

Orchestrating Microbiome Analysis with Bioconductor

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



OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

Challenge: In microbiome data science, there is a growing need for robust, standardized, and scalable methods that support multi-table data and are interoperable with other applications.

Solution: We have developed methods built around the *TreeSummarizedExperiment* class to address these needs. This framework improves support for multi-table microbiome data and integrates seamlessly with the Bioconductor ecosystem. To promote best practices and reproducibility, we provide comprehensive documentation and practical examples in an open-access online book. Thanks to contributions from a global community, the ecosystem continues to expand.



THE PREPRINT SERVER FOR BIOLOGY

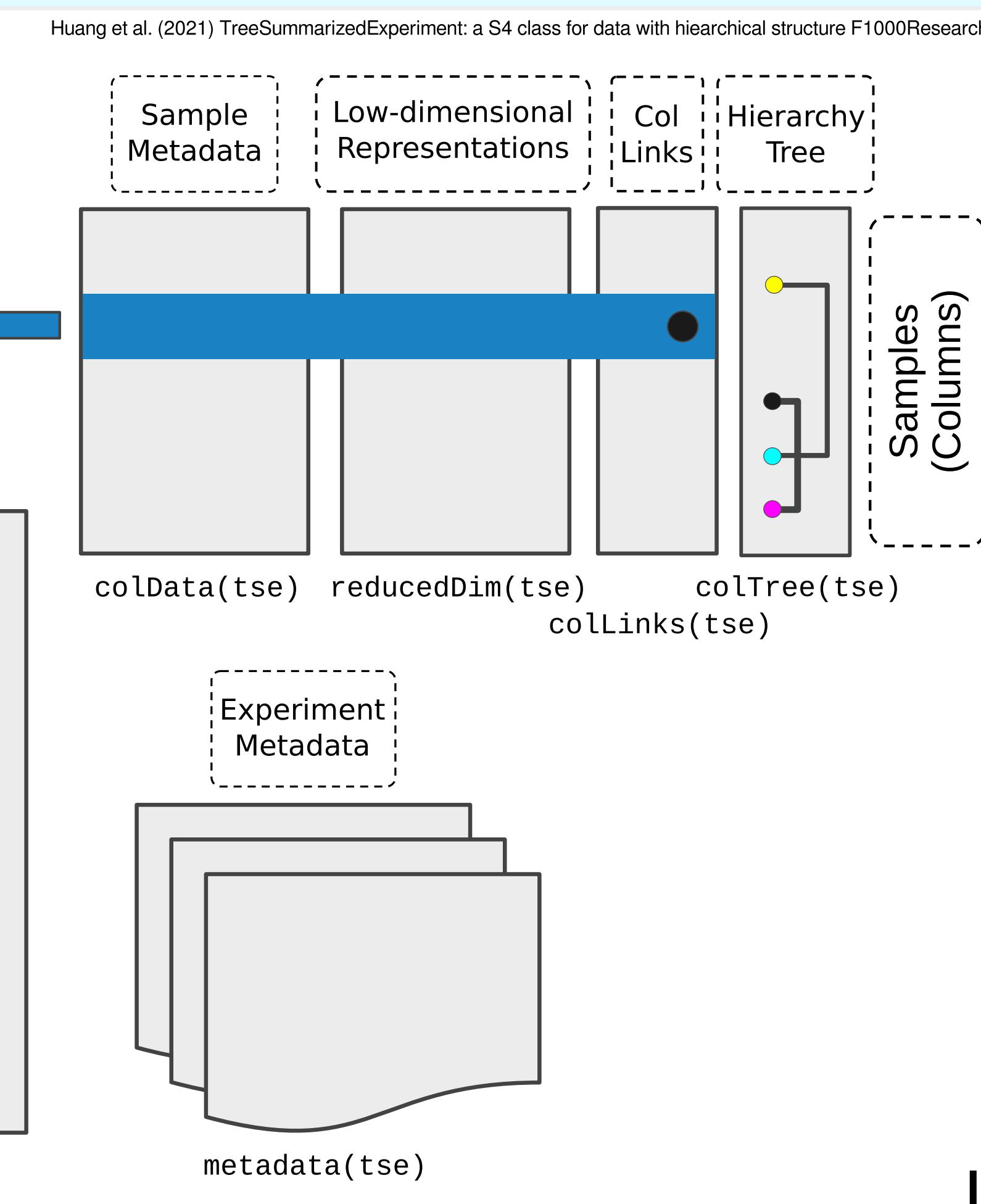
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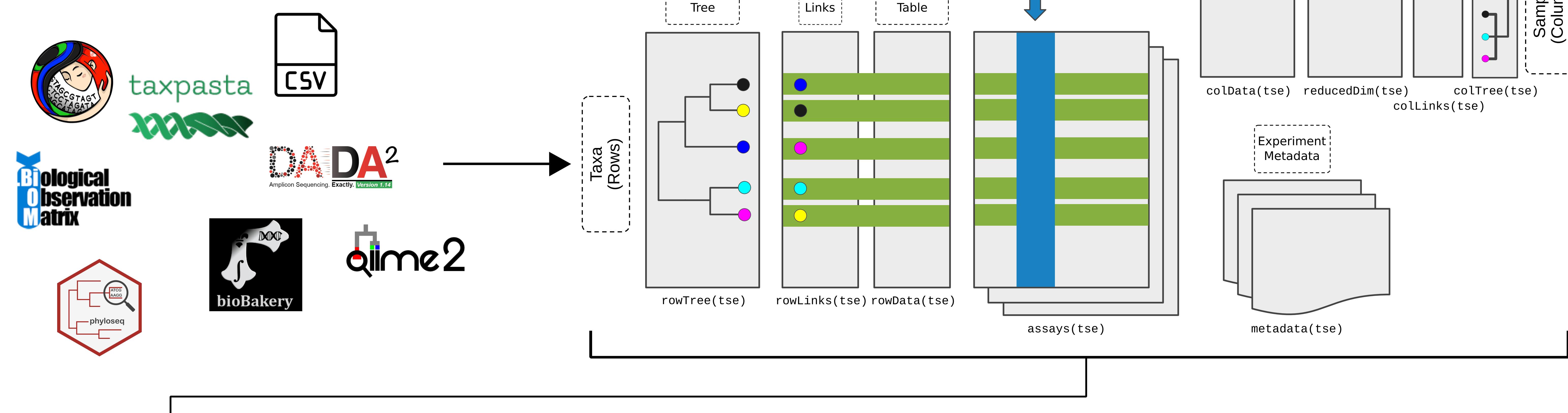
Tuomas Borman, Giulio Benedetti, Geraldson Muluh, Aura Raivo, Benjamin Valderrama, Artur Sannikov, Stefanie Peschel, Yihan Liu, Rasmus Hindström, OMA consortium, Katarina Pärnänen, Christian L. Müller, Aki S. Havulma, Sudarshan Shetty, Marcel Ramos, Domenik J. Bracca, Héctor Corradi Bravo, Felix M. Ernst, Levi Waldron, Thomas F. S. Bastiaansen, Himesh Mallick, Leo Lahti

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Data infrastructure

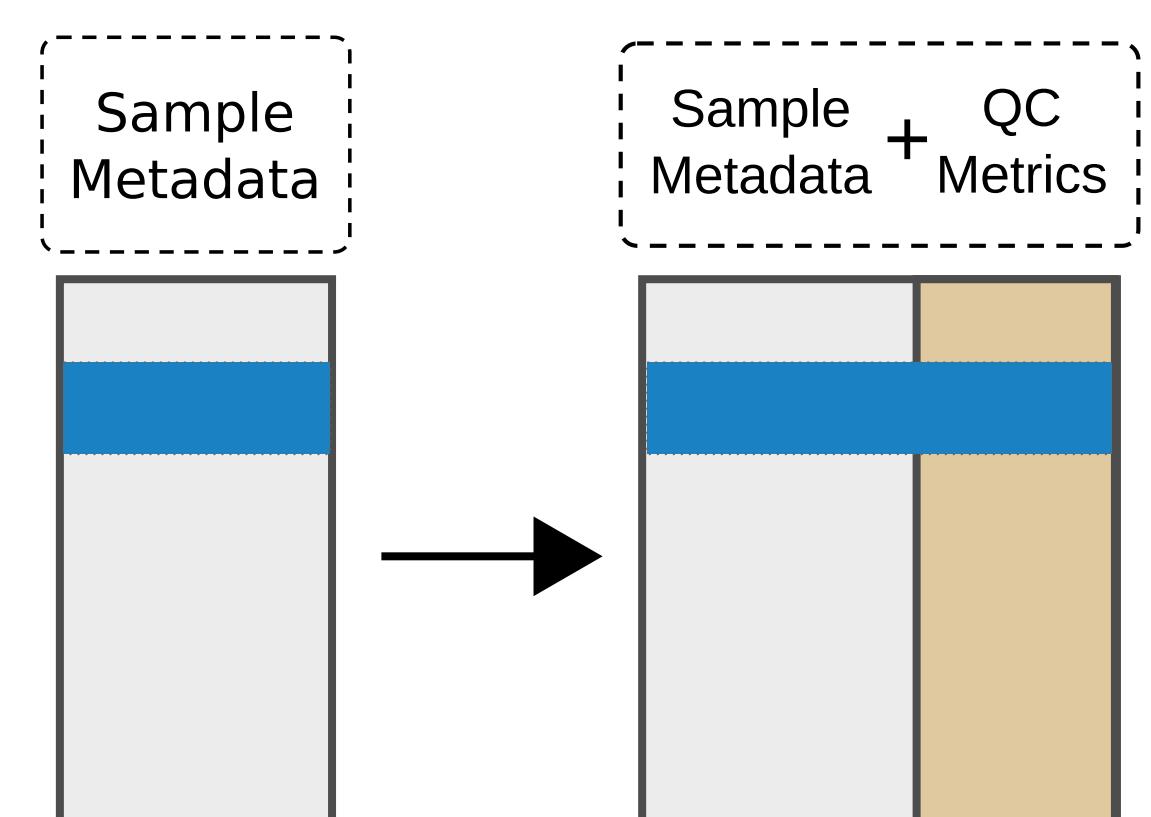
Data can be imported in standard formats using importer functions. In addition, data from multiple public databases — totaling over half a million samples — can be retrieved directly into a *TreeSummarizedExperiment* object.



Downstream analysis

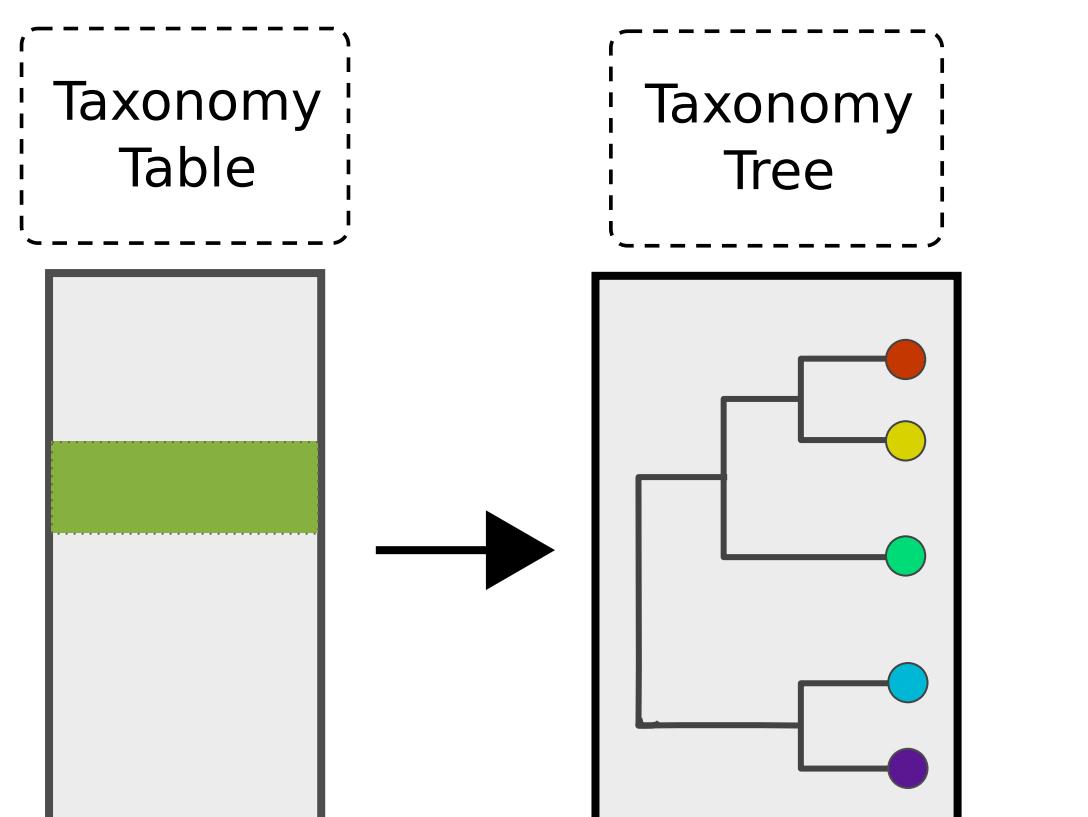
The ecosystem includes a full suite of tools distributed through the *mia* package family.

Quality control



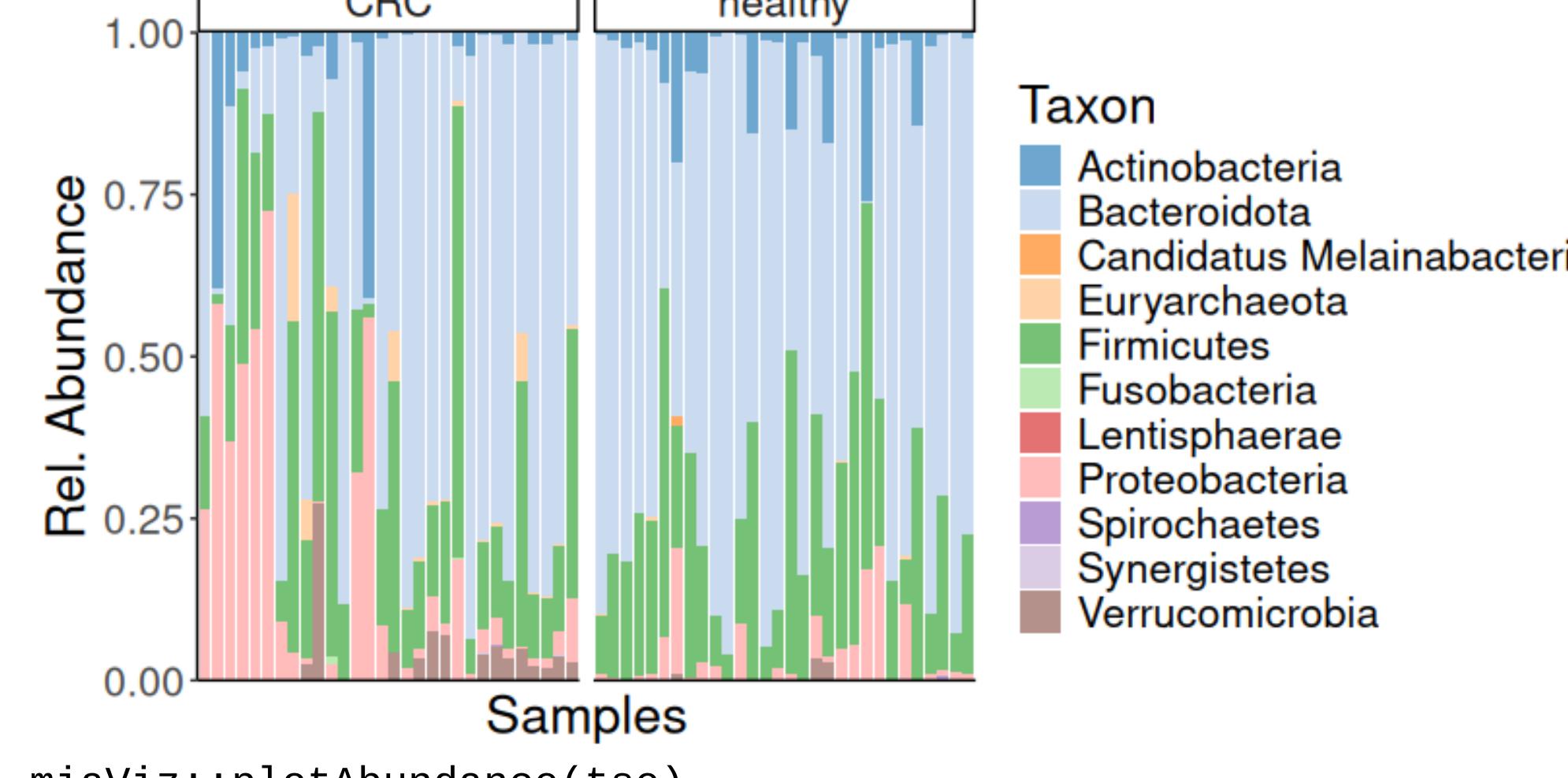
```
tse <- scater::addPerCellQC(tse)
```

Data processing

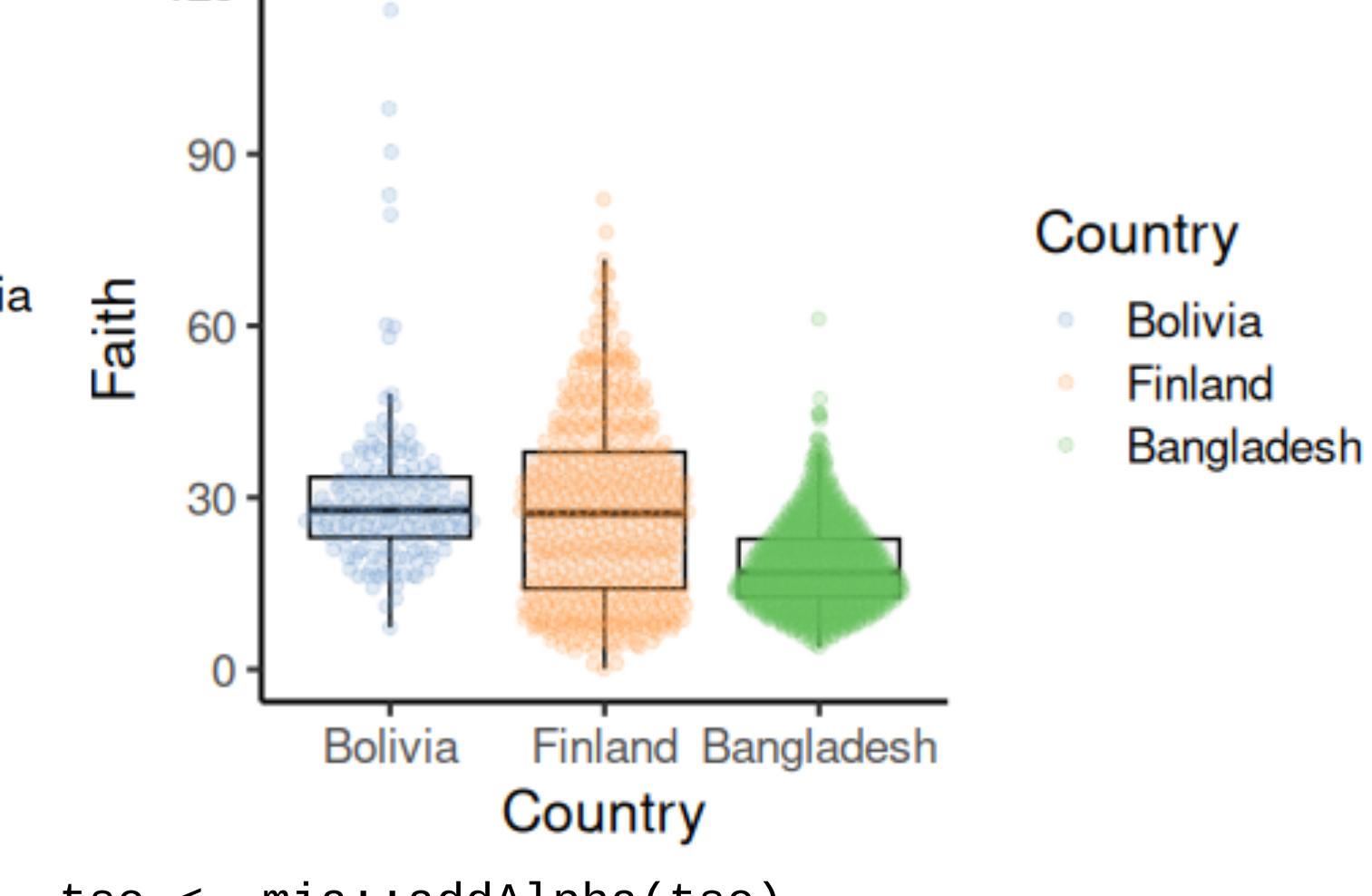


```
tse <- mia::addHierarchyTree(tse)
```

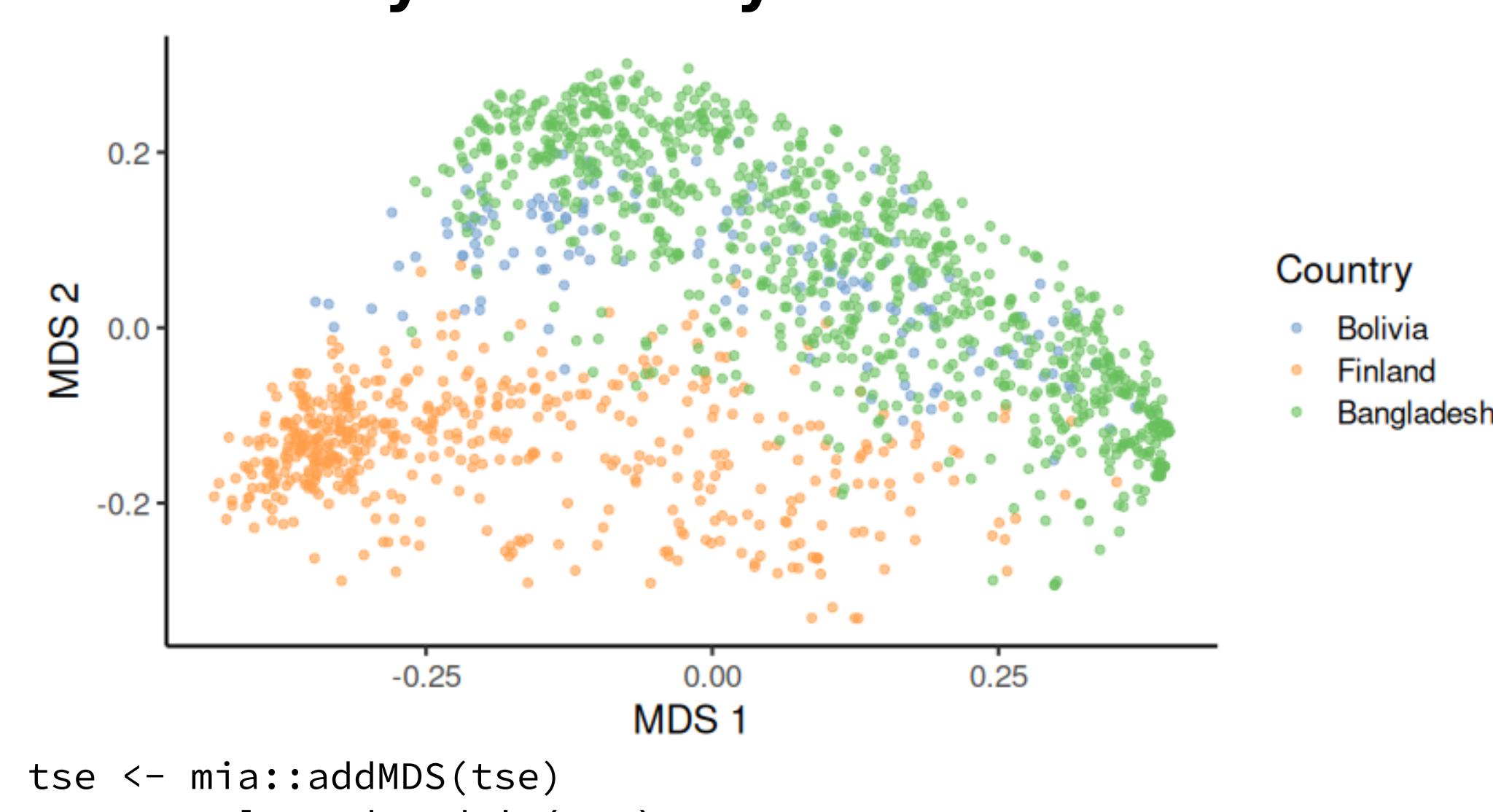
Visualization



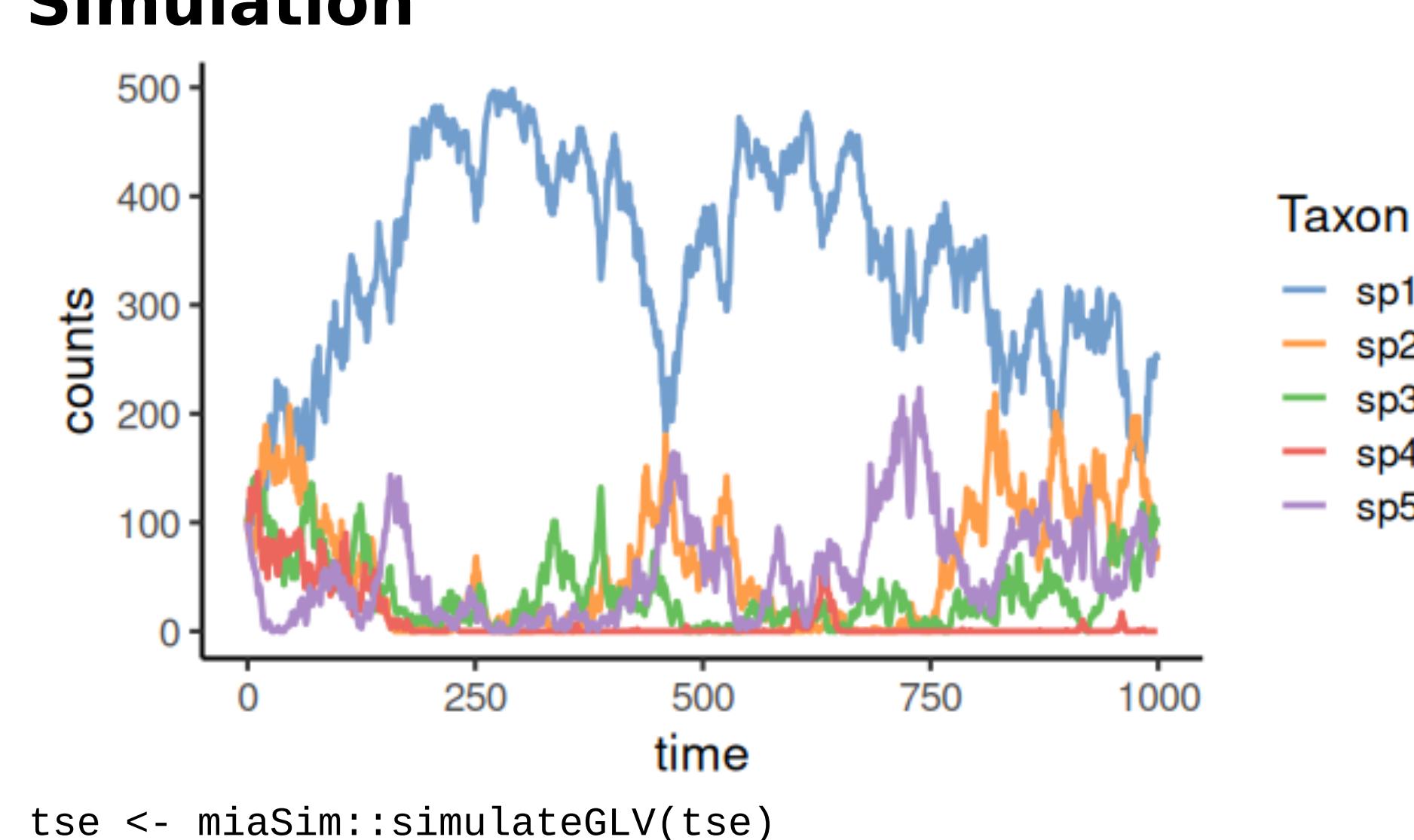
Community indicators



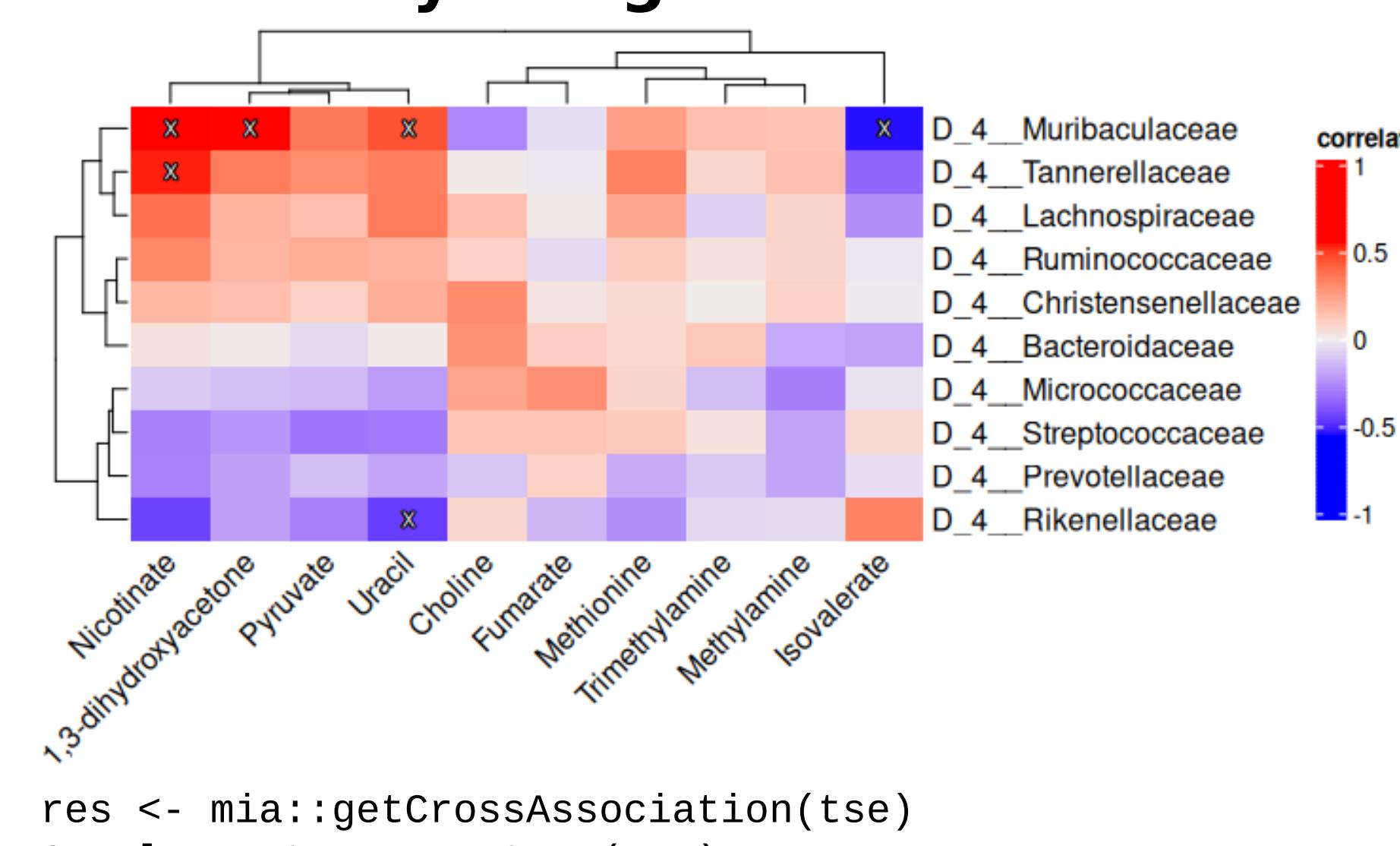
Community similarity



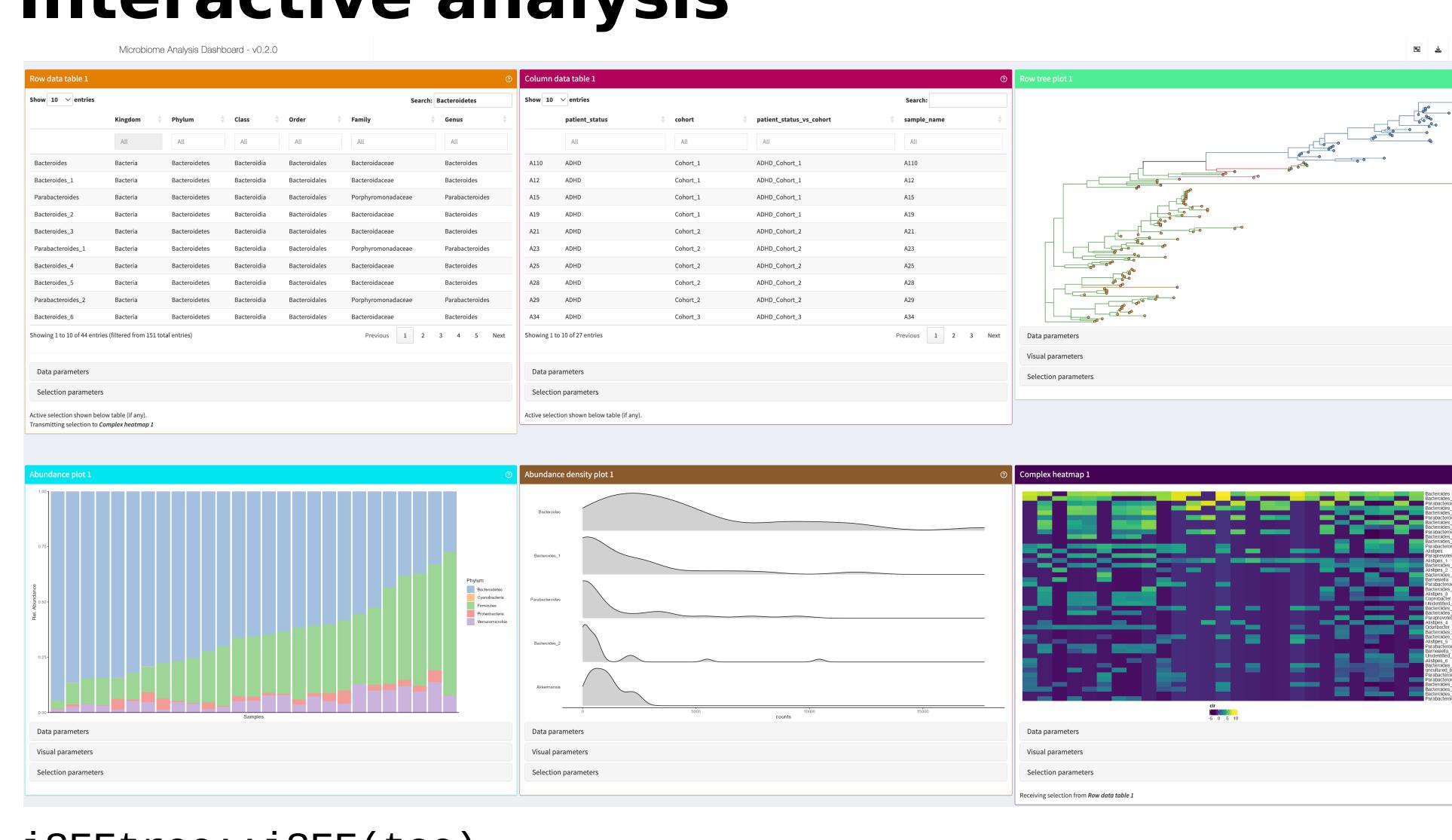
Simulation



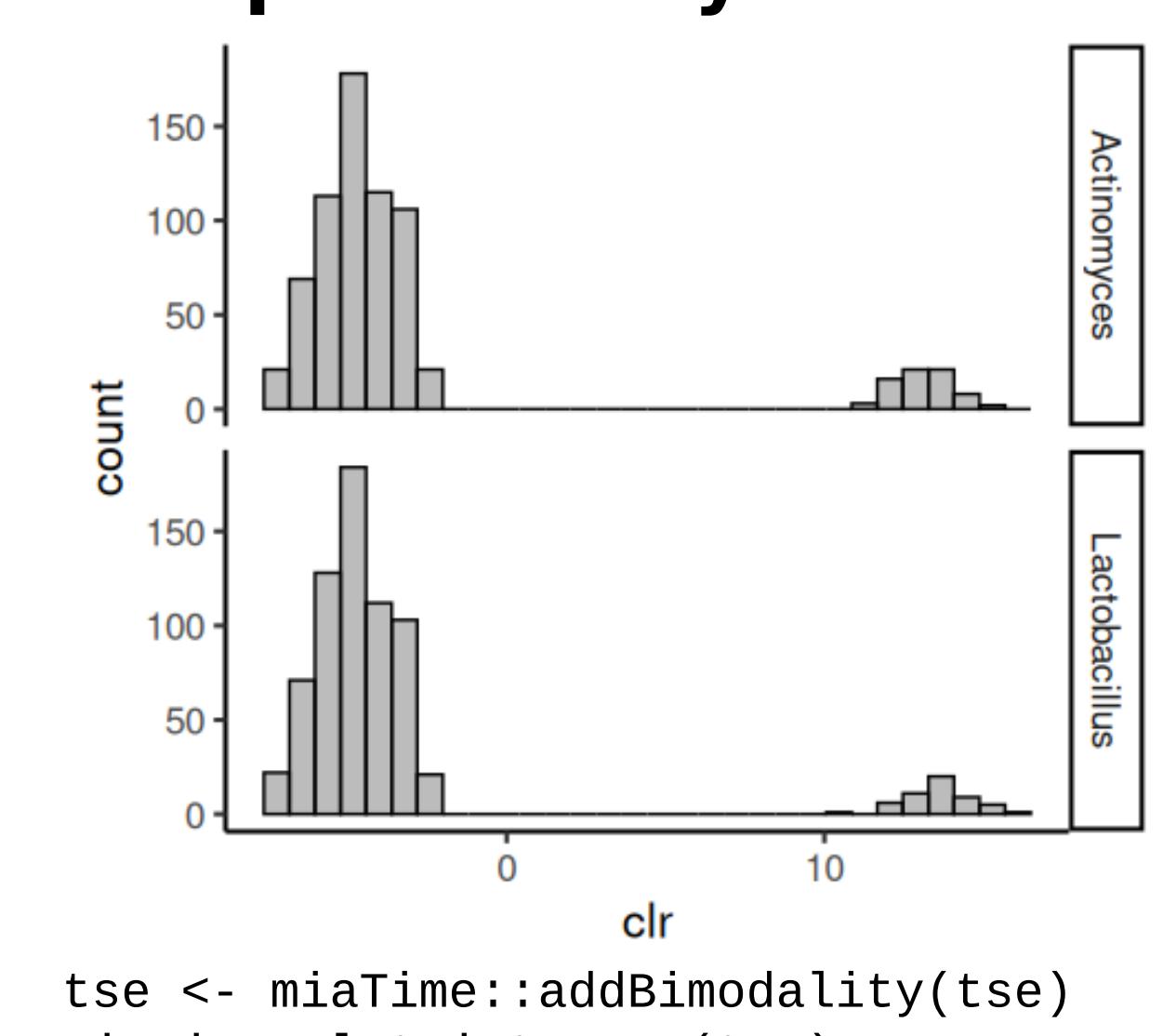
Multi-assay integration



Interactive analysis



Temporal analyses



Online book

To help users adopt the ecosystem, a freely available online book is available.

