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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`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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