Package 'ExperimentSubset'

February 19, 2026

Type Package

Title Manages subsets of data with Bioconductor Experiment objects

Version 1.20.0

Date 2021-05-09

Description
Experiment objects such as the SummarizedExperiment or SingleCellExperiment are data containers for one or more matrix-like assays along with the associated row and column data. Often only a subset of the original data is needed for down-stream analysis. For example, filtering out poor quality samples will require excluding some columns before analysis. The ExperimentSubset object is a container to efficiently manage different subsets of the same data without having to make separate objects for each new subset.

License MIT + file LICENSE

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Depends R (>= 4.0.0), SummarizedExperiment, SingleCellExperiment, SpatialExperiment, TreeSummarizedExperiment

biocViews Infrastructure, Software, DataImport, DataRepresentation

Imports methods, Matrix, S4Vectors

Suggests BiocStyle, knitr, rmarkdown, testthat, covr, stats, scran, scater, scds, TENxPBMCData, airway

VignetteBuilder knitr

Collate 'allClasses.R' 'allGenerics.R' 'ExperimentSubset.R' 'SubsetRangedSummarizedExperiment.R' 'SubsetSingleCellExperiment.R' 'SubsetSummarizedExperiment.R' 'SubsetSpatialExperiment.R' 'SubsetTreeSummarizedExperiment.R'

git_url https://git.bioconductor.org/packages/ExperimentSubset

git_branch RELEASE_3_22

git_last_commit fe8c338

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2026-02-18

Author Irzam Sarfraz [aut, cre] (ORCID:
<https://orcid.org/0000-0001-8121-792X>),
Muhammad Asif [aut, ths] (ORCID:
<https://orcid.org/0000-0003-1839-2527>),
Joshua D. Campbell [aut] (ORCID:
<https://orcid.org/0000-0003-0780-8662>)

Maintainer Irzam Sarfraz <irzam9095@gmail.com>

Contents

AssaySubset . . . 2
AssaySubset-class . . . 3
createSubset . . . 4
ExperimentSubset . . . 5
getSubsetAssay . . . 6
reducedDimNames . . . 7
reducedDimNames<- . . . 8
reducedDims<- . . . 9
reducedDims<-,ANY-method . . . 9
setSubsetAssay . . . 10
subsetAssayCount . . . 11
subsetAssayNames . . . 12
subsetColData . . . 13
subsetColLinks . . . 14
subsetColnames . . . 15
subsetCount . . . 16
subsetDim . . . 17
subsetNames . . . 18
subsetParent . . . 19
SubsetRangedSummarizedExperiment-class . . . 20
subsetRowData . . . 20
subsetRowLinks . . . 21
subsetRownames . . . 22
SubsetSingleCellExperiment-class . . . 23
subsetSpatialCoords . . . 24
subsetSpatialData . . . 24
SubsetSpatialExperiment-class . . . 25
SubsetSummarizedExperiment-class . . . 25
subsetSummary . . . 26
SubsetTreeSummarizedExperiment-class . . . 27

Index **28**

`AssaySubset` *AssaySubset constructor*

Description

Constructor for creating a experiment object internally by the `ExperimentSubset` object. Should not be used directly by the user.

Usage

```
AssaySubset(
  subsetName = "subset",
  rowIndices = NULL,
  colIndices = NULL,
  parentAssay = "counts",
  internalAssay = NULL
)
```

Arguments

subsetName	character(1) Name of the subset.
rowIndices	vector("numeric") Indices of the rows to include in the subset.
colIndices	vector("numeric") Indices of the columns to include in the subset.
parentAssay	character(1) Name of the parent of this subset.
internalAssay	An internal Experiment object to store additional subset data.

Value

A AssaySubset object.

AssaySubset-class *An S4 class to manage subset representation.*

Description

An S4 class to manage subset representation.

Slots

subsetName character(1) Name of the subset.

rowIndices vector("numeric") Indices of the rows to include in the subset.

colIndices vector("numeric") Indices of the columns to include in the subset.

parentAssay character(1) Name of the parent of this subset.

internalAssay SummarizedExperiment An internal experiment object to store additional subset data.

createSubset *Subset creation method for ExperimentSubset objects*

Description

Create a subset from an already available assay in the input ExperimentSubset object by specifying the rows and columns to include in the subset.

Usage

```
createSubset(x, subsetName, rows = NULL, cols = NULL, parentAssay = NULL)

## S4 method for signature 'SubsetRangedSummarizedExperiment'
createSubset(x, subsetName, rows = NULL, cols = NULL, parentAssay = NULL)

## S4 method for signature 'SubsetSingleCellExperiment'
createSubset(x, subsetName, rows = NULL, cols = NULL, parentAssay = NULL)

## S4 method for signature 'SubsetSummarizedExperiment'
createSubset(x, subsetName, rows = NULL, cols = NULL, parentAssay = NULL)

## S4 method for signature 'SubsetSpatialExperiment'
createSubset(x, subsetName, rows = NULL, cols = NULL, parentAssay = NULL)

## S4 method for signature 'SubsetTreeSummarizedExperiment'
createSubset(x, subsetName, rows = NULL, cols = NULL, parentAssay = NULL)
```

Arguments

x	ExperimentSubset Specify the object from which a subset should be created. Input can also be any object inherited from SummarizedExperiment for immediate conversion and subset formation. A list of slots can also be passed to directly construct an ES object from matrices similar to SE and SCE constructors.
subsetName	character(1) Specify the name of the subset to create.
rows	vector("numeric") Specify the rows to include in this subset. If missing or NULL, all rows are included in the subset. Values can be numeric or character. Default NULL.
cols	vector("numeric") Specify the columns to include in this subset. If missing or NULL, all columns are included in the subset. Values can be numeric or character. Default NULL.
parentAssay	character(1) Specify the parent assay of the subset. This parent assay must already be available in the ExperimentSubset object. If NULL, the first available main assay will be marked as parent. Default NULL.

Value

An ExperimentSubset object that now contains the newly created subset.

Examples

```
data(sce_chcl, package = "scds")
es <- ExperimentSubset(sce_chcl)
es <- createSubset(es,
"subset1",
rows = c(10,11,50,56,98,99,102,105,109, 200),
cols = c(20,21,40,45,90,99,100,123,166,299),
parentAssay = "counts")
es
```

`ExperimentSubset` *ExperimentSubset constructor*

Description

This constructor function is used to setup the `ExperimentSubset` object, either through manually specifying the `assays`, `rowData`, `colData` or directly by passing either a `SingleCellExperiment` or `SummarizedExperiment` objects or objects inherited by these classes. A subset can also be directly created by passing a named `list` to the `subset` parameter. This named `list` should have parameter values named as `subsetName`, `rows`, `cols` and `parentAssay`.

Usage

```
ExperimentSubset(
  x,
  subset = list(subsetName = NA, rows = NA, cols = NA, parentAssay = NA)
)
```

Arguments

`x`	An experiment object if direct conversion is required or a list of slots to pass onto `SingleCellExperiment` constructor to generate experiment object from general data.
`subset`	A named `list` if a subset should be created from within the constructor. Named parameters in this list should be `subsetName`, `rows`, `cols` and `parentAssay`.

Value

A `ExperimentSubset` object.

Examples

```
data(sce_chcl, package = "scds")
es <- ExperimentSubset(sce_chcl)
es
```

getSubsetAssay *Get subset assay from an* ExperimentSubset *object.*

Description

Get subset assay from an ExperimentSubset object.

Usage

```
getSubsetAssay(x, subsetName)

## S4 method for signature 'SubsetRangedSummarizedExperiment,character'
getSubsetAssay(x, subsetName)

## S4 method for signature 'SubsetSingleCellExperiment,character'
getSubsetAssay(x, subsetName)

## S4 method for signature 'SubsetSummarizedExperiment,character'
getSubsetAssay(x, subsetName)

## S4 method for signature 'SubsetSpatialExperiment,character'
getSubsetAssay(x, subsetName)

## S4 method for signature 'SubsetTreeSummarizedExperiment,character'
getSubsetAssay(x, subsetName)
```

Arguments

x	Input ExperimentSubset object.
subsetName	Specify 'subset name' or 'subset assay name' to fetch the assay from.

Value

Subset assay

Examples

```
data(sce_chcl, package = "scds")
es <- ExperimentSubset(sce_chcl)
es <- createSubset(es,
"subset1",
rows = c(10,11,50,56,98,99,102,105,109, 200),
cols = c(20,21,40,45,90,99,100,123,166,299),
parentAssay = "counts")
getSubsetAssay(es, "subset1")
```

reducedDimNames *reducedDimNames*

Description

A wrapper to the reducedDimNames from reducedDims method with additional support for subsets.

Usage

```
reducedDimNames(x, ...)

## S4 method for signature 'ANY'
reducedDimNames(x, ...)

## S4 method for signature 'ANY'
reducedDimNames(x, ...)

## S4 method for signature 'ANY'
reducedDimNames(x, ...)
```

Arguments

x	Input ExperimentSubset object or any object supported by reducedDimNames from reducedDims method.
...	Additional arguments to pass to into the SCE method.

Value

The reducedDimNames from the specified subset or same as reducedDimNames from reducedDims when subsetName is missing.

Examples

```
data(sce_chcl, package = "scds")
es <- ExperimentSubset(sce_chcl)
es <- createSubset(es, "subset1",
rows = c(1:1500), cols = c(1:1500),
parentAssay = "counts")
reducedDims(es, subsetName = "subset1") <- list(
PCA_1 = scater::calculatePCA(assay(es, "subset1")),
PCA_2 = scater::calculatePCA(assay(es, "subset1")))
reducedDimNames(es, subsetName = "subset1")
```

reducedDimNames<- *reducedDimNames<-*

Description

A wrapper to the reducedDimNames<- from reducedDims method with additional support for subsets.

Usage

```
reducedDimNames(x, subsetName) <- value

## S4 replacement method for signature 'ANY'
reducedDimNames(x, subsetName) <- value

## S4 replacement method for signature 'ANY'
reducedDimNames(x, subsetName) <- value

## S4 replacement method for signature 'ANY'
reducedDimNames(x, subsetName) <- value
```

Arguments

x	Input ExperimentSubset object or any object supported by reducedDimNames<- from reducedDims method.
subsetName	Specify the name of the subset to which the reducedDimNames<- should be set to. If missing, reducedDimNames<- from reducedDims method is called on the main object.
value	Input value same as reducedDimNames<- from reducedDims method.

Value

Input object with reducedDimNames<- set.

Examples

```
data(sce_chcl, package = "scds")
es <- ExperimentSubset(sce_chcl)
es <- createSubset(es, "subset1",
rows = c(1:1500), cols = c(1:1500),
parentAssay = "counts")
reducedDims(es, subsetName = "subset1") <- list(
PCA_1 = scater::calculatePCA(assay(es, "subset1")),
PCA_2 = scater::calculatePCA(assay(es, "subset1")))
reducedDimNames(es, subsetName = "subset1") <- c("rDim1", "rDim2")
```

reducedDims<- *reducedDims<-*

Description

A wrapper to the reducedDims<- from reducedDims method with additional support for subsets.

Usage

```
reducedDims(x, subsetName) <- value
```

Arguments

x	Input ExperimentSubset object or any object supported by reducedDims<- from reducedDims method.
subsetName	Specify the name of the subset to which the reducedDims should be set to. If missing, reducedDims<- from reducedDims method is called on the main object.
value	A list of values to set to reducedDims.

Value

Updated input object with reducedDims set.

Examples

```
data(sce_chcl, package = "scds")
es <- ExperimentSubset(sce_chcl)
es <- createSubset(es, "subset1",
rows = c(1:1500), cols = c(1:1500),
parentAssay = "counts")
reducedDims(es, subsetName = "subset1") <- list(
PCA_1 = scater::calculatePCA(assay(es, "subset1")),
PCA_2 = scater::calculatePCA(assay(es, "subset1")))
reducedDims(es, subsetName = "subset1")
```

reducedDims<-,ANY-method *reducedDims<-*

Description

A wrapper to the reducedDims<- from reducedDims method with additional support for subsets.

Usage

```
## S4 replacement method for signature 'ANY'
reducedDims(x, subsetName) <- value
```

Arguments

x	Input ExperimentSubset object or any object supported by reducedDims<- from reducedDims method.
subsetName	Specify the name of the subset to which the reducedDims should be set to. If missing, reducedDims<- from reducedDims method is called on the main object.
value	A list of values to set to reducedDims.

Value

Updated input object with reducedDims set.

---

setSubsetAssay *Method for storing new assays inside subsets in ExperimentSubset objects*

Description

Store a new subset assay inside a specified subset in the input ExperimentSubset object.

Usage

```
setSubsetAssay(x, subsetName, inputMatrix, subsetAssayName)

## S4 method for signature
## 'SubsetRangedSummarizedExperiment,character,ANY,character'
setSubsetAssay(x, subsetName, inputMatrix, subsetAssayName)

## S4 method for signature 'SubsetSingleCellExperiment,character,ANY,character'
setSubsetAssay(x, subsetName, inputMatrix, subsetAssayName)

## S4 method for signature 'SubsetSummarizedExperiment,character,ANY,character'
setSubsetAssay(x, subsetName, inputMatrix, subsetAssayName)

## S4 method for signature 'SubsetSpatialExperiment,character,ANY,character'
setSubsetAssay(x, subsetName, inputMatrix, subsetAssayName)

## S4 method for signature
## 'SubsetTreeSummarizedExperiment,character,ANY,character'
setSubsetAssay(x, subsetName, inputMatrix, subsetAssayName)
```

Arguments

x	ExperimentSubset Specify the input object.
subsetName	character(1) Specify the name of the existing subset inside which the new subset assay should be stored.
inputMatrix	dgCMatrix The input subset assay.
subsetAssayName	character(1) Specify the name of the new assay against the inputMatrix parameter.

Value

Updated ExperimentSubset object with the new assay stored inside the specified subset.

Examples

```
data(sce_chcl, package = "scds")
es <- ExperimentSubset(sce_chcl)
es <- createSubset(es, "subset1",
rows = c(10,11,50,56,98,99,102,105,109, 200),
cols = c(20,21,40,45,90,99,100,123,166,299),
parentAssay = "counts")
counts1p <- assay(es, "subset1")
counts1p[,] <- counts1p[,] + 1
es <- setSubsetAssay(es, "subset1", counts1p, "scaledSubset1")
es
```

---

subsetAssayCount *Count method for subset assays in ExperimentSubset objects*

Description

Get the count of the total available subsets and the subset assays inside these subsets in an ExperimentSubset object.

Usage

```
subsetAssayCount(x)

## S4 method for signature 'SubsetRangedSummarizedExperiment'
subsetAssayCount(x)

## S4 method for signature 'SubsetSingleCellExperiment'
subsetAssayCount(x)

## S4 method for signature 'SubsetSummarizedExperiment'
subsetAssayCount(x)

## S4 method for signature 'SubsetSpatialExperiment'
subsetAssayCount(x)

## S4 method for signature 'SubsetTreeSummarizedExperiment'
subsetAssayCount(x)
```

Arguments

x	ExperimentSubset	Input ExperimentSubset object.

Value

A numeric value representing the sum of the subset count and subset assay count.

Examples

```
data(sce_chcl, package = "scds")
es <- ExperimentSubset(sce_chcl)
es <- createSubset(es,
"subset1",
rows = c(10,11,50,56,98,99,102,105,109, 200),
cols = c(20,21,40,45,90,99,100,123,166,299),
parentAssay = "counts")
assay(es, "subset1",
subsetAssayName = "subset1pAssay") <- assay(es, "subset1")[,] + 1
subsetAssayCount(es)
```

---

subsetAssayNames *Name retrieval method for all subset assays in ExperimentSubset objects*

Description

Retrieves the names of all the subsets as well as the subset assays.

Usage

```
subsetAssayNames(x)

## S4 method for signature 'SubsetRangedSummarizedExperiment'
subsetAssayNames(x)

## S4 method for signature 'SubsetSingleCellExperiment'
subsetAssayNames(x)

## S4 method for signature 'SubsetSummarizedExperiment'
subsetAssayNames(x)

## S4 method for signature 'SubsetSpatialExperiment'
subsetAssayNames(x)

## S4 method for signature 'SubsetTreeSummarizedExperiment'
subsetAssayNames(x)
```

Arguments

x	ExperimentSubset	Input ExperimentSubset object.

Value

A vector containing the names of the subsets and the subset assays available in the input ExperimentSubset object.

Examples

```
data(sce_chcl, package = "scds")
es <- ExperimentSubset(sce_chcl)
es <- createSubset(es, "subset1",
rows = c(10,11,50,56,98,99,102,105,109, 200),
cols = c(20,21,40,45,90,99,100,123,166,299),
parentAssay = "counts")
assay(es, "subset1",
subsetAssayName = "subset1pAssay") <- assay(es, "subset1")[,] + 1
subsetAssayNames(es)
```

`subsetColData` *Accessor method for colData from subsets in ExperimentSubset objects*

Description

Get `colData` from a subset.

Set `colData` to a subset.

Usage

```
subsetColData(x, subsetName, parentColData)

subsetColData(x, subsetName) <- value

## S4 method for signature 'SubsetRangedSummarizedExperiment,character'
subsetColData(x, subsetName, parentColData)

## S4 replacement method for signature
## 'SubsetRangedSummarizedExperiment,character,DataFrame'
subsetColData(x, subsetName) <- value

## S4 method for signature 'SubsetSingleCellExperiment,character'
subsetColData(x, subsetName, parentColData)

## S4 replacement method for signature 'SubsetSingleCellExperiment,character,DataFrame'
subsetColData(x, subsetName) <- value

## S4 replacement method for signature 'SubsetSummarizedExperiment,character,DataFrame'
subsetColData(x, subsetName) <- value

## S4 method for signature 'SubsetSummarizedExperiment,character'
subsetColData(x, subsetName, parentColData)

## S4 method for signature 'SubsetSpatialExperiment,character'
subsetColData(x, subsetName, parentColData)

## S4 replacement method for signature 'SubsetSpatialExperiment,character,DataFrame'
subsetColData(x, subsetName) <- value
```

```
## S4 method for signature 'SubsetTreeSummarizedExperiment,character'
subsetColData(x, subsetName, parentColData)

## S4 replacement method for signature 'SubsetTreeSummarizedExperiment,character,DataFrame'
subsetColData(x, subsetName) <- value
```

Arguments

x	ExperimentSubset Input ExperimentSubset object.
subsetName	character(1) Name of the subset to set colData to.
parentColData	logical(1) Logical value indicating if parent colData should be combined or not. Default FALSE.
value	Input DataFrame to store.

Value

The colData from input object.

Input object with colData stored.

Examples

```
data(sce_chcl, package = "scds")
es <- ExperimentSubset(sce_chcl)
es <- createSubset(es,
"subset1",
rows = c(10,11,50,56,98,99,102,105,109, 200),
cols = c(20,21,40,45,90,99,100,123,166,299),
parentAssay = "counts")
subsetColData(es, "subset1")
```

---

subsetColLinks *Accessor method for colLinks from subsets in ExperimentSubset objects*

Description

Get colLinks from a subset.

Usage

```
subsetColLinks(x, subsetName, parentColLinkData)

## S4 method for signature 'SubsetTreeSummarizedExperiment,character'
subsetColLinks(x, subsetName, parentColLinkData)
```

Arguments

x	ExperimentSubset Input ExperimentSubset object.
subsetName	character(1) Name of the subset to get colLinks from.
parentColLinkData	logical(1) Logical value indicating if parent colLinks should be combined or not. Default FALSE.

Value

The colLinks from input object.

---

subsetColnames *subsetColnames*

Description

Get colnames from a subset in the ExperimentSubset object.

Set colnames to a subset in the ExperimentSubset object.

Usage

```
subsetColnames(x, subsetName)

subsetColnames(x, subsetName) <- value

## S4 method for signature 'SubsetRangedSummarizedExperiment,character'
subsetColnames(x, subsetName)

## S4 replacement method for signature 'SubsetRangedSummarizedExperiment,character'
subsetColnames(x, subsetName) <- value

## S4 method for signature 'SubsetSingleCellExperiment,character'
subsetColnames(x, subsetName)

## S4 replacement method for signature 'SubsetSingleCellExperiment,character'
subsetColnames(x, subsetName) <- value

## S4 method for signature 'SubsetSummarizedExperiment,character'
subsetColnames(x, subsetName)

## S4 replacement method for signature 'SubsetSummarizedExperiment,character'
subsetColnames(x, subsetName) <- value

## S4 method for signature 'SubsetSpatialExperiment,character'
subsetColnames(x, subsetName)

## S4 replacement method for signature 'SubsetSpatialExperiment,character'
subsetColnames(x, subsetName) <- value

## S4 method for signature 'SubsetTreeSummarizedExperiment,character'
subsetColnames(x, subsetName)

## S4 replacement method for signature 'SubsetTreeSummarizedExperiment,character'
subsetColnames(x, subsetName) <- value
```

Arguments

x	Input ExperimentSubset object.
subsetName	Name of the subset to set colnames to.
value	Specify the colname values to replace.

Value

A vector of colnames.

Input object with colnames set to a subset.

Examples

```
data(sce_chcl, package = "scds")
es <- ExperimentSubset(sce_chcl)
es <- createSubset(es,
"subset1",
rows = c(10,11,50,56,98,99,102,105,109, 200),
cols = c(20,21,40,45,90,99,100,123,166,299),
parentAssay = "counts")
subsetColnames(es, "subset1")
```

---

subsetCount *Subset count method for ExperimentSubset objects*

Description

Get the total count of the available subsets (excluding subset assays) in an ExperimentSubset object.

Usage

```
subsetCount(x)

## S4 method for signature 'SubsetRangedSummarizedExperiment'
subsetCount(x)

## S4 method for signature 'SubsetSingleCellExperiment'
subsetCount(x)

## S4 method for signature 'SubsetSummarizedExperiment'
subsetCount(x)

## S4 method for signature 'SubsetSpatialExperiment'
subsetCount(x)

## S4 method for signature 'SubsetTreeSummarizedExperiment'
subsetCount(x)
```

Arguments

x	ExperimentSubset Input ExperimentSubset object.

Value

A numeric value representing the total count of the subsets.

Examples

```
data(sce_chcl, package = "scds")
es <- ExperimentSubset(sce_chcl)
es <- createSubset(es,
"subset1",
rows = c(10,11,50,56,98,99,102,105,109, 200),
cols = c(20,21,40,45,90,99,100,123,166,299),
parentAssay = "counts")
subsetCount(es)
```

---

subsetDim *Get dimensions of subsets in ExperimentSubset objects*

Description

Retrieves the dimensions of the specified subset in an ExperimentSubset object.

Usage

```
subsetDim(x, subsetName)

## S4 method for signature 'SubsetRangedSummarizedExperiment,character'
subsetDim(x, subsetName)

## S4 method for signature 'SubsetSingleCellExperiment,character'
subsetDim(x, subsetName)

## S4 method for signature 'SubsetSummarizedExperiment,character'
subsetDim(x, subsetName)

## S4 method for signature 'SubsetSpatialExperiment,character'
subsetDim(x, subsetName)

## S4 method for signature 'SubsetTreeSummarizedExperiment,character'
subsetDim(x, subsetName)
```

Arguments

x	ExperimentSubset Input ExperimentSubset object.
subsetName	character(1) Name of the subset to retrieve the dimensions from.

Value

A vector containing the dimensions of the specified subset i.e. the number of rows and the number of columns in the subset.

Examples

```
data(sce_chcl, package = "scds")
es <- ExperimentSubset(sce_chcl)
es <- createSubset(es,
"subset1",
rows = c(10,11,50,56,98,99,102,105,109, 200),
cols = c(20,21,40,45,90,99,100,123,166,299),
parentAssay = "counts")
subsetDim(es, "subset1")
```

`subsetNames` *Get names of only the subsets in ExperimentSubset objects*

Description

Retrieves the names of the available subsets (not the subset assays) in an `ExperimentSubset` object.

Usage

```
subsetNames(x)

## S4 method for signature 'SubsetRangedSummarizedExperiment'
subsetNames(x)

## S4 method for signature 'SubsetSingleCellExperiment'
subsetNames(x)

## S4 method for signature 'SubsetSummarizedExperiment'
subsetNames(x)

## S4 method for signature 'SubsetSpatialExperiment'
subsetNames(x)

## S4 method for signature 'SubsetTreeSummarizedExperiment'
subsetNames(x)
```

Arguments

`x`	`ExperimentSubset` Specify the input ES object.

Value

A `vector` of subset names.

Examples

```
data(sce_chcl, package = "scds")
es <- ExperimentSubset(sce_chcl)
es <- createSubset(es,
"subset1",
rows = c(10,11,50,56,98,99,102,105,109, 200),
cols = c(20,21,40,45,90,99,100,123,166,299),
```

```
parentAssay = "counts")
subsetNames(es)
```

`subsetParent` *Subset parent hierarchy retrieval method for ExperimentSubset objects*

Description

Retrieves a complete 'subset to parent' link from a specified subset.

Usage

```
subsetParent(x, subsetName)

## S4 method for signature 'SubsetRangedSummarizedExperiment'
subsetParent(x, subsetName)

## S4 method for signature 'SubsetSingleCellExperiment'
subsetParent(x, subsetName)

## S4 method for signature 'SubsetSummarizedExperiment'
subsetParent(x, subsetName)

## S4 method for signature 'SubsetSpatialExperiment'
subsetParent(x, subsetName)

## S4 method for signature 'SubsetTreeSummarizedExperiment'
subsetParent(x, subsetName)
```

Arguments

`x`	`ExperimentSubset` Input `ExperimentSubset` object.
`subsetName`	`character(1)` Specify the name of the subset against which the 'subset to parent link' should be retrieved.

Value

A `list` containing the 'subset to parent' link.

Examples

```
data(sce_chcl, package = "scds")
es <- ExperimentSubset(sce_chcl)
es <- createSubset(es, "subset1",
rows = c(10,11,50,56,98,99,102,105,109, 200),
cols = c(20,21,40,45,90,99,100,123,166,299),
parentAssay = "counts")
assay(es, "subset1",
subsetAssayName = "subset1pAssay") <- assay(es, "subset1")[,] + 1
subsetParent(es, "subset1pAssay")
```

SubsetRangedSummarizedExperiment-class *An S4 class for* RangedSummarizedExperiment *objects with added support for subsets.*

Description

An S4 class for RangedSummarizedExperiment objects with added support for subsets.

Slots

subsets A list of AssaySubset objects.

subsetRowData *Accessor method for rowData from subsets in ExperimentSubset objects*

Description

Get rowData from a subset.

Set rowData to a subset.

Usage

```
subsetRowData(x, subsetName, parentRowData)

subsetRowData(x, subsetName) <- value

## S4 method for signature 'SubsetRangedSummarizedExperiment,character'
subsetRowData(x, subsetName, parentRowData)

## S4 replacement method for signature
## 'SubsetRangedSummarizedExperiment,character,DataFrame'
subsetRowData(x, subsetName) <- value

## S4 method for signature 'SubsetSingleCellExperiment,character'
subsetRowData(x, subsetName, parentRowData)

## S4 replacement method for signature 'SubsetSingleCellExperiment,character,DataFrame'
subsetRowData(x, subsetName) <- value

## S4 replacement method for signature 'SubsetSummarizedExperiment,character,DataFrame'
subsetRowData(x, subsetName) <- value

## S4 method for signature 'SubsetSummarizedExperiment,character'
subsetRowData(x, subsetName, parentRowData)

## S4 method for signature 'SubsetSpatialExperiment,character'
subsetRowData(x, subsetName, parentRowData)
```

```
## S4 replacement method for signature 'SubsetSpatialExperiment,character,DataFrame'
subsetRowData(x, subsetName) <- value

## S4 method for signature 'SubsetTreeSummarizedExperiment,character'
subsetRowData(x, subsetName, parentRowData)

## S4 replacement method for signature 'SubsetTreeSummarizedExperiment,character,DataFrame'
subsetRowData(x, subsetName) <- value
```

Arguments

x	ExperimentSubset Input ExperimentSubset object.
subsetName	character(1) Name of the subset to set rowData to.
parentRowData	logical(1) Logical value indicating if parent rowData should be combined or not. Default FALSE.
value	Input DataFrame to store.

Value

The rowData from input object.

Input object with rowData stored.

Examples

```
data(sce_chcl, package = "scds")
es <- ExperimentSubset(sce_chcl)
es <- createSubset(es,
"subset1",
rows = c(10,11,50,56,98,99,102,105,109, 200),
cols = c(20,21,40,45,90,99,100,123,166,299),
parentAssay = "counts")
subsetRowData(es, "subset1")
```

---

subsetRowLinks *Accessor method for rowLinks from subsets in ExperimentSubset objects*

Description

Get rowLinks from a subset.

Usage

```
subsetRowLinks(x, subsetName, parentRowLinkData)

## S4 method for signature 'SubsetTreeSummarizedExperiment,character'
subsetRowLinks(x, subsetName, parentRowLinkData)
```

Arguments

x	ExperimentSubset Input ExperimentSubset object.
subsetName	character(1) Name of the subset to get rowLinks from.
parentRowLinkData	logical(1) Logical value indicating if parent rowLinks should be combined or not. Default FALSE.

Value

The rowLinks from input object.

---

subsetRownames *subsetRownames*

Description

Get rownames from a subset in the ExperimentSubset object.

Set colnames to a subset in the ExperimentSubset object.

Usage

```
subsetRownames(x, subsetName)

subsetRownames(x, subsetName) <- value

## S4 method for signature 'SubsetRangedSummarizedExperiment,character'
subsetRownames(x, subsetName)

## S4 replacement method for signature 'SubsetRangedSummarizedExperiment,character'
subsetRownames(x, subsetName) <- value

## S4 method for signature 'SubsetSingleCellExperiment,character'
subsetRownames(x, subsetName)

## S4 replacement method for signature 'SubsetSingleCellExperiment,character'
subsetRownames(x, subsetName) <- value

## S4 method for signature 'SubsetSummarizedExperiment,character'
subsetRownames(x, subsetName)

## S4 replacement method for signature 'SubsetSummarizedExperiment,character'
subsetRownames(x, subsetName) <- value

## S4 method for signature 'SubsetSpatialExperiment,character'
subsetRownames(x, subsetName)

## S4 replacement method for signature 'SubsetSpatialExperiment,character'
subsetRownames(x, subsetName) <- value

## S4 method for signature 'SubsetTreeSummarizedExperiment,character'
```

```
subsetRownames(x, subsetName)

## S4 replacement method for signature 'SubsetTreeSummarizedExperiment,character'
subsetRownames(x, subsetName) <- value
```

Arguments

x	Input ExperimentSubset object.
subsetName	Name of the subset to set colnames to.
value	Specify the rownames values to replace.

Value

A vector of colnames.

Input object with rownames set to a subset.

Examples

```
data(sce_chcl, package = "scds")
es <- ExperimentSubset(sce_chcl)
es <- createSubset(es,
"subset1",
rows = c(10,11,50,56,98,99,102,105,109, 200),
cols = c(20,21,40,45,90,99,100,123,166,299),
parentAssay = "counts")
subsetRownames(es, "subset1")
```

SubsetSingleCellExperiment-class

An S4 class for SingleCellExperiment *objects with added support for subsets.*

Description

An S4 class for SingleCellExperiment objects with added support for subsets.

Slots

subsets A list of AssaySubset objects.

subsetSpatialCoords *Accessor method for spatialCoords from subsets in ExperimentSubset objects*

Description

Get spatialCoords from a subset.

Usage

```
subsetSpatialCoords(x, subsetName)

## S4 method for signature 'SubsetSpatialExperiment,character'
subsetSpatialCoords(x, subsetName)
```

Arguments

x	ExperimentSubset Input ExperimentSubset object.
subsetName	character(1) Name of the subset to get spatialCoords from.

Value

The spatialCoords from input object.

subsetSpatialData *Accessor method for spatialData from subsets in ExperimentSubset objects*

Description

Get spatialData from a subset.

Set spatialData to a subset.

Usage

```
subsetSpatialData(x, subsetName, parentSpatialData)

subsetSpatialData(x, subsetName) <- value

## S4 method for signature 'SubsetSpatialExperiment,character'
subsetSpatialData(x, subsetName, parentSpatialData)

## S4 replacement method for signature 'SubsetSpatialExperiment,character,data.frame'
subsetSpatialData(x, subsetName) <- value
```

Arguments

x	ExperimentSubset Input ExperimentSubset object.
subsetName	character(1) Name of the subset to set spatialData to.
parentSpatialData	logical(1) Logical value indicating if parent spatialData should be combined or not. Default FALSE.
value	Input data.frame to store.

Value

The spatialData from input object.

Input object with spatialData stored.

SubsetSpatialExperiment-class

An S4 class for SpatialExperiment *objects with added support for subsets.*

Description

An S4 class for SpatialExperiment objects with added support for subsets.

Slots

subsets A list of AssaySubset objects.

SubsetSummarizedExperiment-class

An S4 class for SummarizedExperiment *objects with added support for subsets.*

Description

An S4 class for SummarizedExperiment objects with added support for subsets.

Slots

subsets A list of AssaySubset objects.

subsetSummary *Method for displaying 'child-parent' link structure of subsets in ExperimentSubset objects*

Description

The function displays the content of an ExperimentSubset object including all available main assays, all subsets and the subset assays inside these subsets. This function also depicts how and in what order the subsets in the object are linked with their parents. Moreover, all supplementary data inside the subsets such as reducedDims and altExps are also displayed against each subset entry.

Usage

```
subsetSummary(x)

## S4 method for signature 'SubsetRangedSummarizedExperiment'
subsetSummary(x)

## S4 method for signature 'SubsetSingleCellExperiment'
subsetSummary(x)

## S4 method for signature 'SubsetSummarizedExperiment'
subsetSummary(x)

## S4 method for signature 'SubsetSpatialExperiment'
subsetSummary(x)

## S4 method for signature 'SubsetTreeSummarizedExperiment'
subsetSummary(x)
```

Arguments

x	ExperimentSubset	Input ExperimentSubset object.

Value

Prints all the available subset information against the input ExperimentSubset object.

Examples

```
data(sce_chcl, package = "scds")
es <- ExperimentSubset(sce_chcl)
es <- createSubset(es,
"subset1",
rows = c(10,11,50,56,98,99,102,105,109, 200),
cols = c(20,21,40,45,90,99,100,123,166,299),
parentAssay = "counts")
assay(es, "subset1",
subsetAssayName = "subset1pAssay") <- assay(es, "subset1")[,] + 1
subsetSummary(es)
```

SubsetTreeSummarizedExperiment-class
An S4 class for TreeSummarizedExperiment *objects with added support for subsets.*

Description

An S4 class for TreeSummarizedExperiment objects with added support for subsets.

Slots

subsets A list of AssaySubset objects.

Index

.AssaySubset *(AssaySubset-class)*, 3
.SubsetRangedSummarizedExperiment *(SubsetRangedSummarizedExperiment-class)*, 20
.SubsetSingleCellExperiment *(SubsetSingleCellExperiment-class)*, 23
.SubsetSpatialExperiment *(SubsetSpatialExperiment-class)*, 25
.SubsetSummarizedExperiment *(SubsetSummarizedExperiment-class)*, 25
.SubsetTreeSummarizedExperiment *(SubsetTreeSummarizedExperiment-class)*, 27

AssaySubset, 2
AssaySubset-class, 3

createSubset, 4
createSubset,SubsetRangedSummarizedExperiment-method *(createSubset)*, 4
createSubset,SubsetSingleCellExperiment-method *(createSubset)*, 4
createSubset,SubsetSpatialExperiment-method *(createSubset)*, 4
createSubset,SubsetSummarizedExperiment-method *(createSubset)*, 4
createSubset,SubsetTreeSummarizedExperiment-method *(createSubset)*, 4

ExperimentSubset, 5

getSubsetAssay, 6
getSubsetAssay,SubsetRangedSummarizedExperiment,character-method *(getSubsetAssay)*, 6
getSubsetAssay,SubsetSingleCellExperiment,character-method *(getSubsetAssay)*, 6
getSubsetAssay,SubsetSpatialExperiment,character-method *(getSubsetAssay)*, 6
getSubsetAssay,SubsetSummarizedExperiment,character-method *(getSubsetAssay)*, 6
getSubsetAssay,SubsetTreeSummarizedExperiment,character-method *(getSubsetAssay)*, 6

reducedDimNames, 7
reducedDimNames,ANY-method *(reducedDimNames)*, 7
reducedDimNames<-, 8
reducedDimNames<-,ANY-method *(reducedDimNames<-)*, 8
reducedDims, *7–10*
reducedDims<-, 9
reducedDims<-,ANY-method, 9

setSubsetAssay, 10
setSubsetAssay,SubsetRangedSummarizedExperiment,charact *(setSubsetAssay)*, 10
setSubsetAssay,SubsetSingleCellExperiment,character,ANY *(setSubsetAssay)*, 10
setSubsetAssay,SubsetSpatialExperiment,character,ANY,ch *(setSubsetAssay)*, 10
setSubsetAssay,SubsetSummarizedExperiment,character,ANY *(setSubsetAssay)*, 10
setSubsetAssay,SubsetTreeSummarizedExperiment,character *(setSubsetAssay)*, 10
subsetAssayCount, 11
subsetAssayCount,SubsetRangedSummarizedExperiment-metho *(subsetAssayCount)*, 11
subsetAssayCount,SubsetSingleCellExperiment-method *(subsetAssayCount)*, 11
subsetAssayCount,SubsetSpatialExperiment-method *(subsetAssayCount)*, 11
subsetAssayCount,SubsetSummarizedExperiment-method *(subsetAssayCount)*, 11
subsetAssayCount,SubsetTreeSummarizedExperiment-method *(subsetAssayCount)*, 11
subsetAssayNames, 12
subsetAssayNames,SubsetRangedSummarizedExperiment-metho *(subsetAssayNames)*, 12
subsetAssayNames,SubsetSingleCellExperiment-method *(subsetAssayNames)*, 12
subsetAssayNames,SubsetSpatialExperiment-method *(subsetAssayNames)*, 12
subsetAssayNames,SubsetSummarizedExperiment-method *(subsetAssayNames)*, 12
subsetAssayNames,SubsetTreeSummarizedExperiment-method *(subsetAssayNames)*, 12
subsetColData, 13

subsetColData,SubsetRangedSummarizedExperiment,character-method (subsetColData), 13
subsetColData,SubsetSingleCellExperiment,character-method (subsetColData), 13
subsetColData,SubsetSpatialExperiment,character-method (subsetColData), 13
subsetColData,SubsetSummarizedExperiment,character-method (subsetColData), 13
subsetColData,SubsetTreeSummarizedExperiment,character-method (subsetColData), 13
subsetColData<- (subsetColData), 13
subsetColData<-,SubsetRangedSummarizedExperiment,character,DataFrame-method (subsetColData), 13
subsetColData<-,SubsetSingleCellExperiment,character,DataFrame-method (subsetColData), 13
subsetColData<-,SubsetSpatialExperiment,character,DataFrame-method (subsetColData), 13
subsetColData<-,SubsetSummarizedExperiment,character,DataFrame-method (subsetColData), 13
subsetColData<-,SubsetTreeSummarizedExperiment,character,DataFrame-method (subsetColData), 13
subsetColLinks, 14
subsetColLinks,SubsetTreeSummarizedExperiment,character-method (subsetColLinks), 14
subsetColnames, 15
subsetColnames,SubsetRangedSummarizedExperiment,character-method (subsetColnames), 15
subsetColnames,SubsetSingleCellExperiment,character-method (subsetColnames), 15
subsetColnames,SubsetSpatialExperiment,character-method (subsetColnames), 15
subsetColnames,SubsetSummarizedExperiment,character-method (subsetColnames), 15
subsetColnames,SubsetTreeSummarizedExperiment,character-method (subsetColnames), 15
subsetColnames<- (subsetColnames), 15
subsetColnames<-,SubsetRangedSummarizedExperiment,character,character-method (subsetColnames), 15
subsetColnames<-,SubsetSingleCellExperiment,character,character-method (subsetColnames), 15
subsetColnames<-,SubsetSpatialExperiment,character,character-method (subsetColnames), 15
subsetColnames<-,SubsetSummarizedExperiment,character,character-method (subsetColnames), 15
subsetColnames<-,SubsetTreeSummarizedExperiment,character,character-method (subsetColnames), 15
subsetCount, 16
subsetCount,SubsetRangedSummarizedExperiment-method (subsetCount), 16
subsetCount,SubsetSingleCellExperiment-method (subsetCount), 16
subsetCount,SubsetSpatialExperiment-method (subsetCount), 16
subsetCount,SubsetSummarizedExperiment-method (subsetCount), 16
subsetCount,SubsetTreeSummarizedExperiment-method (subsetCount), 16
subsetDim, 17
subsetDim,SubsetRangedSummarizedExperiment,character-method (subsetDim), 17
subsetDim,SubsetSingleCellExperiment,character-method (subsetDim), 17
subsetDim,SubsetSpatialExperiment,character-method (subsetDim), 17
subsetDim,SubsetSummarizedExperiment,character-method (subsetDim), 17
subsetDim,SubsetTreeSummarizedExperiment,character-method (subsetDim), 17
subsetNames, 18
subsetNames,SubsetRangedSummarizedExperiment-method (subsetNames), 18
subsetNames,SubsetSingleCellExperiment-method (subsetNames), 18
subsetNames,SubsetSpatialExperiment-method (subsetNames), 18
subsetNames,SubsetSummarizedExperiment-method (subsetNames), 18
subsetNames,SubsetTreeSummarizedExperiment-method (subsetNames), 18
subsetParent, 19
subsetParent,SubsetRangedSummarizedExperiment-method (subsetParent), 19
subsetParent,SubsetSingleCellExperiment-method (subsetParent), 19
subsetParent,SubsetSpatialExperiment-method (subsetParent), 19
subsetParent,SubsetSummarizedExperiment-method (subsetParent), 19
subsetParent,SubsetTreeSummarizedExperiment-method (subsetParent), 19
SubsetRangedSummarizedExperiment-class, 20
subsetRowData, 20
subsetRowData,SubsetRangedSummarizedExperiment,character-method (subsetRowData), 20
subsetRowData,SubsetSingleCellExperiment,character-method (subsetRowData), 20
subsetRowData,SubsetSpatialExperiment,character-method (subsetRowData), 20
subsetRowData,SubsetSummarizedExperiment,character-method (subsetRowData), 20
subsetRowData,SubsetTreeSummarizedExperiment,character-method (subsetRowData), 20
subsetRowData<- (subsetRowData), 20

subsetRowData<-,SubsetRangedSummarizedExperiment,character,DataFrame-method (subsetRowData), 20
subsetRowData<-,SubsetSingleCellExperiment,character,DataFrame-method (subsetRowData), 20
subsetRowData<-,SubsetSpatialExperiment,character,DataFrame-method (subsetRowData), 20
subsetRowData<-,SubsetSummarizedExperiment,character,DataFrame-method (subsetRowData), 20
subsetRowData<-,SubsetTreeSummarizedExperiment,character,DataFrame-method (subsetRowData), 20
subsetRowLinks, 21
subsetRowLinks,SubsetTreeSummarizedExperiment,character-method (subsetRowLinks), 21
subsetRownames, 22
subsetRownames,SubsetRangedSummarizedExperiment,character-method (subsetRownames), 22
subsetRownames,SubsetSingleCellExperiment,character-method (subsetRownames), 22
subsetRownames,SubsetSpatialExperiment,character-method (subsetRownames), 22
subsetRownames,SubsetSummarizedExperiment,character-method (subsetRownames), 22
subsetRownames,SubsetTreeSummarizedExperiment,character-method (subsetRownames), 22
subsetRownames<- (subsetRownames), 22
subsetRownames<-,SubsetRangedSummarizedExperiment,character-method (subsetRownames), 22
subsetRownames<-,SubsetSingleCellExperiment,character-method (subsetRownames), 22
subsetRownames<-,SubsetSpatialExperiment,character-method (subsetRownames), 22
subsetRownames<-,SubsetSummarizedExperiment,character-method (subsetRownames), 22
subsetRownames<-,SubsetTreeSummarizedExperiment,character-method (subsetRownames), 22
SubsetSingleCellExperiment-class, 23
subsetSpatialCoords, 24
subsetSpatialCoords,SubsetSpatialExperiment,character-method (subsetSpatialCoords), 24
subsetSpatialData, 24
subsetSpatialData,SubsetSpatialExperiment,character-method (subsetSpatialData), 24
subsetSpatialData<- (subsetSpatialData), 24
subsetSpatialData<-,SubsetSpatialExperiment,character,data.frame-method (subsetSpatialData), 24
SubsetSpatialExperiment-class, 25
SubsetSummarizedExperiment-class, 25
subsetSummary, 26
subsetSummary,SubsetRangedSummarizedExperiment-method (subsetSummary), 26
subsetSummary,SubsetSingleCellExperiment-method (subsetSummary), 26
subsetSummary,SubsetSpatialExperiment-method (subsetSummary), 26
subsetSummary,SubsetSummarizedExperiment-method (subsetSummary), 26
subsetSummary,SubsetTreeSummarizedExperiment-method (subsetSummary), 26
SubsetTreeSummarizedExperiment-class, 27