

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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Author Martin Morgan, Daniel Van Twisk

Maintainer Bioconductor Package Maintainer <maintainer@bioconductor.org>

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export-methods	<i>Export LoomExperiment to LoomFile</i>
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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 <code>colGraphs<-</code> and <code>rowGraphs<-</code> , value will be the replacement to the slot. For <code>dropHits<-</code> , 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 <code>dropHits</code> , 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 <code>?base::cbind</code> 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 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 efficiently store 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 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
```


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