The Maternal Newborn Oral Microbiome

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## Note: The raw fastq files that support this project can be found within the secure Emory Box location at: <https://emory.app.box.com/folder/48209374654>

# Step 1: Processing fastq files to come up with OTU table.

## Step a) Load packages

library(dada2); packageVersion("dada2")

## Loading required package: Rcpp

## Warning: package 'Rcpp' was built under R version 3.4.4

## [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] '1.36.1'

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'