Session Info

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Load the needed packages

```r
list.of.packages <- c("ggplot2", "reshape2", "dplyr", "ggnewscale", "ggrepel",
                      "lme4", "FSA","car", "grDevices", "devtools", "ggpubr",
                      "vegan", "RColorBrewer", "emmeans", "coin", "devtools",
                      "ggnewscale")
new.packages <- list.of.packages[!(list.of.packages %in% installed.packages()[,"Package"])]
if(length(new.packages)) install.packages(new.packages)

if (!requireNamespace("BiocManager", quietly = TRUE)){
  install.packages("BiocManager")}


list.of.bioc <- c("phyloseq", "grDevices", "microbiome", "mixOmics")
new.packages <- list.of.bioc[!(list.of.bioc %in% installed.packages()[,"Package"])]
if(length(new.packages)) BiocManager::install(new.packages)

library(dplyr)
library(lme4)
library(RColorBrewer)
library(phyloseq)
library(microbiome)
library(ggpubr)
library(ggplot2)
library(reshape2)
library(grDevices)
library(vegan)
library(devtools)
library(ggrepel)
library(ggnewscale)
library(FSA)
library(emmeans)
library(coin)
library(mixOmics)
library(car)

# To install pairwiseAdonis visit the GitHub repos: https://github.com/pmartinezarbizu/pairwiseAdonis
library(pairwiseAdonis)
# to install ggConvexHull visit thte GitHub repo: https://github.com/cmartin/ggConvexHull
library(ggConvexHull)
```

```
sessionInfo()
```

```
## R version 3.6.3 (2020-02-29)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 16.04.7 LTS
##
## Matrix products: default
## BLAS:   /usr/lib/libblas/libblas.so.3.6.0
## LAPACK: /usr/lib/lapack/liblapack.so.3.6.0
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=de_AT.UTF-8        LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=de_AT.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=de_AT.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=de_AT.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
##  [1] ggConvexHull_0.1.0   pairwiseAdonis_0.0.1 cluster_2.1.0
##  [4] car_3.0-10           carData_3.0-3        mixOmics_6.10.9
##  [7] MASS_7.3-53          coin_1.3-1           survival_3.2-7
## [10] emmeans_1.4.5        FSA_0.8.30           ggnewscale_0.4.1
## [13] ggrepel_0.8.1        devtools_2.2.2       usethis_1.5.1
## [16] vegan_2.5-6          lattice_0.20-41      permute_0.9-5
## [19] reshape2_1.4.3       ggpubr_0.2.4         magrittr_1.5
## [22] microbiome_1.8.0     ggplot2_3.2.1        phyloseq_1.30.0
## [25] RColorBrewer_1.1-2   lme4_1.1-21          Matrix_1.2-18
## [28] dplyr_0.8.3
##
## loaded via a namespace (and not attached):
##   [1] readxl_1.3.1         backports_1.1.5     plyr_1.8.5
##   [4] igraph_1.2.6         lazyeval_0.2.2      splines_3.6.3
##   [7] TH.data_1.0-10       digest_0.6.27       foreach_1.5.0
##  [10] htmltools_0.4.0      fansi_0.4.1         memoise_1.1.0
##  [13] openxlsx_4.1.5       remotes_2.1.1       Biostrings_2.54.0
##  [16] matrixStats_0.55.0   rARPACK_0.11-0      sandwich_2.5-1
##  [19] prettyunits_1.0.2    colorspace_1.4-1    haven_2.3.1
##  [22] xfun_0.11            callr_3.4.0         crayon_1.3.4
##  [25] jsonlite_1.6         libcoin_1.0-5       zoo_1.8-7
##  [28] iterators_1.0.12     ape_5.3             glue_1.3.1
##  [31] gtable_0.3.0         zlibbioc_1.32.0     XVector_0.26.0
##  [34] pkgbuild_1.0.6       Rhdf5lib_1.8.0      BiocGenerics_0.32.0
##  [37] abind_1.4-5          scales_1.1.0        mvtnorm_1.0-12
##  [40] Rcpp_1.0.3           xtable_1.8-4        foreign_0.8-76
##  [43] stats4_3.6.3         ellipsis_0.3.0      modeltools_0.2-22
##  [46] pkgconfig_2.0.3      tidyselect_0.2.5    rlang_0.4.6
##  [49] munsell_0.5.0        cellranger_1.1.0    tools_3.6.3
##  [52] cli_2.0.1            ade4_1.7-13         evaluate_0.14
##  [55] biomformat_1.14.0    stringr_1.4.0       yaml_2.2.0
##  [58] processx_3.4.1       knitr_1.26          fs_1.3.1
```

```
##  [61] zip_2.0.4          purrr_0.3.3        nlme_3.1-149
##  [64] compiler_3.6.3     curl_4.3           testthat_2.3.1
##  [67] ggsignif_0.6.0     tibble_2.1.3       stringi_1.4.5
##  [70] ps_1.3.0           desc_1.2.0         RSpectra_0.16-0
##  [73] forcats_0.4.0      nloptr_1.2.1       multtest_2.42.0
##  [76] vctrs_0.3.1        pillar_1.4.3       lifecycle_0.1.0
##  [79] BiocManager_1.30.10 estimability_1.3  data.table_1.12.8
##  [82] corpcor_1.6.9      R6_2.4.1           gridExtra_2.3
##  [85] rio_0.5.16         IRanges_2.20.1     sessioninfo_1.1.1
##  [88] codetools_0.2-16   boot_1.3-24        assertthat_0.2.1
##  [91] pkgload_1.0.2      rhdf5_2.30.1       rprojroot_1.3-2
##  [94] withr_2.1.2        multcomp_1.4-12    S4Vectors_0.24.1
##  [97] mgcv_1.8-33        parallel_3.6.3     hms_0.5.2
## [100] grid_3.6.3         tidyr_1.0.2        coda_0.19-3
## [103] minqa_1.2.4        rmarkdown_2.0      Rtsne_0.15
## [106] Biobase_2.46.0     ellipse_0.4.1
```