# 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, S4Vectors, BiocGenerics, IRanges, GenomeInfoDb, rhdf5

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

**VignetteBuilder** knitr

**RoxygenNote** 7.2.3

**biocViews** DataImport, DataRepresentation

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`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 `saveObject` method for CompressedAtomicLists. |
| `metadata` | Named list of metadata for this object, see `readObjectFile` for details. |
| `...` | Further arguments, to be passed to internal `altReadObject` 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 `saveObject` method for CompressedSplitDataFrameList objects. |
| `metadata` | Named list of metadata for this object, see `readObjectFile` for details. |
| `...` | Further arguments, to be passed to internal `altReadObject` 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

| | |
|---|---|
| `path` | String containing a path to a directory, itself created with the `stageObject` method for GRanges. |
| `metadata` | Named list of metadata for this object, see `readObjectFile` for details. |
| `...` | Further arguments to pass to internal `altReadObject` 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 — *Read a GRangesList from disk*

### 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 `saveObject` method for GRangesLists. |
| metadata | Named list of metadata for this object, see `readObjectFile` for details. |
| ... | Further arguments, to be passed to internal `altReadObject` 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 — *Read a Seqinfo from disk*

### 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 `saveObject` method for Seqinfo objects. |
| metadata | Named list of metadata for this object, see `readObjectFile` 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 CompressedAtomicList 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 CompressedSplitDataFrameList 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 GRanges 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

| | |
|---|---|
| x | A GRangesList 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

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 Seqinfo 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)
```

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