Bioconductor Experiment Classes Cheatsheet

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General

The aim of this file is to provide a schematic organization of the "Bioconductor Experiment" classes in terms of attributes and methods describing them.

The SummarizedExperiment Class

The SummarizedExperiment object is defined in Bioconductor since BioC version 3.2 (R-3.2). It's aim is to flexibly easily provide an instrument for sequencing and microarray data experiments handling.

SummarizedExperiment Refs

1. http://bioconductor.org/packages/release/bioc/html/SummarizedExperiment.html

2. https://bioconductor.org/packages/release/bioc/vignettes/SummarizedExperiment/inst/doc/SummarizedExperiment.html

SummarizedExperiment Cheatsheet

Attribute	Class	Description
assays	list	list of named data matrices
colData	DataFrame	describes samples (columns) units
rowData	DataFrame	describes features (rows) units
Other attribute	Class	Description
elementMetadata	DataFrame	describes additional information on the experiment
metadata	list	list of elementMetadata
NAMES	character_OR_NULL	NOT CLEAR
Method	Output	Description
SummarizedExperiment	SummarizedExperiment	constructor
assays	list	gets/sets a list of assays
assay	matrix	gets/sets the first assay
rowData	DataFrame	gets/sets the rowData structure
colData	DataFrame	gets/sets the colData structure
[	SummarizedExperiment	subsets the object like a matrix/DataFrame
$	DataFrame	operates on the colData columns

The RangedSummarizedExperiment Class

The RagnedSummarizedExperiment class extends the SummarizedExperiment class and is defined in Bioconductor since BioC version 3.2 (R-3.2). It's aim is to provide a more flexible representation of the features in terms of GenomicRanges coordinates.
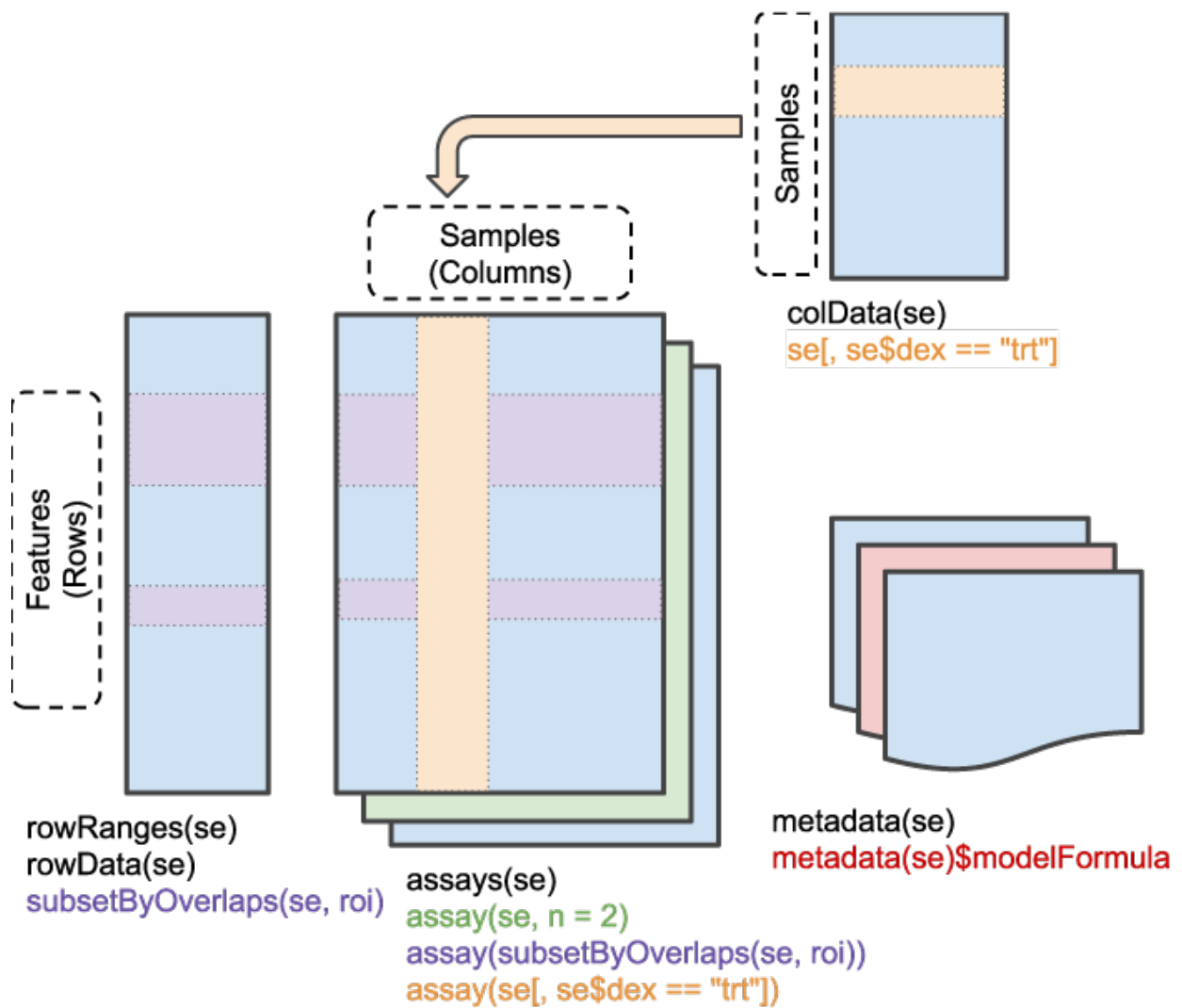
Figure 1: The SummarizedExperiment Representation

RangedSummarizedExperiment Refs

1. http://bioconductor.org/packages/release/bioc/html/SummarizedExperiment.html

2. https://bioconductor.org/packages/release/bioc/vignettes/SummarizedExperiment/inst/doc/SummarizedExperiment.html

RangedSummarizedExperiment Cheatsheet

Attribute	Class	Description
rowRanges	GenomicRanges	describes features as genomic coordinates
Method	Output	Description
SummarizedExperiment	RangedSummarizedExperiment	constructor (give rowRanges)
RangedSummarizedExperiment	RangedSummarizedExperiment	constructor
rowRanges	GenomicRanges	gets/sets the rowRanges structure
subsetByOverlaps	RangedSummarizedExperiment	subsets the object with overlapped ranges

The SingleCellExperiment Class

The SingleCellExperiment object is defined in Bioconductor since BioC version 3.6 (R-3.4) extending the RangedSummarizedExperiment Bioconductor object.

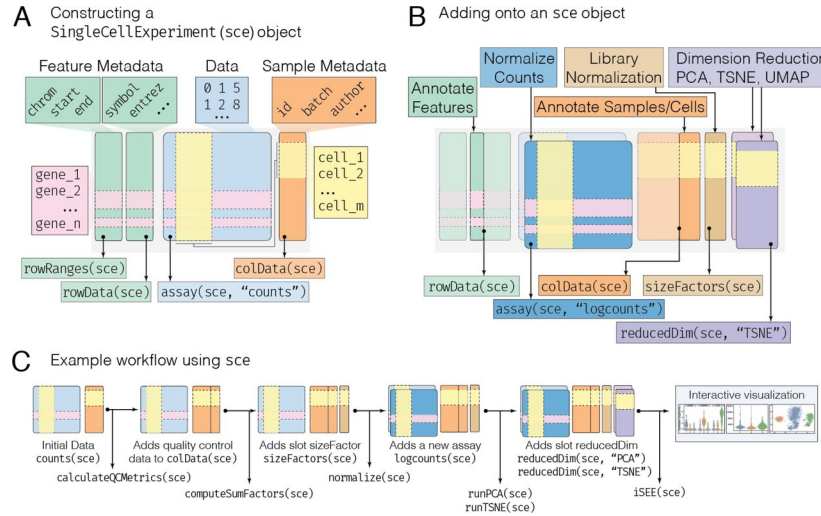For simplicity, exception made when necessary, inherited attributes or methods are not reported.

Figure 2: The SingleCellExperiment Representation

SingleCellExperiment Refs

1. http://bioconductor.org/packages/release/bioc/html/SingleCellExperiment.html

2. https://bioconductor.org/packages/release/bioc/vignettes/SingleCellExperiment/inst/doc/intro.html

SingleCellExperiment Cheatsheet

Attribute	Class	Description
assays	list	list of named data matrices
colData	DataFrame	describes samples (columns) units
rowData	DataFrame	describes features (rows) units
rowRanges	GenomicRanges	describes features as genomic coordinates
int_colData	DataFrame	as colData, but internal (not for direct access)
reducedDims	SimpleList	list of matrices representing reduced dimentions of data
Other attribute	Class	Description
elementMetadata	DataFrame	describes additional information on the experiment
metadata	list	list of elementMetadata
int_metadata	list	see metadata, but internal (not for direct access)
int_elementMetadata	DataFrame	see elementMetadata, but internal (not for direct access)
NAMES	character_OR_NULL	NOT CLEAR
Method	Output	Description
SingleCellExperiment	SingleCellExperiment	constructor
isSpike	logical	gets/sets rows corresponding to spike-in transcripts
spikeNames	character	the spike-ins in the object
sizeFactors	numeric	gets/sets the factors (columns) size (based on reads amount)
clearSizeFactors	SingleCellExperiment	clears size factors and returns the new SingleCellExperiment object
sizeFactorNames	character	gets/sets the names of the sizeFacors (if present)
colData	DataFrame	gets/sets the colData structure
rowData	DataFrame	gets/sets the rowData structure
rowRanges	GenomicRanges	gets/sets the rowRanges structure
reducedDim	matrix	gets/sets one element of reducedDims list
reducedDims	list	gets/sets the reducedDims list
reducedDimNames	character	gets/sets the reducedDims list names