

# Package ‘LoomExperiment’

November 9, 2024

**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** 2024-11-08

## Contents

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

LoomExperiment . . . . .	4
LoomFile . . . . .	6
LoomGraph . . . . .	7
LoomGraphs . . . . .	8

<b>Index</b>	<b>9</b>
--------------	----------

---

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 <code>colGraphs&lt;-</code> and <code>rowGraphs&lt;-</code> , value will be the replacement to the slot. For <code>dropHits&lt;-</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))
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