# Installing R packages for Bayesian approaches

Before starting, update R and RStudio if you use it. Also update existing packages just in case. Basically, the majority of problems appear to be related to having updated versions, installing devtools and Rtools properly.

In general, read the error messages carefully when installing – it quite often appears to be fine, but won’t install something – so check each one to make trouble-shooting easier. Typically, it will say something like non-zero exit status if something goes wrong. The error will often tell you for example if the R version is wrong or another package dependency needs updating.

This gives reasonable advice from a similar course:

<https://bcss.org.my/software/>

If after looking through here, you still have an error, please provide the full error message, and the output from sessionInfo()

## Installing devtools

devtools sometimes doesn't install properly. For windows try:

install.packages("devtools", type = "win.binary")

Search for solutions on Linux or Macs, the default install.packages seems to be problematic for all OS.

If it really doesn’t work, as alternative:

If you can't install devtools, try remotes. remotes::install\_github is the same. Run update.packages() before trying to do anything else though.

## Installing Rtools

This is installed outside of R, from

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

Don’t just install it, follow the instructions. I will summarise them below for Windows, but they will differ for other OS.

It is critical to tell R where R tools is by linking it to the path of Rtools (its location on your hard drive). This is a bit unclear in the instructions. The easiest way is to do this is within R, just type:

writeLines('PATH="**C:\rtools40**\usr\bin;${PATH}"', con = "~/.Renviron")

**Replace only the bit in bold with the location you installed rtools40.**

This will create a hidden text file (or .Renviron file) in your Documents folder linking to R.

Restart the R session.

Check the link by typing in:

Sys.which("make")

This should output (if it works)

> "C:\\rtools40\\usr\\bin\\make.exe"

$Profit$

This should mean you can run all the installed packages.

**If you do this incorrectly, base R will cease to function – don’t worry, just delete the file in Documents. You might have to click ‘View’ in the ribbon then check ‘Hidden files and folders’. Or see below for more details.**

<https://community.rstudio.com/t/stat-package-will-not-load-after-installing-rtools/63265/5>

‘make’ not found errors – indicates that Rtools is not installed or linked properly

## Installing JAGS

Make sure you have JAGS downloaded and installed (it isn't a package)

## Stan

I didn’t have issues but if you did:

Reinstall rstan and StanHeaders packages. There were bugs at one point in the latest versions; they fixed the bugs but did not update the package versions, so update.packages() will not get the new ones.

The error: 'C:/rtools40/usr/mingw\_/bin/g++' not found

Not surprising as the mingw\_ folder does not exist. Make a copy of the C:*/rtools40/mingw64 folder,* move it into *C:/rtools40/usr/* and rename it mingw\_.

Warning message:

In system(paste(CXX, ARGS), ignore.stdout = TRUE, ignore.stderr = TRUE) :

'C:/rtools40/usr/mingw\_/bin/g++' not found

Can be ignored

Or, make a copy of the C:*/rtools40/mingw64 folder, moved it into C:/rtools40/usr/* and renamed it mingw\_

## TMB

TMB and Stan conflict in Ubuntu

make: \*\*\* [/usr/lib/R/etc/Makeconf:181: model8.o] Error 1   
Error in compile("model8.cpp") : Compilation failed

As a quick fix run Stan after TMB not vice versa. There is probably a conflict between the c++ backend of stan and TMB, so this might be problematic if we need to run them together

## Outstanding problems

### Potential bugs

* One person had an issue with 4.0.5; I have been working with 4.0.4 to check this, but everything works for me on R 4.0.4, and very very probably 4.0.5.
* There are some bugs that are OS specific, and some related to RStudio.
* There are also issues if things are linked to network drives.

### Nimble

> out5 <- nimbleMCMC(...)   [line 128]

Failed to create the shared library. Run 'printErrors() to see the compilation errors.

> printErrors()

Warning: In system(cmd) : 'make' not found

> compile("model8.cpp")    [line 201]

Error in compile("model8.cpp") : Compilation failed

Try installing "Rcpp"

### JAGS

> out4 <- jags(data = dataList, inits = inits, parameters.to.save = params, model.file = "model4.txt", n.iter = ni, n.burnin = nb, n.chains = nc, n.thin = nt, n.adapt = na, parallel = TRUE)

Error in makePSOCKcluster(names = spec, ...) :   
  Cluster setup failed. 3 of 3 workers failed to connect.

Try setting parallel = FALSE

<https://stackoverflow.com/questions/62730783/error-in-makepsockclusternames-spec-cluster-setup-failed-3-of-3-work>