Package ‘LoomExperiment’

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Title LoomExperiment container

Description The LoomExperiment package provide a means to easily convert the Bioconductor ``Experiment" classes to loom files and vice versa.

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Contents

`export-methods` *Export LoomExperiment to LoomFile*

Description

Exports a `LoomExperiment` to a `LoomFile`. Note the `colGraph` and `rowGraph` contained within the `LoomExperimnet` object are 1-indexed in `R` and are converted to 0-indexed in the loom file.

Usage

```
## S4 method for signature 'LoomExperiment,LoomFile,ANY'
export(object, con,
   matrix=assayNames(object)[1], rownames_attr="rownames", colnames_attr="colnames")
```

Arguments

`object`	A `LoomExperiment` object to be exported. File must have the `.loom` extension.
`con`	The connection from which data is loaded or to which data is saved. If this is a `character` vector, it is assumed to be a filename and a corresponding file connection is created and then closed after exporting the object. If a `RTLFile` derivative, the data is loaded from or saved to the underlying resource.
`matrix`	A `matrix` in which the column and rows for the Loom file will be derived. The default argument is dervied from the the first assay in the `LoomExperiment` object.
`rownames_attr`	A `character vector` indicating the name of the `rowData` attribute to represent the names `rownames` in the `LoomExperiment` object.
`colnames_attr`	A `character vector` indicating the name of the `colData` attribute to represent the names `colnames` in the `LoomExperiment` object.

Value

An error code indiciating whether the operation was successful.

See Also

`LoomExperiment`, `LoomFile`,

Examples

```
counts <- matrix(rpois(100, lambda = 10), ncol=10, nrow=10)
sce <- SingleCellExperiment(assays = list(counts = counts))
scle <- SingleCellLoomExperiment(sce)
tempfile <- tempfile(fileext=".loom")
export(scle, tempfile)
```

`import-methods` *Import LoomExperiment from LoomFile*

Description

Imports a `LoomExperiment` from a `LoomFile`. Note the `colGraph` and `rowGraph` contained within the 0-indexed loom file will be converted to the 1-indexed represnetation in the resulting `LoomExperiment` object.

Usage

```
## S4 method for signature 'LoomFile,ANY,ANY'
import(con, ...,
   type = c("SingleCellLoomExperiment", "LoomExperiment", "RangedLoomExperiment"),
    rownames_attr=NULL, colnames_attr=NULL)
```

Arguments

`con`	A character indicating the loom file to be created. File must have the `.loom` extension.
`...`	Additional arguments
`type`	Either "SingleCellLoomExperiment", "LoomExperiment", or "RangedLoomExperiment". This value decides what type of object that will be returned by `import`. If left empty `import` will either determine what type of class should be used by the context of the file. If it cannot be determined, the `LoomExperiment` type will default to `SingleCellLoomExperiment`.
`rownames_attr`	A `character vector` indicating the name of the `rowData` attribute to represent the names `rownames` in the `LoomExperiment` object.
`colnames_attr`	A `character vector` indicating the name of the `colData` attribute to represent the names `colnames` in the `LoomExperiment` object.

Value

An object of class `LoomExperiment`

See Also

`LoomExperiment`, `LoomFile`,

Examples

```
l1_file <- system.file("extdata", "L1_DRG_20_example.loom", package = "LoomExperiment")
scle <- import(l1_file, type="SingleCellLoomExperiment")
scle
```

`L1_DRG_20_example.loom` *L1_DRG_20_example.loom*

Description

An example `hdf5` file in the Loom file format obtained from the Linnarson Lab.

The original file was imported using `LoomExperiment` and truncated using the package's subsetting methods. The purpose of this truncation was to reduce the total size of the data as the file's purpose is simply to demonstrate `LoomExperiment`'s functionality.

The data set has dimensions of 20x20. The file contains 7 `rowData` and 103 `colData` entries each corresponding to readings generated by high-throughput sequencing experiments. In addition, a `colGraphs` entry encoding a`LoomGraph` containing two `LoomGraph` objects are also included.

Format

An hdf5 file in the Loom format

Examples

```
## Load L1_DRG_20_example.loom using LoomExperiment's import() method
l1_file <- system.file("extdata", "L1_DRG_20_example.loom", package = "LoomExperiment")
scle <- import(l1_file, type="SingleCellLoomExperiment")
scle
```

`LoomExperiment` *LoomExperiment, RangedLoomExperiment, and SingleCellLoomExperiment classes*

Description

The LoomExperiment family of classes is used as a bridge between Bioconductor's "Experiment" classes and the Linnarson Lab's http://linnarssonlab.org/loompy/index.html. The family of LoomExperiment classes all inherit from the class LoomExperiment as well as their respectively named parent classes. The LoomExperiment class inheirts from `SummarizedExperiment`.

Usage

```
## Constructor

LoomExperiment(..., colGraphs = LoomGraphs(), rowGraphs = LoomGraphs())
RangedLoomExperiment(..., colGraphs = LoomGraphs(), rowGraphs = LoomGraphs())
SingleCellLoomExperiment(..., colGraphs = LoomGraphs(), rowGraphs = LoomGraphs())

## Accessors

## S4 method for signature 'LoomExperiment'
colGraphs(x, ...)
## S4 replacement method for signature 'LoomExperiment'
```

```
colGraphs(x, ...) <- value
## S4 method for signature 'LoomExperiment'
rowGraphs(x, ...)
## S4 replacement method for signature 'LoomExperiment'
rowGraphs(x, ...) <- value

## Subsetting

## S4 method for signature 'LoomExperiment'
x[i, j, ..., drop=TRUE]

## Binding

## S4 method for signature 'LoomExperiment'
rbind(..., deparse.level=1)
## S4 method for signature 'LoomExperiment'
cbind(..., deparse.level=1)
```

Arguments

`x`	A LoomExperiment object
`colGraphs`, `rowGraphs`	LoomGraphs to be placed in either the colGraphs or rowGraphs slot respectively
`value`	For `colGraphs<-` and `rowGraphs<-`, `value` will be the replacement to the slot. For `dropHits<-`, indices to replace selected indices with.
`...`	For constructors, `...` will be passed on to the respective Experiment constructor.
`i`, `j`	For subsetting, indices specifying elements to subset LoomGraph by. For dropHits, numeric indicating the node number
`drop`	For matrices and arrays. If 'TRUE' the result is coerced to the lowest posible dimesnion. This only woeks for extracting elements, not for the replacement.
`deparse.level`	See '?base::cbind' for a description of this argument.

Details

The LoomExperiment class is a virtual class meant to to act as an interface for other `"_LoomExperiment"` classes. It contains two slots:

`colGraphs`: A LoomGraphs object containing `col_graph` data as specified by the loom format.

`rowGraphs`: A LoomGraphs object containing `row_graph` data as specified by the loom format.

The intended use of this class is as an interface that allows various slots and operations necessary for subsequent `"_LoomExperiment"` classes to be defined.

The `colGraphs` and `rowGraphs` slot stores a `LoomGraphs` object that stores a graph of edges between vertices and possibly associated weights. These slots may be `NULL`.

Value

An object of class `LoomExperiment`

Author(s)

Daniel Van Twisk

See Also

`SummarizedExperiment`, `RangedSummarizedExperiment`, `SingleCellExperiment`

Examples

```
## Construction
counts <- matrix(rpois(100, lambda = 10), ncol=10, nrow=10)
sce <- SingleCellExperiment(assays = list(counts = counts))
scle <- SingleCellLoomExperiment(sce)
# OR
scle <- SingleCellLoomExperiment(assays = list(counts = counts))
# OR
scle <- as(sce, "SingleCellLoomExperiment")
scle

## Get and replace rowGraphs and colGraphs
colGraphs(scle)
rowGraphs(scle)

a <- c(1, 2, 3)
b <- c(3, 2, 1)
w <- c(100, 10, 1)
lg <- LoomGraph(a, b, weight=w)
lgs <- LoomGraphs(lg, lg)
names(lgs) <- c('lg1', 'lg2')
lgs

colGraphs(scle) <- lgs
rowGraphs(scle) <- lgs

colGraphs(scle)
rowGraphs(scle)
colGraphs(scle)[[1]]
rowGraphs(scle)[[1]]

## Subsetting
scle2 <- scle[c(1, 3), 1:2]
colGraphs(scle2)[[1]]
rowGraphs(scle2)[[1]]
```

`LoomFile` *LoomFile objects*

Description

A `LoomFile` class represents a loom file based on the Linnarson Lab's http://linnarssonlab.org/loompy/index.html. A loom file is encoded as an hdf5 file. A loom file consists of a main matrix, optional additional layers, a variable number of row and column annotations and sparse graph objects. It is used to efficienctly stroe very large omics datasets.

The `LoomFile` class extends the functionality of the `BiocFile` from the `BiocIO` package.

Author(s)

Daniel Van Twisk

`LoomGraph` *LoomGraph class*

Description

The `LoomGraph` class extends the `SelfHits` class. The `SelfHits` class represents a set of hits between a set of left node and right nodes. Only the Hits are stored in a `SelfHits` `object`. The `LoomGraph` class is meant to store graph information and was created to be used in conjunction with the `LoomExperiment` class. Its purpose is to store either a `col_graph` or `row_graph` as specified by the `loom` file format. Attributes `from` and `to` indicate an edge between two vertices. The `w` column indicates the weight of the corresponding edge and is optional.

Usage

```
LoomGraph(from, to, nnode=max(from, to), ..., weight=NULL)

## S4 method for signature 'LoomGraph'
rbind(..., deparse.level=1)
## S4 method for signature 'LoomGraph'
cbind(..., deparse.level=1)
```

Arguments

`...`	Arguments to pass to the `SelfHits` constructor.
`from`	A numeric vector of nodes indicating one side of the graph's edge.
`to`	A numeric vector of node indicating the second side of the graph's edge.
`nnode`	An integer indicating the maximum number of nodes in the graph.
`weight`	A numeric vector indicating the weight between the prospective edges.
`deparse.level`	See '?base::cbind' for a description of this argument

Value

A LoomGraph object is returned from the constructor.

Author(s)

Daniel Van Twisk

See Also

`LoomExperiment`, `LoomGraphs`, `SelfHits`

Examples

```
## Construction
a <- c(1, 2, 3)
b <- c(3, 2, 1)
w <- c(100, 10, 1)
df <- DataFrame(a, b, w)
lg <- as(df, "LoomGraph")
# OR
```

```
lg <- LoomGraph(a, b, weight=w)
lg

## Subsetting
lg[c(1, 2)]
lg[-c(2)]
```

`LoomGraphs` *LoomGraphs class*

Description

The LoomGraphs class extends the `SimpleList` class. It is meant to store multiple `LoomGraph` objects and was created to be used in conjunction with the `LoomExperiment` class. Its purpose is to store multiple `col_graph` or `row_graph` as specified by the `loom` file format. Only `LoomGraph` obects may be stored in a LoomGraphs object.

Usage

```
LoomGraphs(...)

## S4 method for signature 'LoomGraphs'
rbind(..., deparse.level=1)
## S4 method for signature 'LoomGraphs'
cbind(..., deparse.level=1)
```

Arguments

`...`	`LoomGraph` objects.
`deparse.level`	See '?base::cbind' for a description of this argument

Value

A LoomGraphs object is returned from the constructor.

Author(s)

Daniel Van Twisk

See Also

`LoomExperiment`, `LoomGraph`, `SimpleList`

Examples

```
## Construction
lg1 <- LoomGraph(c(1, 2, 3), c(3, 2, 1), weight=c(4, 7, 8))
lg2 <- LoomGraph(c(3, 3, 1), c(3, 1, 2))
lgs <- LoomGraphs(lg1, lg2)
lgs
```

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