

# Orchestrating Microbiome Analysis with Bioconductor

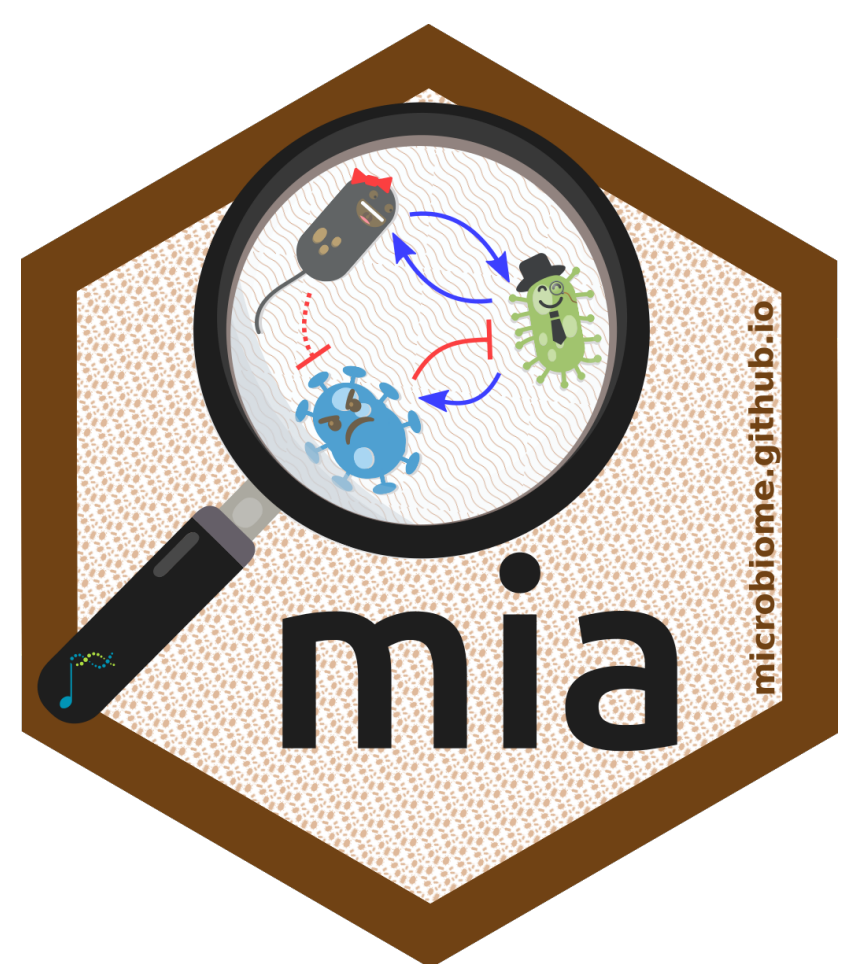
## PRESENTER INFO:

Tuomas Borman  
✉ [tuomas.v.borman@utu.fi](mailto:tuomas.v.borman@utu.fi)

Leo Lahti  
🌐 <https://datascience.utu.fi/>

## CONTRIBUTORS:

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



**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.

bioRxiv  
THE PREPRINT SERVER FOR BIOLOGY

New Results

Follow this preprint

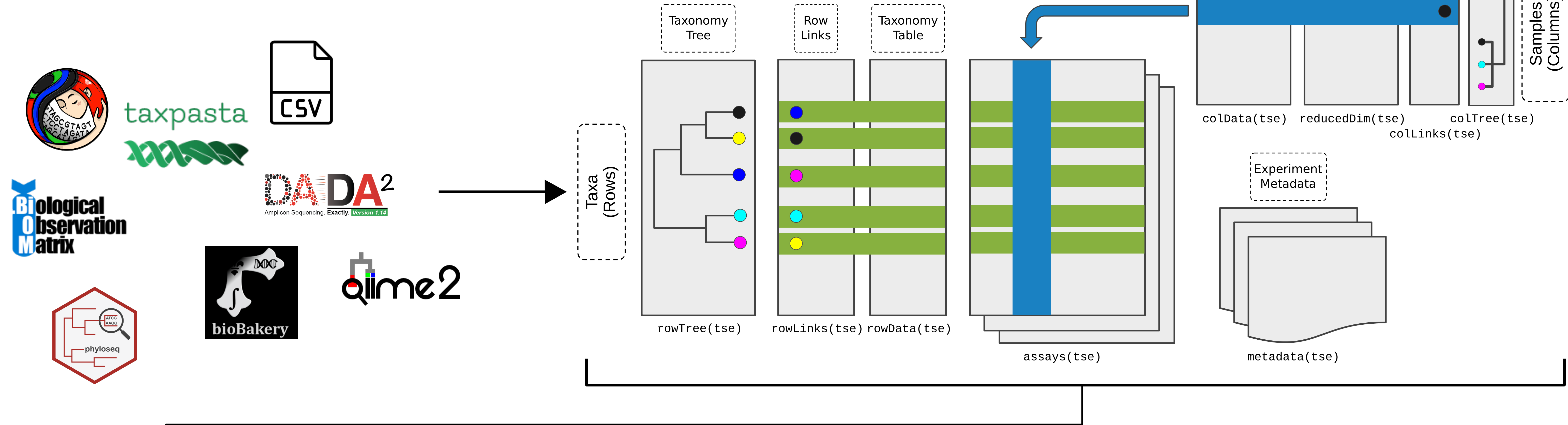
### Orchestrating Microbiome Analysis with Bioconductor

Tuomas Borman, Giulio Benedetti, Geraldson Mulu, Aura Raulo, Benjamin Valderrama, Artur Sannikov, Stefanie Peschel, Yinan Liu, Rasmus Hindström, OMA consortium, Katarina Päämänen, Christian L. Müller, Aki S. Havulinna, Sudarshan Shetty, Marcel Ramos, Domenick J. Braccia, Héctor Corrada Bravo, Felix M. Ernst, Levi Waldron, Thomaz F. S. Bastiaansen, Himel Mallick, Leo Lahti  
doi: <https://doi.org/10.1101/2025.10.29.685036>



## Data infrastructure

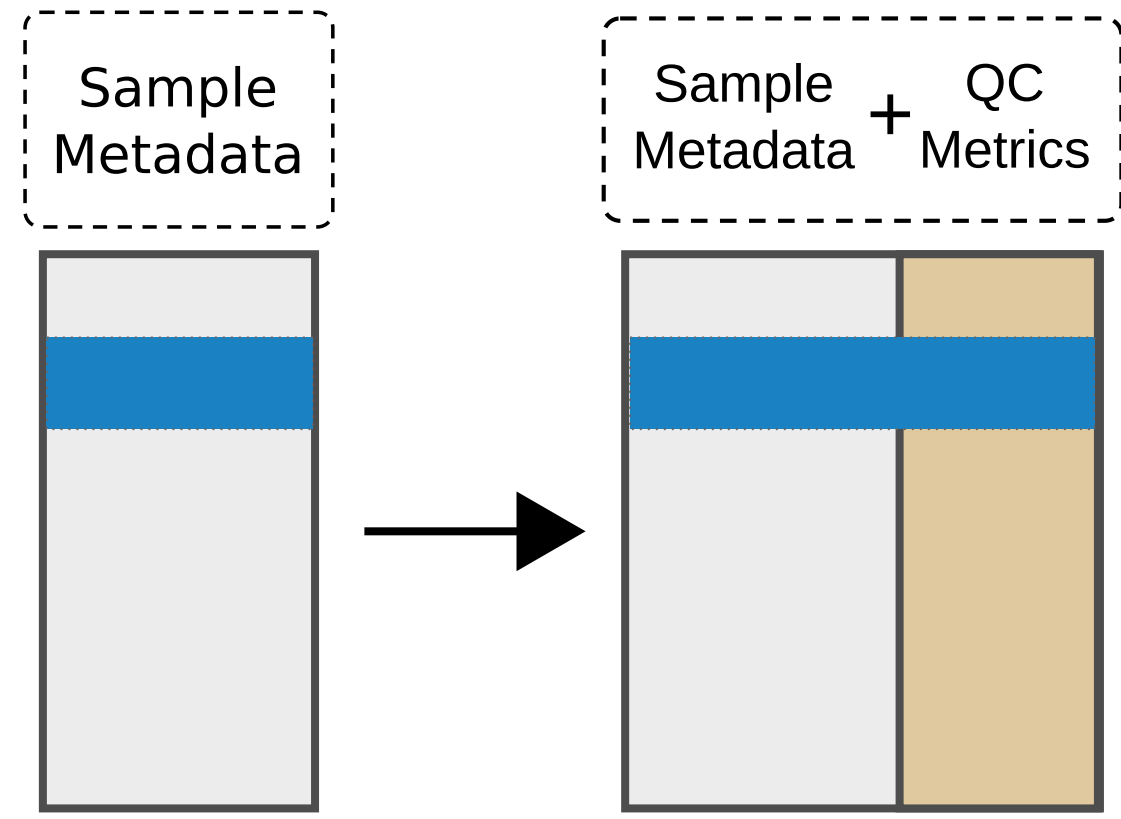
Data can be imported in standard formats using importer functions. In addition, data from multiple public databases — totaling over half a million samples — can be retrieved directly into a *TreeSummarizedExperiment* object.



## Downstream analysis

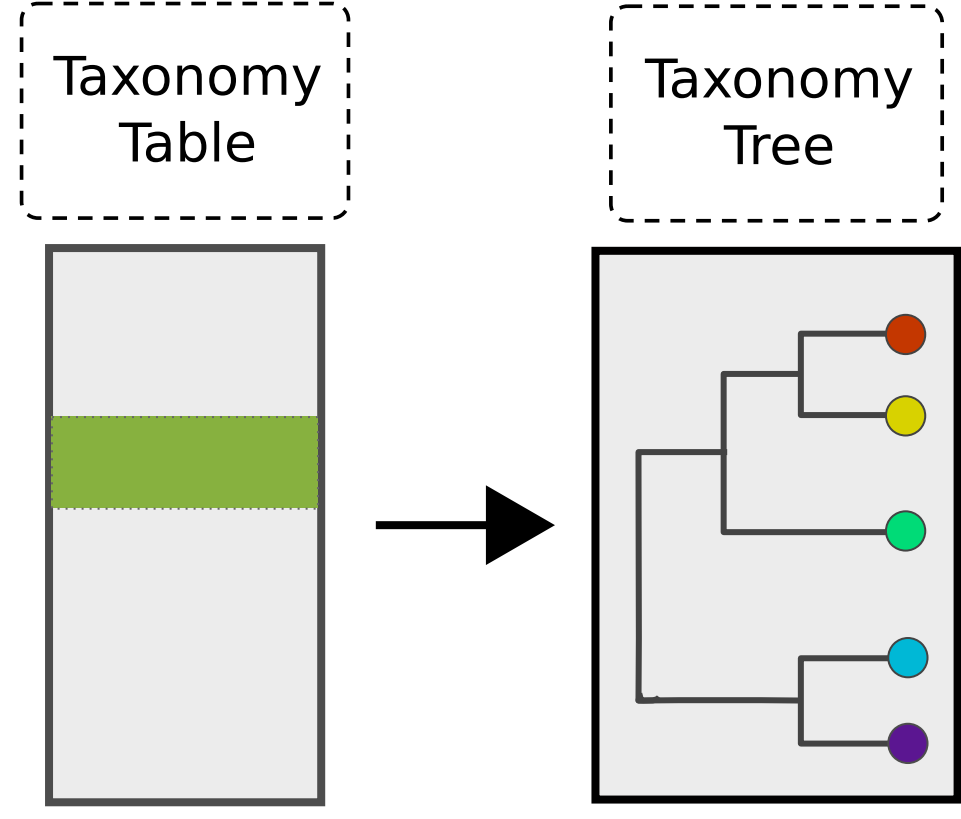
The ecosystem includes a full suite of tools distributed through the *mia* package family.

### Quality control



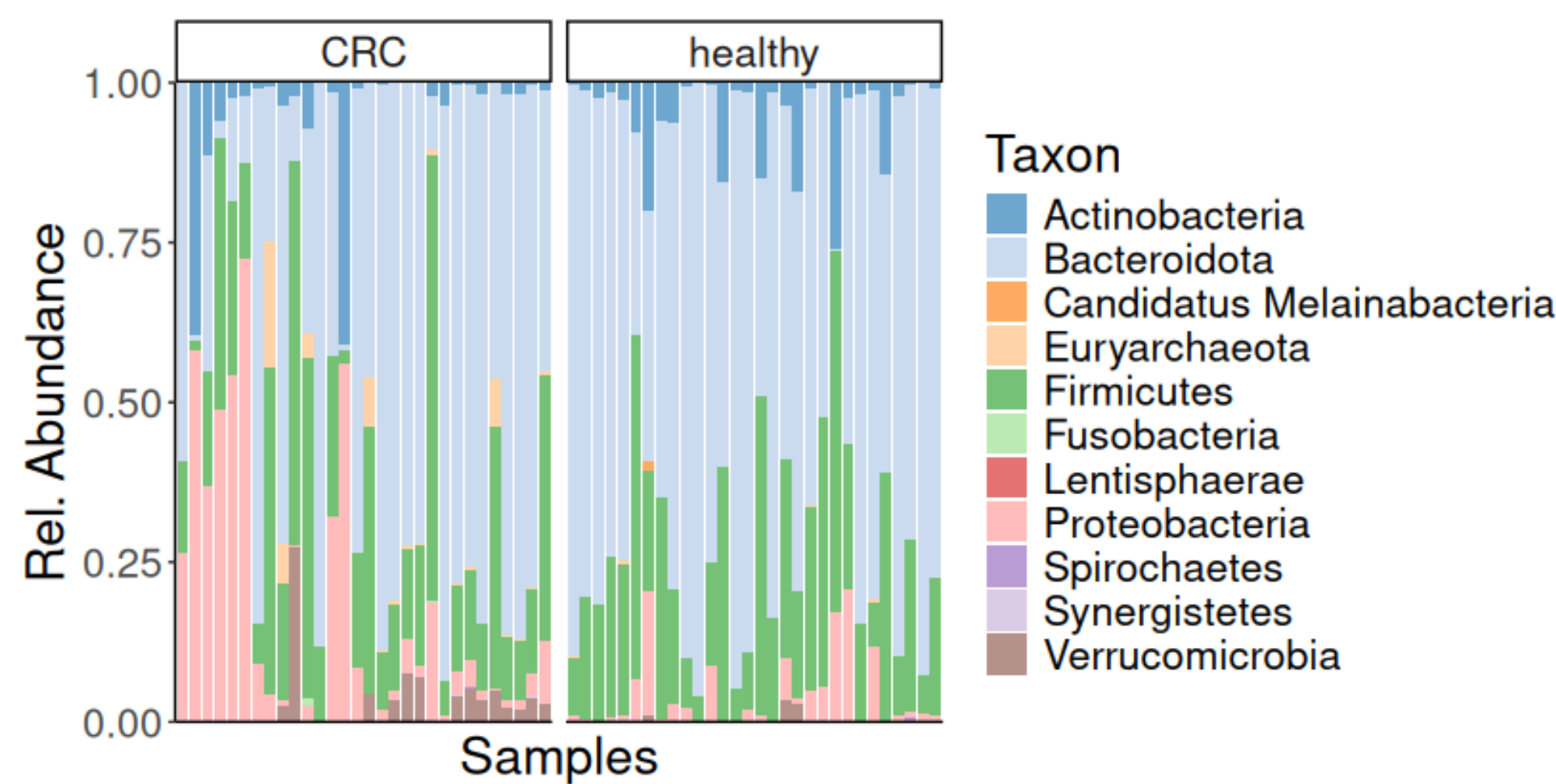
```
tse <- scater::addPerCellQC(tse)
```

### Data processing



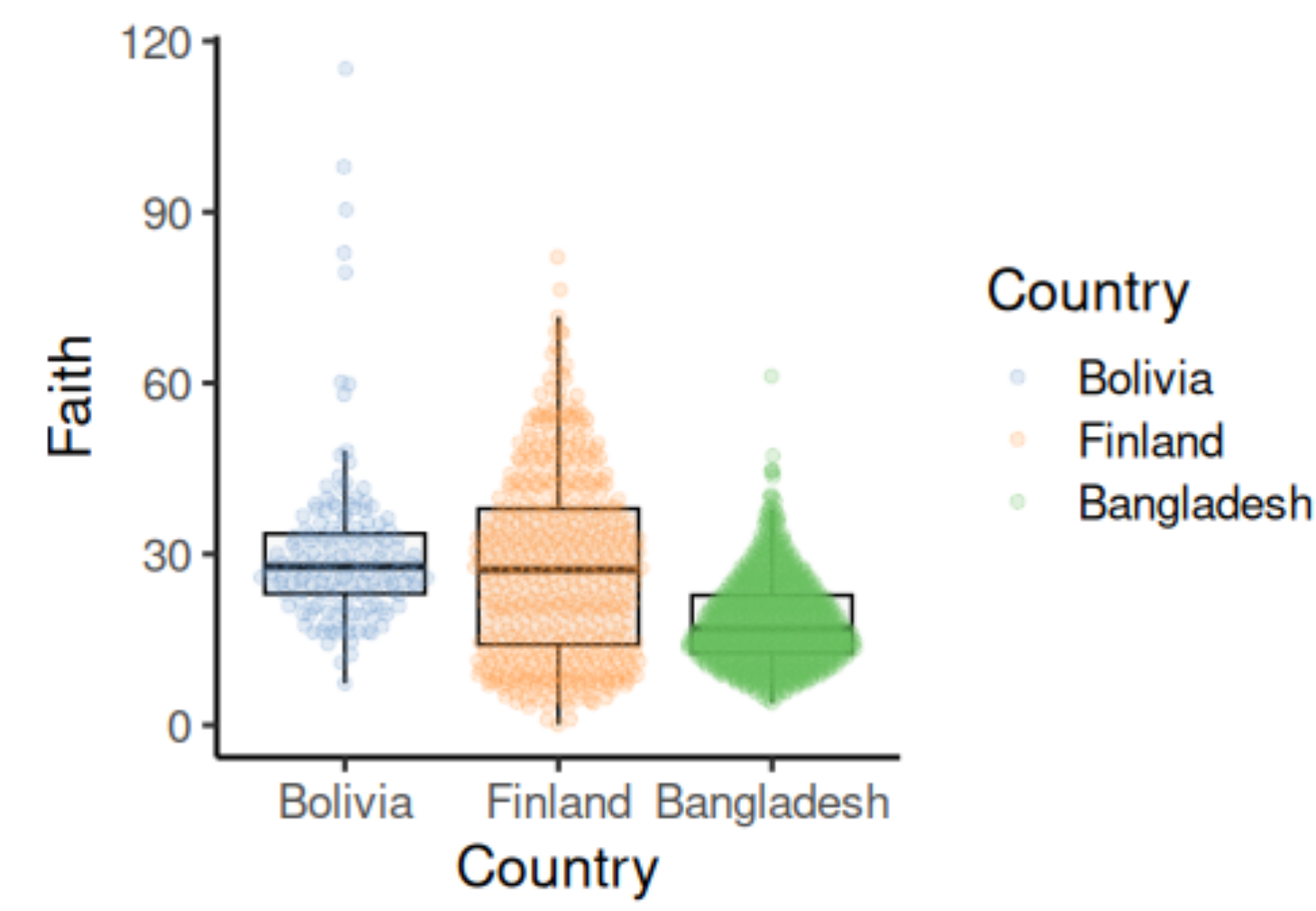
```
tse <- mia::addHierarchyTree(tse)
```

### Visualization



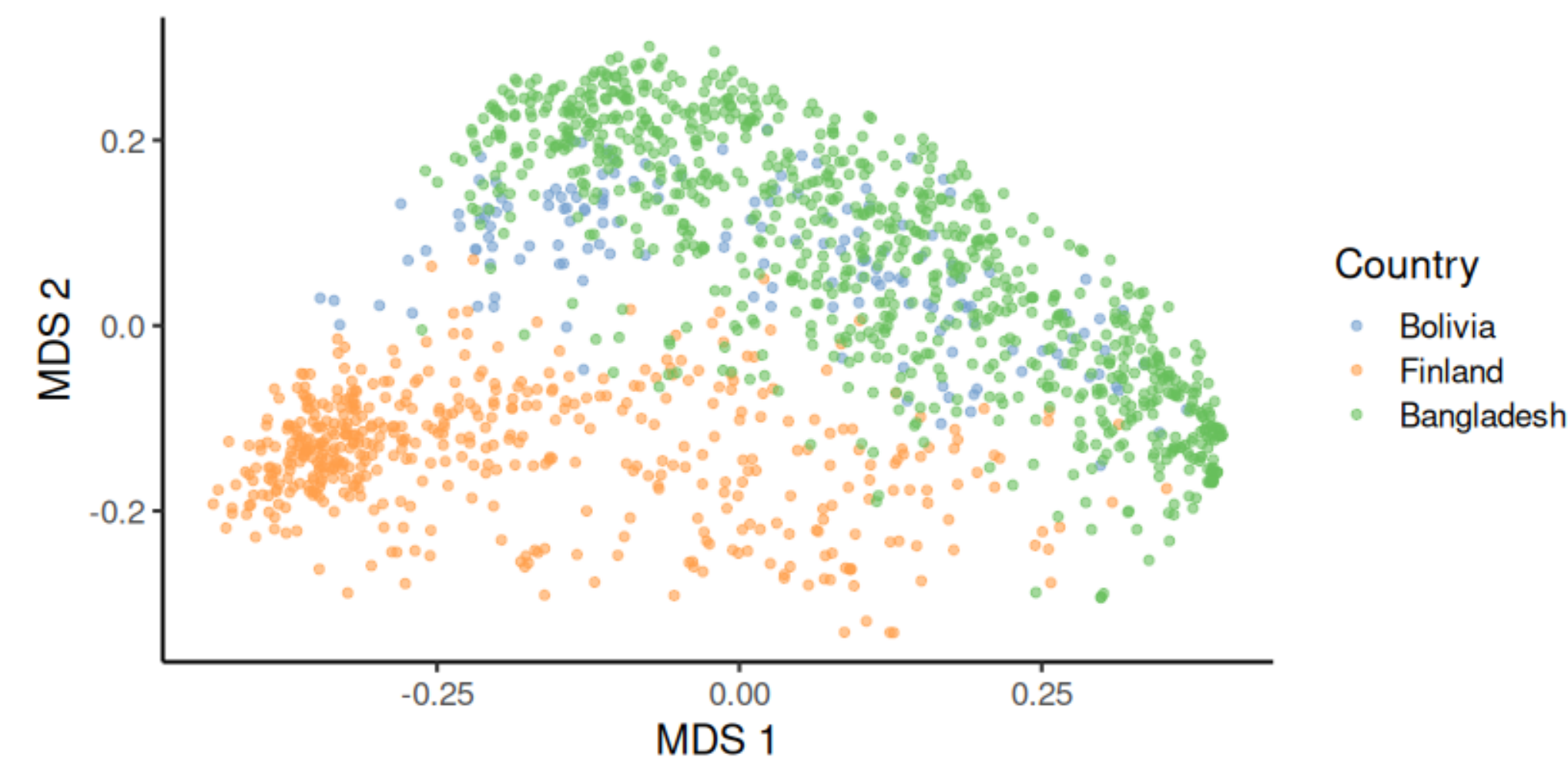
```
miaViz::plotAbundance(tse)
```

### Community indicators



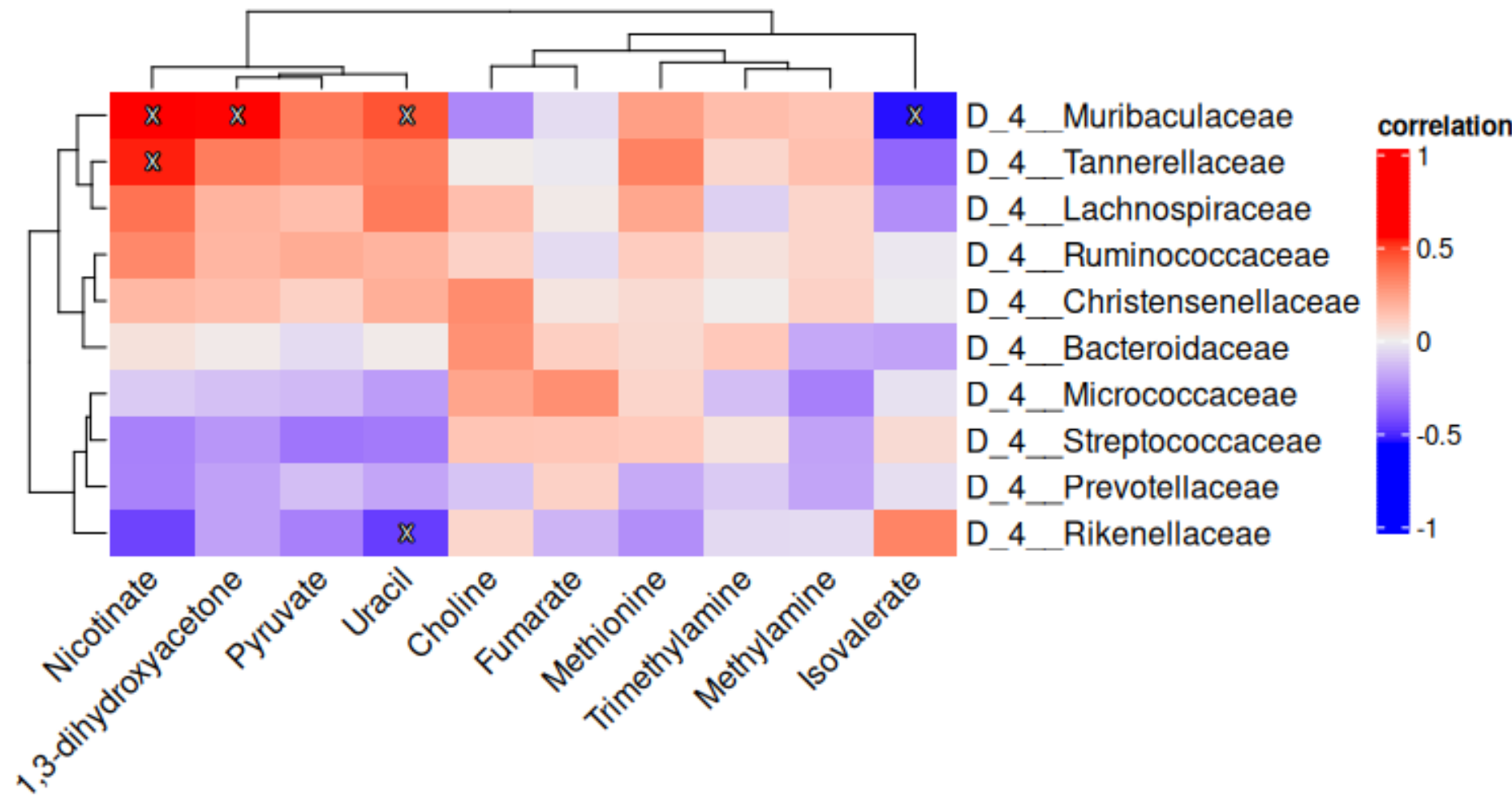
```
tse <- mia::addAlpha(tse)  
scater::plotColData(tse)
```

### Community similarity



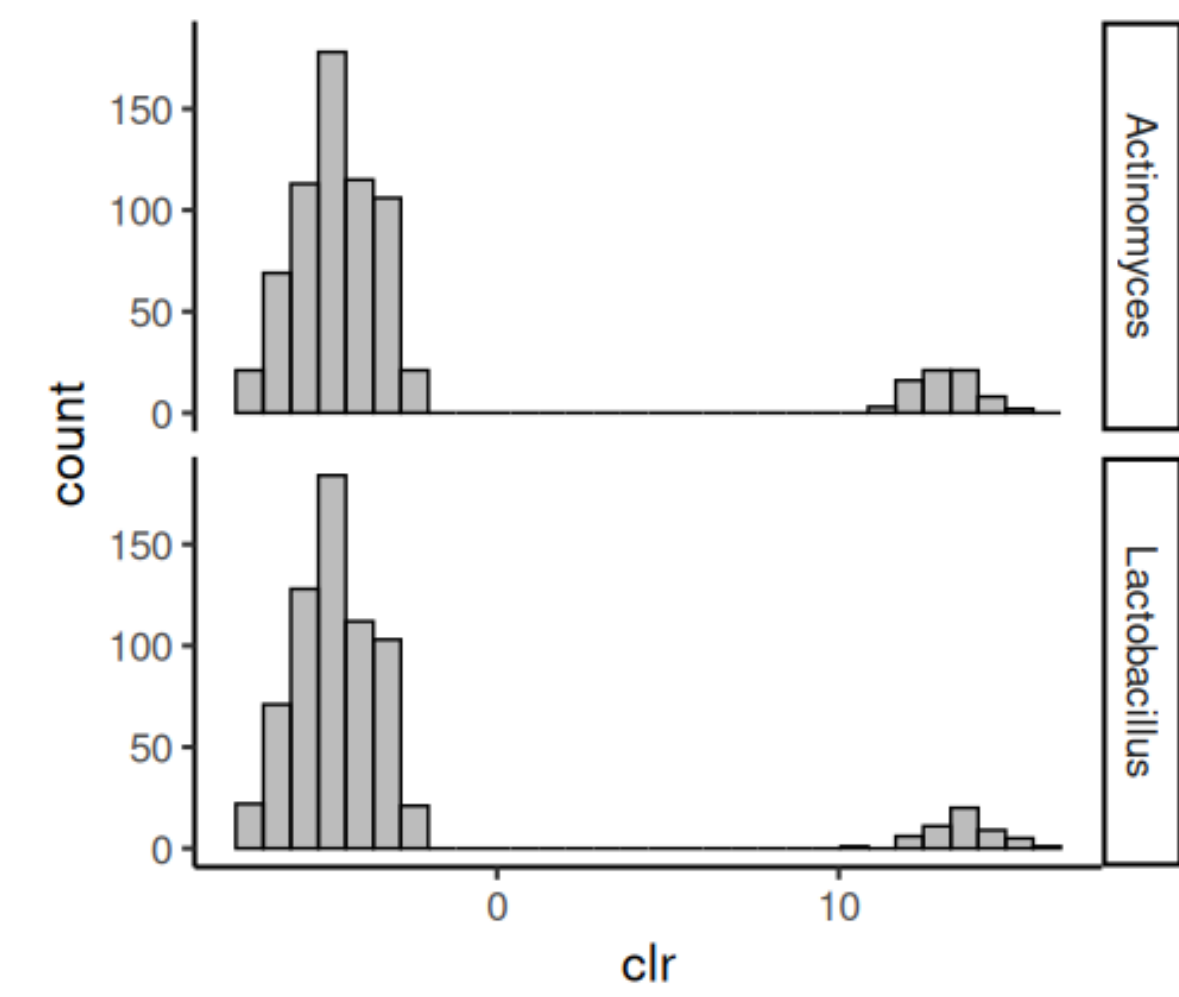
```
tse <- mia::addMDS(tse)  
scater::plotReducedDim(tse)
```

### Multi-assay integration



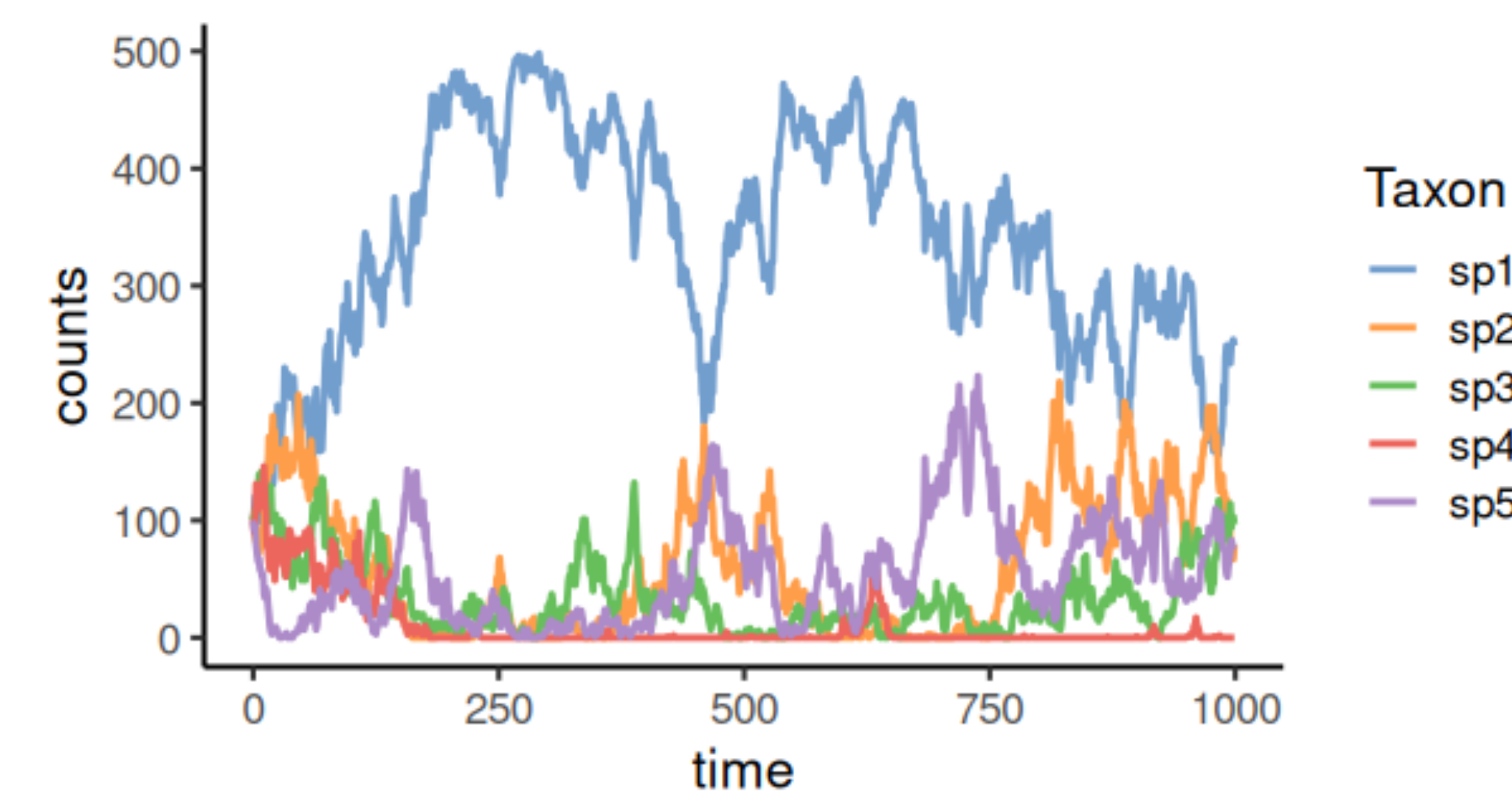
```
res <- mia::getCrossAssociation(tse)  
ComplexHeatmap::Heatmap(res)
```

### Temporal analyses



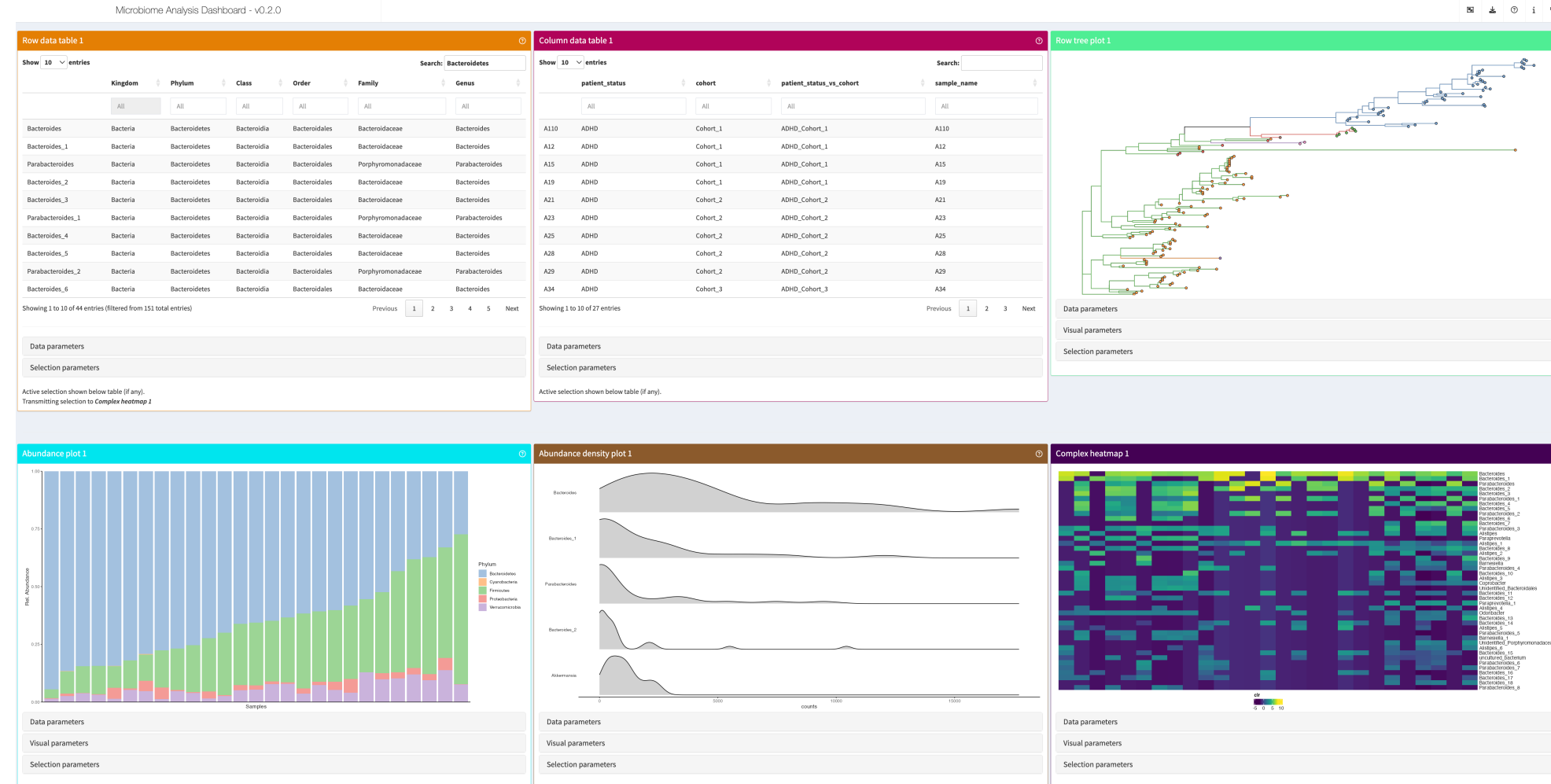
```
tse <- miaTime::addBimodality(tse)  
miaViz::plotHistogram(tse)
```

### Simulation



```
tse <- miaSim::simulateGLV(tse)  
miaViz::plotSeries(tse)
```

### Interactive analysis



```
iSEEtree::iSEE(tse)
```

### Online book

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

