Homework 3

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Proof of Installation

```
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] '1.36.0'

library(ggplot2) ; packageVersion("ggplot2")

## [1] '2.2.1'
```

Proof of Download

```
getwd()

## [1] "/Users/victoriabonisese/Desktop/Spring 2018/NRSG
741/project/MicroBiome"

path <- "/Users/victoriabonisese/Desktop/Spring 2018/NRSG
741/project/MicroBiome"
fns <- list.files(path)
fns

## [1] "Homework 3.Rmd"
## [2] "Homework_3.html"
## [3] "Homework_3.Rmd"
## [4] "MicroBiome.Rproj"
## [5] "MiSeq_SOP"
## [6] "README.md"
## [7] "silva_nr_v132_train_set.fa.gz"
## [8] "silva_species_assignment_v132.fa.gz"
```

```
path2 <- "/Users/victoriabonisese/Desktop/Spring 2018/NRSG
741/project/MicroBiome/MiSeq_SOP"
fns2 <- list.files(path2)
fns2

##  [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"
```

Git Repository

https://github.com/vbonise/MicroBiome.git