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

Index **10**

`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
```

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

BiocFile, *7*

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, *8, 9*
LoomExperiment-class (LoomExperiment), 4
LoomFile, *2, 3*, 7
LoomFile-class (LoomFile), 7
LoomGraph, 7, *9*
LoomGraph-class (LoomGraph), 7
LoomGraphs, *8*, 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

SelfHits, *7, 8*
show,LoomExperiment-method (LoomExperiment), 4
show,RangedLoomExperiment-method (LoomExperiment), 4

show,SingleCellLoomExperiment-method
(LoomExperiment), 4
SimpleList, *8*, *9*
SingleCellExperiment, *6*
SingleCellLoomExperiment
(LoomExperiment), 4
SingleCellLoomExperiment-class
(LoomExperiment), 4
SummarizedExperiment, *4*, *6*