**Directions for installing program MARK and package RMark on a mac**

The R package “RMark” requires that program MARK be installed on your mac (the Mark.exe file), even though you won’t be directly running MARK. As usual, this is a bit more complex on a mac than a pc. Here are the steps to follow:

1. Install the Rmark package in R, and then load the library by typing into your R console:

library(RMark)

1. Install Xcode from the App Store if not already installed on your computer
2. Install GCC builds and gfortran from <http://hpc.sourceforge.net/> by downloading the appropriate pair of tar.gz binary files. For OS X El Capitan & Sierra these would be gcc-7.1-bin.tar.gz & gfortran-7.1-bin.tar.gz. These binaries will download into your ‘Downloads’ folder.
3. From here, run the following lines of code (copy and paste) in Terminal (Terminal is a command line interface that is akin to the Command Prompt in Microsoft Windows; it can be found in the Utilities folder located within your Applications folder). Be sure to pay attention to spaces, and you may be asked for your app installation password.

cd ~/Downloads  
  
gunzip gfortran-7.1-bin.tar.gz  
  
gunzip gcc-7.1-bin.tar.gz  
  
sudo tar -xvf gfortran-7.1-bin.tar -C /  
  
sudo tar -xvf gcc-7.1-bin.tar -C /

1. Now you are ready to download the zipped file containing the build MARK at this link <http://www.phidot.org/software/mark/downloads/files/mark.osx.zip>.
2. Extract the file mark.64.osx from mark.osx.zip (by clicking on the downloaded zip file).
3. Next, rename the file “mark” by deleting the .64.osx extension of the file name.
4. Copy the renamed mark file to the hidden folder /usr/local/bin on your computer. This folder can be accessed by opening your Terminal and copy and pasting:

open -a Finder /usr/local/bin

1. In Terminal, simply type “mark” (without the quotes) to make sure the file is executable. If you get the message “No input file was specified, so MARK job is done”, then everything worked!
2. Now, make sure that RMark in program R can find/use Mark, by running the following lines of code:

data(dipper)

dipper.model=mark(dipper)

1. You should get some model outputs, that start something like this:

Output summary for CJS model

Name : Phi(~1)p(~1)

1. If you do, you are good to go! If not, please get in touch with me, and we will work to figure out what is wrong.