

Clinical microbiome data science

PRESENTER INFO:

Tuomas Borman

✉ tuomas.v.borman@utu.fi

Leo Lahti

✉ leo.lahti@utu.fi



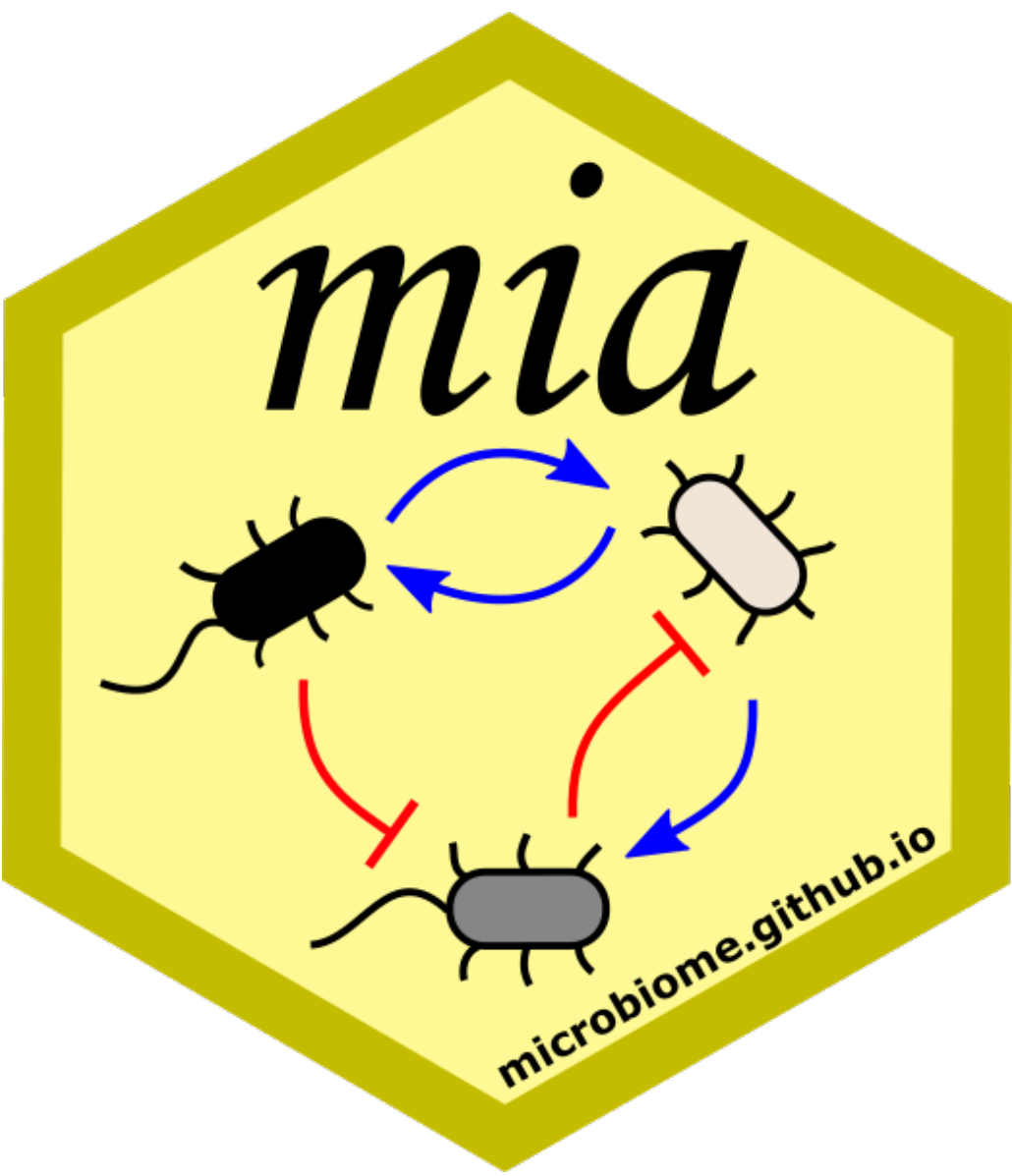
CONTRIBUTORS:

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>



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.

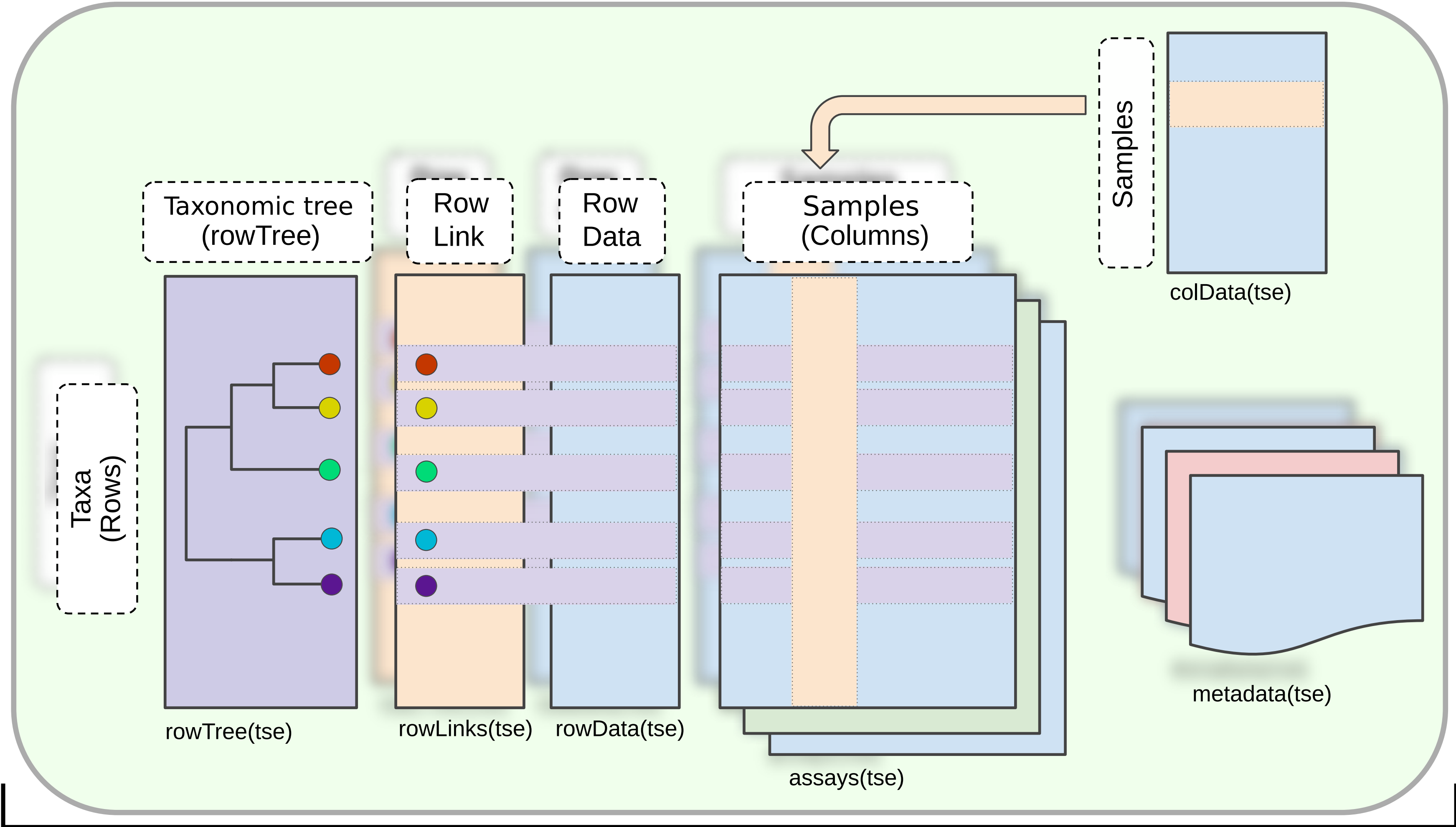
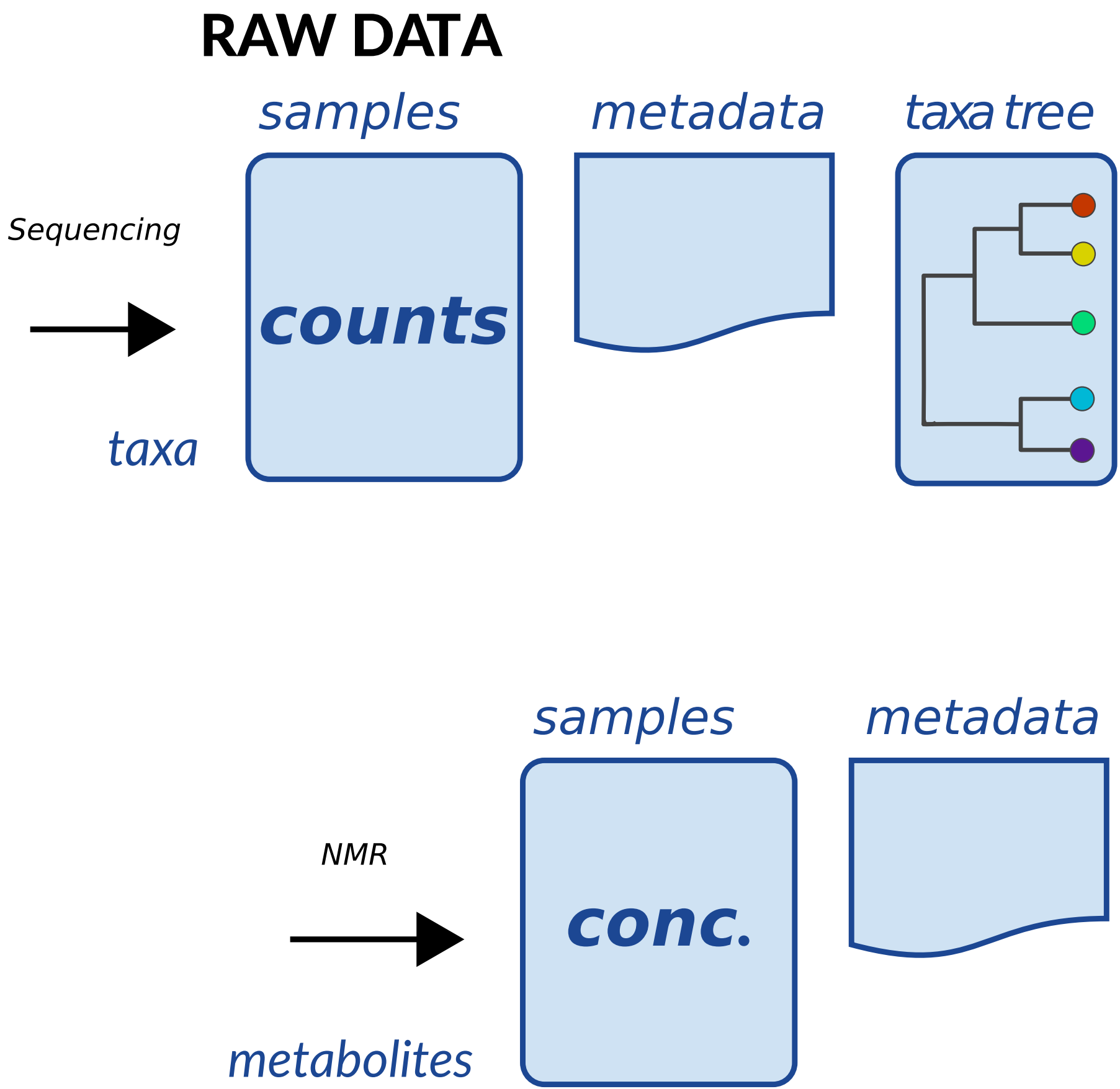
PROPOSAL

- Emerging analysis framework called *miaverse* (M**IC**robiome A**NA**lysis u**Ni**VERSE) 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 *miaverse* pipeline

