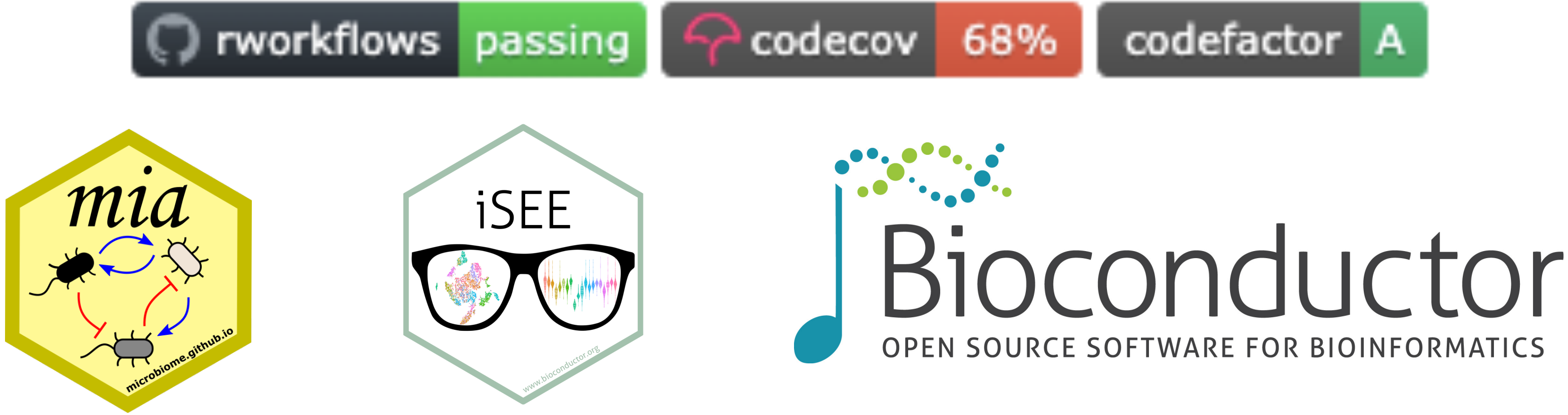


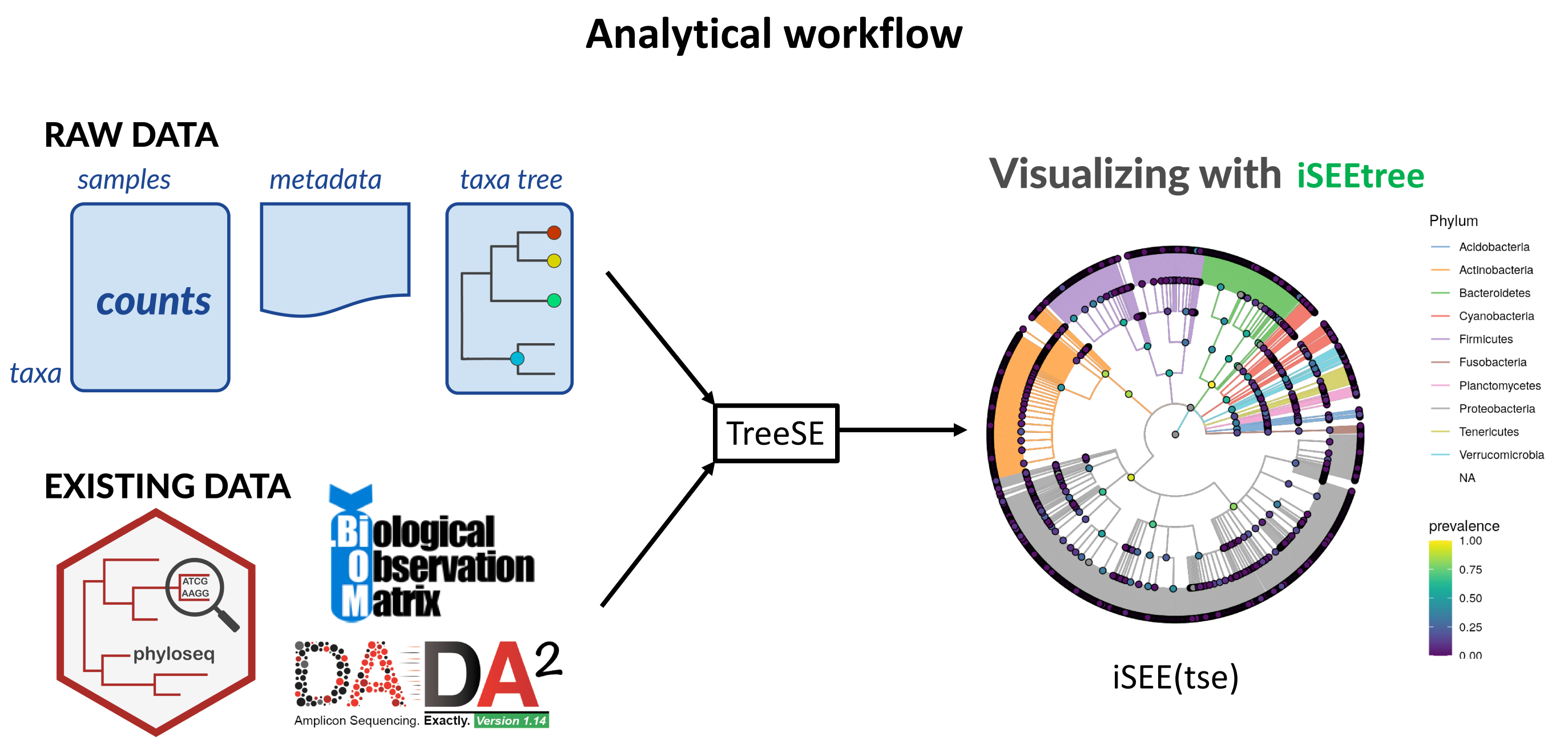
# iSEEtrees: an R package for the interactive visualisation of microbiome data



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## The Problem

Visual exploration is a key step of microbiome data analysis, as it reveals the nature of the data and helps draw informed conclusions from it. However, currently available methods require basic knowledge of R programming and microbiome data structures. Here, we present iSEEtrees, an R/Bioconductor shiny app for the **visualisation and interactive exploration of microbiome data** in the form of TreeSummarizedExperiment (TreeSE).

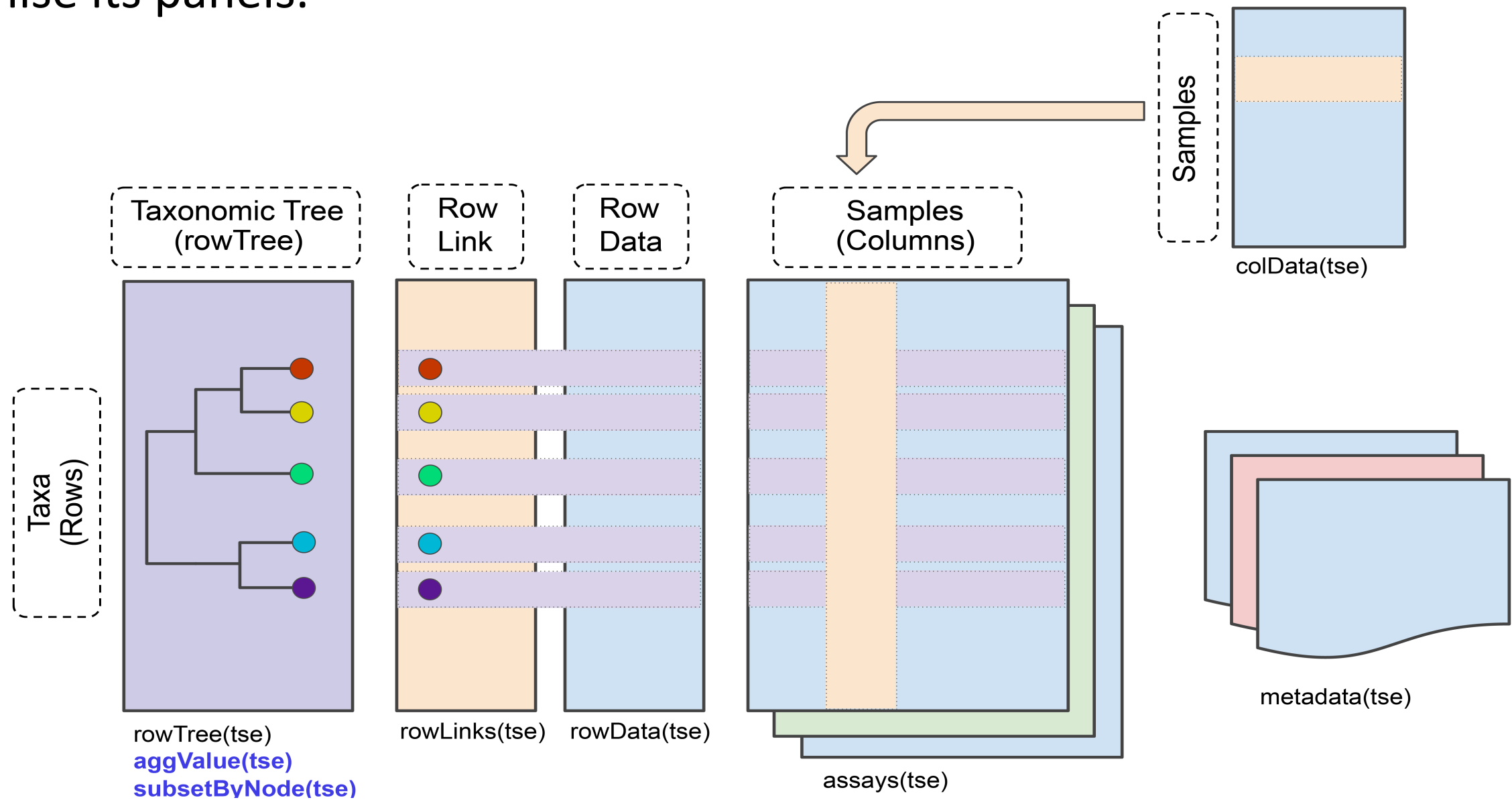


## The App

The iSEEtrees app provides a **customisable set of panels** describing different aspects of the microbiome community under investigation. For each panel, several parameters are available to transform data (*Data parameters*), control aesthetics (*Visual parameters*) and select a subset of the data (*Selection parameters*). Users can also view and modify the underlying R scripts and ultimately download plots as images for publishing and reporting purposes.

## The TreeSE container

TreeSE is a **data structure designed for hierarchical data** such as the microbiome [1]. Its key components include one or more abundance tables (*assays*), sample metadata (*colData*), feature metadata (*rowData*) and a phylogenetic tree (*rowTree*). iSEEtrees uses information from any of those items to generate and customise its panels.



## The Future

We aim to expand the catalogue of iSEEtrees graphics and add more interactive features to the existing panels. Also, a **completely web-based app** (iSEEbug) is under development. Feedback and contributions are welcome!

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