

Session info

Stefano Romano

Before you begin:

These scripts was tailored for the analyses we conducted. They are not meant to be used in other contexts and are reported here as a detailed extension of the method section of our article. Please, use them at your own risk.

If you use any of the material or approaches in these scripts, please, cite: Romano et al, 2020, *Meta-analysis of the gut microbiome of Parkinson's disease patients suggests alterations linked to intestinal inflammation*

Thank you!

```
# Load packages
list.of.packages <- c("ggplot2", "dplyr", "reshape2", "propr", "devtools",
                     "ggpubr", "coin", "data.table", "genodds", "meta", "grid",
                     "doParallel", "foreach", "bbmle", "glmmTMB", "MuMIn")
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("DESeq2", "phyloseq", "zCompositions", "grDevices", "microbiome")
new.packages <- list.of.bioc[!(list.of.bioc %in% installed.packages()[,"Package"])]
if(length(new.packages)) BiocManager::install(new.packages)

source('GMPR.R') # Version: 0.1. Date: 2017/02/07

## Loading required package: matrixStats
devtools::install_github('ggloor/CoDaSeq/CoDaSeq')

## Skipping install of 'CoDaSeq' from a github remote, the SHA1 (6ff864aa) has not changed since last i
## Use `force = TRUE` to force installation

source("ancom_v2.0.R")

## Package 'exactRankTests' is no longer under development.
## Please consider using package 'coin' instead.

##
## Attaching package: 'dplyr'

## The following object is masked from 'package:nlme':
##
## collapse

## The following object is masked from 'package:matrixStats':
```

```

##
##      count
## The following objects are masked from 'package:stats':
##
##      filter, lag
## The following objects are masked from 'package:base':
##
##      intersect, setdiff, setequal, union
library(dplyr)
library(bbmle)

## Loading required package: stats4
##
## Attaching package: 'bbmle'
## The following object is masked from 'package:dplyr':
##
##      slice
library(glmTMB)
library(MuMIn)

##
## Attaching package: 'MuMIn'
## The following object is masked from 'package:bbmle':
##
##      AICc
library(phyloseq)
library(ggpubr)

## Loading required package: ggplot2
## Loading required package: magrittr
library(vegan)

## Loading required package: permute
## Loading required package: lattice
## This is vegan 2.5-6
library(ggplot2)
library(reshape2)
library(microbiome)

##
## microbiome R package (microbiome.github.com)
##
##
##
## Copyright (C) 2011-2019 Leo Lahti,
##      Sudarshan Shetty et al. <microbiome.github.io>
##
## Attaching package: 'microbiome'

```

```

## The following object is masked from 'package:vegan':
##
##     diversity
## The following object is masked from 'package:ggplot2':
##
##     alpha
## The following object is masked from 'package:base':
##
##     transform
library(zCompositions)

## Loading required package: MASS
##
## Attaching package: 'MASS'
## The following object is masked from 'package:dplyr':
##
##     select
## Loading required package: NADA
## Loading required package: survival
##
## Attaching package: 'NADA'
## The following object is masked from 'package:stats':
##
##     cor
## Loading required package: truncnorm
library(propr)

##
## Attaching package: 'propr'
## The following object is masked from 'package:lattice':
##
##     parallel
library(grDevices)
library(devtools)

## Loading required package: usethis
##
## Attaching package: 'devtools'
## The following object is masked from 'package:permute':
##
##     check
library(genodds)
library(data.table)

##
## Attaching package: 'data.table'

```

```
## The following objects are masked from 'package:reshape2':
##
##   dcast, melt
## The following objects are masked from 'package:dplyr':
##
##   between, first, last
```

```
library(meta)
```

```
## Loading 'meta' package (version 4.9-9).
## Type 'help(meta)' for a brief overview.
```

```
library(CoDaSeq)
```

```
## Loading required package: ALDEx2
##
## Attaching package: 'ALDEx2'
## The following object is masked from 'package:propr':
##
##   aldex.glm
## Loading required package: car
## Loading required package: carData
## Registered S3 methods overwritten by 'car':
##   method                from
##   influence.merMod        lme4
##   cooks.distance.influence.merMod lme4
##   dfbeta.influence.merMod   lme4
##   dfbetas.influence.merMod  lme4
##
## Attaching package: 'car'
## The following object is masked from 'package:dplyr':
##
##   recode
```

```
library(doParallel)
```

```
## Loading required package: foreach
## Loading required package: iterators
## Loading required package: parallel
```

```
library(foreach)
```

Report below session info

```
sessionInfo()
```

```
## R version 3.6.2 (2019-12-12)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 16.04.6 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] parallel stats4 stats graphics grDevices utils datasets
## [8] methods base
##
## other attached packages:
## [1] doParallel_1.0.15 iterators_1.0.12 foreach_1.5.0
## [4] CoDaSeq_0.99.6 car_3.0-6 carData_3.0-3
## [7] ALDEx2_1.18.0 meta_4.9-9 data.table_1.12.8
## [10] genodds_1.0.0 devtools_2.2.2 usethis_1.5.1
## [13] propr_4.2.6 zCompositions_1.3.3-1 truncnorm_1.0-8
## [16] NADA_1.6-1 survival_2.43-3 MASS_7.3-51.1
## [19] microbiome_1.8.0 reshape2_1.4.3 vegan_2.5-6
## [22] lattice_0.20-38 permute_0.9-5 ggpubr_0.2.4
## [25] magrittr_1.5 ggplot2_3.2.1 phyloseq_1.30.0
## [28] MuMIn_1.43.17 glmmTMB_1.0.1 bbmle_1.0.23.1
## [31] dplyr_0.8.3 nlme_3.1-137 exactRankTests_0.8-31
## [34] matrixStats_0.55.0
##
## loaded via a namespace (and not attached):
## [1] readxl_1.3.1 backports_1.1.5
## [3] plyr_1.8.5 igraph_1.2.4.2
## [5] lazyeval_0.2.2 TMB_1.7.16
## [7] splines_3.6.2 BiocParallel_1.20.1
## [9] GenomeInfoDb_1.22.0 TH.data_1.0-10
## [11] digest_0.6.23 htmltools_0.4.0
## [13] fansi_0.4.1 memoise_1.1.0
## [15] cluster_2.0.7-1 openxlsx_4.1.5
## [17] remotes_2.1.1 Biostrings_2.54.0
## [19] sandwich_2.5-1 bdsmatrix_1.3-4
## [21] prettyunits_1.0.2 colorspace_1.4-1
## [23] haven_2.3.1 xfun_0.11
## [25] callr_3.4.0 crayon_1.3.4
## [27] RCurl_1.98-1.2 jsonlite_1.6
## [29] lme4_1.1-21 zoo_1.8-7
## [31] ape_5.3 glue_1.3.1
## [33] gtable_0.3.0 zlibbioc_1.32.0
## [35] emmeans_1.4.5 XVector_0.26.0
## [37] DelayedArray_0.12.1 pkgbuild_1.0.6
## [39] Rhdf5lib_1.8.0 BiocGenerics_0.32.0
## [41] abind_1.4-5 scales_1.1.0
## [43] mvtnorm_1.0-12 Rcpp_1.0.3
## [45] xtable_1.8-4 foreign_0.8-71

```

## [47] ellipsis_0.3.0	pkgconfig_2.0.3
## [49] tidyselect_0.2.5	rlang_0.4.6
## [51] cellranger_1.1.0	munsell_0.5.0
## [53] tools_3.6.2	cli_2.0.1
## [55] ade4_1.7-13	evaluate_0.14
## [57] biomformat_1.14.0	stringr_1.4.0
## [59] yaml_2.2.0	processx_3.4.1
## [61] knitr_1.26	fs_1.3.1
## [63] zip_2.0.4	purrr_0.3.3
## [65] compiler_3.6.2	curl_4.3
## [67] testthat_2.3.1	ggsignif_0.6.0
## [69] tibble_2.1.3	stringi_1.4.5
## [71] ps_1.3.0	desc_1.2.0
## [73] forcats_0.4.0	Matrix_1.2-17
## [75] nloptr_1.2.1	multtest_2.42.0
## [77] vctrs_0.3.1	pillar_1.4.3
## [79] lifecycle_0.1.0	BiocManager_1.30.10
## [81] estimability_1.3	bitops_1.0-6
## [83] GenomicRanges_1.38.0	R6_2.4.1
## [85] rio_0.5.16	IRanges_2.20.1
## [87] sessioninfo_1.1.1	codetools_0.2-16
## [89] boot_1.3-24	assertthat_0.2.1
## [91] pkgload_1.0.2	rhdf5_2.30.1
## [93] SummarizedExperiment_1.16.1	rprojroot_1.3-2
## [95] withr_2.1.2	metafor_2.1-0
## [97] multcomp_1.4-12	S4Vectors_0.24.1
## [99] GenomeInfoDbData_1.2.2	mgcv_1.8-28
## [101] hms_0.5.2	grid_3.6.2
## [103] tidyr_1.0.2	coda_0.19-3
## [105] minqa_1.2.4	rmarkdown_2.0
## [107] Rtsne_0.15	numDeriv_2016.8-1.1
## [109] Biobase_2.46.0	