

## Supplementary Figures—“*scater*: pre-processing, quality control, normalisation and visualisation of single-cell RNA-seq data in R”

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Supplementary Figures—an overview of the SCESet class; an overview of the *scater* ecosystem; examples of using the *scater* GUI.

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### Supplementary Figures

### SCESet: an R S4 class for single-cell RNA-seq data

Inherits Bioconductor's ExpressionSet class, so contains all ExpressionSet slots not listed below

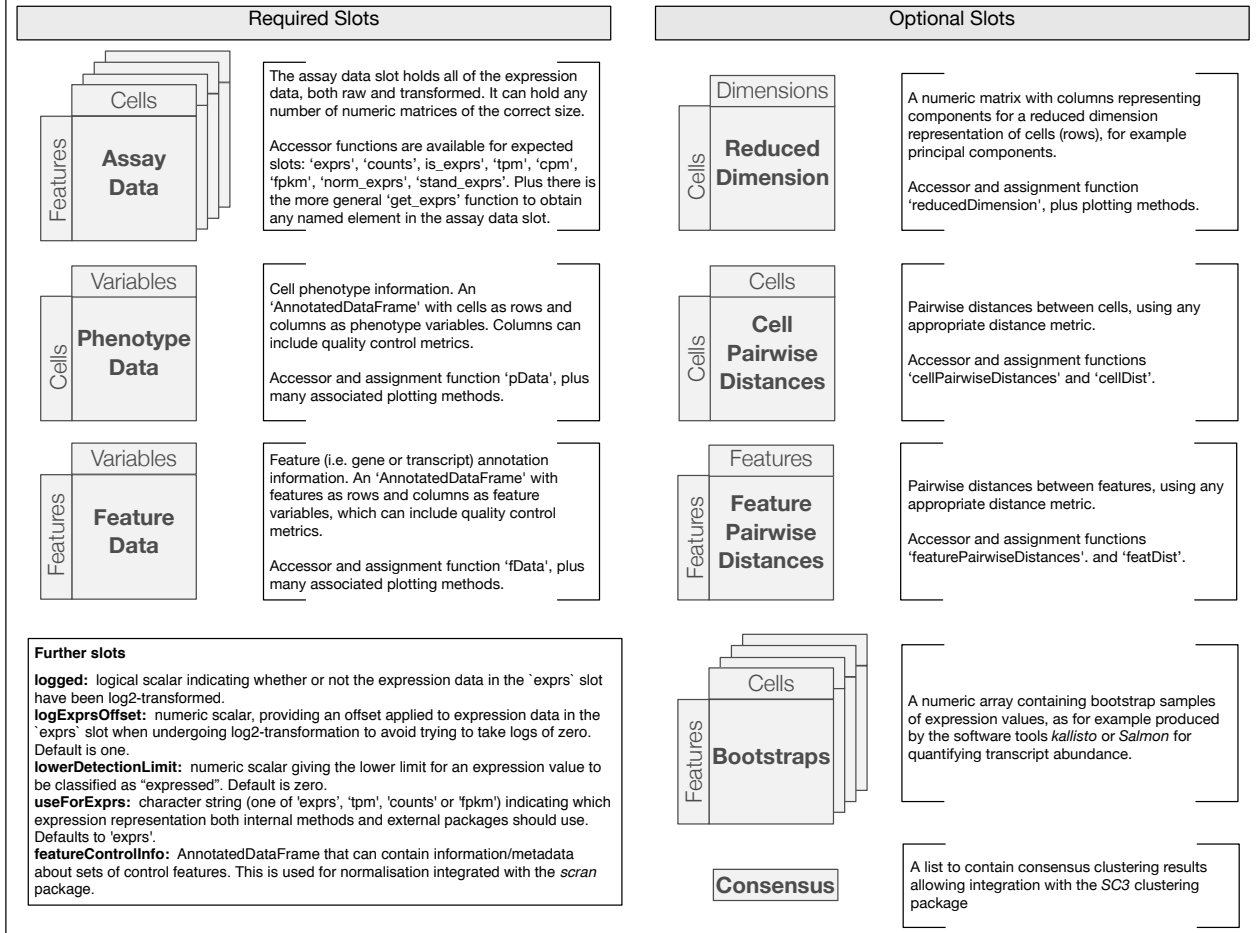


FIG. 1: An overview of the SCESet class that underpins the *scater* package. Building on Bioconductor's ExpressionSet class, it is a fully-featured, sophisticated and flexible data class tailored to scRNA-seq data.

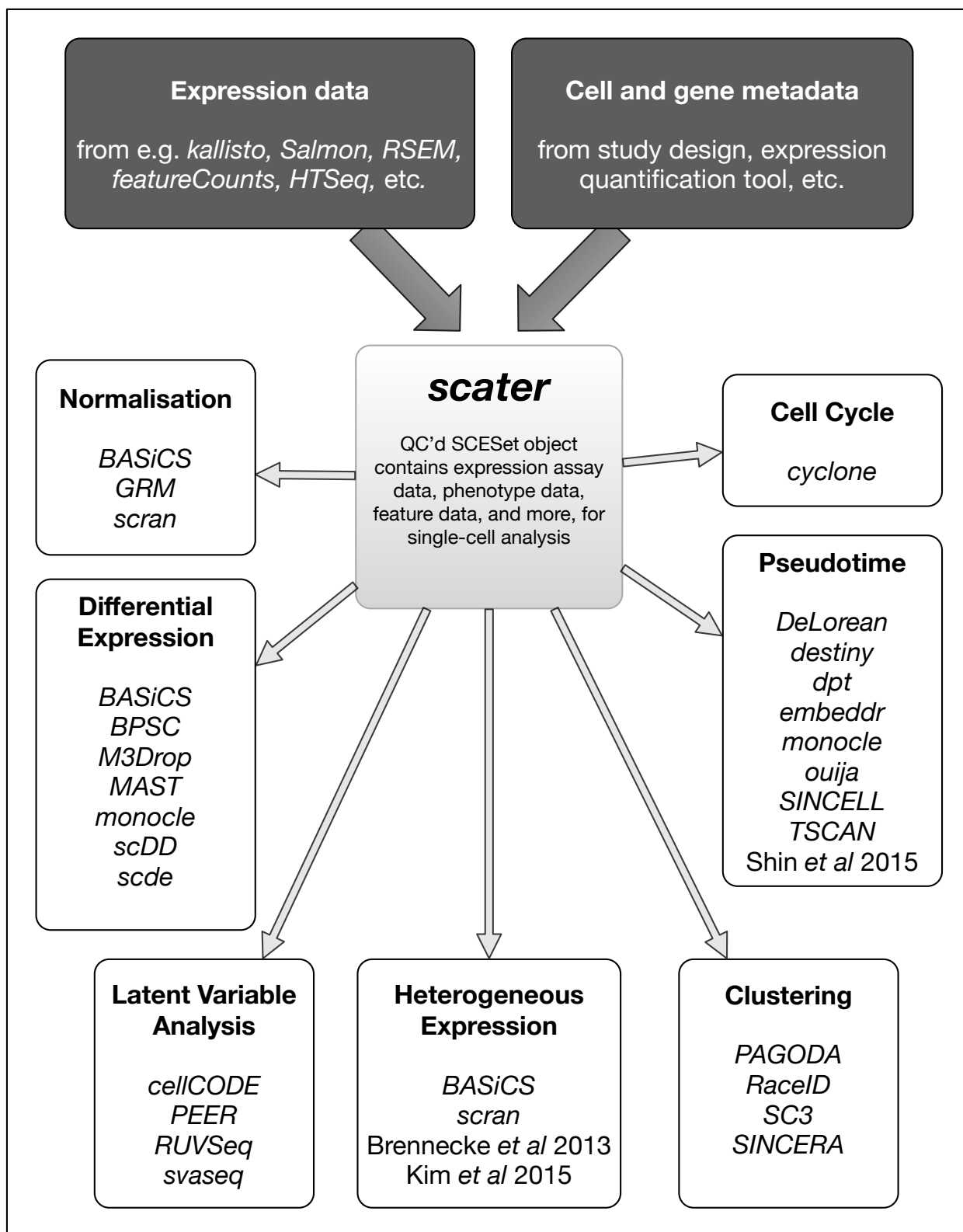


FIG. 2: An overview of the *scater* ecosystem. The SCESet class in *scater* acts as a convenient hub for datasets so that many other methods and tools implemented in R can be applied.

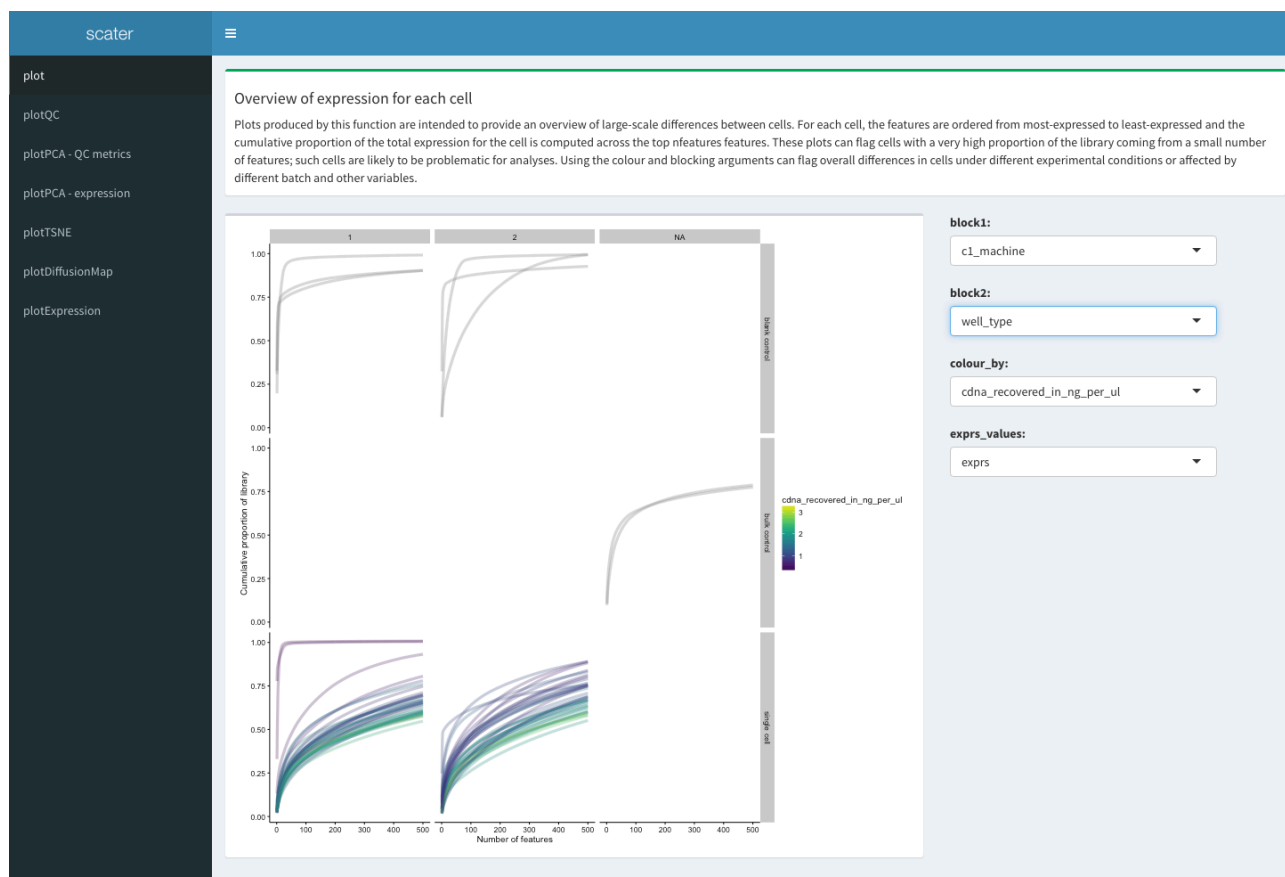


FIG. 3: The landing page for the *scater* graphical user interface (GUI).

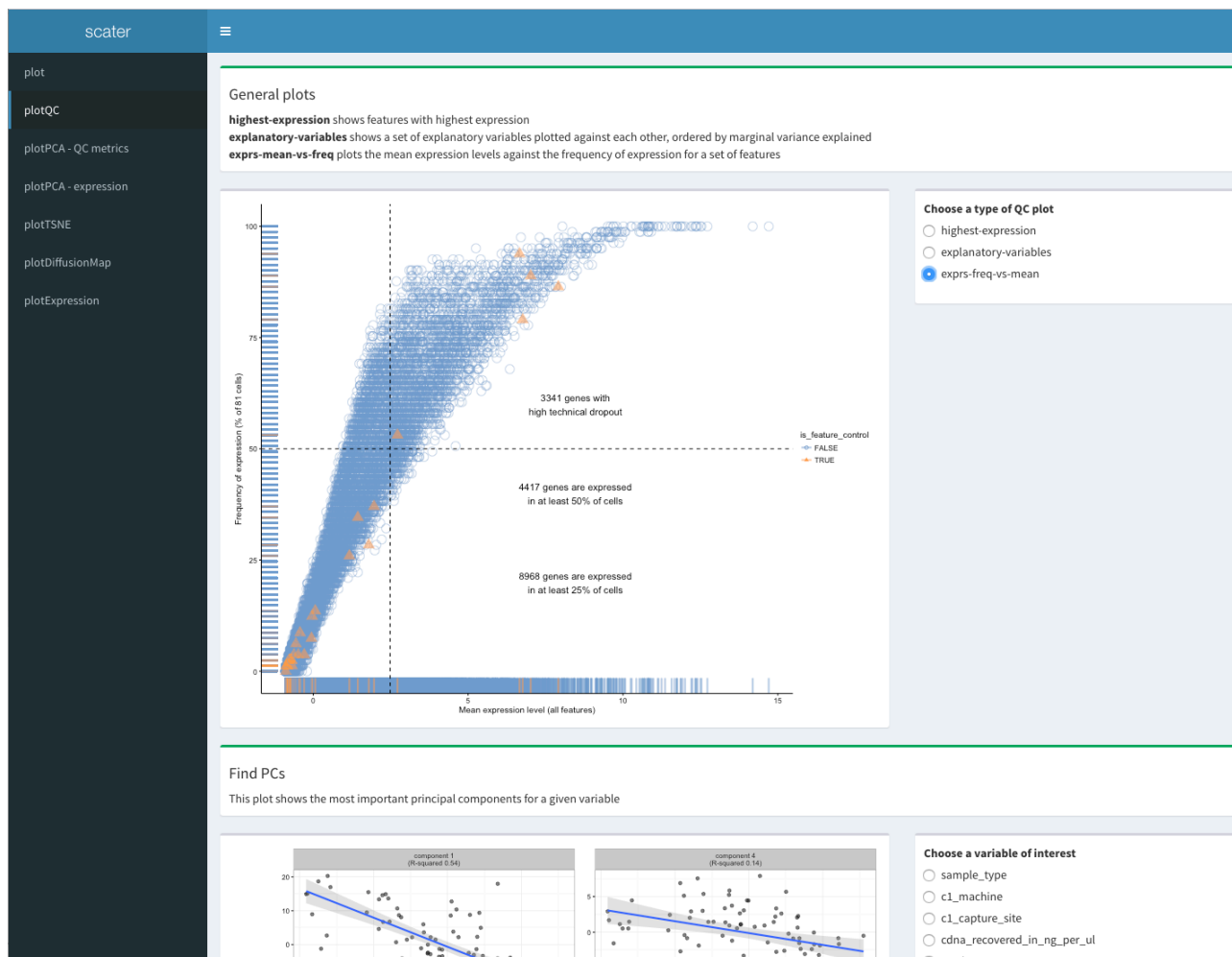


FIG. 4: The plotQC page for the *scater* graphical user interface (GUI).



FIG. 5: The plotPCA - QC (PCA on QC metrics) page for the *scater* graphical user interface (GUI).