

Orchestrating Microbiome Analysis with Bioconductor

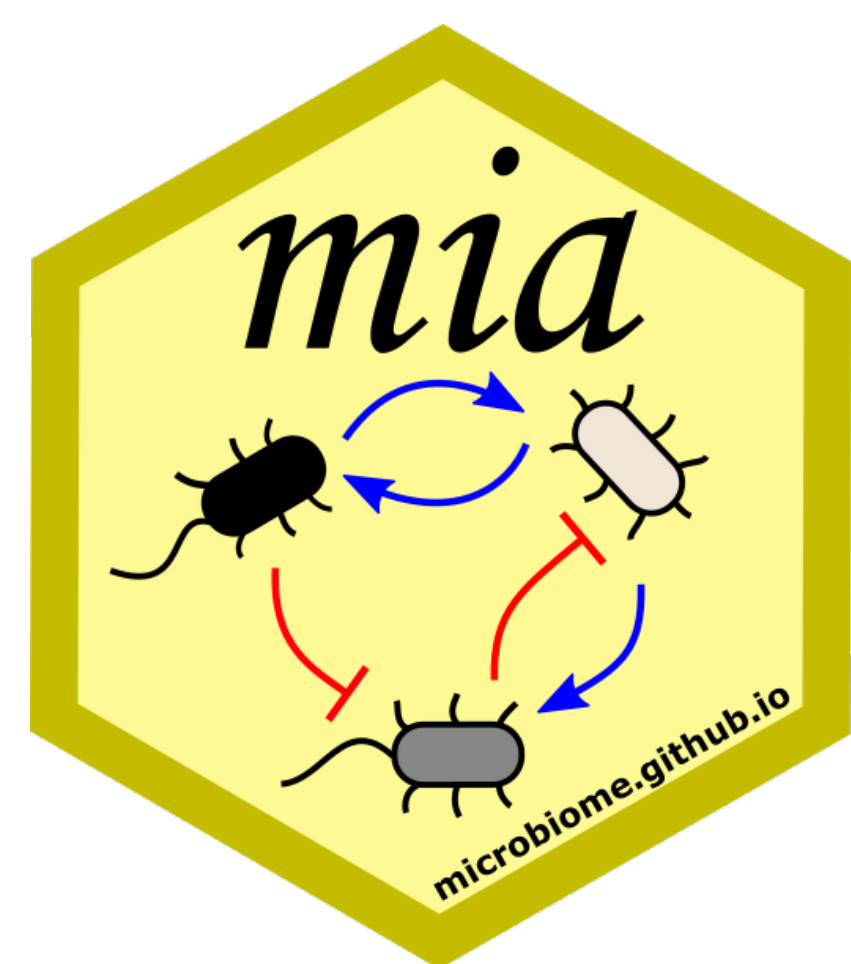
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For full list of contributors, see
OMA (QR code below).

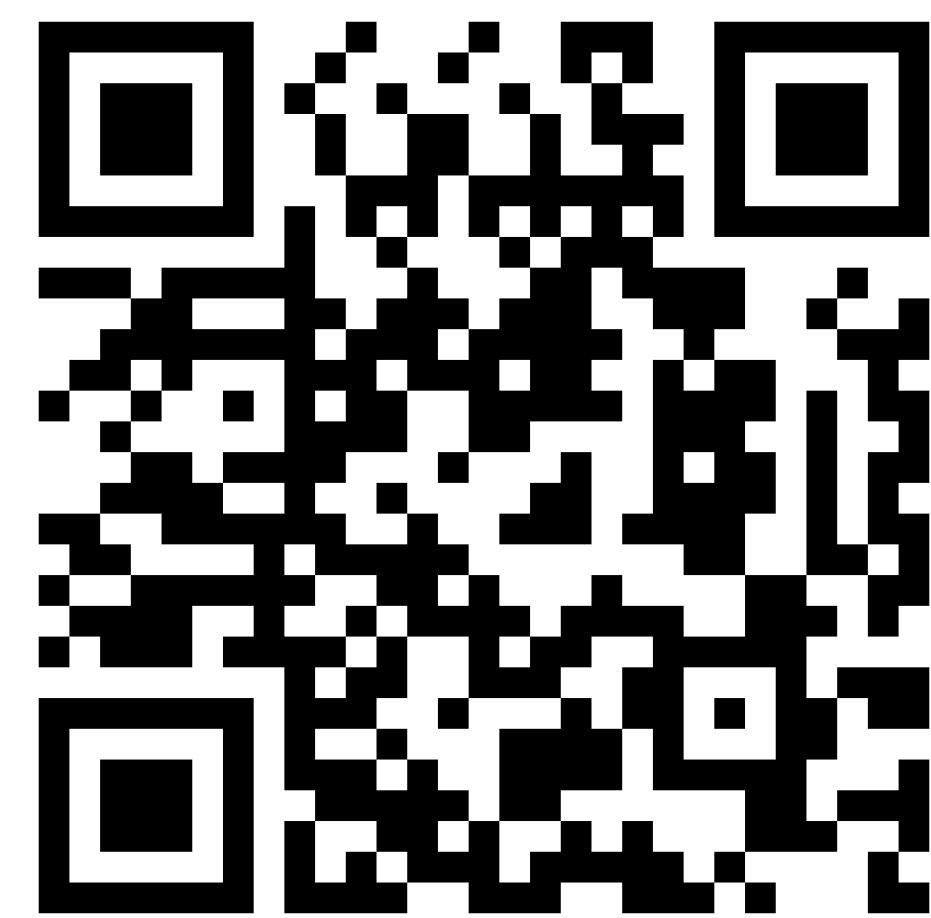


Challenge: The SummarizedExperiment (SE) framework is widely used in Bioconductor and offers significant advantages across various fields. However, microbiome data science has relied on alternative approaches, limiting its integration with these advanced tools.

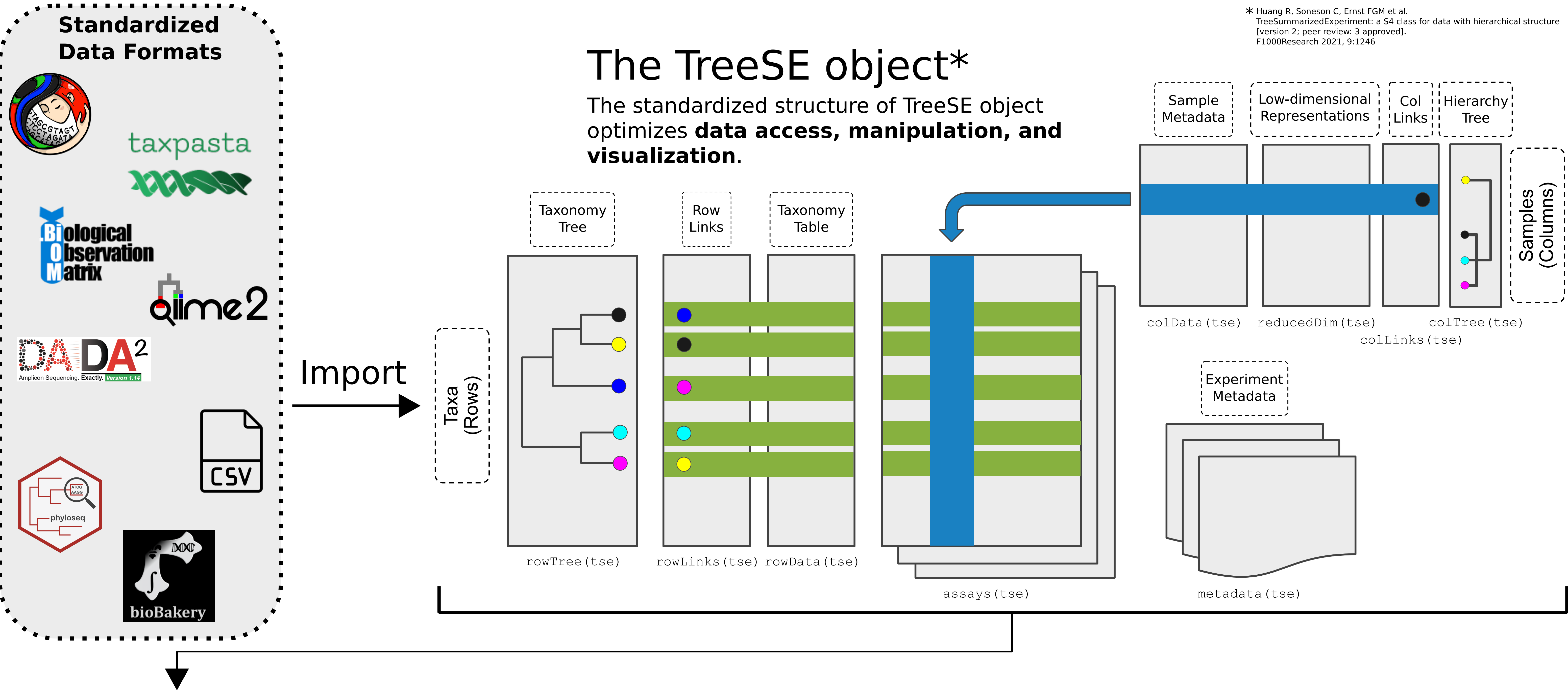
Solution: miaverse (Microbiome Analysis uniVERSE) introduces the TreeSummarizedExperiment (TreeSE), an extension of SE tailored for microbiome data. This collaborative, open-source project offers both tools and an extensive online book to advance and support microbiome data science.

Benefits: By aligning microbiome data science with the established SE framework, miaverse enhances interoperability, reduces duplication, and supports sustainable development in the field.

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

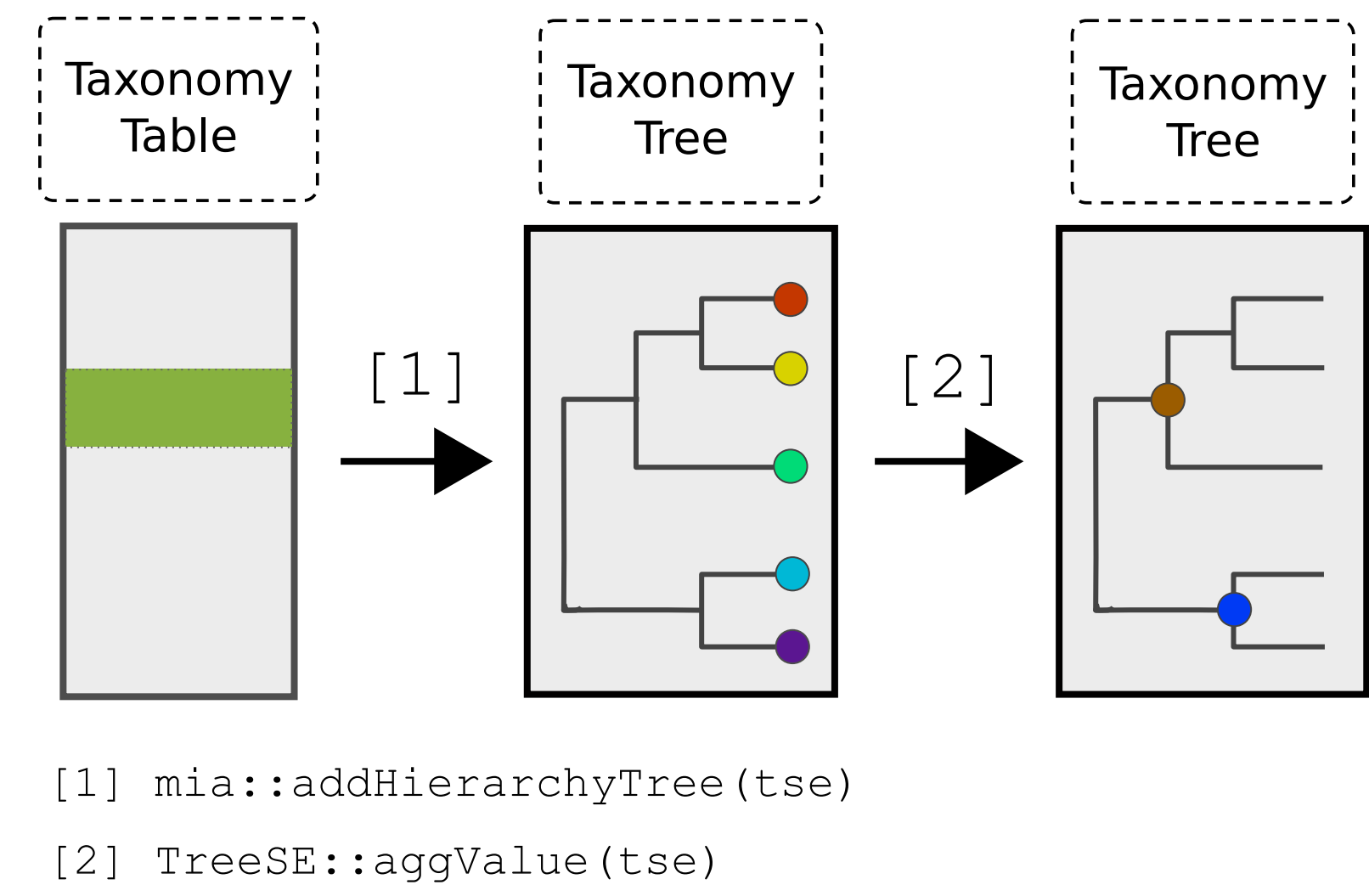


WORKFLOW: TreeSE & miaverse

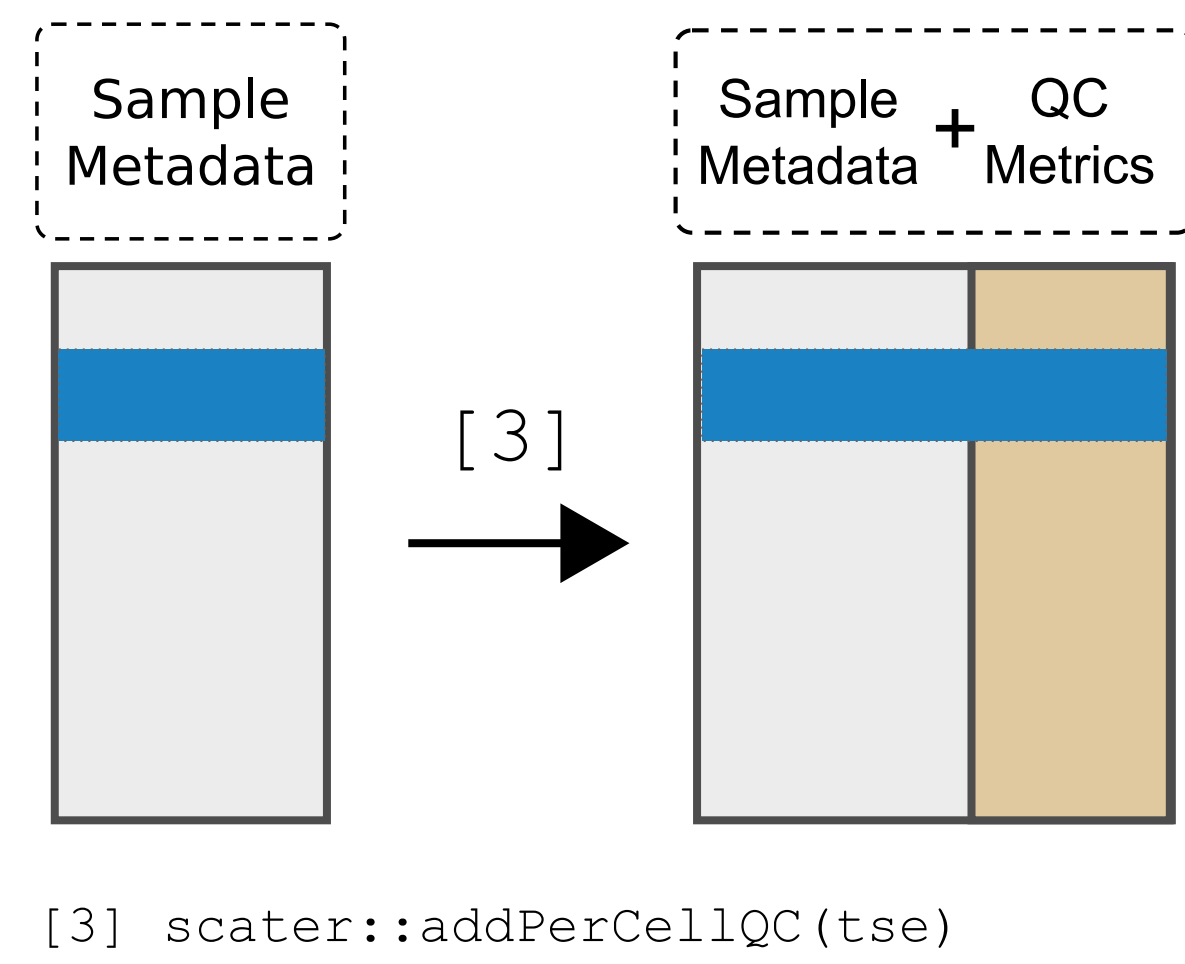


Microbiome data science workflow

Data Wrangling



Quality Control

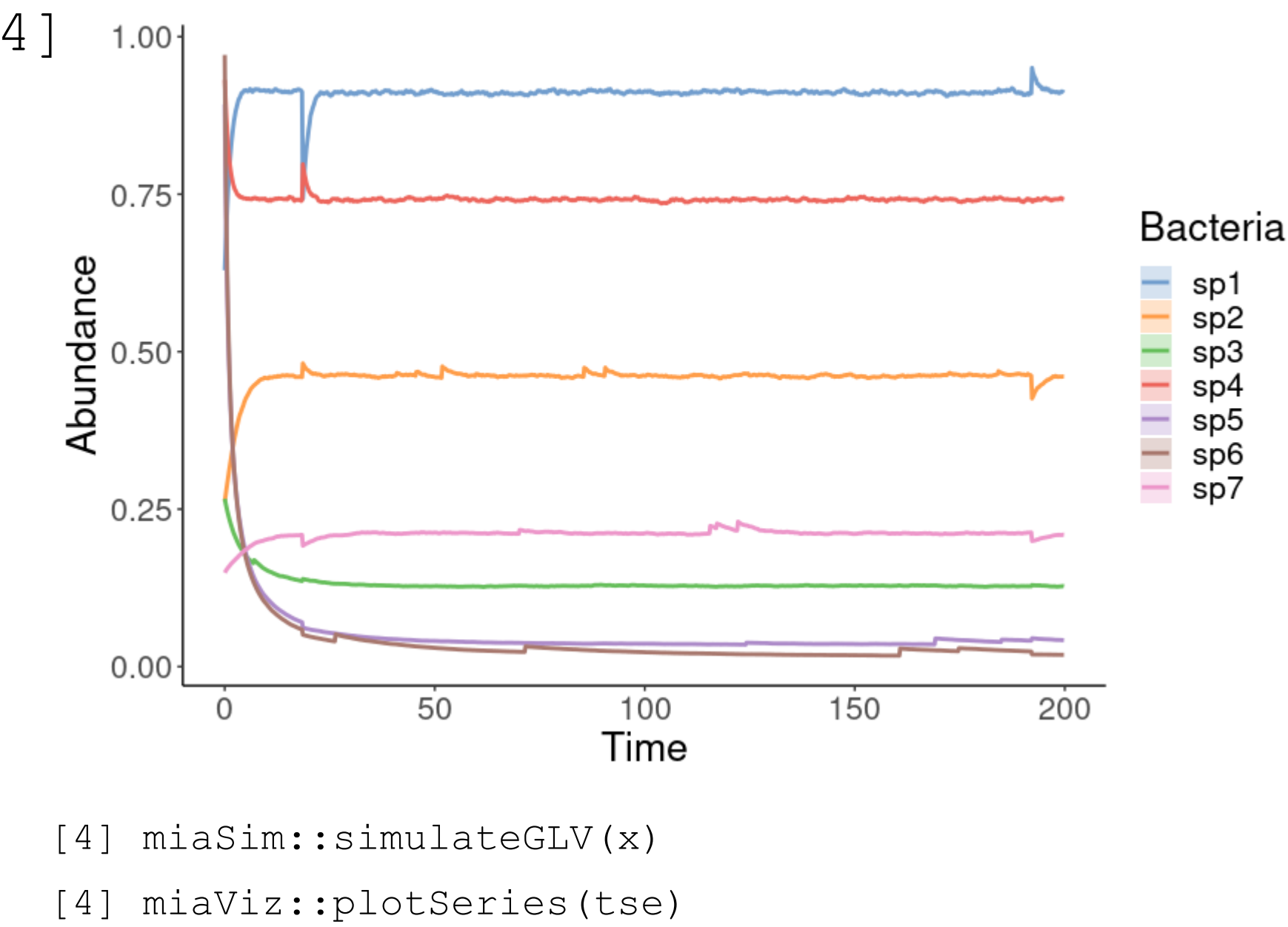


Analysis

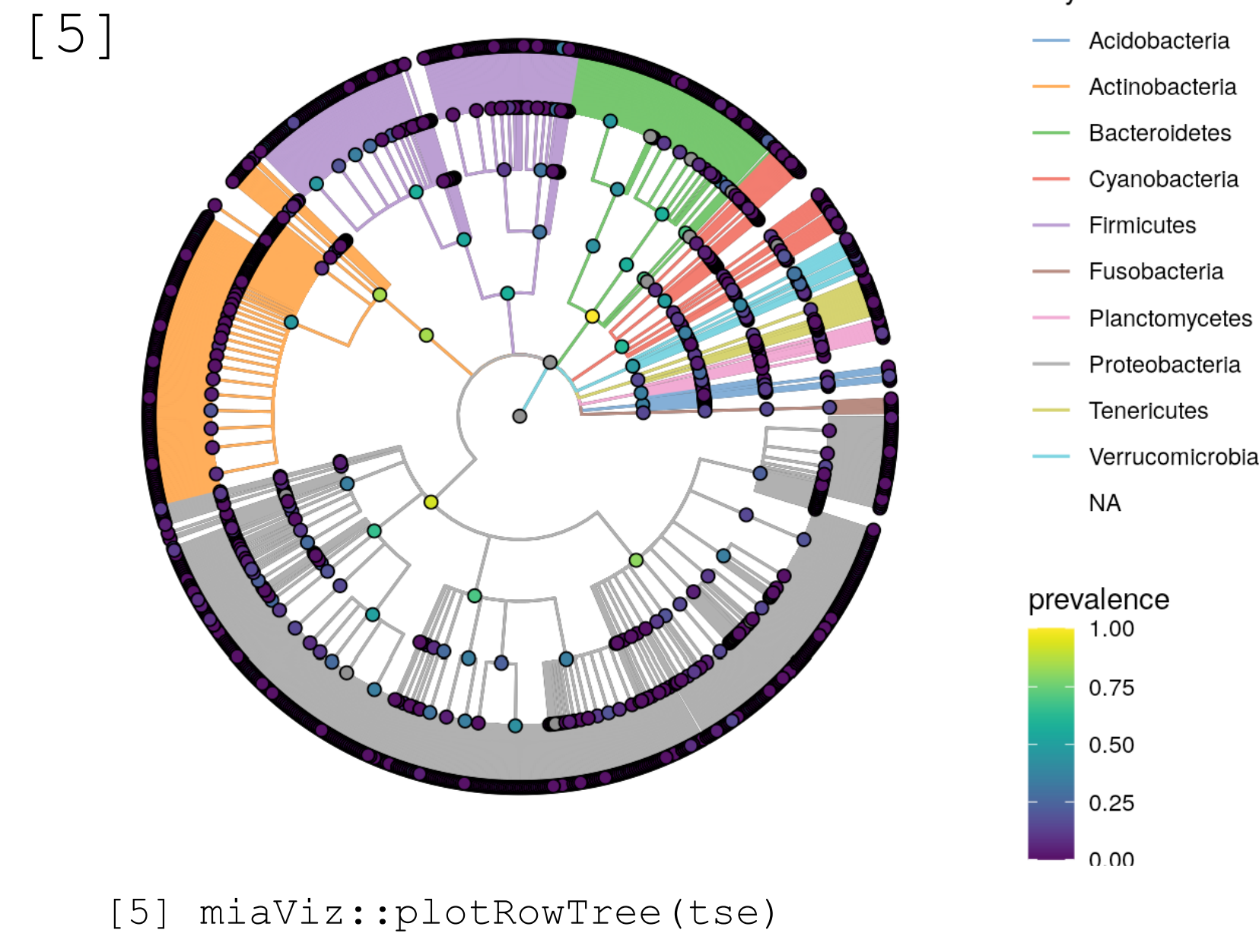
Wide range of methods, including:

- Agglomeration
- Transformation
- Alpha and beta diversity
- Clustering and ordination
- Differential abundance
- Networks and machine learning
- ...

Simulation



Visualization



Expanding ecosystem

The package ecosystem is supported by many independent developers. You can contribute to this community by including support for SE in your R package.

