

Homework 6: Install and Version Verification

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Installing New Packages from Bioconductor

```
#Already have GGPlot2- download the other 3 from bioconductor
source("https://bioconductor.org/biocLite.R")
biocLite("dada2")
biocLite("phyloseq")
biocLite("ShortRead")
```

Installing Related Files

- Installed Fastq File, the RDP training set, the RDP Species Assignment
 - Stored here: /Users/jules/Desktop/NRSG741-Big Data/HW6_files
 - *Note:* No R-code needed

Evidence of Sufficient Install

```
library(dada2); packageVersion("dada2");

## Warning: package 'dada2' was built under R version 3.3.3
## Loading required package: Rcpp
## [1] '1.2.2'

library(phyloseq); packageVersion("phyloseq");

## [1] '1.19.1'

library(ShortRead); packageVersion("ShortRead");

## Warning: package 'ShortRead' was built under R version 3.3.3
## Loading required package: BiocGenerics
## Loading required package: parallel
##
## Attaching package: 'BiocGenerics'
## The following objects are masked from 'package:parallel':
##
##   clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,
##   clusterExport, clusterMap, parApply, parCapply, parLapply,
##   parLapplyLB, parRapply, parSapply, parSapplyLB
## The following objects are masked from 'package:stats':
##
##   IQR, mad, xtabs
```

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## The following objects are masked from 'package:base':
##
##   anyDuplicated, append, as.data.frame, cbind, colnames,
##   do.call, duplicated, eval, evalq, Filter, Find, get, grep,
##   grepl, intersect, is.unsorted, lapply, lengths, Map, mapply,
##   match, mget, order, paste, pmax, pmax.int, pmin, pmin.int,
##   Position, rank, rbind, Reduce, rownames, sapply, setdiff,
##   sort, table, tapply, union, unique, unsplit, which, which.max,
##   which.min
## Loading required package: BiocParallel
## Loading required package: Biostrings
## Loading required package: S4Vectors
## Warning: package 'S4Vectors' was built under R version 3.3.3
## Loading required package: stats4
##
## Attaching package: 'S4Vectors'
## The following objects are masked from 'package:base':
##
##   colMeans, colSums, expand.grid, rowMeans, rowSums
## Loading required package: IRanges
## Warning: package 'IRanges' was built under R version 3.3.3
##
## Attaching package: 'IRanges'
## The following object is masked from 'package:phyloseq':
##
##   distance
## Loading required package: XVector
## Warning: package 'XVector' was built under R version 3.3.3
## Loading required package: Rsamtools
## Loading required package: GenomeInfoDb
## Loading required package: GenomicRanges
## Warning: package 'GenomicRanges' was built under R version 3.3.3
## Loading required package: GenomicAlignments
## Warning: package 'GenomicAlignments' was built under R version 3.3.3
## Loading required package: SummarizedExperiment
## Loading required package: Biobase
## Welcome to Bioconductor
##
##   Vignettes contain introductory material; view with
##   'browseVignettes()'. To cite Bioconductor, see
##   'citation("Biobase")', and for packages 'citation("pkgname)".

```

```

##
## Attaching package: 'Biobase'

## The following object is masked from 'package:phyloseq':
##
##      sampleNames

## [1] '1.32.1'

library(ggplot2); packageVersion("ggplot2");

## [1] '2.2.1'

path2 <- "/Users/jules/Desktop/NRSG741-Big Data/HW6_files/"
fns2 <- list.files(path2)
fns2

## [1] "HW6.htm"                                "MiSeq_SOP"
## [3] "rdp_species_assignment_14.fa.gz" "rdp_train_set_14.fa.gz"

path <- "/Users/jules/Desktop/NRSG741-Big Data/HW6_files/MiSeq_SOP/"
fns <- list.files(path)
fns

## [1] "F3D0_S188_L001_R1_001.fastq" "F3D0_S188_L001_R2_001.fastq"
## [3] "F3D1_S189_L001_R1_001.fastq" "F3D1_S189_L001_R2_001.fastq"
## [5] "F3D141_S207_L001_R1_001.fastq" "F3D141_S207_L001_R2_001.fastq"
## [7] "F3D142_S208_L001_R1_001.fastq" "F3D142_S208_L001_R2_001.fastq"
## [9] "F3D143_S209_L001_R1_001.fastq" "F3D143_S209_L001_R2_001.fastq"
## [11] "F3D144_S210_L001_R1_001.fastq" "F3D144_S210_L001_R2_001.fastq"
## [13] "F3D145_S211_L001_R1_001.fastq" "F3D145_S211_L001_R2_001.fastq"
## [15] "F3D146_S212_L001_R1_001.fastq" "F3D146_S212_L001_R2_001.fastq"
## [17] "F3D147_S213_L001_R1_001.fastq" "F3D147_S213_L001_R2_001.fastq"
## [19] "F3D148_S214_L001_R1_001.fastq" "F3D148_S214_L001_R2_001.fastq"
## [21] "F3D149_S215_L001_R1_001.fastq" "F3D149_S215_L001_R2_001.fastq"
## [23] "F3D150_S216_L001_R1_001.fastq" "F3D150_S216_L001_R2_001.fastq"
## [25] "F3D2_S190_L001_R1_001.fastq" "F3D2_S190_L001_R2_001.fastq"
## [27] "F3D3_S191_L001_R1_001.fastq" "F3D3_S191_L001_R2_001.fastq"
## [29] "F3D5_S193_L001_R1_001.fastq" "F3D5_S193_L001_R2_001.fastq"
## [31] "F3D6_S194_L001_R1_001.fastq" "F3D6_S194_L001_R2_001.fastq"
## [33] "F3D7_S195_L001_R1_001.fastq" "F3D7_S195_L001_R2_001.fastq"
## [35] "F3D8_S196_L001_R1_001.fastq" "F3D8_S196_L001_R2_001.fastq"
## [37] "F3D9_S197_L001_R1_001.fastq" "F3D9_S197_L001_R2_001.fastq"
## [39] "HMP MOCK.v35.fasta" "Mock_S280_L001_R1_001.fastq"
## [41] "Mock_S280_L001_R2_001.fastq" "mouse.dpw.metadata"
## [43] "mouse.time.design" "stability.batch"
## [45] "stability.files"

```