

# Package ‘alabaster.ranges’

March 25, 2024

**Title** Load and Save Ranges-related Artifacts from File

**Version** 1.2.0

**Date** 2023-02-28

**License** MIT + file LICENSE

**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

**git\_url** <https://git.bioconductor.org/packages/alabaster.ranges>

**git\_branch** RELEASE\_3\_18

**git\_last\_commit** c7a063d

**git\_last\_commit\_date** 2023-10-24

**Repository** Bioconductor 3.18

**Date/Publication** 2024-03-25

**Author** Aaron Lun [aut, cre]

**Maintainer** Aaron Lun <[infinite.monkeys.with.keyboards@gmail.com](mailto:infinite.monkeys.with.keyboards@gmail.com)>

## R topics documented:

loadAtomicVectorList . . . . .	2
loadDataFrameList . . . . .	3
loadGRanges . . . . .	3
loadGRangesList . . . . .	4

loadSeqinfo . . . . .	5
stageObject,CompressedAtomicList-method . . . . .	6
stageObject,CompressedSplitDataFrameList-method . . . . .	7
stageObject,GRanges-method . . . . .	8
stageObject,GRangesList-method . . . . .	10
stageObject,Seqinfo-method . . . . .	11

## Index 13

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 <a href="#">?acquireFile</a> . 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	<i>Load a data frame list</i>
-------------------	-------------------------------

---

**Description**

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

**Usage**

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

**Arguments**

<code>info</code>	Named list containing the metadata for this object.
<code>project</code>	Any argument accepted by the acquisition functions, see <code>?acquireFile</code> . 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	<i>Load a GRanges</i>
-------------	-----------------------

---

**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 <a href="#">?acquireFile</a> . 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)
```

---

loadGRangesList	<i>Load a GRanges</i>
-----------------	-----------------------

---

**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 <a href="#">?acquireFile</a> . 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)
gr1 <- split(gr, rep(1:3, length.out=length(gr)))

# Staging it:
tmp <- tempfile()
dir.create(tmp)
info <- stageObject(gr1, 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 <a href="#">?acquireFile</a> . 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

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

---

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 <code>mcols</code> . If NULL, the metadata columns are not saved.
meta.name	String specifying the name of the directory inside path to save <code>metadata(x)</code> . 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"))
```

---

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 <a href="#">GRanges</a> 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 <a href="#">Details</a> .
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 <a href="#">mcols</a> (x). If NULL, per-element metadata is not saved.
meta.name	String specifying the name of the directory inside path to save <a href="#">metadata</a> (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 <a href="#">GRangesList</a> 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 <a href="#">GRangesList</a> groupings.
mcols.name	String specifying the name of the directory inside path to save <a href="#">mcols(x)</a> . If NULL, per-element metadata is not saved.
ranges.name	String containing the name of the directory inside path to save the underlying <a href="#">GRanges</a> (i.e., <a href="#">unlist(x)</a> ).

meta.name	String specifying the name of the directory inside path to save <code>metadata(x)</code> . If NULL, object metadata is not saved.
ranges.args	Further arguments to pass to the <code>stageObject</code> 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 <a href="#">Seqinfo</a> 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 <a href="#">Details</a> .
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)
```

# Index

acquireFile, [2-5](#)

CompressedAtomicList, [2, 6](#)

CompressedSplitDataFrameList, [3, 7](#)

GRanges, [3, 4, 8, 9](#)

GRangesList, [4, 10](#)

loadAtomicVectorList, [2](#)

loadDataFrameList, [3](#)

loadGRanges, [3](#)

loadGRangesList, [4](#)

loadSeqinfo, [5](#)

mcols, [6, 8-11](#)

metadata, [6, 8, 9, 11](#)

Seqinfo, [5, 11, 12](#)

stageObject, [2-6, 11](#)

stageObject, CompressedAtomicList-method,  
[6](#)

stageObject, CompressedSplitDataFrameList-method,  
[7](#)

stageObject, GRanges-method, [8](#)

stageObject, GRangesList-method, [10](#)

stageObject, Seqinfo-method, [11](#)

unlist, [10](#)