

# Package ‘alabaster.ranges’

November 16, 2025

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

**Version** 1.11.0

**Date** 2025-07-22

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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

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

**git\_branch** devel

**git\_last\_commit** 283afd5

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

**Repository** Bioconductor 3.23

**Date/Publication** 2025-11-16

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|                      |                                   |
|----------------------|-----------------------------------|
| readAtomicVectorList | <i>Load an atomic vector list</i> |
|----------------------|-----------------------------------|

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**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 | <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**

|                   |                                                                             |
|-------------------|-----------------------------------------------------------------------------|
| <code>x</code>    | A <a href="#">Seqinfo</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.

**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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