## Clinical microbiome data science

PRESENTER INFO:

Tuomas Borman

Leo Lahti

leo.lahti@utu.fi

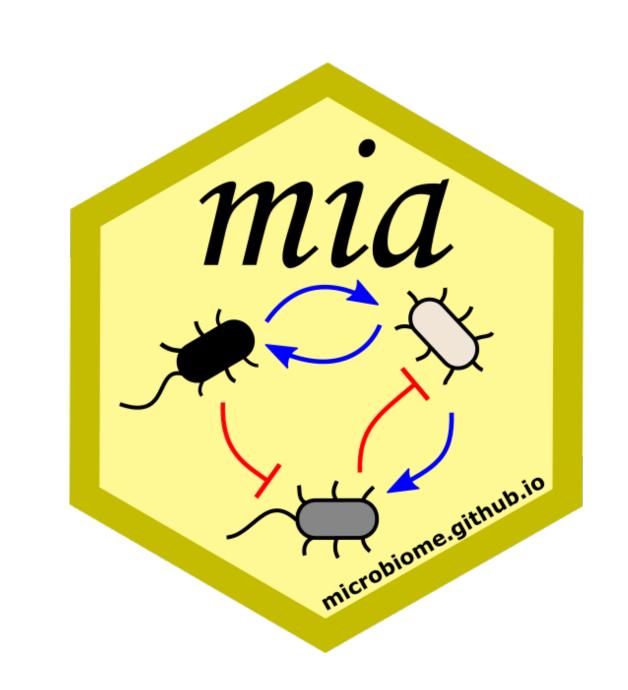
**CONTRIBUTORS:** 

Felix G.M. Ernst, Sudarshan A. Shetty, Ruizhu Huang, Domenick J. Braccia, Héctor Corrada Bravo, The miaverse collective

MORE INFORMATION: Project website:

https://microbiome.github.io







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#### MOTIVATION

- Multi-omics has become more common in microbiome research, because it can support the analysis of microbiome dysbiosis and facilitate the discovery of biomarkers.
- Multi-omics integrates data from multiple sources, for example, microbial abundance data with biomolecular profiling data from blood samples.
- Despite the need, there have not been well-suitable solutions for this kind of analysis that integrate multiple assays.

#### **PROPOSAL**

- Emerging analysis framework called *miaverse* (MIcrobiome Analysis uniVERSE) utilizes a common, **standardized data container**, which enables highly **optimized integration** of multi-assay microbiome profiling data from clinical studies.
- The miaverse contains methods for data analysis and visualization together with comprehensive online documentation and tutorials.
- Common, shared data container enables usage of tools of other disciplines.
- The *miaverse* is a **collaborative open-source project**, and stable version is already available via R/Bioconductor.

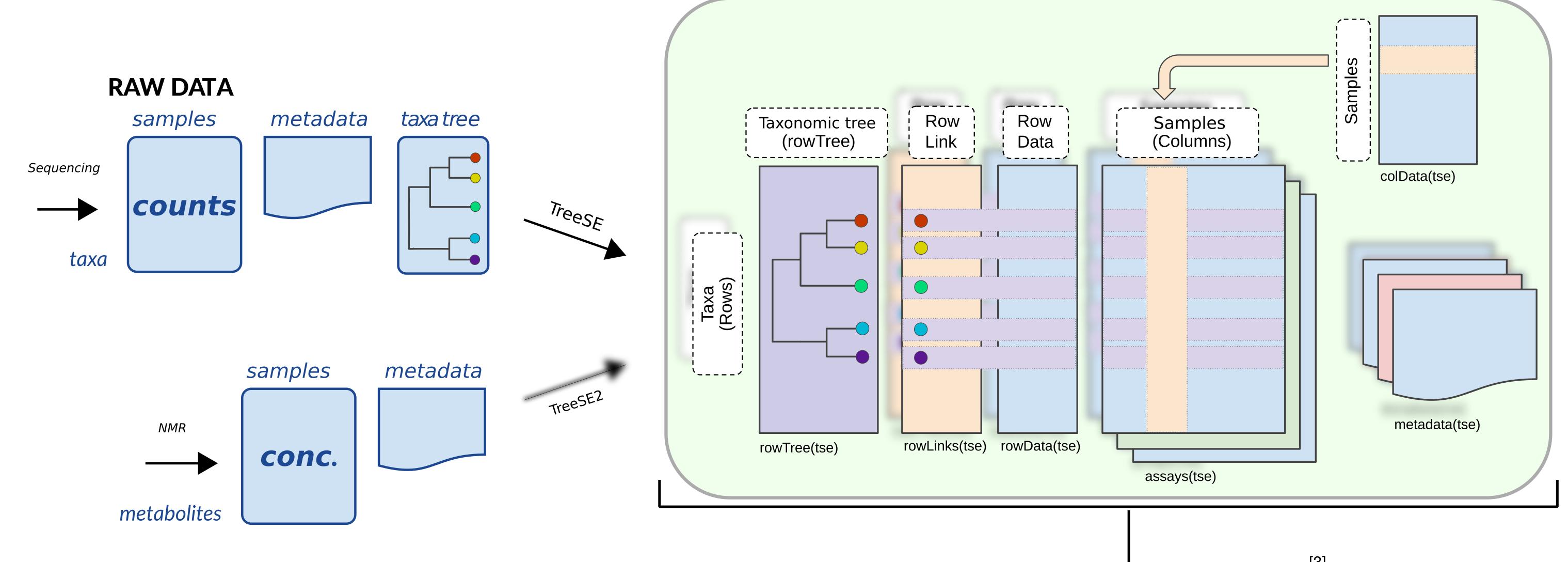
### PROPOSED WORKFLOW: TreeSE & miaverse

Import Data

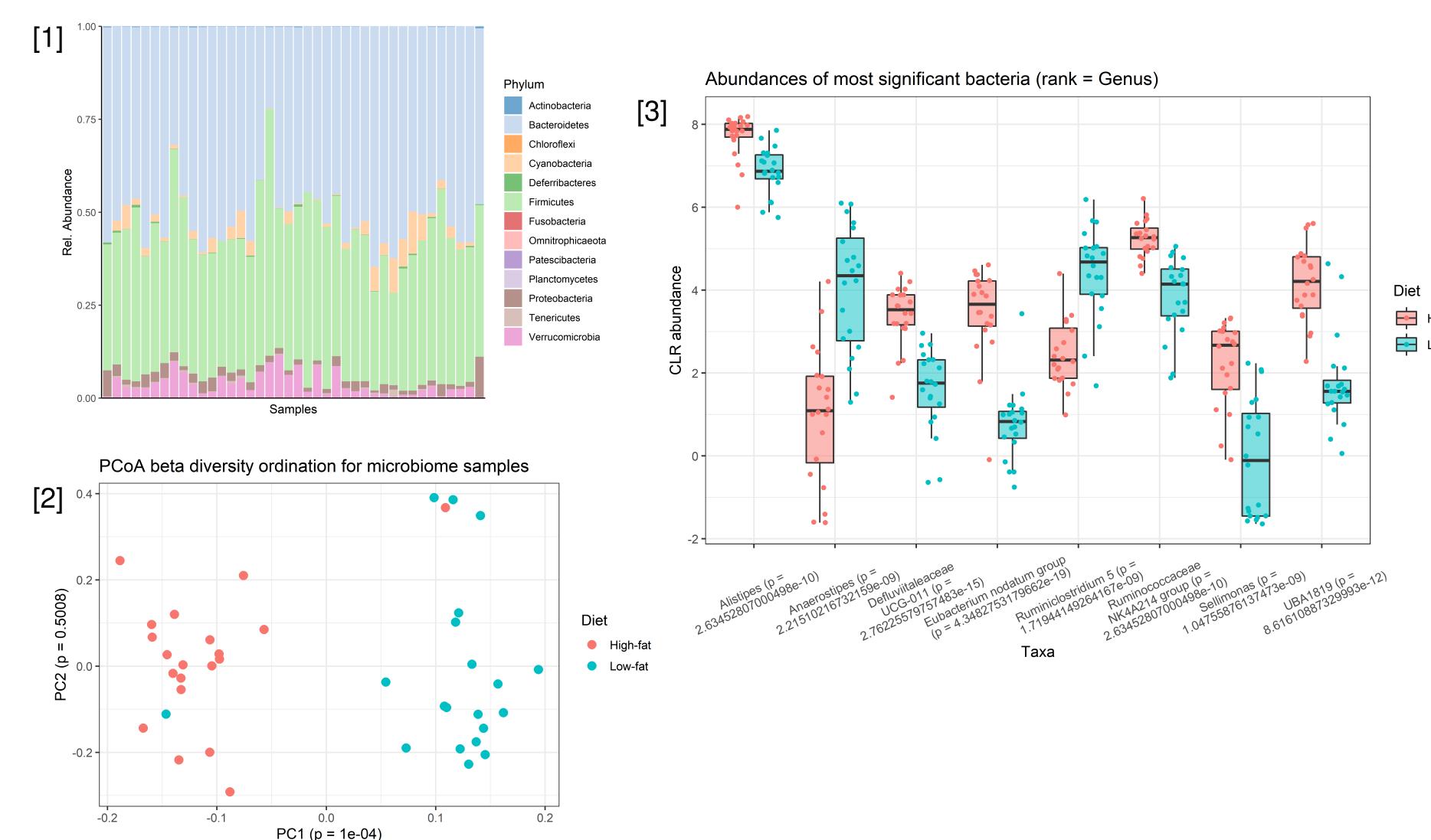
This workflow starts by importing bacterial abundance data and metabolite concentration data into separate TreeSE data containers.

### The TreeSummarizedExperiment object\*

The *TreeSE* object is uniquely positioned to support optimized multi-assay data access, manipulation, and visualization. The separate *TreeSE* objects are linked together with *MultiAssayExperiment (MAE)* data container.

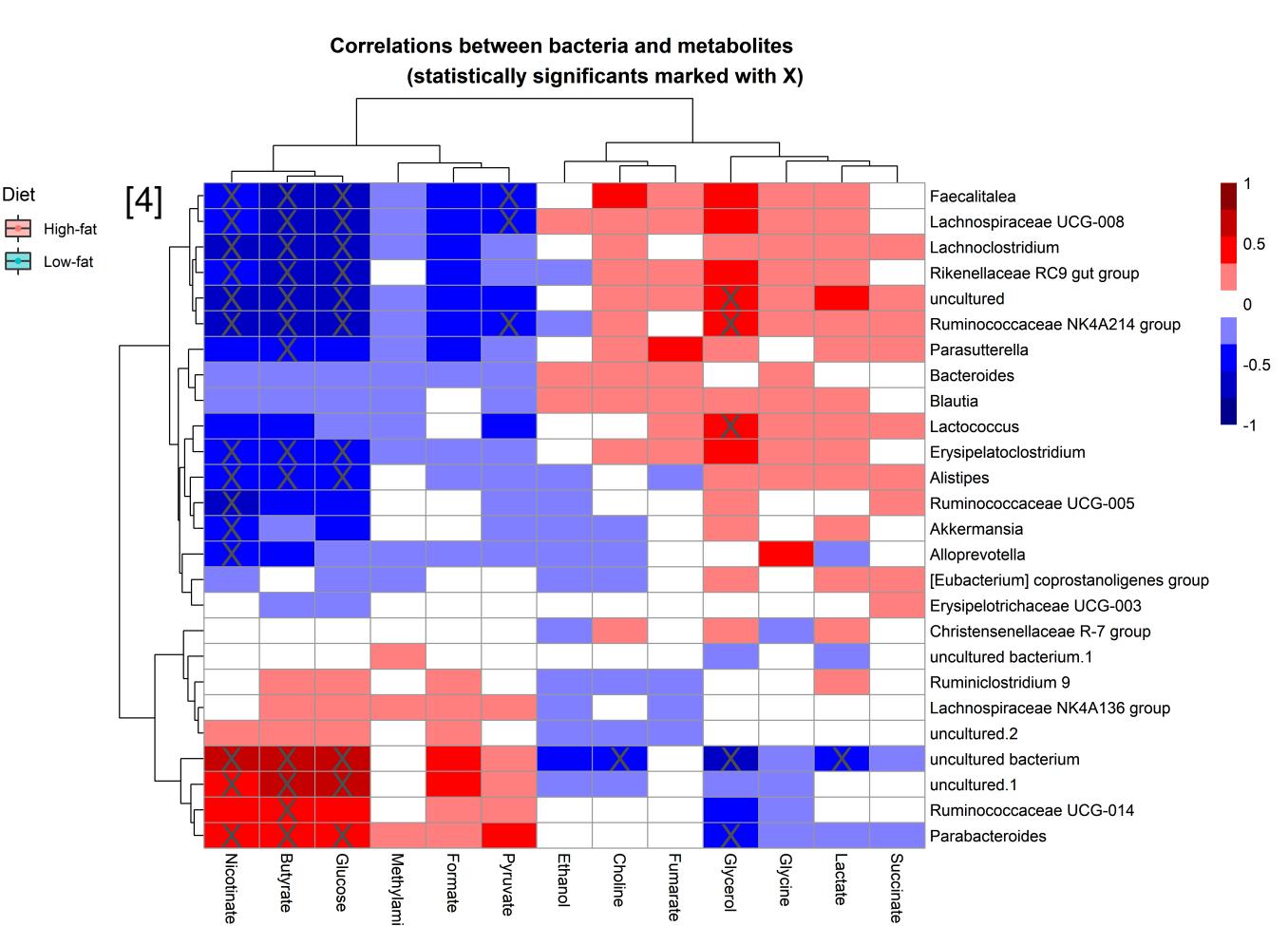






mia::agglomerateByRank(tse, ...)
ancombc::ancombc(tse, ...)
mia::meltAssay(tse, ...)
ggplot2::ggplot(x, ...)

[4]
mia::subsetByPrevalentTaxa(tse, ...)
mia::testCrossCorrelation(mae,, ...)
pheatmap::pheatmap(x, ...)



mia::transformSamples(tse, ...)

scater::plotReducedDim(tse,...)

scater::runMDS(tse,...)