Software Installation Guide

Please read all pages of this document to ensure you have installed a total of **3** software programs (**R, R Studio, Bioconductor** – installed from within R) and **13** *packages* within R. We recommend the use of **R Studio** as a system to organize your analyses in **R**, and will conduct our demonstrations within R Studio. In advance of the workshop, please download and install the latest versions of both R and R Studio, as appropriate for your operating system. More general information about R and R Studio can be found at the following links:

R: http://www.r-project.org/
The software packages that make up the software program R are hosted at a set of mirrored sites around the world, which together make up the Comprehensive R Archive Network (CRAN). For the fastest download speeds, select a CRAN location close to you, such as Revolution Analytics in Dallas, TX.

R Studio: http://www.rstudio.com/products/rstudio/
Select the open-source desktop version of R Studio for our uses.

Quick links for installation:
Windows 7 or 8

> **R**
> Download R version 3.1.0, and follow instructions to install.
>
> **RStudio**
> Download RStudio Desktop v0.98.507 (or higher) for your platform, and follow directions to install.

OS X 10.6+

> **R**
> Download R version 3.1.0, and follow instructions to install.
>
> **RStudio**
> Download RStudio Desktop v0.98.507 (or higher) for your platform, and follow directions to install.

<u>Installing Packages within R</u>
Default installation of R does not include all of the software and *packages* that we will be using during this workshop. Therefore, once you have installed R, you will need to run the program (i.e. open the program) and install the following 13 packages, as well as Bioconductor, for Luciano's workshop session.

To install a package, at the command prompt within R (looks like this: >), type the following:

```
install.packages("PutNameOfPackageHere")
```

And then press return. You should see several lines of red output, and after a time delay, the command prompt will reappear. At this point, you can install the next package. Note that the quotation marks are necessary!

Packages to Install (case-sensitive):
```
ape
geiger
BioGeoBEARS
FD
optimx
snow
Hmisc
car
RColorBrewer
plyr
lattice
latticeExtra
scatterplot3d
```

<u>Installing Bioconductor</u>
Bioconductor runs within R, and is a collection of packages. We will use several collections within Bioconductor that need to be loaded in a separate fashion from the package installation, above. You can find more about Bioconductor here http://www.bioconductor.org/install/

To install Bioconductor, at the command prompt within R, type:

```
source("http://bioconductor.org/biocLite.R")
biocLite()
```

Once Bioconductor is installed, add two additional collections, GenomicFeatures and DESeq2. These may take some time to load.

```
biocLite("GenomicFeatures")
biocLite("DESeq2")
```

The remaining files you will need for the workshop can all be found at the following link:

http://www.acromyrmex.net/OSOSEvolution.html