

HMP_2012_16S_gingival_V35_subset

```
library(MicrobiomeBenchmarkData)
library(magrittr) # must be attached for the functions in functions_da.R to work

## Project directory must be selected in the knitr menu
source("R/functions_da.R")

tse <- getDataset("HMP_2012_16S_gingival_V35_subset", dryrun = FALSE)[[1]]

## Finished HMP_2012_16S_gingival_V35_subset.

## A couple of useful variables
ref <- "subgingival_plaque"
grp <- "hmp_body_subsite"
```

Differential abundance analysis

Trying a few methods for differential abundance analysis

```
DA_filename <- "rmarkdown/HMP_2012_16S_ginivival_V35_subset_DA.rds"

if (file.exists(DA_filename)) {

  cat(paste0("File ", DA_filename, " already exists. Loading it..."))

  DA <- readRDS(DA_filename)

} else {

  cat(paste0("File ", DA_filename, " does not exist. Calculating DA..."))

  dds <- deseq2Poscounts(tse, grp, ref)
  dge <- edgeRtmm(tse, grp, ref)
  lv <- limmaVoomTmm(tse, grp, ref)
  al2 <- aldex2(tse, grp, ref)
  mgs <- metagenomeSeq(tse, grp, ref)
  cc <- corncob(tse, grp, ref, fdr_cutoff = 0.1)
  ambc <- ancom_bc(tse, grp, ref)

  DA <- list(
    dds = dds, dge = dge, lv = lv,
    al2 = al2, mgs = mgs, cc = cc,
    ambc = ambc
  )

  saveRDS(DA, "rmarkdown/HMP_2012_16S_ginivival_V35_subset_DA.rds")
}
```

```
## File rmarkdown/HMP_2012_16S_ginvival_V35_subset_DA.rds already exists. Loading it...
```

Concordance at the top

Enrichment analysis