

Package: S4Arrays (via r-universe)

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Title Foundation of array-like containers in Bioconductor

Description The S4Arrays package defines the Array virtual class to be extended by other S4 classes that wish to implement a container with an array-like semantic. It also provides: (1) low-level functionality meant to help the developer of such container to implement basic operations like display, subsetting, or coercion of their array-like objects to an ordinary matrix or array, and (2) a framework that facilitates block processing of array-like objects (typically on-disk objects).

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URL <https://bioconductor.org/packages/S4Arrays>

BugReports <https://github.com/Bioconductor/S4Arrays/issues>

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aperm2	<i>Generalized permutation of the dimensions of an array</i>
--------	--

Description

aperm2() extends the functionality of base::aperm() by allowing dropping and/or adding *ineffective dimensions* (i.e. dimensions with an extent of 1) from/to the input array, in addition to permuting its dimensions.

Note that, like base::aperm(), aperm2() always preserves the length of the input array. However, unlike with base::aperm(), the array returned by aperm2() doesn't necessarily have the same number of dimensions as the input array.

Usage

```
aperm2(a, perm)
```

Arguments

- | | |
|------|---|
| a | An ordinary array. |
| perm | An integer vector, possibly containing NAs, indicating how the dimensions of the returned array should be mapped to those of the input array.
More precisely, perm can be one of the following: <ul style="list-style-type: none"> A permutation of the seq_along(dim(a)) vector, like for base::aperm(). Note that if the identity permutation is used (i.e. perm=seq_along(dim(a))), then aperm2() is a no-op (like with base::aperm()). A permutation of a <i>subset</i> of the seq_along(dim(a)) vector. In this case the dimensions that are excluded must be <i>ineffective dimensions</i> i.e. each of them must have an extent of 1. In other words, only integers that belong to which(dim(a) == 1) can be missing from perm. In this case, the ineffective dimensions that are excluded will be dropped i.e. they won't be carried over to the returned array. |

- Additionally, any number of NAs can be inserted anywhere in a perm vector like one described above.

In this case, ineffective dimensions will be added to the returned array. These added dimensions will materialize as additional 1's in the `dim()` vector of the returned array, at positions that match the positions of the NAs in `perm`.

Note that if `perm` is missing, then `aperm2(a)` reverses the order of `a`'s dimensions (i.e. `perm` gets set to `rev(seq_along(dim(a)))`), like `base::aperm(a)` does.

Value

An array with one dimension per element in the `perm` argument. The length of the returned array will always be the same as the length of the input array. (Note that for an array `a`, `length(a)` is `prod(dim(a))`.)

Note

The `aperm()` method for `DelayedArray` objects defined in the `DelayedArray` package implements the "aperm2 semantic", that is, it allows dropping and/or adding *ineffective dimensions* from/to the input `DelayedArray` object.

See Also

- `aperm` in the `base` package for the function that `aperm2` is based on.
- `aperm` in the `BiocGenerics` package for the `aperm S4 generic function`.
- `aperm,SVT_SparseArray-method` in the `SparseArray` package and `aperm,DelayedArray-method` in the `DelayedArray` package for `aperm()` methods that implements the "aperm2 semantic".

Examples

```
## -----
## SOME EXAMPLES WITH A 4D ARRAY
## -----

a <- array(1:72, c(3, 6, 1, 4),
           dimnames=list(NULL, letters[1:6], NULL, LETTERS[1:4]))
a

## Permute first two dimensions:
aperm2(a, perm=c(2,1,3,4))

## Permute first and last dimensions:
aperm2(a, perm=c(4,2,3,1))

## Drop 3rd dimension:
aperm2(a, perm=c(1,2,4))

## Drop 3rd dimension and permute 2nd and last:
aperm2(a, perm=c(1,4,2))
```

```

## Drop 3rd dimension and cycle the order of the remaining ones:
aperm2(a, perm=c(2,4,1))

## Add one ineffective dimension:
aperm2(a, perm=c(NA,1,2,3,4))
aperm2(a, perm=c(1,NA,2,3,4))
aperm2(a, perm=c(1,2,NA,3,4))
aperm2(a, perm=c(1,2,3,NA,4))
aperm2(a, perm=c(1,2,3,4,NA))

## Add four ineffective dimensions:
aperm2(a, perm=c(NA,1,2,3,NA,NA,4,NA))

## Permute first and last dimensions and add one ineffective dimension:
aperm2(a, perm=c(4,2,3,NA,1))

## Drop 3rd dimension, cycle the order of the remaining ones, and add
## two ineffective dimensions:
aperm2(a, perm=c(2,4,NA,1,NA))

## No-op:
aperm2(a, perm=seq_along(dim(a)))

## Reverse the order of the dimensions (multidimensional transposition):
aperm2(a) # same as 'aperm2(a, perm=rev(seq_along(dim(a))))'

## -----
## COMPOSING aperm2() TRANSFORMATIONS
## -----

## Applying two successive aperm() transformations, first with 'perm'
## set to 'perm1' then set to 'perm2', is equivalent to applying a
## single aperm() transformation with 'perm' set to 'perm1[perm2]'.
##
## More formally:
##   aperm(aperm(a, perm=perm1), perm=perm2)
## is equivalent to:
##   aperm(a, perm=perm1[perm2])
##
## Note that this also applies to aperm2()!

## Examples with aperm():

perm1 <- c(2,4,3,1)
perm2 <- c(4,3,2,1)
perm3 <- c(2,1,4,3)

a12 <- aperm(aperm(a, perm=perm1), perm=perm2)
stopifnot(identical(a12, aperm(a, perm=perm1[perm2])))

a13 <- aperm(aperm(a, perm=perm1), perm=perm3)
stopifnot(identical(a13, aperm(a, perm=perm1[perm3])))

```

```

a23 <- aperm(aperm(a, perm=perm2), perm=perm3)
stopifnot(identical(a23, aperm(a, perm=perm2[perm3])))

a123 <- aperm(aperm(aperm(a, perm=perm1), perm=perm2), perm=perm3)
stopifnot(identical(a123, aperm(a, perm=perm1[perm2][perm3])))
stopifnot(identical(a123, aperm(a, perm=perm1[perm2[perm3]])))

## Examples with aperm2():

perm1 <- c(2,4,1)
perm2 <- c(1,3,NA,2,NA)
perm3 <- c(5,4,2,1)

a12 <- aperm2(aperm2(a, perm=perm1), perm=perm2)
stopifnot(identical(a12, aperm2(a, perm=perm1[perm2])))

a123 <- aperm2(aperm2(aperm2(a, perm=perm1), perm=perm2), perm=perm3)
stopifnot(identical(a123, aperm2(a, perm=perm1[perm2][perm3])))
stopifnot(identical(a123, aperm2(a, perm=perm1[perm2[perm3]])))

## -----
## REVERSIBILITY OF THE aperm2() TRANSFORMATION
## -----

## An aperm() or aperm2() transformation is always reversible.
## The 'perm' vector to use to achieve the reverse transformation
## can be inferred from the initial 'perm' vector using the following
## helper function ('n' must be the number of dimensions of
## the original array):
build_rev_perm <- function(perm, n=length(perm)) {
  rev_perm <- rep.int(NA_integer_, n)
  na_idx <- which(!is.na(perm))
  rev_perm[perm[na_idx]] <- na_idx
  rev_perm
}

## Examples:

perm <- c(2,4,NA,1,NA)
rev_perm <- build_rev_perm(perm, n=length(dim(a)))
stopifnot(identical(aperm2(aperm2(a, perm=perm), perm=rev_perm), a))

## The "composed" 'perm' vector achieves identity:
perm[rev_perm]

## Sanity checks:

perm <- seq_len(10)
stopifnot(identical(build_rev_perm(perm), perm))

perm <- c(2:5,1L)
rev_perm <- build_rev_perm(perm)

```

```
stopifnot(identical(perm[rev_perm], seq_along(perm)))

perm <- c(5L,NA,2:4,NA,NA,1L)
rev_perm <- build_rev_perm(perm, n=6)
stopifnot(identical(perm[rev_perm], c(1:5,NA)))
```

array selection

*Manipulation of array selections***Description**

NOTE: The tools documented in this man page are primarily intended for developers or advanced users curious about the internals of the **SparseArray** or **DelayedArray** packages. End users typically don't need them for their regular use of [SparseArray](#) or [DelayedArray](#) objects.

An *array selection* is just an index into an array-like object that contains the information of which array elements are selected. This index can take various forms but 3 special forms are particularly useful and extensively used in the context of the **SparseArray** and **DelayedArray** packages: *linear index* (also referred to as *L-index* or *Lindex*), *matrix index* (also referred to as *M-index* or *Mindex*), *N-dimensional index* (also referred to as *N-index* or *Nindex*). See Details section below for more information.

Two utility functions are provided at the moment to convert back and forth between *L-indices* and *M-indices*. More will be added in the future to convert between other types of array indices.

Usage

```
## Convert back and forth between L-indices and M-indices:
Lindex2Mindex(Lindex, dim, use.names=FALSE)
Mindex2Lindex(Mindex, dim, use.names=FALSE, as.integer=FALSE)
```

Arguments

Lindex	An <i>L-index</i> . See Details section below.
Mindex	An <i>M-index</i> . See Details section below. For convenience, Mindex can also be specified as an integer vector with one element per dimension in the underlying array, in which case it will be treated like a 1-row matrix.
dim	An integer vector containing the dimensions of the underlying array. Note that dim can also be an integer matrix, in which case it must have one row per element in Lindex (or per row in Mindex) and one column per dimension in the underlying array.
use.names	Should the names (or rownames) on the input be propagated to the output?
as.integer	Set to TRUE to force Mindex2Lindex to return the L-index as an integer vector. Dangerous! By default, i.e. when as.integer=FALSE, Mindex2Lindex will return the L-index either as an integer or numeric vector. It will choose the former only if it's safe, that is, only if all the values in the L-index "fit" in the integer type. More precisely:

- If `dim` is not a matrix (i.e. is a vector) or if it's a matrix with a single row: `Mindex2Lindex` returns an integer or numeric vector depending on whether `prod(dim)` is \leq `.Machine$integer.max` ($2^{31} - 1$) or not.
- Otherwise `Mindex2Lindex` returns a numeric vector.

Note that with these rules, `Mindex2Lindex` can return a numeric vector even if an integer vector could have been used.

Use `as.integer=TRUE` only in situations where you know that all the L-index values are going to "fit" in the integer type. `Mindex2Lindex` will return garbage if they don't.

Details

The 3 special forms of array indices that are extensively used in the context of the **SparseArray** and **DelayedArray** packages:

1. *Linear index* (or *L-index* or *Lindex*): A numeric vector where each value is ≥ 1 and \leq the length of the array-like object. When using an L-index to subset an array-like object, the returned value is a vector-like object (i.e. no dimensions) of the same length as the L-index.

Example:

```
a <- array(101:124, 4:2)
Lindex <- c(7, 2, 24, 2)
a[Lindex]
```

2. *Matrix index* (or *M-index* or *Mindex*): An integer matrix with one column per dimension in the array-like object and one row per array element in the selection. The values in each column must be ≥ 1 and \leq the extent of the array-like object along the corresponding dimension. When using an M-index to subset an array-like object, the returned value is a vector-like object (i.e. no dimensions) of length the number of rows in the M-index.

Example:

```
a <- array(101:124, 4:2)
Mindex <- rbind(c(3, 2, 1),
                c(2, 1, 1),
                c(4, 3, 2),
                c(2, 1, 1))
a[Mindex]
```

Note that this is the type of index returned by `base::arrayInd`.

3. *N-dimensional* (or *N-index* or *Nindex*): A list with one list element per dimension in the array-like object. Each list element must be a subscript describing the selection along the corresponding dimension of the array-like object. **IMPORTANT:** A `NULL` subscript is interpreted as a *missing* subscript ("missing" like in `a[, , 1:2]`), that is, as a subscript that runs along the full extent of the corresponding dimension of the array-like object. This means that before an N-index can be used in a call to `[`, `[<-`, `[[` or `[[<-`, the `NULL` list elements in it must be replaced with objects of class `"name"`. When using an N-index to subset an array-like object, the returned value is another array-like object of dimensions the lengths of the selections along each dimensions.

Examples:

```

a <- array(101:124, 4:2)

## Normalized N-index (i.e. non-NULL subscripts are integer
## vectors with positive values only):

Nindex <- list(c(1, 4, 1), NULL, 1)
## Same as a[c(1, 4, 1), , 1, drop=FALSE]:
S4Arrays::subset_by_Nindex(a, Nindex)

Nindex <- list(integer(0), NULL, 1)
## Same as a[integer(0), , 1, drop=FALSE]:
S4Arrays::subset_by_Nindex(a, Nindex)

## Non-normalized N-index:

Nindex <- list(-3, NULL, c(TRUE, FALSE, FALSE))
Nindex <- S4Arrays::normalize_Nindex(Nindex, a)
## Same as a[-3, , 1, drop=FALSE]:
S4Arrays::subset_by_Nindex(a, Nindex)

Nindex <- list(IRanges(2, 4), NULL, 1)
Nindex <- S4Arrays::normalize_Nindex(Nindex, a)
## Same as a[2:4, , 1, drop=FALSE]:
S4Arrays::subset_by_Nindex(a, Nindex)

dimnames(a)[[1]] <- LETTERS[1:4]
Nindex <- list(c("D", "B"), NULL, 1)
Nindex <- S4Arrays::normalize_Nindex(Nindex, a)
## Same as a[c("D", "B"), , 1, drop=FALSE]:
S4Arrays::subset_by_Nindex(a, Nindex)

```

Value

Lindex2Mindex returns an M-index.

Mindex2Lindex returns an L-index.

See Also

[arrayInd](#) in the **base** package.

Examples

```

## -----
## M-index vs L-index
## -----

a <- array(101:124, 4:2)

```



```

## The same "array selection" can be represented by an M-index or
## an L-index. Here we use both representations to select the same
## 4 array elements:
Mindex <- rbind(c(3, 2, 1),
               c(2, 1, 1),
               c(4, 3, 2),
               c(2, 1, 1))

a[Mindex]

Lindex <- c(7, 2, 24, 2)
a[Lindex]

## Sanity check:
stopifnot(identical(a[Mindex], a[Lindex]))

## -----
## Convert back and forth between M-index and L-index representation
## -----

Mindex2Lindex(Mindex, dim(a)) # L-index

Lindex2Mindex(Lindex, dim(a)) # M-index

## Sanity checks:
storage.mode(Mindex) <- storage.mode(Lindex) <- "integer"
stopifnot(identical(Mindex2Lindex(Mindex, dim(a)), Lindex))
stopifnot(identical(Lindex2Mindex(Lindex, dim(a)), Mindex))

## -----
## More Mindex2Lindex() examples
## -----

dim <- 4:2
Mindex2Lindex(c(4, 3, 1), dim)
Mindex2Lindex(c(4, 3, 2), dim)

Mindex <- rbind(c(1, 1, 1),
               c(2, 1, 1),
               c(3, 1, 1),
               c(4, 1, 1),
               c(1, 2, 1),
               c(1, 1, 2),
               c(4, 3, 2))

Mindex2Lindex(Mindex, dim)

## With a matrix of dimensions:

dims <- rbind(c(4L, 3L),
              c(5L, 3L),
              c(6L, 3L))

Mindex <- rbind(c(1, 2),

```

```

      c(1, 2),
      c(1, 2))

Mindex2Lindex(Mindex, dims)

## Sanity checks:

dim <- c(33:30, 45L, 30L)
stopifnot(Mindex2Lindex(rep(1, 6), dim) == 1)
stopifnot(Mindex2Lindex(dim, dim) == prod(dim))

stopifnot(identical(Mindex2Lindex(arrayInd(1:120, 6:4), 6:4), 1:120))
stopifnot(identical(Mindex2Lindex(arrayInd(840:1, 4:7), 4:7), 840:1))

```

ArrayGrid-class

ArrayGrid and ArrayViewport objects

Description

A *grid* is a partitioning of an array-like object into block-shaped regions called *viewports*.

The **S4Arrays** package defines two S4 classes to formally represent grids and viewports: the `ArrayGrid` and `ArrayViewport` classes. Note that `ArrayGrid` and `ArrayViewport` objects are used extensively in the context of block processing of array-like objects.

There are two variants of `ArrayGrid` objects:

- `RegularArrayGrid` objects: for grids where all the blocks have the same geometry (except maybe for the edge blocks).
- `ArbitraryArrayGrid` objects: for grids where blocks don't necessarily have the same geometry.

Usage

```

## Constructor functions:
RegularArrayGrid(refdim, spacings=refdim)
ArbitraryArrayGrid(tickmarks)

downsample(x, ratio=1L)

```

Arguments

<code>refdim</code>	An integer vector containing the dimensions of the reference array.
<code>spacings</code>	An integer vector specifying the grid spacing along each dimension.
<code>tickmarks</code>	A list of integer vectors, one along each dimension of the reference array, representing the tickmarks along that dimension. Each integer vector must be sorted in ascending order. NAs or negative values are not allowed.
<code>x</code>	An <code>ArrayGrid</code> object.
<code>ratio</code>	An integer vector specifying the ratio of the downsampling along each dimension. Can be of length 1, in which case the same ratio is used along all the dimensions.

Details

RegularArrayGrid and ArbitraryArrayGrid are concrete subclasses of ArrayGrid, which itself is a virtual class.

Note that an ArrayGrid or ArrayViewport object doesn't store any array data, only the geometry of the grid or viewport. This makes these objects extremely light-weight, even for grids made of millions of blocks.

Value

For RegularArrayGrid(), a RegularArrayGrid instance.

For ArbitraryArrayGrid(), an ArbitraryArrayGrid instance.

For downsample(), an ArrayGrid object on the same reference array than x.

See Also

- [read_block](#) to read a block of data from an array-like object.
- [blockApply](#) and family, in the **DelayedArray** package, for convenient block processing of an array-like object.
- [mapToGrid](#) for mapping reference array positions to grid positions and vice-versa.
- [array](#) and [matrix](#) objects in base R.

Examples

```
## -----
## A. ArrayGrid OBJECTS
## -----

## Create a regularly-spaced grid on top of a 3700 x 100 x 33 array:
grid1 <- RegularArrayGrid(c(3700, 100, 33), c(250, 100, 10))

## Dimensions of the reference array:
refdim(grid1)

## Number of grid elements along each dimension of the reference array:
dim(grid1)

## Total number of grid elements:
length(grid1)

## First element in the grid:
grid1[[1L]]          # same as grid1[[1L, 1L, 1L]]

## Last element in the grid:
grid1[[length(grid1)]] # same as grid1[[15L, 1L, 4L]]

## Dimensions of the grid elements:
dims(grid1)          # one row per grid element

## Lengths of the grid elements:
```

```

lengths(grid1)          # same as rowProds(dims(grid1))
stopifnot(sum(lengths(grid1)) == prod(refdim(grid1)))

maxlength(grid1)        # does not need to compute lengths(grid1) first
                        # so is more efficient than max(lengths(grid1))
stopifnot(maxlength(grid1) == max(lengths(grid1)))

## Create an arbitrary-spaced grid on top of a 15 x 9 matrix:
grid2 <- ArbitraryArrayGrid(list(c(2L, 7:10, 13L, 15L), c(5:6, 6L, 9L)))

refdim(grid2)
dim(grid2)
length(grid2)
grid2[[1L]]             # same as grid2[[1L, 1L]]
grid2[[length(grid2)]] # same as grid2[[15L, 9L]]

dims(grid2)
lengths(grid2)
array(lengths(grid2), dim(grid2)) # display the grid element lengths in
                                   # an array of same shape as grid2

stopifnot(sum(lengths(grid2)) == prod(refdim(grid2)))

maxlength(grid2)        # does not need to compute lengths(grid2) first
                        # so is more efficient than max(lengths(grid2))
stopifnot(maxlength(grid2) == max(lengths(grid2)))

## Max (i.e. highest) resolution grid:
Hgrid <- RegularArrayGrid(6:4, c(1, 1, 1))
Hgrid
dim(Hgrid)             # same as refdim(Hgrid)
stopifnot(identical(dim(Hgrid), refdim(Hgrid)))
stopifnot(all(lengths(Hgrid) == 1))

## Min (i.e. lowest) resolution grid:
Lgrid <- RegularArrayGrid(6:4, 6:4)
Lgrid
stopifnot(all(dim(Lgrid) == 1))
stopifnot(identical(dim(Lgrid[[1L]]), refdim(Lgrid)))
stopifnot(identical(dims(Lgrid), matrix(refdim(Lgrid), nrow=1)))

## -----
## B. ArrayViewport OBJECTS
## -----

## Grid elements are ArrayViewport objects:
grid1[[1L]]
stopifnot(is(grid1[[1L]], "ArrayViewport"))
grid1[[2L]]
grid1[[2L, 1L, 1L]]
grid1[[15L, 1L, 4L]]

## Construction of a standalong ArrayViewport object:

```

```

m0 <- matrix(1:30, ncol=5)
block_dim <- c(4, 3)
viewport1 <- ArrayViewport(dim(m0), IRanges(c(3, 2), width=block_dim))
viewport1

dim(viewport1)      # 'block_dim'
length(viewport1)  # number of array elements in the viewport
ranges(viewport1)

## -----
## C. GRIDS CAN BE TRANSPOSED
## -----

tgrid2 <- t(grid2)
dim(tgrid2)
refdim(tgrid2)

## Use aperm() if the grid has more than 2 dimensions:
tgrid1 <- aperm(grid1)
dim(tgrid1)
refdim(tgrid1)

aperm(grid1, c(3, 1, 2))
aperm(grid1, c(1, 3, 2))
aperm(grid1, c(3, 1))    # some dimensions can be dropped
aperm(grid1, c(3, 2, 3)) # and some can be repeated

## -----
## D. DOWNSAMPLING AN ArrayGrid OBJECT
## -----
## The elements (ArrayViewport) of an ArrayGrid object can be replaced
## with bigger elements obtained by merging adjacent elements. How many
## adjacent elements to merge along each dimension is specified via the
## 'ratio' vector (one integer per dimension). We call this operation
## "downsampling". It can be seen as reducing the "resolution" of a grid
## by the specified ratio (if we think of the grid elements as pixels).
downsample(grid2, 2)
downsample(grid2, 3)
downsample(grid2, 4)

## Downsampling preserves the dimensions of the reference array:
stopifnot(identical(refdim(downsample(grid2, 2)), refdim(grid2)))
stopifnot(identical(refdim(downsample(grid2, 3)), refdim(grid2)))
stopifnot(identical(refdim(downsample(grid2, 4)), refdim(grid2)))

## A big enough ratio will eventually produce the coarsest possible grid
## i.e. a grid with a single grid element covering the entire reference
## array:
grid3 <- downsample(grid2, 7)
length(grid3)
grid3[[1L]]
stopifnot(identical(dim(grid3[[1L]]), refdim(grid3)))

```

```
## Downsampling by a ratio of 1 is a no-op:
stopifnot(identical(downsampling(grid2, 1), grid2))

## Using one ratio per dimension:
downsampling(grid2, c(2, 1))

## Downsample a max resolution grid:
refdim <- c(45, 16, 20)
grid4 <- RegularArrayGrid(refdim, c(1, 1, 1))
ratio <- c(6, 1, 3)
stopifnot(identical(
  downsampling(grid4, ratio),
  RegularArrayGrid(refdim, ratio)
))
```

bind-arrays

Combine multidimensional array-like objects

Description

Bind multidimensional array-like objects along any dimension.

NOTE: This man page is for the `abind` *S4 generic function* defined in the **S4Arrays** package. See `?abind::abind` for the default method (defined in the **abind** package). Bioconductor packages can define specific methods for objects not supported by the default method.

Usage

```
## Bind array-like objects along any dimension:
abind(..., along=NULL, rev.along=NULL)

## Bind array-like objects along their first or second dimension:
arbind(...)
acbind(...)
```

Arguments

```
...           The array-like objects to bind.
along, rev.along
              See ?abind::abind for a description of these arguments.
```

Value

An array-like object, typically of the same class as the input objects if they all have the same class.

See Also

- `abind::abind` in the **abind** package for the default `abind` method.
- `rbind` and `cbind` in the **base** package for the corresponding operations on matrix-like objects.

Examples

```

a1 <- array(1:60, c(3, 5, 4),
           dimnames=list(NULL, paste0("A1y", 1:5), NULL))
a2 <- array(101:240, c(7, 5, 4),
           dimnames=list(paste0("A2x", 1:7), paste0("A2y", 1:5), NULL))
a3 <- array(10001:10100, c(5, 5, 4),
           dimnames=list(paste0("A3x", 1:5), NULL, paste0("A3z", 1:4)))

abind(a1, a2, a3, along=1) # same as 'arbind(a1, a2, a3)'

m2 <- matrix(1:35, nrow=7)
abind(m2, a2, along=3)
abind(a2, m2, along=3)

abind(m2, m2+0.5, rev.along=0) # same as 'abind(m2, m2+0.5, along=3)'

```

is_sparse

Check for sparse representation

Description

is_sparse indicates whether an object (typically array-like) uses a sparse representation of the data or not.

Note that this is about *data representation* and not about the data itself. For example, is_sparse() always returns FALSE on an *ordinary* matrix, even if the matrix contains 99% zeros, because the data in such a matrix is always stored in a dense form. OTOH is_sparse() always returns TRUE on a [SparseArray](#) derivative from the **SparseArray** package, or on a [dgCMatrix](#) object from the **Matrix** package, even if the data contains no zeros, because these objects use a sparse representation of the data.

Usage

```
is_sparse(x)
```

Arguments

x Any object, but will typically be an array-like object.
Examples of array-like objects: ordinary arrays, [SparseArray](#) objects from the **SparseArray** package, [dgCMatrix](#) objects from the **Matrix** package, [DelayedArray](#) objects from the **DelayedArray** package, or any object with an array semantic (i.e. an object for which dim(x) is not NULL).

Value

TRUE or FALSE

See Also

- [read_block](#) to read a block of data from an array-like object.
- [array](#) and [matrix](#) objects in base R.
- [dgCMatrix](#) objects implemented in the **Matrix** package.

Examples

```
m <- matrix(0L, nrow=50, ncol=20)
stopifnot(identical(is_sparse(m), FALSE))

dgc <- as(m + runif(1000), "dgCMatrix")
stopifnot(identical(is_sparse(dgc), TRUE))
```

read_block	<i>Read array blocks</i>
------------	--------------------------

Description

Use `read_block` to read a block of data from an array-like object.

Note that this function is typically used in the context of block processing of on-disk objects (e.g. [DelayedArray](#) objects), often in combination with [write_block](#).

Usage

```
read_block(x, viewport, as.sparse=NA)

## Internal generic function used by read_block() when is_sparse(x)
## is FALSE:
read_block_as_dense(x, viewport)
```

Arguments

<code>x</code>	An array-like object. This can be an ordinary array, a SparseArray object from the SparseArray package, a dgCMatrix object from the Matrix package, a DelayedArray object from the DelayedArray package, or any object with an array semantic (i.e. an object for which <code>dim(x)</code> is not <code>NULL</code>).
<code>viewport</code>	An ArrayViewport object compatible with <code>x</code> , that is, such that <code>refdim(viewport)</code> is identical to <code>dim(x)</code> .
<code>as.sparse</code>	Can be <code>FALSE</code> , <code>TRUE</code> , or <code>NA</code> . If <code>FALSE</code> , the block is returned as an ordinary array (a.k.a. dense array). If <code>TRUE</code> , it's returned as a SparseArray object. If <code>NA</code> (the default), the block is returned as an ordinary array if <code>is_sparse(x)</code> is <code>FALSE</code> and as a SparseArray object otherwise. In other words, using <code>as.sparse=NA</code>

is equivalent to using `as.sparse=is_sparse(x)`. This preserves sparsity and is the most efficient way to read a block.

Note that when returned as a 2D [SparseArray](#) object with numeric or logical data, a block can easily and efficiently be coerced to a [sparseMatrix](#) derivative from the **Matrix** package with `as(block, "sparseMatrix")`. This will return a `dgCMatrix` object if `type(block)` is "double" or "integer", and a `lgCMatrix` object if it's "logical".

Details

`read_block()` delegates to 2 internal generic functions for reading a block:

- `read_block_as_dense`: used when `is_sparse(x)` is FALSE.
- `read_block_as_sparse` (defined in the **SparseArray** package): used when `is_sparse(x)` is TRUE.

Note that these 2 internal generic functions are not meant to be called directly by the end user. The end user should always call the higher-level user-facing `read_block()` function instead.

Value

A block of data. More precisely, the data from `x` that belongs to the block delimited by the specified viewport.

The block of data is returned either as an ordinary (dense) array or as a [SparseArray](#) object from the **SparseArray** package.

Note that the returned block of data is guaranteed to have the same type as `x` and the same dimensions as the viewport. More formally, if `block` is the value returned by `read_block(x, viewport)`, then:

```
identical(type(block), type(x))
```

and

```
identical(dim(block), dim(viewport))
```

are always TRUE.

See Also

- [ArrayGrid](#) for `ArrayGrid` and `ArrayViewport` objects.
- `is_sparse` to check whether an object uses a sparse representation of the data or not.
- [SparseArray](#) objects implemented in the **SparseArray** package.
- `S4Arrays::type` to get the type of the elements of an array-like object.
- The `read_block_as_sparse` internal generic function defined in the **SparseArray** package and used by `read_block()` when `is_sparse(x)` is TRUE.
- `write_block` to write a block of data to an array-like object.
- `blockApply` and family, in the **DelayedArray** package, for convenient block processing of an array-like object.

- `dgCMatrix` and `lgCMatrix` objects implemented in the **Matrix** package.
- `DelayedArray` objects implemented in the **DelayedArray** package.
- `array` and `matrix` objects in base R.

Examples

```
## Please note that, although educative, the examples below are somewhat
## artificial and do not illustrate real-world usage of read_block().
## See '?RealizationSink' in the DelayedArray package for more realistic
## read_block/write_block examples.

## -----
## BASIC EXAMPLE 1: READ A BLOCK FROM AN ORDINARY MATRIX (DENSE)
## -----
m1 <- matrix(1:30, ncol=5)
m1

## Define the viewport on 'm1' to read the data from:
block1_dim <- c(4, 3)
viewport1 <- ArrayViewport(dim(m1), IRanges(c(3, 2), width=block1_dim))
viewport1

## Read the block:
block1 <- read_block(m1, viewport1) # same as m1[3:6, 2:4, drop=FALSE]
block1

## Use 'as.sparse=TRUE' to read the block as sparse object:
block1b <- read_block(m1, viewport1, as.sparse=TRUE)
block1b
is_sparse(block1b) # TRUE
class(block1b)     # an SVT_SparseArray object

## Sanity checks:
stopifnot(identical(type(m1), type(block1)))
stopifnot(identical(dim(viewport1), dim(block1)))
stopifnot(identical(m1[3:6, 2:4, drop=FALSE], block1))
stopifnot(is(block1b, "SparseArray"))
stopifnot(identical(type(m1), type(block1b)))
stopifnot(identical(dim(viewport1), dim(block1b)))
stopifnot(identical(block1, as.array(block1b)))

## -----
## BASIC EXAMPLE 2: READ A BLOCK FROM A SPARSE MATRIX
## -----
m2 <- rsparsematrix(12, 20, density=0.2,
                    rand.x=function(n) sample(25, n, replace=TRUE))
m2
is_sparse(m2) # TRUE

## Define the viewport on 'm2' to read the data from:
block2_dim <- c(2, 20)
viewport2 <- ArrayViewport(dim(m2), IRanges(c(1, 1), width=block2_dim))
```

```

viewport2

## By default, read_block() preserves sparsity:
block2 <- read_block(m2, viewport2)
block2
is_sparse(block2) # TRUE
class(block2)     # an SVT_SparseArray object

## Use 'as.sparse=FALSE' to force read_block() to return an ordinary
## matrix or array:
block2b <- read_block(m2, viewport2, as.sparse=FALSE)
block2b
as(block2b, "sparseMatrix")

## Sanity checks:
stopifnot(is(block2, "SparseArray"))
stopifnot(identical(type(m2), type(block2)))
stopifnot(identical(dim(viewport2), dim(block2)))
stopifnot(identical(type(m2), type(block2b)))
stopifnot(identical(dim(viewport2), dim(block2b)))
stopifnot(identical(block2b, as.array(block2)))

## -----
## BASIC EXAMPLE 3: READ A BLOCK FROM A 3D ARRAY
## -----
a3 <- array(1:60, dim=5:3)

## Define the viewport on 'a3' to read the data from:
block3_dim <- c(2, 4, 1)
viewport3 <- ArrayViewport(dim(a3), IRanges(c(1, 1, 3), width=block3_dim))
viewport3

## Read the block:
block3 <- read_block(a3, viewport3) # same as a3[1:2, 1:4, 3, drop=FALSE]
block3

## Note that unlike [, read_block() never drops dimensions.

## Sanity checks:
stopifnot(identical(type(a3), type(block3)))
stopifnot(identical(dim(viewport3), dim(block3)))
stopifnot(identical(a3[1:2, 1:4, 3, drop=FALSE], block3))

## -----
## BASIC EXAMPLE 4: READ AND PROCESS BLOCKS DEFINED BY A GRID
## -----
a4 <- array(runif(120), dim=6:4)

## Define a grid of 2x3x2 blocks on 'a4':
grid4 <- RegularArrayGrid(dim(a4), spacings=c(2,3,2))
grid4
nblock <- length(grid4) # number of blocks

```

```

## Walk on the grid and print the corresponding blocks:
for (bid in seq_len(nblock)) {
  viewport <- grid4[[bid]]
  block <- read_block(a4, viewport)
  cat("==== Block ", bid, "/", nblock, " =====\n", sep="")
  print(block)
}

## Walk on the grid and compute the sum of each block:
block_sums <- sapply(grid4,
  function(viewport) sum(read_block(a4, viewport))
)
block_sums

## Sanity checks:
stopifnot(identical(length(block_sums), nblock))
stopifnot(all.equal(sum(block_sums), sum(a4)))

## -----
## THE read_block/write_block COMBO
## -----
## See '?write_block' for examples that use the read_block/write_block
## combo.

```

rowsum

Compute column/row sums of a matrix-like object, for groups of rows/columns

Description

rowsum() computes column sums across rows of a numeric matrix-like object for each level of a grouping variable.

colsum() computes row sums across columns of a numeric matrix-like object for each level of a grouping variable.

NOTE: This man page is for the rowsum and colsum *S4 generic functions* defined in the **S4Arrays** package. See `?base::rowsum` for the default rowsum() method (defined in the **base** package). Bioconductor packages can define specific methods for objects (typically matrix-like) not supported by the default methods.

Usage

```
rowsum(x, group, reorder=TRUE, ...)
```

```
colsum(x, group, reorder=TRUE, ...)
```

Arguments

x A numeric matrix-like object.

group, reorder, ...

See `?base::rowsum` for a description of these arguments.

Value

See `?base::rowsum` for the value returned by the default method.

The default `colsum()` method simply does `t(rowsum(t(x), group, reorder=reorder, ...))`.

Specific methods defined in Bioconductor packages should behave as consistently as possible with the default methods.

See Also

- `base::rowsum` for the default rowsum method.
- `showMethods` for displaying a summary of the methods defined for a given generic function.
- `selectMethod` for getting the definition of a specific method.
- `rowsum,DelayedMatrix-method` in the **DelayedArray** package for an example of a specific rowsum method (defined for `DelayedMatrix` objects).

Examples

```
rowsum # note the dispatch on the 'x' arg only
showMethods("rowsum")
selectMethod("rowsum", "ANY") # the default rowsum() method

colsum # note the dispatch on the 'x' arg only
showMethods("colsum")
selectMethod("colsum", "ANY") # the default colsum() method
```

type

Get the type of the elements of an array-like object

Description

The **S4Arrays** package defines a couple of `type()` methods to get the type of the *elements* of a matrix-like or array-like object.

Usage

```
## S4 method for signature 'ANY'
type(x)

## S4 method for signature 'DataFrame'
type(x)
```

Arguments

- `x`
- For the default `type()` method: An array-like object. This can be an ordinary array, a [SparseArray](#) object from the **SparseArray** package, a [dgCMatrix](#) object from the **Matrix** package, a [DelayedArray](#) object from the **DelayedArray** package, or any object with an array semantic (i.e. an object for which `dim(x)` is not `NULL`).
- For the method for [DataFrame](#) objects: A [DataFrame](#) derivative for which `as.data.frame(x)` preserves the number of columns. See below for more information.

Details

Note that for an ordinary matrix or array `x`, `type(x)` is the same as `typeof(x)`.

On an array-like object `x` that is not an ordinary array, `type(x)` is *semantically equivalent* to `typeof(as.array(x))`. However, the actual implementation is careful to avoid turning the full array-like object `x` into an ordinary array, as this would tend to be very inefficient in general. For example, doing so on a big [DelayedArray](#) object could easily eat all the memory available on the machine.

On a [DataFrame](#) object, `type(x)` only works if `as.data.frame(x)` preserves the number of columns, in which case it is *semantically equivalent* to `typeof(as.matrix(as.data.frame(x)))`. Here too, the actual implementation is careful to avoid turning the full object into a data frame, then into a matrix, for efficiency reasons.

Value

A single string indicating the type of the array elements in `x`.

See Also

- The [type](#) generic function defined in the **BiocGenerics** package.
- [SparseArray](#) objects implemented in the **SparseArray** package.
- [DelayedArray](#) objects implemented in the **DelayedArray** package.
- [DataFrame](#) objects implemented in the **S4Vectors** package.

Examples

```
m <- matrix(rpois(54e6, lambda=0.4), ncol=1200)
type(m) # integer

x1 <- as(m, "dgCMatrix")
type(x1) # double

library(SparseArray)
x2 <- SparseArray(m)
type(x2) # integer
```

write_block	<i>Write array blocks</i>
-------------	---------------------------

Description

Use `write_block` to write a block of data to an array-like object.

Note that this function is typically used in the context of block processing of on-disk objects (e.g. [DelayedArray](#) objects), often in combination with [read_block](#).

Usage

```
write_block(sink, viewport, block)
```

Arguments

sink	A **writable** array-like object. This is typically a RealizationSink derivative (<code>RealizationSink</code> is a virtual class defined in the DelayedArray package), but not necessarily. See ?RealizationSink in the DelayedArray package for more information about <code>RealizationSink</code> objects. Although <code>write_block()</code> will typically be used on a <code>RealizationSink</code> derivative, it can also be used on an ordinary array or other in-memory array-like object that supports subassignment (<code>[<-`</code>), like a SparseArray object from the SparseArray package, or a <code>dgCMatrix</code> object from the Matrix package.
viewport	An ArrayViewport object compatible with <code>sink</code> , that is, such that <code>refdim(viewport)</code> is identical to <code>dim(sink)</code> .
block	An array-like object of the same dimensions as <code>viewport</code> .

Value

The modified array-like object `sink`.

See Also

- [ArrayGrid](#) for `ArrayGrid` and `ArrayViewport` objects.
- [SparseArray](#) objects implemented in the **SparseArray** package.
- [read_block](#) to read a block of data from an array-like object.
- [blockApply](#) and family, in the **DelayedArray** package, for convenient block processing of an array-like object.
- [RealizationSink](#) objects implemented in the **DelayedArray** package for more realistic `write_block` examples.
- [array](#) and [matrix](#) objects in base R.

Examples

```

## Please note that, although educative, the examples below are somewhat
## artificial and do not illustrate real-world usage of write_block().
## See '?RealizationSink' in the DelayedArray package for more realistic
## read_block/write_block examples.

## -----
## BASIC EXAMPLE 1: WRITE A BLOCK TO AN ORDINARY MATRIX (DENSE)
## -----
m1 <- matrix(1:30, ncol=5)
m1

## Define the viewport on 'm1' to write the data to:
block1_dim <- c(4, 3)
viewport1 <- ArrayViewport(dim(m1), IRanges(c(3, 2), width=block1_dim))
viewport1

## Data to write:
block1 <- read_block(m1, viewport1) + 1000L

## Write the block:
m1A <- write_block(m1, viewport1, block1)
m1A

## Sanity checks:
stopifnot(identical(`[<-`(m1, 3:6, 2:4, value=block1), m1A))
m1B <- write_block(m1, viewport1, as(block1, "dgCMatrix"))
stopifnot(identical(m1A, m1B))

## -----
## BASIC EXAMPLE 2: WRITE A BLOCK TO A SPARSE MATRIX
## -----
m2 <- rsparsematrix(12, 20, density=0.2,
                    rand.x=function(n) sample(25, n, replace=TRUE))
m2

## Define the viewport on 'm2' to write the data to:
block2_dim <- c(2, 20)
viewport2 <- ArrayViewport(dim(m2), IRanges(c(1, 1), width=block2_dim))
viewport2

## Data to write:
block2 <- matrix(1001:1040, nrow=2)

## Write the block:
m2A <- write_block(m2, viewport2, block2)
m2A

## Sanity checks:
stopifnot(identical(`[<-`(m2, 1:2, , value=block2), m2A))
m2B <- write_block(m2, viewport2, as(block2, "dgCMatrix"))
stopifnot(identical(m2A, m2B))

```



```

## -----
## BASIC EXAMPLE 3: WRITE A BLOCK TO A 3D ARRAY
## -----
a3 <- array(1:60, dim=5:3)

## Define the viewport on 'a3' to write the data to:
block3_dim <- c(2, 4, 1)
viewport3 <- ArrayViewport(dim(a3), IRanges(c(1, 1, 3), width=block3_dim))
viewport3

## Data to write:
block3 <- array(-(1:8), dim=block3_dim)

## Write the block:
a3A <- write_block(a3, viewport3, block3)
a3A

## Sanity checks:
stopifnot(identical(`[<-`(a3, 1:2, , 3, value=block3), a3A))
a3B <- write_block(a3, viewport3, as(block3, "SparseArray"))
stopifnot(identical(a3A, a3B))

## -----
## BASIC EXAMPLE 4: WRITE BLOCKS DEFINED BY A GRID
## -----
a4 <- array(NA_real_, dim=6:4)

## Define a grid of 2x3x2 blocks on 'a4':
grid4 <- RegularArrayGrid(dim(a4), spacings=c(2,3,2))
grid4
nblock <- length(grid4) # number of blocks

## Walk on the grid and write blocks of random data:
for (bid in seq_len(nblock)) {
  viewport <- grid4[[bid]]
  block <- array(runif(length(viewport)), dim=dim(viewport))
  cat("==== Write block ", bid, "/", nblock, " =====\n", sep="")
  a4 <- write_block(a4, viewport, block)
}
a4

## -----
## BASIC EXAMPLE 5: READ, PROCESS, AND WRITE BLOCKS DEFINED BY TWO GRIDS
## -----
## Say we have a 3D array and want to collapse its 3rd dimension by
## summing the array elements that are stacked vertically, that is, we
## want to compute the matrix 'm' obtained by doing 'sum(a[i, j, ])' for
## all valid i and j. There are several ways to do this.

## 1. Here is a solution based on apply():

collapse_3rd_dim <- function(a) apply(a, MARGIN=1:2, sum)

```

```

## 2. Here is a slightly more efficient solution:

collapse_3rd_dim <- function(a) {
  m <- matrix(0, nrow=nrow(a), ncol=ncol(a))
  for (z in seq_len(dim(a)[[3]]))
    m <- m + a[ , , z]
  m
}

## 3. And here is a block-processing solution that involves two grids,
##    one for the sink, and one for the input:

a5 <- array(runif(8000), dim=c(25, 40, 8)) # input
m <- array(NA_real_, dim=dim(a5)[1:2])    # sink

## Since we're going to walk on the two grids simultaneously, read a
## block from 'a5' and write it to 'm', we need to make sure that we
## define grids that are "aligned". More precisely, the two grids must
## have the same number of viewports, and the viewports in one must
## correspond to the viewports in the other one:
m_grid <- RegularArrayGrid(dim(m), spacings=c(10, 10))
a5_grid <- RegularArrayGrid(dim(a5), spacings=c(10, 10, dim(a5)[[3]]))

## Let's check that our two grids are actually "aligned":
stopifnot(identical(length(m_grid), length(a5_grid)))
stopifnot(identical(dims(m_grid), dims(a5_grid)[ , 1:2, drop=FALSE]))

## Walk on the two grids simultaneously, and read/collapse/write blocks:
for (bid in seq_along(m_grid)) {
  ## Read block from 'a5'.
  a5_viewport <- a5_grid[[bid]]
  block <- read_block(a5, a5_viewport)
  ## Collapse it.
  block <- collapse_3rd_dim(block)
  ## Write the collapsed block to 'm'.
  m_viewport <- m_grid[[bid]]
  m <- write_block(m, m_viewport, block)
}

## Sanity checks:
stopifnot(identical(dim(a5)[1:2], dim(m)))
stopifnot(identical(sum(a5), sum(m)))
stopifnot(identical(collapse_3rd_dim(a5), m))

## See '?RealizationSink' in the DelayedArray package for a more
## realistic "array collapse" example where the blocks are written
## to a RealizationSink object.

```

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