

Package ‘ExperimentSubset’

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Type Package

Title Manages subsets of data with Bioconductor Experiment objects

Version 1.0.0

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.

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altExp *Alternative Experiment methods for ExperimentSubset objects*

Description

A wrapper to the altExp from altExps method with additional support for subsets.

Usage

```
altExp(x, e, withColData = FALSE, subsetName)
```

```
## S4 method for signature 'ANY'
```

```
altExp(x, e, withColData = FALSE, subsetName)
```

Arguments

x	ExperimentSubset Input ExperimentSubset object or any object supported by altExp from altExps method.
e	character(1) Same as altExp from altExps.
withColData	logical(1) Same as altExp from altExps. Default FALSE.
subsetName	character(1) Specify the name of the subset from which the altExp should be fetched from. If missing, altExp from altExps method is called on the main object.

Value

The altExp from the specified subset or same as altExp from altExps when subsetName is missing.

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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")
altExp(es, e = "altExample",
  subsetName = "subset1") <- SingleCellExperiment(
  assays = list(counts = assay(es, "subset1")))
altExp(es, subsetName = "subset1")
```

altExp<- *Alternative Experiment methods for ExperimentSubset objects*

Description

A wrapper to the altExp<- from [altExps](#) method with additional support for subsets.

Usage

```
altExp(x, e, withColData = FALSE, subsetName) <- value
```

```
## S4 replacement method for signature 'ANY'
altExp(x, e, withColData = FALSE, subsetName) <- value
```

Arguments

x	ExperimentSubset Input ExperimentSubset object or any object supported by altExp<- from altExps method.
e	character(1) Same as altExp<- from altExps method.
withColData	logical(1) Same as altExp<- from altExps method. Default FALSE.
subsetName	character(1) Specify the name of the subset to which the altExp<- should be set to. If missing, altExp<- from altExps method is called on the main object.
value	SingleCellExperiment Input value same as altExp<- from altExps method.

Value

Input object with altExp<- set.

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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")
altExp(es, e = "altExample",
  subsetName = "subset1") <- SingleCellExperiment(
  assays = list(counts = assay(es, "subset1")))
```

altExpNames *Alternative Experiment methods for ExperimentSubset objects*

Description

A wrapper to the altExpNames from altExps method with additional support for subsets.

Usage

```
altExpNames(x, subsetName)

## S4 method for signature 'ANY'
altExpNames(x, subsetName)
```

Arguments

x	ExperimentSubset Input ExperimentSubset object or any object supported by altExpNames from altExps method.
subsetName	character(1) Specify the name of the subset from which the altExpNames should be fetched from. If missing, altExpNames from altExps method is called on the main object.

Value

The altExpNames from the specified subset or same as altExpNames from altExps when subsetName is missing.

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")
altExp(es, e = "altExample",
  subsetName = "subset1") <- SingleCellExperiment(
  assays = list(counts = assay(es, "subset1")))
altExpNames(es, subsetName = "subset1")
```

altExpNames<- *Alternative Experiment methods for ExperimentSubset objects*

Description

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

Usage

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

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

Arguments

x	ExperimentSubset Input ExperimentSubset object or any object supported by altExpNames<- from altExps method.
subsetName	character(1) Specify the name of the subset to which the altExpNames<- should be set to. If missing, altExpNames<- from altExps method is called on the main object.
value	vector("character") Input value same as altExpNames<- from altExps method.

Value

Input object with altExpNames set.

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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")
altExp(es, e = "altExample",
  subsetName = "subset1") <- SingleCellExperiment(
  assays = list(counts = assay(es, "subset1")))
altExpNames(es, subsetName = "subset1") <- c("altExpSubset1")
```

altExps

Alternative Experiment methods for ExperimentSubset objects

Description

A wrapper to the altExps method with additional support for subsets.

Usage

```
altExps(x, withColData = FALSE, subsetName)

## S4 method for signature 'ANY'
altExps(x, withColData = FALSE, subsetName)
```

Arguments

x	ExperimentSubset Input ExperimentSubset object or any object supported by altExps method.
withColData	logical(1) Same as altExps . Default FALSE.
subsetName	character(1) Specify the name of the subset from which the altExps should be fetched from. If missing, altExps method is called on the main object.

Value

altExps from the specified subset or same as [altExps](#) when subsetName is missing.

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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")
altExps(es, subsetName = "subset1") <- list(
  alt1 = SingleCellExperiment(
    assays = list(
      counts = assay(es, "subset1"))),
  alt2 = SingleCellExperiment(
    assays = list(counts = assay(es, "subset1"))))
altExps(es, subsetName = "subset1")
```

altExps<-

Alternative Experiment methods for ExperimentSubset objects

Description

A wrapper to the altExps<- from [altExps](#) method with additional support for subsets.

Usage

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

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

Arguments

x	ExperimentSubset Input ExperimentSubset object or any object supported by altExps<- from altExps method.
subsetName	character(1) Specify the name of the subset to which the altExps<- should be set to. If missing, altExps<- from altExps method is called on the main object.
value	list() Input value same as altExps<- from altExps method.

Value

Input object with altExps<- set.

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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")
altExps(es, subsetName = "subset1") <- list(
  alt1 = SingleCellExperiment(
    assays = list(counts = assay(es, "subset1"))),
  alt2 = SingleCellExperiment(
    assays = list(counts = assay(es, "subset1"))))
altExpNames(es, subsetName = "subset1")
```

assay,ExperimentSubset,character-method

Accessor method for assays in ExperimentSubset objects

Description

Method to get an assay from an ExperimentSubset object or a subset from an ExperimentSubset object or any object supported by assay from SummarizedExperiment.

Usage

```
## S4 method for signature 'ExperimentSubset,character'
assay(x, i, withDimnames = FALSE, ...)
```

Arguments

x	ExperimentSubset Specify the input object which can be either ExperimentSubset or any object supported by assay from SummarizedExperiment.
i	character(1) Name of an assay or name of a subset or name of a subset assay.
withDimnames	logical(1) Set whether dimnames should be applied to assay. Default FALSE.
...	Additional parameters.

Value

The assay from the input object.

Examples

```

data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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
es

```

assay<- ,ExperimentSubset,character-method

Setter method for assays in ExperimentSubset objects

Description

Method to set an assay to an ExperimentSubset object or a subset from an ExperimentSubset object or any object supported by assay<- from SummarizedExperiment.

Usage

```

## S4 replacement method for signature 'ExperimentSubset,character'
assay(x, i, withDimnames = FALSE, subsetAssayName = NULL, ...) <- value

```

Arguments

x	ExperimentSubset Input ExperimentSubset object or any object supported by assay from SummarizedExperiment.
i	character(1) Name of an assay or name of the subset if storing to an ExperimentSubset object.
withDimnames	logical(1) Set whether dimnames should be applied to assay. Default FALSE.
subsetAssayName	character(1) Name of the assay to store if storing to an ExperimentSubset object.
...	Additional parameters.
value	dgMatrix The assay to store.

Value

Input object with assay stored.

Examples

```

data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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
es

```

 AssaySubset

AssaySubset constructor

Description

Constructor for creating a experiment object internally by the ExperimentSubset object.

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	SummarizedExperiment An internal object to store additional subset data.

Value

A AssaySubset object.

 AssaySubset-class

An S4 class to create subset objects to store inside an ExperimentSubset object.

Description

An S4 class to create subset objects to store inside an ExperimentSubset object.

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.

 colData, ExperimentSubset-method

Accessor method for colData in ExperimentSubset objects

Description

Get colData from a subset of an input object or the object itself.

Usage

```
## S4 method for signature 'ExperimentSubset'
colData(x, subsetName = NULL, ...)
```

Arguments

x	ExperimentSubset Input ExperimentSubset object or any object supported by colData from SummarizedExperiment.
subsetName	character(1) Name of the subset to get colData from. If NULL or missing, colData from main input object is fetched.
...	Additional parameters.

Value

The colData from input object or subset of an input object.

colData<- , ExperimentSubset, DataFrame-method

Setter method for colData in ExperimentSubset objects

Description

Set colData to a subset of an input object or the object itself.

Usage

```
## S4 replacement method for signature 'ExperimentSubset, DataFrame'
colData(x, ..., subsetName) <- value
```

Arguments

x	ExperimentSubset Input ExperimentSubset object or any object supported by colData<- from SummarizedExperiment.
...	Additional parameters.
subsetName	character(1) Name of the subset to set colData to. If NULL or missing, colData to main input object is set.
value	DFrame The colData to store in an object or subset of an object.

Value

Object with colData set.

colnames	<i>Accessor method for colnames in ExperimentSubset objects</i>
----------	---

Description

Get colnames from an ExperimentSubset object or a subset in the ExperimentSubset object or any object supported by colnames in base package.

Usage

```
colnames(object, ...)

## S4 method for signature 'ANY'
colnames(object, subsetName, ...)
```

Arguments

object	ExperimentSubset Input ExperimentSubset object or any object supported by colnames in base package.
...	Additional parameters and subsetName parameter to pass the name of the subset to get colnames from.
subsetName	character(1) Name of the subset to get colnames from. If missing, colnames from main object are returned.

Value

A vector of colnames.

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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")
colnames(es, subsetName = "subset1")
```

colnames<-	<i>Setter method for colnames in ExperimentSubset objects</i>
------------	---

Description

Set colnames to an ExperimentSubset object or a subset in the ExperimentSubset object or any object supported by colnames in base package.

Usage

```
colnames(object, ...) <- value

## S4 replacement method for signature 'ANY'
colnames(object, subsetName, ...) <- value
```

Arguments

object	ExperimentSubset Input ExperimentSubset object or any object supported by colnames in base package.
...	Additional parameters and subsetName parameter to pass the name of the subset to get colnames from.
value	list() A list of colnames to set to the input object.
subsetName	character(1) Name of the subset to get colnames from. If missing, colnames from main object are returned.

Value

Input object with colnames set.

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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")
colnames(es, subsetName = "subset1") <-
paste0("col", seq(subsetDim(es, subsetName = "subset1")[2]))
```

createSubset	<i>Subset creation method for ExperimentSubset objects</i>
--------------	--

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(object, subsetName, rows = NULL, cols = NULL, parentAssay = NULL)

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

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

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

Arguments

object	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.
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_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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
```

dim,ExperimentSubset-method

Dimensions retrieval method for ExperimentSubset objects

Description

Get dimensions of the ExperimentSubset object.

Usage

```
## S4 method for signature 'ExperimentSubset'
dim(x)
```

Arguments

x codeExperimentSubset Input ExperimentSubset object.

Value

A list containing number of rows and number of columns of the object.

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
dim(es)
```

ExperimentSubset	<i>ExperimentSubset constructor</i>
------------------	-------------------------------------

Description

This constructor function is used to setup the ExperimentSubset object 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(
  object,
  subset = list(subsetName = NA, rows = NA, cols = NA, parentAssay = NA)
)
```

Arguments

object	SingleCellExperiment or SummarizedExperiment Specify the root object.
subset	list Specify 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_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
es
```

ExperimentSubset-class

An S4 class to create an ExperimentSubset object with support for subsets.

Description

An S4 class to create an ExperimentSubset object with support for subsets.

Slots

root The root object from which all consequent subsets will be created. This can be any object that is inherited from SummarizedExperiment.

subsets A list of AssaySubset objects.

metadata	<i>Metadata accessor method for ExperimentSubset objects</i>
----------	--

Description

Get metadata from an ExperimentSubset object.

Usage

```
metadata(object, subsetName)

## S4 method for signature 'ANY'
metadata(object, subsetName)
```

Arguments

object	ExperimentSubset Input ExperimentSubset object.
subsetName	character(1) Name of the subset to get the metadata from. If missing, metadata is fetched from the main input object.

Value

A list of metadata elements.

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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")
metadata(es, subsetName = "subset1") <- list(
  meta1 = "This is an example for metadata in subset1")
metadata(es, subsetName = "subset1")
```

metadata<-	<i>Metadata setter method for ExperimentSubset objects</i>
------------	--

Description

Set metadata to an ExperimentSubset object.

Usage

```
metadata(object, subsetName) <- value
```


Arguments

object	ExperimentSubset Input ExperimentSubset object.
subsetName	character(1) Name of the subset to set the metadata to. If missing, metadata is set to the main input object.
value	A list to set to the metadata slot.

Value

Input object with metadata set.

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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")
metadata(es, subsetName = "subset1") <- list(
  meta1 = "This is an example for metadata in subset1")
```

metadata<-,ANY-method *Metadata setter method for ExperimentSubset objects*

Description

Set metadata to an ExperimentSubset object.

Usage

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

Arguments

object	ExperimentSubset Input ExperimentSubset object.
subsetName	character(1) Name of the subset to set the metadata to. If missing, metadata is set to the main input object.
value	list() A list to set to the metadata slot.

Value

Input object with metadata set.

reducedDim *Methods for Reduced Dimensions in ExperimentSubset objects*

Description

A wrapper to the reducedDim from [reducedDims](#) method with additional support for subsets.

Usage

```
reducedDim(object, type, withDimnames, subsetName)
```

```
## S4 method for signature 'ANY'
reducedDim(object, type, withDimnames, subsetName)
```

Arguments

object	ExperimentSubset Input ExperimentSubset object or any object supported by reducedDim from reducedDims method.
type	character(1) Same as type in reducedDim from reducedDims method.
withDimnames	logical(1) Same as withDimnames in reducedDim from reducedDims method.
subsetName	character(1) Specify the name of the subset from which the reducedDim should be fetched from. If missing, reducedDim from reducedDims method is called on the main object.

Value

The reducedDim from the specified subset or same as reducedDim 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")
reducedDim(es, type = "PCA",
  subsetName = "subset1") <- scater::calculatePCA(
  assay(es, "subset1"))
reducedDim(es, type = "PCA", subsetName = "subset1")
```

reducedDim<- *Methods for Reduced Dimensions in ExperimentSubset objects*

Description

A wrapper to the reducedDim<- from [reducedDims](#) method with additional support for subsets.

Usage

```
reducedDim(object, type, subsetName) <- value
```

Arguments

object	ExperimentSubset Input ExperimentSubset object or any object supported by reducedDim<- from reducedDims method.
type	character(1) Same as type in reducedDim<- from reducedDims method.
subsetName	character(1) Specify the name of the subset to which the reducedDim should be set to. If missing, reducedDim<- from reducedDims method is called on the main object.
value	matrix Value to set to reducedDim.

Value

Updated input object with reducedDim set.

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
es <- createSubset(es, "subset1",
  rows = c(1:1500), cols = c(1:1500),
  parentAssay = "counts")
reducedDim(es, type = "PCA",
  subsetName = "subset1") <- scater::calculatePCA(
  assay(es, "subset1"))
```

reducedDim<-,ANY-method

Methods for Reduced Dimensions in ExperimentSubset objects

Description

A wrapper to the reducedDim<- from [reducedDims](#) method with additional support for subsets.

Usage

```
## S4 replacement method for signature 'ANY'
reducedDim(object, type, subsetName) <- value
```

Arguments

object	ExperimentSubset Input ExperimentSubset object or any object supported by reducedDim<- from reducedDims method.
type	character(1) Same as type in reducedDim<- from reducedDims method.
subsetName	character(1) Specify the name of the subset to which the reducedDim should be set to. If missing, reducedDim<- from reducedDims method is called on the main object.
value	matrix Value to set to reducedDim.

Value

Updated input object with reducedDim set.

reducedDimNames	<i>Methods for Reduced Dimensions in ExperimentSubset objects</i>
-----------------	---

Description

A wrapper to the reducedDimNames from [reducedDims](#) method with additional support for subsets.

Usage

```
reducedDimNames(x, subsetName)

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

Arguments

x	ExperimentSubset Input ExperimentSubset object or any object supported by reducedDimNames from reducedDims method.
subsetName	character(1) Specify the name of the subset from which the reducedDimNames should be fetched from. If missing, reducedDimNames from reducedDims method is called on the main object.

Value

The reducedDimNames from the specified subset or same as reducedDimNames from [reducedDims](#) when subsetName is missing.

reducedDimNames<-	<i>Methods for Reduced Dimensions in ExperimentSubset objects</i>
-------------------	---

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
```

Arguments

x	ExperimentSubset Input ExperimentSubset object or any object supported by reducedDimNames<- from reducedDims method.
subsetName	character(1) 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	vector("character") Input value same as reducedDimNames<- from reduced-Dims method.

Value

Input object with reducedDimNames<- set.

reducedDims	<i>Methods for Reduced Dimensions in ExperimentSubset objects</i>
-------------	---

Description

A wrapper to the [reducedDims](#) method with additional support for subsets.

Usage

```
reducedDims(object, withDimnames, subsetName)
```

```
## S4 method for signature 'ANY'
reducedDims(object, withDimnames, subsetName)
```

Arguments

object	ExperimentSubset Input ExperimentSubset object or any object supported by reducedDims method.
withDimnames	logical(1) Same as withDimnames in reducedDims method.
subsetName	character(1) Specify the name of the subset from which the reducedDims should be fetched from. If missing, reducedDims method is called on the main object.

Value

The reducedDims from the specified subset or same as link[SingleCellExperiment]reducedDims when subsetName is missing.

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
es <- createSubset(es, "subset1",
  rows = c(1:1500), cols = c(1:1500),
  parentAssay = "counts")
reducedDim(es, type = "PCA_1",
  subsetName = "subset1") <- scater::calculatePCA(
  assay(es, "subset1"))
```

```
reducedDim(es, type = "PCA_2",
subsetName = "subset1") <- scater::calculatePCA(
assay(es, "subset1"))
reducedDims(es, subsetName = "subset1")
```

reducedDims<-

Methods for Reduced Dimensions in ExperimentSubset objects

Description

A wrapper to the reducedDims<- from [reducedDims](#) method with additional support for subsets.

Usage

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

Arguments

object	ExperimentSubset Input ExperimentSubset object or any object supported by reducedDims<- from reducedDims method.
subsetName	character(1) 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	list() A list of values to set to reducedDims.

Value

Updated input object with reducedDims set.

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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

Methods for Reduced Dimensions in ExperimentSubset objects

Description

A wrapper to the reducedDims<- from [reducedDims](#) method with additional support for subsets.

Usage

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

Arguments

object	ExperimentSubset Input ExperimentSubset object or any object supported by reducedDims<- from reducedDims method.
subsetName	character(1) 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	list() A list of values to set to reducedDims.

Value

Updated input object with reducedDims set.

rowData,ExperimentSubset-method

Accessor method for rowData in ExperimentSubset objects

Description

Get rowData from a subset of an input object or the object itself.

Usage

```
## S4 method for signature 'ExperimentSubset'
rowData(x, subsetName = NULL, ...)
```

Arguments

x	ExperimentSubset Input ExperimentSubset object or any object supported by rowData from SummarizedExperiment.
subsetName	character(1) Name of the subset to get rowData from. If NULL or missing, rowData from main input object is fetched.
...	Additional parameters.

Value

The rowData from input object or subset of an input object.

```
rowData<- ,ExperimentSubset-method
```

Setter method for rowData in ExperimentSubset objects

Description

Set rowData to a subset of an input object or the object itself.

Usage

```
## S4 replacement method for signature 'ExperimentSubset'
rowData(x, ..., subsetName) <- value
```

Arguments

x	ExperimentSubset Input ExperimentSubset object or any object supported by rowData<- from SummarizedExperiment.
...	Additional parameters.
subsetName	character(1) Name of the subset to set rowData to. If NULL or missing, rowData to main input object is set.
value	DFrame The rowData to store in an object or subset of an object.

Value

Object with rowData set.

```
rownames
```

Accessor method for rownames in ExperimentSubset objects

Description

Get rownames from an ExperimentSubset object or a subset in the ExperimentSubset object or any object supported by rownames in base package.

Usage

```
rownames(object, ...)
```

```
## S4 method for signature 'ANY'
rownames(object, subsetName, ...)
```

Arguments

object	ExperimentSubset Input ExperimentSubset object or any object supported by rownames in base package.
...	Additional parameters and subsetName parameter to pass the name of the subset to get rownames from.
subsetName	character(1) Name of the subset to get rownames from. If missing, rownames from main object are returned.

Value

A vector of rownames.

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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")
rownames(es, subsetName = "subset1")
```

rownames<-

Setter method for rownames in ExperimentSubset objects

Description

Set rownames to an ExperimentSubset object or a subset in the ExperimentSubset object or any object supported by rownames in base package.

Usage

```
rownames(object, ...) <- value

## S4 replacement method for signature 'ANY'
rownames(object, subsetName, ...) <- value
```

Arguments

object	ExperimentSubset Input ExperimentSubset object or any object supported by rownames in base package.
...	Additional parameters and subsetName parameter to pass the name of the subset to get rownames from.
value	codelist() A list of rownames to set to the input object.
subsetName	character(1) Name of the subset to get rownames from. If missing, rownames from main object are returned.

Value

Input object with rownames set.

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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")
rownames(es, subsetName = "subset1") <-
paste0("row", seq(subsetDim(es, subsetName = "subset1")[1]))
```

show, ExperimentSubset-method

Display method for ExperimentSubset objects

Description

Show the ExperimentSubset object

Usage

```
## S4 method for signature 'ExperimentSubset'
show(object)
```

Arguments

object ExperimentSubset Input ExperimentSubset object.

Value

Displays the overall contents of the ExperimentSubset object.

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
es
```

storeSubset

Method for storing new assays in ExperimentSubset objects

Description

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

Usage

```
storeSubset(object, subsetName, inputMatrix, subsetAssayName)
```

```
## S4 method for signature 'ExperimentSubset'
storeSubset(object, subsetName, inputMatrix, subsetAssayName = NULL)
```

Arguments

object	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	dgMatrix The input subset assay.
subsetAssayName	character(1) Specify the name of the new assay against the inputMatrix parameter. If NULL, a new subset is created internally using the createSubset function. Default NULL.

Value

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

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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 <- storeSubset(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(object)

## S4 method for signature 'ExperimentSubset'
subsetAssayCount(object)
```

Arguments

object ExperimentSubset Input ExperimentSubset object.

Value

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

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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	<i>Name retrieval method for all subset assays in ExperimentSubset objects</i>
------------------	--

Description

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

Usage

```
subsetAssayNames(object)

## S4 method for signature 'ExperimentSubset'
subsetAssayNames(object)
```

Arguments

object 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_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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	<i>Accessor method for colData from subsets in ExperimentSubset objects</i>
---------------	---

Description

Get colData from a subset.

Usage

```
subsetColData(object, subsetName)

## S4 method for signature 'ExperimentSubset,character'
subsetColData(object, subsetName)
```

Arguments

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

Value

The colData from input object.

subsetCount	<i>Subset count method for ExperimentSubset objects</i>
-------------	---

Description

Get the total count of the available subsets in an ExperimentSubset object.

Usage

```
subsetCount(object)

## S4 method for signature 'ExperimentSubset'
subsetCount(object)
```

Arguments

object ExperimentSubset Input ExperimentSubset object.

Value

A numeric value representing the total count of the subsets.

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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	<i>Get dimensions of subsets in ExperimentSubset objects</i>
-----------	--

Description

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

Usage

```
subsetDim(object, subsetName)

## S4 method for signature 'ExperimentSubset,character'
subsetDim(object, subsetName)
```

Arguments

object	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_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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	<i>Get names of subsets in ExperimentSubset objects</i>
-------------	---

Description

Retrieves the names of the available subsets in an ExperimentSubset object.

Usage

```
subsetNames(object)

## S4 method for signature 'ExperimentSubset'
subsetNames(object)
```

Arguments

object ExperimentSubset Specify the input object.

Value

A vector of subset names.

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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	<i>Subset parent hierarchy retrieval method for ExperimentSubset objects</i>
--------------	--

Description

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

Usage

```
subsetParent(object, subsetName)
```

```
## S4 method for signature 'ANY'
subsetParent(object, subsetName)
```

Arguments

object 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 parent link of the subset.

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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")
```

subsetRowData	<i>Accessor method for rowData from subsets in ExperimentSubset objects</i>
---------------	---

Description

Get rowData from a subset.

Usage

```
subsetRowData(object, subsetName)
```

```
## S4 method for signature 'ExperimentSubset,character'
subsetRowData(object, subsetName)
```

Arguments

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

Value

The rowData from input object.

subsetSummary	<i>Method for displaying child-parent link structure of subsets in ExperimentSubset objects</i>
---------------	---

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(object)
```

```
## S4 method for signature 'ExperimentSubset'
subsetSummary(object)
```

Arguments

object	ExperimentSubset Input ExperimentSubset object.
--------	---

Value

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

Examples

```
data(sce_chc1, package = "scds")
es <- ExperimentSubset(sce_chc1)
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)
```

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