iSEETheBook

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Preface

This book compiles essential knowledge about *iSEE*, an R package released through the Bioconductor project.

This book covers essential knowledge for three main groups of users:

- End users interacting with the graphical user interface in their web browser.
- Developers of scripted web-applications using iSEE to showcase data sets.
- Developers of extensions contributing new functionality and packages to the iSEE ecosystem.

See Rue-Albrecht et al. (2018) for the original publication.

1 Introduction

iSEE is a Bioconductor package designed to produce interactive web applications for the visualisation of biological assays (Figure 1.1).
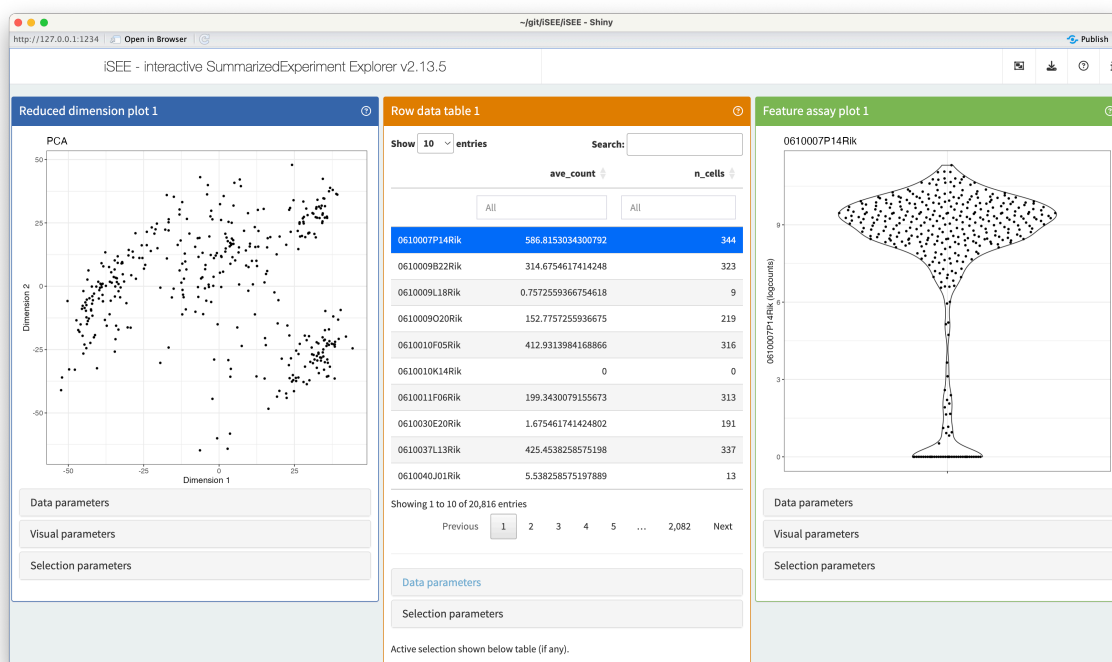

Figure 1.1: The iSEE app interface.

Initiated in 2017 with single-cell RNA-sequencing in mind, *iSEE* was designed in such a way that it naturally handles any biological assay that can be stored in a rectangular matrix of features (in rows) and samples (in columns).

What makes *iSEE* stand out from other interactive web-application is its focus on the *SummarizedExperiment* class (Figure 1.2), a data structure is widely used throughout the Bioconductor project, from bulk to single-cell experiments.

The well-defined and stable *SummarizedExperiment* data structure makes it easy for *iSEE* to automatically detect information commonly stored in dedicated components of *Summarized-*
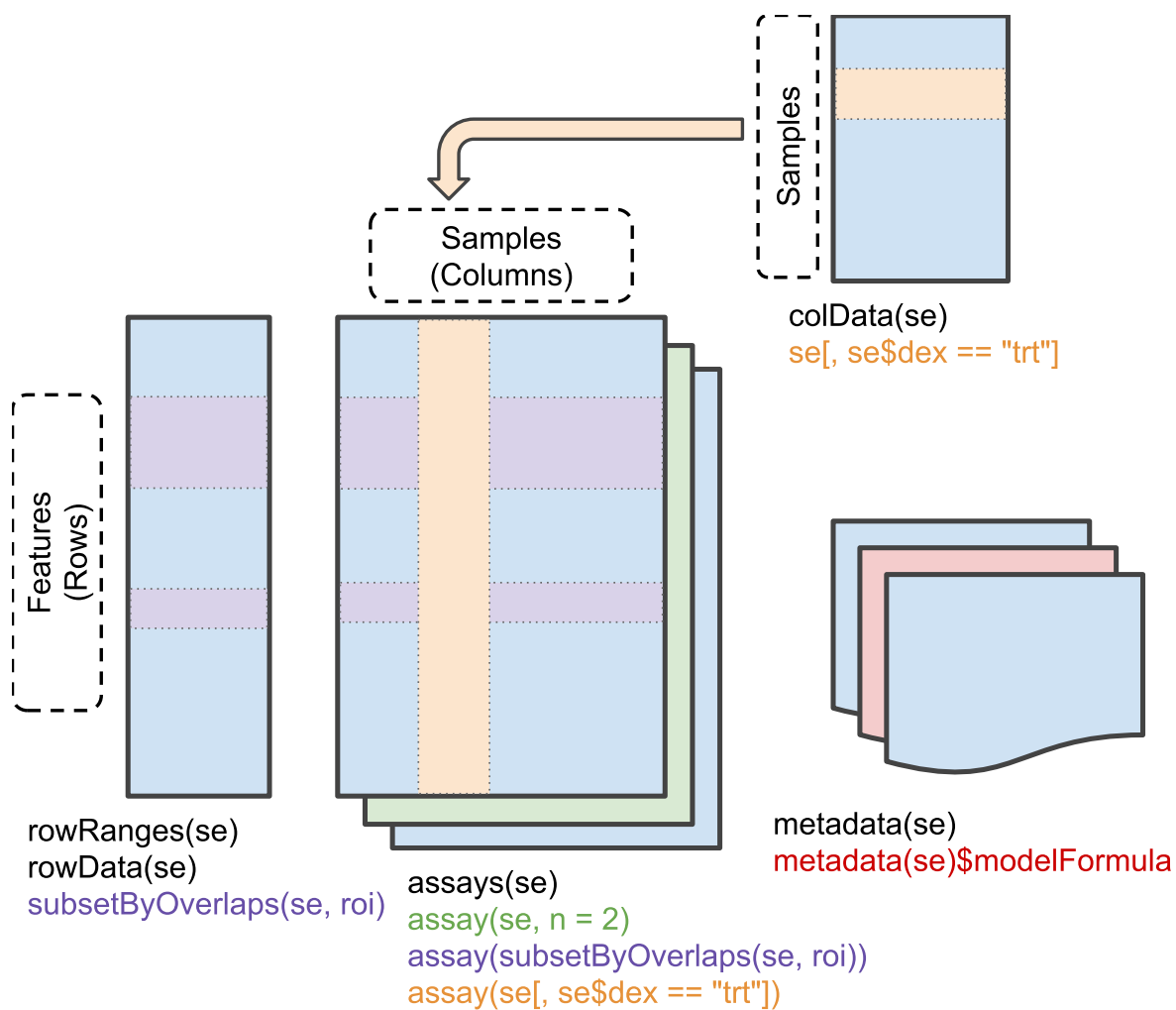
Figure 1.2: Schematic representation of the SummarizedExperiment class (reproduced from the vignette of the *SummarizedExperiment* package).

Experiment objects and display that information in a range of interactive panels, including tables and plots.

2 The user interface

In this chapter, we describe the contents and layout of a standard *iSEE* app.

Specifically, we focus on the appearance of the interactive point-and-click interface presented to end-users who come to simply explore the data set without any programming knowledge required.

Illustrative screenshots are taken from the *iSEE* app produced by the example code given in the help page of the `iSEE()` function, which can be access from an *R* console by typing either `help(iSEE)` or `?iSEE`.

Under entirely default settings, data sets loaded into the *iSEE* app are automatically parsed for standard information stored in *SummarizedExperiment* objects. Based on the information available and a set of eight core panel types designed to display different pieces of information, the `iSEE()` function automatically populates the interface with one panel of each type for which the relevant information is available.

The example code given in the help page of the `iSEE()` function produces an *iSEE* app that showcases all eight core panel types:
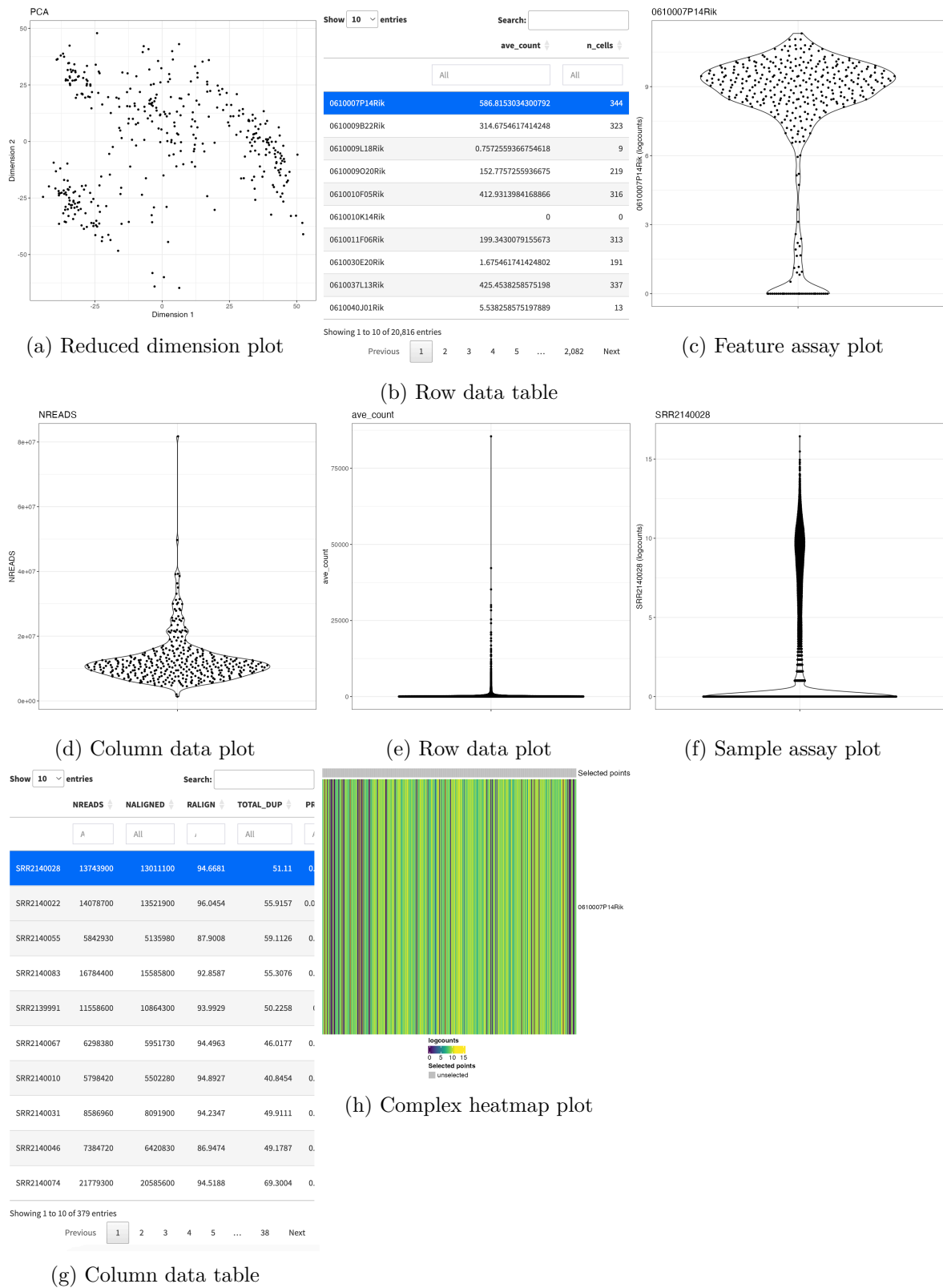
(a) Reduced dimension plot

(b) Row data table

(c) Feature assay plot

(d) Column data plot

(e) Row data plot

(f) Sample assay plot

(g) Column data table

(h) Complex heatmap plot

Figure 2.1: Core panel types in the *iSEE* package.

References

Rue-Albrecht, Kevin, Federico Marini, Charlotte Soneson, and Aaron T. L. Lun. 2018. "ISEE: Interactive Summarizedexperiment Explorer." *F1000Research* 7: 741. https://doi.org/10.12688/f1000research.14966.1.