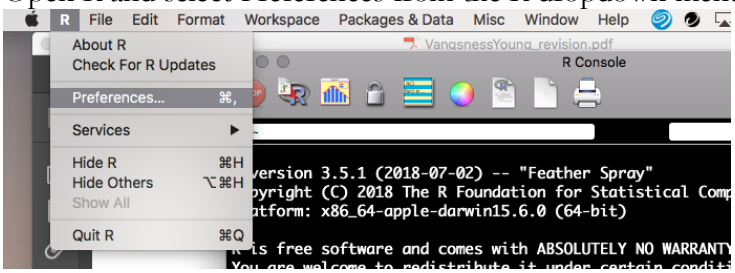
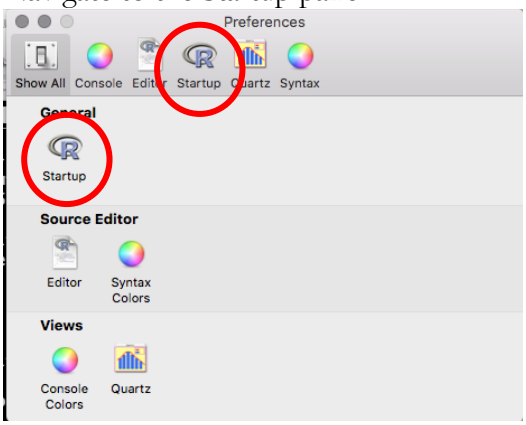
(Created by Lisa Vangsness – do not distribute without her permission)
For Mac

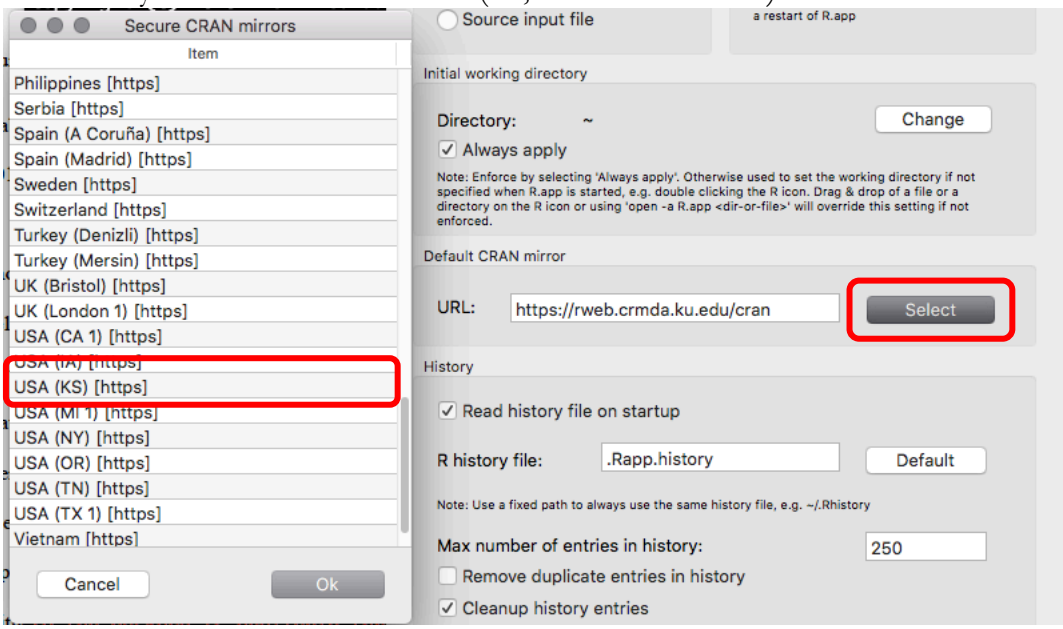
1. Navigate to the CRAN and install the version of R that is appropriate for your OS.
2. Open R and select Preferences from the R dropdown menu:



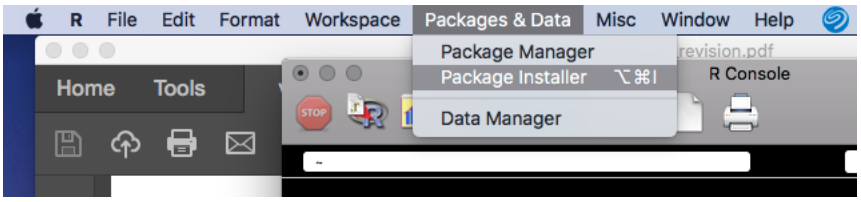
3. Navigate to the Startup pane:



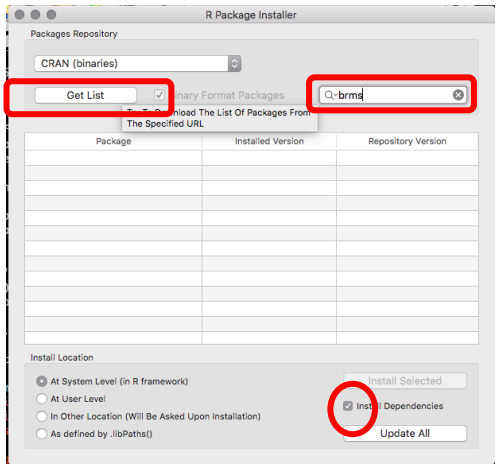
4. Set KU as your default CRAN mirror (i.e., download location):



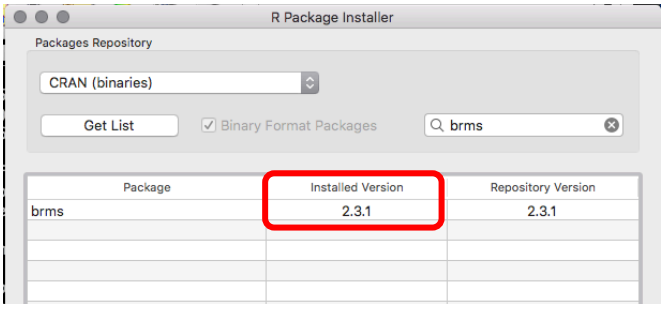
5. Navigate to the Package Installer from the Packages & Data dropdown menu:



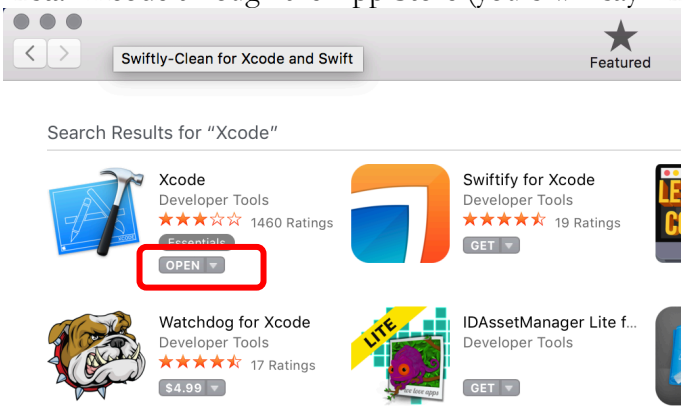
6. Check "install dependencies" before searching for and installing the following packages:
    a. Brms
    b. BH
    c. RcppEigen



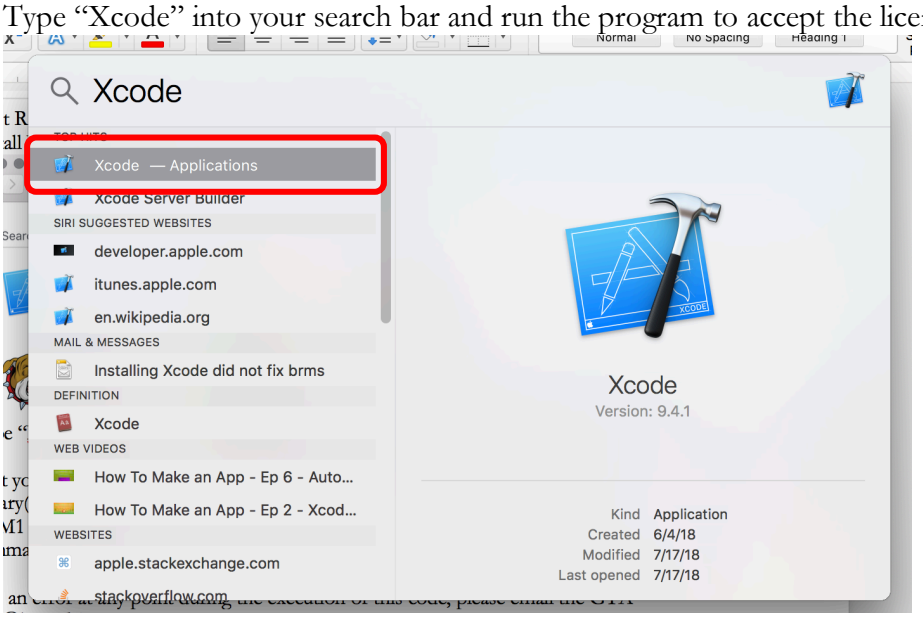
You will know that you've successfully installed a package when the search screen looks like this:



7. Quit R
8. Install Xcode through the App Store (yours will say "install"):



9. Type "Xcode" into your search bar and run the program to accept the license:



10. Open R and test your installation using the following code (paste 1 line at a time and *be sure to use the same capitalization*):

```
> library(brms)
> BRM1 <- brm(weight ~ Diet, data = ChickWeight)
> summary(BRM1)
```

For Windows

BRMS Installation for Windows Computers using RStudio

Instructions courtesy of Kelsey Panfil

In the command window of R studio, type:

```
> Install.packages("brms", dependencies=TRUE)
```

This installs the brms package and all other packages that it uses. This step takes 5-10 minutes. A large amount of red text appears; this is normal. All the dependent packages will unpack next. Then the brms package will unpack. Add this package to your library now:

```
> Library(brms)
```

The brms package requires a C++ compiler to run Bayesian models. R tools includes a C++ compiler and can be downloaded from CRAN (https://cran.r-project.org/mirrors.html). Choose the location closest to you. Then select "Download R for Windows" and then "Rtools." Choose the version of R tools that matches your original R download.

Once you have downloaded R tools from CRAN, begin the installation process. Your computer will take you through a series of steps where you hit "next" multiple times. One of these prompts will ask you to edit the system path. There is an unchecked box followed by a long string of text. YOU MUST CLICK THE BOX! This step is crucial because this puts R tools in your path for R to use. Then finish clicking through the prompts and install.

After R tools is installed, close R studio and open it again. In the command window, type:

```
> sys.getenv("PATH")
```

This generates another long string of text. Towards the beginning of this string, "Rtools" should be in the path. This indicates that you have installed R tools properly. To double check this, type:

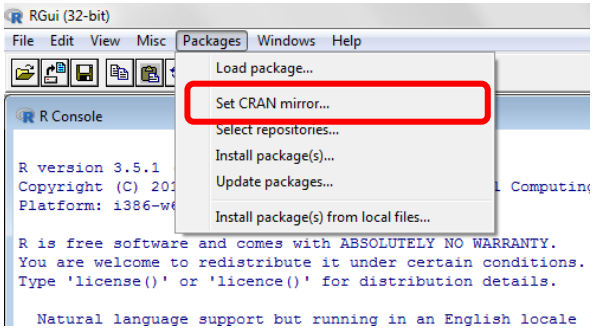
```
> system('g++ -v')
```

This command should not throw any errors. If no error message appears, then you successfully installed brms and are ready to begin Bayesian data analysis.

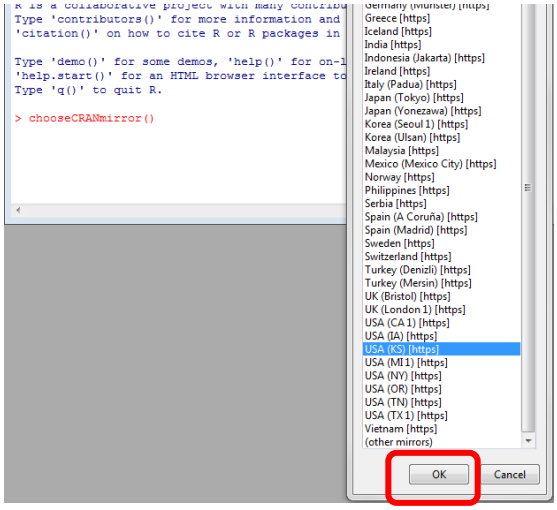
For Windows

BRMS Installation for Windows Computers using R's Command Interface

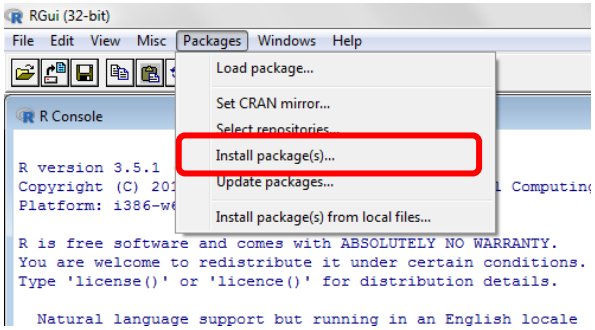
1. Navigate to the CRAN and install the version of R that is appropriate for your version of Windows.
2. Open R and select "Set CRAN mirror…" from the Packages menu:



3. Set KU as your default CRAN mirror (i.e., download location):

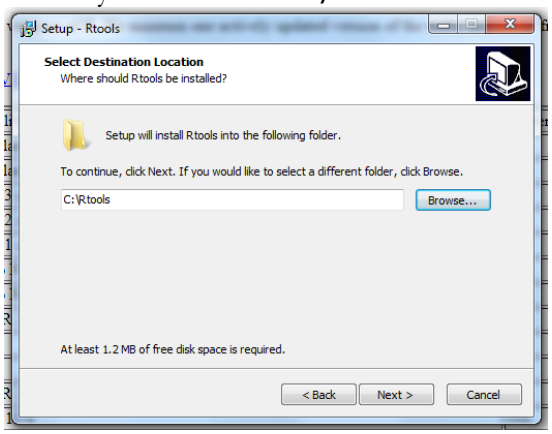


4. Select "Install package(s)…" from the Packages menu:

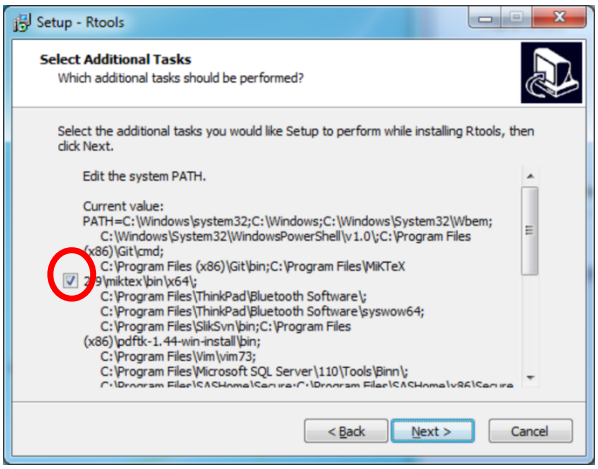


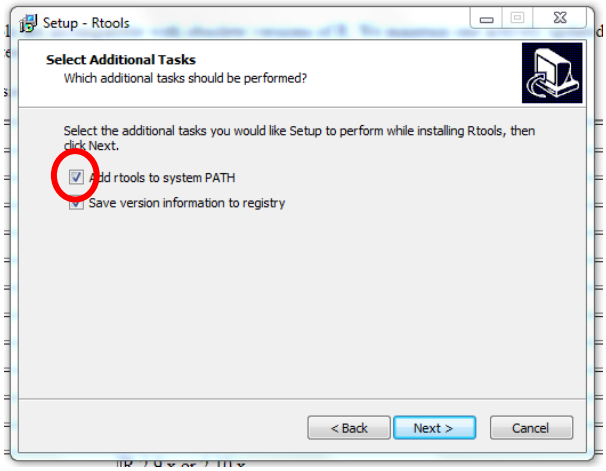
5. Scroll down to select the following packages for installation:
   a. brms
6. Quit R.

7. Install the appropriate version of Rtools from the CRAN.
    a. **During the installation process**, you will be asked where you would like to install Rtools. Be sure that you install it to **C:/Rtools**:

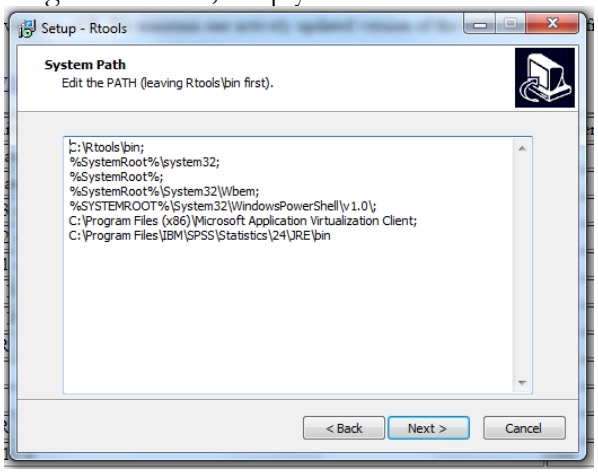


    b. **During the installation process**, you will also see a screen entitled "Select Additional Tasks." This screen will allow you to edit the system path to ensure that R communicates with the C++ compiler in Rtools. Simply check the box next to this option (*note: the formatting of this screen may depend upon your version of Windows*):





    c. **Depending on your version of Windows**, you may receive an additional prompt to manually change the PATH; simply leave it as is:



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```
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> BRM1 <- brm(weight ~ Diet, data = ChickWeight)
> summary(BRM1)
```