

MicrobiomeExperiment and the emerging R ecosystem for microbiome research

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MORE INFO @ EuroBioc2020:

Short Talk: Wednesday, 16:40 - 16:50 CET

Workshop: Friday, 17:05 - 18:05 CET

CONTRIBUTING AUTHORS:

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Check out the miaBook on GitHub:



MOTIVATION

- Existing microbiome workflows in Bioconductor are largely unsupported by the rich and versatile SummarizedExperiment (SE) family of classes.
- Recently contributed packages now provide tools for multiomic and time-series analyses which work alongside both new and old tools for metagenomic analyses.

PROPOSAL

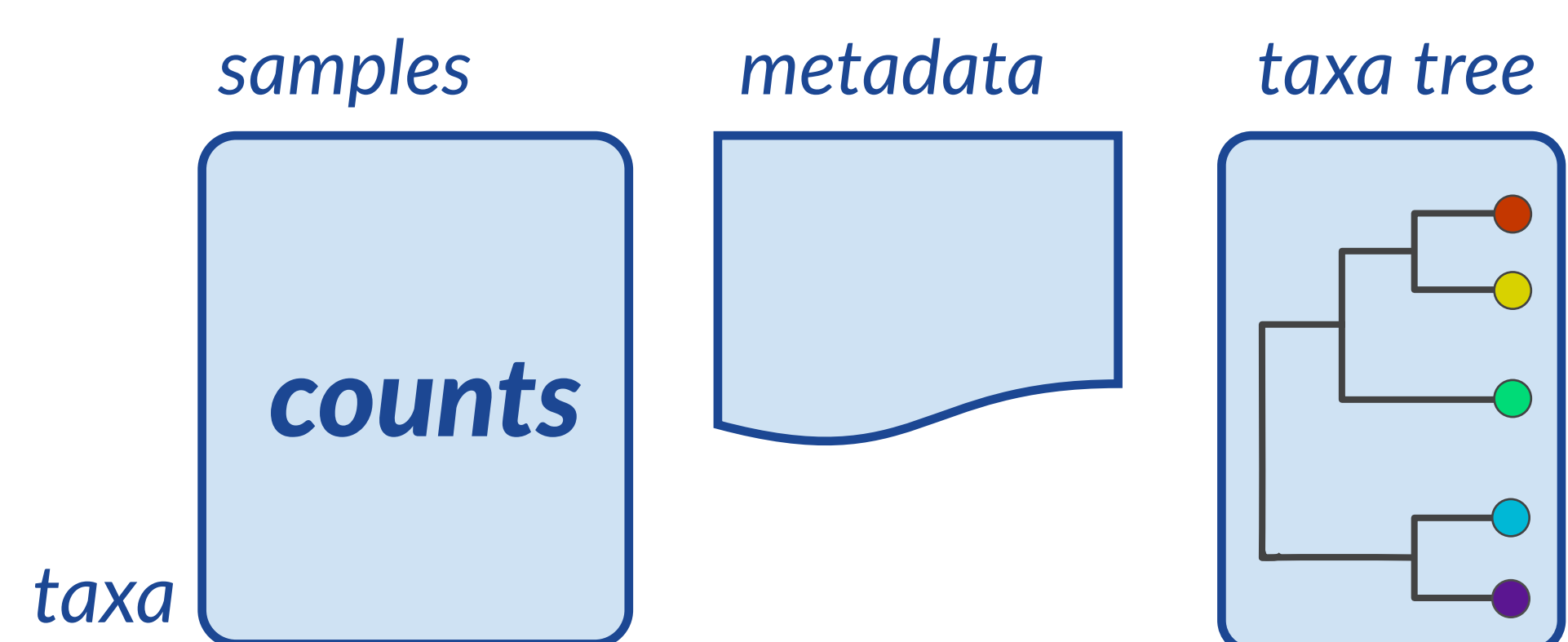
- We propose a pipeline using TreeSummarizedExperiment (TreeSE) and the Microbiome Analysis package (mia) for computational metagenomics with multi-omic data.
- We hope to reduce overlapping efforts, improve interoperability and ensure the long-term sustainability of microbiome research for the R and Bioconductor community.

PROPOSED WORKFLOW: TreeSE & mia

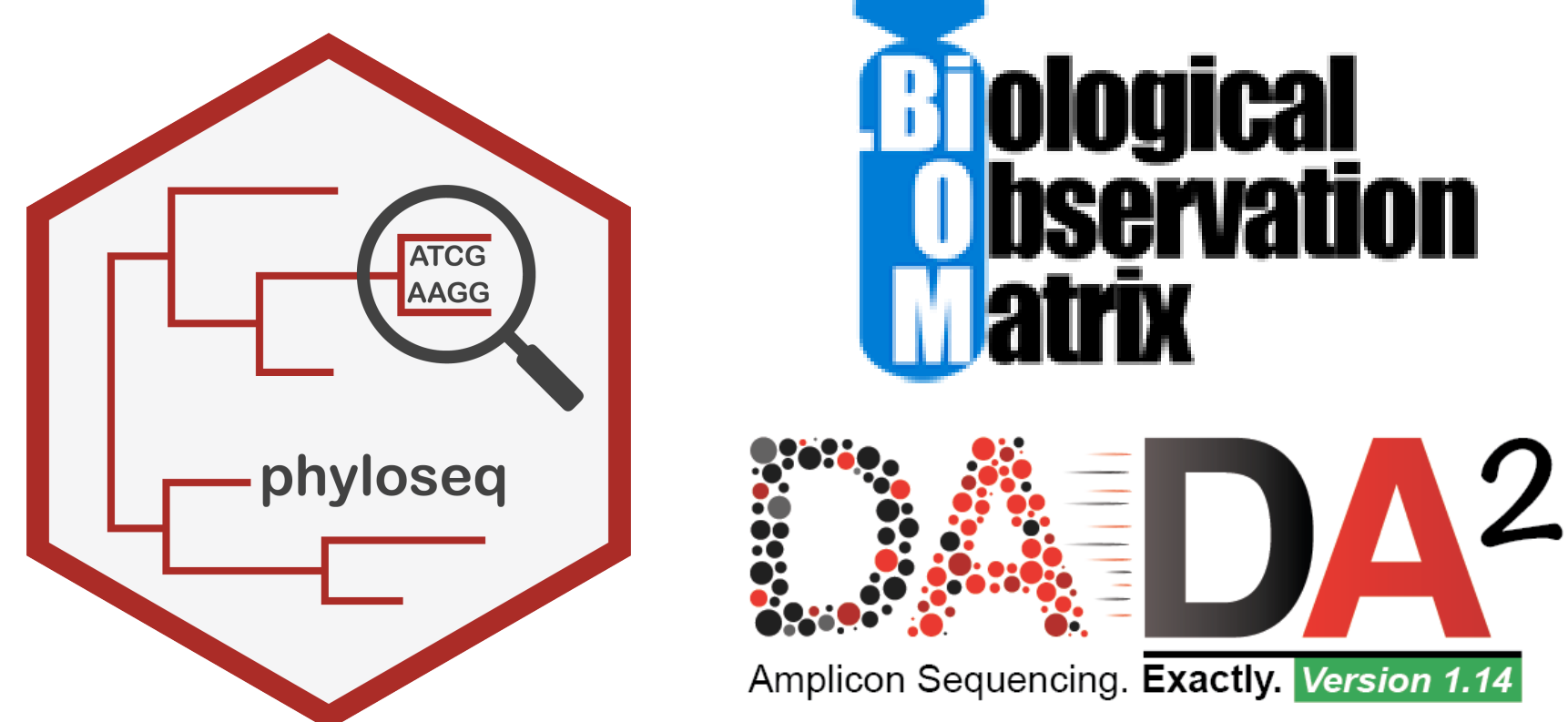
Import Data

This workflow starts with either raw data directly from relative abundance estimation or taxonomic classification OR pre-existing data objects from widely used tools.

RAW DATA

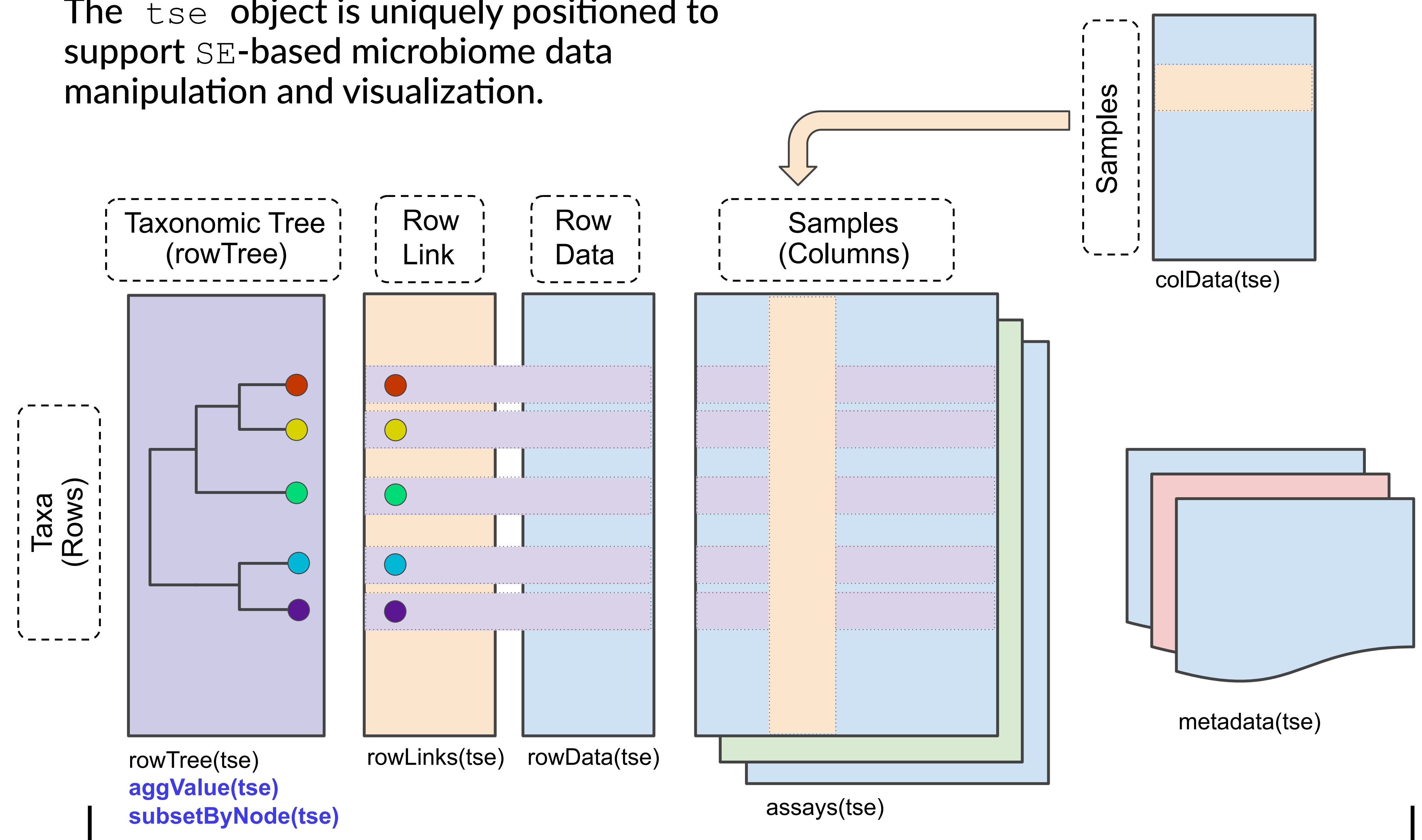


EXISTING DATA



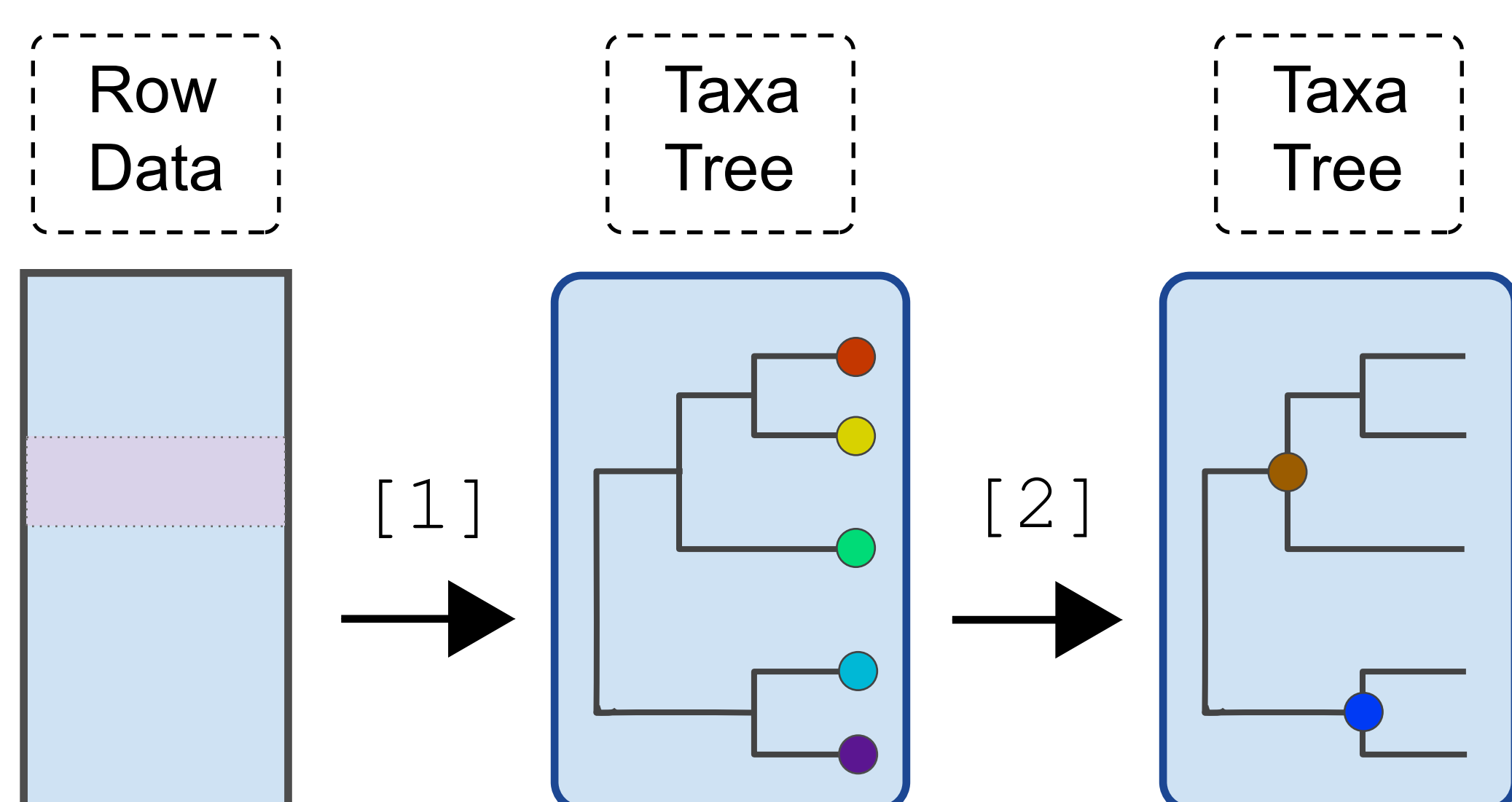
The TreeSE object

The tse object is uniquely positioned to support SE-based microbiome data manipulation and visualization.



The mia Pipeline

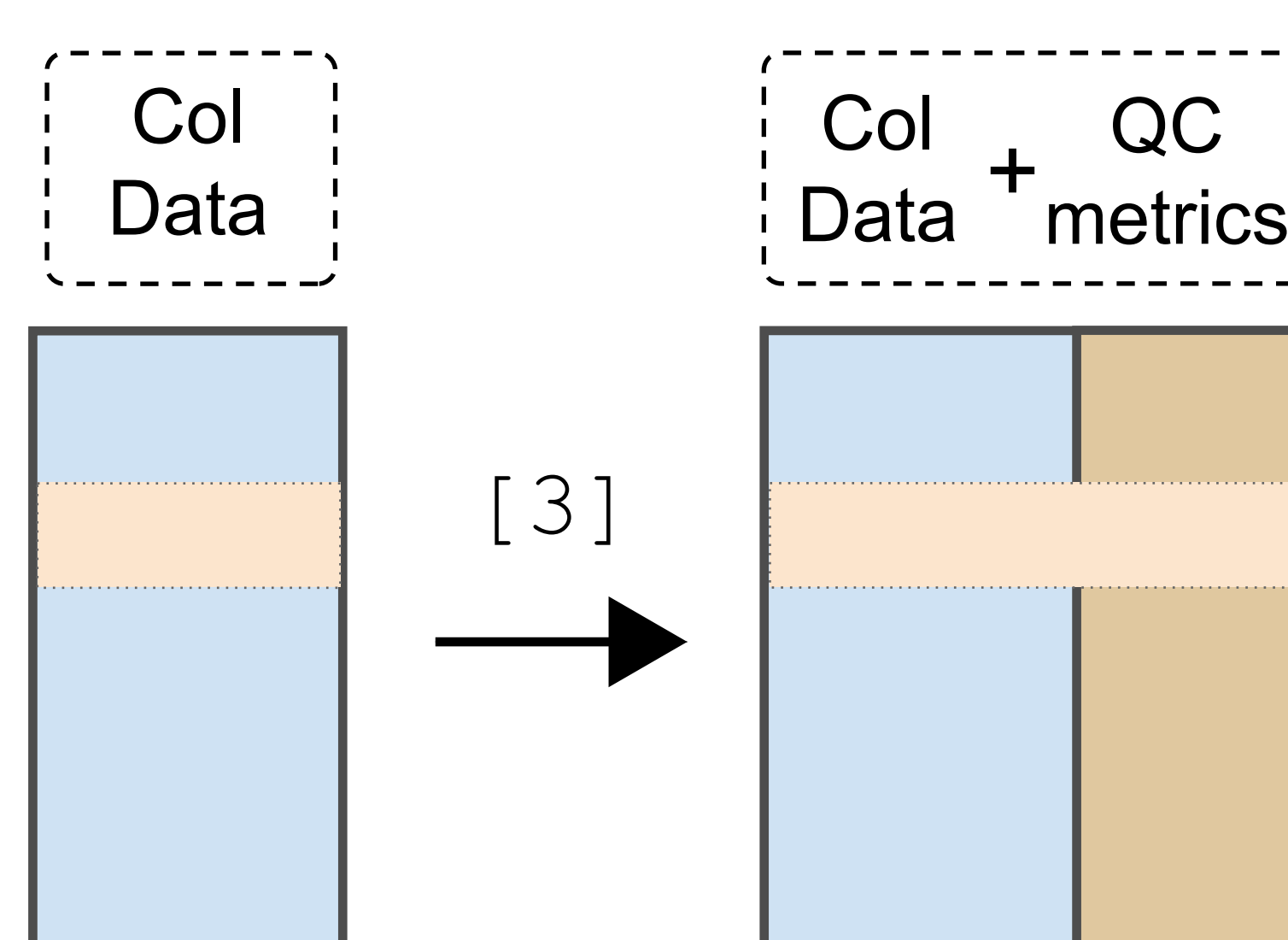
Accessing Taxonomic Info.



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

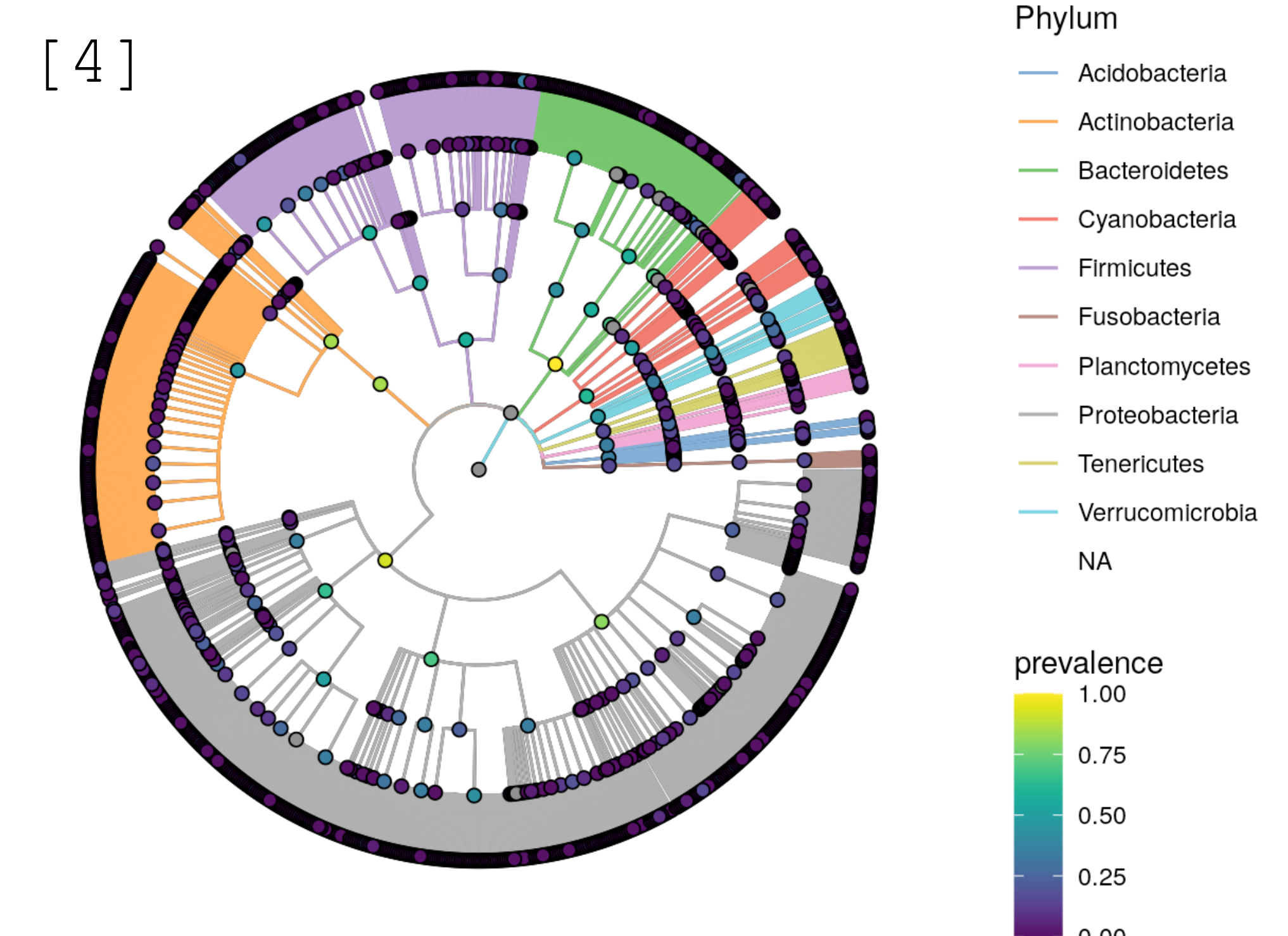
[2] `TreeSE::aggValue(tse)`

Quality Control



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

Visualizing with miaViz



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