

Package ‘LoomExperiment’

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Title LoomExperiment container

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

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| | |
|----------------------------------|---|
| export-methods | 2 |
| import-methods | 3 |
| L1_DRG_20_example.loom | 4 |
| LoomExperiment | 4 |
| LoomFile | 6 |
| LoomGraph | 7 |
| LoomGraphs | 8 |

| | |
|----------------|--|
| export-methods | <i>Export LoomExperiment to LoomFile</i> |
|----------------|--|

Description

Exports a LoomExperiment to a LoomFile. Note the colGraph and rowGraph contained within the LoomExperiment 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 derived 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 indicating 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 representation 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

| | |
|----------------------------|---|
| <code>con</code> | A character indicating the loom file to be created. File must have the .loom extension. |
| <code>...</code> | Additional arguments |
| <code>type</code> | Either "SingleCellLoomExperiment", "LoomExperiment", or "RangedLoomExperiment". This value decides what type of object that will be returned by <code>import</code> . If left empty <code>import</code> 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. |
| <code>rownames_attr</code> | A character vector indicating the name of the rowData attribute to represent the names rownames in the LoomExperiment object. |
| <code>colnames_attr</code> | 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")  
scl <- import(l1_file, type="SingleCellLoomExperiment")  
scl
```

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")
scl <- import(l1_file, type="SingleCellLoomExperiment")
scl
```

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 inherits 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

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

Details

The LoomExperiment class is a virtual class meant 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 Linnarsson 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 efficiently store very large omics datasets.

The LoomFile class extends the functionality of the [RTLFile](#) from the `rtracklayer` 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

| | |
|----------------------------|--|
| <code>...</code> | Arguments to pass to the <code>SelfHits</code> constructor. |
| <code>from</code> | A numeric vector of nodes indicating one side of the graph's edge. |
| <code>to</code> | A numeric vector of node indicating the second side of the graph's edge. |
| <code>nnode</code> | An integer indicating the maximum number of nodes in the graph. |
| <code>weight</code> | A numeric vector indicating the weight between the prospective edges. |
| <code>deparse.level</code> | See <code>'?base::cbind'</code> 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 objects 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
```

Index

- * **datasets**
 - L1_DRG_20_example.loom, 4
 - [,LoomExperiment,ANY,ANY,ANY-method (LoomExperiment), 4
 - [,LoomExperiment,ANY-method (LoomExperiment), 4
 - [,LoomExperiment-method (LoomExperiment), 4
 - [,RangedLoomExperiment,ANY,ANY,ANY-method (LoomExperiment), 4
 - [,RangedLoomExperiment,ANY-method (LoomExperiment), 4
 - [,RangedLoomExperiment-method (LoomExperiment), 4
 - [,SingleCellLoomExperiment,ANY,ANY,ANY-method (LoomExperiment), 4
 - [,SingleCellLoomExperiment,ANY-method (LoomExperiment), 4
 - [,SingleCellLoomExperiment-method (LoomExperiment), 4
- cbind,LoomExperiment-method (LoomExperiment), 4
- cbind,LoomGraph-method (LoomGraph), 7
- cbind,LoomGraphs-method (LoomGraphs), 8
- cbind,SingleCellLoomExperiment-method (LoomExperiment), 4
- colGraphs (LoomExperiment), 4
- colGraphs,LoomExperiment-method (LoomExperiment), 4
- colGraphs<- (LoomExperiment), 4
- colGraphs<- ,LoomExperiment-method (LoomExperiment), 4
- export (export-methods), 2
- export,LoomExperiment,LoomFile,ANY-method (export-methods), 2
- export-methods, 2
- import (import-methods), 3
- import,LoomFile,ANY,ANY-method (import-methods), 3
- import-methods, 3
- L1_DRG_20_example
 - (L1_DRG_20_example.loom), 4
- L1_DRG_20_example.loom, 4
- LoomExperiment, 2, 3, 4, 7, 8
- LoomExperiment-class (LoomExperiment), 4
- LoomFile, 2, 3, 6
- LoomFile-class (LoomFile), 6
- LoomGraph, 7, 8
- LoomGraph-class (LoomGraph), 7
- LoomGraphs, 7, 8
- LoomGraphs-class (LoomGraphs), 8
- RangedLoomExperiment (LoomExperiment), 4
- RangedLoomExperiment-class (LoomExperiment), 4
- RangedSummarizedExperiment, 6
- rbind,LoomExperiment-method (LoomExperiment), 4
- rbind,LoomGraph-method (LoomGraph), 7
- rbind,LoomGraphs-method (LoomGraphs), 8
- rbind,SingleCellLoomExperiment-method (LoomExperiment), 4
- rowGraphs (LoomExperiment), 4
- rowGraphs,LoomExperiment-method (LoomExperiment), 4
- rowGraphs<- (LoomExperiment), 4
- rowGraphs<- ,LoomExperiment-method (LoomExperiment), 4
- RTLFile, 6
- SelfHits, 7
- show,LoomExperiment-method (LoomExperiment), 4
- show,RangedLoomExperiment-method (LoomExperiment), 4
- show,SingleCellLoomExperiment-method (LoomExperiment), 4
- SimpleList, 8
- SingleCellExperiment, 6
- SingleCellLoomExperiment (LoomExperiment), 4
- SingleCellLoomExperiment-class (LoomExperiment), 4
- SummarizedExperiment, 4, 6