

# *miaverse* – microbiome analytics framework in *SummarizedExperiment* family

## PRESENTER INFO:

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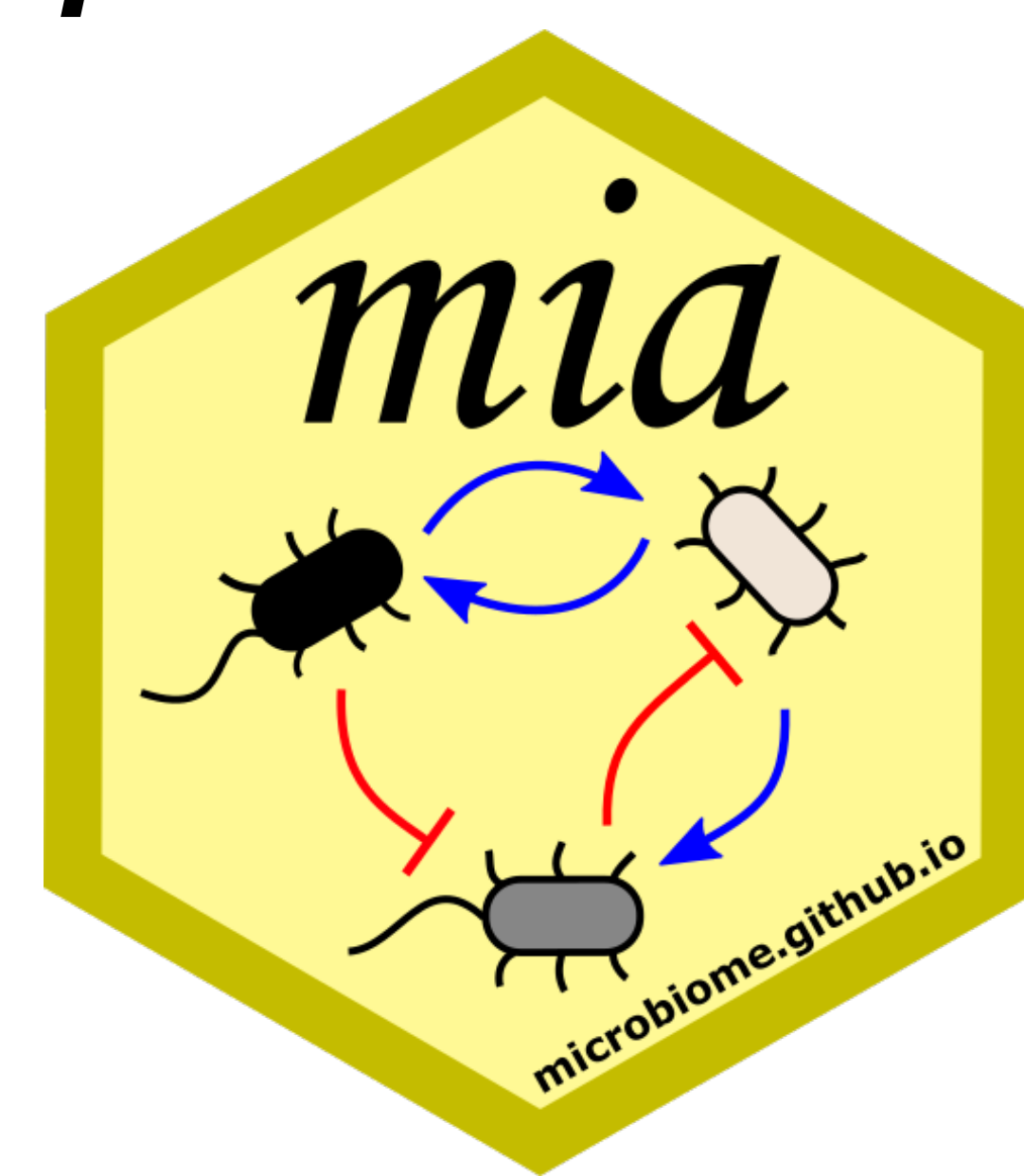
Felix G.M. Ernst, Sudarshan A. Shetty, Ruizhu Huang, Domenick J. Braccia, Héctor Corrada Bravo, The miaverse collective



## MORE INFORMATION:

Project website:

<https://microbiome.github.io>



Remember: Package demo @EuroBioC2023 Thursday 13:30 CEST

## MOTIVATION

- Existing microbiome workflows in Bioconductor has been largely unsupported by the **rich and versatile SummarizedExperiment (SE) family** of classes.
- Shared data container can reduce overlapping efforts, improve interoperability and ensure longterm sustainability.
- As sample size get bigger and multiomics approach is applied, more **efficient data management, handling and wrangling** methods are needed.

## PROPOSAL

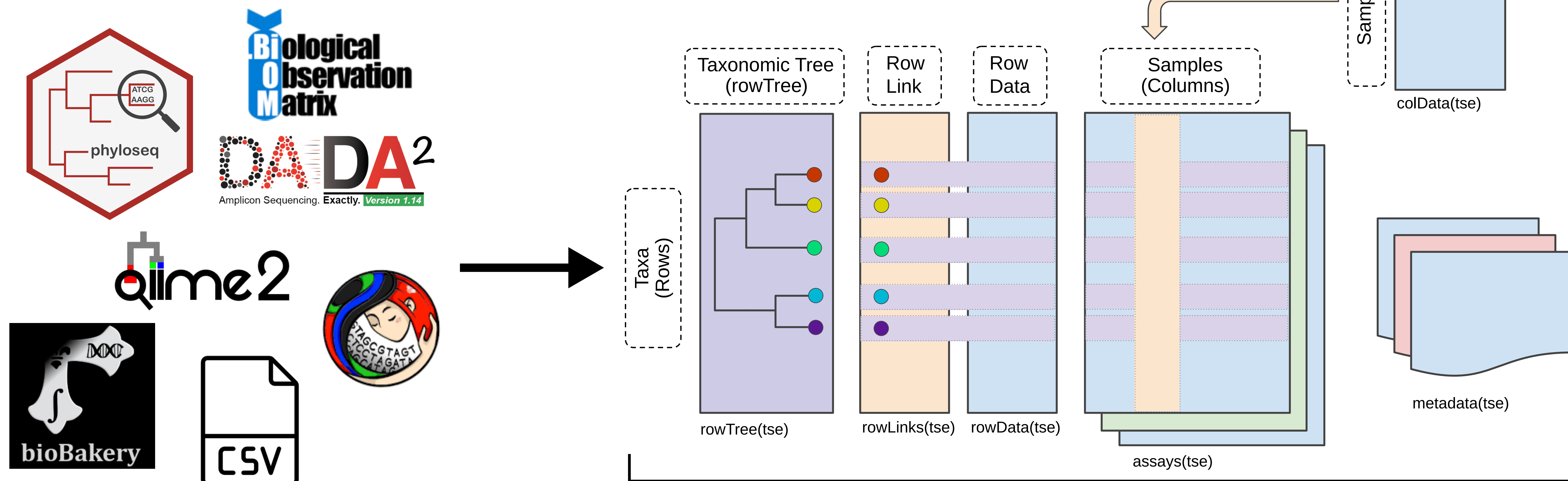
- Emerging analysis framework called *miaverse* (Microbiome Analysis uniVERSE) utilizes a common, **standardized data container**, *TreeSummarizedExperiment*.
- The miaverse contains **methods for data analysis and visualization** together with comprehensive **online tutorial book**, **Orchestrating Microbiome Analysis (OMA)**.
- Common, **shared data container** enables usage of **tools of other disciplines** such as single-cell analytics.
- The *miaverse* is a **collaborative open-source project**, and stable version is already available via R/Bioconductor.

\* 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

## PROPOSED WORKFLOW: *TreeSE* & *miaverse*

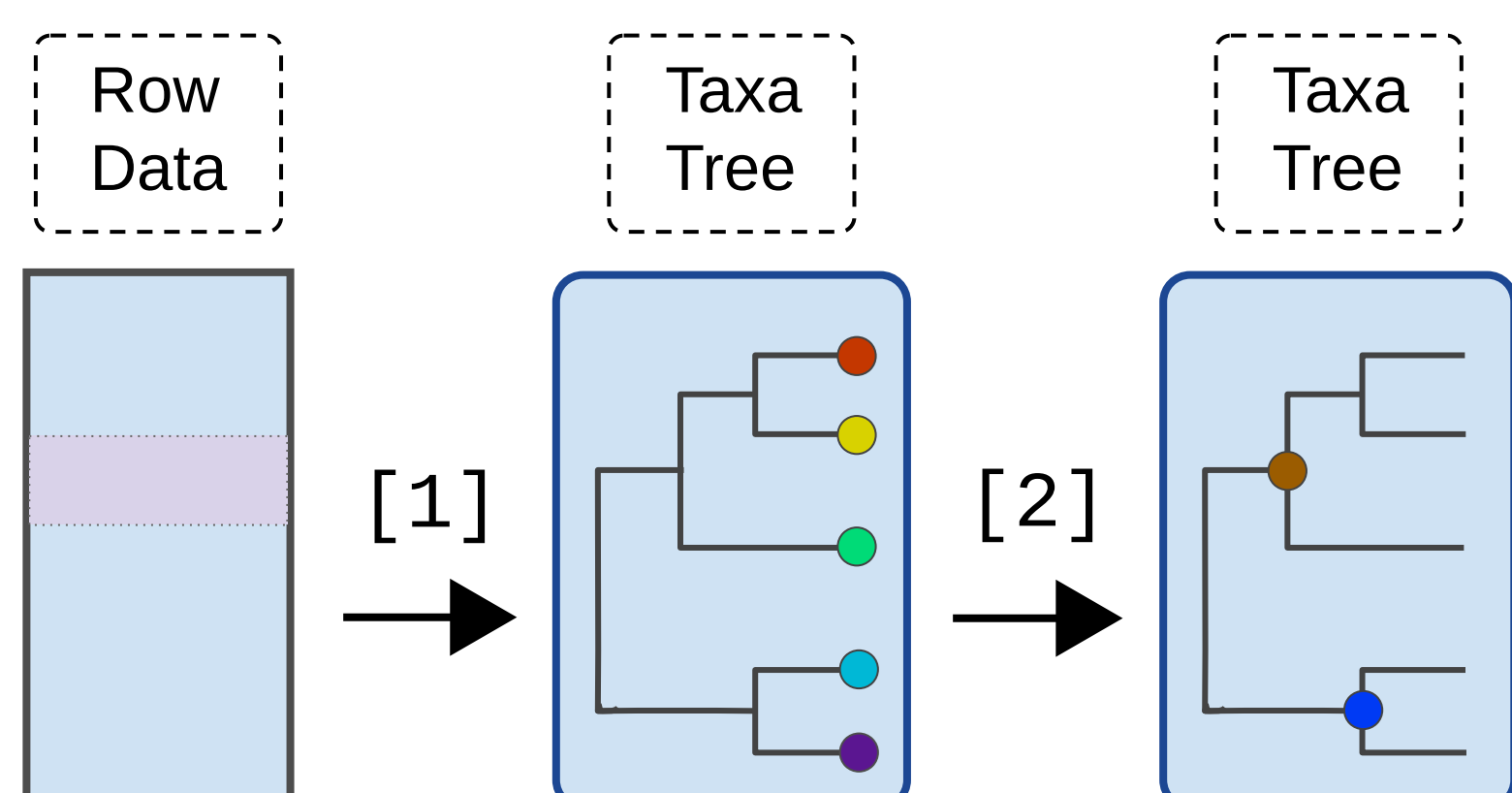
### Import Data

This workflow starts by importing bacterial abundance data into ***TreeSE* data container**.



## The *miaverse* pipeline

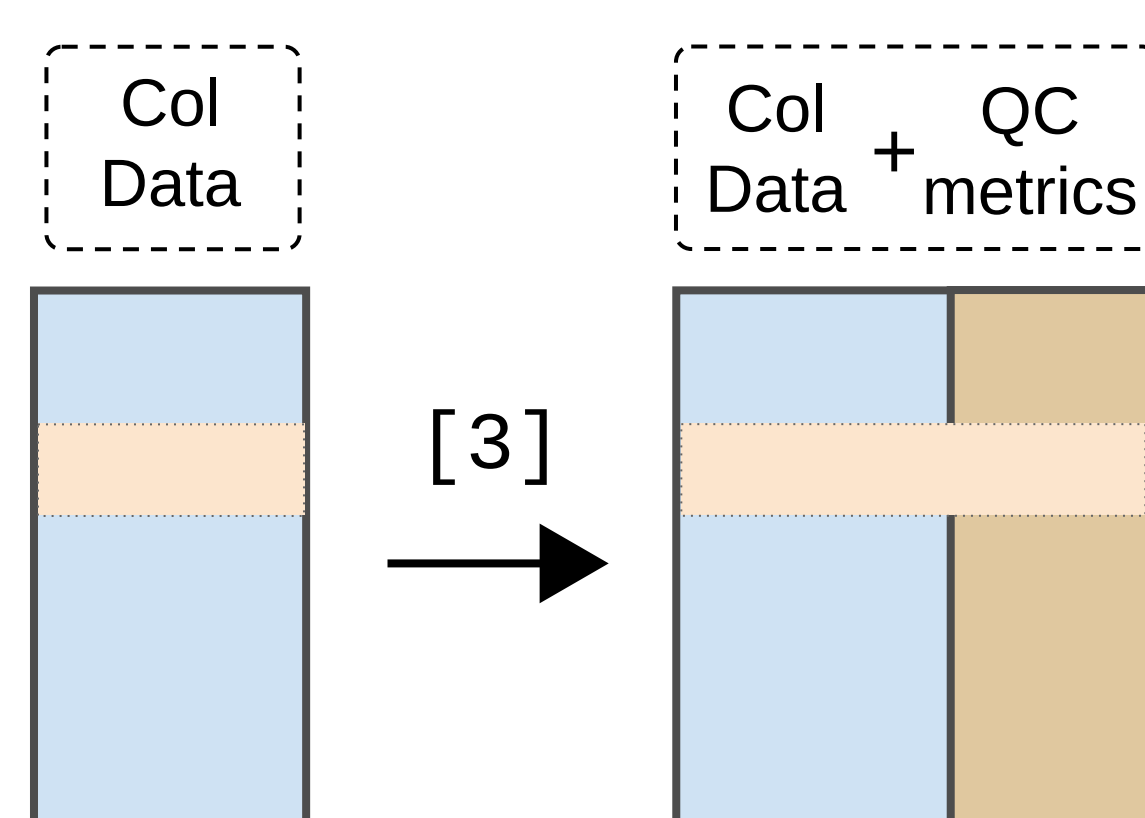
### Accessing Taxonomic Info



[1] `mia::addTaxonomyTree(tse)`

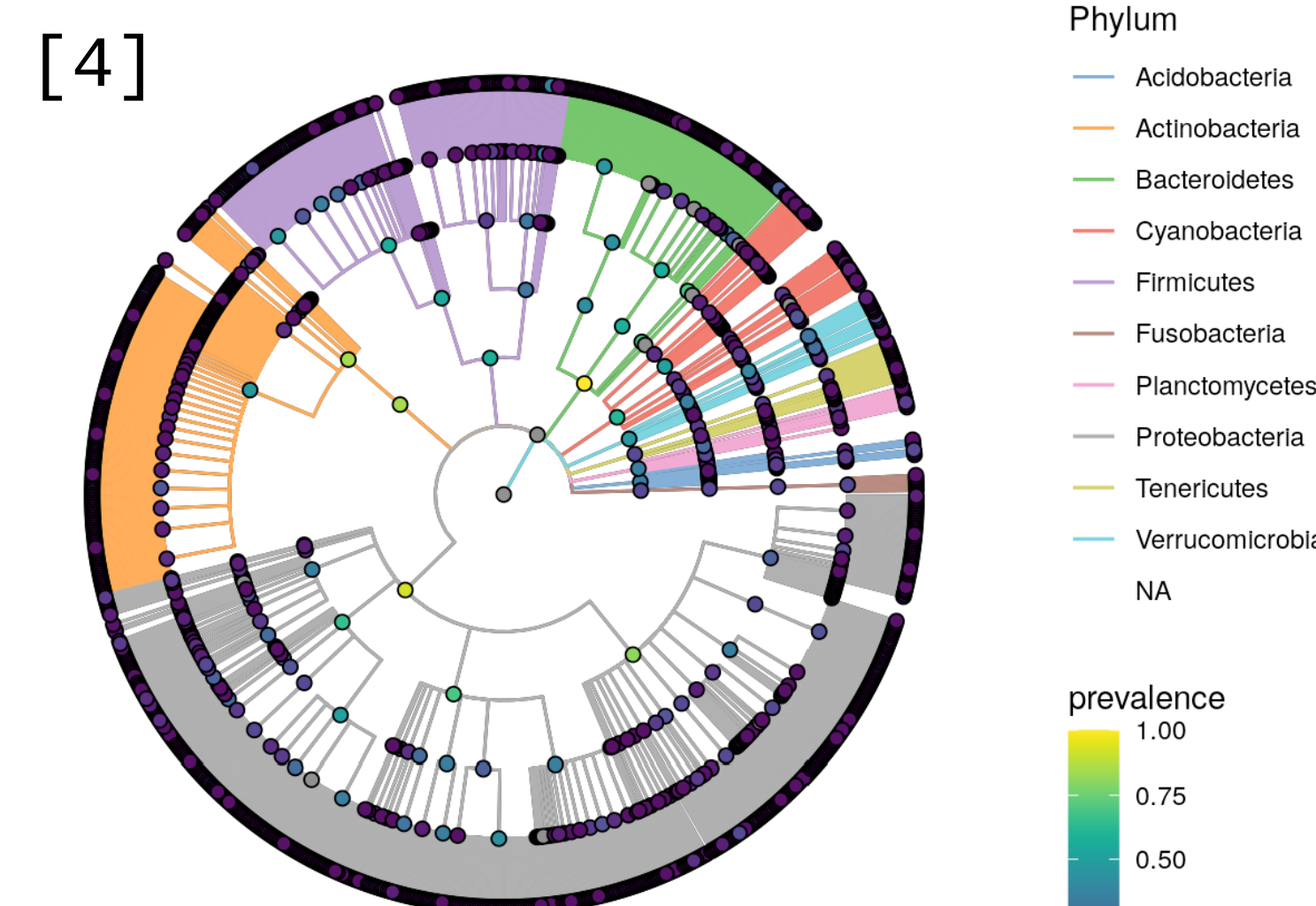
[2] `TreeSE::aggValue(tse)`

### Quality Control



[3] `scater::addPerCellQC(tse)`

### Visualizing with miaViz



[4] `miaViz::plotRowTree(tse)`