

This document describes how to install msbayes in detail. You should be able to compile the C source codes for this program under many architectures. We have confirmed that it works under a unix-like system, such as linux and Mac OS-X. Let us know if you have difficulty in compiling.

Install GSL (including headers), R (and add-on pkgs: locfit, KernSmooth, akima). Then compile by "make all". Location of installation can be specified by PREFIX (e.g., make PREFIX=/usr/local install).

If this doesn't make sense, keep reading. We assume that you are not accustomed to the unix environment and command line. So below we describe the blow-by-blow installation procedure.

1 ## REQUIREMENTS:

C compiler:

we use gcc, but it should compile with any standard C compiler. For Mac OS-X, the compiler may not be installed by default. You need to install XCode appropriate to your OS version.

GSL (GNU Scientific library) <<http://www.gnu.org/software/gsl/>>
GSL is available for many architectures. If you are using RedHat like system, you need to install rpm packages for gsl and gsl-devel (needed for compilation, but not required to run the program). "yum install gsl gsl-devel" as a root will take care of it. With Mac OS-X, you can install it with fink, or compile from the source code. see Naoki's site for FINK and Xtools info:
<<http://www.faculty.uaf.edu/ffnt/teaching/programming/setupPC.html>>

make:

GNU make is preferred, but I think it works with any modern make.

2 ## COMPILATION and INSTALLATION

If you have downloaded the binary distribution skip this section and go to section "BINARY INSTALLATION"

I assume that you have downloaded the source code file and saved it to your "home directory" (e.g. usually /home/name in unix and /Users/name in Mac OS-X if your username is name).

Open the command-line terminal (e.g. Terminal.app in Mac OS-X), and type following commands (we use "\$" to indicate the command line prompt, so do not actually type "\$" character):

```
$ cd
$ ls msbayes*
```

cd (change directory) will bring you to your home directory, and ls

(list) should show you the file name. If "ls" command shows you the correct file name, you are in the correct directory. If not, find the downloaded source code with "cd" and "ls". For example, if you downloaded the file to your Desktop in Mac OS-X,

```
$ cd
$ cd Desktop
$ ls msbayes*
```

should work.

- 2.1. unpack the source (replace xxx with the appropriate version number).

```
$ tar xzvf msbayes-xxx.tgz
```

This command creates a directory called msbayes-xxx, which contains all source code.

- 2.2. go inside of src directory in the unpacked directory by using cd (change directory).

```
$ cd msbayes/src
```

- 2.3 Compile by typing the following commands:

```
$ make install; make
(if using mac OS X: $make mac lean; make mac)
```

Hopefully, this successfully compiled the programs. If there is an error, make sure GSL is installed correctly (see above)

- 2.4. Now let's install all components into appropriate places

```
$ make install
```

By default, this will install the programs into your home directory (e.g. /Users/name/bin and /Users/name/lib/msbayes). The following files will be installed:

```
In "bin" directory,
msbayes.pl
acceptRej.pl
msprior
msDQH
sumstatsvector
In "lib/msbayes" directory,
acceptRej.r
make_pd2005.r
loc2plot.r
```

If your system is used by multiple users, you might want to install them into the directory accessible by all users. To do this, you need to have root (super user) access.

```
$ sudo make PREFIX=/usr/local install
```

OR

```
$ su
```

```
Password: Give_the_root_password
```

```
$ PREFIX=/usr/local make install
```

With Mac OS-X, you probably want to do the "sudo ...". You can specify where ever you want to install the program by changing PREFIX=... In this example, it will install executable files in /usr/local/bin/ and /usr/local/lib/msbayes/. Note that acceptRej.r need to use the three R-scripts installed in "lib/msbayes" directory. Preserve the relative relationship of the location of the files, or you can put the R-scripts in the same directory as acceptRej.r.

3 ## BINARY INSTALLATION

- 3.1 linux RPM

As a super user, you can install by

```
$ rpm -ivh msbayes-xxx-x.i386.rpm
```

Or you can recompile the source RPM (SRPM) and install by

```
$ rpmbuild --rebuild msbayes-xxx-x.src.rpm
```

```
$ rpm -ivh /usr/src/redhat/RPM/*/msbayes*
```

- 3.2 Mac OS-X tgz

unpack the binary (StuffIt Expander). Then move the two directory (bin and lib) into your Home directory. So you will have:

```
/Users/name/bin/msbayes.pl and four other files
```

and

```
/Users/name/lib/msbayes/acceptRej.r and two other files.
```

4 ## SETTING UP EXECUTION PATH

Let's check if it is working.

Type:

```
$ msbayes.pl -h
```

If it complains that "command not found", you need to setup your execution PATH. If it gives the usage of the program (-h for

'h'elp), you can skip to the next step.

To check if the directory you installed the executable files is under your execution PATH:

```
$ echo $PATH
```

will tell you your execution PATH (delimited by ":"). If the directory is not listed, you need to add it to your environment file. Type the following command:

If you installed the programs into your home directory

```
$ echo 'export PATH=$PATH:$HOME/bin' >> ~/.bash_profile
```

Or if you used PREFIX=/usr/local/bin

```
$ echo 'export PATH=$PATH:/usr/local/bin' >> ~/.bash_profile
```

*** You need to log out and log in again. ***

```
## 5 ## INSTALLATION OF R AND R ADD-ON PACKAGES
```

```
- 5.1. Make sure R <http://www.r-project.org/> is installed.
```

```
- 5.2. Additionally, the following R packages should be installed for plotting the posterior samples using acceptRej.pl:
```

```
locfit  
KernSmooth  
akima  
VGAM
```

To install these packages, you can use one of the following methods.

(A)

```
- Download the three "packages sources" from:  
<http://cran.us.r-project.org/src/contrib/PACKAGES.html>  
- In the command line, type:
```

```
$ R CMD INSTALL locfit_xxx.tar.gz KernSmooth_xxx.tar.gz akima_xxx.tar.gz  
VGAM_xxx.tar.gz
```

Note that the version numbers of each package may slightly different (xxx). Use the filenames which match with the actual files you downloaded

```
** You probably need to execute this command as root (super user),  
or use "sudo R CMD INSTALL ..." in Mac OS-X
```

(B) Alternatively, packages can be automatically downloaded and installed from inside of R.

```
- Start R in the command line by typing:
```

\$ R

Since a regular non-administrator account generally cannot install the add-on packages, you probably need to start R as the root (super user), or you need to type "sudo R" instead of "R" in Mac OS-X.

- After R start up, type the following command in R (don't type '>', which indicate the R prompt(:

```
> install.packages(c("locfit", "KernSmooth", "akima"), dependencies=TRUE)
```

It will ask where you want to download the packages from. Click whatever the closest mirror site.

Details of installing add-on packages can be found in "R Installation and Administration"
<<http://cran.r-project.org/doc/manuals/R-admin.html>>, section "Add-on" packages".
and also in <<http://www.biostat.jhsph.edu/bit/R-personal-library.html>> or <<http://csg.sph.umich.edu/docs/R/localpackages.html>>

6 ## DONE

Keep reading README to learn how to use the program