

## **RMark Workshop**

**Semester:** Spring 2024

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## Software Installation to Complete Before the Course

We will use three free programs in this course: [Program R](#), [RStudio](#), and [Program MARK](#). These are three separate installations detailed below. In step 4 you'll install several R packages.

### 1st step: Install Program R

R is a free and open-source programming language and software environment for statistical computing and graphics. The exercises for this workshop will be based in R.

- [Windows](#)
  - Click "Download R 4.3.2 for Windows" and install. Default installation settings are okay.
- [Mac OS](#)
  - Click the ".pkg" file that matches your version of Mac OS and install. R-4.3.2 is the latest version, but prior versions may work if your OS version isn't compatible with the latest R version. Default installation settings are okay.

### 2nd step: Install RStudio

RStudio is a free and open-source integrated development environment (IDE) for R. You can opt to run R directly without an IDE, but I recommend RStudio.

- [Windows or Mac](#)
  - Scroll down past the table comparing license options to the section called "All Installers."
  - Click the link that corresponds to your OS and install. Default installation settings are okay.

### 3rd step: Install Program MARK

Program MARK is a free program for parameter estimation from marked individuals (e.g., capture-mark-recapture). We will run MARK from within R, but you must have the standalone Program MARK installed.

- [Windows](#)
  - Click "setup.exe" and install. You may get a security prompt. Default settings are okay.
- [Mac OS](#)
  - MARK was written for Windows, but scroll down to the Apple logo for Mac options. We will be running MARK using the RMark interface, so that option may work for you.

### 4th step: Install add-on R Packages

Launch RStudio, and run the following line in the R console to install.

```
install.packages(c("ggplot2", "tidyverse", "RMark"))
```

Installing Program MARK on **mac OS** can be a challenge!

For instance, if you have a mac, you likely will need to download the appropriate gcc and gfortran binaries for your particular version of OS (and processor) as well as change the terminal code to reflect the appropriate file names.

**So...for those with mac OS, give the below instructions a try.**

These instructions worked for the following system and compilers, but should work for others as well:

System information: Mac OSX Ventura ver. 13.1 with M1 Chip

Compilers downloaded (Instructions 1, step 1b): gcc-9.2-bin.tar.gz and gfortran-9.2-bin.tar.gz (identical to instructions).

Instructions #1: <http://www.phidot.org/forum/viewtopic.php?f=21&t=4075>

Instructions #2: <https://oliviergimenez.github.io/popdyn-workshop/tutorials/rmark-mac.html>

**Three things to note before getting started.**

1. These instructions worked with the newest operating system (as of Feb 2023), but students have also had success with older versions of the gcc and gfortran libraries. It may be suggested to download the versions that most closely match your OS, but it doesn't appear to be fatal (if you don't).
2. Make sure you remove any old files that you previously downloaded for this (mark.64.osx, gcc, gfortran, etc.) from your desktop and downloads folders.
3. When you unzip the gcc and gfortran libraries, terminal may respond with the following: gunzip: gcc-9.2-bin.tar: unknown suffix – ignored. This doesn't appear to be a true error, as previous students were able to proceed just fine.

Follow the steps as in Instructions #1. However, after you download and unzip the mark file, it will be named "mark.64.osx". **This needs to be changed to simply "mark". Students re-named the file after moving it into the bin finder window, but I think this can be done earlier, when the mark file is still on the desktop, immediately following step 2d of Instructions #1.** If you download the ver. 9.2 gcc and gfortran libraries, you should not need to alter any of the code provided in Instructions #1, assuming you changed the mark file name.

This mistake was caught by someone else and the full process is documented in Instructions #2. These instructions state that Xcode (developer tools) needs to be downloaded from the app store. However, some students only found these instructions later and some did not have Xcode, but mark still seemed to work fine. Some students had a newer machine and Xcode capabilities may come standard. Others had an older

Mac but already had Xcode dependencies installed (e.g., if they used JAGS frequently). So if you use JAGS, you can probably ignore this step.

Once you get through the installations process, go to R Studio, install the RMark package, and load the library. From the dipper() help page, copy and paste the last chunk of code into a new script and run it. If everything is installed correctly the code should run fine. I.e., summary(mymodel) will provide a model summary and not throw an error.

Here's the code:

```
# Here is an example of user specified links for each real parameter
data(dipper)
dipper.proc=process.data(dipper)
dipper.ddl=make.design.data(dipper.proc)
# dummy run of make.mark.model to get links and design data.
# parm.specific set to TRUE so it will create a link for
# each parameter because for this model they are all the
# same (logit) and if this was not specified you'd get a vector with one element
dummy=make.mark.model(dipper.proc,dipper.ddl,simplify=FALSE,parm.specific=TRUE)
input.links=dummy$links
# get model indices for p where time=4
log.indices=dipper.ddl$p$model.index[dipper.ddl$p$time==4]
# assign those links to log
input.links[log.indices]="Log"
# Now these can be used with any call to mark
mymodel=mark(dipper.proc,dipper.ddl,input.links=input.links,delete=TRUE)
summary(mymodel)
```

**For those with mac OS, give the above instructions a try. Thank you!**

Finally, the following link may be helpful if you get a Terminal error "Operation not permitted": <https://iboysoft.com/howto/operation-not-permitted-mac-terminal.html>