

All used packages, cleanup, and directory structure

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Contents

1. Load packages	1
2. Clean up global environment	3
3. Directory structure (do only once)	3

1. Load packages

```
library(phyloseq)
library(microbiome)
library(microbiomeutilities) # format_to_besthit()
library(ggpubr) # ggarrange()
library(plyr)
library(dplyr)
library(ape)
library(reshape2)
library(scales)
library(knitr)
library(ggrepel)
library(nlme)
library(lme4)
library(sciplot) # se() function
library(apeglm)
library(pheatmap)
library(picante)
library(emmeans)
library(multcomp)
library(multcompView)
library(purrr) # functions for lists
library(car) # Anova() function (for glmer)
library(ggvegan) # customize PRC plot

# colour palettes
library(viridis)
library(RColorBrewer)
```

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  utils      datasets  methods    base
##
## other attached packages:
## [1] RColorBrewer_1.1-2          viridis_0.5.1
## [3] viridisLite_0.3.0          ggvegan_0.1-0
## [5] car_3.0-7                   carData_3.0-3
## [7] purrr_0.3.3                 multcompView_0.1-8
## [9] multcomp_1.4-12            TH.data_1.0-10
## [11] MASS_7.3-49                 survival_3.1-11
## [13] mvtnorm_1.1-0               emmeans_1.4.5
## [15] picante_1.8.1               vegan_2.5-6
## [17] lattice_0.20-35             permute_0.9-5
## [19] pheatmap_1.0.12            apeglm_1.2.1
## [21] sciplot_1.2-0               lme4_1.1-21
## [23] Matrix_1.2-14               nlme_3.1-137
## [25] ggrepel_0.8.2               knitr_1.28
## [27] scales_1.1.0                reshape2_1.4.3
## [29] ape_5.3                     dplyr_0.8.5
## [31] plyr_1.8.6                  ggpubr_0.2.5
## [33] magrittr_1.5                microbiomeutilities_0.99.02
## [35] microbiome_1.2.1            ggplot2_3.3.0
## [37] phyloseq_1.24.2
##
## loaded via a namespace (and not attached):
## [1] minqa_1.2.4                  colorspace_1.4-1
## [3] ggsignif_0.6.0               rio_0.5.16
## [5] estimability_1.3             XVector_0.20.0
## [7] GenomicRanges_1.32.7         codetools_0.2-15
## [9] splines_3.5.0                ade4_1.7-15
## [11] jsonlite_1.6.1               nloptr_1.2.2.1
## [13] cluster_2.0.7-1              compiler_3.5.0
## [15] assertthat_0.2.1             htmltools_0.4.0
## [17] tools_3.5.0                  igraph_1.2.4.2
## [19] coda_0.19-3                  gtable_0.3.0
## [21] glue_1.3.2                   GenomeInfoDbData_1.1.0
## [23] Rcpp_1.0.3                   bbmle_1.0.23.1
## [25] Biobase_2.40.0               cellranger_1.1.0
## [27] vctrs_0.2.4                  Biostrings_2.48.0
## [29] multtest_2.36.0              iterators_1.0.12
```

```
## [31] xfun_0.12                stringr_1.4.0
## [33] openxlsx_4.1.4           lifecycle_0.2.0
## [35] zlibbioc_1.26.0          zoo_1.8-7
## [37] hms_0.5.3                parallel_3.5.0
## [39] SummarizedExperiment_1.10.1 biomformat_1.8.0
## [41] sandwich_2.5-1           rhdf5_2.24.0
## [43] yaml_2.2.1               curl_4.3
## [45] gridExtra_2.3            emdbook_1.3.12
## [47] bdsmatrix_1.3-4          stringi_1.4.6
## [49] S4Vectors_0.18.3         foreach_1.4.8
## [51] BiocGenerics_0.26.0      zip_2.0.4
## [53] boot_1.3-20              BiocParallel_1.14.2
## [55] GenomeInfoDb_1.16.0     rlang_0.4.5
## [57] pkgconfig_2.0.3          matrixStats_0.56.0
## [59] bitops_1.0-6             evaluate_0.14
## [61] Rhdf5lib_1.2.1           tidyselect_1.0.0
## [63] R6_2.4.1                 IRanges_2.14.12
## [65] DelayedArray_0.6.6       pillar_1.4.3
## [67] haven_2.2.0              foreign_0.8-70
## [69] withr_2.1.2              mgcv_1.8-23
## [71] abind_1.4-5              RCurl_1.98-1.1
## [73] tibble_2.1.3             crayon_1.3.4
## [75] rmarkdown_2.1            readxl_1.3.1
## [77] grid_3.5.0              data.table_1.12.8
## [79] forcats_0.5.0           digest_0.6.25
## [81] xtable_1.8-4            tidyr_1.0.2
## [83] numDeriv_2016.8-1.1     stats4_3.5.0
## [85] munsell_0.5.0
```

2. Clean up global environment

If memory and computing speed are needed. The commands will empty the Global Environment of the R-project, and `gc()` will cause a garbage collection to take place and report the memory usage.

```
rm(list = ls())
gc()
```

3. Directory structure (do only once)

```
# Create Folders as following
#Tables
dir.create("tables")

# Figures
dir.create("figures")

# Phyloseq objects
dir.create("phyobjects")
```