

# Homework 3 - Answer Key

*Melinda Higgins & Vicki Hertzberg*

*February 21, 2018*

**Problem 1 - Document that you have installed dada2 and phyloseq, as well as shortread and ggplot2.**

Yes, I successfully installed these packages. Here is proof that `dada2` is working.

NOTE, the following versions should have been installed:

- `dada2` version 1.6.x - see <https://www.bioconductor.org/packages/release/bioc/html/dada2.html>
- `ggplot2` version 2.2.x - see <https://cran.r-project.org/web/packages/ggplot2/index.html>
- `ShortRead` version 1.36.x - see <https://www.bioconductor.org/packages/release/bioc/html/ShortRead.html>
- `phyloseq` version 1.22.x - see <https://www.bioconductor.org/packages/release/bioc/html/phyloseq.html>

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

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

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

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

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

```
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

## 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)".

## 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] '1.36.0'
```

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

```
##
## Attaching package: 'phyloseq'

## The following object is masked from 'package:SummarizedExperiment':
##
##     distance

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

## The following object is masked from 'package:GenomicRanges':
##
##     distance

## The following object is masked from 'package:IRanges':
##
##     distance

## [1] '1.22.3'
```

**Problem 2 - Please document that you have downloaded the THREE additional files:**

- the fastq files from the Mothur MiseqSOP walkthrough
- silva\_nr\_v132\_train\_set.fa.gz
- silva\_species\_assignment\_v132.fa.gz

```
# the ~ should work on a Mac
# path <- "~/MiSeq_SOP"

# if you are on a Windows OS computer (like me), use
# . instead of ~
path <- "./MiSeq_SOP"

# list the files in the
# /MiSeq_SOP directory
fns <- list.files(path)
fns
```

```
## [1] "F3D0_S188_L001_R1_001.fastq"
## [2] "F3D0_S188_L001_R2_001.fastq"
## [3] "F3D1_S189_L001_R1_001.fastq"
## [4] "F3D1_S189_L001_R2_001.fastq"
## [5] "F3D141_S207_L001_R1_001.fastq"
## [6] "F3D141_S207_L001_R2_001.fastq"
## [7] "F3D142_S208_L001_R1_001.fastq"
## [8] "F3D142_S208_L001_R2_001.fastq"
## [9] "F3D143_S209_L001_R1_001.fastq"
## [10] "F3D143_S209_L001_R2_001.fastq"
## [11] "F3D144_S210_L001_R1_001.fastq"
## [12] "F3D144_S210_L001_R2_001.fastq"
## [13] "F3D145_S211_L001_R1_001.fastq"
## [14] "F3D145_S211_L001_R2_001.fastq"
## [15] "F3D146_S212_L001_R1_001.fastq"
## [16] "F3D146_S212_L001_R2_001.fastq"
## [17] "F3D147_S213_L001_R1_001.fastq"
## [18] "F3D147_S213_L001_R2_001.fastq"
## [19] "F3D148_S214_L001_R1_001.fastq"
## [20] "F3D148_S214_L001_R2_001.fastq"
## [21] "F3D149_S215_L001_R1_001.fastq"
## [22] "F3D149_S215_L001_R2_001.fastq"
## [23] "F3D150_S216_L001_R1_001.fastq"
## [24] "F3D150_S216_L001_R2_001.fastq"
## [25] "F3D2_S190_L001_R1_001.fastq"
## [26] "F3D2_S190_L001_R2_001.fastq"
## [27] "F3D3_S191_L001_R1_001.fastq"
## [28] "F3D3_S191_L001_R2_001.fastq"
## [29] "F3D5_S193_L001_R1_001.fastq"
## [30] "F3D5_S193_L001_R2_001.fastq"
## [31] "F3D6_S194_L001_R1_001.fastq"
## [32] "F3D6_S194_L001_R2_001.fastq"
## [33] "F3D7_S195_L001_R1_001.fastq"
## [34] "F3D7_S195_L001_R2_001.fastq"
## [35] "F3D8_S196_L001_R1_001.fastq"
```

```
## [36] "F3D8_S196_L001_R2_001.fastq"
## [37] "F3D9_S197_L001_R1_001.fastq"
## [38] "F3D9_S197_L001_R2_001.fastq"
## [39] "filtered"
## [40] "HMP MOCK.v35.fasta"
## [41] "Mock_S280_L001_R1_001.fastq"
## [42] "Mock_S280_L001_R2_001.fastq"
## [43] "mouse.dpw.metadata"
## [44] "mouse.time.design"
## [45] "silva_nr_v132_train_set.fa.gz"
## [46] "silva_species_assignment_v132.fa.gz"
## [47] "stability.batch"
## [48] "stability.files"
```