

# Package ‘alabaster.ranges’

December 1, 2025

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

**Version** 1.10.0

**Date** 2025-07-22

**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, Seqinfo, 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** RELEASE\_3\_22

**git\_last\_commit** e35375b

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.22

**Date/Publication** 2025-12-01

**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**

|                       |                                                                                                                                                |
|-----------------------|------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>path</code>     | String containing a path to a directory, itself created with the <a href="#">saveObject</a> method for <a href="#">CompressedAtomicLists</a> . |
| <code>metadata</code> | Named list of metadata for this object, see <a href="#">readObjectFile</a> for details.                                                        |
| <code>...</code>      | 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 | <i>Load a data frame list</i> |
|-------------------|-------------------------------|

---

## 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 | <i>Read a GRanges from disk</i> |
|-------------|---------------------------------|

---

## 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 <a href="#">stageObject</a> method for <a href="#">GRanges</a> . |
| metadata | Named list of metadata for this object, see <a href="#">readObjectFile</a> for details.                                           |
| ...      | 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)
grl <- split(gr, rep(1:3, length.out=length(gr)))

tmp <- tempfile()
saveObject(grl, 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](#)

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, 6](#)

readDataFrameList, [3, 7](#)

readGRanges, [4, 8](#)

readGRangesList, [5, 9](#)

readObject, [2–5](#)

readObjectFile, [2–5](#)

readSeqinfo, [5, 10](#)

saveObject, [2, 3, 5](#)

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](#)