

# Used package versions

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## Load packages and retrieve R and package versions

```
library(ape)
library(car)
library(dplyr)
library(emmeans)
library(ggpubr)
library(knitr)
library(lme4)
library(magrittr)
library(microbiome)
library(microbiomeutilities)
library(multcompView)
library(nlme)
library(phyloseq)
library(picante)
library(plyr)
library(purrr)
library(reshape2)
library(sciplot)
library(tinytex)
library(vegan)
library(viridis)

sessionInfo()
```

```
## R version 3.5.0 (2018-04-23)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 18363)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=English_Netherlands.1252 LC_CTYPE=English_Netherlands.1252
## [3] LC_MONETARY=English_Netherlands.1252 LC_NUMERIC=C
## [5] LC_TIME=English_Netherlands.1252
##
## attached base packages:
## [1] stats      graphics  grDevices datasets  utils      methods    base
```

```
##
## other attached packages:
## [1] viridis_0.5.1          viridisLite_0.3.0
## [3] tinytex_0.20           sciplot_1.2-0
## [5] reshape2_1.4.3        purrr_0.3.4
## [7] plyr_1.8.6            picante_1.8.1
## [9] vegan_2.5-6           lattice_0.20-41
## [11] permute_0.9-5         nlme_3.1-152
## [13] multcompView_0.1-8    microbiomeutilities_0.99.02
## [15] microbiome_1.2.1      phyloseq_1.24.2
## [17] lme4_1.1-26          Matrix_1.2-18
## [19] knitr_1.31            ggpubr_0.2.5
## [21] magrittr_2.0.1        ggplot2_3.3.0
## [23] emmeans_1.4.5         dplyr_1.0.4
## [25] car_3.0-7             carData_3.0-3
## [27] ape_5.3
##
## loaded via a namespace (and not attached):
## [1] RColorBrewer_1.1-2    tools_3.5.0          utf8_1.1.4
## [4] R6_2.5.0              mgcv_1.8-23          BiocGenerics_0.26.0
## [7] colorspace_1.4-1     ade4_1.7-15          withr_2.1.2
## [10] gridExtra_2.3         tidyselect_1.1.0     curl_4.3
## [13] compiler_3.5.0       Biobase_2.40.0       scales_1.1.0
## [16] mvtnorm_1.1-0        stringr_1.4.0        digest_0.6.27
## [19] foreign_0.8-70       minqa_1.2.4          rmarkdown_2.1
## [22] rio_0.5.16           XVector_0.20.0       pkgconfig_2.0.3
## [25] htmltools_0.4.0      rlang_0.4.10         readxl_1.3.1
## [28] generics_0.1.0       jsonlite_1.6.1       zip_2.0.4
## [31] biomformat_1.8.0     Rcpp_1.0.6           munsell_0.5.0
## [34] S4Vectors_0.18.3    Rhdf5lib_1.2.1       fansi_0.4.2
## [37] abind_1.4-5          lifecycle_1.0.0      stringi_1.5.3
## [40] yaml_2.2.1           MASS_7.3-53.1        zlibbioc_1.26.0
## [43] rhdf5_2.24.0         grid_3.5.0           ggrepel_0.8.2
## [46] parallel_3.5.0       forcats_0.5.0        crayon_1.4.1
## [49] Biostrings_2.48.0    haven_2.2.0          splines_3.5.0
## [52] multtest_2.36.0      hms_0.5.3            pillar_1.5.0
## [55] igraph_1.2.4.2       boot_1.3-27          estimability_1.3
## [58] ggsignif_0.6.0       codetools_0.2-15     stats4_3.5.0
## [61] glue_1.4.2           evaluate_0.14        data.table_1.12.8
## [64] renv_0.13.0-9        vctrs_0.3.6          nloptr_1.2.2.1
## [67] foreach_1.4.8        cellranger_1.1.0     tidyr_1.1.3
## [70] gtable_0.3.0         xfun_0.21            openxlsx_4.1.4
## [73] xtable_1.8-4         survival_3.1-11      pheatmap_1.0.12
## [76] tibble_3.1.0         iterators_1.0.12     IRanges_2.14.12
## [79] cluster_2.0.7-1      statmod_1.4.35       ellipsis_0.3.1
```