

Using R for Stable Isotope Statistics

(1) INSTALLING PROGRAM R, R STUDIO, & JAGS

Installing Program R: if you do not already have Program R installed on your computer, please use the following link to do so. Free download link: <https://www.r-project.org>

Installing R Studio: we would also **highly** recommend installing R Studio. R Studio is a 'Integrative Development Environment', which basically means it makes running analyses in R much more intuitive and user friendly. The rest of this user guide will be predicated around the use of R Studio. Free download link: <https://www.rstudio.com>

Installing JAGS: The SIMMR package uses a program called JAGS (Just Another Gibbs Sampler) to run the stable isotope mixing model. Before you install SIMMR, you will also need to visit the JAGS website and download and install JAGS for your operating system. Free download link: <https://sourceforge.net/projects/mcmc-jags/files/>

(2) INSTALLING THE STATISTICAL TOOLS, OR 'PACKAGES' WITHIN R.

We will be working with/conducting the following analyses:

- (1) **SIBER** – a packages for quantifying standard and Bayesian estimates of isotopic 'space' occupied by a population/species. Developed and maintained by Andrew Parnell. For details on the SIBER package: <https://cran.r-project.org/web/packages/SIBER/SIBER.pdf>
- (2) **SIMMR** – a stable isotope mixing model package developed and maintained by Andrew Parnell. For details on the SIMMR package: <https://cran.r-project.org/web/packages/simmr/simmr.pdf>
- (3) **Essential Amino Acid 'Fingerprinting'** – currently there is no specific package for these analyses. Instead researchers make use of traditional ecological analyses such as LDA and PCA to conduct these. Here, we will be using the R packages 'MASS' and 'ellipse'.

To install the packages necessary for completing these analyses:

- (1) Open R Studio
- (2) Create a new R Script: You can either do this by going under 'File' or using the shortcut button at the top left of the program
- (3) Copy and paste the commands below (next page) into your script
- (4) Run the commands by selecting them with your mouse and then hitting the 'Run' button. Alternatively, you can copy them directly into the Console of R Studio and hit return.

```
# installing the necessary packages for SIBER, SIMMR, and EAA Fingerprinting Analyses
install.packages('SIBER')
install.packages('rjags')
install.packages('simmr')
install.packages('MASS')
install.packages('ellipse')
install.packages('compostions')
install.packages('devtools')
install.packages('ggplot2')
install.packages('vegan')
```

Now that we've installed the necessary packages, we need to load them. Note that this needs to happen in the exact order shown below as 'rjags' is necessary for SIMMR to load.

```
# loading packages
library(SIBER)
library(rjags)
library(simr)
library(MASS)
library(ellipse)
library(compositions)
library(devtools)
library(ggplot2)
library(vegan)
```

(3) CHECKING THE INSTALL

Now to make sure all the packages have installed properly, we will do a search for the necessary functions. As an example, we will show a search for the main SIBER function 'createSiberObject()'

```
## Checking to make sure all the packages have installed and loaded properly
?createSiberObject()
```

If you see the following error message in the Console then there has been a problem with the package installation OR the loading of the necessary library:

```
> ?createSiberObject()
Error in .helpForCall(topicExpr, parent.frame()) :
  no methods for 'createSiberObject' and no documentation for it as a function
```

Instead, you should see the following appear in the 'Help' tab of your RStudio Environment. This means that the SIBER package has installed properly and R is able to access the necessary functions.

createSiberObject {SIBER} R Documentation

Read in SIBER format data and generate the SIBER object

Description

This function takes raw isotope data and creates a SIBER object which contains information in a structured manner that enables other functions to loop over groups and communities, fit Bayesian ellipses, and afterwards, generate various plots, and additional analyses on the posterior distributions.

Usage

```
createSiberObject(data.in)
```

Continue checking the following functions for the SIMMR and MASS packages. If you don't receive any error messages then you should be good to go!

```
# Check the primary SIMMR function
```

```
?simmr_Load()
```

```
?lda()
```

```
?ellipse()
```

```
?ggplot2()
```