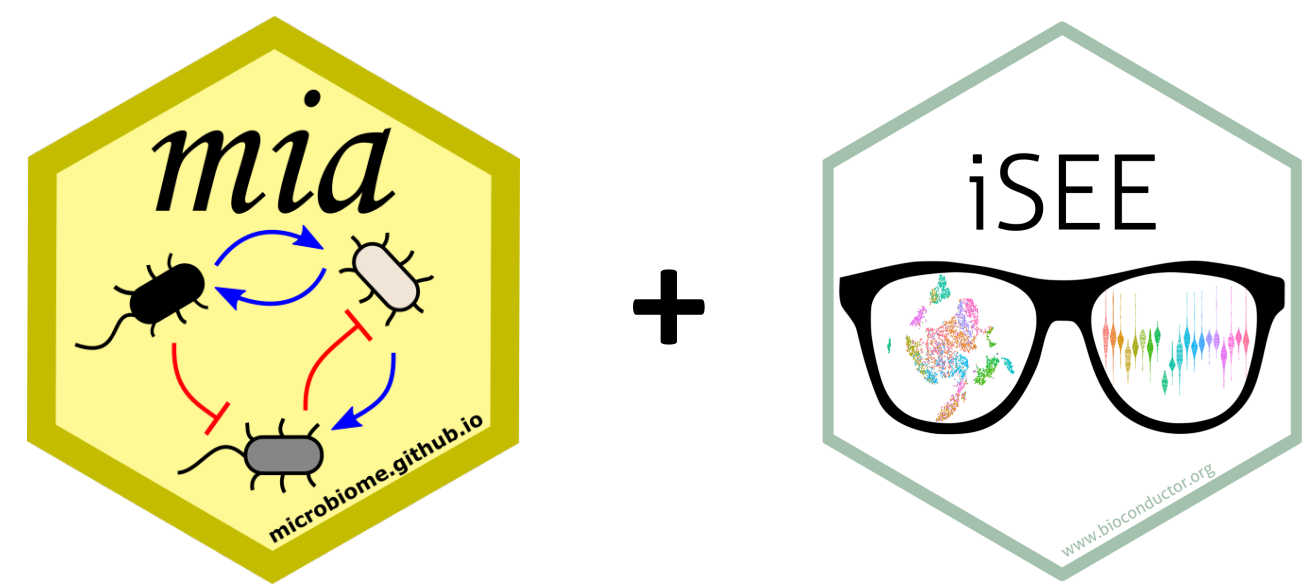


miaDash: a web app for reproducible and interactive microbiome analysis and visualisation

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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

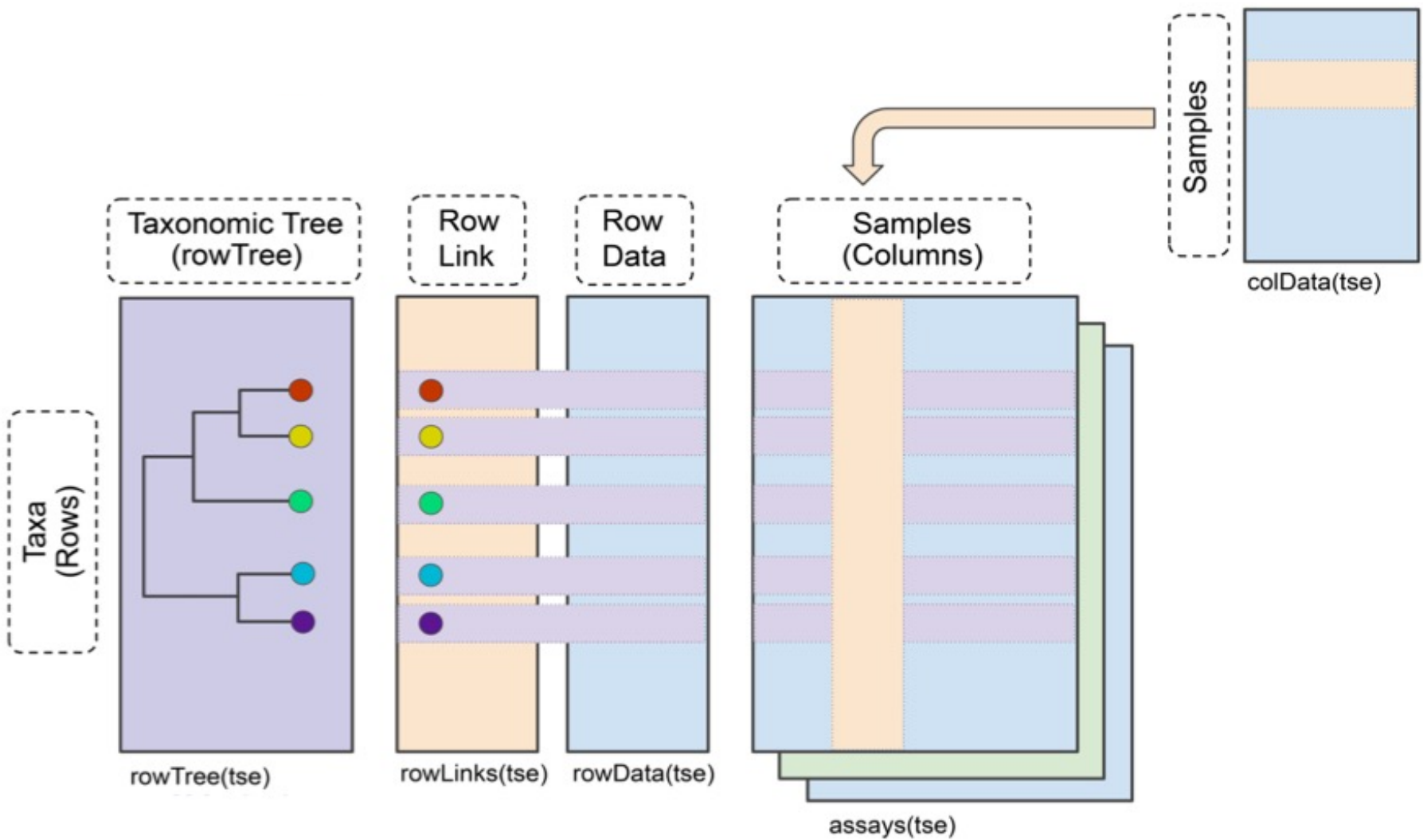
miaDash provides an intuitive graphical user interface reflecting the four common steps of microbiome data analysis: *Import* a dataset from several available sources; *Manipulate* data with routine operations; *Estimate* quality and diversity metrics; and *Visualise* multiple aspects of the dataset 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.

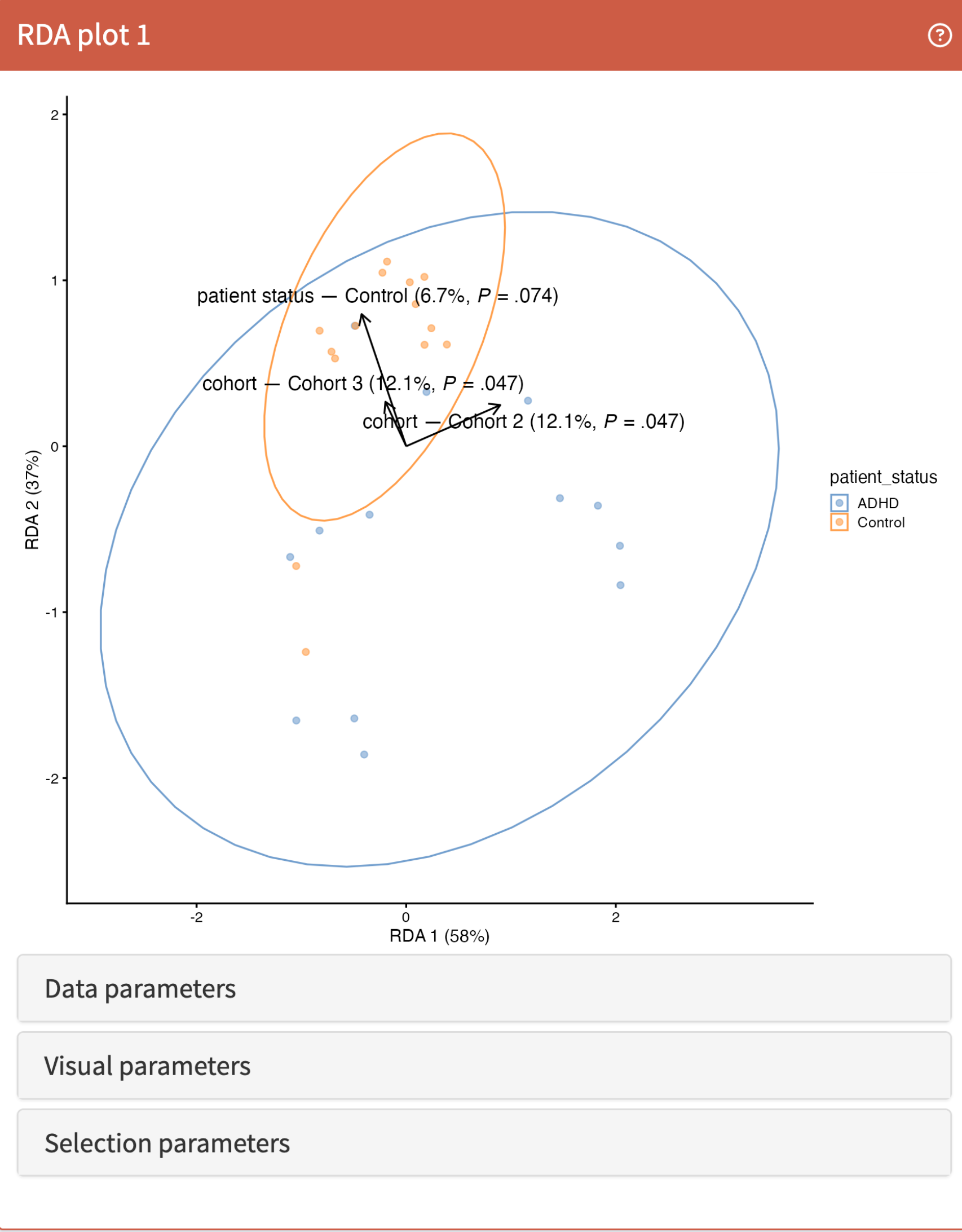
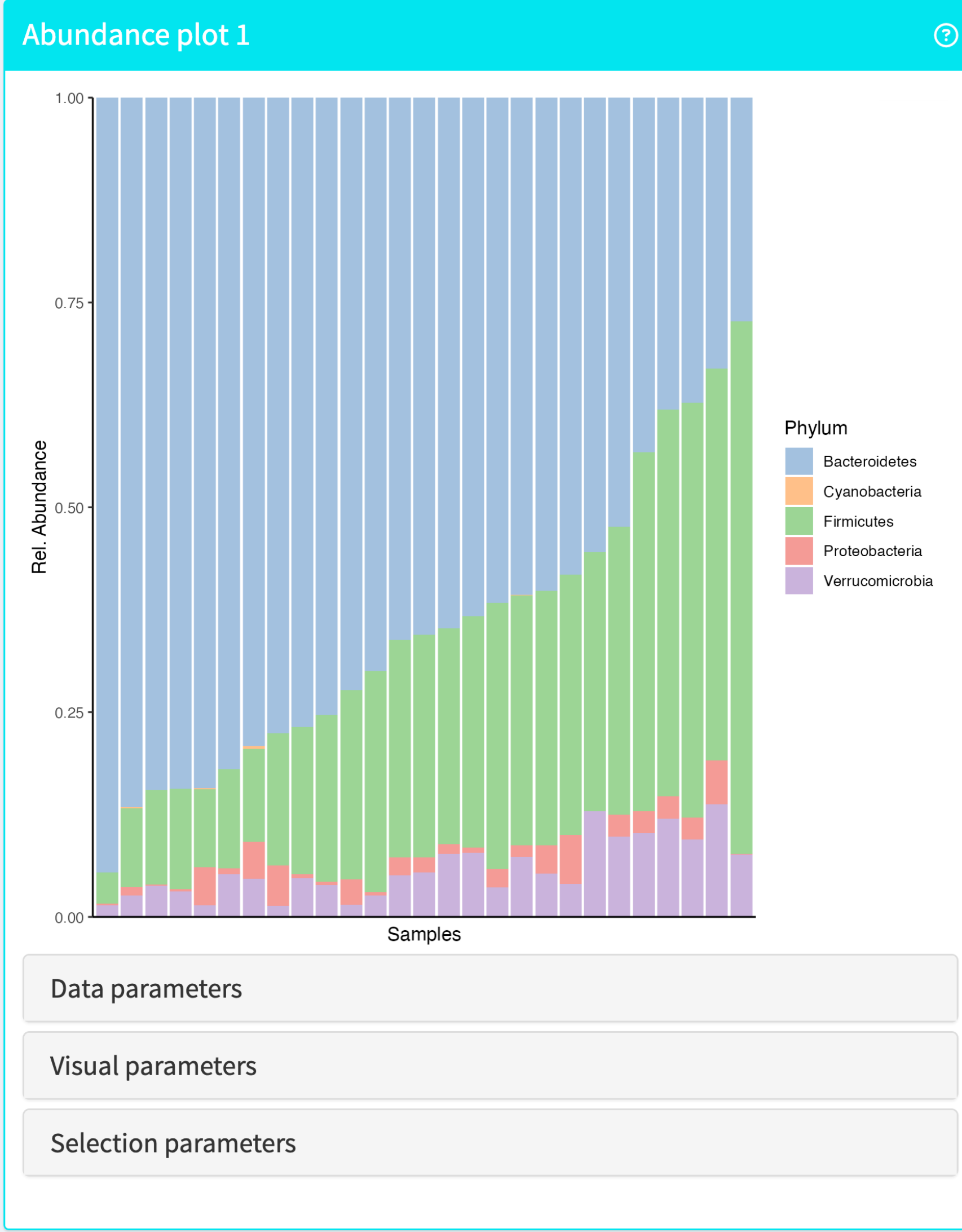
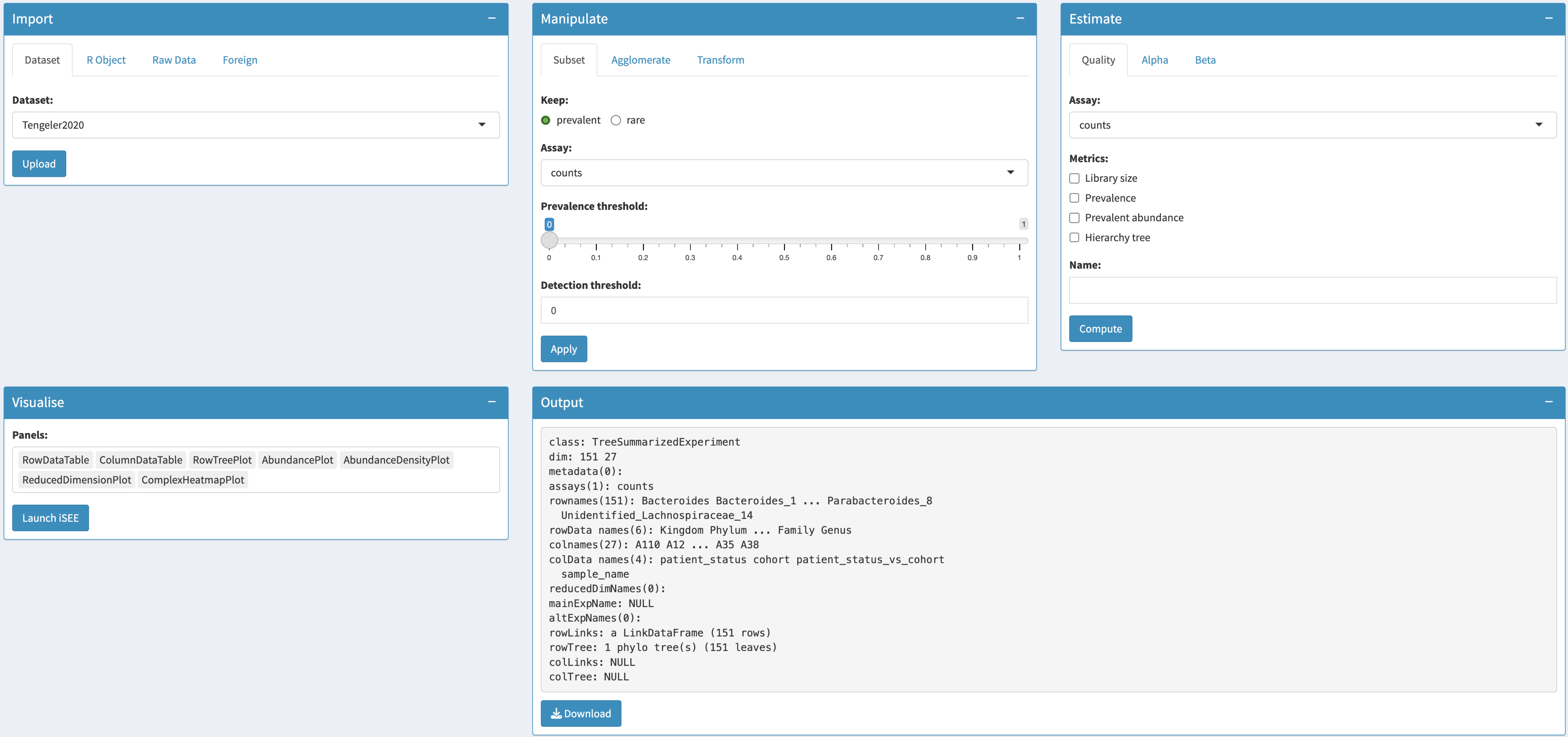
The TreeSE data container

Under the hood, miaDash uses a TreeSummarizedExperiment (TreeSE) object to store and modify microbiome datasets. TreeSE is an all-in-one data container designed for hierarchical data [3]. It can store assays, side information on features and samples, hierarchy trees, alternative experiments and reduced dimensions.



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References:
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2. Rue-Albrecht K, Marini F, Sonesson C, Lun ATL (2018). "iSEE: Interactive SummarizedExperiment Explorer." *F1000Research*, 7, 741.
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