ms\_bacteria\_fungi package versions

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# packages used for HEU\_manusript analysis  
library(plyr)  
library(dplyr)  
library(ggplot2)  
library(phyloseq)  
library(DESeq2)

## Warning: package 'S4Vectors' was built under R version 3.3.3

## Warning: package 'IRanges' was built under R version 3.3.3

## Warning: package 'GenomicRanges' was built under R version 3.3.3

library(reshape2)  
library(vegan)

# now get the versions of all packages used  
sessionInfo()

## R version 3.3.2 (2016-10-31)  
## Platform: x86\_64-apple-darwin13.4.0 (64-bit)  
## Running under: macOS 10.15.4  
##   
## locale:  
## [1] en\_CA.UTF-8/en\_CA.UTF-8/en\_CA.UTF-8/C/en\_CA.UTF-8/en\_CA.UTF-8  
##   
## attached base packages:  
## [1] parallel stats4 stats graphics grDevices utils datasets   
## [8] methods base   
##   
## other attached packages:  
## [1] vegan\_2.4-5 lattice\_0.20-38   
## [3] permute\_0.9-5 reshape2\_1.4.3   
## [5] DESeq2\_1.14.1 SummarizedExperiment\_1.4.0  
## [7] Biobase\_2.34.0 GenomicRanges\_1.26.4   
## [9] GenomeInfoDb\_1.10.3 IRanges\_2.8.2   
## [11] S4Vectors\_0.12.2 BiocGenerics\_0.20.0   
## [13] phyloseq\_1.19.1 ggplot2\_3.1.0   
## [15] dplyr\_0.8.0.1 plyr\_1.8.4   
##   
## loaded via a namespace (and not attached):  
## [1] bit64\_0.9-7 jsonlite\_1.6 splines\_3.3.2   
## [4] foreach\_1.4.4 Formula\_1.2-3 assertthat\_0.2.0   
## [7] latticeExtra\_0.6-28 blob\_1.1.1 yaml\_2.2.0   
## [10] RSQLite\_2.1.1 backports\_1.1.3 pillar\_1.3.1   
## [13] glue\_1.3.1 digest\_0.6.18 checkmate\_1.9.1   
## [16] RColorBrewer\_1.1-2 XVector\_0.14.1 colorspace\_1.4-0   
## [19] htmltools\_0.3.6 Matrix\_1.2-12 XML\_3.98-1.19   
## [22] pkgconfig\_2.0.2 genefilter\_1.56.0 zlibbioc\_1.20.0   
## [25] xtable\_1.8-3 purrr\_0.3.1 scales\_1.0.0   
## [28] BiocParallel\_1.8.2 annotate\_1.52.1 htmlTable\_1.13.1   
## [31] tibble\_2.0.1 mgcv\_1.8-20 withr\_2.1.2   
## [34] nnet\_7.3-12 lazyeval\_0.2.1 survival\_2.43-3   
## [37] magrittr\_1.5 crayon\_1.3.4 memoise\_1.1.0   
## [40] evaluate\_0.13 nlme\_3.1-131 MASS\_7.3-51.1   
## [43] foreign\_0.8-71 tools\_3.3.2 data.table\_1.12.0   
## [46] stringr\_1.4.0 locfit\_1.5-9.1 munsell\_0.5.0   
## [49] cluster\_2.0.6 AnnotationDbi\_1.36.2 Biostrings\_2.42.1   
## [52] ade4\_1.7-10 rlang\_0.4.6 rhdf5\_2.18.0   
## [55] grid\_3.3.2 RCurl\_1.95-4.12 iterators\_1.0.10   
## [58] biomformat\_1.2.0 rstudioapi\_0.9.0 htmlwidgets\_1.3   
## [61] igraph\_1.1.2 bitops\_1.0-6 base64enc\_0.1-3   
## [64] rmarkdown\_1.12 gtable\_0.2.0 codetools\_0.2-16   
## [67] multtest\_2.30.0 DBI\_1.0.0 R6\_2.4.0   
## [70] gridExtra\_2.3 knitr\_1.22 bit\_1.1-14   
## [73] Hmisc\_4.1-1 ape\_5.0 stringi\_1.4.3   
## [76] Rcpp\_1.0.0 geneplotter\_1.52.0 rpart\_4.1-13   
## [79] acepack\_1.4.1 tidyselect\_0.2.5 xfun\_0.5