ms\_gc\_package\_versions

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# packages used for ms\_global\_cohort\_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(cowplot)  
library(splines)  
library(pheatmap)  
library(igraph)  
library(plotrix)  
library(dunn.test)  
library(tidyr)

# 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] splines parallel stats4 stats graphics grDevices utils   
## [8] datasets methods base   
##   
## other attached packages:  
## [1] tidyr\_0.8.3 dunn.test\_1.3.5   
## [3] plotrix\_3.7-4 igraph\_1.1.2   
## [5] pheatmap\_1.0.12 usethis\_1.6.1   
## [7] devtools\_2.0.1 vegan\_2.4-5   
## [9] permute\_0.9-5 cowplot\_0.9.4   
## [11] mixOmics\_6.3.1 lattice\_0.20-38   
## [13] MASS\_7.3-51.1 reshape2\_1.4.3   
## [15] missForest\_1.4 itertools\_0.1-3   
## [17] iterators\_1.0.10 foreach\_1.4.4   
## [19] randomForest\_4.6-12 DESeq2\_1.14.1   
## [21] SummarizedExperiment\_1.4.0 Biobase\_2.34.0   
## [23] GenomicRanges\_1.26.4 GenomeInfoDb\_1.10.3   
## [25] IRanges\_2.8.2 S4Vectors\_0.12.2   
## [27] BiocGenerics\_0.20.0 phyloseq\_1.19.1   
## [29] ggplot2\_3.1.0 dplyr\_0.8.0.1   
## [31] 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 geneplotter\_1.52.0   
## [15] knitr\_1.22 pkgload\_1.0.2   
## [17] ade4\_1.7-10 Formula\_1.2-3   
## [19] jsonlite\_1.6 annotate\_1.52.1   
## [21] cluster\_2.0.6 shiny\_1.2.0   
## [23] backports\_1.1.3 assertthat\_0.2.0   
## [25] Matrix\_1.2-12 lazyeval\_0.2.1   
## [27] cli\_1.0.1 later\_0.8.0   
## [29] prettyunits\_1.0.2 acepack\_1.4.1   
## [31] htmltools\_0.3.6 tools\_3.3.2   
## [33] gtable\_0.2.0 glue\_1.3.1   
## [35] Rcpp\_1.0.0 Biostrings\_2.42.1   
## [37] multtest\_2.30.0 ape\_5.0   
## [39] nlme\_3.1-131 crosstalk\_1.0.0   
## [41] xfun\_0.5 stringr\_1.4.0   
## [43] ps\_1.3.0 testthat\_2.0.1   
## [45] mime\_0.6 miniUI\_0.1.1.1   
## [47] XML\_3.98-1.19 zlibbioc\_1.20.0   
## [49] scales\_1.0.0 promises\_1.0.1   
## [51] biomformat\_1.2.0 rhdf5\_2.18.0   
## [53] RColorBrewer\_1.1-2 yaml\_2.2.0   
## [55] memoise\_1.1.0 gridExtra\_2.3   
## [57] rpart\_4.1-13 latticeExtra\_0.6-28   
## [59] stringi\_1.4.3 RSQLite\_2.1.1   
## [61] genefilter\_1.56.0 desc\_1.2.0   
## [63] checkmate\_1.9.1 pkgbuild\_1.0.2   
## [65] BiocParallel\_1.8.2 manipulateWidget\_0.10.0  
## [67] rlang\_0.4.6 pkgconfig\_2.0.2   
## [69] bitops\_1.0-6 matrixStats\_0.54.0   
## [71] rgl\_0.100.19 evaluate\_0.13   
## [73] purrr\_0.3.1 htmlwidgets\_1.3   
## [75] processx\_3.3.0 bit\_1.1-14   
## [77] tidyselect\_0.2.5 magrittr\_1.5   
## [79] R6\_2.4.0 Hmisc\_4.1-1   
## [81] DBI\_1.0.0 pillar\_1.3.1   
## [83] foreign\_0.8-71 withr\_2.1.2   
## [85] mgcv\_1.8-20 survival\_2.43-3   
## [87] RCurl\_1.95-4.12 nnet\_7.3-12   
## [89] tibble\_2.0.1 crayon\_1.3.4   
## [91] rARPACK\_0.11-0 ellipse\_0.4.1   
## [93] rmarkdown\_1.12 locfit\_1.5-9.1   
## [95] grid\_3.3.2 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 httpuv\_1.4.5.1   
## [103] munsell\_0.5.0 sessioninfo\_1.1.1