

Package ‘LoomExperiment’

January 20, 2025

Title LoomExperiment container

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

Version 1.24.0

Encoding UTF-8

Author Martin Morgan, Daniel Van Twisk

Maintainer Bioconductor Package Maintainer <maintainer@bioconductor.org>

Depends R (>= 3.5.0), S4Vectors, SingleCellExperiment, SummarizedExperiment, methods, rhdf5, BiocIO

Imports DelayedArray, GenomicRanges, HDF5Array, Matrix, stats, stringr, utils

Suggests testthat, BiocStyle, knitr, rmarkdown, reticulate

Collate AllGenerics.R utils.R SharedMethods.R LoomGraph-class.R LoomExperiment-class.R RangedLoomExperiment-class.R SingleCellLoomExperiment-class.R LoomFile-class.R export-method.R import-method.R

License Artistic-2.0

VignetteBuilder knitr

biocViews ImmunoOncology, DataRepresentation, DataImport, Infrastructure, SingleCell

RoxygenNote 7.1.1

git_url <https://git.bioconductor.org/packages/LoomExperiment>

git_branch RELEASE_3_20

git_last_commit 046fa8f

git_last_commit_date 2024-10-29

Repository Bioconductor 3.20

Date/Publication 2025-01-20

Contents

export-methods	2
import-methods	3
L1_DRG_20_example.loom	4

LoomExperiment	4
LoomFile	6
LoomGraph	7
LoomGraphs	8

Index	9
--------------	----------

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))
scl <- SingleCellLoomExperiment(sce)
tempfile <- tempfile(fileext=".loom")
export(scl, 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 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.
<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, <code>...</code> 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))
scl <- SingleCellLoomExperiment(sce)
# OR
scl <- SingleCellLoomExperiment(assays = list(counts = counts))
# OR
scl <- as(sce, "SingleCellLoomExperiment")
scl

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

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(scl) <- lgs
rowGraphs(scl) <- lgs

colGraphs(scl)
rowGraphs(scl)
colGraphs(scl)[[1]]
rowGraphs(scl)[[1]]

## Subsetting
scl2 <- scl[c(1, 3), 1:2]
colGraphs(scl2)[[1]]
rowGraphs(scl2)[[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
```


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, 6

- 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

- 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