



2015 Harvard Workshop on Metagenomics

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Local install: R and RStudio

This should not be necessary unless you wish to run the R exercises on your local machine. All items are installed and configured on the Amazon instance.

R Installation:

To download:

- Windows download <https://cran.r-project.org/bin/windows/base/>
- MacOSX download <https://cran.r-project.org/bin/windows/base/> (please ensure you select the version appropriate to your OS version)

Install the packages as you would any other program

RStudio Installation:

To download visit <https://www.rstudio.com/products/rstudio/download/>

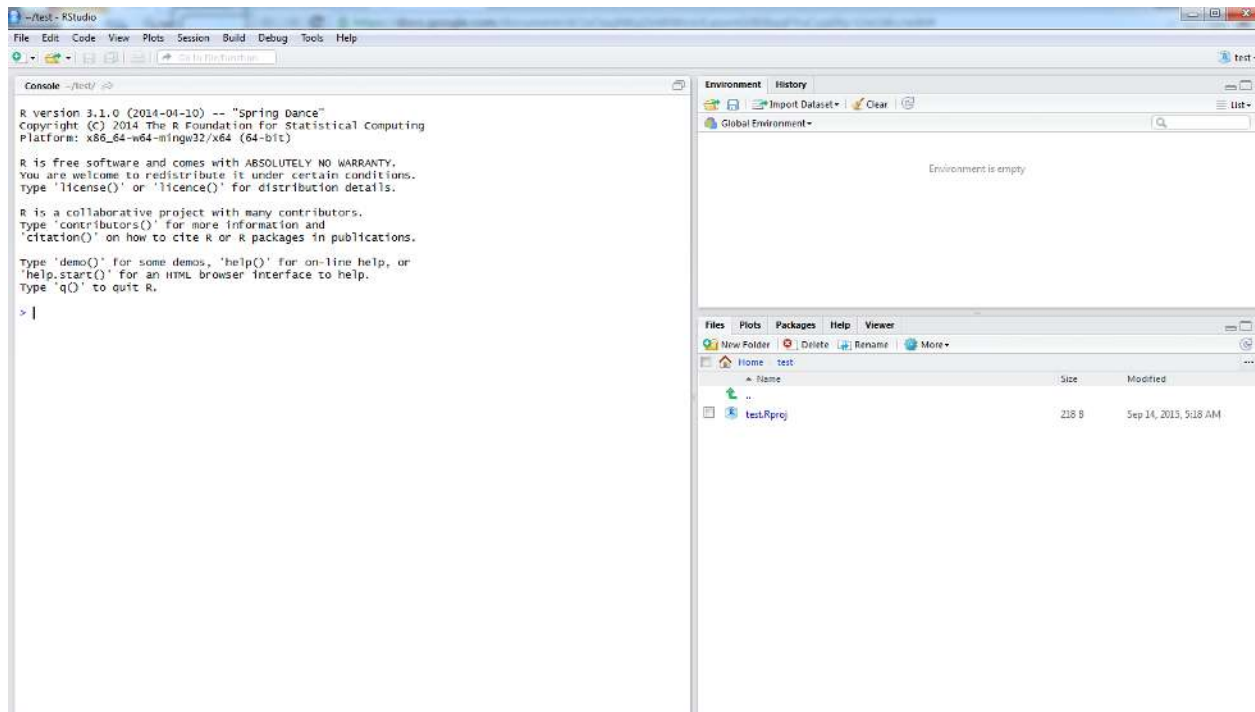
Installers for Supported Platforms

Installers	Size	Date	MD5
RStudio 0.99.484 - Windows Vista/7/8/10	73.9 MB	2015-09-08	84eea3025538c811c0542c195c2f16e3
RStudio 0.99.484 - Mac OS X 10.6+ (64-bit)	56.2 MB	2015-09-08	a0ce0ad1f983d134b394358e3f4485e2
RStudio 0.99.484 - Ubuntu 12.04+/Debian 8+ (32-bit)	77.4 MB	2015-09-08	fe0c5d879c128c5d3d035bec73150fcc
RStudio 0.99.484 - Ubuntu 12.04+/Debian 8+ (64-bit)	83.9 MB	2015-09-08	ee2a2ab6fce06e3936afd4b5968f7d0c
RStudio 0.99.484 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (32-bit)	76.8 MB	2015-09-08	61dcfadd2eb5135e2ff0482dcae3e385
RStudio 0.99.484 - Fedora 19+/RedHat 7+/openSUSE 13.1+ (64-bit)	77.7 MB	2015-09-08	5ff067f87907caa001a8d15deda2c3d6

Select the version appropriate to your operating system and install as you normally would.

Starting RStudio:

Find the program on your machine and start RStudio.



Cut and paste the following into the left-hand window to install some packages which we need for the PhyloSeq part of the course. Note that this may take up to 20 minutes depending on what you may already have installed.

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

install <- function(pkg){
  for(i in pkg){
    if(!require(i,character.only=TRUE)){
      biocLite(i,quiet=TRUE,suppressUpdates=TRUE)
      library(i,character.only=TRUE)
    }
  }
}

packages = c("phyloseq",
```

```
"metagenomeSeq",  
"interactiveDisplay",  
"devtools",  
"qvalue",  
"shiny",  
"genefilter",  
"msd16s",  
"matrixStats",  
"ShortRead",  
"downloader")
```

```
install.packages)
```

```
install_github("benjjneb/dada2")  
install_github("joey711/biomformat")
```