

Clinical microbiome data science

PRESENTER INFO:

Tuomas Borman

✉ tuomas.v.borman@utu.fi

Leo Lahti

✉ leo.lahti@utu.fi



Bioinformatics Day 2022
Espoo, Finland
2 June 2022

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>

EuroBioc2020 poster:

<https://f1000research.com/posters/9-1459>

TreeSummarizedExperiment:

<https://f1000research.com/articles/9-1246/v2>



* Huang R, Soneson C, Ernst FGM et al. TreeSummarizedExperiment: a S4 class for data with hierarchical structure [version 2; peer review: 3 approved]. F1000Research 2021, 9:1246

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 integrate 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 integrates 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.

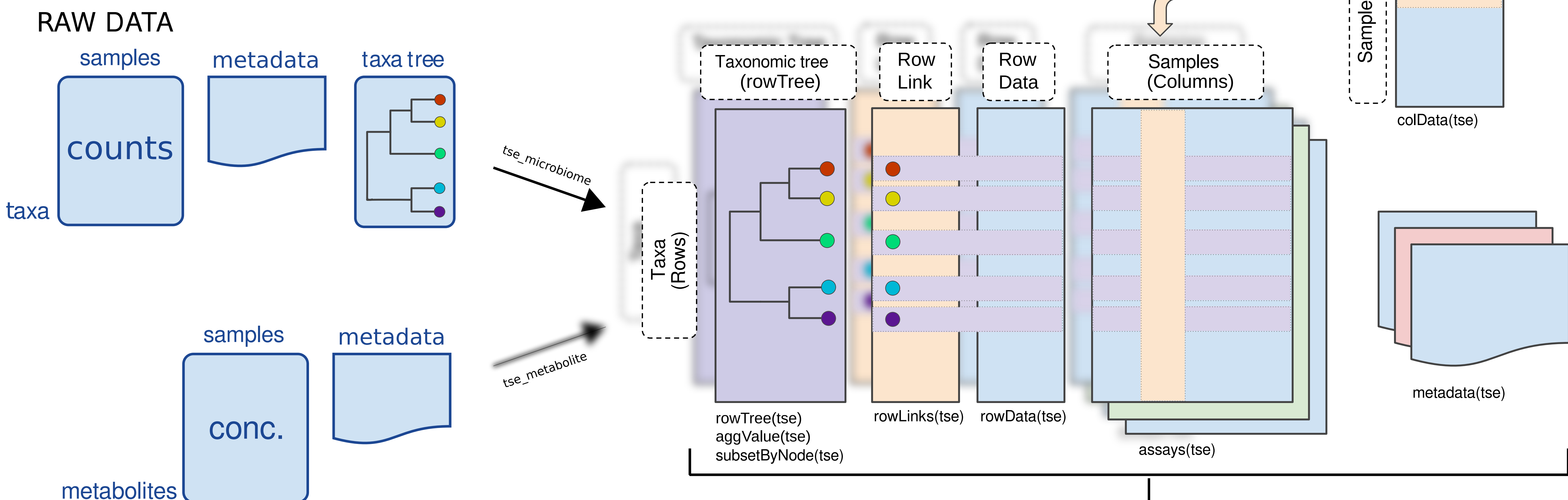
• Common, shared data container enables usage of tools of other disciplines.

• The *miaverse* is a collaborative open-source project, and stable version is already available via Bioconductor.

PROPOSED WORKFLOW:

Import Data

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



The *miaverse* pipeline

