

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

**Maintainer** Irzam Sarfraz <[irzam9095@gmail.com](mailto:irzam9095@gmail.com)>

**R topics documented:**

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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 <a href="#">altExps</a> method.  |
| e           | character(1) Same as altExp from <a href="#">altExps</a> .   |
| withColData | logical(1) Same as altExp from <a href="#">altExps</a> . Default FALSE.  |
| subsetName  | character(1) Specify the name of the subset from which the altExp should be fetched from. If missing, altExp from <a href="#">altExps</a> 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 <a href="#">altExps</a> method.  |
| e           | character(1) Same as altExp<- from <a href="#">altExps</a> method.   |
| withColData | logical(1) Same as altExp<- from <a href="#">altExps</a> method. Default FALSE.  |
| subsetName  | character(1) Specify the name of the subset to which the altExp<- should be set to. If missing, altExp<- from <a href="#">altExps</a> method is called on the main object. |
| value       | SingleCellExperiment Input value same as altExp<- from <a href="#">altExps</a> 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_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")
```

---

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 <a href="#">altExps</a> method.   |
| withColData | logical(1) Same as <a href="#">altExps</a> . Default FALSE.   |
| subsetName  | character(1) Specify the name of the subset from which the altExps should be fetched from. If missing, <a href="#">altExps</a> 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 <a href="#">altExps</a> method.   |
| subsetName | character(1) Specify the name of the subset to which the altExps<- should be set to. If missing, altExps<- from <a href="#">altExps</a> method is called on the main object. |
| value      | list() Input value same as altExps<- from <a href="#">altExps</a> 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&lt;- ,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      *ExperimentSubset constructor*

---

**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 <a href="#">reducedDims</a> method.  |
| type         | character(1) Same as type in reducedDim from <a href="#">reducedDims</a> method.   |
| withDimnames | logical(1) Same as withDimnames in reducedDim from <a href="#">reducedDims</a> method.   |
| subsetName   | character(1) Specify the name of the subset from which the reducedDim should be fetched from. If missing, reducedDim from <a href="#">reducedDims</a> 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 <a href="#">reducedDims</a> method.  |
| type       | character(1) Same as type in reducedDim<- from <a href="#">reducedDims</a> method.   |
| subsetName | character(1) Specify the name of the subset to which the reducedDim should be set to. If missing, reducedDim<- from <a href="#">reducedDims</a> 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 <a href="#">reducedDims</a> method.  |
| type       | character(1) Same as type in reducedDim<- from <a href="#">reducedDims</a> method.   |
| subsetName | character(1) Specify the name of the subset to which the reducedDim should be set to. If missing, reducedDim<- from <a href="#">reducedDims</a> 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 <a href="#">reducedDims</a> method.   |
| subsetName | character(1) Specify the name of the subset from which the reducedDimNames should be fetched from. If missing, reducedDimNames from <a href="#">reducedDims</a> 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 <a href="#">reducedDims</a> method.   |
| subsetName | character(1) Specify the name of the subset to which the reducedDimNames<- should be set to. If missing, reducedDimNames<- from <a href="#">reducedDims</a> method is called on the main object. |
| value      | vector("character") Input value same as reducedDimNames<- from <a href="#">reduced-Dims</a> method.  |

**Value**

Input object with reducedDimNames<- set.

---

reducedDims

*Methods for Reduced Dimensions in ExperimentSubset objects*


---

**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 <a href="#">reducedDims</a> method.   |
| withDimnames | logical(1) Same as withDimnames in <a href="#">reducedDims</a> method.  |
| subsetName   | character(1) Specify the name of the subset from which the reducedDims should be fetched from. If missing, <a href="#">reducedDims</a> 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 <a href="#">reducedDims</a> method.   |
| subsetName | character(1) Specify the name of the subset to which the reducedDims should be set to. If missing, reducedDims<- from <a href="#">reducedDims</a> 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 <a href="#">reducedDims</a> method.   |
| subsetName | character(1) Specify the name of the subset to which the reducedDims should be set to. If missing, reducedDims<- from <a href="#">reducedDims</a> 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               dgCMatrx 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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