Package ‘alabaster.ranges’

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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, Seqinfo, rhdf5

Suggests testthat, knitr, BiocStyle, jsonlite

VignetteBuilder knitr

RoxygenNote 7.2.3

biocViews DataImport, DataRepresentation

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Contents

`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

`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` *Read a GRangesList from disk*

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` *Read a Seqinfo from disk*

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

`x`	A GRangesList 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

`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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