

Package: alabaster.ranges (via r-universe)

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Title Load and Save Ranges-related Artifacts from File

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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, GenomeInfoDb, rhdf5

Suggests testthat, knitr, BiocStyle, jsonlite

VignetteBuilder knitr

RoxygenNote 7.2.3

biocViews DataImport, DataRepresentation

Repository <https://bioc.r-universe.dev>

RemoteUrl <https://github.com/bioc/alabaster.ranges>

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readAtomicVectorList *Load an atomic vector list*

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 *Load a data frame list*

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

| | |
|-----------------------|---|
| <code>path</code> | String containing a path to a directory, itself created with the stageObject method for GRanges . |
| <code>metadata</code> | Named list of metadata for this object, see readObjectFile for details. |
| <code>...</code> | 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> |
|-----------------|-------------------------------------|

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)
gr1 <- split(gr, rep(1:3, length.out=length(gr)))

tmp <- tempfile()
saveObject(gr1, tmp)
readObject(tmp)
```

| | |
|-------------|---------------------------------|
| readSeqinfo | <i>Read a Seqinfo from disk</i> |
|-------------|---------------------------------|

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

| | |
|------|---|
| x | A Seqinfo 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.

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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