ms\_HEU\_package\_versions

Nelly Amenyogbe

7/16/2020

# 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(missForest)  
library(reshape2)  
library(mixOmics)  
library(cowplot)  
library(vegan)  
library(devtools)  
library(ggbiplot)  
library(cowplot)

# 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] grid parallel stats4 stats graphics grDevices utils   
## [8] datasets methods base   
##   
## other attached packages:  
## [1] ggbiplot\_0.55 scales\_1.0.0   
## [3] usethis\_1.6.1 devtools\_2.0.1   
## [5] vegan\_2.4-5 permute\_0.9-5   
## [7] cowplot\_0.9.4 mixOmics\_6.3.1   
## [9] lattice\_0.20-38 MASS\_7.3-51.1   
## [11] reshape2\_1.4.3 missForest\_1.4   
## [13] itertools\_0.1-3 iterators\_1.0.10   
## [15] foreach\_1.4.4 randomForest\_4.6-12   
## [17] DESeq2\_1.14.1 SummarizedExperiment\_1.4.0  
## [19] Biobase\_2.34.0 GenomicRanges\_1.26.4   
## [21] GenomeInfoDb\_1.10.3 IRanges\_2.8.2   
## [23] S4Vectors\_0.12.2 BiocGenerics\_0.20.0   
## [25] phyloseq\_1.19.1 ggplot2\_3.1.0   
## [27] dplyr\_0.8.0.1 plyr\_1.8.4   
##   
## loaded via a namespace (and not attached):  
## [1] colorspace\_1.4-0 rprojroot\_1.3-2   
## [3] htmlTable\_1.13.1 corpcor\_1.6.9   
## [5] XVector\_0.14.1 fs\_1.4.1   
## [7] base64enc\_0.1-3 rstudioapi\_0.9.0   
## [9] remotes\_2.0.2 bit64\_0.9-7   
## [11] RSpectra\_0.12-0 AnnotationDbi\_1.36.2   
## [13] codetools\_0.2-16 splines\_3.3.2   
## [15] geneplotter\_1.52.0 knitr\_1.22   
## [17] pkgload\_1.0.2 ade4\_1.7-10   
## [19] Formula\_1.2-3 jsonlite\_1.6   
## [21] annotate\_1.52.1 cluster\_2.0.6   
## [23] shiny\_1.2.0 backports\_1.1.3   
## [25] assertthat\_0.2.0 Matrix\_1.2-12   
## [27] lazyeval\_0.2.1 cli\_1.0.1   
## [29] later\_0.8.0 prettyunits\_1.0.2   
## [31] acepack\_1.4.1 htmltools\_0.3.6   
## [33] tools\_3.3.2 igraph\_1.1.2   
## [35] gtable\_0.2.0 glue\_1.3.1   
## [37] Rcpp\_1.0.0 Biostrings\_2.42.1   
## [39] multtest\_2.30.0 ape\_5.0   
## [41] nlme\_3.1-131 crosstalk\_1.0.0   
## [43] xfun\_0.5 stringr\_1.4.0   
## [45] ps\_1.3.0 testthat\_2.0.1   
## [47] mime\_0.6 miniUI\_0.1.1.1   
## [49] XML\_3.98-1.19 zlibbioc\_1.20.0   
## [51] promises\_1.0.1 biomformat\_1.2.0   
## [53] rhdf5\_2.18.0 RColorBrewer\_1.1-2   
## [55] yaml\_2.2.0 memoise\_1.1.0   
## [57] gridExtra\_2.3 rpart\_4.1-13   
## [59] latticeExtra\_0.6-28 stringi\_1.4.3   
## [61] RSQLite\_2.1.1 genefilter\_1.56.0   
## [63] desc\_1.2.0 checkmate\_1.9.1   
## [65] pkgbuild\_1.0.2 BiocParallel\_1.8.2   
## [67] manipulateWidget\_0.10.0 rlang\_0.4.6   
## [69] pkgconfig\_2.0.2 bitops\_1.0-6   
## [71] matrixStats\_0.54.0 rgl\_0.100.19   
## [73] evaluate\_0.13 purrr\_0.3.1   
## [75] htmlwidgets\_1.3 processx\_3.3.0   
## [77] bit\_1.1-14 tidyselect\_0.2.5   
## [79] magrittr\_1.5 R6\_2.4.0   
## [81] Hmisc\_4.1-1 DBI\_1.0.0   
## [83] pillar\_1.3.1 foreign\_0.8-71   
## [85] withr\_2.1.2 mgcv\_1.8-20   
## [87] survival\_2.43-3 RCurl\_1.95-4.12   
## [89] nnet\_7.3-12 tibble\_2.0.1   
## [91] crayon\_1.3.4 rARPACK\_0.11-0   
## [93] ellipse\_0.4.1 rmarkdown\_1.12   
## [95] locfit\_1.5-9.1 data.table\_1.12.0   
## [97] callr\_3.1.1 blob\_1.1.1   
## [99] digest\_0.6.18 webshot\_0.5.1   
## [101] xtable\_1.8-3 tidyr\_0.8.3   
## [103] httpuv\_1.4.5.1 munsell\_0.5.0   
## [105] sessioninfo\_1.1.1