

# Homework 3 2018

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The following is documentation that I have installed and loaded the necessary packages and files for class on 2/28.

1. Document that you have installed `dada2` and `phyloseq`, as well as `shortread` and `ggplot2`.

```
# First make sure you have the latest version of R and Bioconductor, then install the  
current release of dada2 (packageVersion 1.6.0), phyloseq (packageVersion 1.22.3), and  
ShortRead (packageVersion 1.36.1) from bioconductor
```

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

```
## Bioconductor version 3.6 (BiocInstaller 1.28.0), ?biocLite for help
```

```
biocLite("dada2")
```

```
## BioC_mirror: https://bioconductor.org
```

```
## Using Bioconductor 3.6 (BiocInstaller 1.28.0), R 3.4.3 (2017-11-30).
```

```
## Installing package(s) 'dada2'
```

```
##  
## The downloaded binary packages are in  
## /var/folders/mg/s57ddz_97p37v2hwyq6ybsbw0000gn/T//RtmpVl3433/downloaded_packages
```

```
## Old packages: 'GenomicRanges', 'pillar'
```

```
biocLite("phyloseq")
```

```
## BioC_mirror: https://bioconductor.org
```

```
## Using Bioconductor 3.6 (BiocInstaller 1.28.0), R 3.4.3 (2017-11-30).
```

```
## Installing package(s) 'phyloseq'
```

```
##  
## The downloaded binary packages are in  
## /var/folders/mg/s57ddz_97p37v2hwyq6ybsbw0000gn/T//RtmpVl3433/downloaded_packages
```

```
## Old packages: 'GenomicRanges', 'pillar'
```

```
biocLite("ShortRead")
```

```
## BioC_mirror: https://bioconductor.org
```

```
## Using Bioconductor 3.6 (BiocInstaller 1.28.0), R 3.4.3 (2017-11-30).
```

```
## Installing package(s) 'ShortRead'
```

```
##  
## The downloaded binary packages are in  
## /var/folders/mg/s57ddz_97p37v2hwyq6ybsbw0000gn/T//RtmpVl3433/downloaded_packages
```

```
## Old packages: 'GenomicRanges', 'pillar'
```

```
# If you already have these packages, load them  
library(dada2); packageVersion("dada2")
```

```
## Loading required package: Rcpp
```

```
## [1] '1.6.0'
```

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

```
## [1] '1.22.3'
```

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

```
## 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, sd, var, xtabs
```

```
## The following objects are masked from 'package:base':  
##  
##   anyDuplicated, append, as.data.frame, cbind, colMeans,  
##   colnames, colSums, 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,  
##   rowMeans, rownames, rowSums, 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
```

```
## Loading required package: stats4
```

```
##  
## Attaching package: 'S4Vectors'
```

```
## The following object is masked from 'package:base':  
##  
##   expand.grid
```

```
## Loading required package: IRanges
```

```
##  
## Attaching package: 'IRanges'
```

```
## The following object is masked from 'package:phyloseq':  
##  
## distance
```

```
## Loading required package: XVector
```

```
##  
## Attaching package: 'Biostrings'
```

```
## The following object is masked from 'package:base':  
##  
## strsplit
```

```
## Loading required package: Rsamtools
```

```
## Loading required package: GenomeInfoDb
```

```
## Loading required package: GenomicRanges
```

```
## Loading required package: GenomicAlignments
```

```
## 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
```

```
## Loading required package: DelayedArray
```

```
## Loading required package: matrixStats
```

```
##  
## Attaching package: 'matrixStats'
```

```
## The following objects are masked from 'package:Biobase':  
##  
##      anyMissing, rowMedians
```

```
##  
## Attaching package: 'DelayedArray'
```

```
## The following objects are masked from 'package:matrixStats':  
##  
##      colMaxs, colMins, colRanges, rowMaxs, rowMins, rowRanges
```

```
## The following object is masked from 'package:Biostrings':  
##  
##      type
```

```
## The following object is masked from 'package:base':  
##  
##      apply
```

```
## [1] '1.36.1'
```

```
#Also load ggplot2 (packageVersion 2.2.1)  
library(ggplot2); packageVersion("ggplot2")
```

```
## [1] '2.2.1'
```

2. Please document that you have downloaded THREE additional files as follows:

- fastq files from the Mothur MiseqSOP walkthrough
- RDP training set
- RDP species assignment set

```
path <- "~/Desktop/N741/2018week6/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"
```

```
path2 <- "~/Desktop/N741/2018week6/RDP Data"
fns2 <- list.files(path2)
```

```
fns2
```

```
## [1] "silva_nr_v132_train_set.fa.zip"
## [2] "silva_species_assignment_v132.fa.zip"
```