

# Package ‘alabaster.ranges’

April 25, 2024

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

**Version** 1.3.3

**Date** 2024-01-25

**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, S4Vectors, BiocGenerics, IRanges, GenomeInfoDb, rhdf5

**Suggests** testthat, knitr, BiocStyle, jsonlite

**VignetteBuilder** knitr

**RoxygenNote** 7.2.3

**biocViews** DataImport, DataRepresentation

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

**git\_branch** devel

**git\_last\_commit** 773a02a

**git\_last\_commit\_date** 2024-03-23

**Repository** Bioconductor 3.19

**Date/Publication** 2024-04-25

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

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

## Contents

readAtomicVectorList . . . . .	2
readDataFrameList . . . . .	3
readGRanges . . . . .	4
readGRangesList . . . . .	5

readSeqinfo . . . . .	5
saveObject,CompressedAtomicList-method . . . . .	6
saveObject,CompressedSplitDataFrameList-method . . . . .	7
saveObject,GRanges-method . . . . .	8
saveObject,GRangesList-method . . . . .	9
saveObject,Seqinfo-method . . . . .	10

## Index 11

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 <a href="#">saveObject</a> method for <a href="#">CompressedAtomicLists</a> .
metadata	Named list of metadata for this object, see <a href="#">readObjectFile</a> for details.
...	Further arguments, to be passed to internal <a href="#">altReadObject</a> 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 <a href="#">saveObject</a> method for <a href="#">CompressedSplitDataFrameList</a> objects.
metadata	Named list of metadata for this object, see <a href="#">readObjectFile</a> for details.
...	Further arguments, to be passed to internal <a href="#">altReadObject</a> 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 <a href="#">stageObject</a> method for <a href="#">GRanges</a> .
<code>metadata</code>	Named list of metadata for this object, see <a href="#">readObjectFile</a> for details.
<code>...</code>	Further arguments to pass to internal <a href="#">altReadObject</a> 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 <a href="#">saveObject</a> method for <a href="#">GRangesLists</a> .
metadata	Named list of metadata for this object, see <a href="#">readObjectFile</a> for details.
...	Further arguments, to be passed to internal <a href="#">altReadObject</a> 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 <a href="#">saveObject</a> method for Seqinfo objects.
metadata	Named list of metadata for this object, see <a href="#">readObjectFile</a> 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 <a href="#">CompressedAtomicList</a> 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 <a href="#">CompressedSplitDataFrameList</a> 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 <a href="#">GRanges</a> 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 <a href="#">GRangesList</a> 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 <a href="#">Seqinfo</a> 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)
```

# Index

altReadObject, 2–5

CompressedAtomicList, 2, 6, 7

CompressedSplitDataFrameList, 3, 7

GRanges, 4, 8

GRangesList, 5, 9

loadAtomicVectorList  
(readAtomicVectorList), 2

loadDataFrameList (readDataFrameList), 3

loadGRanges (readGRanges), 4

loadGRangesList (readGRangesList), 5

loadSeqinfo (readSeqinfo), 5

readAtomicVectorList, 2, 7

readDataFrameList, 3, 7

readGRanges, 4, 8

readGRangesList, 5, 9

readObject, 2–5

readObjectFile, 2–6

readSeqinfo, 5, 10

saveObject, 2, 3, 5, 6

saveObject, CompressedAtomicList-method,  
6

saveObject, CompressedSplitDataFrameList-method,  
7

saveObject, GRanges-method, 8

saveObject, GRangesList-method, 9

saveObject, Seqinfo-method, 10

Seqinfo, 5, 6, 10

stageObject, 4

stageObject, CompressedAtomicList-method  
(saveObject, CompressedAtomicList-method),  
6

stageObject, CompressedSplitDataFrameList-method  
(saveObject, CompressedSplitDataFrameList-method),  
7

stageObject, GRanges-method  
(saveObject, GRanges-method), 8

stageObject, GRangesList-method  
(saveObject, GRangesList-method),  
9

stageObject, Seqinfo-method  
(saveObject, Seqinfo-method), 10