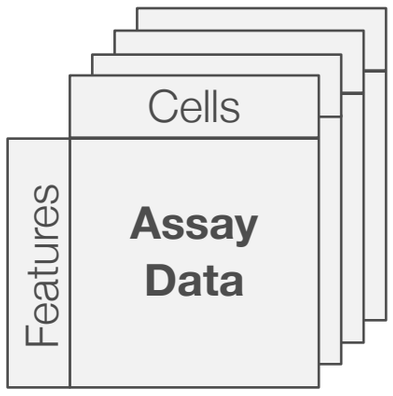
SCESet: an R S4 class for single-cell RNA-seq data

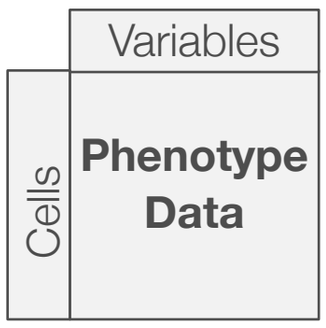
Inherits Bioconductor's ExpressionSet class, so contains all ExpressionSet slots not listed below

Required Slots



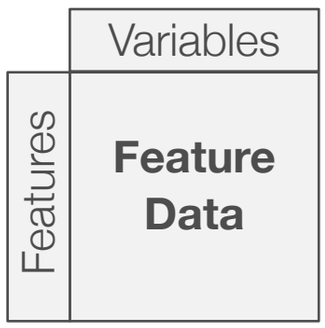
The assay data slot holds all of the expression data, both raw and transformed. It can hold any number of numeric matrices of the correct size.

Accessor functions are available for expected slots: ‘exprs', ‘counts’, is_exprs', ‘tpm', ‘cpm', ‘fpkm', ‘norm_exprs', ‘stand_exprs’. Plus there is the more general ‘get_exprs’ function to obtain any named element in the assay data slot.



Cell phenotype information. An ‘AnnotatedDataFrame' with cells as rows and columns as phenotype variables. Columns can include quality control metrics.

Accessor and assignment function ‘pData', plus many associated plotting methods.



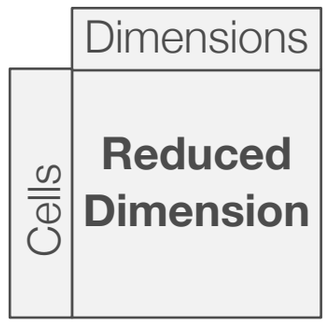
Feature (i.e. gene or transcript) annotation information. An ‘AnnotatedDataFrame' with features as rows and columns as feature variables, which can include quality control metrics.

Accessor and assignment function ‘fData', plus many associated plotting methods.

Further slots

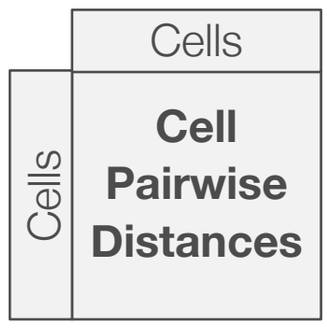
logged: logical scalar indicating whether or not the expression data in the `exprs` slot have been log2-transformed.
logExprsOffset: numeric scalar, providing an offset applied to expression data in the `exprs` slot when undergoing log2-transformation to avoid trying to take logs of zero. Default is one.
lowerDetectionLimit: numeric scalar giving the lower limit for an expression value to be classified as “expressed”. Default is zero.
useForExprs: character string (one of 'exprs’, ‘tpm', 'counts' or 'fpkm') indicating which expression representation both internal methods and external packages should use. Defaults to 'exprs'.
featureControlInfo: AnnotatedDataFrame that can contain information/metadata about sets of control features. This is used for normalisation integrated with the *scran* package.

Optional Slots



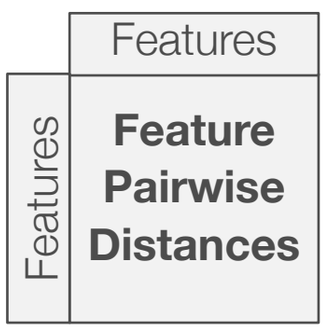
A numeric matrix with columns representing components for a reduced dimension representation of cells (rows), for example principal components.

Accessor and assignment function ‘reducedDimension', plus plotting methods.



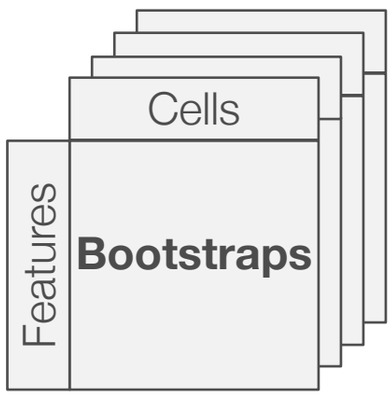
Pairwise distances between cells, using any appropriate distance metric.

Accessor and assignment functions ‘cellPairwiseDistances' and ‘cellDist’.



Pairwise distances between features, using any appropriate distance metric.

Accessor and assignment functions ‘featurePairwiseDistances'. and ‘featDist’.



A numeric array containing bootstrap samples of expression values, as for example produced by the software tools *kallisto* or *Salmon* for quantifying transcript abundance.

Consensus

A list to contain consensus clustering results allowing integration with the *SC3* clustering package