

# CmdStan User's Guide

Version 2.28

Stan Development Team

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# Introduction

This document is a user's guide for CmdStan, the command-line interface to the Stan statistical modeling language. CmdStan provides the tools to compile a statistical model written in the Stan probabilistic programming language into a C++ executable program which can then be run to either: do inference on data, producing an estimate of the posterior; generate new quantities of interest from an existing estimate; or generate data from the model according to a given set of parameters

CmdStan provides the programs and tools to compile Stan programs into C++ executables that can be run directly from the command line, together with a few utilities to check and summarize the resulting outputs.

The packages CmdStanR and CmdStanPy which provide interfaces to CmdStan from R and Python, respectively, similarly, JuliaStan also interfaces with CmdStan.

## *Stan home page*

For links to up-to-date code, examples, manuals, bug reports, feature requests, and everything else Stan related, see the Stan home page:

<http://mc-stan.org/>

## *Licensing*

CmdStan, Stan, and the Stan Math Library are licensed under the new BSD license (3-clause). See the Stan Reference Manual Licenses section for licensing terms for Stan and the dependent packages Boost, Eigen, Sundials, and Intel TBB.

## *Stan documentation: user's guide and reference manuals*

The Stan user's guide provides example models and programming techniques for coding statistical models in Stan. It also serves as an example-driven introduction to Bayesian modeling and inference:

<http://mc-stan.org/docs/stan-users-guide>

Stan's modeling language is shared across all of its interfaces. The Stan Language Reference Manual provides a concise definition of the language syntax for all elements in the language.

<http://mc-stan.org/docs/reference-manual>

The Stan Functions Reference provides definitions and examples for all the functions defined in the Stan math library and available in the Stan programming language, including all probability distributions.

<http://mc-stan.org/docs/functions-reference>.

### *Benefits of CmdStan*

- With every new Stan release, there is a corresponding CmdStan release, therefore CmdStan provides access to the latest version of Stan, and can be used to run the development version of Stan as well.
- Of the Stan interfaces, CmdStan has the lightest memory footprint, therefore it can fit larger and more complex models. It has the fewest dependencies, which makes it easier to run in limited environments such as clusters.
- The output generated is in CSV format and can be post-processed using other Stan interfaces or general tools.

# QuickStart Guide

This section is designed to help users install CmdStan and get acquainted with the CmdStan interface.



# 1. CmdStan Installation

## 1.1. Installation via conda

CmdStan can be installed via the package management system conda via the conda-forge channel. This will install a pre-built version of CmdStan along with the required dependencies (i.e. a C++ compiler, a version of Make, and required libraries) detailed below under Source installation.

One can create a new conda environment (named `stan-env`) and install CmdStan with the following command.

```
conda create -n stan-env -c conda-forge cmdstan
```

or install it in an existing environment with

```
conda install -c conda-forge cmdstan
```

The conda installation is designed so one can use the R or Python bindings to CmdStan seamlessly. Additionally, it provides the command `cmdstan_model` to activate the CmdStan makefile from anywhere. To enable either of these, ensure your environment is activated<sup>1</sup> with `conda activate <env>`, where `<env>` is the name of the environment CmdStan was installed into. In the first command above, the environment was named `stan-env`, but any name may be used so long as you are consistent.

You can check which version of CmdStan is installed in your current environment by running the following command.

```
conda list cmdstan
```

Finally, you can specify a different version for installation by adding `=VERSION` to the end of the above commands.<sup>2</sup> For example,

```
conda install -c conda-forge cmdstan=2.27.0
```

Please report conda-specific install problems directly to the conda-forge issue tracker, [here](#).

---

<sup>1</sup>A special environment, called `base`, is activated automatically by conda on startup. Installing software directly in `base` is not recommended by conda, but may be appropriate for some users who do not intend to use multiple environments

<sup>2</sup>You can view available versions with the command `conda search -c conda-forge cmdstan`

## 1.2. Source installation

To install CmdStan from source you need:

- A modern C++11 compiler. Supported versions are
  - Linux: g++ 4.9.3 or clang 6.0
  - macOS: the XCode version of clang
  - Windows: g++ 8.1 (available with RTools 4.0) is recommended; alternatively, g++ 4.9.3 (available with RTools 3.5).
- The GNU-Make utility program or the Windows equivalent mingw32-make. On macOS, this is part of the XCode command line tools installed via command `xcode-select --install`. On Windows, mingw32-make is installed as part of RTools: <https://cran.rstudio.com/bin/windows/Rtools/>.
- The CmdStan C++ source code and libraries.
  - CmdStan releases are available from GitHub as a compressed tarfile containing all C++ source code and libraries. The most recent CmdStan release is always available as <https://github.com/stan-dev/cmdstan/releases/latest>.
  - To use the current development version you can clone the GitHub repo.

The CmdStan release unpacks into a directory called `cmdstan-<version>` where the version string consists of the major.minor.patch version numbers, e.g. `cmdstan-2.23.0`. Cloning CmdStan from GitHub creates a directory simply called `cmdstan`. Throughout this manual, we refer to this top-level CmdStan source directory as `<cmdstan-home>`.

### Installing the C++ toolchain

The C++ toolchain consists of a modern C++ compiler and the GNU-Make utility, described in greater detail in the following section.

#### *Linux: g++ and make*

On Linux, the C++ compiler command `g++` and the GNU-Make command is `make`. These are often installed by default. To check, run commands:

```
g++ --version
make --version
```

If these are at least at g++ version 4.9.3 or later and make version 3.81 or later, no additional installations are necessary. It may still be desirable to update the C++ compiler g++, because later versions are faster.

To install the latest version of these tools (or upgrade an older version), use the following commands or their equivalent for your distribution, install via the commands:

```
sudo apt install g++  
sudo apt install make
```

If you can't run `sudo`, you will need to ask your sysadmin or cluster administrator to install these tools for you.

*MacOS: clang++ and make*

To install a C++ development environment on a Mac, use Apple's Xcode development environment <https://developer.apple.com/xcode/>.

From the Xcode home page View in Mac App Store.

- From the App Store, click Install, enter an Apple ID, and wait for Xcode to finish installing.
- Open the Xcode application, click top-level menu Preferences, click top-row button Downloads, click button for Components, click on the Install button to the right of the Command Line Tools entry, then wait for it to finish installing.
- Click the top-level menu item Xcode, then click item Quit Xcode to quit.

To test, open the Terminal application and enter:

```
clang++ --version  
make --version
```

If you have installed XCode, but don't have make, you can install the XCode command-line tools via command:

```
xcode-select --install
```

*Note* MacOS installations may include old version of the g++ compiler which is a version 4.2.1. CmdStan requires g++ at 4.9.3 or later. Trying to install later versions of g++ using homebrew or macports is no longer recommended; use the XCode toolchain.

*Windows: g++ and mingw32-make*

The Windows toolchain consists of programs g++, the C++ compiler, and mingw32-make, the GNU-Make utility. To check if these are present, open a command shell <sup>3</sup> and type:

```
g++ --version
mingw32-make --version
```

## Rtools C++ Development Environment

The simplest way to install a full C++ build environment that will work for CmdStan is to use the Rtools package designed for R developers on Windows (even if you don't plan to use R).

If you don't have RTools, the latest version is Rtools40 (released April 2020) which can be downloaded from:

- <https://cran.r-project.org/bin/windows/Rtools/>

After installation is complete, you need to perform one more step: you need to add the location of the Rtools compiler and make utilities to the PATH environment variable. If you have Rtools40, these should be:

```
C:\RTools\RTools40\usr\bin
C:\RTools\RTools40\mingw64\bin
```

If you have an earlier version of RTools, use RTools35:

```
C:\RTools\RTools35\usr\bin
C:\RTools\RTools35\mingw64\bin
```

See these instructions for details on changing the PATH.

## 32-bit Builds

CmdStan defaults to a 64-bit build. On a 32-bit operating system, you must specify the make variable BIT=32 as part of the make command, described in the next section.

---

<sup>3</sup>To open a Windows command shell, first open the **Start Menu**, (usually in the lower left of the screen), select option **All Programs**, then option **Accessories**, then program **Command Prompt**. Alternatively, enter [Windows+r] (both keys together on the keyboard), and enter cmd into the text field that pops up in the Run window, then press [Return] on the keyboard to run.

## GNU-Make utility

CmdStan relies on the GNU-make utility to build both the Stan model executables and the CmdStan tools.

GNU-Make builds executable programs and libraries from source code by reading files called Makefiles which specify how to derive the target program. A Makefile consists of a set of recursive rules where each rule specifies a target, its dependencies, and the specific operations required to build the target. Specifying dependencies for a target provides a way to control the build process so that targets which depend on other files will be updated as needed *only* when there are changes to those other files. Thus Make provides an efficient way to manage complex software.

The CmdStan Makefile is in the <cmdstan-home> directory and is named `makefile`. This is one of the default GNU Makefile names, which allows you to omit the `-f makefile` argument to the Make command. Because the CmdStan Makefile includes several other Makefiles, **Make only works properly when invoked from the <cmdstan-home> directory**; attempts to use this Makefile from another directory by specifying the full path to the file `makefile` won't work. For example, trying to call Make from another directory by specifying the full path the the `makefile` results in the following set of error messages:

```
make -f ~/github/stan-dev/cmdstan/makefile
/Users/mitzi/github/stan-dev/cmdstan/makefile:58: make/stanc: No such file or directory
/Users/mitzi/github/stan-dev/cmdstan/makefile:59: make/program: No such file or directory
/Users/mitzi/github/stan-dev/cmdstan/makefile:60: make/tests: No such file or directory
/Users/mitzi/github/stan-dev/cmdstan/makefile:61: make/command: No such file or directory
make: *** No rule to make target `make/command'. Stop.
```

Makefile syntax allows general pattern rules based on file suffixes. Stan programs must be stored in files with suffix `.stan`; the CmdStan makefile rules specify how to transform the Stan source code into a binary executable. For example, to compile the Stan program `my_program.stan` in directory `../my_dir/`, the make target is `../my_dir/my_program` or `../my_dir/my_program.exe` (on Windows).

To call Make, you invoke the utility name, either `make` or `mingw32-make`, followed by, in order:

- zero or more Make program options, then specify any Make variables as a series of
- zero or more Make variables, described below

- zero or more *target* names; the set of names is determined by the Makefile rules.

```
make <flags> <variables> <targets>
```

## Makefile Variables

Make targets can be preceded by any number of Makefile variable name=value pairs. For example, to compile `../my_dir/my_program.stan` for an OpenCL (GPU) machine, set the makefile variable `STAN_OPENCL` to `TRUE`:

```
> make STAN_OPENCL=TRUE ../my_dir/my_program    # on Windows use mingw32-make
```

Makefile variables can also be set by creating a file named `local` in the `CmdStan` make subdirectory which contains a list of `<VARIABLE>=<VALUE>` pairs, one per line. For example, if you are working on a 32-bit machine, you would put the line `BIT=32` into the file `<cmdstan-home>/make/local` so that all `CmdStan` programs and `Stan` models compile properly.

The complete set of Makefile variables can be found in file `<cmdstan-home>/cmdstan/stan/lib/stan_math/make/compiler_flags`.

## Make Targets

When invoked without any arguments at all, `Make` prints a help message:

```
> make    # on Windows use mingw32-make
```

```
-----
CmdStan v2.23.0 help
```

```
Build CmdStan utilities:
```

```
> make build
```

```
This target will:
```

1. Install the Stan compiler `bin/stanc` from `stanc3` binaries.
2. Build the print utility `bin/print` (deprecated; will be removed in v3).
3. Build the `stansummary` utility `bin/stansummary`
4. Build the diagnose utility `bin/diagnose`
5. Build all libraries and object files compile and link an executable S

```
Note: to build using multiple cores, use the -j option to make, e.g.,
for 4 cores:
```

```
> make build -j4
```

Build a Stan program:

Given a Stan program at `foo/bar.stan`, build an executable by typing:

```
> make foo/bar
```

This target will:

1. Install the Stan compiler (`bin/stanc`), as needed.
2. Use the Stan compiler to generate C++ code, `foo/bar.hpp`.
3. Compile the C++ code using `cc .` to generate `foo/bar`

Additional make options:

`STANCFLAGS`: defaults to `""`. These are extra options passed to `bin/stanc` when generating C++ code. If you want to allow undefined functions in Stan program, either add this to `make/local` or the command line:

```
STANCFLAGS = --allow_undefined
```

`USER_HEADER`: when `STANCFLAGS` has `--allow_undefined`, this is the name of header file that is included. This defaults to `"user_header.hpp"` in the directory of the Stan program.

Example - bernoulli model: `examples/bernoulli/bernoulli.stan`

1. Build the model:

```
> make examples/bernoulli/bernoulli
```

2. Run the model:

```
> examples/bernoulli/bernoulli sample data file=examples/bernoulli/be
```

3. Look at the samples:

```
> bin/stansummary output.csv
```

Clean CmdStan:

Remove the built CmdStan tools:

```
> make clean-all
```

---

## Clone the GitHub CmdStan repository

This section can be skipped if you want to build CmdStan using the release tarfile, which contains all source files and libraries needed to build CmdStan. However, if you wish to use the current (stable) development version of CmdStan, you must clone the CmdStan GitHub repo.

The CmdStan repo contains just the `cmdstan` module; the Stan inference engine algorithms and Stan math library functions are specified as submodules and stored in the GitHub repositories `stan` and `math`, respectively. By cloning the CmdStan repository with argument `--recursive`, Git automatically initializes and updates each submodule in the repository, including nested submodules if any of the submodules in the repository have submodules themselves.

The following sequence of commands will check out the current CmdStan develop branch on GitHub and assemble and build the command line interface and supporting libraries:

```
> git clone https://github.com/stan-dev/cmdstan.git --recursive
> cd cmdstan
> make build      # on Windows use mingw32-make
```

The resulting set of directories should have the same structure as the release:

- directory `cmdstan/stan` contains the sub-module `stan` (<https://github.com/stan-dev/stan>)
- directory `cmdstan/stan/lib/stan_math` contains the sub-module `math` (<https://github.com/stan-dev/math>)

## Building CmdStan

Building CmdStan involves preparing a set of executable programs and compiling the command line interface and supporting libraries. The CmdStan tools are:

- `stanc`: the Stan compiler (translates Stan language to C++).
- `stansummary`: a basic posterior analysis tool. The `stansummary` utility processes one or more output files from a run or set of runs of Stan's HMC sampler. For all parameters and quantities of interest in the Stan program, `stansummary` reports a set of statistics including mean, standard deviation, percentiles, effective number of samples, and  $\hat{R}$  values.
- `diagnose`: a basic sampler diagnostic tool which checks for indications that the HMC sampler was unable to sample from the full posterior.



CmdStan releases include pre-built binaries of the Stan language compiler <https://github.com/stan-dev/stanc3>: `bin/linux-stanc`, `bin/mac-stanc` and `bin/windows-stanc`. The CmdStan makefile build task copies the appropriate binary to `bin/stanc`. For CmdStan installations which have been cloned or downloaded from the CmdStan GitHub repository, the makefile task will download the appropriate OS-specific binary from the stanc3 repository's nightly release.

Steps to build CmdStan:

- Download the latest release from <https://github.com/stan-dev/cmdstan/releases/latest> or clone the GitHub repo.
- Open a command-line terminal window and change directories to the CmdStan home directory.
- Run the makefile target `build` which instantiates the CmdStan utilities and compiles all necessary C++ libraries.

```
> cd <cmdstan-home>
> make build      # on Windows use mingw32-make
```

If your computer has multiple cores and sufficient ram, the build process can be parallelized by providing the `-j` option. For example, to build on 4 cores, type:

```
> make -j4 build      # on Windows use mingw32-make
```

When `make build` is successful, the directory `<cmdstan-home>/bin/` will contain the executables `stanc`, `stansummary`, and `diagnose` (on Windows, corresponding `.exe` files) and the final lines of console output will show the version of CmdStan that has just been built, e.g.:

```
--- CmdStan v2.23.0 built ---
```

**Warning:** *The Make program may take 10+ minutes and consume 2+ GB of memory to build CmdStan.*

**Windows only:** CmdStan requires that the Intel TBB library, which is built by the above command, can be found by the Windows system. This requires that the directory `<cmdstan-home>/stan/lib/stan_math/lib/tbb` is part of the `PATH` environment variable. To permanently make this setting for the current user, you may execute:

```
> mingw32-make install-tbb
```

After changing the `PATH` environment variable, you must open a new shell in order to these setting to take effect. (This is not necessary on Mac and Linux systems

because they can use the absolute path to the Intel TBB library when linking into Stan programs.)

### 1.3. Checking the Stan compiler

To check that the CmdStan installation is complete and in working order, run the following series of commands from the folder which CmdStan was installed.

On Linux/macOS:

```
# compile the example
> make examples/bernoulli/bernoulli

# fit to provided data (results of 10 trials, 2 out of 10 successes)
> ./examples/bernoulli/bernoulli sample data file=examples/bernoulli/bernoulli.json

# default output written to file `output.csv`,
# default num_samples is 1000, output file should have approx. 1050 lines
> ls -l output.csv

# run the `bin/stansummary` utility to summarize parameter estimates
> bin/stansummary output.csv
```

On Windows:

```
# compile the example
> mingw32-make examples/bernoulli/bernoulli.exe

# fit to provided data (results of 10 trials, 2 out of 10 successes)
> ./examples/bernoulli/bernoulli.exe sample data file=examples/bernoulli/bernoulli.json

# run the `bin/stansummary.exe` utility to summarize parameter estimates
> bin/stansummary.exe output.csv
```

The sample data in file `bernoulli.json` specifies 2 out of 10 successes, therefore the range  $\text{mean}(\theta) \pm \text{sd}(\theta)$  should include 0.2.

### 1.4. Troubleshooting the installation

Updates to CmdStan, changes in compiler options, or updates to the C++ toolchain may result in errors when trying to compile a Stan program. Often, these problems can be resolved by removing the existing CmdStan binaries and recompiling. To do

this, you must run the makefile commands from the `<cmdstan-home>` directory:

```
> cd <cmdstan-home>
> make clean-all      # on Windows use mingw32-make
> make build
```

## Common problems

This section contains solutions to problems reported on <https://discourse.mc-stan.org>

### Compiler error message about PCH file

To speed up compilation, the Stan makefile pre-compiles parts of the core Stan library. If these pre-compiled files are out of sync with the compiled model, the compiler will complain, e.g.:

```
error: PCH file uses an older PCH format that is no longer supported
```

In this case, clean and rebuild CmdStan, as shown in the previous section.

### Windows: ‘mingw32-make’ is not recognised

If the C++ toolchain has been installed but not properly registered, then the call to `mingw32-make` will result in error message:

```
'mingw32-make' is not recognised as an internal or external command
```

To fix this, you should make sure that the RTools installation is in your PATH environment variable, as described in the RTools section.

In addition, if you have the RTools 4.0 toolchain, then call the utility `pacman` to register the right version of `make`:

```
pacman -Sy mingw-w64-x86_64-make
```

See: <https://discourse.mc-stan.org/t/cmdstan-installation-on-windows/11287/6>

### Windows: ‘g++’ or ‘cut’ is not recognized

The CmdStan makefile uses a few shell utilities which might not be present in Windows, resulting in the error message:

```
'cut' is not recognized as an internal or external command, operable program
```

The solution is to add `mingw_64/bin` directory to the user PATH environment variable.

See: <https://discourse.mc-stan.org/t/errors-when-using-cmdstan-model/14984/21>

## 2. Example Model and Data

The following is a simple, complete Stan program for a Bernoulli model of binary data.<sup>1</sup> The model assumes the binary observed data  $y[1], \dots, y[N]$  are i.i.d. with Bernoulli chance-of-success  $\theta$ .

```
data {  
  int<lower=0> N;  
  array[N] int<lower=0, upper=1> y;  
}  
parameters {  
  real<lower=0, upper=1> theta;  
}  
model {  
  theta ~ beta(1, 1); // uniform prior on interval 0,1  
  y ~ bernoulli(theta);  
}
```

The input data file contains definitions for the two variables  $N$  and  $y$  which are specified in the data block of program `bernoulli.stan` (above).

A data set of  $N=10$  observations is included in the example Bernoulli model directory in both JSON notation and Rdump data format where 8 out of 10 trials had outcome 0 (failure) and 2 trials had outcome 1 (success). In JSON, this data is:

```
{  
  "N" : 10,  
  "y" : [0,1,0,0,0,0,0,0,0,1]  
}
```

---

<sup>1</sup>The model is available with the CmdStan distribution at the path `<cmdstan-home>/examples/bernoulli/bernoulli.stan`.

## 3. Compiling a Stan Program

A Stan program must be in a file with extension `.stan`. The CmdStan makefile rules specify all necessary steps to translate files with suffix `.stan` to a CmdStan executable program. This is a two-stage process:

- first the Stan program is translated to C++ by the `stanc` compiler
- then the C++ compiler compiles all C++ sources and links them together with the CmdStan interface program and the Stan and math libraries.

### 3.1. Invoking the Make utility

To compile Stan programs, you must invoke the Make program from the `<cmdstan-home>` directory. The Stan program can be in a different directory, but the directory path names cannot contain spaces - this limitation is imposed by Make.

```
> cd <cmdstan_home>
```

In the call to the Make program, the target is name of the CmdStan executable corresponding to the Stan program file. On Mac and Linux, this is the name of the Stan program with the `.stan` omitted. On Windows, replace `.stan` with `.exe`, and make sure that the path is given with slashes and not backslashes. To build the Bernoulli example, on Mac and Linux:

```
> make examples/bernoulli/bernoulli
```

On Windows, the command is the same with the addition of `.exe` at the end of the target (*note the use of forward slashes*):

```
> make examples/bernoulli/bernoulli.exe
```

The generated C++ code (`bernoulli.hpp`), object file (`bernoulli.o`) and the compiled executable will be placed in the same directory as the Stan program.

The compiled executable consists of the Stan model and the CmdStan command line interface which provides inference algorithms to do MCMC sampling, optimization, and variational inference. The following sections provide examples of doing inference using each method on the example model and data file.

### 3.2. Dependencies

When executing a Make target, all its dependencies are checked to see if they are up to date, and if they are not, they are rebuilt. If the you call Make with target `bernoulli` twice in a row, without any editing `bernoulli.stan` or otherwise changing the system, on the second invocation, Make will determine that the executable is already newer than the Stan source file and will not recompile the program:

```
> make examples/bernoulli/bernoulli
make: `examples/bernoulli/bernoulli' is up to date.
```

If the file containing the Stan program is updated, the next call to make will rebuild the CmdStan executable.

### 3.3. Compiler errors

The Stan probabilistic programming language is a programming language with a rich syntax, as such, it is often the case that a carefully written program contains errors.

The simplest class of errors are simple syntax errors such as forgetting the semi-colon statement termination marker at the end of a line, or typos such as a misspelled variable name. For example, if in the `bernoulli.stan` program, we introduce a typo on line 9 by writing `thata` instead of `theta`, the Make command fails with the following

```
--- Translating Stan model to C++ code ---
bin/stanc --o=bernoulli.hpp bernoulli.stan
```

```
Semantic error in 'bernoulli.stan', line 9, column 2 to column 7:
```

```
-----
 7:  }
 8:  model {
 9:    thata ~ beta(1, 1);  // uniform prior on interval 0, 1
    ^
10:    y ~ bernoulli(theta);
11:  }
-----
```

```
Identifier 'thata' not in scope.
```

```
make: *** [bernoulli.hpp] Error 1
```

Stan is a strongly-typed language; and the compiler will throw an error if statements or expressions violate the type rules. The following trivial program `foo.stan` contains an illegal assignment statement:

```
data {
  real x;
}
transformed data {
  int y = x;
}
```

The Make command fails with the following:

Semantic error in 'foo.stan', line 5, column 2 to column 12:

```
-----
3:  }
4:  transformed data {
5:    int y = x;
   ^
6:  }
-----
```

Ill-typed arguments supplied to assignment operator =: lhs has type int and

The Stan Reference Manual provides a complete specification of the Stan programming language. The Stan User's Guide also contains a full description of the errors and warnings stanc can emit.

### 3.4. Troubleshooting C++ compiler or linker errors

If the stanc compiler successfully translates a Stan program to C++, the resulting C++ code should be valid C++ which can be compiled into an executable. The stanc compiler is also a program, and while it has been extensively tested, it may still contain errors such that the generated C++ code fails to compile.

The Make command prints the following message to the terminal at the point when it compiles and links the C++ file:

```
--- Compiling, linking C++ code ---
```

If the program fails to compile for any reason, the C++ compiler and linker will most likely print a long series of error messages to the console.

If this happens, please report the error, together with the Stan program on either the Stan Forums or on the Stan compiler GitHub issues tracker.

### 3.5. C++ compilation and linking flags

Users can set flags for the C++ compiler and linker and compiler to optimize their executables. We advise users to only do this once they are sure their basic setup of Cmdstan without flags works.

The CXXFLAGS and LDFLAGS makefile variables can be used to set compiler and linker flags respectively. We recommend setting these in the `make/local` file.

For example:

```
CXXFLAGS = -O2
```

A recommend a set of CXXFLAGS and LDFLAGS flags can be turned on by setting `STAN_CPP_OPTIMS=true` in the `make/local` file. These are tested compiler and link-time optimizations that can speed up execution of certain models. We have observed speedups up to 15 percent, but this depends on the model, operating system and hardware used. The use of these flags does considerably slow down compilation, so they are not used by default.

#### Optimizing by ignoring range checks

When assigning or reading from with vectors, `row_vectors`, matrices or arrays using indexing, Stan performs checks that a supplied index is valid (not out of range). These check avoids segmentation faults and other runtime errors that can be difficult to debug.

For some models these checks can represent a significant part of the models execution time. By setting the `STAN_NO_RANGE_CHECKS=true` makefile flag in the `make/local` file the range checks can be removed. Use this flag with caution (only once the indexing has been validated). In case of any unexpected behavior remove the flag for easier debugging.



## 4. MCMC Sampling

### 4.1. Running the sampler

To generate a sample from the posterior distribution of the model conditioned on the data, we run the executable program with the argument `sample` or `method=sample` together with the input data. The executable can be run from any directory. Here, we run it in the directory which contains the Stan program and input data, `<cmdstan-home>/examples/bernoulli`:

```
> cd examples/bernoulli
```

To execute sampling of the model under Linux or Mac, use:

```
> ./bernoulli sample data file=bernoulli.data.json
```

In Windows, the `./` prefix is not needed:

```
> bernoulli.exe sample data file=bernoulli.data.json
```

The output is the same across all supported platforms. First, the configuration of the program is echoed to the standard output:

```
method = sample (Default)
  sample
    num_samples = 1000 (Default)
    num_warmup = 1000 (Default)
    save_warmup = 0 (Default)
    thin = 1 (Default)
  adapt
    engaged = 1 (Default)
    gamma = 0.050000000000000003 (Default)
    delta = 0.80000000000000004 (Default)
    kappa = 0.75 (Default)
    t0 = 10 (Default)
    init_buffer = 75 (Default)
    term_buffer = 50 (Default)
    window = 25 (Default)
  algorithm = hmc (Default)
    hmc
```

```

    engine = nuts (Default)
      nuts
        max_depth = 10 (Default)
    metric = diag_e (Default)
    metric_file = (Default)
    stepsize = 1 (Default)
    stepsize_jitter = 0 (Default)
id = 0 (Default)
data
  file = bernoulli.data.json
init = 2 (Default)
random
  seed = 3252652196 (Default)
output
  file = output.csv (Default)
  diagnostic_file = (Default)
  refresh = 100 (Default)

```

After the configuration has been displayed, a short timing message is given.

```

Gradient evaluation took 1.2e-05 seconds
1000 transitions using 10 leapfrog steps per transition would take 0.12 seconds
Adjust your expectations accordingly!

```

Next, the sampler reports the iteration number, reporting the percentage complete.

```

Iteration:    1 / 2000 [  0%]  (Warmup)
....
Iteration: 2000 / 2000 [100%]  (Sampling)

```

Finally, the sampler reports timing information:

```

Elapsed Time: 0.007 seconds (Warm-up)
              0.017 seconds (Sampling)
              0.024 seconds (Total)

```

## 4.2. Running multiple chains

A Markov chain generates samples from the target distribution only after it has converged to equilibrium. In theory, convergence is only guaranteed asymptotically as the number of draws grows without bound. In practice, diagnostics must be applied to monitor convergence for the finite number of draws actually available. One way to monitor whether a chain has converged to the equilibrium distribution is

to compare its behavior to other randomly initialized chains. For robust diagnostics, we recommend running 4 chains.

There are two different ways of running multiple chains, with the `num_chains` argument using a single executable and by using the Unix and DOS shell to run multiple executables. The former is currently supported and recommended when using the NUTS sampling algorithm with either the diagonal (`diag_e`) or dense (`dense_e`) metric.

### Using the `num_chains` argument to run multiple chains

The `num_chains` argument can be used with the NUTS sampling algorithm with either the diagonal (`diag_e`) or dense (`dense_e`) metric.

Example that will run 4 chains:

```
./bernoulli sample num_chains=4 data file=bernoulli.data.json output file=ou
```

If the model was not compiled with `STAN_THREADS=true`, the above command will run 4 chains sequentially and will produce the sample in `output_1.csv`, `output_2.csv`, `output_3.csv`, `output_4.csv`. A suffix with the chain id is appended to the provided output filename (`output.csv` in the above command).

If the model was compiled with `STAN_THREADS=true`, the chains can run in parallel, with the `num_threads` argument defining the maximum number of threads used to run the chains. If the model uses no within-chain parallelization (`map_rect` or `reduce_sum` calls), the below command will run 4 chains in parallel, provided there are cores available:

```
./bernoulli sample num_chains=4 data file=bernoulli.data.json output file=ou
```

If the model uses within-chain parallelization (`map_rect` or `reduce_sum` calls), the threads are automatically scheduled to run the parallel parts of a single chain or run the sequential parts of another chains. The below call starts 4 chains that can use 16 threads. At a given moment a single chain may use all 16 threads, 1 thread, anything in between, or can wait for a thread to be available. The scheduling is left to the Threading Building Blocks scheduler.

```
./bernoulli_par sample num_chains=4 data file=bernoulli.data.json output fil
```

### Using shell for running multiple chains

To run multiple chains given a model and data, either sequentially or in parallel, we can also use the Unix or DOS shell `for` loop to set up index variables needed to

identify each chain and its outputs.

On MacOS or Linux, the for-loop syntax for both the bash and zsh interpreters is:

```
for NAME [in LIST]; do COMMANDS; done
```

The list can be a simple sequence of numbers, or you can use the shell expansion syntax `{1..N}` which expands to the sequence from 1 to  $N$ , e.g. `{1..4}` expands to 1 2 3 4. Note that the expression `{1..N}` cannot contain spaces.

To run 4 chains for the example bernoulli model on MacOS or Linux:

```
> for i in {1..4}
do
    ./bernoulli sample data file=bernoulli.data.json \
    output file=output_${i}.csv
done
```

The backslash (\) indicates a line continuation in Unix. The expression `${i}` substitutes in the value of loop index variable `i`. To run chains in parallel, put an ampersand (&) at the end of the nested sampler command:

```
> for i in {1..4}
do
    ./bernoulli sample data file=bernoulli.data.json \
    output file=output_${i}.csv &
done
```

This pushes each process into the background which allows the loop to continue without waiting for the current chain to finish.

On Windows, the DOS for-loop syntax is one of:

```
for %i in (SET) do COMMAND COMMAND-ARGUMENTS
for /l %i in (START, STEP, END) do COMMAND COMMAND-ARGUMENTS
```

To run 4 chains in parallel on Windows:

```
>for /l %i in (1, 1, 4) do start /b bernoulli.exe sample ^
    data file=bernoulli.data.json my_data ^
    output file=output_%i.csv
```

The caret (^) indicates a line continuation in DOS.

### 4.3. Stan CSV output file

Each execution of the model results in draws from a single Markov chain being written to a file in comma-separated value (CSV) format. The default name of the output file is `output.csv`.

The first part of the output file records the version of the underlying Stan library and the configuration as comments (i.e., lines beginning with the pound sign (#)).

```
# stan_version_major = 2
# stan_version_minor = 23
# stan_version_patch = 0
# model = bernoulli_model
# method = sample (Default)
#   sample
#     num_samples = 1000 (Default)
#     num_warmup = 1000 (Default)
...
# output
#   file = output.csv (Default)
#   diagnostic_file = (Default)
#   refresh = 100 (Default)
```

This is followed by a CSV header indicating the names of the values sampled.

```
lp__,accept_stat__,stepsize__,treedepth__,n_leapfrog__,divergent__,energy__,
```

The first output columns report the HMC sampler information:

- `lp__` - the total log probability density (up to an additive constant) at each sample
- `accept_stat__` - the average Metropolis acceptance probability over each simulated Hamiltonian trajectory
- `stepsize__` - integrator step size
- `treedepth__` - depth of tree used by NUTS (NUTS sampler)
- `n_leapfrog__` - number of leapfrog calculations (NUTS sampler)
- `divergent__` - has value 1 if trajectory diverged, otherwise 0. (NUTS sampler)
- `energy__` - value of the Hamiltonian
- `int_time__` - total integration time (static HMC sampler)

Because the above header is from the NUTS sampler, it has columns `treedepth__`, `n_leapfrog__`, and `divergent__` and doesn't have column `int_time__`. The remaining columns correspond to model parameters. For the Bernoulli model, it is just

the final column, theta.

The header line is written to the output file before warmup begins. If option `save_warmup` is set to 1, the warmup draws are output directly after the header. The total number of warmup draws saved is `num_warmup` divided by `thin`, rounded up (i.e., ceiling).

Following the warmup draws (if any), are comments which record the results of adaptation: the stepsize, and inverse mass metric used during sampling:

```
# Adaptation terminated
# Step size = 0.884484
# Diagonal elements of inverse mass matrix:
# 0.535006
```

The default sampler is NUTS with an adapted step size and a diagonal inverse mass matrix. For this example, the step size is 0.884484, and the inverse mass contains the single entry 0.535006 corresponding to the parameter theta.

Draws from the posterior distribution are printed out next, each line containing a single draw with the columns corresponding to the header.

```
-6.84097,0.974135,0.884484,1,3,0,6.89299,0.198853
-6.91767,0.985167,0.884484,1,1,0,6.92236,0.182295
-7.04879,0.976609,0.884484,1,1,0,7.05641,0.162299
-6.88712,1,0.884484,1,1,0,7.02101,0.188229
-7.22917,0.899446,0.884484,1,3,0,7.73663,0.383596
...
```

The output ends with timing details:

```
# Elapsed Time: 0.007 seconds (Warm-up)
#               0.017 seconds (Sampling)
#               0.024 seconds (Total)
```

#### 4.4. Summarizing sampler output(s) with `stansummary`

The `stansummary` utility processes one or more output files from a run or set of runs of Stan's HMC sampler given a model and data. For all columns in the Stan CSV output file `stansummary` reports a set of statistics including mean, standard deviation, percentiles, effective number of samples, and  $\hat{R}$  values.

To run `stansummary` on the output files generated by the for loop above, by the above run of the `bernoulli` model on Mac or Linux:

```
<cmdstan-home>/bin/stansummary output_*.csv
```

On Windows, use backslashes to call the stansummary.exe.

```
<cmdstan-home>\bin\stansummary.exe output_*.csv
```

The stansummary output consists of one row of statistics per column in the Stan CSV output file. Therefore, the first rows in the stansummary report statistics over the sampler state. The final row of output summarizes the estimates of the model variable `theta`:

```
Inference for Stan model: bernoulli_model
```

```
4 chains: each with iter=(1000,1000,1000,1000); warmup=(0,0,0,0); thin=(1,1,
```

```
Warmup took (0.0070, 0.0070, 0.0070, 0.0070) seconds, 0.028 seconds total
```

```
Sampling took (0.020, 0.017, 0.021, 0.019) seconds, 0.077 seconds total
```

	Mean	MCSE	StdDev	5%	50%	95%	N_Eff	N_Eff/s
lp__	-7.3	1.8e-02	0.75	-8.8	-7.0	-6.8	1.8e+03	2.4e+04
accept_stat__	0.89	2.7e-03	0.17	0.52	0.96	1.0	3.9e+03	5.1e+04
stepsize__	1.1	7.5e-02	0.11	0.93	1.2	1.2	2.0e+00	2.6e+01
treedepth__	1.4	8.1e-03	0.49	1.0	1.0	2.0	3.6e+03	4.7e+04
n_leapfrog__	2.3	1.7e-02	0.98	1.0	3.0	3.0	3.3e+03	4.3e+04
divergent__	0.00	nan	0.00	0.00	0.00	0.00	nan	nan
energy__	7.8	2.6e-02	1.0	6.8	7.5	9.9	1.7e+03	2.2e+04
theta	0.25	2.9e-03	0.12	0.079	0.23	0.46	1.7e+03	2.1e+04

Samples were drawn using `hmc` with `nuts`.

For each parameter, `N_Eff` is a crude measure of effective sample size, and `R_hat` is the potential scale reduction factor on split chains (at convergence, `R_hat=1`).

In this example, we conditioned the model on a dataset consisting of the outcomes of 10 bernoulli trials, where only 2 trials reported success. The 5%, 50%, and 95% percentile values for `theta` reflect the uncertainty in our estimate, due to the small amount of data, given the prior of `beta(1, 1)`

## 5. Optimization

The CmdStan executable can run Stan's optimization algorithms for penalized maximum likelihood estimation which provide a deterministic method to find the posterior mode. If the posterior is not convex, there is no guarantee Stan will be able to find the global mode as opposed to a local optimum of log probability.

The executable does not need to be recompiled in order to switch from sampling to optimization, and the data input format is the same. The following is a minimal call to Stan's optimizer using defaults for everything but the location of the data file.

```
> ./bernoulli optimize data file=bernoulli.data.json
```

Executing this command prints both output to the console and to a csv file.

The first part of the console output reports on the configuration used. The above command uses all default configurations, therefore the optimizer used is the L-BFGS optimizer and its default initial stepsize and tolerances for monitoring convergence:

```
./bernoulli optimize data file=bernoulli.data.json
method = optimize
  optimize
    algorithm = lbfgs (Default)
      lbfgs
        init_alpha = 0.001 (Default)
        tol_obj = 1e-12 (Default)
        tol_rel_obj = 10000 (Default)
        tol_grad = 1e-08 (Default)
        tol_rel_grad = 10000000 (Default)
        tol_param = 1e-08 (Default)
        history_size = 5 (Default)
      iter = 2000 (Default)
      save_iterations = 0 (Default)
    id = 0 (Default)
  data
    file = bernoulli.data.json
  init = 2 (Default)
  random
    seed = 87122538 (Default)
```



```

output
  file = output.csv (Default)
  diagnostic_file = (Default)
  refresh = 100 (Default)

```

The second part of the output indicates how well the algorithm fared, here converging and terminating normally. The numbers reported indicate that it took 5 iterations and 8 gradient evaluations. This is, not surprisingly, far fewer iterations than required for sampling; even fewer iterations would be used with less stringent user-specified convergence tolerances. The alpha value is for step size used. In the final state the change in parameters was roughly 0.002 and the length of the gradient roughly  $3\text{e-}05$  (0.00003).

```

Initial log joint probability = -6.85653
      Iter      log prob      ||dx||      ||grad||      alpha      alpha0
        5      -5.00402      0.00184936      3.35074e-05          1          1

```

Optimization terminated normally:

Convergence detected: relative gradient magnitude is below tolerance

The output from optimization is written into the file `output.csv` by default. The output follows the same pattern as the output for sampling, first dumping the entire set of parameters used as comment lines:

```

# stan_version_major = 2
# stan_version_minor = 23
# stan_version_patch = 0
# model = bernoulli_model
# method = optimize
#   optimize
#     algorithm = lbfgs (Default)
...

```

Following the config information, are two lines of output: the CSV headers and the recorded values:

```

lp__,theta
-5.00402,0.200003

```

Note that everything is a comment other than a line for the header, and a line for the values. Here, the header indicates the unnormalized log probability with `lp__` and the model parameter `theta`. The maximum log probability is -5.0 and the posterior mode for `theta` is 0.20. The mode exactly matches what we would expect from the

data.<sup>1</sup>

Because the prior was uniform, the result 0.20 represents the maximum likelihood estimate (MLE) for the very simple Bernoulli model. Note that no uncertainty is reported.

All of the optimizers stream per-iteration intermediate approximations to the command line console. The sub-argument `save_iterations` specifies whether or not to save the intermediate iterations to the output file. Allowed values are 0 or 1, corresponding to False and True respectively. The default value is 0, i.e., intermediate iterations are not saved to the output file. Running the optimizer with `save_iterations=1` writes both the initial log joint probability and values for all iterations to the output CSV file.

Running the example model with option `save_iterations=1`, i.e., the command

```
> ./bernoulli optimize save_iterations=1 data file=bernoulli.data.json
```

produces CSV file output rows:

```
lp__,theta
-6.85653,0.493689
-6.10128,0.420936
-5.02953,0.22956
-5.00517,0.206107
-5.00403,0.200299
-5.00402,0.200003
```

---

<sup>1</sup>The Jacobian adjustment included for the sampler's log probability function is not applied during optimization, because it can change the shape of the posterior and hence the solution.

## 6. Variational Inference

CmdStan can approximate the posterior distribution using variational inference. The approximation is a Gaussian in the unconstrained variable space. Stan implements two variational algorithms. The `algorithm=meanfield` option uses a fully factorized Gaussian for the approximation. The `algorithm=fullrank` option uses a Gaussian with a full-rank covariance matrix for the approximation.

The executable does not need to be recompiled in order to switch to variational inference, and the data input format is the same. The following is a minimal call to Stan's variational inference algorithm using defaults for everything but the location of the data file.

```
> ./bernoulli variational data file=bernoulli.data.R
```

Executing this command prints both output to the console and to a csv file.

The first part of the console output reports on the configuration used. Here it indicates the default mean-field setting of the variational inference algorithm. It also indicates the default parameter sizes and tolerances for monitoring the algorithm's convergence.

```
method = variational
  variational
    algorithm = meanfield (Default)
      meanfield
    iter = 10000 (Default)
    grad_samples = 1 (Default)
    elbo_samples = 100 (Default)
    eta = 1 (Default)
    adapt
      engaged = 1 (Default)
      iter = 50 (Default)
    tol_rel_obj = 0.01 (Default)
    eval_elbo = 100 (Default)
    output_samples = 1000 (Default)
id = 0 (Default)
data
  file = bernoulli.data.json
```

```

init = 2 (Default)
random
  seed = 3323783840 (Default)
output
  file = output.csv (Default)
  diagnostic_file = (Default)
  refresh = 100 (Default)

```

After the configuration has been displayed, informational and timing messages are output:

```

-----
EXPERIMENTAL ALGORITHM:

```

```

  This procedure has not been thoroughly tested and may be unstable
  or buggy. The interface is subject to change.
-----

```

```

Gradient evaluation took 2.1e-05 seconds
1000 transitions using 10 leapfrog steps per transition would take 0.21 seconds
Adjust your expectations accordingly!

```

The rest of the output describes the progression of the algorithm. An adaptation phase finds a good value for the step size scaling parameter  $\eta$ . The evidence lower bound (ELBO) is the variational objective function and is evaluated based on a Monte Carlo estimate. The variational inference algorithm in Stan is stochastic, which makes it challenging to assess convergence. That is, while the algorithm appears to have converged in  $\sim 250$  iterations, the algorithm runs for another few thousand iterations until mean change in ELBO drops below the default tolerance of 0.01.

Begin  $\eta$  adaptation.

```

Iteration:   1 / 250 [  0%] (Adaptation)
Iteration:  50 / 250 [ 20%] (Adaptation)
Iteration: 100 / 250 [ 40%] (Adaptation)
Iteration: 150 / 250 [ 60%] (Adaptation)
Iteration: 200 / 250 [ 80%] (Adaptation)
Success! Found best value [eta = 1] earlier than expected.

```

Begin stochastic gradient ascent.

iter	ELBO	delta_ELBO_mean	delta_ELBO_med	notes
100	-6.131	1.000	1.000	

200	-6.458	0.525	1.000	
300	-6.300	0.359	0.051	
400	-6.137	0.276	0.051	
500	-6.243	0.224	0.027	
600	-6.305	0.188	0.027	
700	-6.289	0.162	0.025	
800	-6.402	0.144	0.025	
900	-6.103	0.133	0.025	
1000	-6.314	0.123	0.027	
1100	-6.348	0.024	0.025	
1200	-6.244	0.020	0.018	
1300	-6.293	0.019	0.017	
1400	-6.250	0.017	0.017	
1500	-6.241	0.015	0.010	MEDIAN ELBO CON

Drawing a sample of size 1000 from the approximate posterior...  
COMPLETED.

The output from variational is written into the file `output.csv` by default. The output follows the same pattern as the output for sampling, first dumping the entire set of parameters used as CSV comments:

```
# stan_version_major = 2
# stan_version_minor = 23
# stan_version_patch = 0
# model = bernoulli_model
# method = variational
#   variational
#     algorithm = meanfield (Default)
#       meanfield
#         iter = 10000 (Default)
#         grad_samples = 1 (Default)
#         elbo_samples = 100 (Default)
#         eta = 1 (Default)
#       adapt
#         engaged = 1 (Default)
#         iter = 50 (Default)
#         tol_rel_obj = 0.01 (Default)
#         eval_elbo = 100 (Default)
#         output_samples = 1000 (Default)
```

...

Next is the column header line, followed more CSV comments reporting the adapted value for the stepsize, followed by the values. The first line is special: it is the mean of the variational approximation. The rest of the output contains `output_samples` number of samples drawn from the variational approximation.

```
lp__,log_p__,log_g__,theta
# Stepsize adaptation complete.
# eta = 1
0,0,0,0.236261
0,-6.82318,-0.0929121,0.300415
0,-6.89701,-0.158687,0.321982
0,-6.99391,-0.23916,0.343643
0,-7.35801,-0.51787,0.401554
0,-7.4668,-0.539473,0.123081
...
```

The header indicates the unnormalized log probability with `lp__`. This is a legacy feature that we do not use for variational inference. The ELBO is not stored unless a diagnostic option is given.

For further details, see Kucukelbir, Alp, Rajesh Ranganath, Andrew Gelman, and David M. Blei. 2015. *Automatic Variational Inference in Stan*. arXiv 1506.03431. <http://arxiv.org/abs/1506.03431>.

## 7. Generating Quantities of Interest from a Fitted Model

The generated quantities block computes *quantities of interest* (QOIs) based on the data, transformed data, parameters, and transformed parameters. It can be used to:

- generate simulated data for model testing by forward sampling
- generate predictions for new data
- calculate posterior event probabilities, including multiple comparisons, sign tests, etc.
- calculating posterior expectations
- transform parameters for reporting
- apply full Bayesian decision theory
- calculate log likelihoods, deviances, etc. for model comparison

The `generate_quantities` method allows you to generate additional quantities of interest from a fitted model without re-running the sampler. Instead, you write a modified version of the original Stan program and add a generated quantities block or modify the existing one which specifies how to compute the new quantities of interest. Running the `generate_quantities` method on the new program together with sampler outputs (i.e., a set of draws) from the fitted model runs the generated quantities block of the new program using the existing sample by plugging in the per-draw parameter estimates for the computations in the generated quantities block. See the Stan User's Guide section Stand-alone generated quantities and ongoing prediction for further details.

To illustrate how this works we use the `generate_quantities` method to do posterior predictive checks using the estimate of `theta` given the example bernoulli model and data, following the posterior predictive simulation procedure in the Stan User's Guide.

We write a program `bernoulli_ppc.stan` which contains the following generated quantities block, with comments to explain the procedure:

```
generated quantities {  
  real<lower=0, upper=1> theta_rep;  
  array[N] int y_sim;  
  // use current estimate of theta to generate new sample
```

```

for (n in 1:N) {
  y_sim[n] = bernoulli_rng(theta);
}
// estimate theta_rep from new sample
theta_rep = sum(y_sim) * 1.0 / N;
}

```

The rest of the program is the same as in `bernoulli.stan`.

The `generate_method` requires the sub-argument `fitted_params` which takes as its value the name of a Stan CSV file. The per-draw parameter estimates from the `fitted_params` file will be used to run the generated quantities block.

If we run the `bernoulli.stan` program for a single chain to generate a sample in file `bernoulli_fit.csv`:

```
> ./bernoulli sample data file=bernoulli.data.json output file=bernoulli_fit
```

Then we can run the `bernoulli_ppc.stan` to carry out the posterior predictive checks:

```
> ./bernoulli_ppc generate_quantities fitted_params=bernoulli_fit.csv \
    data file=bernoulli.data.json \
    output file=bernoulli_ppc.csv
```

The output file `bernoulli_ppc.csv` consists of just the values for the variables declared in the generated quantities block, i.e., `theta_rep` and the elements of `y_sim`:

```

# model = bernoulli_ppc_model
# method = generate_quantities
#   generate_quantities
#     fitted_params = bernoulli_fit.csv
# id = 0 (Default)
# data
#   file = bernoulli.data.json
# init = 2 (Default)
# random
#   seed = 2135140492 (Default)
# output
#   file = bernoulli_ppc.csv
#   diagnostic_file = (Default)
#   refresh = 100 (Default)

```



```

theta_rep,y_sim.1,y_sim.2,y_sim.3,y_sim.4,y_sim.5,y_sim.6,y_sim.7,y_sim.8,y_
0.2,0,0,1,0,0,0,0,0,1,0
0.3,1,0,0,1,0,1,0,0,0,0
0.8,1,0,1,1,1,1,1,1,1,0
0.1,0,0,0,0,0,1,0,0,0,0
0.3,0,0,0,0,0,0,1,1,1,0

```

*Note:* the only relevant analysis of the resulting CSV output is computing per-column statistics; this can easily be done in Python, R, Excel or similar, or you can use the CmdStanPy and CmdStanR interfaces which provide a better user experience for this workflow.

Given the current implementation, to see the fitted parameter values for each draw, create a copy variable in the generated quantities block, e.g.:

```

generated quantities {
  real<lower=0, upper=1> theta_cp = theta;
  real<lower=0, upper=1> theta_rep;
  array[N] int y_sim;
  // use current estimate of theta to generate new sample
  for (n in 1:N) {
    y_sim[n] = bernoulli_rng(theta);
  }
  // estimate theta_rep from new sample
  theta_rep = sum(y_sim) * 1.0 / N;
}

```

Now the output is slightly more interpretable: `theta_cp` is the same as the `theta` used to generate the values `y_sim[1]` through `y_sim[1]`. Comparing columns `theta_cp` and `theta_rep` allows us to see how the uncertainty in our estimate of `theta` is carried forward into our predictions:

```

theta_cp,theta_rep,y_sim.1,y_sim.2,y_sim.3,y_sim.4,y_sim.5,y_sim.6,y_sim.7,y_
0.102391,0,0,0,0,0,0,0,0,0,0,0
0.519567,0.2,0,1,0,0,1,0,0,0,0,0
0.544634,0.6,1,0,0,0,0,1,1,1,1,1
0.167651,0,0,0,0,0,0,0,0,0,0,0
0.167651,0.1,1,0,0,0,0,0,0,0,0,0

```

# Reference Manual

This section provides a complete reference for all CmdStan methods:

- `sample`
- `optimize`
- `variational`
- `generate_quantities`
- `diagnose`
- `help`

## 8. Command-Line Interface Overview

A CmdStan executable is built from the Stan model concept and the CmdStan command line parser. The command line argument syntax consists of sets of keywords and keyword-value pairs. Arguments are grouped by the following keywords:

- `method` - specifies the kind of inference done on the model. Each kind of inference requires further configuration via sub-arguments. The `method` argument is required. It can be specified overtly as the a keyword-value pair `method=<inference>` or implicitly as one of the following:
  - `sample` - obtain a sample from the posterior using HMC
  - `optimize` - penalized maximum likelihood estimation
  - `variational` - automatic variational inference
  - `generate_quantities` - run model's generated quantities block on existing sample to obtain new quantities of interest.
  - `diagnose` - compute and compare sampler gradient calculations to finite differences.
- `data` - specifies the input data file, if any.
- `output` - specifies program outputs, both disk files and terminal window outputs.
- `init` - specifies initial values for the model parameters, if any.
- `random` - specifies the seed for the pseudo-random number.

The remainder of this chapter covers the general configuration options used for all processing. The following chapters cover the per-inference configuration options.

### 8.1. Input data argument

The values for all variables declared in the data block of the model are read in from an input data file in either JSON or Rdump format. The syntax for the input data argument is:

```
data file=<filepath>
```

The keyword `data` must be followed directly by the keyword-value pair `file=<filepath>`. If the model doesn't declare any data variables, this argument is ignored.

The input data file must contain definitions for all data variables declared in the data block. If one or more data block variables are missing from the input data file, the program prints an error message to `stderr` and returns a non-zero return code. For example, the model `bernoulli.stan` defines two data variables `N` and `y`. If the input data file doesn't include both variables, or if the data variable doesn't match the declared type and dimensions, the program will exit with an error message at the point where it first encounters missing data.

For example if the input data file doesn't include the definition for variable `y`, the executable exits with the following message:

```
Exception: variable does not exist; processing stage=data initialization; va
```

## 8.2. Output control arguments

The output keyword is used to specify non-default options for output files and messages written to the terminal window. The output keyword takes several keyword-value pair sub-arguments.

The keyword value pair `file=<filepath>` specifies the location of the Stan CSV output file. If unspecified, the output file is written to a file named `output.csv` in the current working directory.

The keyword value pair `diagnostic_file=<filepath>` specifies the location of the auxiliary output file. By default, no auxiliary output file is produced. This option is only valid for the iterative algorithms `sample` and `variational`.

The keyword value pair `refresh=<int>` specifies the number of iterations between progress messages written to the terminal window. The default value is 100 iterations.

The keyword value pair `sig_figs=<int>` specifies the number of significant digits for all numerical values in the output files. Allowable values are between 1 and 18, which is the maximum amount of precision available for 64-bit floating point arithmetic. The default value is 6. **Note:** increasing `sig_figs` above the default will increase the size of the output CSV files accordingly.

The keyword value pair `profile_file=<filepath>` specifies the location of the output file for profiling data. If the model uses no profiling, the output profile file is not produced. If the model uses profiling and `profile_file` is unspecified,

the profiling data is written to a file named `profile.csv` in the current working directory.

### 8.3. Initialize model parameters argument

Initialization is only applied to parameters defined in the parameters block. By default, all parameters are initialized to random draws from a uniform distribution over the range  $[-2, 2]$ . These values are on the unconstrained scale, so must be inverse transformed back to satisfy the constraints declared for parameters. Because zero is chosen to be a reasonable default initial value for most parameters, the interval around zero provides a fairly diffuse starting point. For instance, unconstrained variables are initialized randomly in  $(-2, 2)$ , variables constrained to be positive are initialized roughly in  $(0.14, 7.4)$ , variables constrained to fall between 0 and 1 are initialized with values roughly in  $(0.12, 0.88)$ .

The initialization argument is specified as keyword-value pair with keyword `init`. The value can be one of the following:

- positive real number  $x$ . All parameters will be initialized to random draws from a uniform distribution over the range  $[-x, x]$ .
- 0 - All parameters will be initialized to zero values on the unconstrained scale. The transforms are arranged in such a way that zero initialization provides reasonable variable initializations: 0 for unconstrained parameters; 1 for parameters constrained to be positive; 0.5 for variables to constrained to lie between 0 and 1; a symmetric (uniform) vector for simplexes; unit matrices for both correlation and covariance matrices; and so on.
- filepath - A data file in JSON or Rdump format containing initial parameters values for some or all of the model parameters. User specified initial values must satisfy the constraints declared in the model (i.e., they are on the constrained scale). Parameters which aren't explicitly initialized will be initialized randomly over the range  $[-2, 2]$ .

### 8.4. Random number generator arguments

The random-number generator's behavior is determined by the unsigned seed (positive integer) it is started with. If a seed is not specified, or a seed of 0 or less is specified, the system time is used to generate a seed. The seed is recorded and included with Stan's output regardless of whether it was specified or generated randomly from the system time.

The syntax for the random seed argument is:

```
random seed=<int>
```

The keyword `random` must be followed directly by the keyword-value pair `seed=<int>`.

## 8.5. Chain identifier argument: `id`

The chain identifier argument is used in conjunction with the `random seed` argument when running multiple Markov chains for sampling. The chain identifier is used to advance the random number generator a very large number of random variates so that two chains with the same seed and different identifiers draw from non-overlapping subsequences of the random-number sequence determined by the seed. Together, the seed and chain identifier determine the behavior of the random number generator.

The syntax for the random seed argument is:

```
id=<int>
```

The default value is 0.

When running a set of chains from the command line with a specified seed, this argument should be set to the chain index. E.g., when running 4 chains, the value should be 1,...,4, successively. When running multiple chains from a single command, Stan's interfaces manage the chain identifier arguments automatically.

For complete reproducibility, every aspect of the environment needs to be locked down from the OS and version to the C++ compiler and version to the version of Stan and all dependent libraries. See the Stan Reference Manual Reproducibility chapter for further details.

## 8.6. Command line help

CmdStan provides a `help` and `help-all` mechanism that displays either the available top-level or keyword-specific key-value argument pairs. To display top-level help, call the CmdStan executable with keyword `help`:

```
> ./bernoulli help
```

```
Usage: ./bernoulli <arg1> <subarg1_1> ... <subarg1_m> ... <arg_n> <subarg_n_1> ...
```

Begin by selecting amongst the following inference methods and diagnostics,  
`sample`            Bayesian inference with Markov Chain Monte Carlo

```

optimize      Point estimation
variational   Variational inference
diagnose      Model diagnostics
generate_quantities  Generate quantities of interest

```

Or see help information with

```

help          Prints help
help-all     Prints entire argument tree

```

Additional configuration available by specifying

```

id            Unique process identifier
data          Input data options
init          Initialization method: "x" initializes randomly between [-x, x]
random        Random number configuration
output        File output options

```

See `./bernoulli <arg1> [ help | help-all ]` for details on individual arguments.

## 8.7. Error messages and return codes

CmdStan executables and utility programs use streams standard output (stdout) and standard error (stderr) to report information and error messages, respectively. Some methods also generate warning messages when the algorithm detects potential problems with the inference. Depending on the method, these messages are sent to either standard out or standard error.

All program executables provide a return code between 0 and 255:

- 0 - Program ran to termination as expected.
- value in range [1 : 125] - Method invoked could not run due to problems with model or data.
- value > 128 - Fatal error during execution, process terminated by signal. To determine the signal number, subtract 128 from the return value, e.g. return code 139 results from termination signal 11 (segmentation violation).

A non-zero return code or outputs sent to stderr indicate problems with the inference. However, a return code of zero and absence of error messages doesn't necessarily mean that the inference is valid, it is still necessary to validate the inferences using all available summary and diagnostic techniques.

## 9. MCMC Sampling using Hamiltonian Monte Carlo

The `sample` method provides Bayesian inference over the model conditioned on data using Hamiltonian Monte Carlo (HMC) sampling. By default, the inference engine used is the No-U-Turn sampler (NUTS), an adaptive form of Hamiltonian Monte Carlo sampling. For details on HMC and NUTS, see the Stan Reference Manual chapter on MCMC Sampling.

The full set of configuration options available for the `sample` method is reported at the beginning of the sampler output file as CSV comments. When the example model `bernoulli.stan` is run via the command line with all default arguments, the resulting Stan CSV file header comments show the complete set of default configuration options:

```
# model = bernoulli_model
# method = sample (Default)
#   sample
#     num_samples = 1000 (Default)
#     num_warmup = 1000 (Default)
#     save_warmup = 0 (Default)
#     thin = 1 (Default)
#     adapt
#       engaged = 1 (Default)
#       gamma = 0.05 (Default)
#       delta = 0.8 (Default)
#       kappa = 0.75 (Default)
#       t0 = 10 (Default)
#       init_buffer = 75 (Default)
#       term_buffer = 50 (Default)
#       window = 25 (Default)
#     algorithm = hmc (Default)
#       hmc
#         engine = nuts (Default)
#         nuts
#           max_depth = 10 (Default)
```



```
#      metric = diag_e (Default)
#      metric_file = (Default)
#      stepsize = 1 (Default)
#      stepsize_jitter = 0 (Default)
```

## 9.1. Iterations

At every sampler iteration, the sampler returns a set of estimates for all parameters and quantities of interest in the model. During warmup, the NUTS algorithm adjusts the HMC algorithm parameters `metric` and `stepsize` in order to efficiently sample from *typical set*, the neighborhood substantial posterior probability mass through which the Markov chain will travel in equilibrium. After warmup, the fixed `metric` and `stepsize` are used to produce a set of draws.

The following keyword-value arguments control the total number of iterations:

- `num_samples`
- `num_warmup`
- `save_warmup`
- `thin`

The values for arguments `num_samples` and `num_warmup` must be a non-negative integer. The default value for both is 1000.

For well-specified models and data, the sampler may converge faster and this many warmup iterations may be overkill. Conversely, complex models which have difficult posterior geometries may require more warmup iterations in order to arrive at good values for the step size and metric.

The number of sampling iterations to runs depends on the effective sample size (EFF) reported for each parameter and the desired precision of your estimates. An EFF of at least 100 is required to make a viable estimate. The precision of your estimate is  $\sqrt{N}$ ; therefore every additional decimal place of accuracy increases this by a factor of 10.

Argument `save_warmup` takes values 0 or 1, corresponding to `False` and `True` respectively. The default value is 0, i.e., warmup draws are not saved to the output file. When the value is 1, the warmup draws are written to the CSV output file directly after the CSV header line.

Argument `thin` controls the number of draws from the posterior written to the output file. Some users familiar with older approaches to MCMC sampling might be used to thinning to eliminate an expected autocorrelation in the samples. HMC is not

nearly as susceptible to this autocorrelation problem and thus thinning is generally not required nor advised, as HMC can produce *anticorrelated* draws, which increase the effective sample size beyond the number of draws from the posterior. Thinning should only be used in circumstances where storage of the samples is limited and/or RAM for later processing the samples is limited.

The value of argument `thin` must be a positive integer. When `thin` is set to value  $N$ , every  $N^{th}$  iteration is written to the output file. Should the value of `thin` exceed the specified number of iterations, the first iteration is saved to the output. This is because the iteration counter starts from zero and whenever the counter modulo the value of `thin` equals zero, the iteration is saved to the output file. Since zero modulo any positive integer is zero, the first iteration is always saved. When `num_sampling=M` and `thin=N`, the number of iterations written to the output CSV file will be  $\text{ceiling}(M/N)$ . If `save_warmup=1`, thinning is applied to the warmup iterations as well.

## 9.2. Adaptation

The `adapt` keyword is used to specify non-default options for the sampler adaptation schedule and settings.

Adaptation can be turned off by setting sub-argument `engaged` to value 0. If `engaged=0`, no adaptation will be done, and all other adaptation sub-arguments will be ignored. Since the default argument is `engaged=1`, this keyword-value pair can be omitted from the command.

There are two sets of adaptation sub-arguments: step size optimization parameters and the warmup schedule. These are described in detail in the Reference Manual section Automatic Parameter Tuning.

### Step size optimization configuration

The Stan User's Guide section on model conditioning and curvature provides a discussion of adaptation and stepsize issues. The Stan Reference Manual section on HMC algorithm parameters explains the NUTS-HMC adaptation schedule and the tuning parameters for setting the step size.

The following keyword-value arguments control the settings used to optimize the step size:

- `delta` - The target Metropolis acceptance rate. The default value is 0.8. Its value must be strictly between 0 and 1. Increasing the default value forces the

algorithm to use smaller step sizes. This can improve sampling efficiency (effective sample size per iteration) at the cost of increased iteration times. Raising the value of `delta` will also allow some models that would otherwise get stuck to overcome their blockages. Models with difficult posterior geometries may require increasing the `delta` argument closer to 1; we recommend first trying to raise it to 0.9 or at most 0.95. Values about 0.95 are strong indication of bad geometry; the better solution is to change the model geometry through reparameterization which could yield both more efficient and faster sampling.

- `gamma` - Adaptation regularization scale. Must be a positive real number, default value is 0.05. This is a parameter of the Nesterov dual-averaging algorithm. We recommend always using the default value.
- `kappa` - Adaptation relaxation exponent. Must be a positive real number, default value is 0.75. This is a parameter of the Nesterov dual-averaging algorithm. We recommend always using the default value.
- `t_0` - Adaptation iteration offset. Must be a positive real number, default value is 10. This is a parameter of the Nesterov dual-averaging algorithm. We recommend always using the default value.

### Warmup schedule configuration

When adaptation is engaged, the warmup schedule is specified by sub-arguments, all of which take positive integers as values:

- `init_buffer` - The number of iterations spent tuning the step size at the outset of adaptation.
- `window` - The initial number of iterations devoted to tune the metric, will be doubled successively.
- `term_buffer` - The number of iterations used to re-tune the step size once the metric has been tuned.

The specified values may be modified slightly in order to ensure alignment between the warmup schedule and total number of warmup iterations.

The following figure is taken from the Stan Reference Manual, where label “I” correspond to `init_buffer`, the initial “II” corresponds to `window`, and the final “III” corresponds to `term_buffer`:

**Warmup Epochs Figure.** *Adaptation during warmup occurs in three stages: an initial fast adaptation interval (I), a series of expanding slow adaptation intervals (II), and a final fast adaptation interval (III). For HMC, both the fast and slow intervals are used*

for adapting the step size, while the slow intervals are used for learning the (co)variance necessitated by the metric. Iteration numbering starts at 1 on the left side of the figure and increases to the right.



### 9.3. Algorithm

The `algorithm` keyword-value pair specifies the algorithm used to generate the sample. There are two possible values: `hmc`, which generates from an HMC-driven Markov chain; and `fixed_param` which generates a new sample without changing the state of the Markov chain. The default argument is `algorithm=hmc`.

#### Samples from a set of fixed parameters

If a model doesn't specify any parameters, then argument `algorithm=fixed_param` is mandatory.

The fixed parameter sampler generates a new sample without changing the current state of the Markov chain. This can be used to write models which generate pseudo-data via calls to RNG functions in the transformed data and generated quantities blocks.

#### HMC samplers

All HMC algorithms have three parameters:

- step size
- metric
- integration time - the number of steps taken along the Hamiltonian trajectory

See the Stan Reference Manual section on HMC algorithm parameters for further details.

### Step size

The HMC algorithm simulates the evolution of a Hamiltonian system. The step size parameter controls the resolution of the sampler. Low step sizes can get HMC samplers unstuck that would otherwise get stuck with higher step sizes.

The following keyword-value arguments control the step size:

- `stepsize` - How far to move each time the Hamiltonian system evolves forward. Must be a positive real number, default value is 1.
- `stepsize_jitter` - Allows step size to be “jittered” randomly during sampling to avoid any poor interactions with a fixed step size and regions of high curvature. Must be a real value between 0 and 1. The default value is 0. Setting `stepsize_jitter` to 1 causes step sizes to be selected in the range of 0 to twice the adapted step size. Jittering below the adapted value will increase the number of steps required and will slow down sampling, while jittering above the adapted value can cause premature rejection due to simulation error in the Hamiltonian dynamics calculation. We strongly recommend always using the default value.

### Metric

All HMC implementations in Stan utilize quadratic kinetic energy functions which are specified up to the choice of a symmetric, positive-definite matrix known as a *mass matrix* or, more formally, a *metric* Betancourt (2017).

The `metric` argument specifies the choice of Euclidean HMC implementations:

- `metric=unit` specifies unit metric (diagonal matrix of ones).
- `metric=diag_e` specifies a diagonal metric (diagonal matrix with positive diagonal entries). This is the default value.
- `metric=dense_e` specifies a dense metric (a dense, symmetric positive definite matrix).

By default, the metric is estimated during warmup. However, when `metric=diag_e` or `metric=dense_e`, an initial guess for the metric can be specified with the `metric_file` argument whose value is the filepath to a JSON or Rdump file which contains a single variable `inv_metric`. For a `diag_e` metric the `inv_metric` value must be a vector of positive values, one for each parameter in the system. For a `dense_e` metric, `inv_metric` value must be a positive-definite square matrix with number of rows and columns equal to the number of parameters in the model.

The `metric_file` option can be used with and without adaptation enabled. If adaptation is enabled, the provided metric will be used as the initial guess in the adaptation process. If the initial guess is good, then adaptation should not change it much. If the metric is no good, then the adaptation will override the initial guess.

If adaptation is disabled, both the `metric_file` and `stepsize` arguments should be specified.

### *Integration time*

The total integration time is determined by the argument `engine` which take possible values:

- `nuts` - the No-U-Turn Sampler which dynamically determines the optimal integration time.
- `static` - an HMC sampler which uses a user-specified integration time.

The default argument is `engine=nuts`.

The NUTS sampler generates a proposal by starting at an initial position determined by the parameters drawn in the last iteration. It then evolves the initial system both forwards and backwards in time to form a balanced binary tree. The algorithm is iterative; at each iteration the tree depth is increased by one, doubling the number of leapfrog steps thus effectively doubling the computation time. The algorithm terminates in one of two ways: either the NUTS criterion (i.e., a U-turn in Euclidean space on a subtree) is satisfied for a new subtree or the completed tree; or the depth of the completed tree hits the maximum depth allowed.

When `engine=nuts`, the subargument `max_depth` can be used to control the depth of the tree. The default argument is `max_depth=10`. In the case where a model has a difficult posterior from which to sample, `max_depth` should be increased to ensure that the NUTS tree can grow as large as necessary.

When the argument `engine=static` is specified, the user must specify the integration time via keyword `int_time` which takes as a value a positive number. The default value is  $2\pi$ .

## **9.4. Sampler diagnostic file**

The output keyword sub-argument `diagnostic_file=<filepath>` specifies the location of the auxiliary output file which contains sampler information for each

draw, and the gradients on the unconstrained scale and log probabilities for all parameters in the model. By default, no auxiliary output file is produced.

## 9.5. Examples

The Quickstart Guide MCMC Sampling chapter section on multiple chains showed how to run multiple chains given a model and data, using the minimal required command line options: the method, the name of the data file, and a chain-specific name for the output file.

To run 4 chains in parallel on Mac OS and Linux, the syntax in both bash and zsh is the same:

```
> for i in {1..4}
do
    ./bernoulli sample data file=my_model.data.json \
        output file=output_${i}.csv &
done
```

The backslash (\) indicates a line continuation in Unix. The expression `${i}` substitutes in the value of loop index variable `i`. The ampersand (&) pushes each process into the background which allows the loop to continue without waiting for the current chain to finish.

On Windows the corresponding loop is:

```
>for /l %i in (1, 1, 4) do start /b bernoulli.exe sample ^
    data file=my_model.data.json my_data ^
    output file=output_%i.csv
```

The caret (^) indicates a line continuation in DOS. The expression `%i` is the loop index.

In the following examples, we focus on just the nested sampler command for Unix.

### Running multiple chains with a specified RNG seed

For reproducibility, we specify the same RNG seed across all chains and use the chain id argument to specify the RNG offset.

The RNG seed is specified by `random seed=<int>` and the offset is specified by `id=<loop index>`, so the call to the sampler is:

```
./my_model sample data file=my_model.data.json \
    output file=output_${i}.csv \
```

```
random seed=12345 id=${i}
```

### Changing the default warmup and sampling iterations

The warmup and sampling iteration keyword-value arguments must follow the `sample` keyword. The call to the sampler which overrides the default warmup and sampling iterations is:

```
./my_model sample num_warmup=500 num_sampling=500 \  
    data file=my_model.data.json \  
    output file=output_${i}.csv
```

### Saving warmup draws

To save warmup draws as part of the Stan CSV output file, use the keyword-value argument `save_warmup=1`. This must be grouped with the other `sample` keyword sub-arguments.

```
./my_model sample num_warmup=500 num_sampling=500 save_warmup=1 \  
    data file=my_model.data.json \  
    output file=output_${i}.csv
```

### Initializing parameters

By default, all parameters are initialized on an unconstrained scale to random draws from a uniform distribution over the range  $[-2, 2]$ . To initialize some or all parameters to good starting points on the constrained scale from a data file in JSON or Rdump format, use the keyword-value argument `init=<filepath>`:

```
./my_model sample init=my_param_inits.json data file=my_model.data.json \  
    output file=output_${i}.csv
```

To verify that the specified values will be used by the sampler, you can run the sampler with option `algorithm=fixed_param`, so that the initial values are used to generate the sample. Since this generates a set of identical draws, setting `num_warmup=0` and `num_samples=1` will save unnecessary iterations. As the output values are also on the constrained scale, the set of reported values will match the set of specified initial values.

For example, if we run the example Bernoulli model with specified initial value for parameter “theta”:

```
{ "theta" : 0.5 }
```



via command:

```
./bernoulli sample algorithm=fixed_param num_warmup=0 num_samples=1 \
    init=bernoulli.init.json data file=bernoulli.data.json
```

The resulting output CSV file contains a single draw:

```
lp__,accept_stat__,theta
0,0,0.5
#
# Elapsed Time: 0 seconds (Warm-up)
#               0 seconds (Sampling)
#               0 seconds (Total)
#
```

### Specifying the metric and stepsize

An initial guess for the metric can be specified with the `metric_file` argument whose value is the filepath to a JSON or Rdump file which contains a single variable `inv_metric`. The `metric_file` option can be used with and without adaptation enabled.

By default, the metric is estimated during warmup adaptation. If the initial guess is good, then adaptation should not change it much. If the metric is no good, then the adaptation will override the initial guess. For example, the JSON file `bernoulli.diag_e.json`, contents

```
{ "inv_metric" : [0.296291] }
```

can be used as the initial metric as follows:

```
../my_model sample algorithm=hmc metric_file=bernoulli.diag_e.json \
    data file=my_model.data.json \
    output file=output_${i}.csv
```

If adaptation is disabled, both the `metric_file` and `stepsize` arguments should be specified.

```
../my_model sample adapt engaged=0 \
    algorithm=hmc stepsize=0.9 \
    metric_file=bernoulli.diag_e.json \
    data file=my_model.data.json \
    output file=output_${i}.csv
```

The resulting output CSV file will contain the following set of comment lines:

```
# Adaptation terminated
# Step size = 0.9
# Diagonal elements of inverse mass matrix:
# 0.296291
```

### Changing the NUTS-HMC adaptation parameters

The keyword-value arguments for these settings are grouped together under the `adapt` keyword which itself is a sub-argument of the `sample` keyword.

Models with difficult posterior geometries may required increasing the `delta` argument closer to 1.

```
./my_model sample adapt delta=0.95 \
    data file=my_model.data.json \
    output file=output_${i}.csv
```

To skip adaptation altogether, use the keyword-value argument `engaged=0`. Disabling adaptation disables both metric and stepsize adaptation, so a stepsize should be provided along with a metric to enable efficient sampling.

```
../my_model sample adapt engaged=0 \
    algorithm=hmc stepsize=0.9 \
    metric_file=bernoulli.diag_e.json \
    data file=my_model.data.json \
    output file=output_${i}.csv
```

Even with adaptation disabled, it is still advisable to run warmup iterations in order to allow the initial parameter values to be adjusted to estimates which fall within the typical set.

To skip warmup altogether requires specifying both `num_warmup=0` and `adapt engaged=0`.

```
../my_model sample num_warmup=0 adapt engaged=0 \
    algorithm=hmc stepsize=0.9 \
    metric_file=bernoulli.diag_e.json \
    data file=my_model.data.json \
    output file=output_${i}.csv
```

### Increasing the tree-depth

Models with difficult posterior geometries may required increasing the `max_depth` argument from its default value 10. This requires specifying a series of keyword-

argument pairs:

```
./my_model sample adapt delta=0.95 \  
    algorithm=hmc engine=nuts max_depth=15 \  
    data file=my_model.data.json \  
    output file=output_${i}.csv
```

### Capturing Hamiltonian diagnostics and gradients

The output keyword sub-argument `diagnostic_file=<filepath>` write the sampler parameters and gradients of all model parameters for each draw to a CSV file:

```
./my_model sample data file=my_model.data.json \  
    output file=output_${i}.csv \  
    diagnostic_file=diagnostics_${i}.csv
```

### Suppressing progress updates to the console

The output keyword sub-argument `refresh=<int>` specifies the number of iterations between progress messages written to the terminal window. The default value is 100 iterations. The progress updates look like:

```
Iteration:    1 / 2000 [ 0%] (Warmup)  
Iteration:  100 / 2000 [ 5%] (Warmup)  
Iteration:  200 / 2000 [10%] (Warmup)  
Iteration:  300 / 2000 [15%] (Warmup)
```

For simple models which fit quickly, such updates can be annoying; to suppress them altogether, set `refresh=0`. This only turns off the `Iteration:` messages; the configuration and timing information are still written to the terminal.

```
./my_model sample data file=my_model.data.json \  
    output file=output_${i}.csv \  
    refresh=0
```

For complicated models which take a long time to fit, setting the refresh rate to a low number, e.g. 10 or even 1, provides a way to more closely monitor the sampler.

### Everything example

The `CmdStan` argument parser requires keeping sampler config sub-arguments together; interleaving sampler config with the inputs, outputs, inits, RNG seed and chain id config results in an error message such as the following:

```
./bernoulli sample data file=bernoulli.data.json adapt delta=0.95
adapt is either mistyped or misplaced.
```

Perhaps you meant one of the following valid configurations?

```
method=sample sample adapt
method=variational variational adapt
```

Failed to parse arguments, terminating Stan

The following example provides a template for a call to the sampler which specifies input data, initial parameters, initial step-size and metric, adaptation, output, and RNG initialization.

```
./my_model sample num_warmup=2000 \
    init=my_param_inits.json \
    adapt delta=0.95 init_buffer=100 \
    window=50 term_buffer=100 \
    algorithm=hmc engine=nuts max_depth=15 \
    metric=dense_e metric_file=my_metric.json \
    stepsize=0.6555 \
    data file=my_model.data.json \
    output file=output_${i}.csv refresh=10 \
    random seed=12345 id=${i}
```

The keywords `sample`, `data`, `output`, and `random` are the top-level argument groups. Within the `sample` config arguments, the keyword `adapt` groups the adaptation algorithm parameters and the keyword-value `algorithm=hmc` groups the NUTS-HMC parameters.

The top-level groups can be freely ordered with respect to one another. The following is also a valid command:

```
./my_model random seed=12345 id=${i} \
    data file=my_model.data.json \
    output file=output_${i}.csv refresh=10 \
    sample num_warmup=2000 \
    init=my_param_inits.json \
    algorithm=hmc engine=nuts max_depth=15 \
    metric=dense_e metric_file=my_metric.json \
    stepsize=0.6555 \
    adapt delta=0.95 init_buffer=100 \
    window=50 term_buffer=100
```

## 10. Maximum Likelihood Estimation

The `optimize` method finds the mode of the posterior distribution, assuming that there is one. If the posterior is not convex, there is no guarantee Stan will be able to find the global mode as opposed to a local optimum of log probability. For optimization, the mode is calculated without the Jacobian adjustment for constrained variables, which shifts the mode due to the change of variables. Thus modes correspond to modes of the model as written.

The full set of configuration options available for the `optimize` method is reported at the beginning of the sampler output file as CSV comments. When the example model `bernoulli.stan` is run with `method=optimize` via the command line with all default arguments, the resulting Stan CSV file header comments show the complete set of default configuration options:

```
# model = bernoulli_model
# method = optimize
#   optimize
#     algorithm = lbfgs (Default)
#       lbfgs
#         init_alpha = 0.001 (Default)
#         tol_obj = 9.999999999999998e-13 (Default)
#         tol_rel_obj = 10000 (Default)
#         tol_grad = 1e-08 (Default)
#         tol_rel_grad = 10000000 (Default)
#         tol_param = 1e-08 (Default)
#         history_size = 5 (Default)
#     iter = 2000 (Default)
#     save_iterations = 0 (Default)
```

### 10.1. Optimization algorithms

The `algorithm` argument specifies the optimization algorithm. This argument takes one of the following three values:

- `lbfgs` A quasi-Newton optimizer. This is the default optimizer and also much faster than the other optimizers.
- `bfgs` A quasi-Newton optimizer.

- `newton` A Newton optimizer. This is the least efficient optimization algorithm, but has the advantage of setting its own stepsize.

See the Stan Reference Manual's Optimization chapter for a description of these algorithms.

All of the optimizers stream per-iteration intermediate approximations to the command line console. The sub-argument `save_iterations` specifies whether or not to save the intermediate iterations to the output file. Allowed values are 0 or 1, corresponding to `False` and `True` respectively. The default value is 0, i.e., intermediate iterations are not saved to the output file.

## 10.2. The quasi-Newton optimizers

For both BFGS and L-BFGS optimizers, convergence monitoring is controlled by a number of tolerance values, any one of which being satisfied causes the algorithm to terminate with a solution. See the BFGS and L-BFGS configuration chapter for details on the convergence tests.

Both BFGS and L-BFGS have the following configuration arguments:

- `init_alpha` - The initial step size parameter. Must be a positive real number. Default value is 0.001
- `tol_obj` - Convergence tolerance on changes in objective function value. Must be a positive real number. Default value is  $1^{-12}$ .
- `tol_rel_obj` - Convergence tolerance on relative changes in objective function value. Must be a positive real number. Default value is  $1^4$ .
- `tol_grad` - Convergence tolerance on the norm of the gradient. Must be a positive real number. Default value is  $1^{-8}$ .
- `tol_rel_grad` - Convergence tolerance on the relative norm of the gradient. Must be a positive real number. Default value is  $1^7$ .
- `tol_param` - Convergence tolerance on changes in parameter value. Must be a positive real number. Default value is  $1^{-8}$ .

The `init_alpha` argument specifies the first step size to try on the initial iteration. If the first iteration takes a long time (and requires a lot of function evaluations), set `init_alpha` to be the roughly equal to the `alpha` used in that first iteration. The default value is very small, which is reasonable for many problems but might be too large or too small depending on the objective function and initialization. Being too

big or too small just means that the first iteration will take longer (i.e., require more gradient evaluations) before the line search finds a good step length.

In addition to the above, the L-BFGS algorithm has argument `history_size` which controls the size of the history it uses to approximate the Hessian. The value should be less than the dimensionality of the parameter space and, in general, relatively small values (5-10) are sufficient; the default value is 5.

If L-BFGS performs poorly but BFGS performs well, consider increasing the history size. Increasing history size will increase the memory usage, although this is unlikely to be an issue for typical Stan models.

### 10.3. The Newton optimizer

There are no configuration parameters for the Newton optimizer. It is not recommended because of the slow Hessian calculation involving finite differences.

## 11. Variational Inference Algorithm: ADVI

CmdStan can approximate the posterior distribution using variational inference. The approximation is a Gaussian in the unconstrained variable space.

Stan implements an automatic variational inference algorithm, called Automatic Differentiation Variational Inference (ADVI) Kucukelbir et al. (2015). ADVI uses Monte Carlo integration to approximate the variational objective function, the ELBO (evidence lower bound). ADVI optimizes the ELBO in the real-coordinate space using stochastic gradient ascent. The measures of convergence are similar to the relative tolerance scheme of Stan's optimization algorithms.

The algorithm progression consists of an adaptation phase followed by a sampling phase. The adaptation phase finds a good value for the step size scaling parameter  $\eta$ . The evidence lower bound (ELBO) is the variational objective function and is evaluated based on a Monte Carlo estimate. The variational inference algorithm in Stan is stochastic, which makes it challenging to assess convergence. The algorithm runs until the mean change in ELBO drops below the specified tolerance.

The full set of configuration options available for the variational method is reported at the beginning of the sampler output file as CSV comments. When the example model `bernoulli.stan` is run with `method=variational` via the command line with all default arguments, the resulting Stan CSV file header comments show the complete set of default configuration options:

```
# method = variational
#   variational
#     algorithm = meanfield (Default)
#       meanfield
#     iter = 10000 (Default)
#     grad_samples = 1 (Default)
#     elbo_samples = 100 (Default)
#     eta = 1 (Default)
#     adapt
#       engaged = 1 (Default)
#       iter = 50 (Default)
#     tol_rel_obj = 0.01 (Default)
#     eval_elbo = 100 (Default)
```



```
#      output_samples = 1000 (Default)
```

The console output includes a notice that this algorithm is considered to be experimental:

#### EXPERIMENTAL ALGORITHM:

This procedure has not been thoroughly tested and may be unstable or buggy. The interface is subject to change.

## 11.1. Variational algorithms

Stan implements two variational algorithms. The `algorithm` argument specifies the variational algorithm.

- `algorithm=meanfield` - Use a fully factorized Gaussian for the approximation. This is the default algorithm.
- `algorithm=fullrank` Use a Gaussian with a full-rank covariance matrix for the approximation.

## 11.2. Configuration

- `iter=<int>` Maximum number of iterations. Must be  $< 0$ . Default is 10000.
- `grad_samples=<int>` Number of samples for Monte Carlo estimate of gradients. Must be  $< 0$ . Default is 1.
- `elbo_samples=<int>` Number of samples for Monte Carlo estimate of ELBO (objective function). Must be  $< 0$ . Default is 100.
- `eta=<double>` Stepsize weighting parameter for adaptive stepsize sequence. Must be  $< 0$ . Default is 1.0.
- `adapt` Warmup Adaptation keyword, takes sub-arguments:
  - `engaged=<boolean>` Adaptation engaged? Valid values: (0, 1). Default is 1.
  - `iter=<int>` Maximum number of adaptation iterations. Must be  $< 0$ . Default is 50.
- `tol_rel_obj=<double>` Convergence tolerance on the relative norm of the objective. Must be  $< 0$ . Default is 0.01.
- `eval_elbo=<int>` Evaluate ELBO every Nth iteration. Must be  $< 0$ . Default is 100.

- `output_samples=<int>` Number of posterior samples to draw and save. Must be  $< 0$ . Default is 1000.

### 11.3. CSV output

The output file consists of the following pieces of information:

- The full set of configuration options available for the variational method is reported at the beginning of the sampler output file as CSV comments.
- The first three output columns are labelled `lp__`, `log_p__`, `log_g__`, the rest are the model parameters.
- The stepsize adaptation information is output as CSV comments following column header row.
- The following line contains the mean of the variational approximation.
- The rest of the output contains `output_samples` number of samples drawn from the variational approximation.

To illustrate, we call Stan's variational inference on the example model and data:

```
> ./bernoulli variational data file=bernoulli.data.R
```

By default, the output file is `output.csv`. Lines 1 - 28 contain configuration information:

```
# stan_version_major = 2
# stan_version_minor = 23
# stan_version_patch = 0
# model = bernoulli_model
# method = variational
#   variational
#     algorithm = meanfield (Default)
#       meanfield
#     iter = 10000 (Default)
#     grad_samples = 1 (Default)
#     elbo_samples = 100 (Default)
#     eta = 1 (Default)
#     adapt
#       engaged = 1 (Default)
#       iter = 50 (Default)
#     tol_rel_obj = 0.01 (Default)
```

```
#      eval_elbo = 100 (Default)
#      output_samples = 1000 (Default)
...
```

The column header row is:

```
lp__,log_p__,log_g__,theta
```

The stepsize adaptation information is:

```
# Stepsize adaptation complete.
# eta = 1
```

The reported mean variational approximations information is:

```
0,0,0,0.214911
```

That is, the estimate for `theta` given the data is 0.2.

The following is a sample based on this approximation:

```
0,-14.0252,-5.21718,0.770397
0,-7.05063,-0.10025,0.162061
0,-6.75031,-0.0191099,0.241606
...
```

## 12. Standalone Generate Quantities

The `generate_quantities` method allows you to generate additional quantities of interest from a fitted model without re-running the sampler. For an overview of the uses of this feature, see the QuickStart Guide section and the Stan User's Guide section on Stand-alone generated quantities and ongoing prediction.

This method requires sub-argument `fitted_params` which takes as its value an existing Stan CSV file that contains a sample from an equivalent model, i.e., a model with the same parameters, transformed parameters, and model blocks, conditioned on the same data.

If we run the `bernoulli.stan` program for a single chain to generate a sample in file `bernoulli_fit.csv`:

```
> ./bernoulli sample data file=bernoulli.data.json output file=bernoulli_fit.csv
```

Then we can run the `bernoulli_ppc.stan` to carry out the posterior predictive checks:

```
> ./bernoulli_ppc generate_quantities fitted_params=bernoulli_fit.csv \  
    data file=bernoulli.data.json \  
    output file=bernoulli_ppc.csv
```

The `fitted_params` file must be a Stan CSV file; attempts to use a regular CSV file will result an error message of the form:

```
Error reading fitted param names from sample csv file <filename.csv>
```

The `fitted_params` file must contain columns corresponding to legal values for all parameters defined in the model. If any parameters are missing, the program will exit with an error message of the form:

```
Error reading fitted param names from sample csv file <filename.csv>
```

The parameter values of the `fitted_params` are on the constrained scale and must obey all constraints. For example, if we modify the contents of the first reported draw in `bernoulli_fit.csv` so that the value of `theta` is outside the declared bounds `real<lower=0, upper=1>`, the program will return the following error message:

```
Exception: lub_free: Bounded variable is 1.21397, but must be in the interval
```

## 13. Diagnosing HMC by Comparison of Gradients

CmdStan has a basic diagnostic feature that will calculate the gradients of the initial state and compare them with gradients calculated by finite differences. Discrepancies between the two indicate that there is a problem with the model or initial states or else there is a bug in Stan.

To allow for the possibility of adding other kinds of diagnostic tests, the `diagnose` method argument configuration has subargument `test` which currently only takes value `gradient`. There are two available gradient test configuration arguments:

- `epsilon` - The finite difference step size. Must be a positive real number. Default value is  $10^{-6}$
- `error` - The error threshold. Must be a positive real number. Default value is  $10^{-6}$

To run on the different platforms with the default configuration, use one of the following.

Mac OS and Linux

```
> ./my_model diagnose data file=my_data
```

Windows

```
> my_model diagnose data file=my_data
```

To relax the test threshold, specify the `error` argument as follows:

```
> ./my_model diagnose test=gradient error=0.0001 data file=my_data
```

To see how this works, we run diagnostics on the example `bernoulli` model:

```
> ./bernoulli diagnose data file=bernoulli.data.R
```

Executing this command prints output to the console and as a series of comment lines to the output csv file. The console output is:

```
method = diagnose
  diagnose
    test = gradient (Default)
```

```

    gradient
      epsilon = 9.999999999999995e-07 (Default)
      error = 9.999999999999995e-07 (Default)
id = 0 (Default)
data
  file = bernoulli.data.json
init = 2 (Default)
random
  seed = 2152196153 (Default)
output
  file = output.csv (Default)
  diagnostic_file = (Default)
  refresh = 100 (Default)

```

TEST GRADIENT MODE

Log probability=-8.42814

param idx	value	model	finite diff	error
0	0.0361376	-3.1084	-3.1084	-2.37554e-10

The same information is printed to the output file as csv comments, i.e., each line is prefixed with a pound sign #.

## 14. Parallelization

Stan provides three ways of parallelizing execution of a Stan model:

- multi-threading with Intel Threading Building Blocks (TBB),
- multi-processing with Message Passing Interface (MPI) and
- manycore processing with OpenCL.

### 14.1. Multi-threading with TBB

In order to exploit multi-threading in a Stan model, the models must be rewritten to use the `reduce_sum` and `map_rect` functions. For instructions on how to rewrite Stan models to use these functions see Stan's User guide chapter on parallelization, the `reduce_sum` case study or the Multithreading and Map-Reduce tutorial.

#### Compiling

Once a model is rewritten to use the above-mentioned functions, the model must be compiled with the `STAN_THREADS` makefile flag. The flag can be supplied in the `make` call but we recommend writing the flag to the `make/local` file.

An example of the contents of `make/local` to enable threading with TBB:

```
STAN_THREADS=true
```

The model is then compiled as normal:

```
make path/to/model
```

#### Running

Before running a multi-threaded model, we need to specify the maximum number of threads the program can run (total threads for all chains). This is done by setting the `num_threads` argument. Valid values for `num_threads` are positive integers and -1. If `num_threads` is set to -1, all available cores will be used.

Generally, this number should not exceed the number of available cores for best performance.

Example:

```
./model sample data file=data.json num_threads=4 ...
```

When the model is compiled with `STAN_THREADS` we can sample with multiple chains with a single executable (see section running multiple chains for cases when this is available). When running multiple chains `num_threads` is the maximum number of threads that can be used by all the chains combined. The exact number of threads that will be used for each chain at a given point in time is determined by the TBB scheduler. The following example start 2 chains with 8 total threads available:

```
./model sample num_chains=2 data file=data.json num_threads=8 ...
```

## 14.2. Multi-processing with MPI

In order to use multi-processing with MPI in a Stan model, the models must be rewritten to use the `map_rect` function. By using MPI, the model can be parallelized across multiple cores or a cluster. MPI with Stan is supported on MacOS and Linux.

### Dependencies

Compiling and running Stan models with MPI requires that the system has an MPI implementation installed. For Unix systems the most commonly used implementations are MPICH and OpenMPI.

### Compiling

Once a model is rewritten to use `map_rect`, additional makefile flags must be written to the `make/local`. These are:

- `STAN_MPI`: Enables the use of MPI with Stan if `true`.
- `CXX`: The name of the MPI C++ compiler wrapper. Typically `mpicxx`.
- `TBB_CXX_TYPE`: The C++ compiler the MPI wrapper wraps. Typically `gcc` on Linux and `clang` on MacOS.

An example of `make/local` on Linux:

```
STAN_MPI=true  
CXX=mpicxx  
TBB_CXX_TYPE=gcc
```

The model is then compiled as normal:

```
make path/to/model
```



## Running

The Stan model compiled with `STAN_MPI` is run using an MPI launcher. The MPI standard suggests using `mpiexec`, but a vendor wrapper for the launcher like `mpirun` can also be used. The launcher is supplied the path to the built executable and the number of processes to start: `-n X` for `mpiexec` or `-np X` for `mpirun` where `X` is replaced by the integer representing the number of processes.

Example for running a model with six processes:

```
mpiexec -n 6 path/to/model sample data file=data.json ...
```

## 14.3. OpenCL

### Dependencies

OpenCL is supported on most modern CPUs and GPUs. In order to run OpenCL-enabled Stan models, an OpenCL runtime for the target device must be installed. This subsection lists installation instructions for OpenCL runtimes of the commonly-found devices.

In order to check if any OpenCL-enabled device and its runtime is already present use the `clinfo` tool. On Linux, `clinfo` can typically be installed with the default package manager (for example `sudo apt-get install clinfo` on Ubuntu). For Windows, pre-built `clinfo` binary can be found [here](#).

Also use `clinfo` to verify successful installation of OpenCL runtimes.

### NVIDIA GPU

- Linux:

Install the NVIDIA GPU driver and the NVIDIA CUDA Toolkit. On Ubuntu the commands to install both is:

```
sudo apt update
```

```
sudo apt install nvidia-driver-460 nvidia-cuda-toolkit
```

Replace the driver version (460 in the above case) with the latest number at the time of installation.

- Windows:

Install the NVIDIA GPU Driver and CUDA Toolkit.

### *AMD GPU*

- Linux:  
Install Radeon Software for Linux available [here](#).
- Windows:  
We recommend installing the open source OCL-SDK.

### *AMD CPU*

Install the open source PoCL.

### *Intel CPU/GPU*

Follow Intel's install instructions given [here](#) (requires registration).

## **Compiling**

In order to enable the OpenCL backend the model must be compiled with the `STAN_OPENCL` makefile flag. The flag can be supplied in the make call but we recommend writing the flag to the `make/local` file.

An example of the contents of `make/local` to enable parallelization with OpenCL:

```
STAN_OPENCL=true
```

The model is then compiled as normal:

```
make path/to/model
```

## **Running**

The Stan model compiled with `STAN_OPENCL` can also be supplied the OpenCL platform and device IDs of the target device. These IDs determine the device on which to run the OpenCL-supported functions on. You can list the devices on your system using the `clinfo` program. If the system has one GPU and no OpenCL CPU runtime, the platform and device IDs of the GPU are typically 0. In that case you can also omit the OpenCL IDs as the default 0 IDs are used in that case.

We supply these IDs when starting the executable as shown below:

```
path/to/model sample data file=data.json opencl platform=0 device=1
```

# CmdStan Tools

This section provides a reference for the CmdStan tools:

- `stanc`
- `stansummary`
- `diagnose`
- `print` (deprecated)

## 15. `stanc`: Translating Stan to C++

CmdStan translates Stan programs to C++ using the Stan compiler program which is included in the CmdStan release `bin` directory as program `stanc`. One can view the complete `stanc` documentation in the Stan User’s Guide.

As of release 2.22, the CmdStan Stan to C++ compiler is written in OCaml. This compiler is called “`stanc3`” and has its own repository <https://github.com/stan-dev/stanc3>, from which pre-built binaries for Linux, Mac, and Windows can be downloaded.

### 15.1. Instantiating the `stanc` binary

Before the Stan compiler can be used, the binary `stanc` must be created. This can be done using the `makefile` as follows. For Mac and Linux:

```
make bin/stanc
```

For Windows:

```
make bin/stanc.exe
```

This is also done as part of the `make build` command.

### 15.2. The Stan compiler program

The Stan compiler program `stanc` converts Stan programs to C++ concepts. If the compiler encounters syntax errors in the program, it will provide an error message indicating the location in the input where the failure occurred and reason for the failure. The following example illustrates a fully qualified call to `stanc` to generate the C++ translation of the example model `bernoulli.stan`. For Linux and Mac:

```
> cd <cmdstan-home>
> bin/stanc --o=bernoulli.hpp examples/bernoulli/bernoulli.stan
```

For Windows:

```
> cd <cmdstan-home>
> bin/stanc.exe --o=bernoulli.hpp examples/bernoulli/bernoulli.stan
```

The base name of the Stan program file determines the name of the C++ model class. Because this name is the name of a C++ class, it must start with an alphabetic

character (a--z or A--Z) and contain only alphanumeric characters (a--z, A--Z, and 0--9) and underscores (\_) and should not conflict with any C++ reserved keyword.

The C++ code implementing the class is written to the file `bernoulli.hpp` in the current directory. The final argument, `bernoulli.stan`, is the file from which to read the Stan program.

In practice, `stanc` is invoked indirectly, via the GNU Make utility, which contains rules that compile a Stan program to its corresponding executable. To build the simple Bernoulli model via `make`, we specify the name of the target executable file. On Mac and Linux, this is the name of the Stan program with the `.stan` omitted. On Windows, replace `.stan` with `.exe`, and make sure that the path is given with slashes and not backslashes. For Linux and Mac:

```
> make examples/bernoulli/bernoulli
```

For Windows:

```
> make examples/bernoulli/bernoulli.exe
```

The makefile rules first invoke the `stanc` compiler to translate the Stan model to C++ , then compiles and links the C++ code to a binary executable. The makefile variable `STANCFLAGS` can be used to to override the default arguments to `stanc`, e.g.,

```
> make STANCFLAGS="--include-paths=~/foo" examples/bernoulli/bernoulli
```

## 16. stansummary: MCMC Output Analysis

The CmdStan `stansummary` program reports statistics for one or more sampler chains over all sampler and model parameters and quantities of interest. The statistics reported include both summary statistics of the estimates and diagnostic statistics on the sampler chains, reported in the following order:

- Mean - sample mean
- MCSE - Monte Carlo Standard Error, a measure of the amount of noise in the sample
- StdDev - sample standard deviation
- Quantiles - default 5%, 50%, 95%
- $N_{\text{eff}}$  - effective sample size - the number of independent draws in the sample
- $N_{\text{eff}}/S$  - the number of independent draws per second
- $\hat{R}$  -  $\hat{R}$  statistic, a measure of chain equilibrium, must be within 0.05 of 1.0.

When reviewing the `stansummary` output, it is important to check the final three output columns first - these are the diagnostic statistics on chain convergence and number of independent draws in the sample. A  $\hat{R}$  statistic of greater than 1.05 indicates that the chain has not converged and therefore the sample is not drawn from the posterior, thus the estimates of the mean and all other summary statistics are invalid.

Estimation by sampling produces an approximate value for the model parameters; the MCSE statistic indicates the amount of noise in the estimate. Therefore MCSE column is placed next to the sample mean column, in order to make it easy to compare this sample with others.

For more information, see the Posterior Analysis chapter of the Stan Reference Manual which describes both the theory and practice of MCMC estimation techniques. The summary statistics and the algorithms used to compute them are described in sections Notation for samples and Effective Sample Size.

### 16.1. Building the `stansummary` command

The CmdStan makefile task `build` compiles the `stansummary` utility into the `bin` directory. It can be compiled directly using the makefile as follows:

```
> cd <cmdstan-home>
```

```
> make bin/stansummary
```

## 16.2. Running the stansummary program

The stansummary utility processes one or more output files from a set of chains from one run of the HMC sampler. To run stansummary on the output file or files generated by a run of the sampler, on Mac or Linux:

```
<cmdstan-home>/bin/stansummary <file_1.csv> ... <file_N.csv>
```

On Windows, use backslashes to call the stansummary.exe.

```
<cmdstan-home>\bin\stansummary.exe <file_1.csv> ... <file_N.csv>
```

For example, after running 4 chains to fit the example model `eight_schools.stan` to the supplied example data file, we run stansummary on the resulting Stan CSV output files to get the following report:

```
> bin/stansummary eight_*.csv
```

```
Input files: eight_1.csv, eight_2.csv, eight_3.csv, eight_4.csv
```

```
Inference for Stan model: eight_schools_model
```

```
4 chains: each with iter=(1000,1000,1000,1000); warmup=(0,0,0,0); thin=(1,1,
```

```
Warmup took (0.048, 0.060, 0.047, 0.045) seconds, 0.20 seconds total
```

```
Sampling took (0.057, 0.058, 0.061, 0.066) seconds, 0.24 seconds total
```

	Mean	MCSE	StdDev	5%	50%	95%	N_Eff	N_Eff/s
lp__	-18	0.33	5.1	-26	-19	-9.1	233	963
accept_stat__	0.88	1.6e-02	0.23	0.21	0.98	1.00	203	838
stepsize__	0.18	2.2e-02	0.031	0.14	0.20	0.22	2.0	8.3
treedepth__	3.8	5.9e-02	0.78	2.0	4.0	5.0	175	724
n_leapfrog__	18	1.3e+00	9.4	7.0	15	31	51	212
divergent__	0.015	4.1e-03	0.12	0.00	0.00	0.00	865	3576
energy__	23	3.4e-01	5.5	13	23	32	258	1066
mu	7.9	0.16	5.1	-0.23	7.9	16	1021	4221
theta[1]	12	0.30	8.6	-0.48	11	28	837	3459
theta[2]	7.8	0.15	6.4	-2.7	7.7	18	1717	7096
theta[3]	6.1	0.19	7.7	-6.5	6.5	18	1684	6958
theta[4]	7.5	0.15	6.7	-3.1	7.4	18	2026	8373
theta[5]	4.7	0.17	6.4	-6.7	5.3	15	1391	5747

theta[6]	5.9	0.16	6.7	-5.8	6.2	16	1673	6915
theta[7]	11	0.22	7.0	0.057	10	23	1069	4419
theta[8]	8.3	0.20	7.9	-4.2	8.0	22	1503	6209
tau	7.2	0.26	5.2	1.5	5.9	17	401	1657

Samples were drawn using `hmc` with `nuts`.

For each parameter, `N_Eff` is a crude measure of effective sample size, and `R_hat` is the potential scale reduction factor on split chains (at convergence, `R_hat=1`).

The console output information consists of

- Model, chains, and timing summaries
- Sampler parameter statistics
- Model parameter statistics
- Sampling algorithm - either `nuts` (shown here) or static HMC.

There is one row per parameter and the row order in the summary report corresponds to the column order in the Stan CSV output file.

## Sampler parameters

The initial Stan CSV columns provide information on the sampler state for each draw:

- `lp__` - the total log probability density (up to an additive constant) at each sample
- `accept_stat__` - the average Metropolis acceptance probability over each simulated Hamiltonian trajectory
- `stepsize__` - integrator step size
- `treedepth__` - depth of tree used by NUTS (NUTS sampler)
- `n_leapfrog__` - number of leapfrog calculations (NUTS sampler)
- `divergent__` - has value 1 if trajectory diverged, otherwise 0. (NUTS sampler)
- `energy__` - value of the Hamiltonian
- `int_time__` - total integration time (static HMC sampler)

Because we ran the NUTS sampler, the above summary reports sampler parameters `treedepth__`, `n_leapfrog__`, and `divergent__`; the static HMC sampler would report `int_time__` instead.



## Model parameters and quantities of interest

The remaining Stan CSV columns report the values of all parameters, transformed parameters, and generated quantities in the order in which these variables are declared in the Stan program. For container variables, i.e., vector, row\_vector, matrix, and array variables, the statistics for each element are reported separately, in row-major order. The `eight_schools.stan` program parameters block contains the following parameter variable declarations:

```
real mu;
array[J] real theta;
real<lower=0> tau;
```

In the example data, `J` is 8; therefore the `stansummary` listing reports on `theta[1]` through `theta[8]`.

## 16.3. Command-line options

The `stansummary` command syntax provides a set of flags to customize the output which must precede the list of filenames. When invoked with no arguments or with the `-h` or `--help` option, the program prints the usage message to the console and exits.

Report statistics for one or more Stan CSV files from a HMC sampler run.

Example: `stansummary model_chain_1.csv model_chain_2.csv`

Options:

<code>-a, --autocorr [n]</code>	Display the chain autocorrelation for the <code>n</code> -th input file, in addition to statistics.
<code>-c, --csv_filename [file]</code>	Write statistics to a CSV file.
<code>-h, --help</code>	Produce help message, then exit.
<code>-p, --percentiles [values]</code>	Percentiles to report as ordered set of comma-separated integers from (1,99), inclusive. Default is 5,50,95.
<code>-s, --sig_figs [n]</code>	Significant figures reported. Default is 2. Must be an integer from (1, 18), inclusive.

Both short and long option names are allowed. Short names are specified as `<o>` `<value>`; long option names can be specified either as `--<option>=<value>` or `--<option> <value>`.

The amount of precision in the sampler output limits the amount of real precision in the summary report. CmdStan's command line interface also has output argument

`sig_figs`. The default sampler output precision is 6. The `--sig_figs` argument to the `stansummary` program should not exceed the `sig_figs` argument to the sampler.

## 17. diagnose: Diagnosing Biased Hamiltonian Monte Carlo Inferences

CmdStan is distributed with a utility that is able to read in and analyze the output of one or more Markov chains to check for the following potential problems:

- Divergent transitions
- Transitions that hit the maximum treedepth
- Low E-BFMI values
- Low effective sample sizes
- High  $\hat{R}$  values

The meanings of several of these problems are discussed in <https://arxiv.org/abs/1701.02434>.

### 17.1. Building the diagnose command

The CmdStan makefile task `build` compiles the `diagnose` utility into the `bin` directory. It can be compiled directly using the makefile as follows:

```
> cd <cmdstan-home>
> make bin/diagnose
```

### 17.2. Running the diagnose command

The `diagnose` command is executed on one or more output files, which are provided as command-line arguments separated by spaces. If there are no apparent problems with the output files passed to `diagnose`, it outputs a message that all transitions are within treedepth limit and that no divergent transitions were found. If problems are detected, it outputs a summary of the problem along with possible ways to mitigate it.

To fully exercise the `diagnose` command, we run 4 chains to sample from the Neal's funnel distribution, discussed in the Stan User's Guide reparameterization section <https://mc-stan.org/docs/stan-users-guide/reparameterization-section.html>. This program defines a distribution which exemplifies the difficulties of sampling from some hierarchical models:

```

parameters {
  real y;
  vector[9] x;
}
model {
  y ~ normal(0, 3);
  x ~ normal(0, exp(y / 2));
}

```

This program is available on GitHub: <https://github.com/stan-dev/example-models/blob/master/misc/funnel/funnel.stan>

Stan has trouble sampling from the region where  $y$  is small and thus  $x$  is constrained to be near 0. This is due to the fact that the density's scale changes with  $y$ , so that a step size that works well when  $y$  is large is inefficient when  $y$  is small and vice-versa.

Running 4 chains produces output files `output_1.csv`, ..., `output_4.csv`. We run `diagnose` command on this fileset:

```
> bin/diagnose output_*.csv
```

The output is printed to the terminal window:

```
Processing csv files: output_1.csv, output_2.csv, output_3.csv, output_4.csv
```

```
Checking sampler transitions treedepth.
```

```
9 of 4000 (0.23%) transitions hit the maximum treedepth limit of 10, or 2^10
```

```
Trajectories that are prematurely terminated due to this limit will result in
```

```
For optimal performance, increase this limit.
```

```
Checking sampler transitions for divergences.
```

```
9 of 4000 (0.23%) transitions ended with a divergence.
```

```
These divergent transitions indicate that HMC is not fully able to explore t
```

```
Try increasing adapt delta closer to 1.
```

```
If this doesn't remove all divergences, try to reparameterize the model.
```

```
Checking E-BFMI - sampler transitions HMC potential energy.
```

```
The E-BFMI, 0.078, is below the nominal threshold of 0.3 which suggests that
```

```
If possible, try to reparameterize the model.
```

```
Effective sample size satisfactory.
```

The following parameters had split R-hat greater than 1.1:

y

Such high values indicate incomplete mixing and biased estimation.

You should consider regularizing your model with additional prior information.

Processing complete.

In this example, changing the model to use a non-centered parameterization is the only way to correct these problems. In this second model, the parameters `x_raw` and `y_raw` are sampled as independent standard normals, which is easy for Stan.

```
parameters {
  real y_raw;
  vector[9] x_raw;
}
transformed parameters {
  real y;
  vector[9] x;

  y = 3.0 * y_raw;
  x = exp(y / 2) * x_raw;
}
model {
  y_raw ~ std_normal(); // implies y ~ normal(0, 3)
  x_raw ~ std_normal(); // implies x ~ normal(0, exp(y / 2))
}
```

This program is available on GitHub: [https://github.com/stan-dev/example-models/blob/master/misc/funnel/funnel\\_reparam.stan](https://github.com/stan-dev/example-models/blob/master/misc/funnel/funnel_reparam.stan)

We compile the program and run 4 chains, as before. Now the diagnose command doesn't detect any problems:

Processing csv files: output\_1.csv, output\_2.csv, output\_3.csv, output\_4.csv

Checking sampler transitions treedepth.

Treedepth satisfactory for all transitions.

Checking sampler transitions for divergences.

No divergent transitions found.

Checking E-BFMI - sampler transitions HMC potential energy.

E-BFMI satisfactory for all transitions.

Effective sample size satisfactory.

Split R-hat values satisfactory all parameters.

Processing complete, no problems detected.

### 17.3. diagnose warnings and recommendations

#### Divergent transitions after warmup

Stan uses Hamiltonian Monte Carlo (HMC) to explore the target distribution — the posterior defined by a Stan program + data — by simulating the evolution of a Hamiltonian system. In order to approximate the exact solution of the Hamiltonian dynamics we need to choose a step size governing how far we move each time we evolve the system forward. That is, the *step size controls the resolution of the sampler*.

Unfortunately, for particularly hard problems there are features of the target distribution that are too small for this resolution. Consequently the sampler misses those features and returns biased estimates. Fortunately, this mismatch of scales manifests as *divergences* which provide a practical diagnostic. If there are any divergences after warmup, then the samples may be biased.

If the divergent transitions cannot be eliminated by increasing the `adapt_delta` parameter, we have to find a different way to write the model that is logically equivalent but simplifies the geometry of the posterior distribution. This problem occurs frequently with hierarchical models and one of the simplest examples is Neal’s Funnel, which is discussed in the reparameterization section of the Stan User’s Guide.

#### Maximum treedepth exceeded

Warnings about hitting the maximum treedepth are not as serious as warnings about divergent transitions. While divergent transitions are a *validity* concern, hitting the maximum treedepth is an *efficiency* concern. Configuring the No-U-Turn-Sampler (the variant of HMC used by Stan) requires putting a cap on the depth of the trees that it evaluates during each iteration (for details on this see the *Hamiltonian Monte Carlo Sampling* chapter in the Stan Reference Manual. When the maximum allowed tree depth is reached it indicates that NUTS is terminating prematurely to avoid excessively long execution time.

This is controlled through the `max_depth` argument. If the number of transitions which exceed maximum treedepth is low, increasing `max_depth` may correct this problem.

### **Low E-BFMI values - sampler transitions HMC potential energy.**

The sampler csv output column `energy__` is used to diagnose the accuracy of any Hamiltonian Monte Carlo sampler. If the standard deviation of `energy` is much larger than  $\sqrt{D/2}$ , where  $D$  is the number of *unconstrained* parameters, then the sampler is unlikely to be able to explore the posterior adequately. This is usually due to heavy-tailed posteriors and can sometimes be remedied by reparameterizing the model.

The warning that some number of chains had an estimated Bayesian Fraction of Missing Information (BFMI) that was too low implies that the adaptation phase of the Markov Chains did not turn out well and those chains likely did not explore the posterior distribution efficiently. For more details on this diagnostic, see <https://arxiv.org/abs/1604.00695>. Should this occur, you can either run the sampler for more iterations, or consider reparameterizing your model.

### **Low effective sample sizes**

Roughly speaking, the effective sample size (ESS) of a quantity of interest captures how many independent draws contain the same amount of information as the dependent sample obtained by the MCMC algorithm. Clearly, the higher the ESS the better. Stan uses  $\hat{R}$  adjustment to use the between-chain information in computing the ESS. For example, in case of multimodal distributions with well-separated modes, this leads to an ESS estimate that is close to the number of distinct modes that are found.

Bulk-ESS refers to the effective sample size based on the rank normalized draws. This does not directly compute the ESS relevant for computing the mean of the parameter, but instead computes a quantity that is well defined even if the chains do not have finite mean or variance. Overall bulk-ESS estimates the sampling efficiency for the location of the distribution (e.g. mean and median).

Often quite smaller ESS would be sufficient for the desired estimation accuracy, but the estimation of ESS and convergence diagnostics themselves require higher ESS. We recommend requiring that the bulk-ESS is greater than 100 times the number of chains. For example, when running four chains, this corresponds to having a rank-normalized effective sample size of at least 400.

**High  $\hat{R}$** 

$\hat{R}$  (R-hat) convergence diagnostic compares the between- and within-chain estimates for model parameters and other univariate quantities of interest. If chains have not mixed well (ie, the between- and within-chain estimates don't agree),  $\hat{R}$  is larger than 1. We recommend running at least four chains by default and only using the sample if  $\hat{R}$  is less than 1.01. Stan reports  $\hat{R}$  which is the maximum of rank normalized split-R-hat and rank normalized folded-split-R-hat, which works for thick tailed distributions and is sensitive also to differences in scale. For more details on this diagnostic, see <https://arxiv.org/abs/1903.08008>.

There is further discussion in <https://arxiv.org/abs/1701.02434>; however the correct resolution is necessarily model specific, hence all suggestions general guidelines only.



## 18. `print` (deprecated): MCMC Output Analysis

The `print` utility is deprecated, but is still available until CmdStan v3.0. Use the `stansummary` utility instead.

# Appendices

This section contains the following appendices:

- Stan CSV File Format
- JSON format
- RDump data format
- Using external C++ code from within a Stan program

## 19. Stan CSV File Format

The output from all CmdStan methods is in CSV format. A Stan CSV file is a data table where the columns are the method and model parameters and quantities of interest. Each row contains one record's worth of data in plain-text format using the comma character (',') as the field delimiter (hence the name).

For the Stan CSV files, data is strictly numerical, however, possible values include both positive and negative infinity and “Not-a-Number” which are represented as the strings NaN, inf, +inf, -inf. All other values are written in decimal notation with at most 6 digits of precision.

Stan CSV files have a header row containing the column names. They also make extensive use of CSV comments, i.e., lines which begin with the # character. In addition to initial and final comment rows, some methods also put comment rows in the middle of the data table, which makes it difficult to use many of the commonly used CSV parser packages.

### 19.1. CSV column names and order

The data table is laid out with zero or more method-specific columns followed by the Stan program variables declared in the parameter block, then the variables in the transformed parameters block, finally variables declared in the generated quantities, in declaration order.

Stan provides three types of container objects: arrays, vectors, and matrices. In order to output all elements of a container object, it is necessary to choose an indexing notation and a serialization order. The Stan CSV file indexing notation is

- The column name consists of the variable name followed by the element indices.
- Indices are delimited by periods (':').
- Indexing is 1-based, i.e., given a dimension of size  $N$ , the first element index is 1 and the last element index is  $N$ .

Container variables are serialized in column major order, a.k.a. “Fortran” order. In column major-order, all elements of column 1 are listed in ascending order, followed by all elements of column 2, thus the first index changes the slowest and the last index changes the fastest.

To see how this works, consider a 3-dimensional variable with dimension sizes 2, 3, and 4, e.g., an array of matrices, a 2-D array of vectors or `row_vectors`, or a 3-D array of scalars. Given a Stan program with model parameter variable:

```
array[2, 3, 4] real foo;
```

The Stan CSV file will require 24 columns to output the elements of `foo`. The first 6 columns will be labeled:

```
foo.1.1.1, foo.1.1.2, foo.1.1.3, foo.1.1.4, foo.1.2.1, foo.1.2.2
```

The final 6 columns will be labeled:

```
foo.2.2.3, foo.2.2.4, foo.2.3.1, foo.2.3.2, foo.2.3.3, foo.2.3.4
```

## 19.2. MCMC sampler CSV output

The sample method produces both a Stan CSV output file and a diagnostic file which contains the sampler parameters together with the gradients on the unconstrained scale and log probabilities for all parameters in the model.

To see how this works, we show snippets of the output file resulting from the following command:

```
./bernoulli sample save_warmup=1 num_warmup=200 num_samples=100 \
    data file=bernoulli.data.json \
    output file=bernoulli_samples.csv
```

### Sampler Stan CSV output file

The sampler output file contains the following:

- Initial comment rows listing full CmdStan argument configuration.
- Header row
- Data rows containing warmup draws, if run with option `save_warmup=1`
- Comment rows for adaptation listing step size and metric used for sampling
- Sampling draws
- Comment rows giving timing information

#### Initial comments rows: argument configuration

All configuration arguments are listed, one per line, indented according to CmdStan's hierarchy of arguments and sub-arguments. Arguments not overtly specified on the command line are annotated as (Default).

In the above example the `num_samples`, `num_warmup`, and `save_warmup` arguments were specified, whereas subargument `thin` is left at its default value, as seen in the initial comment rows:

```
# stan_version_major = 2
# stan_version_minor = 24
# stan_version_patch = 0
# model = bernoulli_model
# method = sample (Default)
#   sample
#     num_samples = 100
#     num_warmup = 200
#     save_warmup = 1
#     thin = 1 (Default)
#   adapt
#     engaged = 1 (Default)
#     gamma = 0.050000000000000003 (Default)
#     delta = 0.80000000000000004 (Default)
#     kappa = 0.75 (Default)
#     t0 = 10 (Default)
#     init_buffer = 75 (Default)
#     term_buffer = 50 (Default)
#     window = 25 (Default)
#   algorithm = hmc (Default)
#     hmc
#       engine = nuts (Default)
#       nuts
#         max_depth = 10 (Default)
#         metric = diag_e (Default)
#         metric_file = (Default)
#         stepsize = 1 (Default)
#         stepsize_jitter = 0 (Default)
# id = 0 (Default)
# data
#   file = bernoulli.data.json
# init = 2 (Default)
# random
#   seed = 2991989946 (Default)
# output
#   file = bernoulli_samples.csv
```

```
# diagnostic_file = bernoulli_diagnostics.csv
# refresh = 100 (Default)
```

Note that when running multi-threaded programs which use `reduce_sum` for high-level parallelization, the number of threads used will also be included in this initial comment header.

### Column headers

The CSV header row lists all sampler parameters, model parameters, transformed parameters, and quantities of interest. The sampler parameters are described in detail in the output file section of the Quickstart Guide chapter on MCMC Sampling. The example model `bernoulli.stan` only contains one parameter `theta`, therefore the CSV file data table consists of 7 sampler parameter columns and one column for the model parameter:

```
lp__,accept_stat__,stepsize__,treedepth__,n_leapfrog__,divergent__,energy__,
```

As a second example, we show the output of the `eight_schools.stan` model on run on example dataset. This model has 3 parameters: `mu`, `theta` a vector whose length is dependent on the input data, here  $N = 8$ , and `tau`. The initial columns are for the 7 sampler parameters, as before. The column headers for the model parameters are:

```
mu,theta.1,theta.2,theta.3,theta.4,theta.5,theta.6,theta.7,theta.8,tau
```

### Data rows containing warmup draws

When run with option `save_warmup=1`, the thinned warmup draws are written to the CSV output file directly after the CSV header line. Since the default option is `save_warmup=0`, this section is usually not present in the output file.

Here we specified `num_warmup=200` and left `thin` at the default value 1, therefore the next 200 lines are data rows containing the sampler and model parameter values for each warmup draw.

```
-6.74827,1,1,1,1,0,6.75348,0.247195
-6.74827,4.1311e-103,14.3855,1,1,0,6.95087,0.247195
-6.74827,1.74545e-21,2.43117,1,1,0,7.67546,0.247195
-6.77655,0.99873,0.239791,2,7,0,6.81982,0.280619
-6.7552,0.999392,0.323158,1,3,0,6.79175,0.26517
```

### Comment rows for adaptation

During warmup, the sampler adjusts the stepsize and the metric. At the end warmup, the sampler outputs this information as comments.

```
# Adaptation terminated
# Step size = 0.813694
# Diagonal elements of inverse mass matrix:
# 0.592879
```

As the example bernoulli model only contains a single parameter, and as the default metric is `diag_e`, the inverse mass matrix is a  $1 \times 1$  matrix, and the length of the diagonal vector is also 1.

In contrast, if we run the eight schools example model with metric `dense_e`, the adaptation comments section lists both the stepsize and the full  $10 \times 10$  inverse mass matrix:

```
# Adaptation terminated
# Step size = 0.211252
# Elements of inverse mass matrix:
# 25.6389, 17.3379, 13.9455, 15.9036, 15.1953, 8.73729, 16.9486, 14.4231, 17.4969,
# 17.3379, 79.8719, 12.2989, -1.28006, 9.92895, -3.51622, 10.073, 22.0196, 17.4969,
# 13.9455, 12.2989, 36.1572, 12.8734, 11.9446, 9.09582, 9.74519, 10.9539, 12.1204,
# 15.9036, -1.28006, 12.8734, 59.9998, 10.245, 8.03461, 16.9754, 3.13443, 9.68292,
# 15.1953, 9.92895, 11.9446, 10.245, 43.548, 15.3403, 13.0537, 7.69818, 10.1093,
# 8.73729, -3.51622, 9.09582, 8.03461, 15.3403, 39.981, 12.7695, 1.16248, 6.13749,
# 16.9486, 10.073, 9.74519, 16.9754, 13.0537, 12.7695, 45.8884, 11.6074, 8.96413,
# 14.4231, 22.0196, 10.9539, 3.13443, 7.69818, 1.16248, 11.6074, 49.4083, 18.9169,
# 17.4969, 19.8151, 12.1204, 9.68292, 10.1093, 6.13749, 8.96413, 18.9169, 68.15946,
# 0.518757, 4.71028, 0.211353, -1.36097, 0.155245, -2.08507, -1.15946, 3.15625
```

*Note that when the sampler is run with arguments `algorithm=fixed_param`, this section will be missing.*

### Data rows containing sampling draws

The output file contains the values for the thinned set draws during sampling. Here we specified `num_sampling=100` and left `thin` at the default value 1, therefore the next 100 lines are data rows containing the sampler and model parameter values for each sampling iteration.

```
-8.76921,0.796814,0.813694,1,1,0,9.75854,0.535093
-6.79143,0.979604,0.813694,1,3,0,9.13092,0.214431
-6.79451,0.955359,0.813694,2,3,0,7.19149,0.289341
```

### Timing information

Upon successful completion, the sampler writes timing information to the output CSV file as a series of final comment lines:

```
#
# Elapsed Time: 0.005 seconds (Warm-up)
#               0.002 seconds (Sampling)
#               0.007 seconds (Total)
#
```

### Diagnostic CSV output file

The diagnostic file contains the following:

- Initial comment rows listing full CmdStan argument configuration.
- Header row
- Data rows containing warmup draws, if run with option `save_warmup=1`
- Sampling draws
- Comment rows giving timing information

The columns in this file contain, in order: - all sampler parameters - all model parameter estimates - the latent Hamiltonian for each parameter - the gradient for each parameters

The labels for the latent Hamiltonian columns are the parameter column label with prefix `p_` and the labels for the gradient columns are the parameter column label with prefix `g_`.

These are the column labels from the file `bernoulli_diagnostic.csv`:

```
lp__,accept_stat__,stepsize__,treedepth__,n_leapfrog__,divergent__,energy__,
```

### Profiling CSV output file

The profiling information is stored in a plain CSV format with no meta information in the comments.

Each row represents timing information collected in a `profile` statement for a given thread. It is possible that some `profile` statements have only one entry (if they were only executed by one thread) and others have multiple entries (if they were executed by multiple threads).

The columns are as follows:

- `name`, The name of the `profile` statement that is being timed
- `thread_id`, The thread that executed the `profile` statement



- `total_time`, The combined time spent executing statements inside the profile which includes calculation with and without automatic differentiation
- `forward_time`, The time spent in the profile statement during the forward pass of a reverse mode automatic differentiation calculation or during a calculation without automatic differentiation
- `reverse_time`, The time spent in the profile statement during the reverse (backward) pass of reverse mode automatic differentiation
- `chain_stack`, The number of objects allocated on the chaining automatic differentiation stack. There is a function call for each of these objects in the reverse pass
- `no_chain_stack`, The number of objects allocated on the non-chaining automatic differentiation stack
- `autodiff_calls`, The total number of times the profile statement was executed with automatic differentiation
- `no_autodiff_calls` - The total number of times the profile statement was executed without automatic differentiation

### 19.3. Optimization output

- Config as comments
- Header row
- Penalized maximum likelihood estimate

### 19.4. Variational inference output

- Config as comments
- Header row
- Adaptation as comments
- Variational estimate
- Sample draws from estimate of the posterior

### 19.5. Generate quantities outputs

- Header row
- Quantities of interest

### 19.6. Diagnose method outputs

- Header row
- Gradients

## 20. JSON Format for CmdStan

CmdStan can use JSON format for input data for both model data and parameters. Model data is read in by the model constructor. Model parameters are used to initialize the sampler and optimizer.

### 20.1. Creating JSON files

You can create the JSON file yourself using the guidelines below, but a more convenient way to create a JSON file for use with CmdStan is to use the `write_stan_json()` function provided by the CmdStanR interface.

### 20.2. JSON syntax summary

JSON is a data interchange notation, defined by an ECMA standard. JSON data files must in Unicode. JSON data is a series of structural tokens, literal tokens, and values:

- Structural tokens are the left and right curly bracket `{}`, left and right square bracket `[]`, the semicolon `;`, and the comma `,`.
- Literal tokens must always be in lowercase. There are three literal tokens: `true`, `false`, `null`.
- A primitive value is a single token which is either a literal, a string, or a number.
- A string consists of zero or more Unicode characters enclosed in double quotes, e.g. `"foo"`. A backslash is used to escape the double quote character as well as the backslash itself. JSON allows the use of Unicode character escapes, e.g. `"\\uHHHH"` where HHHH is the Unicode code point in hex.
- All numbers are decimal numbers. Scientific notation is allowed. The following are examples of numbers: `17`, `17.2`, `-17.2`, `-17.2e8`, `17.2e-8`. *Note:* The concepts of positive and negative infinity as well as “not a number” cannot be expressed as numbers in JSON, but they can be encoded as strings `"+inf"`, `"-inf"`, and `"NaN"`, respectively, which can be mixed with numbers.
- A JSON array is an ordered, comma-separated list of zero or more JSON values enclosed in square brackets. The elements of an array can be of any type. The following are examples of arrays: `[]`, `[1]`, `[0.2, "-inf", true]`.

- A name-value pair consists of a string followed by a colon followed by a value, either primitive or compound.
- A JSON object is a comma-separated series of zero or more name-value pairs enclosed in curly brackets. Each name-value pair is a member of the object. Membership is unordered. Member names are not required to be unique. The following are examples of objects: { }, {"foo": null}, {"bar" : 17, "baz" : [14,15,16.6] }.

### 20.3. Stan data types in JSON notation

Stan follows the JSON standard. A Stan input file in JSON notation consists of single JSON object which contains zero or more name-value pairs. This structure corresponds to a Python data dictionary object. The following is an example of JSON data for the simple Bernoulli example model:

```
{ "N" : 10, "y" : [0,1,0,0,0,0,0,0,0,1] }
```

Matrix data and multi-dimensional arrays are indexed in row-major order. For a Stan program which has data block:

```
data {
  int d1;
  int d2;
  int d3;
  array[d1, d2, d3] int ar;
}
```

the following JSON input would be valid:

```
{ "d1" : 2,
  "d2" : 3,
  "d3" : 4,
  "ar" : [[[0,1,2,3], [4,5,6,7], [8,9,10,11]],
           [[12,13,14,15], [16,17,18,19], [20,21,22,23]]]
}
```

JSON ignores whitespace. In the above examples, the spaces and newlines are only used to improve readability and can be omitted.

All data inputs are encoded as name-value pairs. The following table provides more examples of JSON data. The left column contains a Stan data variable declaration and the right column contains valid JSON data inputs.

Stan variable	JSON data
<code>int i</code>	<code>"i": 17</code>
<code>real a</code>	<code>"a" : 17</code> <code>"a" : 17.2</code> <code>"a" : "NaN"</code> <code>"a" : "+inf"</code> <code>"a" : "-inf"</code>
<code>array[5] int</code>	<code>"a" : [1, 2, 3, 4, 5]</code>
<code>array[5] real a</code>	<code>"a" : [ 1, 2, 3.3, "NaN", 5 ]</code>
<code>vector[5] a</code>	<code>"a" : [ 1, 2, 3.3, "NaN", 5 ]</code>
<code>row_vector[5] a</code>	<code>"a" : [ 1, 2, 3.3, "NaN", 5 ]</code>
<code>array[5] real a</code>	<code>"a" : [ 1, 2, 3.3, "NaN", 5 ]</code>
<code>matrix[2, 3] a</code>	<code>"a" : [ [ 1, 2, 3 ], [ 4, 5, 6 ] ]</code>

### Empty arrays in JSON

JSON notation is not able to distinguish between multi-dimensional arrays where any dimension is 0, e.g., a 2-D array with dimensions (1, 0), i.e., an array which contains a single array which is empty, has JSON representation `[ ]`. To see how this works, consider the following Stan program data block:

```
data {
  int d;
  array[d] int ar_1d;
  array[d, d] int ar_2d;
  array[d, d, d] int ar_3d;
}
```

In the case where variable `d` is 1, all arrays will contain a single value. If array variable `ar_d1` contains value 7, 2-D array variable `ar_d2` contains (an array which contains) value 8, and 3-D array variable `ar_d3` contains (an array which contains an array which contains) value 9, the JSON representation is:

```
{ "ar_d1" : [7],
  "ar_d2" : [[8]],
  "ar_d3" : [[[9]]]
}
```

However, in the case where variable `d` is 0, `ar_d1` is empty, i.e., it contains no values, as is `ar_d2`, `ar_d3`, and the JSON representation is

```
{ "d" : 0,  
  "ar_d1" : [ ],  
  "ar_d2" : [ ],  
  "ar_d3" : [ ]  
}
```

## 21. RDump Format for CmdStan

**NOTE:** Although the RDump format is still supported, I/O with JSON is faster and recommended. See the chapter on JSON for more details.

RDump format can be used to represent values for Stan variables. This format was introduced in SPLUS and is used in R, JAGS, and in BUGS (but with a different ordering).

A dump file is structured as a sequence of variable definitions. Each variable is defined in terms of its dimensionality and its values. There are three kinds of variable declarations: - scalars - sequences - general arrays

### 21.1. Creating dump files

Dump files can be created from R using RStan, via the `rstan` package function `stan_rdump`. Stan RDump files must be created via `stan_rdump` and not by R's native `dump` function because R's `dump` function uses a richer syntax than is supported by the underlying Stan i/o libraries.

### 21.2. Scalar variables

A simple scalar value can be thought of as having an empty list of dimensions. Its declaration in the dump format follows the SPLUS assignment syntax. For example, the following would constitute a valid dump file defining a single scalar variable `y` with value 17.2:

```
y <- 17.2
```

### 21.3. Sequence variables

One-dimensional arrays may be specified directly using the SPLUS sequence notation. The following example defines an integer-value and a real-valued sequence.

```
n <- c(1,2,3) y <- c(2.0,3.0,9.7)
```

Arrays are provided without a declaration of dimensionality because the reader just counts the number of entries to determine the size of the array.

Sequence variables may alternatively be represented with R's colon-based notation. For instance, the first example above could equivalently be written as

```
n <- 1:3
```

The sequence denoted by `1:3` is of length 3, running from 1 to 3 inclusive. The colon notation allows sequences going from high to low. The following are equivalent:

```
n <- 2:-2
```

```
n <- c(2,1,0,-1,-2)
```

As a special case, a sequence of zeros can also be represented in the dump format by `integer(x)` and `double(x)`, for type `int` and `double`, respectively. Here `x` is a non-negative integer to specify the length. If `x` is 0, it can be omitted. The following are some examples.

```
x1 <- integer()
```

```
x2 <- integer(0)
```

```
x3 <- integer(2)
```

```
y1 <- double()
```

```
y2 <- double(0)
```

```
y3 <- double(2)
```

## 21.4. Array variables

For more than one dimension, the dump format uses a dimensionality specification. For example, the following defines a  $2 \times 3$  array:

```
y <- structure(c(1,2,3,4,5,6), .Dim = c(2,3))
```

Data is stored column-major, thus the values for `y` will be:

```
y[1, 1] = 1
```

```
y[1, 2] = 3
```

```
y[1, 3] = 5
```

```
y[2, 1] = 2
```

```
y[2, 2] = 4
```

```
y[2, 3] = 6
```

The `structure` keyword just wraps a sequence of values and a dimensionality declaration, which is itself just a sequence of non-negative integer values. The product of the dimensions must equal the length of the array.

If the values happen to form a contiguous sequence of integers, they may be written with colon notation. Thus the example above is equivalent to the following.

```
y <- structure(1:6, .Dim = c(2,3))
```

Sequence notation can be used within any call to the generic `c()` function in R. In the above example, `c(2,3)` could be written as `c(2:3)`.

The generalization of column-major indexing is last-index major indexing. Arrays of more than two dimensions are written in a last-index major form. For example,

```
z <- structure(1:24, .Dim = c(2,3,4))
```

produces a three-dimensional `int` (assignable to `real`) array `z` with values:

```
z[1, 1, 1] = 1
z[2, 1, 1] = 2
z[1, 2, 1] = 3
z[2, 2, 1] = 4
z[1, 3, 1] = 5
z[2, 3, 1] = 6
z[1, 1, 2] = 7
z[2, 1, 2] = 8
z[1, 2, 2] = 9
z[2, 2, 2] = 10
z[1, 3, 2] = 11
z[2, 3, 2] = 12
z[1, 1, 3] = 13
z[2, 1, 3] = 14
z[1, 2, 3] = 15
z[2, 2, 3] = 16
z[1, 3, 3] = 17
z[2, 3, 3] = 18
z[1, 1, 4] = 19
z[2, 1, 4] = 20
z[1, 2, 4] = 21
z[2, 2, 4] = 22
z[1, 3, 4] = 23
z[2, 3, 4] = 24
```

If the underlying 3-D array is stored as a 1-D array in last-index major format, the innermost array elements will be contiguous.

The sequence of values inside `structure` can also be `integer(x)` or `double(x)`. In particular, if one or more dimensions is zero, `integer()` can be put inside `structure`. For instance, the following example is supported by the dump format.



```
y <- structure(integer(), .Dim = c(2,0))
```

## 21.5. Matrix- and vector-valued variables

The dump format for matrices and vectors, including arrays of matrices and vectors, is the same as that for arrays of the same shape.

### Vector dump format

The following three declarations have the same dump format for their data.

```
array[K] real a;  
vector[K] b;  
row_vector[K] c;
```

### Matrix dump format

The following declarations have the same dump format.

```
array[M, N] real a;  
matrix[M, N] b;
```

### Arrays of vectors and matrices

The key to understanding arrays is that the array indexing comes before any of the container indexing. That is, an array of vectors is just that: each array element is a vector. See the chapter on array and matrix types in the user's guide section of the language manual for more information.

For the dump data format, the following declarations have the same arrangement.

```
array[M, N] real a;  
matrix[M, N] b;  
array[M] vector[N] c;  
array[M] row_vector[N] d;
```

Similarly, the following also have the same dump format.

```
array[P, M, N] real a;  
array[P] matrix[M, N] b;  
array[P, M] vector[N] c;  
array[P, M] row_vector[N] d;
```

## 21.6. Integer- and real-valued variables

There is no declaration in a dump file that distinguishes integer versus continuous values. If a value in a dump file's definition of a variable contains a decimal point (e.g., 132.3) or uses scientific notation (e.g.,  $1.323e2$ ), Stan assumes that the values are real.

For a single value, if there is no decimal point, it may be assigned to an `int` or `real` variable in Stan. An array value may only be assigned to an `int` array if there is no decimal point or scientific notation in any of the values. This convention is compatible with the way R writes data.

The following dump file declares an integer value for `y`.

```
y <- 2
```

This definition can be used for a Stan variable `y` declared as `real` or as `int`. Assigning an integer value to a real variable automatically promotes the integer value to a real value.

Integer values may optionally be followed by `L` or `l`, denoting long integer values. The following example, where the type is explicit, is equivalent to the above.

```
y <- 2L
```

The following dump file provides a real value for `y`.

```
y <- 2.0
```

Even though this is a round value, the occurrence of the decimal point in the value, `2.0`, causes Stan to infer that `y` is real valued. This dump file may only be used for variables `y` declared as `real` in Stan.

### Scientific notation

Numbers written in scientific notation may only be used for real values in Stan. R will write out the integer one million as  $1e + 06$ .

### Infinite and not-a-number values

Stan's reader supports infinite and not-a-number values for scalar quantities (see the section of the reference manual section of the language manual for more information on Stan's numerical data types). Both infinite and not-a-number values are supported by Stan's dump-format readers.

	Value	Preferred Form	Alternative Forms
positive infinity	Inf		Infinity, infinity
negative infinity	-Inf		-Infinity, -infinity
not a number	NaN		

These strings are not case sensitive, so `inf` may also be used for positive infinity, or `NAN` for not-a-number.

## 21.7. Quoted variable names

In order to support JAGS data files, variables may be double quoted. For instance, the following definition is legal in a dump file.

```
"y" <- c(1,2,3) \end{Verbatim}
```

## 21.8. Line breaks

The line breaks in a dump file are required to be consistent with the way R reads in data. Both of the following declarations are legal.

```
y <- 2
y <-
3
```

Also following R, breaking before the assignment arrow are not allowed, so the following is invalid.

```
y
<- 2 # Syntax Error
```

Lines may also be broken in the middle of sequences declared using the `c(...)` notation., as well as between the comma following a sequence definition and the dimensionality declaration. For example, the following declaration of a  $2 \times 2 \times 3$  array is valid.

```
y <-
structure(c(1,2,3,
4,5,6,7,8,9,10,11,
12), .Dim = c(2,2,
3))
```

Because there are no decimal points in the values, the resulting dump file may be used for three-dimensional array variables declared as `int` or `real`.

## 21.9. BNF grammar for dump data

A more precise definition of the dump data format is provided by the following (mildly templated) Backus-Naur form grammar.

```
definition ::= name <- value optional_semicolon
```

```
name ::= char*          | ''' char* '''      | ''' char* '''
```

```
value ::= value<int> | value<double>
```

```
value<T> ::= T          | seq<T>              | zero_array<T>          |
'structure' '(' seq<T> ',' ".Dim" '=' seq<int> ')' | 'structure'
 '(' zero_array<T> ',' ".Dim" '=' seq<int> ')'
```

```
seq<int> ::= int ':' int          | cseq<int>
```

```
zero_array<int> ::= "integer" '(' <non-negative int>? ')'
```

```
zero_array<real> ::= "double" '(' <non-negative int>? ')'
```

```
seq<real> ::= cseq<real>
```

```
cseq<T> ::= 'c' '(' vseq<T> ')'
```

```
vseq<T> ::= T          | T ',' vseq<T>
```

The template parameters `T` will be set to either `int` or `real`. Because Stan allows promotion of integer values to real values, an integer sequence specification in the dump data format may be assigned to either an integer- or real-based variable in Stan.

## 22. Using external C++ code

The `--allow_undefined` flag can be passed to the call to `stanc`, which will allow undefined functions in the Stan language to be parsed without an error. We can then include a definition of the function in a C++ header file. This requires specifying two makefile variables: `- STANCFLAGS=--allow_undefined - USER_HEADER=<header_file.hpp>`, where `<header_file.hpp>` is the name of a header file that defines a function with the same name and signature in a namespace that is formed by concatenating the `class_name` argument to `stanc` documented above to the string `_namespace`

As an example, consider the following variant of the Bernoulli example

```
functions {
  real make_odds(real theta);
}
data {
  int<lower=0> N;
  array[N] int<lower=0, upper=1> y;
}
parameters {
  real<lower=0, upper=1> theta;
}
model {
  theta ~ beta(1, 1); // uniform prior on interval 0, 1
  y ~ bernoulli(theta);
}
generated quantities {
  real odds;
  odds = make_odds(theta);
}
```

Here the `make_odds` function is declared but not defined, which would ordinarily result in a parser error. However, if you put `STANCFLAGS = --allow_undefined` into the `make/local` file or into the `stanc` call, then the `stanc` compiler will translate this program to C++, but the generated C++ code will not compile unless you write a file such as `examples/bernoulli/make_odds.hpp` with the following lines

```
namespace bernoulli_model_namespace {  
    template <typename T0__> inline typename  
        boost::math::tools::promote_args<T0__>::type make_odds(const T0__  
theta, std::ostream* pstream__) {  
        return theta / (1 - theta); }  
}
```

Given the above, the following make invocation should work

```
> make STANFLAGS=--allow_undefined USER_HEADER=examples/bernoulli/make_odds
```

Alternatively, you could put STANFLAGS and USER\_HEADER into the make/local file instead of specifying them on the command-line.

If the function were more complicated and involved functions in the Stan Math Library, then you would need to prefix the function calls with `stan::math::`. The `pstream__` argument is mandatory in the signature but need not be used if your function does not print any output. To see the necessary boilerplate look at the corresponding lines in the generated C++ file.

For more details about how to write C++ code using the Stan Math Library, see <https://arxiv.org/abs/1509.07164>.

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