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, utils, S4Vectors, BiocGenerics, IRanges, GenomeInfoDb

Suggests testthat, knitr, BiocStyle, jsonlite

VignetteBuilder knitr

RoxygenNote 7.2.1

biocViews DataImport, DataRepresentation

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R topics documented:

`loadAtomicVectorList` *Load an atomic vector list*

Description

Load a list of atomic vectors as a CompressedAtomicList, typically from files created by the corresponding `stageObject` method.

Usage

```
loadAtomicVectorList(info, project)
```

Arguments

`info`	Named list containing the metadata for this object.
`project`	Any argument accepted by the acquisition functions, see `?acquireFile`. By default, this should be a string containing the path to a staging directory.

Value

A CompressedAtomicList of the relevant type.

Author(s)

Aaron Lun

Examples

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

# Staging this object:
tmp <- tempfile()
dir.create(tmp)
info <- stageObject(X, tmp, path="test1")

# Loading the object:
loadAtomicVectorList(info, tmp)
```

loadDataFrameList *Load a data frame list*

Description

Load a list of data frames as a CompressedSplitDataFrameList, typically from files created by the corresponding `stageObject` method.

Usage

```
loadDataFrameList(info, project)
```

Arguments

`info`	Named list containing the metadata for this object.
`project`	Any argument accepted by the acquisition functions, see ?`acquireFile`. By default, this should be a string containing the path to a staging directory.

Value

A CompressedSplitDataFrameList.

Author(s)

Aaron Lun

Examples

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

tmp <- tempfile()
dir.create(tmp)
info <- stageObject(Y, tmp, path="test2")

loadDataFrameList(info, tmp)
```

loadGRanges *Load a GRanges*

Description

Load a GRanges object based on the metadata saved by the corresponding `stageObject` method.

Usage

```
loadGRanges(info, project)
```

Arguments

info	Named list containing the metadata for this object.
project	Any argument accepted by the acquisition functions, see ?acquireFile. By default, this should be a string containing the path to a staging directory.

Value

A GRanges object.

Examples

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

# Staging it:
tmp <- tempfile()
dir.create(tmp)
info <- stageObject(gr, tmp, path="ranges")

# Now loading it back in:
loadGRanges(info, tmp)
```

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loadGRangesList *Load a GRanges*

Description

Load a GRangesList object based on the metadata saved by the corresponding stageObject method.

Usage

```
loadGRangesList(info, project)
```

Arguments

info	Named list containing the metadata for this object.
project	Any argument accepted by the acquisition functions, see ?acquireFile. By default, this should be a string containing the path to a staging directory.

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)))

# Staging it:
tmp <- tempfile()
dir.create(tmp)
info <- stageObject(grl, tmp, path="ranges")

# Now loading it back in:
loadGRangesList(info, tmp)
```

`loadSeqinfo` *Load a Seqinfo*

Description

Load a Seqinfo object based on the metadata saved by the corresponding `stageObject` method.

Usage

```
loadSeqinfo(info, project)
```

Arguments

`info`	Named list containing the metadata for this object.
`project`	Any argument accepted by the acquisition functions, see `?acquireFile`. By default, this should be a string containing the path to a staging directory.

Value

A Seqinfo object.

Examples

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

# Staging it:
tmp <- tempfile()
dir.create(tmp)
info <- stageObject(si, tmp, path="seqinfo")

# Now loading it back in:
loadSeqinfo(info, tmp)
```

stageObject,CompressedAtomicList-method

Stage a compressed list of atomic vectors

Description

Stage a CompressedAtomicList object.

Usage

```
## S4 method for signature 'CompressedAtomicList'
stageObject(
  x,
  dir,
  path,
  child = FALSE,
  group.name = "grouping",
  concat.name = "concatenated",
  mcols.name = "mcols",
  meta.name = "other"
)
```

Arguments

x	A Bioconductor object of the specified class.
dir	String containing the path to the staging directory.
path	String containing a prefix of the relative path inside dir where x is to be saved. The actual path used to save x may include additional components, see Details.
child	Logical scalar indicating whether x is a child of a larger object.
group.name	String containing the name of the file inside path to save the list groupings.
concat.name	String containing the extension-less name of the file inside path to save the concatenated elements.
mcols.name	String specifying the name of the directory inside path to save the mcols. If NULL, per-element metadata is not saved.
meta.name	String specifying the name of the directory inside path to save metadata(x). If NULL, object metadata is not saved.

Details

The staging process will save both the interval groupings and the concatenated vector into separate files. The concatenated vector is coerced into a DataFrame and staged with the corresponding stageObject method. The CompressedList may also be decorated with metadata for each list element in its mcols, which is saved to mcols.name. No file is created at mcols.name if mcols(x) is NULL or has no columns.

Value

A named list containing the metadata for `x`. The contents of `x` are saved inside `path` and referenced from the metadata.

Author(s)

Aaron Lun

Examples

```
tmp <- tempfile()
dir.create(tmp)

library(S4Vectors)
X <- splitAsList(LETTERS, sample(3, 26, replace=TRUE))
stageObject(X, tmp, path="test1")
list.files(file.path(tmp, "test1"))
```

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stageObject,CompressedSplitDataFrameList-method

Stage compressed lists of DataFrames

Description

Stage CompressedSplitDataFrameList objects.

Usage

```
## S4 method for signature 'CompressedSplitDataFrameList'
stageObject(
  x,
  dir,
  path,
  child = FALSE,
  group.name = "grouping.csv",
  concat.name = "concatenated",
  mcols.name = "mcols",
  meta.name = "other"
)
```

Arguments

`x`	A CompressedList containing DataFrames with the same columns.
`dir`	String containing the path to the staging directory.
`path`	String containing a prefix of the relative path inside `dir` where `x` is to be saved. The actual path used to save `x` may include additional components, see Details.

child	Logical scalar indicating whether x is a child of a larger object.
group.name	String containing the name of the file inside path to save the list groupings.
concat.name	String containing the extension-less name of the file inside path to save the concatenated elements.
mcols.name	String specifying the name of the directory inside path to save the mcols. If NULL, the metadata columns are not saved.
meta.name	String specifying the name of the directory inside path to save metadata(x). If NULL, object metadata is not saved.

Details

The staging process will save both the interval groupings and the concatenated DataFrame into separate files. The CompressedList may also be decorated with metadata for each list element in its mcols, which is saved to mcols.name. No file is created at mcols.name if mcols(x) is NULL or has no columns.

Value

A named list containing the metadata for x. The contents of x are saved inside path and referenced from the metadata.

Author(s)

Aaron Lun

Examples

```
tmp <- tempfile()
dir.create(tmp)

library(S4Vectors)
Y <- splitAsList(DataFrame(Xxx=LETTERS, Yyy=1:26), sample(3, 26, replace=TRUE))
stageObject(Y, tmp, path="test2")
list.files(file.path(tmp, "test2"))
```

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stageObject,GRanges-method

Stage a GRanges object

Description

Stage a GRanges object containing genomic intervals.

Usage

```
## S4 method for signature 'GRanges'
stageObject(
  x,
  dir,
  path,
  child = FALSE,
  coord.name = "ranges",
  seqinfo.name = "seqinfo",
  mcols.name = "mcols",
  meta.name = "other"
)
```

Arguments

x	A GRanges object or one of its subclasses.
dir	String containing the path to the staging directory.
path	String containing a prefix of the relative path inside dir where x is to be saved. The actual path used to save x may include additional components, see Details.
child	Logical scalar indicating whether x is a child of a larger object.
coord.name	String containing the name of the file inside path to save the genomic coordinates.
seqinfo.name	String containing the name of the file inside path to save the sequence information.
mcols.name	String specifying the name of the directory inside path to save mcols(x). If NULL, per-element metadata is not saved.
meta.name	String specifying the name of the directory inside path to save metadata(x). If NULL, object metadata is not saved.

Details

Setting mcols.name=NULL and meta.name=NULL will skip the staging of the mcols and metadata. This is primarily useful for use in staging RangedSummarizedExperiments where the mcols have already been saved as part of the rowData.

Value

A named list containing the metadata for x. The contents of x are saved into various files inside file.path(dir, path).

Author(s)

Aaron Lun

Examples

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

tmp <- tempfile()
dir.create(tmp)
stageObject(gr, tmp, path="ranges")
list.files(tmp, recursive=TRUE)
```

`stageObject,GRangesList-method`
Stage a GRangesList object

Description

Stage a GRangesList object containing groups of genomic intervals.

Usage

```
## S4 method for signature 'GRangesList'
stageObject(
  x,
  dir,
  path,
  child = FALSE,
  group.name = "grouping",
  mcols.name = "mcols",
  ranges.name = "ranges",
  meta.name = "other",
  ranges.args = list()
)
```

Arguments

`x`	A GRangesList object or one of its subclasses.
`dir`	String containing the path to the staging directory.
`path`	String containing a prefix of the relative path inside `dir` where `x` is to be saved. The actual path used to save `x` may include additional components, see Details.
`child`	Logical scalar indicating whether `x` is a child of a larger object.
`group.name`	String containing the name of the file inside `path` to save the GRangesList groupings.
`mcols.name`	String specifying the name of the directory inside `path` to save `mcols(x)`. If `NULL`, per-element metadata is not saved.
`ranges.name`	String containing the name of the directory inside `path` to save the underlying GRanges (i.e., `unlist(x)`).

meta.name	String specifying the name of the directory inside path to save metadata(x). If NULL, object metadata is not saved.
ranges.args	Further arguments to pass to the stageObject method when saving the underlying GRanges.

Details

Setting mcols.name=NULL and meta.name=NULL will skip the staging of the mcols and metadata. This is primarily useful for use in staging RangedSummarizedExperiments where the mcols have already been saved as part of the rowData.

Value

A named list containing the metadata for x. The contents of x are saved into various files inside file.path(dir, path).

Author(s)

Aaron Lun

Examples

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

tmp <- tempfile()
dir.create(tmp)
stageObject(grl, tmp, path="GRL")
list.files(tmp, recursive=TRUE)
```

---

stageObject,Seqinfo-method

Stage a Seqinfo object

Description

Stage a Seqinfo object containing genomic information.

Usage

```
## S4 method for signature 'Seqinfo'
stageObject(x, dir, path, child = FALSE)
```

Arguments

x	A Seqinfo object.
dir	String containing the path to the staging directory.
path	String containing a prefix of the relative path inside dir where x is to be saved. The actual path used to save x may include additional components, see Details.
child	Logical scalar indicating whether x is a child of a larger object.

Value

A named list containing the metadata for x. The contents of x are saved into various files inside file.path(dir, path).

Examples

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

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

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