

# 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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| 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**

|               |  |
|---------------|--|
| 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 aLoomGraph 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 SingleCellLoomEx-
                    periment 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 [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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