miaverse

Microbiome analysis framework in SummarizedExperiment family

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MOTIVATION

CONTRIBUTORS:

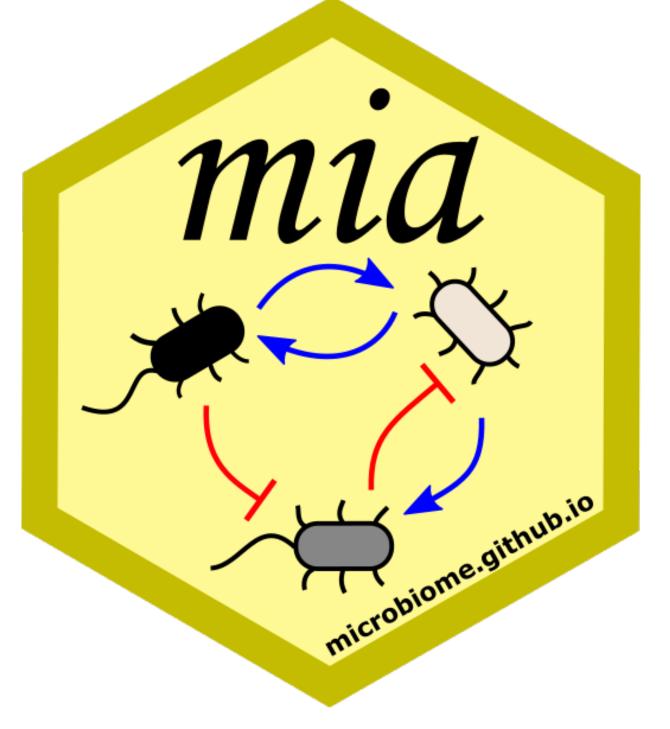
The miaverse collective. For the full list of contributors, see the project website.

MORE INFORMATION:

Go to project website. Join #miaverse BioC Slack channel.

Project website microbiome.github.io





Remember: Package demo @EuroBioC2023 Thursday 13:30 CEST

UNIVERSITY OF TURKU

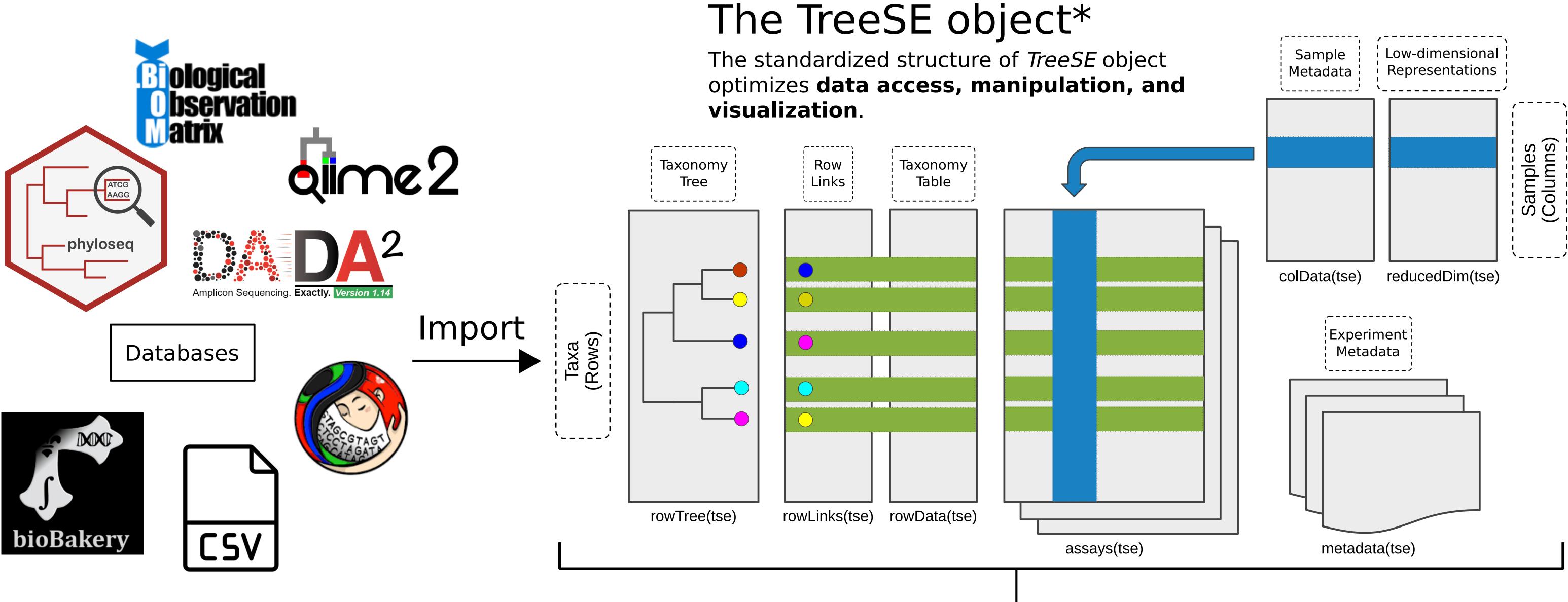
- Existing microbiome workflows in Bioconductor has been largely unsupported by the rich and versatile SummarizedExperiment (SE) family of classes.
- Shared data container can reduce overlapping efforts, improve interoperability and ensure longterm sustainability.
- As sample size get bigger and multiomics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

METHODS

- Emerging analysis framework called miaverse (MIcrobiome Analysis uniVERSE) utilizes a common, standardized data container, TreeSummarizedExperiment.
- miaverse contains methods for data analysis and visualization together with the comprehensive online tutorial book.
- The miaverse is a collaborative open-source project, and stable version is available via R/Bioconductor.

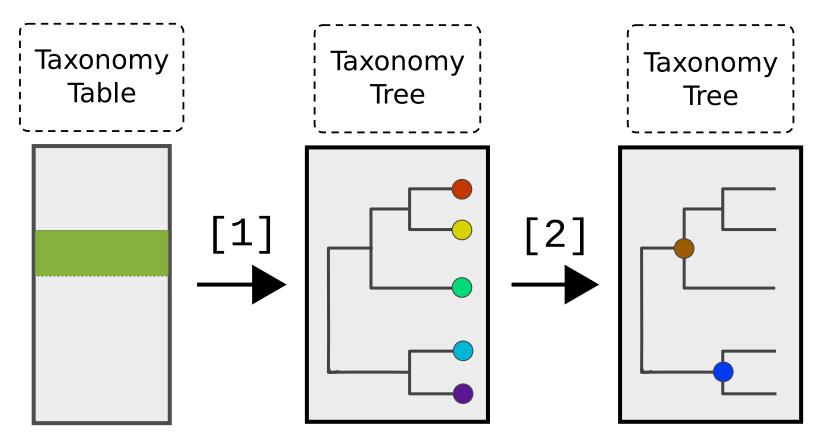
riment: a S4 class for data with hierarchical structure

WORKFLOW: TreeSummarizedExperiment (TreeSE) & miaverse



The miaverse pipeline

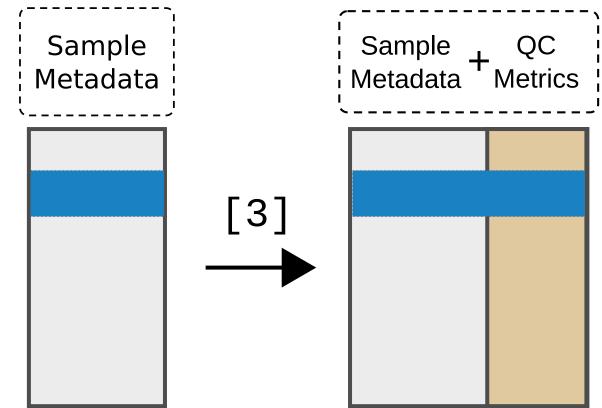
Data Wrangling



mia::addTaxonomyTree(tse)

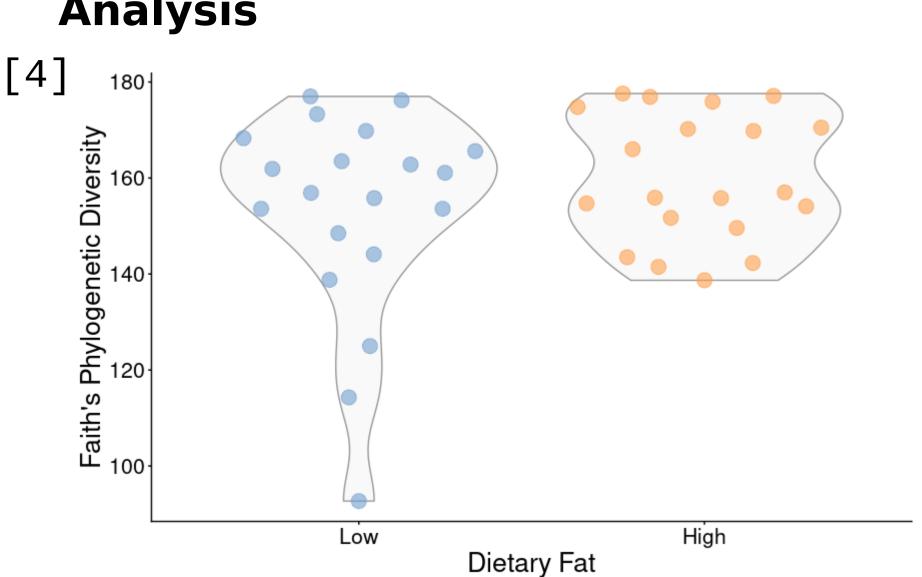
[2] TreeSE::aggValue(tse)

Quality Control



scater::addPerCellQC(tse)

Analysis



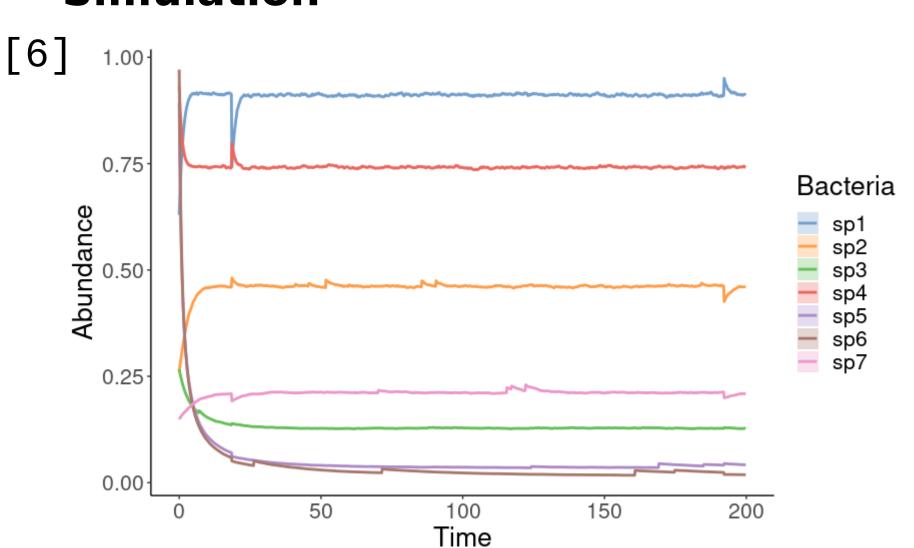
[4] mia::estimateDiversity(tse)

[4] scater::plotColData(tse)

Check Orchestrating Microbiome Analysis (OMA) tutorial book for more examples and information.

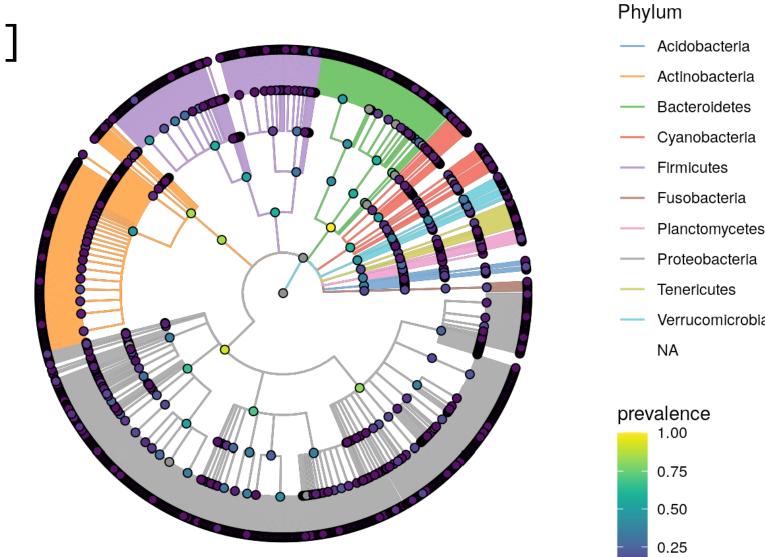


Simulation



miaSim::simulateGLV(x) miaViz::plotSeries(tse)

Visualization [7]



[7] miaViz::plotRowTree(tse)