



# benchdamic: benchmarking of differential abundance methods on microbiome data

## RATIONALE

### Issue:

Many approaches have been proposed for Differential Abundance (DA) analysis in metagenomics, it is widely recognised that the perfect method does not exist.

### Solution:

A careful exploratory data analysis is necessary to address methodological choices. We benchmarked methods from bulk RNA-seq, metagenomics, and single-cell RNA-seq on metagenomics data.

### Application:

benchdamic is a new R/Bioconductor package that provides a computational framework to guide researchers in the selection of the method that best fits their data.

## IMPLEMENTATION

### Goodness of fit

**Question:** Which are the parametric distributions that are able to fit both the proportion of zeros and the counts in your data?

**Input:** phyloseq or TreeSummarizedExperiment objects

**Working function:** FitModels

**Output:** plotRMSE, plotMD

### Type I Error Control

**Question:** Which are the DA methods that are able to control the number of false positives in your data?

**Input:** phyloseq or TreeSummarizedExperiment objects

**Working function:** createMocks, runMocks, createTIEC

**Output:** plotFPR, plotFDR, plotKS, plotQQ, plotLogP

### Concordance

**Question:** If multiple DA methods are run on the same data, would they be concordant?

**Input:** phyloseq or TreeSummarizedExperiment objects

**Working function:** createSplits, runSplits, createConcordance

**Output:** plotConcordance

### Enrichment

**Question:** If some prior knowledge about your experiment is available, would the findings be coherent with that knowledge?

**Input:** phyloseq or TreeSummarizedExperiment objects

**Working function:** runDA, createEnrichment, createPositives

**Output:** plotEnrichment, plotContingency, plotMutualFindings, plotPositives

