

Package ‘alabaster.ranges’

November 14, 2025

Title Load and Save Ranges-related Artifacts from File

Version 1.11.0

Date 2025-07-22

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Description Save GenomicRanges, IRanges and related data structures into file artifacts, and load them back into memory.
This is a more portable alternative to serialization of such objects into RDS files. Each artifact is associated with metadata for further interpretation; downstream applications can enrich this metadata with context-specific properties.

Depends GenomicRanges, alabaster.base

Imports methods, S4Vectors, BiocGenerics, IRanges, Seqinfo, rhdf5

Suggests testthat, knitr, BiocStyle, jsonlite

VignetteBuilder knitr

RoxygenNote 7.2.3

biocViews DataImport, DataRepresentation

git_url <https://git.bioconductor.org/packages/alabaster.ranges>

git_branch devel

git_last_commit 283afd5

git_last_commit_date 2025-10-29

Repository Bioconductor 3.23

Date/Publication 2025-11-14

Author Aaron Lun [aut, cre]

Maintainer Aaron Lun <infinite.monkeys.with.keyboards@gmail.com>

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readAtomicVectorList	<i>Load an atomic vector list</i>
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Description

Load a list of atomic vectors as a [CompressedAtomicList](#) from its on-disk representation. This is usually not directly called by users, but is instead called by dispatch in [readObject](#).

Usage

```
readAtomicVectorList(path, metadata, ...)
```

Arguments

path	String containing a path to a directory, itself created with the saveObject method for CompressedAtomicLists .
metadata	Named list of metadata for this object, see readObjectFile for details.
...	Further arguments, to be passed to internal altReadObject calls.

Value

A [CompressedAtomicList](#) of the relevant type.

Author(s)

Aaron Lun

See Also

["saveObject,CompressedAtomicList-method"](#), to save an object to disk.

Examples

```
library(S4Vectors)
X <- splitAsList(LETTERS, sample(3, 26, replace=TRUE))

tmp <- tempfile()
saveObject(X, tmp)
readObject(tmp)
```

readDataFrameList	<i>Load a data frame list</i>
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Description

Load a list of data frames as a [CompressedSplitDataFrameList](#) from its on-disk representation. This is usually not directly called by users, but is instead called by dispatch in [readObject](#).

Usage

```
readDataFrameList(path, metadata, ...)
```

Arguments

path	String containing a path to a directory, itself created with the saveObject method for CompressedSplitDataFrameList objects.
metadata	Named list of metadata for this object, see readObjectFile for details.
...	Further arguments, to be passed to internal altReadObject calls.

Value

A [CompressedSplitDataFrameList](#).

Author(s)

Aaron Lun

See Also

"[saveObject,CompressedSplitDataFrameList-method](#)", to save an object to disk.

Examples

```
library(S4Vectors)
Y <- splitAsList(DataFrame(Xxx=LETTERS, Yyy=1:26), sample(3, 26, replace=TRUE))

tmp <- tempfile()
saveObject(Y, tmp)
readObject(tmp)
```

readGRanges

Read a GRanges from disk

Description

Read a [GRanges](#) object from its on-disk representation. This is usually not directly called by users, but is instead called by dispatch in [readObject](#).

Usage

```
readGRanges(path, metadata, ...)
```

Arguments

path	String containing a path to a directory, itself created with the stageObject method for GRanges .
metadata	Named list of metadata for this object, see readObjectFile for details.
...	Further arguments to pass to internal altReadObject calls.

Value

A [GRanges](#) object.

Author(s)

Aaron Lun

See Also

"[saveObject,GRanges-method](#)", to save a [GRanges](#) to disk.

Examples

```
gr <- GRanges(c("chrA", "chrB"), IRanges(c(1, 5), c(100, 200)))
seqlengths(gr) <- c(chrA=1000, chrB=2000)

tmp <- tempfile()
saveObject(gr, tmp)
readObject(tmp)
```

readGRangesList	<i>Read a GRangesList from disk</i>
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Description

Read a [GRangesList](#) object from its on-disk representation.

Usage

```
readGRangesList(path, metadata, ...)
```

Arguments

path	String containing a path to a directory, itself created with the saveObject method for GRangesLists .
metadata	Named list of metadata for this object, see readObjectFile for details.
...	Further arguments, to be passed to internal altReadObject calls.

Value

A [GRangesList](#) object.

Examples

```
gr <- GRanges(c("chrA", "chrB"), IRanges(c(1, 5), c(100, 200)))
seqlengths(gr) <- c(chrA=1000, chrB=2000)
grl <- split(gr, rep(1:3, length.out=length(gr)))

tmp <- tempfile()
saveObject(grl, tmp)
readObject(tmp)
```

readSeqinfo	<i>Read a Seqinfo from disk</i>
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Description

Read a [Seqinfo](#) object from its on-disk representation. This is usually not directly called by users, but is instead called by dispatch in [readObject](#).

Usage

```
readSeqinfo(path, metadata, ...)
```

Arguments

path	String containing a path to a directory, itself created with the saveObject method for Seqinfo objects.
metadata	Named list of metadata for this object, see readObjectFile for details.
...	Further arguments, ignored.

Value

A [Seqinfo](#) object.

See Also

"[saveObject,Seqinfo-method](#)" for the corresponding saving method.

Examples

```
si <- Seqinfo(c("chrA", "chrB"), c(1000, 2000))

tmp <- tempfile()
saveObject(si, tmp)
readObject(tmp)
```

saveObject,CompressedAtomicList-method

Save compressed list of atomic vectors to disk

Description

Save a [CompressedAtomicList](#) object to its on-disk representation.

Usage

```
## S4 method for signature 'CompressedAtomicList'
saveObject(x, path, ...)
```

Arguments

x	A CompressedAtomicList object.
path	String containing the path to a directory in which to save x.
...	Further arguments to pass to specific methods.

Value

x is saved to path, and NULL is invisibly returned.

Author(s)

Aaron Lun

See Also[readAtomicVectorList](#), to read a [CompressedAtomicList](#) from disk.**Examples**

```
library(S4Vectors)
X <- splitAsList(LETTERS, sample(3, 26, replace=TRUE))

tmp <- tempfile()
saveObject(X, tmp)
list.files(tmp, recursive=TRUE)
```

`saveObject,CompressedSplitDataFrameList-method`*Save compressed lists of data frames to disk*

Description

Save a [CompressedSplitDataFrameList](#) object to its on-disk representation.

Usage

```
## S4 method for signature 'CompressedSplitDataFrameList'
saveObject(x, path, ...)
```

Arguments

x	A CompressedSplitDataFrameList object.
path	String containing the path to a directory in which to save x.
...	Further arguments to pass to specific methods.

Value

x is saved to path, and NULL is invisibly returned.

Author(s)

Aaron Lun

See Also[readDataFrameList](#), to read a [CompressedSplitDataFrameList](#) from disk.

Examples

```
library(S4Vectors)
Y <- splitAsList(DataFrame(Xxx=LETTERS, Yyy=1:26), sample(3, 26, replace=TRUE))

tmp <- tempfile()
saveObject(Y, tmp)
list.files(tmp, recursive=TRUE)
```

saveObject,GRanges-method

Save a GRanges object to disk

Description

Save a [GRanges](#) object to its on-disk representation .

Usage

```
## S4 method for signature 'GRanges'
saveObject(x, path, ...)
```

Arguments

x	A GRanges object or one of its subclasses.
path	String containing the path to a directory in which to save x.
...	Further arguments to pass to specific methods.

Value

x is saved to path, and NULL is invisibly returned.

Author(s)

Aaron Lun

See Also

[readGRanges](#), to read a [GRanges](#) from disk.

Examples

```
gr <- GRanges(c("chrA", "chrB"), IRanges(c(1, 5), c(100, 200)))
seqlengths(gr) <- c(chrA=1000, chrB=2000)

tmp <- tempfile()
saveObject(gr, tmp)
list.files(tmp, recursive=TRUE)
```

`saveObject,GRangesList-method`*Save a GRangesList object to disk*

Description

Save a [GRangesList](#) object to its on-disk representation.

Usage

```
## S4 method for signature 'GRangesList'
saveObject(x, path, ...)
```

Arguments

<code>x</code>	A GRangesList object.
<code>path</code>	String containing the path to a directory in which to save <code>x</code> .
<code>...</code>	Further arguments to pass to specific methods.

Value

`x` is saved to `path`, and `NULL` is invisibly returned.

Author(s)

Aaron Lun

See Also

[readGRangesList](#), to read a [GRangesList](#) from disk.

Examples

```
gr <- GRanges("chrA", IRanges(1:100, width=1))
grl <- split(gr, rep(1:3, length.out=length(gr)))

tmp <- tempfile()
saveObject(grl, tmp)
list.files(tmp, recursive=TRUE)
```

`saveObject,Seqinfo-method`*Save a Seqinfo object to disk*

Description

Save a [Seqinfo](#) object to its on-disk representation.

Usage

```
## S4 method for signature 'Seqinfo'
saveObject(x, path, ...)
```

Arguments

<code>x</code>	A Seqinfo object.
<code>path</code>	String containing the path to a directory in which to save <code>x</code> .
<code>...</code>	Further arguments to pass to specific methods.

Value

`x` is saved to `path`, and `NULL` is invisibly returned.

See Also

[readSeqinfo](#), to read a [Seqinfo](#) from disk.

Examples

```
si <- Seqinfo(c("chrA", "chrB"), c(1000, 2000))

tmp <- tempfile()
dir.create(tmp)
saveObject(si, tmp, path="seqinfo")
list.files(tmp, recursive=TRUE)
```

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