used then P is the number of processors in this partition; see [this section](#) for an explanation of the -partition command-line switch.

If P is large and prime, a grid such as 1 x P x 1 will be required, which may incur extra communication costs.

### Restrictions:

This command must be used before the simulation box is defined by a [read\\_sites](#) or [create\\_box](#) command.

**Related commands:** none

### Default:

SPPARKS chooses Px, Py, Pz

## read\_sites command

### Syntax:

```
read_sites file
```

- file = name of data file to read in

### Examples:

```
read_sites data.potts
read_sites ../run7/data.potts.gz
```

### Description:

Read in a data file containing information SPPARKS needs to setup an [on-lattice or off-lattice application](#). The file can be ASCII text or a gzipped text file (detected by a .gz suffix). This is one of 2 ways to specify event sites ; see the [create\\_sites](#) command for another method.

A data file has a header and a body, as described below. The body of the file contains up to 3 sections: Sites, Neighbors, Values. Sites defines the coordinates of event sites. Neighbors define the neighbors of each site (only for on-lattice applications). Values assign per-site values to each site, which can also be done via the [set](#) command.

The read\_sites command can be used in one of 3 scenarios:

If a simulation box has not already been created and no event sites exist, then the data file defines the box size (in the header), and it must define Sites. It must also define Neighbors for on-lattice applications. The Values section is optional, since these can be set later via the [set](#) command.

If a simulation box has already been defined (by the "create\_box" command or a previous read\_sites command), but no sites have previously been defined, then the data file must define Sites. It must also define Neighbors for on-lattice applications. The Values section is optional.

If a simulation box has already been defined, and sites have previously been defined (by the "create\_sites" command or a previous read\_sites command), then no Sites or Neighbors can be specified, but the Values section may be used. This is a means of restarting a simulation using per-site info written out by the [dump](#) command and reformatted into a data file so it can be input by this command.

Note that the periodicity of the simulation box, as defined by the [boundary](#) command is not considered by this command when defining sites or neighbors. It is up to you to insure sites are not duplicated on a periodic boundary, or that a site's neighbor list does not include sites that are on the other side of the simulation box, across a non-periodic boundary. This is in contrast to the [create\\_sites](#) command which accounts for both of these issues when creating sites and neighbor lists.

---

The first line of the header of the data file is always skipped; it typically contains a description of the file. Then lines are read one at a time. Lines can have a trailing comment starting with '#' that is ignored. If the line is blank (only whitespace after comment is deleted), it is skipped. If the line contains a header keyword, the corresponding value(s) is read from the line. If it doesn't contain a header keyword, the line begins the body of the file.

The body of the file contains zero or more sections. The first line of a section has only a keyword. The next line is skipped. The remaining lines of the section contain values. The number of lines depends on the section keyword as described below. Zero or more blank lines can be used between sections. Sections can appear in any order, with a few exceptions as noted below.

The formatting of individual lines in the data file (indentation, spacing between words and numbers) is not important except that header and section keywords (e.g. dimension, xlo xhi, Sites, Values) must be capitalized as shown and can't have extra white space between their words - e.g. two spaces or a tab between "xlo and "xhi" is not valid.

---

These are the recognized header keywords. Header lines can come in any order. The value(s) are read from the beginning of the line. Thus the keyword *sites* should be in a line like "1000 sites"; the keyword *ylo yhi* should be in a line like "-10.0 10.0 ylo yhi". All these settings have a default value of 0, except the lo/hi box size defaults which are -0.5 and 0.5. A line need only appear if the value is different than the default. If the keyword values have already been defined (e.g. box sizes for a previously created simulation box), then the values in the data file must match.

- *dimension* = dimension of system = 1,2,3
- *sites* = number of sites
- *max neighbors* = max # of neighbors of any site
- *xlo xhi* = simulation box boundaries in x dimension
- *ylo yhi* = simulation box boundaries in y dimension
- *zlo zhi* = simulation box boundaries in z dimension

The *max neighbors* setting is only needed if the file contains a Neighbors section, which is only used for on-lattice applications.

The simulation box size is determined by the lo/hi settings. For 2d simulations, the *zlo zhi* values should be set to bound the z coords for atoms that appear in the file; the default of -0.5 0.5 is valid if all z coords are 0.0. The same rules hold for *ylo and yhi* for 1d simulations.

---

These are the possible section keywords for the body of the file: *Sites*, *Neighbors*, *Values*.

Each section is listed below. The format of each section is described including the number of lines it must contain and rules (if any) for where it can appear in the data file.

Any individual line in the various sections can have a trailing comment starting with "#" for annotation purposes. E.g. in the Sites section:

```
10 10.0 5.0 6.0 # impuity site
```

---

*Sites* section:

- one line per site
- line syntax: ID x y z

ID = global site ID (1-N)  
x y z = coordinates of site

- example:

```
101 7.0 0.0 3.0
```

There must be N lines in this section where N = number of sites and is defined by the *sites* keyword in the header section of the file. The lines can appear in any order.

---

*Neighbors* section:

- one line per site
- line syntax: ID n1 n2 n3 ...

ID = global site ID (1-N)  
n1 n2 n3 ... = IDs of neighbor sites

- example:

```
101 7 32 15 1004 ...
```

There must be N lines in this section where N = number of sites and is defined by the *sites* keyword in the header section of the file. The lines can appear in any order.

The number of neighbors can vary from site to site, but there can be no more than *max neighbors* for any one site. The neighbors of an individual site can be listed in any order.

---

*Values* section:

- one line per site
- line syntax: ID i1 i2 ... iN d1 d2 ... dN

ID = global site ID (1-N)  
i1,i2,...iN = integer values for the site  
d1,d2,...dN = floating point values for the site

- example:

```
101 1 3 4.0
```

There must be N lines in this section where N = number of sites and is defined by the *sites* keyword in the header section of the file. The lines can appear in any order.

The number of values per site that should be listed depends on the application which defines the number of integer and floating-point values per site. These are listed in order, with the integer values first, followed by the floating-point values.

---

### Restrictions:

To write gzipped dump files, you must compile SPPARKS with the -DSPPARKS\_GZIP option - see the [Making SPPARKS](#) section of the documentation.

### Related commands:

[create\\_box](#), [create\\_sites](#), [set](#)

**Default:** none

## region command

### Syntax:

```
region ID style args keyword value ...
```

- ID = user-assigned name for the region
- style = *block* or *cylinder* or *sphere* or *union* or *intersect*

```
block args = xlo xhi ylo yhi zlo zhi
    xlo,xhi,ylo,yhi,zlo,zhi = bounds of block in all dimensions (distance units)
cylinder args = dim c1 c2 radius lo hi
    dim = x or y or z = axis of cylinder
    c1,c2 = coords of cylinder axis in other 2 dimensions (distance units)
    radius = cylinder radius (distance units)
    lo,hi = bounds of cylinder in dim (distance units)
sphere args = x y z radius
    x,y,z = center of sphere (distance units)
    radius = radius of sphere (distance units)
union args = N reg-ID1 reg-ID2 ...
    N = # of regions to follow, must be 2 or greater
    reg-ID1,reg-ID2, ... = IDs of regions to jointogether
intersect args = N reg-ID1 reg-ID2 ...
    N = # of regions to follow, must be 2 or greater
    reg-ID1,reg-ID2, ... = IDs of regions to intersect
```

- zero or more keyword/value pairs may be appended
- keyword = *side*

```
side value = in or out
    in = the region is inside the specified geometry
    out = the region is outside the specified geometry
```

### Examples:

```
region 1 block -3.0 5.0 INF 10.0 INF INF
region 2 sphere 0.0 0.0 0.0 5 side out
region void cylinder y 2 3 5 -5.0 EDGE
region outside union 4 side1 side2 side3 side4
```

### Description:

This command defines a geometric region of space. Various other commands use regions. For example, the region can be filled with sites via the [create\\_sites](#) command.

The distance units used to define the region are setup by the [lattice](#) command which must be used before any regions are defined. The lattice command defines a lattice spacing and regions are defined in terms of this length scale. For example, if the lattice spacing is 3.0 and the region sphere radius is 2.5, then the size of the sphere is  $2.5 \times 3.0 = 7.5$ .

Commands which use regions typically test whether a lattice site is contained in the region or not. For this purpose, coordinates exactly on the region boundary are considered to be interior to the region. This means, for example, for a spherical region, a lattice site on the sphere surface would be part of the region if the sphere were defined with the *side in* keyword, but would not be part of the region if it were defined using the *side out* keyword. See more details on the *side* keyword below.

The lo/hi values for the *block* or *cylinder* styles can be specified as EDGE or INF. EDGE means they extend all the way to the global simulation box boundary. Note that this is the current box boundary; if the box changes size during a simulation, the region does not. INF means a large negative or positive number ( $1.0\text{e}20$ ), so it should encompass the simulation box even if it changes size. If a region is defined before the simulation box has been created (via [create\\_box](#) or [read\\_sites](#) commands), then an EDGE or INF parameter cannot be used.

**IMPORTANT NOTE:** Regions in SPPARKS are always 3d geometric objects, regardless of whether the [dimension](#) of the lattice is 1d or 2d or 3d. Thus when using regions in a 2d simulation, for example, you should be careful to define the region so that its intersection with the 2d x-y plane of the simulation has the 2d geometric extent you want. Also note that for 2d simulations, SPPARKS expects lattice sites to lie in the  $z=0$  plane, and similarly for 1d ( $y = z = 0$ ), so the regions you define as input to the [create\\_box](#) command should reflect that.

For style *cylinder*, the c1,c2 params are coordinates in the 2 other dimensions besides the cylinder axis dimension. For dim = x,  $c1/c2 = y/z$ ; for dim = y,  $c1/c2 = x/z$ ; for dim = z,  $c1/c2 = x/y$ . Thus the third example above specifies a cylinder with its axis in the y-direction located at  $x = 2.0$  and  $z = 3.0$ , with a radius of 5.0, and extending in the y-direction from -5.0 to the upper box boundary.

The *union* style creates a region consisting of the volume of all the listed regions combined. The *intersect* style creates a region consisting of the volume that is common to all the listed regions.

The *side* keyword determines whether the region is considered to be inside or outside of the specified geometry. Using this keyword in conjunction with *union* and *intersect* regions, complex geometries can be built up. For example, if the interior of two spheres were each defined as regions, and a *union* style with *side* = out was constructed listing the region-IDs of the 2 spheres, the resulting region would be all the volume in the simulation box that was outside both of the spheres.

**Restrictions:** none

**Related commands:**

[lattice](#), [create\\_sites](#)

**Default:**

The option defaults are *side* = in.



## reset\_time command

### Syntax:

```
reset_time time
```

- time = new time

### Examples:

```
reset_time 0.0  
reset_time 100.0
```

### Description:

Set the current time to the specified value. This can be useful if a preliminary run was performed and you wish to reset the time before performing a subsequent run.

**Restrictions:** none

**Related commands:** none

**Default:** none

## run command

### Syntax:

```
run delta keyword values ...
```

- delta = run simulation for this amount of time (seconds)
- zero or more keyword/value pairs may be appended
- keyword = *upto* or *pre* or *post*

```
upto value = none
pre value = no or yes
post value = no or yes
```

### Examples:

```
run 100.0
run 10000.0 upto
run 1000 pre no post yes
```

### Description:

This command runs a Monte Carlo application for the specified number of seconds of simulation time. If multiple run commands are used, the simulation is continued, possibly with new settings which were specified between the successive run commands.

The [application](#) defines Monte Carlo events and probabilities which determine the amount of physical time associated with each event.

A value of delta = 0.0 is acceptable; only the status of the system is computed and printed without making any Monte Carlo moves.

The *upto* keyword means to perform a run starting at the current time up to the specified time. E.g. if the current time is 10.0 and "run 100.0 upto" is used, then an additional 90.0 seconds will be run. This can be useful for very long runs on a machine that allocates chunks of time and terminate your job when time is exceeded. If you need to restart your script multiple times (reading in the last restart file), you can keep restarting your script with the same run command until the simulation finally completes.

The *pre* and *post* keywords can be used to streamline the setup, clean-up, and associated output to the screen that happens before and after a run. This can be useful if you wish to do many short runs in succession (e.g. SPPARKS is being called as a library which is doing other computations between successive short SPPARKS runs).

By default (pre and post = *yes*), SPPARKS initializes data structures and computes propensities before every run. After every run it gathers and prints timings statistics. If a run is just a continuation of a previous run, the data structure initialization is not necessary. So if *pre* is specified as *no* then the initialization is skipped. Propensities are still re-computed since commands between runs or a driver program may have changed the system, e.g. by altering lattice values. Note that if *pre* is set to *no* for the very 1st run SPPARKS performs, then it is overridden, since the initialization must be done.

If *post* is specified as *no*, the full timing summary is skipped; only a one-line summary timing is printed.

**Restrictions:** none

**Related commands:** none

**Default:**

The option defaults are pre = yes and post = yes.

## sector command

### Syntax:

```
sector flag keyword value ...
```

- flag = *yes* or *no* or *N* where  $N = 2, 4, 8$
- zero or more keyword/value pairs may be appended
- keyword = *tstop* or *nstop*

```
tstop value = dt
dt = elapsed time for events to perform within sector (seconds)
nstop value = N
N = average number of events per site to perform within sector
```

### Examples:

```
sector no
sector yes
sector 4
sector yes nstop 0.5
sector yes tstop 5.0
```

### Description:

This command partitions the portion of the simulation domain owned by each processor into sectors or sub-domains. It can only be used for [on-lattice applications](#). Typically, it is used in a parallel simulation, to enable parallelism, but it can also be used on a single processor.

If sectoring is enabled via the *yes* setting, then for 1d lattices, each processor's sub-domain is partitioned into 2 halves, for 2d lattices, each processor's sub-domain is partitioned into 4 quadrants, and for 3d lattices it is partitioned into 8 octants. If the *N* setting is used instead, then the number of sectors can be specified directly. This may be useful in some models to reduce communication. A 3d lattice can use 2 (x only) or 4 sectors (x and y), instead of the default 8 (x and y and z). A 2d lattice can use 2 sectors (x only), instead of the default 4 (x and y). Note that if no sectors are used in a dimension, then there must be only one processor assigned to that dimension of the simulation box (see the [app\\_style procs](#) command). For example, if "sector 2" is used for a 2d lattice, then the processor layout must be Px1, where P is the total number of processors.

If sectors are turned on, then a kinetic Monte Carlo (KMC) or rejection KMC (rKMC) algorithm is performed in the following manner. Events or sites are selected within the first sector on each processor, via a [solver](#) or [sweeping method](#). Communication is then done between processors to update sector boundaries. Then all processors move to the next sector, and the process is repeated. Thus a single sweep over the entire lattice is performed in 2 (or 4 or 8) stages for 1d (of 2d or 3d) lattices, as sectors are processed one at a time, followed by the appropriate communication. This procedure insure events occurring on one processor do not conflict with events performed by other processors.

The optional keywords determine how much time is spent on each sector (i.e. how many events are performed) before moving to the next sector. See the discussion below for what they mean when sectoring is set to *no*.

Note that using sectors turns an exact KMC or rKMC algorithm into an approximate one, in the spirit of [Amar](#). This is because events are occurring within a sector while the state of the system on the boundary of the sector is held frozen. If the time-per-sector is too large, this will require less communication but will induce incorrect

dynamics at the sector boundaries. Conversely, if the time-per-sector is too small, the simulation will perform few events per sector and spend too much time communicating.

If the *tstop* keyword is set to a value  $> 0.0$ , it sets the time per sector to the specified value. For a KMC algorithm, events are performed until this time threshold is reached. The final event, whose time  $\geq tstop$ , is not accepted. For a rKMC algorithm, the time per attempted event  $= dt\_sweep$  is defined by the application, and the number of attempted events in each sector is set to  $nsite * \text{int}(tstop/dt\_sweep)$ . Because of integer truncation, the simulation time increment in rKMC may differ slightly from the specified *tstop*.

If the *nstop* keyword is set to a value  $> 0.0$ , it sets the average number of events (or attempts) per site. For example, an *nstop* value of 2.0 means attempt 2 events per site for a rKMC algorithm. For a KMC algorithm, this is converted into a time using  $pmax =$  the maximum propensity per site. At the start of each visit to a sector, the per-site propensity for the sector  $= psect$ , is computed. *Psect* is the total propensity of the sector divided by the total number of active sites, which are those with propensity greater than zero. After all sectors have been visited, *pmax* is set to the largest value of *psect* across all processors and sectors, and the threshold time for the next visit to each sector is set to  $nstop/pmax$ .

In the KMC case, this means that if the total propensity of the system decreases as the simulation proceeds (e.g. grain growth occurs), then the effective time per sweep will increase in an adaptive way. Said another way, the number of events per sweep will remain roughly constant, as the time per event increases. In the rKMC case, the time per attempt is constant due to the use of a null-bin, so there is no adaptivity.

If neither the *tstop* or *nstop* keywords are specified, a default value of *nstop* = 1.0 is used, meaning one event per site is performed or attempted in the KMC or rKMC algorithm in each sector. This should give good behavior in many applications, meaning high accuracy is achieved with good parallel performance due to a modest amount of communication being performed.

Note that it makes no sense to specify both *tstop* and *nstop* since they define the time-per-sector in different ways. When *tstop* is specified, it sets *nstop* to 0.0. Likewise when *nstop* is specified, it sets *tstop* to 0.0. Thus if both are used, the last setting takes precedence.

If sectors are turned off via the *no* setting, then the *nstop* or *tstop* settings still have an effect for rKMC simulations where the *sweep* style is set to *color*. They determine how many times the sites associated with each color are looped over before moving to the next color. Normally, this should just be 1, which is the *nstop* default, but this can be changed if desired.

### Restrictions:

This command can only be used as part of on-lattice applications as specified by the *app\_style* command.

### Related commands:

*app\_style*, *solve\_style*, *sweep*

### Default:

The default for sectoring is *no* and the option defaults are *nstop* = 1.0 and *tstop* = 0.0.

---

(Amar) Shin and Amar, Phys Rev B, 71, 125432-1-125432-13 (2005).

## seed command

### Syntax:

```
seed Nvalue
```

- Nvalue = seed for a random number generator (positive integer)

### Examples:

```
seed 5838959
```

### Description:

This command sets the random number seed for a master random number generator which is used by SPPARKS to initialize auxiliary random number generators which in turn are used for all operations in the code requiring random numbers. Thus this command is needed to perform any simulation with SPPARKS.

**Restrictions:** none

**Related commands:** none

**Default:** none

## set command

### Syntax:

```
set label style args keyword values ...
```

- *label* = *site* or *iN* or *dN* or *x* or *y* or *z* or *xyz*
- *style* = *value* or *range* or *displace*

```
value arg = nvalue
    nvalue = value to set sites to
range args = lo hi
    lo,hi = range of values to set sites to
unique args = none
displace arg = delta
    delta = max distance to displace the site
```

- zero or more keyword/value pairs may be appended
- *keyword* = *fraction* or *region* or *loop* or *if*

```
fraction value = frac
    frac = number > 0 and <= 1.0
region args = region-ID
    region-ID = ID of region that sites must be part of
loop arg = all or local
    all = loop over all sites
    local = loop over only sites I own
if args = label2 op nvalue2
    label2 = id or iN or dN or x or y or z
    op = "=" or "<=" or ">" or "!="
    nvalue2 = value to compare site value to
```

### Examples:

```
set i1 value 2 fraction 0.5
set d1 range 1.0 2.0 loop local
set xyz displace 0.2
set i1 range 1 50 if x <20 if i2 = 3
```

### Description:

Reset a per-site value for one or more sites. Each on-lattice or off-lattice application defines what per-site values are stored with each site in its model. When sites are created by the [create\\_sites](#) or [read\\_sites](#) commands, their per-site values may be set to zero or to values specified by those commands. This command enables the values to be changed, either before the first [run](#), or between runs.

The *label* determines which per-site quantity is set. *iN* and *dN* mean the Nth integer or floating-point quantity, with  $1 \leq N \leq N_{\max}$ .  $N_{\max}$  is defined by the application. If *label* is specified as *site* it is the same as *i1*. For off-lattice applications, the *x* or *y* or *z* or *xyz* coordinates of each site can be adjusted.

For label *iN* or *dN* or *site*, the styles *value* or *range* can be used.

For style *value*, the per-site quantity is set to the specified *nvalue*, which should be either an integer or floating-point numeric value, depending on what kind of per-site quantity is being set.

For style *range*, the per-site quantity is set to a random value between *lo* and *hi* (inclusive). Both *lo* and *hi* should be either integer or floating-point numeric values, depending on what kind of per-site quantity is being set.

For style *unique*, the per-site quantity is set to the site ID, which is effectively a value unique to each site. This can be useful, for example, for setting the initial spin of each site to a unique value.

NOTE: The *displace* style is not yet implemented but will be soon. The following text explains how it will work for off-lattice applications.

For label *x* or *y* or *z* or *xyz*, the style *displace* must be used. For *x* or *y* or *z*, the corresponding coordinate of each site is displaced by a random distance between *-delta* and *delta*. For *xyz* the site is displaced to a new random point within a sphere of radius *delta* surrounding the site (or a circle for 2d models, or a line segment for 1d models).

---

The optional keywords enables selection of sites whose *label* quantity will be reset to a new value. Note that these optional keywords can be used in various combinations, and the *if* keyword can be used multiple times, to select desired sites.

The keyword *fraction* means that only a fraction of the sites will be reset, where  $0 < \textit{frac} \leq 1.0$ . For each site a random number *R* is generated and the reset only occurs if  $R < \textit{frac}$ .

The keyword *region* means that only sites in the specified region will be reset. Note that a defined region can be a union or intersection of several regions and can be either inside or outside a geometric boundary; see the [region](#) command for details.

The keyword *loop* determines how sites in the simulation box are looped over when their per-site quantity is reset. In general, each processor will own some subset *Nlocal* of the total number of sites *Nglobal* in the simulation box. The entire set of sites are assumed to have IDs from 1 to *Nglobal*. For *loop all*, each processor performs a loop from 1 to *Nglobal* and generates the new value for that site. If it owns the site, then it resets its value. This means that the changes to per-site values will be the same, independent of which processor owns which site. For *loop local*, each processor loops over only its sites from 1 to *Nlocal*. This may be faster, but if random numbers are used to determine new per-site values, it will give different answers depending on the the number of processors used.

The keyword *if* sets a condition that must be met in order for the per-site quantity to be reset. The per-site quantity specified by *label2* is compared to the numeric *nvalue2* and if the condition is not met, then the site is skipped.

**Restrictions:** none

**Related commands:**

[create\\_sites](#), [read\\_sites](#)

**Default:**

The default values for the optional keywords is *fraction* 1.0 and *loop* all. No region is defined by default nor are any *if*-tests.



## shell command

### Syntax:

```
shell style args
```

- style = *cd* or *mkdir* or *mv* or *rm* or *rmdir*

```
cd arg = dir
    dir = directory to change to
mkdir args = dir1 dir2 ...
    dir1,dir2 = one or more directories to create
mv args = old new
    old = old filename
    new = new filename
rm args = file1 file2 ...
    file1,file2 = one or more filenames to delete
rmdir args = dir1 dir2 ...
    dir1,dir2 = one or more directories to delete
```

### Examples:

```
shell cd sub1
shell cd ..
shell mkdir tmp1 tmp2 tmp3
shell rmdir tmp1
shell mv log.lammps hold/log.1
shell rm TMP/file1 TMP/file2
```

### Description:

Execute a shell command. Only a few simple file-based shell commands are supported, in Unix-style syntax. With the exception of *cd*, all commands are executed by only a single processor, so that files/directories are not being manipulated by multiple processors.

The *cd* style executes the Unix "cd" command to change the working directory. All subsequent SPPARKS commands that read/write files will use the new directory. All processors execute this command.

The *mkdir* style executes the Unix "mkdir" command to create one or more directories.

The *mv* style executes the Unix "mv" command to rename a file and/or move it to a new directory.

The *rm* style executes the Unix "rm" command to remove one or more files.

The *rmdir* style executes the Unix "rmdir" command to remove one or more directories. A directory must be empty to be successfully removed.

### Restrictions:

SPPARKS does not detect errors or print warnings when any of these Unix commands execute. E.g. if the specified directory does not exist, executing the *cd* command will silently not do anything.

**Related commands:** none

**Default:** none

## app\_style command

### Syntax:

```
app_style style args
```

- style = application style name
- args = args

### Examples:

```
app_style ising 100 100  
app_style potts 1000 1000 4
```

### Description:

This command ...

**Restrictions:** none

### Related commands:

[variable](#), ...

**Default:** none

## app\_style command

### Syntax:

```
app_style style args
```

- style = application style name
- args = args

### Examples:

```
app_style ising 100 100  
app_style potts 1000 1000 4
```

### Description:

This command ...

**Restrictions:** none

### Related commands:

[variable](#), ...

**Default:** none

## solve\_style command

### Syntax:

```
solve_style style args keyword value ...
```

- style = *linear* or *tree* or *group* or *none*

```
linear arg = none
tree arg = none
group args = hi lo
    hi,lo = range of allowed probabilities
none arg = none
```

- zero or more keyword/value pairs may be appended
- keyword = *ngroup*

```
ngroup value = N
    N = # of groups to use
```

### Examples:

```
solve_style linear
solve_style tree
solve_style group 1.0 1.0e-6
solve_style group 100.0 1.0 ngroup 10
```

### Description:

Choose a kinetic Monte Carlo (KMC) solver to use in your [application](#). If no [sweeper](#) is used then a solver is required.

A KMC solver picks events for your application to perform from a list of events and their associated probabilities. It does this using the standard [Gillespie](#) or [BKL](#) algorithm which also computes a timestep during which the chosen event occurs. The only difference between the various solver styles is the algorithm they use to select events which affects their speed and scalability as a function of the number of events they choose from. The *linear* solver may be suitable for simulations with few events; the *tree* or *group* solver should be used for larger simulations.

The *linear* style chooses an event by scanning the list of events in a linear fashion. Hence the cost to pick an event scales as  $O(N)$ , where  $N$  is the number of events.

The *tree* style chooses an event by creating a binary tree of probabilities and their sums, as in the [Gibson/Bruck](#) implementation of the Gillespie direct method algorithm. Its cost to pick an event scales as  $O(\log N)$ .

The *group* style chooses an event using the composition and rejection (CR) algorithm described originally in [Devroye](#) and discussed in [Slepoy](#). Its cost to pick an event scales as  $O(1)$  as it is a constant time algorithm. It requires that you bound the *hi* and *lo* probabilities for any event that will be considered with the solver. Note that for on-lattice applications this is typically the total probability of all events associated with a site. The value of *lo* must be  $> 0.0$  and *lo* cannot be  $\geq hi$ . For efficiency purposes it is good to choose bounds that are reasonably tight.

By default, the *group* style will create groups whose boundaries cascade downward in powers of 2 from *hi* to *lo*. I.e. the first group is from  $hi/2$  to  $hi$ , the second group is from  $hi/4$  to  $hi/2$ , and continuing until *lo* is reached. Note that for  $hi/lo = 1.0e6$ , there would thus be about 20 groups.

If the *ngroup* keyword is used, then it specifies the number of groups to use between *lo* and *hi* and they will be equal in extent. E.g. for *ngroup* = 3, the first group is from  $lo$  to  $lo + (hi-lo)/3$ , the second group is from  $lo + 2*(hi-lo)/3$ , and the third group is from  $lo + 2*(hi-lo)/3$  to  $hi$ .

**IMPORTANT NOTE:** For the *group* style, if an event is generated that has a probability = 0.0 (e.g. a site has no possible event), that is not a violation of the *lo* bound. However if an event is generated with a non-zero probability and the probability is less than *lo* or greater than *hi*, then the probability is reset by the solver to the *lo* or *hi* bound. If this occurs during a run, SPPARKS will print out a warning message (either before the run, or at the end of the script), since it indicates events have been selected using (slightly) different probabilities than the model generated. This allows you to set a different *lo* or *hi* bound and re-run the simulation.

The *none* style deletes any KMC solver previously defined. This may be useful for transitioning from a KMC solver in one run to a [sweeping method](#) with a rejection-KMC solver in a subsequent run.

### Restrictions:

The *ngroup* keyword can only be used with style *group*.

### Related commands:

[app\\_style](#), [sweep\\_style](#)

**Default:** none

---

**(Gillespie)** Gillespie, J Comp Phys, 22, 403-434 (1976); Gillespie, J Phys Chem, 81, 2340-2361 (1977).

**(BKL)** Bortz, Kalos, Lebowitz, J Comp Phys, 17, 10 (1975).

**(Gibson)** Gibson and Bruck, J Phys Chem, 104, 1876 (2000).

**(Devroye)** Devroye, [Non-Uniform Random Variate Generation](#), Springer-Verlag, New York (1986).

**(Slepoy)** Slepoy, Thompson, Plimpton, J Chem Phys, 128, 205101 (2008).

## app\_style command

### Syntax:

```
app_style style args
```

- style = application style name
- args = args

### Examples:

```
app_style ising 100 100  
app_style potts 1000 1000 4
```

### Description:

This command ...

**Restrictions:** none

### Related commands:

[variable](#), ...

**Default:** none

## stats command

### Syntax:

```
stats delta keyword values ...
```

- delta = time increment between statistical output (seconds)
- zero or more keyword/value pairs may be appended
- keyword = *delay* or *logfreq* or *loglinfreq*

```
delay value = tdelay
    tdelay = delay stats until at least this time (seconds)
logfreq or loglinfreq values = N factor
    N = number of repetitions per interval
    factor = scale factor between intervals
```

### Examples:

```
stats 0.1
stats 0.1 delta 0.5
stats 1.0 loglinfreq 7 10.0
```

### Description:

Print statistics to the screen and log file every so many seconds during a simulation. A value of 0.0 for delta means only print stats at the beginning and end of the run, in which case no optional keywords can be used.

The quantities printed are elapsed CPU time followed by those provided by the [application](#), followed by those provided by any [diagnostics](#) you have defined.

Typically the application reports only the number of events or sweeps executed, followed by the simulation time, but other application-specific quantities may also be reported. Quantities such as the total energy of the system can be included in the output by creating diagnostics via the [diag\\_style](#) command.

The *delay* keyword will suppress output until *tdelay* time has elapsed.

Using the *logfreq* or *loglinfreq* keyword will produce statistical output at progressively larger intervals during the course of a simulation. There will be *N* outputs per interval where the size of the interval is initially *delta* and then scales up by *factor* each time. With *loglinfreq*, output times increase arithmetically within an interval; with *logfreq* the output times increase geometrically.

For example, this command

```
stats 0.1 loglinfreq 7 10.0
```

will produce output at times:

```
t = 0, 0.1, 0.2, ..., 0.7, 1, 2, ..., 7, 10, 20, ....
```

This command

```
stats 0.1 logfreq 1 2.0
```



will produce output at times:

$t = 0, 0.1, 0.2, 0.4, 0.8, 1.6, \dots$

This command

```
stats 1.0 logfreq 10 10.0
```

will produce output at times:

$t = 0, 1.0, 1.26, 1.58, 2.00, 2.51, 3.16, 3.98, 5.01, 6.31, 7.94, 10.0, \dots$

Note that in the above examples the times are the earliest times that output will be produced. In practice, because time is incremented in discrete jumps, output will be produced at times somewhat later than these times.

If  $N$  is specified as 0, then this will turn off logarithmic output, and revert to regular output every *delta* seconds.

---

### **Restrictions:**

See the doc pages for quantities provided by particular [app\\_style](#) and [diag\\_style](#) commands for further details.

### **Related commands:**

[dump](#), [diag\\_style](#)

### **Default:**

The default stats delta is 0.0. The keyword defaults are delay = 0.0 and no logarithmic output.

## sweep command

### Syntax:

```
sweep style keyword value ...
```

- style = *random* or *raster* or *color* or *color/strict* or *none*
- zero or more keyword/value pairs may be appended
- keyword = *mask*

```
mask value = yes or no
yes/no = mask out sites than cannot change
```

### Examples:

```
sweep random
sweep raster mask yes ...
```

### Description:

Use a rejection kinetic Monte Carlo (rKMC) algorithm for an [on-lattice application](#). If rKMC is not used then a kinetic Monte Carlo (KMC) algorithm must be used as defined by the [solve\\_style](#) command.

The rKMC algorithm in SPPARKS selects sites on a lattice in an order determined by this command and requests that the application perform events. The application defines the geometry and connectivity of the lattice, what the possible events are, and defines their rates and acceptance/rejection criteria.

The ordering of selected sites is also affected by the [sector](#) command, which partitions each processor's portion of the simulation domain into sectors which are quadrants (2d) or octants (3d). In this case, the ordering described below is within each sector. Sectors are looped over one at a time, interleaved by communication of lattice values inbetween.

For the *random* style, sites are chosen randomly, one at a time.

For the *raster* style, a sweep of the lattice is done, as a loop over all sites in a pre-determined order, e.g. a triple loop over i,j,k for a 3d cubic lattice.

For the *color* style, lattice sites are partitioned into sub-groups or colors which are non-interacting in the sense that events on two sites of the same color can be performed simultaneously without conflict. This enables parallelism since events on all sites of the same color can be attempted simultaneously. Similar to sectors, the colors are looped over, interleaved by communication of lattice values inbetween.

The *color/strict* style is the same as the *color* style except that random numbers are generated in a way that is independent of the processor which generates them. Thus SPPARKS should produce the same answer, independent of how many processors are used. This can be useful in debugging an application.

If the application supports it, the *mask* keyword can be set to *yes* to skip sites which cannot perform an event due to the current value of the site and its neighbors. Enabling masking should not change the answer given by a simulation (in a statistical sense); it only offers a computational speed-up. For example, sites in the interior of grains in a Potts grain-growth model may have no potential of flipping their value. Masking can only be set to *yes* if the [temperature](#) is set to 0.0, since otherwise there is a finite probability of any site performing an event.

The *none* style deletes any rKMC sweeping algorithm previously defined. This may be useful for transitioning from a rKMC solver in one run to a [KMC solver](#) in a subsequent run.

**Restrictions:**

This command can only be used as part of on-lattice applications as specified by the [app\\_style](#) command.

Not all lattice styles and applications support the *color* and *color/strict* styles. Not all applications support the *mask* option.

**Related commands:**

[app\\_style](#), [solve\\_style](#), [sector](#)

**Default:**

The option defaults are mask = no.

## temperature command

### Syntax:

```
temperature T
```

- T = value of temperature for the Monte Carlo simulation (energy units)

### Examples:

```
temperature 2.0
```

### Description:

This command sets the temperature as used in various applications. The typical usage would be as part of a Boltzmann factor that alters the propabilities of event acceptance and rejection.

The units of the specfied temperature should be consistent with how the application defines energy. E.g. if used in a Boltzmann factor where a  $kT$  factor scales the energy of a Hamiltonian defined by the application, then this command is really defining  $kT$  and the specified value should have the units of energy as computed by the Hamiltonian.

**Restrictions:** none

This command can only be used as part of applications that allow for a temperature to be specified. See the doc pages for individual applications defined by the [app\\_style](#) command for further details.

**Related commands:** none

### Default:

The default temperature is 0.0.

## undump command

### Syntax:

```
undump dump-ID
```

- dump-ID = ID of previously defined dump

### Examples:

```
undump mine  
undump 2
```

### Description:

Turn off a previously defined [dump](#) command so that it is no longer active. This closes the file associated with the dump.

**Restrictions:** none

**Related commands:**

[dump](#)

**Default:** none

## update\_only command

### Syntax:

```
update_only keyword
```

keyword = *yes* or *no*

### Examples:

```
update_only yes  
update_only no
```

### Description:

On-lattice applications have the ability to run a separate update command that updates the site array values separate to those changes which occur during a KMC or rKMC iteration. That update can run in conjunction with a KMC or rKMC iteration or with this command one can run the update routine while skipping any normal KMC or rKMC iterations. One can run the user\_update by itself by running "update\_only yes" or run it in conjunction with the KMC or rKMC iterations by running "update\_only no". Currently there are no applications which use this command but it has been made available for custom built applications.

---

### Restrictions:

This command must be run with an [app\\_style](#) that supports it.

### Related commands:

[app\\_style](#)

### Default:

The default value is set to "no" so that the user\_update runs in conjunction with the KMC or rKMC iterations.

## variable command

### Syntax:

variable name style args ...

- name = name of variable to define
- style = *index* or *loop* or *world* or *universe* or *uloop* or *equal* or *atom*

*index* args = one or more strings  
*loop* args = N = integer size of loop  
*world* args = one string for each partition of processors  
*universe* args = one or more strings  
*uloop* args = N = integer size of loop  
*equal* args = one formula containing numbers, math operations, variable references  
  numbers = 0.0, 100, -5.4, 2.8e-4, etc  
  constants = PI  
  keywords = time, nglobal  
  math operations = (), -x, x+y, x-y, x\*y, x/y, x^y,  
                  sqrt(x), exp(x), ln(x), log(x),  
                  sin(x), cos(x), tan(x), asin(x), acos(x), atan(x),  
                  ceil(x), floor(x), round(x)  
  other variables = v\_abc, v\_n

### Examples:

```
variable x index run1 run2 run3 run4 run5 run6 run7 run8
variable LoopVar loop $n
variable MyValue equal 5.0*exp(v_energy/(v_boltz*v_Temp))
variable beta equal v_temp/3.0
variable temp world 300.0 310.0 320.0 ${Tfinal}
variable x universe 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
variable x uloop 15
```

### Description:

This command assigns one or more strings to a variable name for evaluation later in the input script or during a simulation.

Variables can be used in several ways in SPPARKS. A variable can be referenced elsewhere in an input script to become part of a new input command. For variable styles that store multiple strings, the [next](#) command can be used to increment which string is assigned to the variable. Variables of style *equal* can be evaluated to produce a single numeric value which can be output directly via the [print](#) command.

In the discussion that follows, the "name" of the variable is the arbitrary string that is the 1st argument in the variable command. This name can only contain alphanumeric characters and underscores. The "string" is one or more of the subsequent arguments. The "string" can be simple text as in the 1st example above, it can contain other variables as in the 2nd example, or it can be a formula as in the 3rd example. The "value" is the numeric quantity resulting from evaluation of the string. Note that the same string can generate different values when it is evaluated at different times during a simulation.

**IMPORTANT NOTE:** When a variable command is encountered in the input script and the variable name has already been specified, the command is ignored. This means variables can NOT be re-defined in an input script (with 2 exceptions, read further). This is to allow an input script to be processed multiple times without resetting

the variables; see the [jump](#) or [include](#) commands. It also means that using the [command-line switch](#) `-var` will override a corresponding variable setting in the input script.

There are two exceptions to this rule. First, variables of style *equal* ARE redefined each time the command is encountered. This allows them to be reset, when their formulas contain a substitution for another variable, e.g. `$x`. This can be useful in a loop. This also means an *equal*-style variable will re-define a command-line switch `-var` setting, so an *index*-style variable should be used for such settings instead, as in `bench/in.lj`.

Second, as described below, if a variable is iterated on to the end of its list of strings via the [next](#) command, it is removed from the list of active variables, and is thus available to be re-defined in a subsequent variable command.

---

[This section](#) of the manual explains how occurrences of a variable name in an input script line are replaced by the variable's string. The variable name can be referenced as `$x` if the name "x" is a single character, or as `${LoopVar}` if the name "LoopVar" is one or more characters.

As described below, for variable styles *index*, *loop*, *universe*, and *uloop*, which string is assigned to a variable can be incremented via the [next](#) command. When there are no more strings to assign, the variable is exhausted and a flag is set that causes the next [jump](#) command encountered in the input script to be skipped. This enables the construction of simple loops in the input script that are iterated over and then exited from.

---

For the *index* style, one or more strings are specified. Initially, the 1st string is assigned to the variable. Each time a [next](#) command is used with the variable name, the next string is assigned. All processors assign the same string to the variable.

*Index* style variables with a single string value can also be set by using the command-line switch `-var`; see [this section](#) for details.

The *loop* style is identical to the *index* style except that the strings are the integers from 1 to N. This allows generation of a long list of runs (e.g. 1000) without having to list N strings in the input script. Initially, the string "1" is assigned to the variable. Each time a [next](#) command is used with the variable name, the next string ("2", "3", etc) is assigned. All processors assign the same string to the variable.

For the *world* style, one or more strings are specified. There must be one string for each processor partition or "world". See [this section](#) of the manual for information on running SPPARKS with multiple partitions via the `"-partition"` command-line switch. This variable command assigns one string to each world. All processors in the world are assigned the same string. The next command cannot be used with *equal* style variables, since there is only one value per world. This style of variable is useful when you wish to run different simulations on different partitions.

For the *universe* style, one or more strings are specified. There must be at least as many strings as there are processor partitions or "worlds". See [this page](#) for information on running SPPARKS with multiple partitions via the `"-partition"` command-line switch. This variable command initially assigns one string to each world. When a [next](#) command is encountered using this variable, the first processor partition to encounter it, is assigned the next available string. This continues until all the variable strings are consumed. Thus, this command can be used to run 50 simulations on 8 processor partitions. The simulations will be run one after the other on whatever partition becomes available, until they are all finished. *Universe* style variables are incremented using the files `"tmp.spparks.variable"` and `"tmp.spparks.variable.lock"` which you will see in your directory during such a SPPARKS run.

The *uloop* style is identical to the *universe* style except that the strings are the integers from 1 to N. This allows generation of long list of runs (e.g. 1000) without having to list N strings in the input script.

---



For the *equal* style, a single string is specified which represents a formula that will be evaluated afresh each time the variable is used. If you want spaces in the string, enclose it in double quotes so the parser will treat it as a single argument. For *equal* style variables the formula computes a scalar quantity, which becomes the value of the variable whenever it is evaluated.

Note that *equal* variables can produce different values at different stages of the input script or at different times during a run.

The next command cannot be used with *equal* style variables, since there is only one string.

The formula for an *equal* variable can contain a variety of quantities. The syntax for each kind of quantity is simple, but multiple quantities can be nested and combined in various ways to build up formulas of arbitrary complexity. For example, this is a valid (though strange) variable formula:

```
variable x equal "2.0 + v_MyTemp / pow(v_Volume,1/3) "
```

Specifically, an formula can contain numbers, math operations, and references to other variables.

Number	0.2, 100, 1.0e20, -15.4, etc
Constants	PI
Keywords	time, nglobal
Math operations	(), -x, x+y, x-y, x*y, x/y, x^y, sqrt(x), exp(x), ln(x), log(x), sin(x), cos(x), tan(x), asin(x), acos(x), atan(x), ceil(x), floor(x), round(x)
Other variables	v_abc, v_n

The keywords currently allowed in a formula are *time* and *nglobal*. *Time* is the current simulation time. *Nglobal* is the number of sites in the model.

Math operations are written in the usual way, where the "x" and "y" in the examples above can be another section of the formula. Operators are evaluated left to right and have the usual precedence: unary minus before exponentiation ("^"), exponentiation before multiplication and division, and multiplication and division before addition and subtraction. Parenthesis can be used to group one or more portions of a formula and enforce a desired order of operations. Additional math operations can be specified as keywords followed by a parenthesized argument, e.g. sqrt(v\_ke). Note that ln() is the natural log; log() is the base 10 log. The ceil(), floor(), and round() operations are those in the C math library. Ceil() is the smallest integer not less than its argument. Floor() is the largest integer not greater than its argument. Round() is the nearest integer to its argument.

The current values of other variables can be accessed by prepending a "v\_" to the variable name. This will cause that variable to be evaluated.

**IMPORTANT NOTE:** If you define variables in circular manner like this:

```
variable a equal v_b
variable b equal v_a
print $a
```

then SPPARKS will run for a while when the print statement is invoked!

Another way to reference a variable in a formula is using the \$x form instead of v\_x. There is a subtle difference between the two references that has to do with when the evaluation of the included variable is done.

Using a `$x`, the value of the include variable is substituted for immediately when the line is read from the input script, just as it would be in other input script command. This could be the desired behavior if a static value is desired. Or it could be the desired behavior for an equal-style variable if the variable command appears in a loop (see the [jump](#) and [next](#) commands), since the substitution will be performed anew each time thru the loop as the command is re-read. Note that if the variable formula is enclosed in double quotes, this prevents variable substitution and thus an error will be generated when the variable formula is evaluated.

Using a `v_x`, the value of the included variable will not be accessed until the variable formula is evaluated. Thus the value may change each time the evaluation is performed. This may also be desired behavior.

As an example, if the current simulation box volume is 1000.0, then these lines:

```
variable x equal vol
variable y equal 2*$x
```

will associate the equation string "2\*1000.0" with variable y.

By contrast, these lines:

```
variable x equal vol
variable y equal 2*v_x
```

will associate the equation string "2\*v\_x" with variable y.

Thus if the variable y were evaluated periodically during a run where the box volume changed, the resulting value would always be 2000.0 for the first case, but would change dynamically for the second case.

---

### Restrictions:

All *universe*- and *uloop*-style variables defined in an input script must have the same number of values.

### Related commands:

[next](#), [jump](#), [include](#), [print](#)

**Default:** none

## volume command

### Syntax:

```
volume V
```

- V = volume of system (liters)

### Examples:

```
volume 1.0e-10
```

### Description:

This command sets the volume of the system for use in the [app\\_style chemistry](#) application.

For example, it could be the volume of a biological cell within which biochemical reactions are taking place.

### Restrictions:

This command can only be used as part of the [app\\_style chemistry](#) application.

### Related commands:

[app\\_style chemistry](#)

**Default:** none