Orchestrating Microbiome Analysis with Bioconductor

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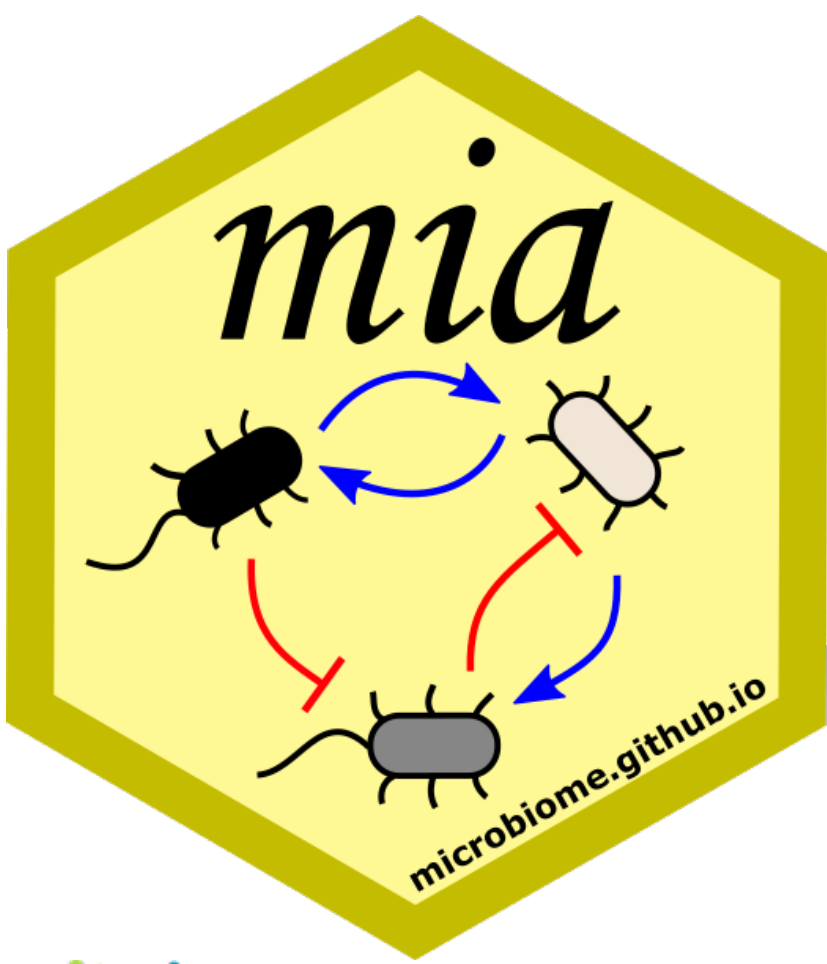
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FindingPheno

CONTRIBUTORS:

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

Research Council of Finland

Bioconductor
OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

mia
microbiome.github.io

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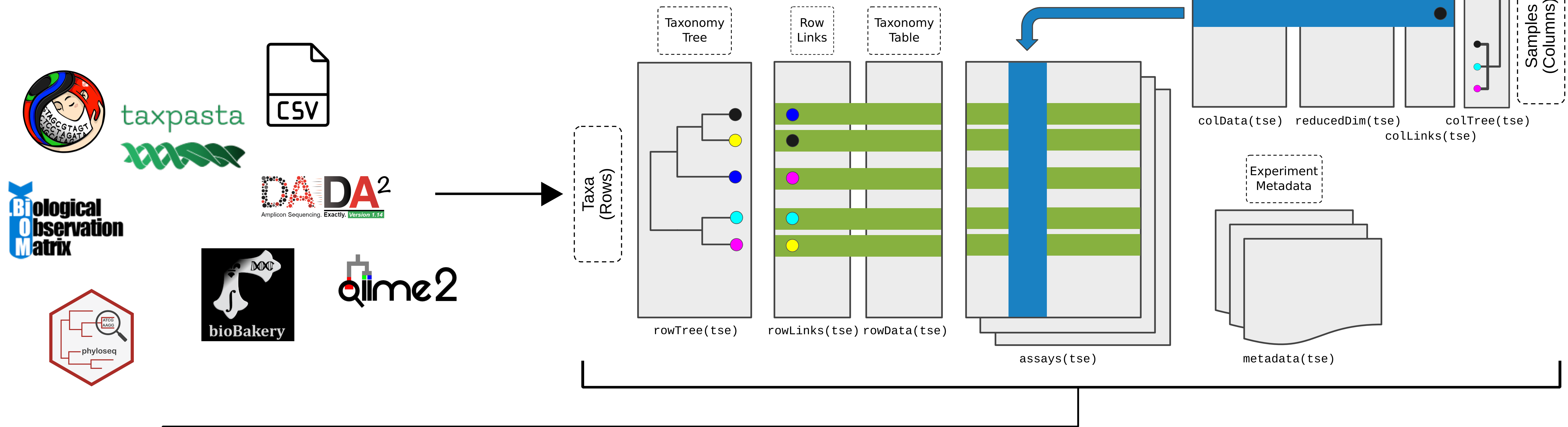
Solution: We have developed methods built around the *TreeSummarizedExperiment* class to address these needs. This framework improves support for multi-table microbiome data and integrates seamlessly with the Bioconductor ecosystem. To promote best practices and reproducibility, we provide comprehensive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

Check **Orchestrating Microbiome Analysis (OMA) online book**.

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.

Huang et al. (2021) TreeSummarizedExperiment: a S4 class for data with hiearchical structure F1000Research


```
rowTree(tse)    rowLinks(tse) rowData(tse)    assays(tse)    metadata(tse)
```

```
colData(tse)  reducedDim(tse)    colTree(tse)
                    colLinks(tse)
```

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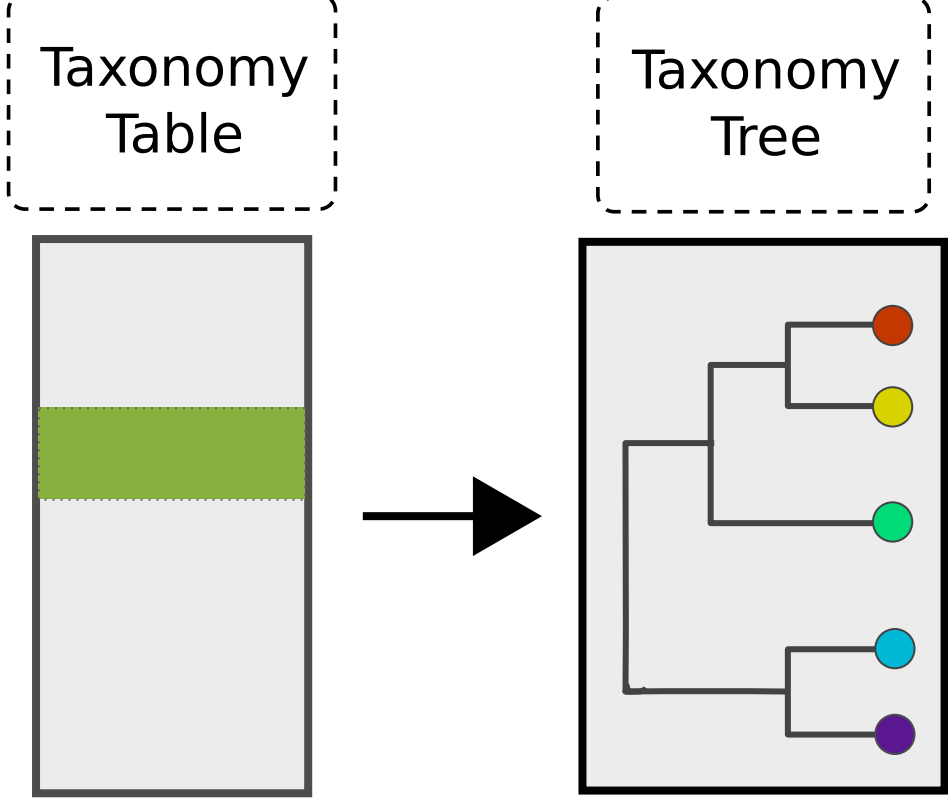
The ecosystem includes a full suite of tools distributed through the *mia* package family.

Quality control
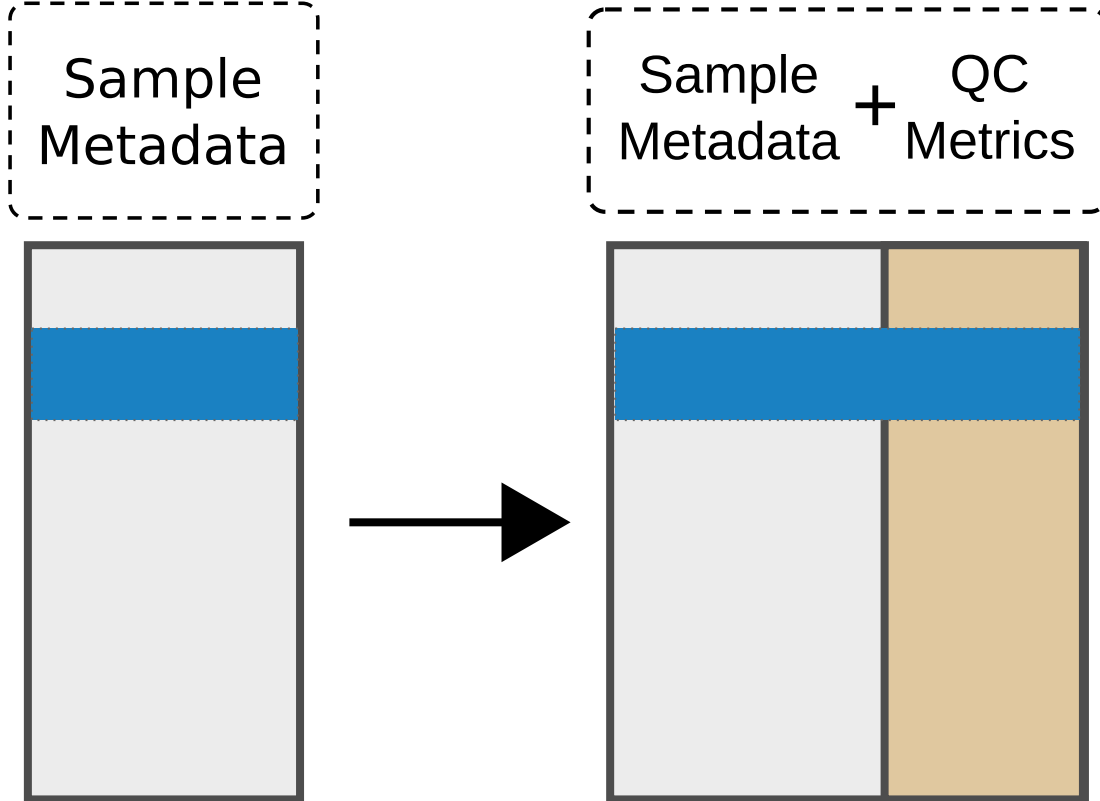

```
tse <- scater::addPerCellQC(tse)
```
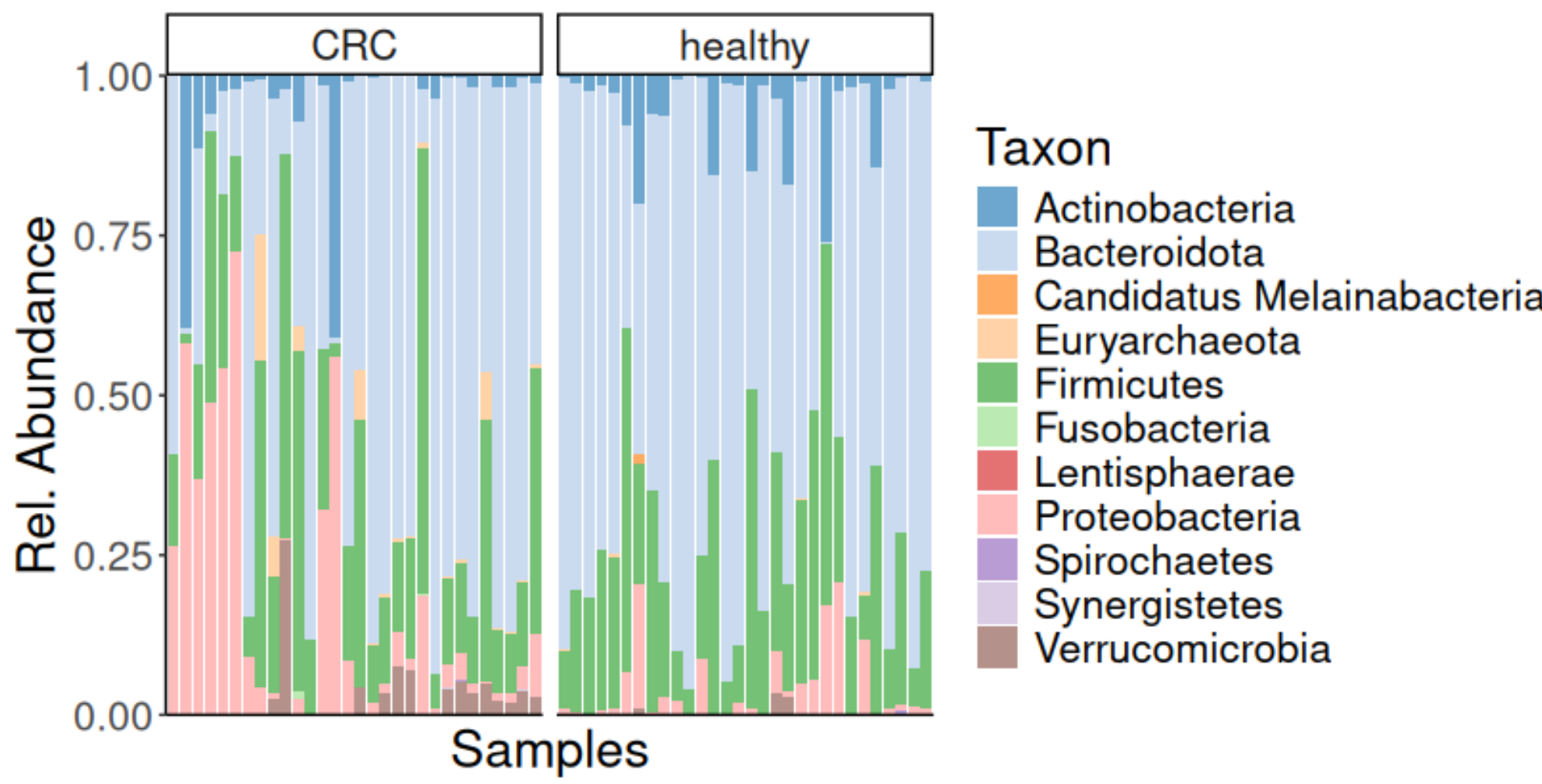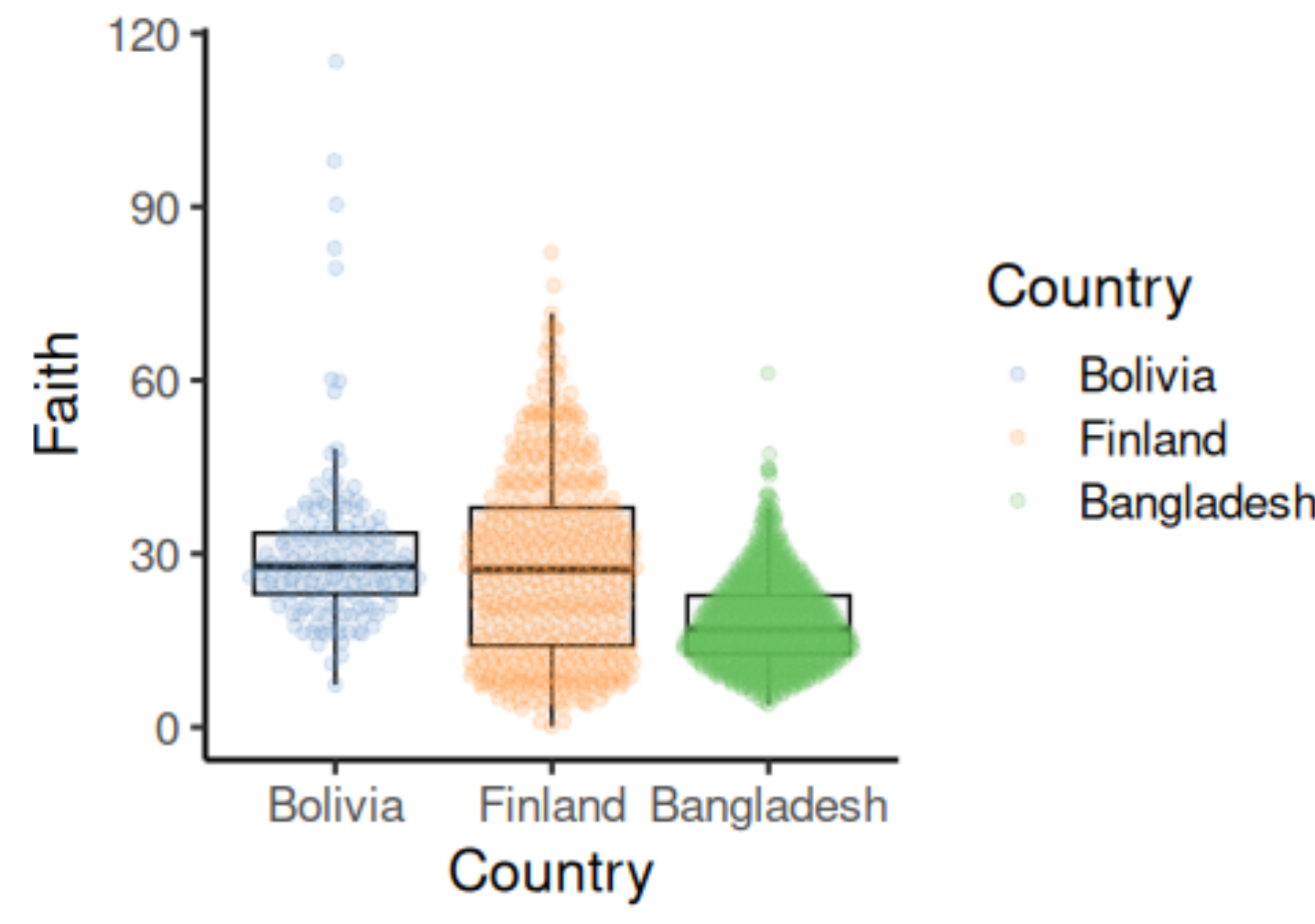
Data processing


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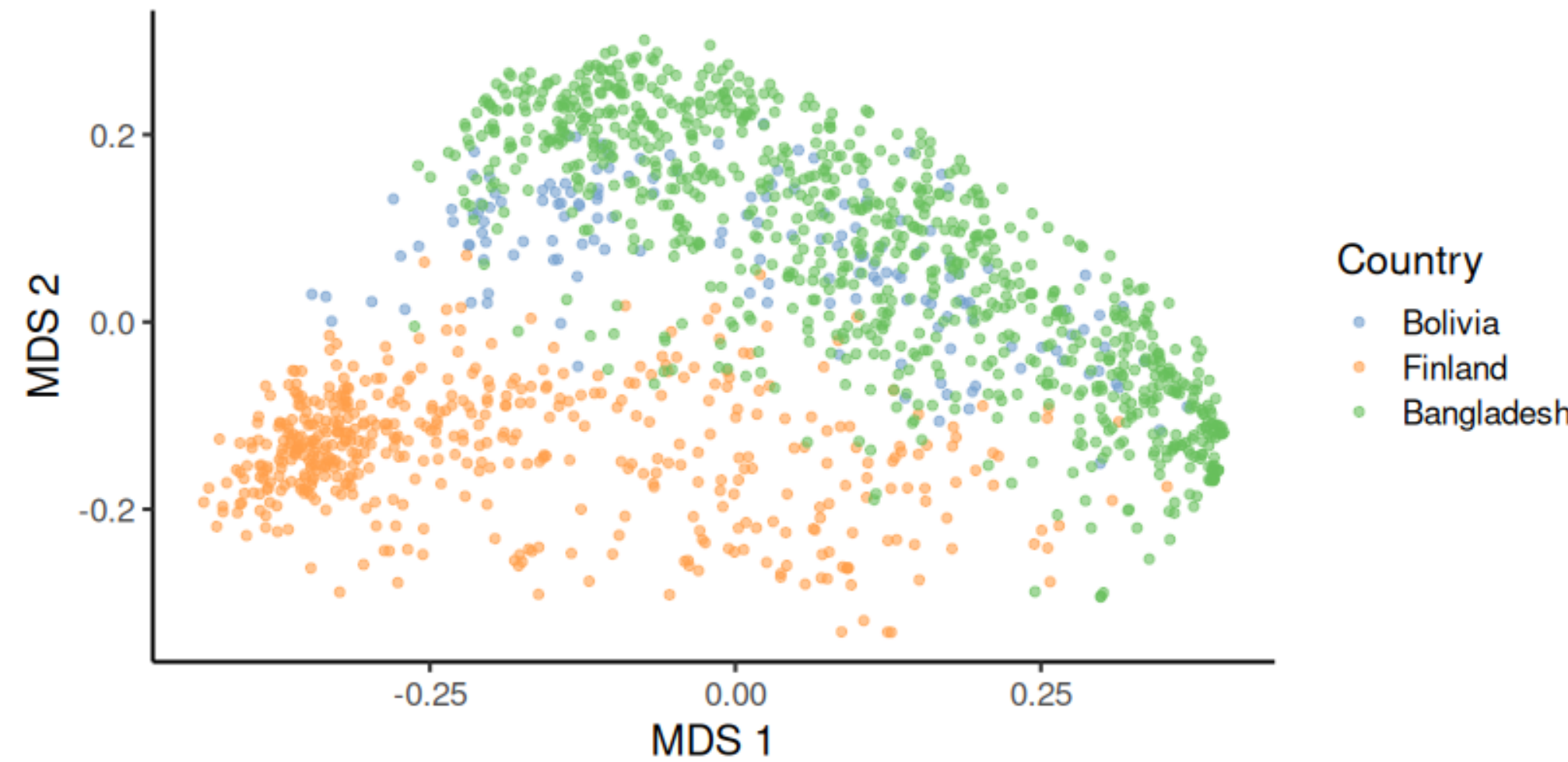
Visualization


```
miaViz::plotAbundance(tse)
```
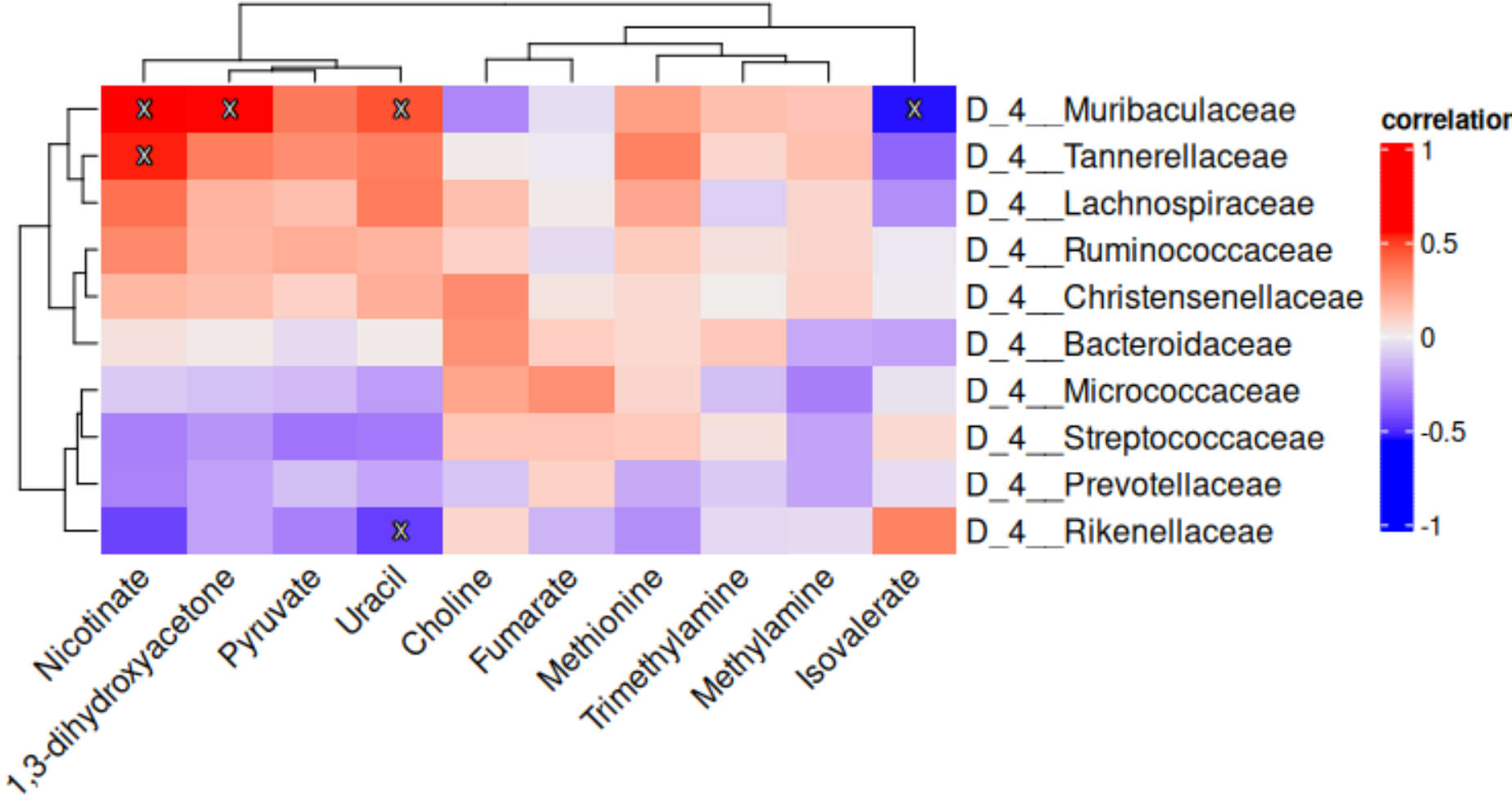
Community indicators


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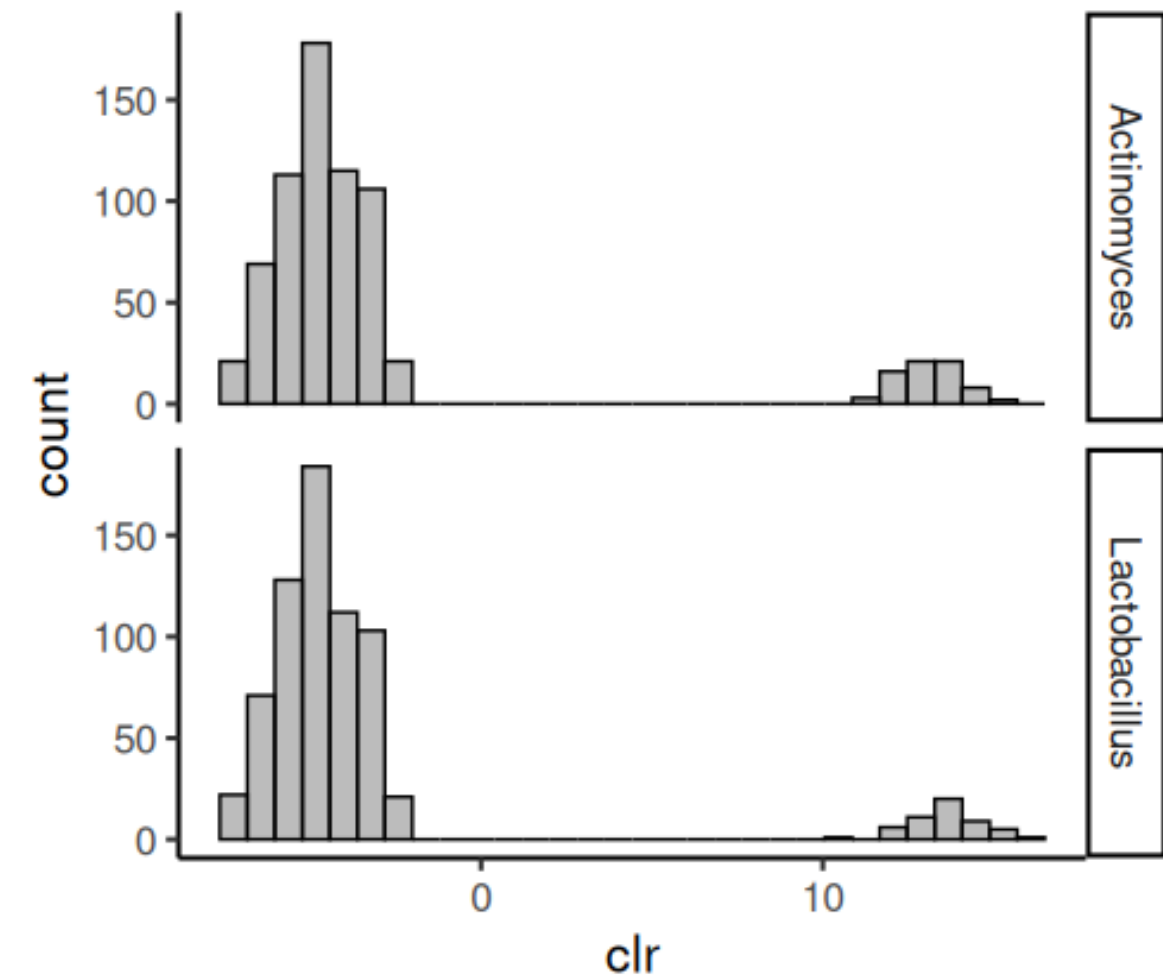
Community similarity


```
tse <- mia::addMDS(tse)
scater::plotReducedDim(tse)
```
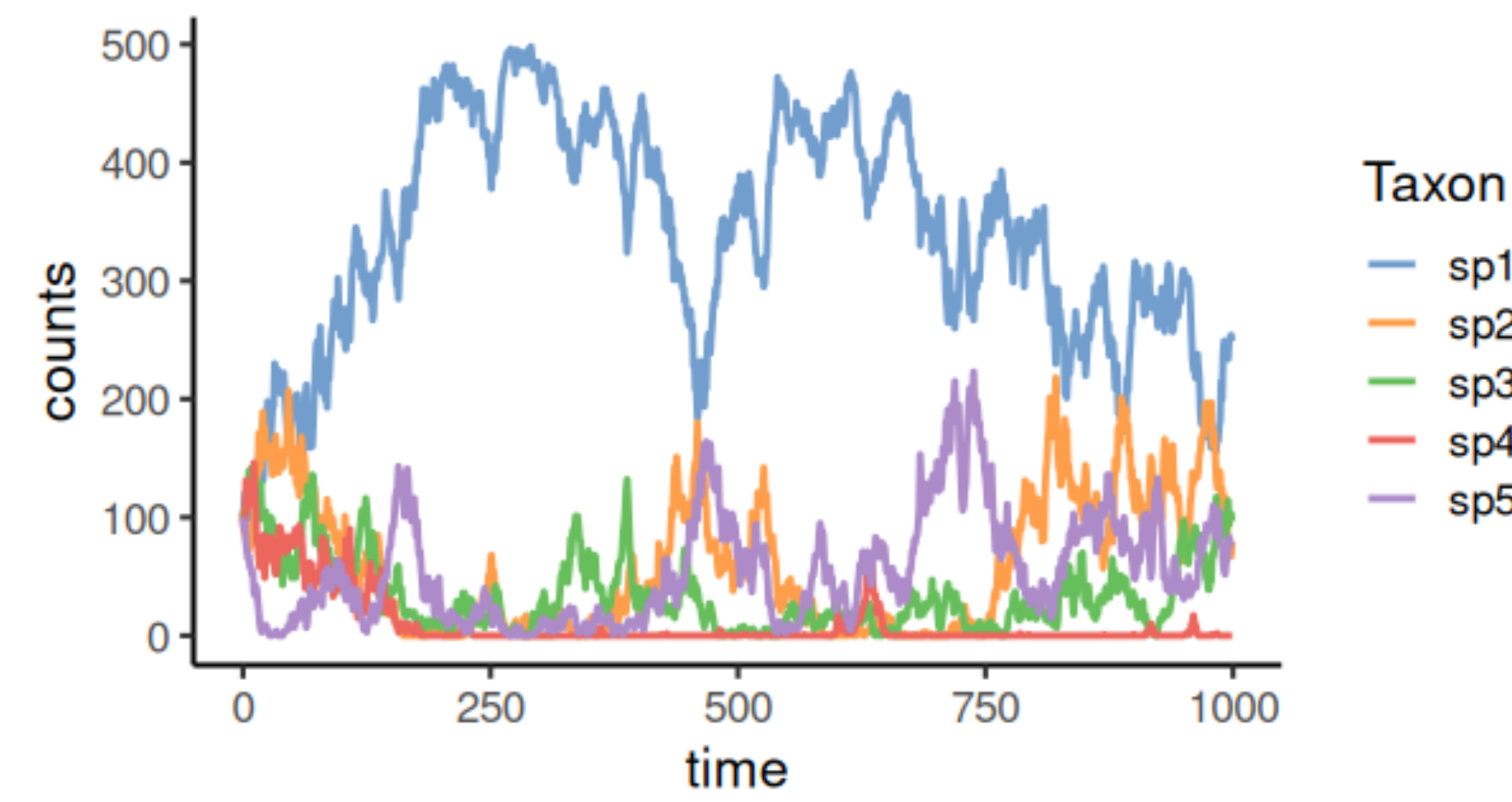
Multi-assay integration


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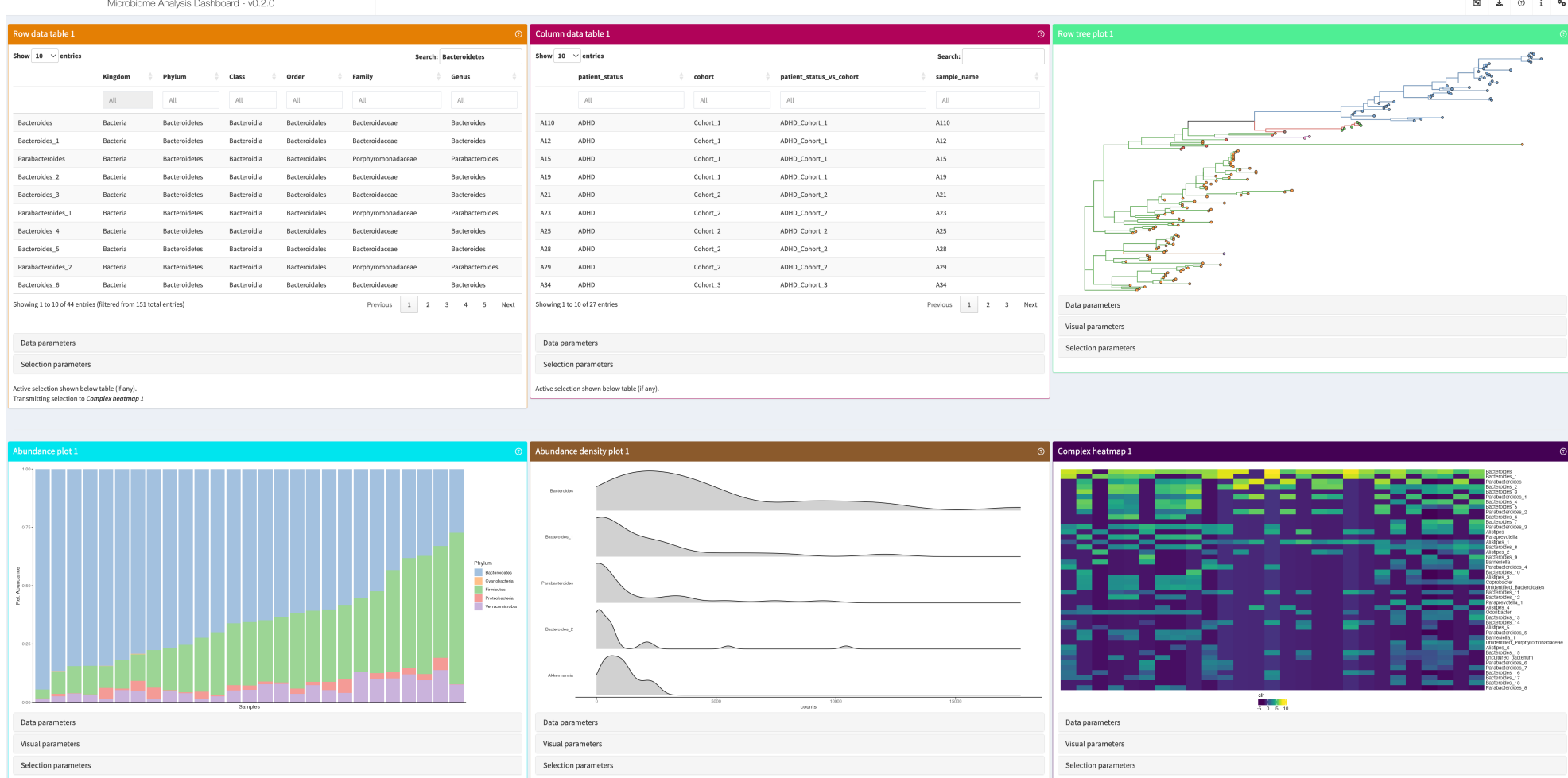
Temporal analyses


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

Simulation


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

Interactive analysis


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

Expanding ecosystem

The ecosystem is continuously growing thanks to contributions from a global community.