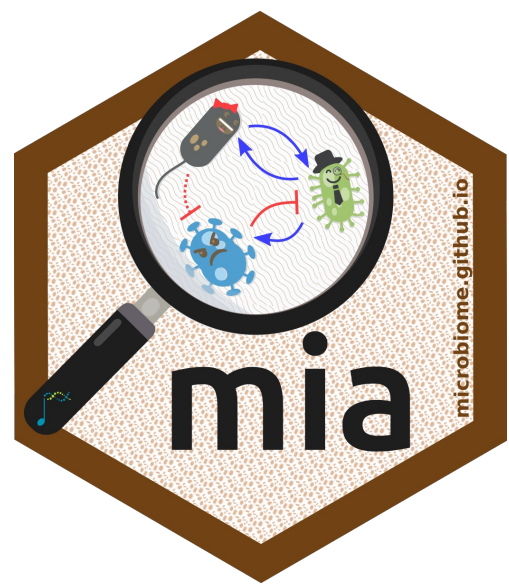


miaDash: a web app for reproducible and interactive microbiome analysis and visualisation

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Try miaDash

The problem

Microbes are everywhere and are essential for keeping ecosystems in balance. As microbiome research advances, microbiome datasets continue to grow. The Bioconductor framework provides methods for microbiome data analysis, but they are not yet accessible to non-programmers. To lower the entry threshold, we developed miaDash, a web app to interactively analyse and visualise microbiome data. Our goal is to **make microbiome data science accessible** to anyone who needs it, with or without programming skills.

The solution

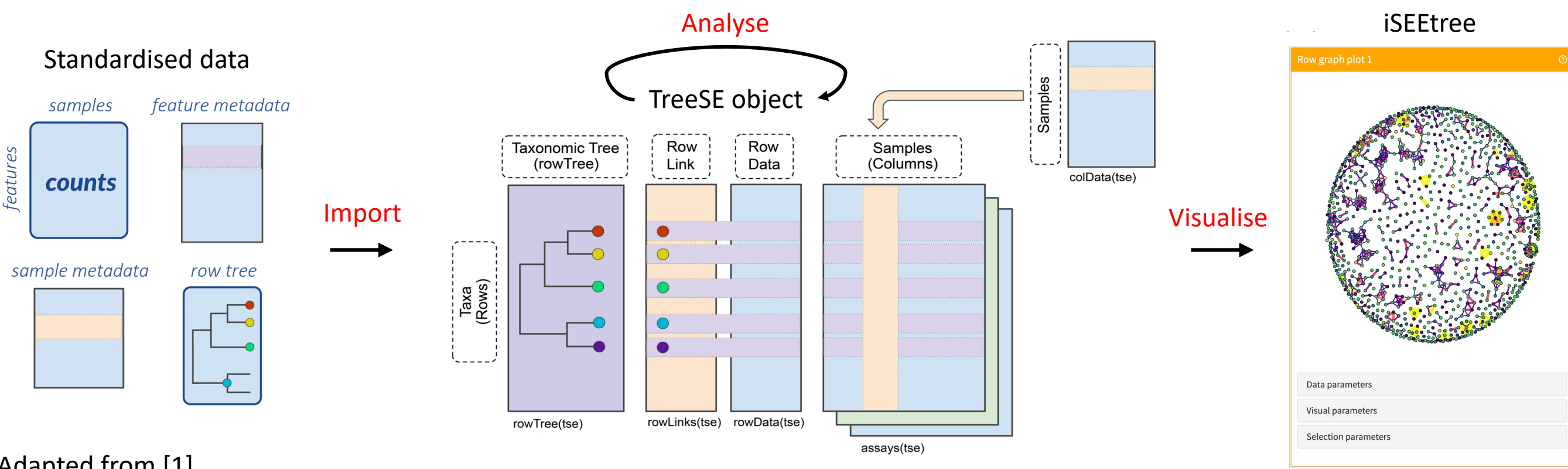
miaDash provides an intuitive graphical user interface reflecting the four common steps of microbiome data analysis: *Import* a dataset from several available sources; *Manipulate* data with routine operations; *Estimate* quality and diversity metrics; and *Visualise* multiple aspects of the dataset using iSEEtree [1, 2]. For each panel, users can transform data (*Data params*), control aesthetics (*Visual params*) and subset data (*Selection params*). Data, plots and R scripts can then be downloaded.

The future

In the upcoming versions of miaDash, we aim to enhance **method coverage**, **accessibility** and **reproducibility** by expanding the analytical toolkit, making panels more interactive and generating R scripts that completely replicate the analyses.

The framework

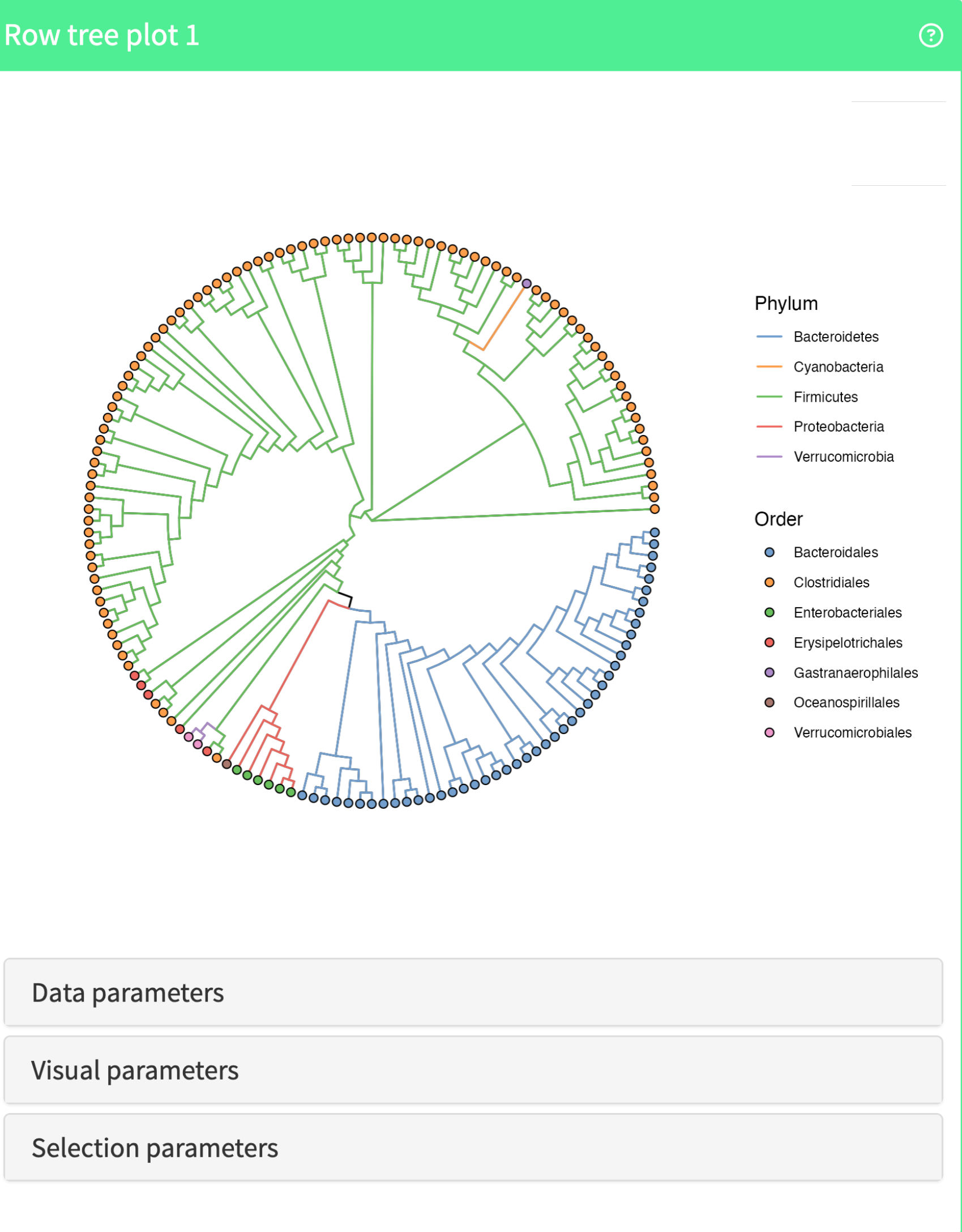
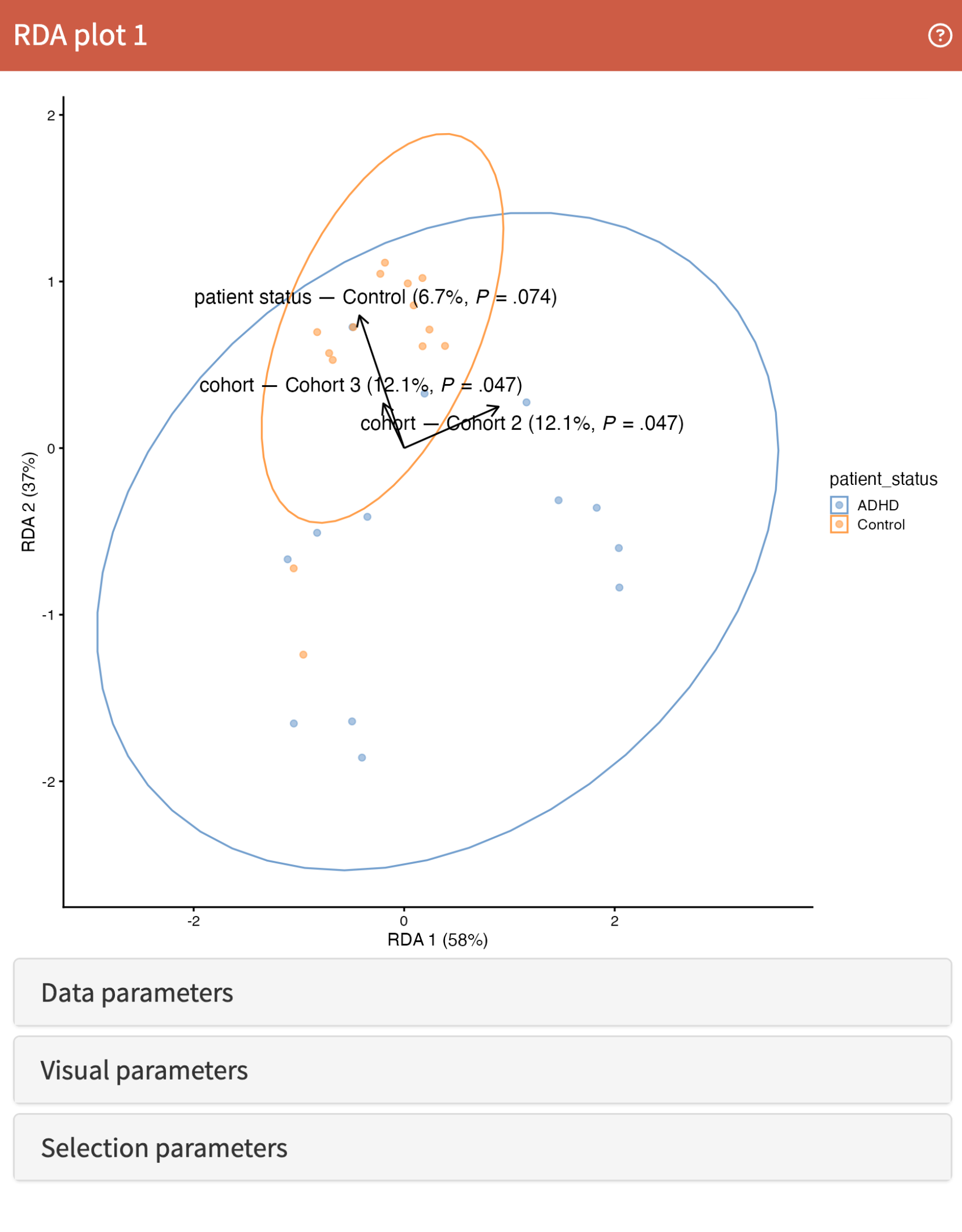
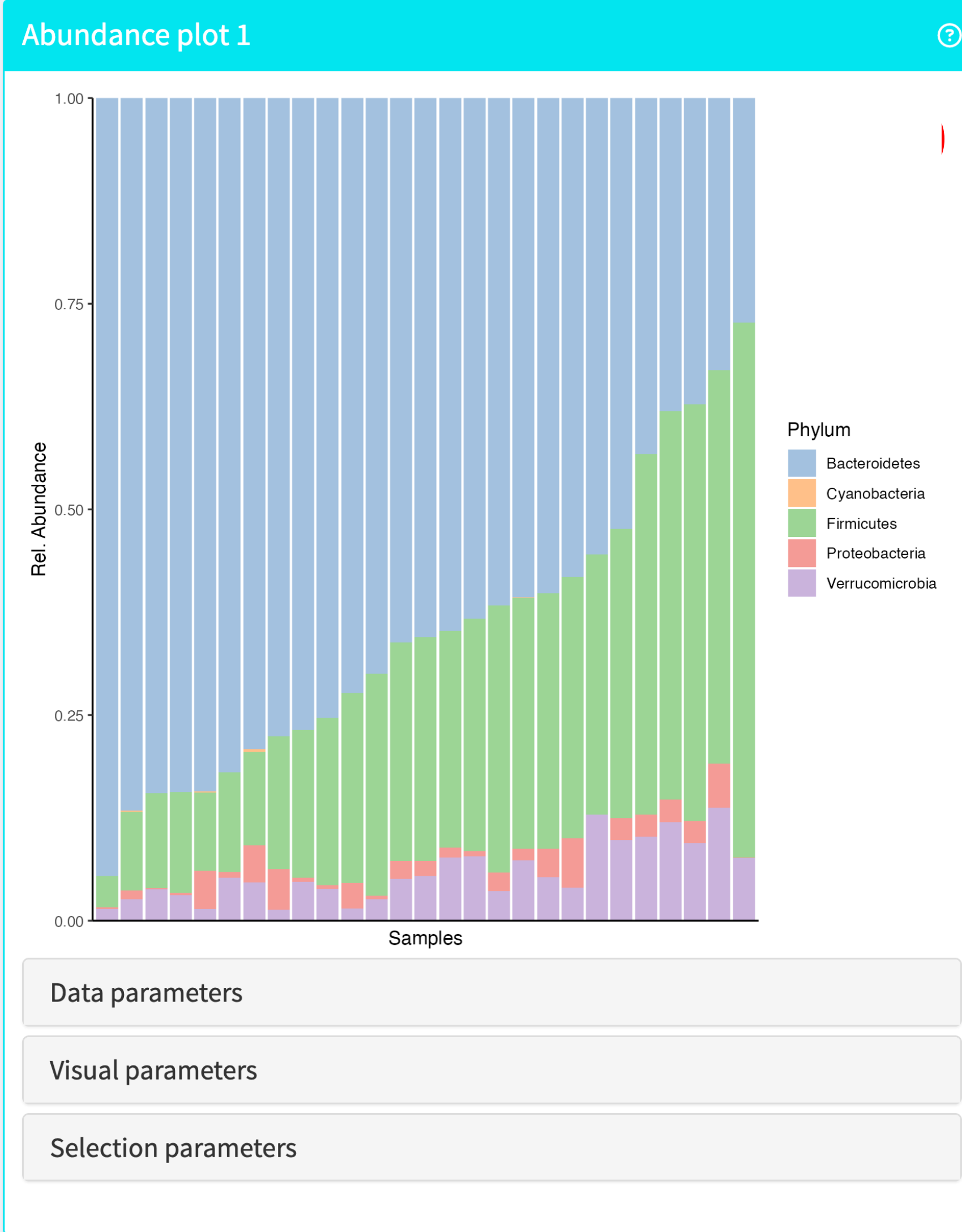
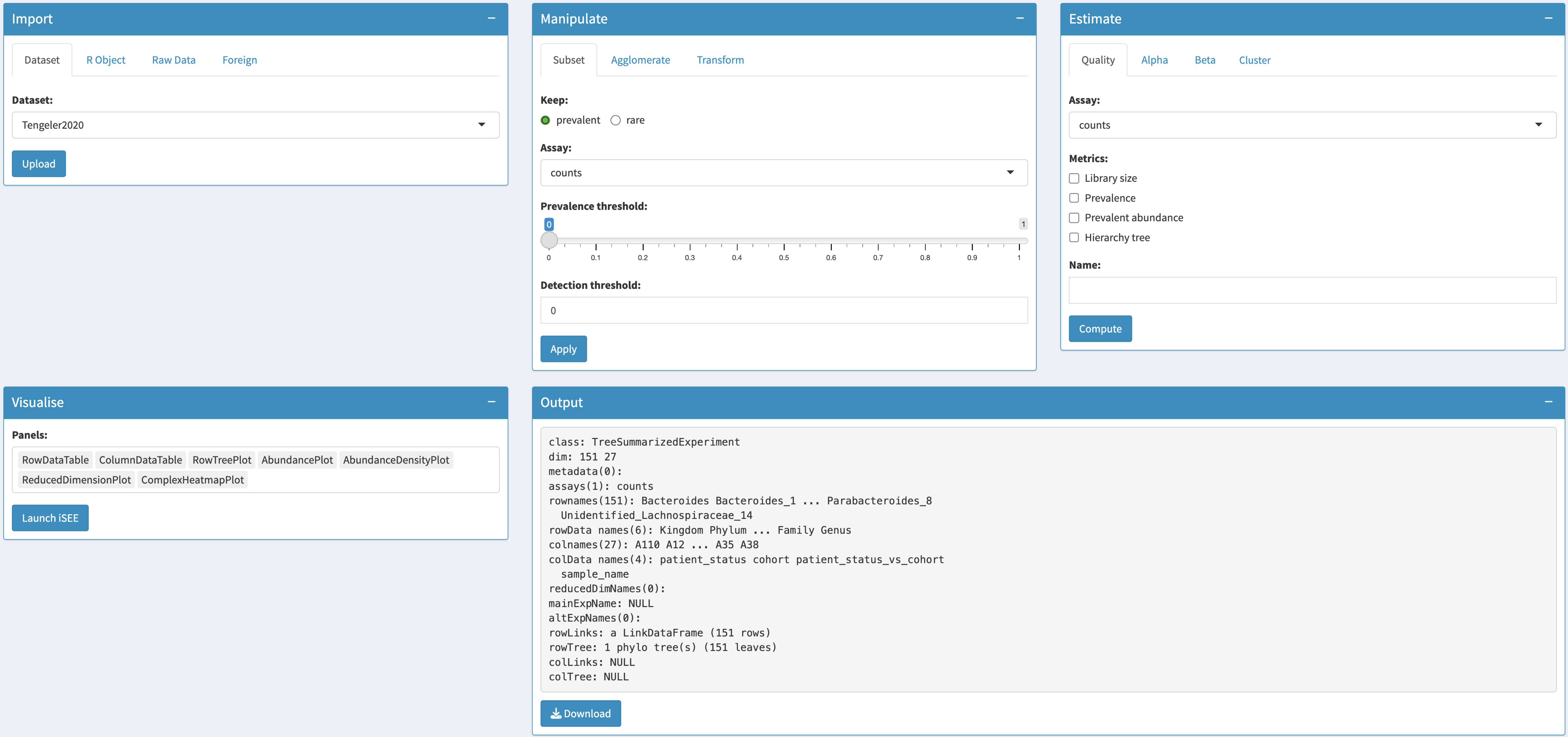
miaDash emerges from the combination of three key packages: **mia**, **iSEE** and **TreeSummarizedExperiment** (TreeSE). mia provides the toolkit for microbiome analysis, iSEE creates the graphical user interface and the TreeSE data container stores all the elements of a microbiome dataset, including assays, side information on features and samples, hierarchy trees, alternative experiments and reduced dimensions [3]. This framework promotes data integration and reproducibility.



Adapted from [1].

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