

NRSG 741 Homework 3

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^aRepository available at (https://github.com/tommyflynn/N741_Homework) [https://github.com/tommyflynn/N741_Homework]

Abstract

```
## Loading required package: Rcpp

## 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
```

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```

##
## 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

(packageVersion("dada2"))

## [1] '1.6.0'
```