Homework 3

Jasmine Nakayama

February 23, 2018

Note: I did not sync this with a GitHub repository, since the files are large. However, there is a copy of this PDF in [https://github.com/jynakay/Assignments (https://github.com/jynakay/Assignments)] (https://github.com/jynakay/Assignments (https://github.com/jynakay/Assignments)).

Proof of downloaded packages:

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

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

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

```
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'
```

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

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

Proof of downloaded files:

```
path <- "./MiSeq_SOP"
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] "HMP_MOCK.v35.fasta"
## [40] "Mock_S280_L001_R1_001.fastq"
## [41] "Mock_S280_L001_R2_001.fastq"
## [42] "mouse.dpw.metadata"
## [43] "mouse.time.design"
## [44] "silva_nr_v132_train_set.fa.gz"
## [45] "silva_species_assignment_v132.fa.gz"
## [46] "stability.batch"
## [47] "stability.files"
```