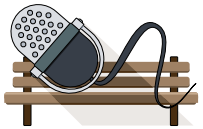


benchdamic: benchmarking of differential abundance methods on microbiome data

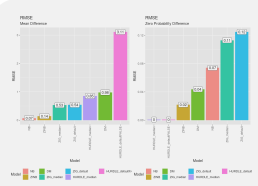
RATIONALE

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.

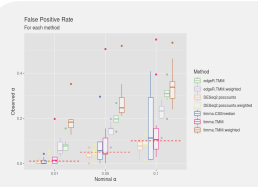
Application:
benchdamic is a new R/ Bioconductor package that provides a computational framework to guide researchers in the selection of the method that best fits their data.

IMPLEMENTATION



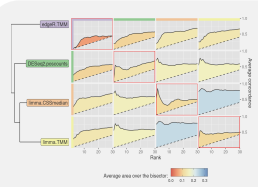
Goodness of fit

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`



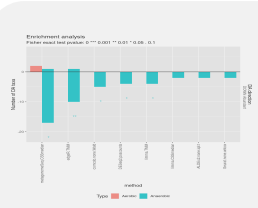
Type I Error Control

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`