

Package ‘broadcast’

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Title Broadcasted Array Operations Like 'NumPy'

Version 0.1.9.8

Description Implements efficient 'NumPy'-like broadcasted operations for atomic and recursive arrays. In the context of operations involving 2 (or more) arrays, “broadcasting” (AKA singleton expansion) refers to efficiently recycling array dimensions, without making copies.

Besides linking to 'Rcpp',

'broadcast' does not use any external libraries in any way;

'broadcast' was essentially made from scratch and can be installed out-of-the-box.

The implementations available in 'broadcast' include, but are not limited to, the following.

1) Broadcasted element-wise operations on any 2 arrays;

they support a large set of

relational, arithmetic, Boolean, string, and bit-wise operations.

2) A faster, more memory efficient, and broadcasted abind-like function,

for binding arrays along an arbitrary dimension.

3) Broadcasted ifelse-like and apply-like functions.

4) Casting functions,

that cast subset-

groups of an array to a new dimension, cast nested lists to dimensional lists, and vice-versa.

5) A few linear algebra functions for statistics.

The functions in the 'broadcast' package strive to minimize computation time and memory usage

(which is not just better for efficient computing, but also for the environment).

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<https://tony-aw.github.io/broadcast/>

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Description

`broadcast`:
Broadcasted Array Operations Like 'NumPy'

Implements efficient 'NumPy'-like broadcasted operations for atomic and recursive arrays.

In the context of operations involving 2 (or more) arrays, “broadcasting” (AKA singleton expansion) refers to efficiently recycling array dimensions, without making copies.

Besides linking to 'Rcpp', 'broadcast' does not use any external libraries in any way; 'broadcast' was essentially made from scratch and can be installed out-of-the-box.

The implementations available in 'broadcast' include, but are not limited to, the following:

1. Broadcasted element-wise operations on any 2 arrays; they support a large set of relational, arithmetic, Boolean, string, and bit-wise operations.
2. A faster, more memory efficient, and broadcasted `abind`-like function, for binding arrays along an arbitrary dimension.
3. Broadcasted `ifelse`-like and `apply`-like functions.
4. Casting functions, that cast subset-groups of an array to a new dimension, cast nested lists to dimensional lists, and vice-versa.
5. A few linear algebra functions for statistics.

The functions in the 'broadcast' package strive to minimize computation time and memory usage (which is not just better for efficient computing, but also for the environment).

Links to Get Started

- The Quick-Start Guide, Vignettes, Benchmarks, and more can be found on the [website](#).
- GitHub main page: <https://github.com/tony-aw/broadcast>
- Reporting Issues or Giving Suggestions: <https://github.com/tony-aw/broadcast/issues>

Functions

Broadcasted Operators

Base 'R' comes with relational (`==`, `!=`, etc.), arithmetic (`+`, `-`, `*`, `/`, etc.), and logical/bit-wise (`&`, `|`) operators.

'broadcast' provides 2 ways to use these operators with broadcasting.

The first (and simple) way is to use the [broadcaster](#) class, which comes with it's own method dispatch for the above mentioned operators.

This method support operator precedence, and for the average 'R' user, this is sufficient.

The second way is to use the large set of `bc.` - functions.

These offer much greater control and more operators than the previous method, and has less risk of running into conflicting methods.

But it does not support operator precedence.

More information about both methods can be found here:

[broadcast_operators](#).

Binding Arrays

'broadcast' provides the [bind_array](#) function, to bind arrays along an arbitrary dimension, with support for broadcasting.

See [bind_array](#).

Casting Functions

'broadcast' provides several "casting" functions.

These can facility complex forms of broadcasting that would normally not be possible.

But these "casting" functions also have their own merit, beside empowering complex broadcasting.

More information about the casting functions can be found here:

[broadcast_casting](#).

General Pairwise Broadcasted Functions

'broadcast' also comes with a few general pairwise broadcasted functions:

- [bc_ifelse](#): Broadcasted version of [ifelse](#).
- [bcapply](#): Broadcasted `apply`-like function.
- [bc_strep](#): Broadcasted version of [strep](#).

Other functions

'broadcast' provides [type-casting](#) functions, which preserve names and dimensions - convenient for arrays.

'broadcast' also provides [simple linear algebra functions for statistics](#).

And 'broadcast' comes with some helper functions:

[checkNA](#), [checkNULL](#),
[bc_dim](#), [ndim](#), [lst.ndim](#), [rep_dim](#),
[vector2array](#).

Supported Structures

'broadcast' supports atomic/recursive arrays (up to 16 dimensions), and atomic/recursive vectors. As in standard Linear Algebra convention, dimensionless vectors are interpreted as column-vectors in broadcasted array operations.

Author(s)

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References

Harris, C.R., Millman, K.J., van der Walt, S.J. et al. *Array programming with NumPy*. Nature 585, 357–362 (2020). doi:[10.1038/s4158602026492](https://doi.org/10.1038/s4158602026492). ([Publisher link](#)).

aaa01_broadcast_operators

Details on Broadcasted Operators

Description

Base 'R' comes with relational, arithmetic and logical/bit-wise (&, |) operators. 'broadcast' provides 2 ways to use these operators with broadcasting.

The first (and simple) way is to use the [broadcaster](#) class, which comes with its own method dispatch for the above mentioned operators.

This approach supports operator precedence, and for the average 'R' user, this is sufficient.

The second way is to use the large set of `bc. -` functions.

These offer much greater control and more operators than the previous method, and has less risk of running into conflicting methods.

But they do not support operator precedence.

Operators Overloaded via Broadcaster Class

The 'broadcast' package provides the [broadcaster](#) class, which comes with its own method dispatch for the base operators.

If at least one of the 2 arguments of the base operators has the [broadcaster](#) class attribute, and no other class (like `bit64`) interferes, broadcasting will be used.

The following operators have a 'broadcaster' method:

```

+, -, *, /, ^, %, %%
==, !=, <, >, <=, >=
&, |

```

See also the Examples section below.

Available bc. functions

'broadcast' provides a set of functions for broadcasted element-wise binary operations with broadcasting.

These functions use an API similar to the [outer](#) function.

The following functions for simple operations are available:

- [bc.rel](#): General relational operations (`==`, `!=`, `<`, `>`, `<=`, `>=`).
The various other bc. methods below have specialised relational operators available for specialised needs.
- [bc.b](#): Boolean (i.e. logical) operations;
- [bc.i](#): integer arithmetic operations;
- [bc.d](#): decimal arithmetic operations;
- [bc.cplx](#): complex arithmetic operations;
- [bc.str](#): string (in)equality, concatenation, and distance operations;
- [bc.raw](#): operations that take in arrays of type `raw` and return an array of type `raw`;
- [bc.bit](#): BIT-WISE operations, supporting the `raw` and `integer` types;
- [bc.list](#): apply any 'R' function to 2 recursive arrays with broadcasting.

Attribute Handling

The bc. functions and the overloaded operators generally do **not** preserve attributes, unlike the base 'R' operators, except for names, dimnames, comment (if appropriate), and the [broadcaster](#) class attribute (and related attributes).

Broadcasting often results in an object with more dimensions, larger dimensions, and/or larger length than the original objects.

This is relevant as some class-specific attributes are only appropriate for certain dimensions or lengths.

Custom matrix classes, for example, presumes an object to have exactly 2 dimensions.

And the various classes provided by the 'bit' package have length-related attributes.

So class attributes cannot be guaranteed to hold for the resulting objects when broadcasting is involved.

Almost all functions provided by 'broadcast' are S3 or S4 generics; methods can be written for them for specific classes, so that class-specific attributes can be supported when needed.

Unary operations (i.e. $+x$, $-x$) return the original object, with only the sign adjusted.

Examples

```
# maths ====
```

```
x <- 1:10
y <- 1:10
dim(x) <- c(10, 1)
dim(y) <- c(1, 10)
broadcaster(x) <- TRUE
broadcaster(y) <- TRUE
```

```
x + y / x
(x + y) / x
```

```
(x + y) * x
```

```
# relational operators ====
```

```
x <- 1:10
y <- array(1:10, c(1, 10))
broadcaster(x) <- TRUE
broadcaster(y) <- TRUE
```

```
x == y
x != y
x < y
x > y
x <= y
x >= y
```

```
# maths ====
```

```
x <- sample(1:10)
y <- sample(1:10)
dim(x) <- c(10, 1)
dim(y) <- c(1, 10)
mbroadcasters(c("x", "y"), TRUE)
```

```

x + y / x
(x + y) / x

(x + y) * x

# relational operators ====
x <- 1:10
y <- array(1:10, c(1, 10))
mbroadcasters(c("x", "y"), TRUE)

x == y
x != y
x < y
x > y
x <= y
x >= y

```

aaa02_broadcast_casting

Details on Casting Functions

Description

'broadcast' provides several "casting" functions. These can facilitate complex forms of broadcasting that would normally not be possible. But these "casting" functions also have their own merit, beside empowering complex broadcasting.

The following casting functions are available:

- [acast](#):
Casts group-based subsets of an array into a new dimension.
Useful for, for example, performing **grouped** broadcasted operations.
- [cast_hier2dim](#):
Casts a nested/hierarchical list into a dimensional list (i.e. array of type list).
Useful because one cannot broadcast through nesting, but one **can** broadcast along dimensions.
- [hier2dim](#), [hiernames2dimnames](#):
Helper functions for [cast_hier2dim](#).
- [cast_dim2hier](#):
Casts a dimensional list into a nested/hierarchical list; the opposite of [cast_hier2dim](#).
- [cast_shallow2atomic](#):
Casts a (dimensional) shallow (i.e. non-nested) list into an atomic vector or array.
Useful because atomic vectors/arrays have access to many vectorized (broadcasted) operations that may not be available for vectors/arrays of type list.

- **cast_dim2flat:**
Casts a dimensional list into a flattened list, but with names that indicate their original dimensional positions.
Mostly useful for printing or summarizing dimensional lists.
- **dropnests:**
Drop redundant nesting in lists; mostly used for facilitating the above casting functions.
- The **reorient_vector** (%orientbc<-%) operator:
Changes the orientation of an oriented vector.
Oriented vectors can be used to modify an array along a dimension.

Shared argument recurse_all

The **dropnests**, **hier2dim**, **hiernames2dimnames**, and **cast_hier2dim** methods all have the **recurse_all** argument.

By default **recurse_all** = FALSE, meaning these methods do not recurse through dimensional or classed lists (like **data.frames**).

Setting **recurse_all** = TRUE allows these methods to recurse through all list objects, even if they are dimensional and/or classed.

Shared Argument in2out

The **hier2dim**, **hiernames2dimnames**, **cast_hier2dim**, and **cast_dim2hier** methods all have the **in2out** argument.

in2out: TRUE;

By default **in2out** is TRUE.

This means the call

```
y <- cast_hier2dim(x)
```

will cast the elements of the deepest valid depth of **x** to the rows of **y**, and elements of the depth above that to the columns of **y**, and so on until the surface-level elements of **x** are cast to the last dimension of **y**.

Similarly, the call

```
x <- cast_dim2hier(y)
```

will cast the rows of **y** to the inner most elements of **x**, and the columns of **y** to one depth above that, and so on until the last dimension of **y** is cast to the surface-level elements of **x**.

Consider the nested list **x** with a depth of 3, and the recursive array **y** with 3 dimensions, where their relationship can be described as the following code:

```
y <- cast_hier2dim(x)
```

```
x <- cast_dim2hier(y).
```

Then it holds that:

```
x[[i]][[j]][[k]] corresponds to y[[k, j, i]],
```

$\forall(i, j, k)$, provided $x[[i]][[j]][[k]]$ exists.

in2out: FALSE;

If `in2out = FALSE`, the call

```
y <- cast_hier2dim(x, in2out = FALSE)
```

will cast the surface-level elements of x to the rows of y , and elements of the depth below that to the columns of y , and so on until the elements of the deepest valid depth of x are cast to the last dimension of y .

Similarly, the call

```
x <- cast_dim2hier(y, in2out = FALSE)
```

will cast the rows of y to the surface-level elements of x , and the columns of y to one depth below that, and so on until the last dimension of y is cast to the inner most elements of x .

Consider the nested list x with a depth of 3, and the recursive array y with 3 dimensions, where their relationship can be described with the following code:

```
y <- cast_hier2dim(x, in2out = FALSE)
```

```
x <- cast_dim2hier(y, in2out = FALSE).
```

Then it holds that :

$x[[i]][[j]][[k]]$ corresponds to $y[[i, j, k]]$,

$\forall(i, j, k)$, provided $x[[i]][[j]][[k]]$ exists.

Examples

```
# recurse_all demonstration ====
```

```
x <- list(
  a = list(list(list(list(1:10)))),
  b = data.frame(month.abb, month.name),
  c = data.frame(month.abb),
  d = array(list(1), c(1,1,1))
)
```

```
dropnests(x) # by default, recurse_all = FALSE
```

```
dropnests(x, recurse_all = TRUE) # recurse_all = TRUE
```

```
# in2out demonstration ====
```

```
x <- list(
  group1 = list(
    class1 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    ),
    class2 = list(
      height = rnorm(10, 170),
```

```

      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    )
  ),
  group2 = list(
    class1 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    ),
    class2 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    )
  )
)

# in2out = TRUE (default):
x2 <- cast_hier2dim(x)
dimnames(x2) <- hiernames2dimnames(x)
print(x2)
cast_dim2flat(x2[1,1,,drop = FALSE])

# in2out = FALSE:
x2 <- cast_hier2dim(x, in2out = FALSE)
dimnames(x2) <- hiernames2dimnames(x, in2out = FALSE)
print(x2)
cast_dim2flat(x2[1,1,,drop = FALSE])

```

acast

*Simple and Fast Casting/Pivoting of an Array***Description**

The `acast()` function spreads subsets of an array margin over a new dimension.

Roughly speaking, `acast()` can be thought of as the "array" analogy to `data.table::dcast()`. But note 2 important differences:

- `acast()` works on arrays instead of data.tables.
- `acast()` casts into a completely new dimension (namely `ndim(x) + 1`), instead of casting into new columns.

Usage

```
acast(x, ...)
```

```
## Default S3 method:
```

```
acast(x, margin, grp, fill = FALSE, fill_val, ...)
```

Arguments

<code>x</code>	an atomic or recursive array.
<code>...</code>	further arguments passed to or from methods.
<code>margin</code>	a scalar integer, specifying the margin to cast from.
<code>grp</code>	a factor, where <code>length(grp) == dim(x)[margin]</code> , with at least 2 unique values, specifying which indices of <code>dim(x)[margin]</code> belong to which group. Each group will be cast onto a separate index of dimension <code>ndim(x) + 1</code> . Unused levels of <code>grp</code> will be dropped. Any NA values or levels found in <code>grp</code> will result in an error.
<code>fill</code>	Boolean. When factor <code>grp</code> is unbalanced (i.e. has unequally sized groups) the result will be an array where some slices have missing values, which need to be filled. If <code>fill = TRUE</code> , an unbalanced <code>grp</code> factor is allowed, and missing values will be filled with <code>fill_val</code> . If <code>fill = FALSE</code> (default), an unbalanced <code>grp</code> factor is not allowed, and providing an unbalanced factor for <code>grp</code> produces an error.
<code>fill_val</code>	scalar of the same type of <code>x</code> , giving value to use to fill in the gaps when <code>fill = TRUE</code> . The <code>fill_val</code> argument is ignored when <code>fill = FALSE</code> . If <code>fill_val</code> is missing, it is specified as follows: • If <code>x</code> is of type <code>raw</code> and <code>fill = TRUE</code>, <code>fill_val</code> is not allowed to be missing, and an error is returned; • If <code>x</code> is atomic but not <code>raw</code>, <code>fill_val</code> is set to <code>NA</code>; • If <code>x</code> is of type <code>list</code>, <code>fill_val</code> is set to <code>list(NULL)</code>.

Details

For the sake of illustration, consider a matrix `x` and a grouping factor `grp`. Let the integer scalar `k` represent a group in `grp`, such that `k ∈ 1:nlevels(grp)`. Then the code

```
out <- acast(x, margin = 1, grp = grp)
```

essentially performs the following for every group `k`:

- copy-paste the subset `x[grp == k, ]` to the subset `out[, , k]`.

Please see the examples section to get a good idea on how this function casts an array.

Value

An array with dimensions `c(dim(x), max(tabulate(grp)))`.

Back transformation

From the casted array,
`out <- acast(x, margin, grp)`,
 one can get the original `x` back by using
`back <- asplit(out, ndim(out)) |> bind_array(along = margin)`.
 Note, however, the following about the back-transformed array `back`:

- `back` will be ordered by `grp` along dimension `margin`;
- if the levels of `grp` did not have equal frequencies, then `dim(back)[margin] > dim(x)[margin]`, and `back` will have more missing values than `x`.

See Also

[broadcast_casting](#)

Examples

```
# balanced acasting ====
x <- cbind(id = rep(1:3, each = 2), grp = rep(1:2, 3), val = rnorm(6))
print(x)

grp <- as.factor(x[, 2])
levels(grp) <- c("a", "b")
margin <- 1L

acast(x, margin, grp)

# unbalanced acasting ====
x <- cbind(id = c(rep(1:3, each = 2), 1), grp = c(rep(1:2, 3), 2), val = rnorm(7))
print(x)

grp <- as.factor(x[, 2])
levels(grp) <- c("a", "b")
margin <- 1L

acast(x, margin, grp, fill = TRUE)

# unbalanced acasting with raw array ====
x <- cbind(id = c(rep(1:3, each = 2), 1), grp = c(rep(1:2, 3), 2), val = sample(1:7))
x <- as_raw(x)
print(x)
```

```

grp <- x[, 2] |> as.integer() |> as.factor()
levels(grp) <- c("a", "b")
margin <- 1L

(fill_val <- as.raw(255))
acast(x, margin, grp, fill = TRUE, fill_val = fill_val)

```

bc.b

*Broadcasted Boolean Operations***Description**

The `bc.b()` method performs broadcasted logical (or Boolean) operations on 2 arrays.

Please note that these operations will treat the input as logical.

Therefore, something like `bc.b(1, 2, "==")` returns `TRUE`, because both 1 and 2 are `TRUE` when treated as logical.

For regular relational operators, see [bc.rel](#).

Usage

```

bc.b(x, y, op, ...)

## S4 method for signature 'ANY'
bc.b(x, y, op)

```

Arguments

<code>x, y</code>	conformable vectors/arrays of type <code>logical</code> , <code>numeric</code> , or <code>raw</code> . Note that input with type of <code>double</code> will be coerced to <code>integer</code> .
<code>op</code>	a single string, giving the operator. Supported Boolean operators: <code>&</code> , <code> </code> , <code>xor</code> Supported relational operators: <code>==</code> , <code>!=</code> .
<code>...</code>	further arguments passed to or from methods.

Value

Normally:

A logical array/vector as a result of the broadcasted Boolean operation.

If both x and y are type of raw:

A raw array/vector as a result of the broadcasted Boolean operation, where 01 codes for TRUE and 00 codes for FALSE.

This is convenient as raw requires less memory space than logical.

See Also

[broadcast_operators](#)

Examples

```
x.dim <- c(4:2)
x.len <- prod(x.dim)
x.data <- sample(c(TRUE, FALSE, NA), x.len, TRUE)
x <- array(x.data, x.dim)
y <- array(1:50, c(4,1,1))

bc.b(x, y, "&")
bc.b(x, y, "|")
bc.b(x, y, "xor")
bc.b(x, y, "==")
bc.b(x, y, "!=")
```

bc.bit

Broadcasted Bit-wise Operations

Description

The `bc.bit()` method performs broadcasted bit-wise operations on pairs of arrays, where both arrays are of type raw or both arrays are of type integer.

Usage

```
bc.bit(x, y, op, ...)

## S4 method for signature 'ANY'
bc.bit(x, y, op)
```

Arguments

x, y	conformable raw or integer (32 bit) vectors/arrays.
op	a single string, giving the operator. Supported bit-wise operators: &, , xor, nand, nor, «, », ==, !=, <, >, <=, >=. "nand" is defined as bit-wise $!(x \& y)$, and "nor" is defined as bit-wise $!(x y)$.
...	further arguments passed to or from methods.

Details

The "&", "|", "xor", "nand", and "nor" operators given in `bc.bit()` perform BIT-WISE AND, OR, XOR, NAND, and NOR operations, respectively.

The relational operators given in `bc.bit()` perform BIT-WISE relational operations:

- "==" is equivalent to bit-wise $!xor(x, y)$, but faster;
- "!=" is equivalent to bit-wise $xor(x, y)$;
- "<" is equivalent to bit-wise $!(x \& y)$, but faster;
- ">" is equivalent to bit-wise $(x \& !y)$, but faster;
- "<=" is equivalent to bit-wise $!(x | y)$, but faster;
- ">=" is equivalent to bit-wise $(x | !y)$, but faster.

The "«" and "»" operators perform bit-wise left-shift and right-shift, respectively, on x by unit y. For these shift operations, y being larger than the number of bits of x results in an error. Shift operations are only supported for type of raw.

Value

For bit-wise operators:

An array of the same type as x and y, as a result of the broadcasted bit-wise operation.

Note

`bc.bit(x, x, "nand")` and `bc.bit(x, x, "nor")` are equivalent to bit-wise negation of x.

I.e.:

$!x$ if x is type of raw, or `bitwNot(x)` if x is type of integer.

See Also[broadcast_operators](#)**Examples**

```

x.dim <- c(4:2)
x.len <- prod(x.dim)
x.data <- as.raw(0:10)
y.data <- as.raw(10:0)
x <- array(x.data, x.dim)
y <- array(y.data, c(4,1,1))

bc.bit(x, y, "&")
bc.bit(x, y, "|")
bc.bit(x, y, "xor")

```

bc.cplx

*Broadcasted Complex Numeric Operations***Description**

The `bc.cplx()` method performs broadcasted complex numeric operations on pairs of arrays.

Usage

```

bc.cplx(x, y, op, ...)

## S4 method for signature 'ANY'
bc.cplx(x, y, op)

```

Arguments

<code>x, y</code>	conformable vectors/arrays of type complex.
<code>op</code>	a single string, giving the operator. Supported arithmetic operators: +, -, *, /. Supported relational operators: ==, !=.
<code>...</code>	further arguments passed to or from methods.

Details

For the `*` and `/` operators, `bc.cplx()` uses more strict NA checks than base 'R':
If for an iteration, `re(x)`, `im(x)`, `re(y)`, and/or `im(y)` contains NA, than the result for that iteration is necessarily `NA_complex_`.

Value

For arithmetic operators:

A complex array as a result of the broadcasted arithmetic operation.

For relational operators:

A logical array as a result of the broadcasted relational comparison.

See Also

[broadcast_operators](#)

Examples

```
x.dim <- c(4:2)
x.len <- prod(x.dim)
gen <- function() sample(c(rnorm(20), NA, NaN, Inf, -Inf))
x <- array(gen() + gen() * -1i, x.dim)
y <- array(gen() + gen() * -1i, c(4,1,1))

bc.cplx(x, y, "==")
bc.cplx(x, y, "!=")

bc.cplx(x, y, "+")

bc.cplx(array(gen() + gen() * -1i), array(gen() + gen() * -1i), "==")
bc.cplx(array(gen() + gen() * -1i), array(gen() + gen() * -1i), "!=")

x <- array(gen() + gen() * -1i)
y <- array(gen() + gen() * -1i)
bcr(x) <- bcr(y) <- TRUE
out <- x * y
bind_array(list(x = x, y = y, `x*y` = x*y, out = out), 2L)
```

Description

The `bc.d()` method performs broadcasted decimal numeric operations on 2 numeric or logical arrays.

Usage

```
bc.d(x, y, op, ...)

## S4 method for signature 'ANY'
bc.d(x, y, op, tol = sqrt(.Machine$double.eps))
```

Arguments

x, y	conformable vectors/arrays of type logical or numeric.
op	a single string, giving the operator. Supported arithmetic operators: +, -, *, /, ^, pmin, pmax. Supported relational operators: ==, !=, <, >, <=, >=, d==, d!=, d<, d>, d<=, d>=.
...	further arguments passed to or from methods.
tol	a single number between 0 and 0.1, giving the machine tolerance to use for the relational operators. Only relevant for the following operators: d==, d!=, d<, d>, d<=, d>= See the %d==%, %d!=%, %d<%, %d>%, %d<=%, %d>= operators from the 'tinycodet' package for details.

Value

For arithmetic operators:
A numeric array as a result of the broadcasted decimal arithmetic operation.

For relational operators:
A logical array as a result of the broadcasted decimal relational comparison.

See Also

[broadcast_operators](#)

Examples

```
x.dim <- c(4:2)
x.len <- prod(x.dim)
x.data <- sample(c(NA, 1.1:1000.1), x.len, TRUE)
x <- array(x.data, x.dim)
y <- array(1:50, c(4,1,1))

bc.d(x, y, "+")
bc.d(x, y, "-")
bc.d(x, y, "*")
```

```

bc.d(x, y, "/" )
bc.d(x, y, "^" )

bc.d(x, y, "==" )
bc.d(x, y, "!=" )
bc.d(x, y, "<" )
bc.d(x, y, ">" )
bc.d(x, y, "<=" )
bc.d(x, y, ">=" )

```

bc.i	<i>Broadcasted Integer Numeric Operations with Extra Overflow Protection</i>
------	--

Description

The `bc.i()` method performs broadcasted integer numeric operations on 2 numeric or logical arrays.

Please note that these operations will treat the input as (double typed) integers, and will efficiently truncate when necessary.

Therefore, something like `bc.i(1, 1.5, "==")` returns TRUE, because `trunc(1.5)` equals 1.

For regular relational operators, see [bc.rel](#).

Usage

```

bc.i(x, y, op, ...)

## S4 method for signature 'ANY'
bc.i(x, y, op)

```

Arguments

x, y	conformable vectors/arrays of type logical or numeric.
op	a single string, giving the operator. Supported simple arithmetic operators: +, -, *, ^, pmin, pmax. Supported special division arithmetic operators: gcd, %%, %/%. Supported relational operators: ==, !=, <, >, <=, >=. The "gcd" operator performs the "Greatest Common Divisor" operation, using the Euclidean algorithm.
...	further arguments passed to or from methods.

Value

For arithmetic operators:

A numeric array of whole numbers, as a result of the broadcasted arithmetic operation.

Base 'R' supports integers from -2^{53} to 2^{53} , which thus range from approximately -9 quadrillion to +9 quadrillion.

Values outside of this range will be returned as -Inf or Inf, as an extra protection against integer overflow.

For relational operators:

A logical array as a result of the broadcasted integer relational comparison.

See Also

[broadcast_operators](#)

Examples

```
x.dim <- c(4:2)
x.len <- prod(x.dim)
x.data <- sample(c(NA, 1.1:1000.1), x.len, TRUE)
x <- array(x.data, x.dim)
y <- array(1:50, c(4,1,1))

bc.i(x, y, "+")
bc.i(x, y, "-")
bc.i(x, y, "*")
bc.i(x, y, "gcd") # greatest common divisor
bc.i(x, y, "^")

bc.i(x, y, "==")
bc.i(x, y, "!=")
bc.i(x, y, "<")
bc.i(x, y, ">")
bc.i(x, y, "<=")
bc.i(x, y, ">=")
```

Description

The `bc.list()` method performs broadcasted operations on 2 Recursive arrays.

Usage

```
bc.list(x, y, f, ...)

## S4 method for signature 'ANY'
bc.list(x, y, f)
```

Arguments

<code>x, y</code>	conformable Recursive vectors/arrays (i.e. vectors/arrays of type <code>list</code>).
<code>f</code>	a function that takes in exactly 2 arguments, and returns a result that can be stored in a single element of a list.
<code>...</code>	further arguments passed to or from methods.

Value

A recursive array.

See Also

[broadcast_operators](#)

Examples

```
x.dim <- c(10, 2, 2)
x.len <- prod(x.dim)

gen <- function(n) sample(list(letters, month.abb, 1:10), n, TRUE)

x <- array(gen(10), x.dim)
y <- array(gen(10), c(10, 1, 1))

bc.list(
  x, y, \(x, y) x %in% y
)
```

Description

The `bc.raw()` method performs broadcasted operations on arrays of type `raw`, and the return type is **always** `raw`.

For bit-wise operations, use [bc.bit](#).

For relational operations with logical (TRUE/FALSE/NA) results, use [bc.rel](#).

Usage

```
bc.raw(x, y, op, ...)
```

```
## S4 method for signature 'ANY'
bc.raw(x, y, op)
```

Arguments

<code>x, y</code>	conformable vectors/arrays of type <code>raw</code> .
<code>op</code>	a single string, giving the operator. Supported operators: <code>==</code> , <code>!=</code> , <code><</code> , <code>></code> , <code><=</code> , <code>>=</code> , <code>pmin</code> , <code>pmax</code> , <code>diff</code> . The relational operators work the same as in bc.rel , but with the following difference: a TRUE result is replaced with <code>01</code> , and a FALSE result is replaced with <code>00</code> . The "diff" operator performs the byte equivalent of <code>abs(x - y)</code> .
<code>...</code>	further arguments passed to or from methods.

Value

`bc.raw()` **always** returns an array of type `raw`.

For the relational operators, `01` codes for TRUE results, and `00` codes for FALSE results.

See Also

[broadcast_operators](#)

Examples

```
x <- array(
  sample(as.raw(1:100)), c(5, 3, 2)
)
y <- array(
  sample(as.raw(1:100)), c(5, 1, 1)
)
```

```
cond <- bc.raw(x, y, "!=")
print(cond)

bc_ifelse(cond, yes = x, no = y)
```

`bc.rel`*Broadcasted General Relational Operators*

Description

The `bc.rel()` method performs broadcasted general relational operations on 2 arrays.

Usage

```
bc.rel(x, y, op, ...)

## S4 method for signature 'ANY'
bc.rel(x, y, op)
```

Arguments

<code>x, y</code>	conformable vectors/arrays of any atomic type.
<code>op</code>	a single string, giving the relational operator. Supported relational operators: <code>==</code> , <code>!=</code> , <code><</code> , <code>></code> , <code><=</code> , <code>>=</code> .
<code>...</code>	further arguments passed to or from methods.

Value

A logical array as a result of the broadcasted general relational operation.

See Also

[broadcast_operators](#)

Examples

```
x.dim <- c(4:2)
x.len <- prod(x.dim)
x.data <- sample(c(NA, 1.1:1000.1), x.len, TRUE)
x <- array(x.data, x.dim)
y <- array(1:50, c(4,1,1))
```

```
bc.rel(x, y, "==")
bc.rel(x, y, "!=")
bc.rel(x, y, "<")
bc.rel(x, y, ">")
bc.rel(x, y, "<=")
bc.rel(x, y, ">=")
```

bc.str

*Broadcasted String Operations***Description**

The `bc.str()` method performs broadcasted string operations on pairs of arrays.

Usage

```
bc.str(x, y, op, ...)

## S4 method for signature 'ANY'
bc.str(x, y, op)
```

Arguments

<code>x, y</code>	conformable vectors/arrays of type character.
<code>op</code>	a single string, giving the operator. Supported concatenation operators: <code>+</code> . Supported relational operators: <code>==</code> , <code>!=</code> . Supported distance operators: <code>levenshtein</code> , <code>lcss</code> . "levenshtein" is a distance measure of remoteness (i.e. greater distance = higher levenshtein). "lcss" stands for Longest Common Sub-String, and is a distance measure of closeness (i.e. smaller distance = higher lcss).
<code>...</code>	further arguments passed to or from methods.

Value

For concatenation operation:

A character array as a result of the broadcasted concatenation operation.

For relational operation:

A logical array as a result of the broadcasted relational comparison.

For distance operation:

An integer array as a result of the broadcasted distance measurement.

References

The 'C++' code for the Levenshtein edit string distance is based on the code found in https://rosettacode.org/wiki/Levenshtein_distance#C++

See Also

[broadcast_operators](#)

Examples

```
# string concatenation:
x <- array(letters, c(10, 2, 1))
y <- array(letters, c(10,1,1))
bc.str(x, y, "+")

# string (in)equality:
bc.str(array(letters), array(letters), "==")
bc.str(array(letters), array(letters), "!=")

# string distances:
x <- setNames(month.name, month.name) |> vector2array(1L)
y <- setNames(month.abb, month.abb) |> vector2array(2L)
bc.str(x, y, "levenshtein") # levenshtein
bc.str(x, y, "lcss") # longest common sub-string
```

bcapply

Apply Function to Pair of Arrays with Broadcasting

Description

The `bcapply()` method applies a function to 2 arrays element-wise with broadcasting.

Usage

```
bcapply(x, y, f, ...)

## S4 method for signature 'ANY'
bcapply(x, y, f, v = NULL)
```

Arguments

x, y	conformable atomic or recursive vectors/arrays.
f	a function that takes in exactly 2 arguments, and returns a result that can be stored in a single element of a recursive or atomic array.
...	further arguments passed to or from methods.
v	either NULL, or single string, giving the scalar type for a single iteration. If NULL (default) or "list", the result will be a recursive array. If it is certain that, for every iteration, f() always results in a single atomic scalar of exactly a specific type, the user can specify the type in v to pre-allocate the result. Pre-allocating the results leads to slightly faster and more memory efficient code. NOTE: Incorrectly specifying v leads to undefined behaviour; when unsure, leave v at its default value.

Value

An atomic or recursive array with dimensions `bc_dim(x, y)`.
 Preserves some of the attributes of x and y similar to broadcasted infix operators, as explained in [broadcast_operators](#).

Examples

```
# check for each element in one recursive array if values are present in another:
mylist <- list(
  as.raw(0:255),
  sample(c(TRUE, FALSE, NA), 100, TRUE),
  0:255,
  rnorm(10),
  rnorm(10) + rnorm(10) * -1i,
  sample(month.abb)
)
mylist <- c(mylist, list(mylist))
x <- array(sample(mylist, 50, TRUE), c(5, 5, 2))
y <- array(sample(mylist, 50, TRUE), c(5, 5, 2))
```

```

bcapply(x, y, `~in%`) # returns a dimensional list / recursive array

bcapply(x, y, \(x, y) any(x %in% y), v = "logical") # returns logical array

bcapply(x, y, \(x, y) all(x %in% y), v = "logical") # returns logical array


# calculate quartiles for each list item, and return numeric array of quartiles:
x <- list(
  a = 1:10,
  beta = exp(-3:3),
  logic = c(TRUE,FALSE,FALSE,TRUE)
)
print(x)
quantiles <- array(c(1:3/4), c(1, 3))
colnames(quantiles) <- paste0("q = ", quantiles)
print(quantiles)

out <- bcapply(x, quantiles, \(x, y) quantile(x, probs = y), v = "double")
print(out)
typeof(out)

```

bc_dim

Predict Broadcasted Dimensions

Description

bc_dim(x, y) gives the dimensions an array would have, as the result of an broadcasted binary element-wise operation between 2 arrays x and y.

Usage

```
bc_dim(x, y)
```

Arguments

x, y an atomic or recursive array.

Value

Returns an integer vector giving the broadcasted dimension sizes of the result, or the length of the result if its dimensions will be NULL.

Examples

```
x.dim <- c(4:2)
x.len <- prod(x.dim)
x.data <- sample(c(TRUE, FALSE, NA), x.len, TRUE)
x <- array(x.data, x.dim)
y <- array(1:50, c(4,1,1))

dim(bc.b(x, y, "&")) == bc_dim(x, y)
dim(bc.b(x, y, "|")) == bc_dim(x, y)
```

bc_ifelse

Broadcasted Ifelse

Description

The `bc_ifelse()` method performs a broadcasted form of [ifelse](#).

Usage

```
bc_ifelse(test, yes, no, ...)

## S4 method for signature 'ANY'
bc_ifelse(test, yes, no)
```

Arguments

test	a vector or array, with the type logical, integer, or raw, and a length equal to <code>prod(bc_dim(yes, no))</code> . If yes / no are of type raw, test is not allowed to contain any NAs.
yes, no	conformable vectors/arrays of the same type. All atomic types are supported. Recursive arrays of type list are also supported.
...	further arguments passed to or from methods.

Value

The output, here referred to as `out`, will be an array of the same type as `yes` and `no`.
If `test` has the same dimensions as `bc_dim(yes, no)`, then `out` will also have the same dimnames as `test`.
If `test` is a [broadcaster](#), then `out` will also be a [broadcaster](#).

After broadcasting `yes` against `no`, given any element index `i`, the following will hold for the output:

- when `test[i] == TRUE`, `out[i]` is `yes[i]`;
- when `test[i] == FALSE`, `out[i]` is `no[i]`;
- when `test[i]` is `NA`, `out[i]` is `NA` when `yes` and `no` are atomic, and `out[i]` is `list(NULL)` when `yes` and `no` are recursive.

Examples

```
x.dim <- c(5, 3, 2)
x.len <- prod(x.dim)

x <- array(sample(1:100), x.dim)
y <- array(sample(1:100), c(5, 1, 1))

cond <- bc.i(x, y, ">")

bc_ifelse(cond, yes = x^2, no = -y)
```

bc_strep

Broadcasted strep

Description

The `bc_strep()` method is a broadcasted form of [strep](#).

Usage

```
bc_strep(x, y, ...)

## S4 method for signature 'ANY'
bc_strep(x, y)
```

Arguments

<code>x</code>	vector/array of type character.
<code>y</code>	vector/array of type integer.
<code>...</code>	further arguments passed to or from methods.

Value

A character array as a result of the broadcasted repetition operation.

Examples

```
x <- array(sample(month.abb), c(10, 2))
y <- array(sample(1:10), c(10, 2, 3))

print(x)
print(y)

bc_strrep(x, y)
```

bind_array

*Dimensional Binding of Arrays with Broadcasting***Description**

`bind_array()` binds (atomic/recursive) arrays along a dimension.
Allows for broadcasting.

Usage

```
bind_array(
  input,
  along,
  rev = FALSE,
  ndim2bc = 16L,
  name_along = TRUE,
  comnames_from = 1L
)
```

Arguments

input	a list of arrays; both atomic and recursive arrays are supported, and can be mixed. If argument <code>input</code> has length 0, or it contains exclusively objects where one or more dimensions are 0, an error is returned. <code>input</code> may not contain more than $2^{31} - 1$ objects, and no less than 2 objects. If the user wishes to include vectors to bind in <code>input</code>, the vectors must be turned into arrays; for example using vector2array.
along	a single integer, indicating the dimension along which to bind the dimensions. I.e. use <code>along = 1</code> for row-binding, <code>along = 2</code> for column-binding, etc. Specifying <code>along = 0</code> will bind the arrays on a new dimension before the first, making <code>along</code> the new first dimension. Specifying <code>along = N + 1</code>, with $N = \max(\text{lst.ndim}(\text{input}))$, will create an additional dimension ($N + 1$) and bind the arrays along that new dimension.

rev	Boolean, indicating if along should be reversed, counting backwards. If FALSE (default), along works like normally; if TRUE, along is reversed. I.e. <code>along = 0, rev = TRUE</code> is equivalent to <code>along = N+1, rev = FALSE</code>; and <code>along = N+1, rev = TRUE</code> is equivalent to <code>along = 0, rev = FALSE</code>; with <code>N = max(1st.ndim(input))</code>.
ndim2bc	a single non-negative integer; specify here the maximum number of dimensions that are allowed to be broadcasted when binding arrays. If <code>ndim2bc = 0L</code>, no broadcasting will be allowed at all.
name_along	Boolean, indicating if dimension along should be named. Please run the code in the examples section to get a demonstration of the naming behaviour.
comnames_from	either an integer scalar or NULL. Indicates which object in input should be used for naming the shared dimension. If NULL, no communal names will be given. For example: When binding columns of matrices, the matrices will share the same rownames. Using <code>comnames_from = 10</code> will then result in <code>bind_array()</code> using <code>rownames(input[[10]])</code> for the rownames of the output.

Details

The API of `bind_array()` is inspired by the fantastic `abind::abind()` function by Tony Plare & Richard Heiberger (2016).

But `bind_array()` differs considerably from `abind::abind` in that `bind_array()` allows for broadcasting, `bind_array()` is generally faster and more memory-efficient, and `bind_array()` can handle recursive arrays.

Note that, unlike `abind::abind()`, `bind_array()` only binds (atomic/recursive) arrays and matrices;

`bind_array()` does not attempt to convert things to arrays when they are not arrays, but will give an error instead.

This saves computation time and prevents unexpected results.

Value

An array as a result from the (broadcasted) binding.

The type of the result is determined from the highest type of any of the non-empty inputs.

The hierarchy of types is:

`raw < logical < integer < double < complex < character < list` .

If one of the input arrays is a [broadcaster](#), the result will also be a [broadcaster](#).

References

Plate T, Heiberger R (2016). *abind: Combine Multidimensional Arrays*. R package version 1.4-5, <https://CRAN.R-project.org/package=abind>.

Examples

```
# Simple example ====
x <- array(1:20, c(5, 4))
y <- array(-1:-15, c(5, 3))
z <- array(21:40, c(5, 4))
input <- list(x, y, z)
# column binding:
bind_array(input, 2L)

#####

# Broadcasting example ====
x <- array(1:20, c(5, 4))
y <- array(-1:-5, c(1, 5)) # rows will be broadcasted from 1 to 5
z <- array(21:40, c(5, 4))
input <- list(x, y, z)
bind_array(input, 2L)

#####

# Mixing types ====
# here, atomic and recursive arrays are mixed,
# resulting in recursive arrays

# creating the arrays:
x <- c(
  lapply(1:3, \(x)sample(c(TRUE, FALSE, NA))),
  lapply(1:3, \(x)sample(1:10)),
  lapply(1:3, \(x)rnorm(10)),
  lapply(1:3, \(x)sample(letters))
) |> matrix(4, 3, byrow = TRUE)
dimnames(x) <- list(letters[1:4], LETTERS[1:3])
print(x)

y <- matrix(1:12, 4, 3)
print(y)
z <- matrix(letters[1:12], c(4, 3))

# column-binding:
input <- list(x = x, y = y, z = z)
bind_array(input, along = 2L)
```

```
#####

# Illustrating `along` argument ====
# using recursive arrays for clearer visual distinction
input <- list(x = x, y = y)

bind_array(input, along = 0L) # binds on new dimension before first
bind_array(input, along = 1L) # binds on first dimension (i.e. rows)
bind_array(input, along = 2L)
bind_array(input, along = 3L) # bind on new dimension after last

bind_array(input, along = 0L, TRUE) # binds on new dimension after last
bind_array(input, along = 1L, TRUE) # binds on last dimension (i.e. columns)
bind_array(input, along = 2L, TRUE)
bind_array(input, along = 3L, TRUE) # bind on new dimension before first

#####

# binding, with empty arrays ====
emptyarray <- array(numeric(0L), c(0L, 3L))
dimnames(emptyarray) <- list(NULL, paste("empty", 1:3))
print(emptyarray)
input <- list(x = x, y = emptyarray)
bind_array(input, along = 1L, comnames_from = 2L) # row-bind

#####

# Illustrating `name_along` ====
x <- array(1:15, c(5, 3), list(NULL, LETTERS[1:3]))
y <- array(-1:-15, c(5, 3))
z <- array(-1:-15, c(5, 3))

bind_array(list(a = x, b = y, z), 2L)
bind_array(list(x, y, z), 2L)
bind_array(list(a = unname(x), b = y, c = z), 2L)
bind_array(list(x, a = y, b = z), 2L)
input <- list(x, y, z)
names(input) <- c("", NA, "")
bind_array(input, 2L)

#####

# binding vectors and arrays ====
x <- setNames(1:4, letters[1:4]) |> vector2array(orient = 2L, ndim = 2L)
y <- array(1:20, c(5, 4), list(NULL, LETTERS[1:4]))
input <- list(x, y)
```

```

bind_array(input, 1L, comnames_from = 1L) # row-bind, with names from vector `x`

#####

# start with empty vector, and bind arrays from there (handy in loops) ====
y <- array(-1:-15, c(5, 3))
z <- array(-1:-15, c(5, 3))
input <- list(y, z)
init <- vector2array(raw(0L), 1L, 2L)
for(i in input) {
  init <- bind_array(list(init, i), 2L)
}
print(init)

#####

# type of the result is independent of the types of empty arrays ====
# make regular arrays of type `integer`:
y <- array(-1:-15, c(5, 3))
z <- array(-1:-15, c(5, 3))

# make empty array of type `list`:
emptyarray <- array(vector("list", 0L), c(0L, 3L))
dimnames(emptyarray) <- list(NULL, paste("empty", 1:3))
print(emptyarray)
typeof(emptyarray) # type of list, the highest type
length(emptyarray) # but also empty, so it's type does NOT affect result type!

# bind results:
input <- list(y = y, z = z, e = emptyarray)
out <- bind_array(input, along = 1L, comnames_from = 2L) # row-bind
typeof(out) # `integer`, NOT `list`, because empty arrays don't count

```

broadcaster

Check or Set if an Array is a Broadcaster

Description

`broadcaster()` checks if an array or vector is marked as a "broadcaster".
`bcr()` is a short-hand alias for `broadcaster()`.

`broadcaster()<-` (or `bcr()<-`) marks or un-marks the object as a "broadcaster".

`mbroadcasters()` marks or un-marks multiple objects in an environment as broadcaster.
`mbroadcasters()` may be more memory efficient for large arrays than `broadcaster()<-`, as `mbroadcasters()` calls `class(x)<-` directly in the given environment.

The `broadcaster` class attribute exists purely to overload the arithmetic, Boolean, bit-wise, and relational infix operators, to support broadcasting.

This makes mathematical expressions with multiple variables, where precedence may be important, far more convenient.

Like in the following calculation:

$x / (y + z)$

See [broadcast_operators](#) for more information.

Usage

`broadcaster(x)`

`broadcaster(x) <- value`

`mbroadcasters(nms, value, env = NULL)`

`bcr(x)`

`bcr(x) <- value`

Arguments

<code>x</code>	object to check or mark. Only S3 vectors and arrays are supported, and only up to 16 dimensions.
<code>value</code>	set to TRUE to make an array a broadcaster, or FALSE to remove the broadcaster class attribute from an array.
<code>nms</code>	a character vector of variable names.
<code>env</code>	the environment where to look for the variable names specified in <code>nms</code> . If NULL, the environment from which the function was called is used.

Value

For `broadcaster()`:

TRUE if an array or vector is a broadcaster, or FALSE if it is not.

For `broadcaster()<-`:

Returns nothing, but marks (if right hand side is TRUE) or un-marks (if right hand side is FALSE) the object as a "broadcaster".

For `mbroadcasters()`:

Returns nothing, but marks (if value is TRUE) or un-marks (if value is FALSE) the objects as broadcasters.

If value = TRUE, objects that cannot become a broadcaster or are already a broadcaster will be ignored.

If value = FALSE, objects that are not broadcasters (according to `broadcaster()`) will be ignored.

Note

The 'broadcaster' class will make arithmetic and relational operators operate with broadcasting. Functions that rely on non-broadcasted functionality of these operators will produce unexpected results.

Thus functions like `pmin()` and `pmax()`, and some functions from the 'tinypilot' package, are **not** compatible with 'broadcaster' vectors/arrays.

Please ensure an object is not a 'broadcaster' before applying these functions on it.

See Also

[broadcast_operators](#)

Examples

```
# maths ====

x <- 1:10
y <- 1:10
dim(x) <- c(10, 1)
dim(y) <- c(1, 10)
broadcaster(x) <- TRUE
broadcaster(y) <- TRUE


x + y / x
(x + y) / x

(x + y) * x


# relational operators ====
x <- 1:10
y <- array(1:10, c(1, 10))
broadcaster(x) <- TRUE
broadcaster(y) <- TRUE

x == y
x != y
```

```

x < y
x > y
x <= y
x >= y

# maths ====

x <- sample(1:10)
y <- sample(1:10)
dim(x) <- c(10, 1)
dim(y) <- c(1, 10)
mbroadcasters(c("x", "y"), TRUE)

x + y / x
(x + y) / x

(x + y) * x

# relational operators ====
x <- 1:10
y <- array(1:10, c(1, 10))
mbroadcasters(c("x", "y"), TRUE)

x == y
x != y
x < y
x > y
x <= y
x >= y

```

cast_dim2flat

Cast Dimensional List into a Flattened List

Description

cast_dim2flat() casts a dimensional list (i.e. recursive array) into a flat list (i.e. recursive vector), but with names that indicate the original dimensional positions of the elements.

Primary purpose for this function is to facilitate printing or summarizing dimensional lists.

Usage

```
cast_dim2flat(x, ...)
```

```
## Default S3 method:  
cast_dim2flat(x, ...)
```

Arguments

x	a list
...	further arguments passed to or from methods.

Value

A flattened list, with names that indicate the original dimensional positions of the elements.

See Also

[broadcast_casting](#)

Examples

```
x <- array(  
  sample(list(letters, month.name, 1:10 ~ "foo"), prod(4:2), TRUE),  
  dim = 4:2,  
  dimnames = list(NULL, LETTERS[1:3], c("x", "y"))  
)  
  
# summarizing ====  
summary(x) # dimensional information is lost  
  
# In the following instances, dimensional position info is retained:  
cast_dim2flat(x) |> summary()  
  
cast_dim2flat(x[1:3, 1:2, 2, drop = FALSE]) |> summary()  
  
cast_dim2flat(x[1:3, 1:2, 2, drop = TRUE]) |> summary()  
  
# printing ====  
print(x) # too compact  
cast_dim2flat(x) |> print() # much less compact
```

cast_dim2hier

Cast Dimensional List into Hierarchical List

Description

cast_dim2hier() casts a dimensional list (i.e. an array of type list) into a hierarchical/nested list.

Usage

```
cast_dim2hier(x, ...)
```

```
## Default S3 method:
```

```
cast_dim2hier(x, in2out = TRUE, distr.names = TRUE, ...)
```

Arguments

x an array of type list.

... further arguments passed to or from methods.

in2out see [broadcast_casting](#).

distr.names TRUE or FALSE, indicating if dimnames from x should be distributed over the nested elements of the output.
See examples section for demonstration.

Value

A nested list.

See Also

[broadcast_casting](#)

Examples

```
x <- array(c(as.list(1:24), as.list(letters)), 4:2)
dimnames(x) <- list(
  letters[1:4],
  LETTERS[1:3],
  month.abb[1:2])
```

```

)
print(x)

# cast `x` from in to out, and distribute names:
x2 <- cast_dim2hier(x, distr.names = TRUE)
head(x2, n = 2)

# cast `x` from out to in, and distribute names:
x2 <- cast_dim2hier(x, in2out = FALSE, distr.names = TRUE)
head(x2, n = 2)

```

cast_hier2dim

*Cast Hierarchical List into Dimensional list***Description**

cast_hier2dim() casts a hierarchical/nested list into a dimensional list (i.e. an array of type list).

This method comes with 2 helper functions:

[hier2dim](#) and [hiernames2dimnames](#) methods.

See their help page for details.

Usage

```

cast_hier2dim(x, ...)

## Default S3 method:
cast_hier2dim(
  x,
  in2out = TRUE,
  maxdepth = 16L,
  recurse_all = FALSE,
  padding = list(NULL),
  direction.names = 0L,
  ...
)

```

Arguments

x	a nested list. If x has redundant nesting, it is advisable (though not necessary) to reduce the redundant nesting using dropnests .
...	further arguments passed to or from methods.

in2out, recurse_all	see broadcast_casting .
maxdepth	a single, positive integer, giving the maximum depth to recurse into the list. The surface-level elements of a list is depth 1.
padding	a list of length 1, giving the padding value to use when padding is required. Padding is used to ensure every all slices of the same dimension in the output have equal number of elements (for example, all rows must have the same number of columns).
direction.names	see argument <code>direction</code> from the hiernames2dimnames method.

Value

An array of type `list`, with the dimensions given by [hier2dim](#).

If the output needs padding (indicated by [hier2dim](#)), the output will have more elements than `x`, filled with a padding value (as specified in the `padding` argument).

If `direction.names = 0` (default), the result will not have any `dimnames`; the `dimnames` can then still be constructed using [hiernames2dimnames](#).

If `direction.names` is 1 or -1, the result *will* have `dimnames`.

See Also

[broadcast_casting](#), [hier2dim](#), [hiernames2dimnames](#)

Examples

```
# Example 1: Basics ====
x <- list(
  group1 = list(
    class1 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    ),
    class2 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    )
  ),
  group2 = list(
    class1 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
```

```

        sex = sample(c("M", "F", NA), 10, TRUE)
      ),
      class2 = list(
        height = rnorm(10, 170),
        weight = rnorm(10, 80),
        sex = sample(c("M", "F", NA), 10, TRUE)
      )
    )
  )

# predict what dimensions `x` would have if casted as dimensional:
hier2dim(x)

x2 <- cast_hier2dim(x) # cast as dimensional

# since the original list uses the same names for all elements within the same depth,
# dimnames can be set easily:
dimnames(x2) <- hiernames2dimnames(x)

print(x2)

#####

# Example 2: Cast from outside to inside ===
x <- list(
  group1 = list(
    class1 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    ),
    class2 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    )
  ),
  group2 = list(
    class1 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    ),
    class2 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    )
  )
)

```

```

# by default, `in2out = TRUE`;
# for this example, `in2out = FALSE` is used

# predict what dimensions `x` would have if casted as dimensional:
hier2dim(x, in2out = FALSE)

x2 <- cast_hier2dim(x, in2out = FALSE) # cast as dimensional

# since the original list uses the same names for all elements within the same depth,
# dimnames can be set easily:
# because in2out = FALSE, go from the shallow names to the deeper names:
dimnames(x2) <- hiernames2dimnames(x, in2out = FALSE)

print(x2)

#####

# Example 3: padding ===

# For Example 3, take the same list as before, but remove x$group1$class2:

x <- list(
  group1 = list(
    class1 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    )
  ),
  group2 = list(
    class1 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    ),
    class2 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    )
  )
)

hier2dim(x) # as indicated here, dimension 2 (i.e. columns) will have padding

# casting this to a dimensional list will resulting in padding with `NULL`:
x2 <- cast_hier2dim(x)
print(x2)
# The `NULL` values are added for padding.
# This is because all slices of the same dimension need to have the same number of elements.

```

```
# For example, all rows need to have the same number of columns.

# one can also use custom padding:
x2 <- cast_hier2dim(x, padding = list(~ "this is padding"))
print(x2)

dimnames(x2) <- hiernames2dimnames(x)

print(x2)

# we can also use in2out = FALSE:
x2 <- cast_hier2dim(x, in2out = FALSE, padding = list(~ "this is padding"))
dimnames(x2) <- hiernames2dimnames(x, in2out = FALSE)
print(x2)
```

cast_shallow2atomic	<i>Cast Shallow List to Atomic Object</i>
---------------------	---

Description

cast_shallow2atomic() casts a shallow (i.e. non-nested) list to an atomic vector/array.

Usage

```
cast_shallow2atomic(x, ...)

## Default S3 method:
cast_shallow2atomic(x, arrangement = 0L, padding = NA, comnames_from = 1L, ...)
```

Arguments

x	a shallow (i.e. non-nested) list. The attributes of the objects inside the list will be ignored, except for names.
...	further arguments passed to or from methods.
arrangement	see the Details and Examples sections.
padding	an atomic scalar, and only relevant if arrangement is 1 or -1. This gives the padding value to use when padding is required. Padding is used to ensure every all slices of the same dimension in the output have equal number of elements (for example, all rows must have the same number of columns).

`comnames_from` an integer scalar or NULL, and only relevant if `arrangement` is 1 or -1.
 This gives which element of `x` to use for the communal names.
 If NULL, no communal names will be given.
 For example:
 If `x` is a 1d (or dimensionless) list, `cast_shallow2atomic(x, 1, arrangement = 1)` will produce an atomic matrix.
 The column names of the matrix will be `names(x)`.
 The row names, however, will be taken from `names(x[[comnames_from]])`, provided that `x[[comnames_from]]` has the proper length.
 See also the Examples section.

Details

If `arrangement = 0L`,
`cast_shallow2atomic()` works like `unlist()`, except that `cast_shallow2atomic()` guarantees an atomic vector result.

If `arrangement = 1L`,
`cast_shallow2atomic()` will produce an atomic array, with the elements arranged such that the dimensions are `c(max(lengths(x)), dim(x))`.
 If `x` has no dimensions, `dim(x)` is replaced with `length(x)`, thus treating `x` as an 1d array.
 This will therefore always produce an atomic array with at least 2 dimensions.
 The `dimnames`, if possible to construct, will be `c(dimnames(x[[comnames_from]]), dimnames(x))`.

If `arrangement = -1L`,
`cast_shallow2atomic()` will produce an atomic array, with the elements arranged such that the dimensions are `c(dim(x), max(lengths(x)))`.
 If `x` has no dimensions, `dim(x)` is replaced with `length(x)`, thus treating `x` as an 1d array.
 This will therefore always produce an atomic array with at least 2 dimensions.
 The `dimnames`, if possible to construct, will be `c(dimnames(x), names(x[[comnames_from]]))`.

In all cases, the result will be atomic.

Value

If `arrangement = 0L`:
 An atomic vector.

If `arrangement = 1L`:
 An atomic array.

If `arrangement = -1L`:
 An atomic array.

The type of the result is determined from the highest atomic type of any of the list elements (including elements of length zero).
 The hierarchy of atomic types is:

raw < logical < integer < double < complex < character.

List elements that are not atomic but language expressions, like formulas, will be coerced to type of character.

Back transformation

From the casted atomic object,
`out <- cast_shallow2atomic(x, ...)`,
 one can get an *approximation* of the original shallow list back using just base 'R' functions.
 This section describes how to do so.

If `arrangement = 0L`,
 one can transform an atomic object `out` back to a shallow list using:
`back <- as.list(out)`
`names(back) <- names(out)`

If `arrangement = 1L`,
 one can transform an atomic object `out` back to a shallow list using:
`asplit(out, seq(2, ndim(out)))`

If `arrangement = -1L`,
 one can transform an atomic object `out` back to a shallow list using:
`asplit(out, seq(1, ndim(out) - 1L))`

See Also

[broadcast_casting](#)

Examples

```
# recursive vector ====
x <- list(
  setNames(1:11, letters[1:11]), 1:10, 1:9, 1:8, 1:7, 1:6, 1:5, 1:4, 1:3, 1:2, 1L, integer(0L)
)
names(x) <- month.abb
print(x)

cast_shallow2atomic(x, 0L)
cast_shallow2atomic(x, 1L, comnames_from = 1L)
cast_shallow2atomic(x, -1L, comnames_from = 1L)

# recursive matrix ====
x <- list(
```

```

  setNames(1:11, letters[1:11]), 1:10, 1:9, 1:8, 1:7, 1:6, 1:5, 1:4, 1:3, 1:2, 1L, integer(0L)
) |> rev()
dim(x) <- c(3, 4)
dimnames(x) <- list(month.abb[1:3], month.name[1:4])
print(x)

cast_shallow2atomic(x, 0L)
cast_shallow2atomic(x, 1L, comnames_from = length(x))
cast_shallow2atomic(x, -1L, comnames_from = length(x))

```

checkmissing

Efficiently Check for (Non-)Missing Values

Description

The `checkNULL()` function efficiently checks for the presence (or absence) of `NULL` in every element of a list.

The `checkNA()` function efficiently checks for the presence (or absence) of `NA/NaN` in every element of an atomic vector.

Usage

```

checkNA(x, ...)

## Default S3 method:
checkNA(x, op, inv = FALSE, ...)

checkNULL(x, ...)

## Default S3 method:
checkNULL(x, op, inv = FALSE, ...)

```

Arguments

<code>x</code>	an object. For <code>checkNULL()</code>: a recursive vector or array (i.e. type of <code>list</code>). For <code>checkNA()</code>: an atomic vector or array (raw type not supported).
<code>...</code>	further arguments passed to or from methods.
<code>op</code>	a single string, giving the operation to use. The following operations are supported: "logical": checks for every element of <code>x</code> the presence/absence of missing values; returns a logical vector/array.

- "raw": same as operation "logical", except the result will be a raw vector/array (01 = TRUE, 00 = FALSE), which requires less memory.
- "any": checks if any element is (not) missing.
- "all": checks if all elements are (not) missing.
- "count" or "sum": counts the number of elements that are (not) missing.
- "which": gives the element indices that are (not) missing.
- "first": gives the element index of the first (non-) missing element.
- "last": gives the element index of the last (non-) missing element.

inv

Boolean, indicating if the check should be inverted.

If inv = FALSE (default), the operations check for missing elements.

If inv = TRUE, the operations check for NOT missing elements.

Value

Output depends on the specification of argument op:

- "logical": logical vector with the same length, names, and dimensions as x.
- "raw": raw vector with the same length, names, and dimensions as x.
- "any": TRUE or FALSE.
- "all": TRUE or FALSE.
- "count" or "sum": 53 bit integer scalar.
- "which": vector of indices.
- "first": the first index found, or 0 otherwise.
- "last": the last index found, or 0 otherwise.

Examples

```
# checkNA ====
x <- array(
  sample(c(-10:10, NA, NaN)), dim = 4:2
)
y <- array(
  sample(c(-10:10, NA, NaN)), dim = c(4,1,1)
)
broadcaster(x) <- broadcaster(y) <- TRUE

mx <- checkNA(x, "raw")
my <- checkNA(y, "raw")
bc.b(mx, my, "&")
bc.b(mx, my, "xor")
bc.b(mx, my, "==")
bc.b(mx, my, "!=")
bc_ifelse(bc.b(mx, my, "|"), -1000L, x + y)
```

```
# checkNULL ====
x <- array(
  sample(list(letters, LETTERS, month.abb, month.name, NULL)), dim = 4:2
)
y <- array(
  sample(list(letters, LETTERS, month.abb, month.name, NULL)), dim = c(4,1,1)
)
broadcaster(x) <- broadcaster(y) <- TRUE

mx <- checkNULL(x, "raw")
my <- checkNULL(y, "raw")
bc.b(mx, my, "&")
bc.b(mx, my, "xor")
bc.b(mx, my, "==")
bc.b(mx, my, "!=")
bc_ifelse(bc.b(mx, my, "|"), list(~ "Nothing"), bc.list(x, y, paste0))
```

dropnests

Drop Redundant List Nesting

Description

dropnests() drops redundant nesting of a list.
 It is the hierarchical equivalent to the dimensional base::drop() function.

Usage

```
dropnests(x, ...)

## Default S3 method:
dropnests(x, maxdepth = 16L, recurse_all = FALSE, ...)
```

Arguments

x	a list
...	further arguments passed to or from methods.
maxdepth	a single, positive integer, giving the maximum depth to recurse into the list. The surface-level elements of a list is depth 1. dropnests(x, maxdepth = 1) will return x unchanged.
recurse_all	see broadcast_casting .

Value

A list without redundant nesting.
Attributes are preserved.

See Also

[broadcast_casting](#)

Examples

```
x <- list(
  a = list(list(list(list(1:10)))),
  b = list(1:10)
)

print(x)

dropnests(x)

# recurse_all demonstration ====
x <- list(
  a = list(list(list(list(1:10)))),
  b = data.frame(month.abb, month.name),
  c = data.frame(month.abb),
  d = array(list(1), c(1,1,1))
)

dropnests(x) # by default, recurse_all = FALSE

dropnests(x, recurse_all = TRUE)

# maxdepth demonstration ====
x <- list(
  a = list(list(list(list(1:10)))),
  b = list(1:10)
)
print(x)

dropnests(x) # by default, maxdepth = 16

dropnests(x, maxdepth = 3L)

dropnests(x, maxdepth = 1L) # returns `x` unchanged
```

hier2dim

Helper Functions For cast_hier2dim

Description

hier2dim() takes a hierarchical/nested list, and predicts what dimensions the list would have, if casted by the [cast_hier2dim](#) function.

hiernames2dimnames() takes a hierarchical/nested list, and intelligently tries to compose dimnames for the result of [cast_hier2dim](#).

Usage

```
hier2dim(x, ...)

hiernames2dimnames(x, ...)

## Default S3 method:
hier2dim(x, in2out = TRUE, maxdepth = 16L, recurse_all = FALSE, ...)

## Default S3 method:
hiernames2dimnames(
  x,
  in2out = TRUE,
  maxdepth = 16L,
  recurse_all = FALSE,
  direction = 1,
  ...
)
```

Arguments

x	a nested list. If x has redundant nesting, it is advisable (though not necessary) to reduce the redundant nesting using dropnests .
...	further arguments passed to or from methods.
in2out, recurse_all	see broadcast_casting .
maxdepth	a single, positive integer, giving the maximum depth to recurse into the list. The surface-level elements of a list is depth 1.

direction A single number, giving the direction in which to search for names.
 Must be either 1 (to search from start to end) or -1 (to search from end to start).
 If set to 0, the result will simply be NULL.

Value

For `hier2dim()`:

An integer vector, giving the dimensions `x` would have, if casted by `cast_hier2dim()`.

The names of the output indicates if padding is required (name "padding"), or no padding is required (no name) for that dimension;

Padding will be required if not all list-elements at a certain depth have the same length.

For `hiernames2dimnames()`:

A list of dimnames; these can be assigned to the dimnames of the result of `cast_hier2dim`.

See Also

[broadcast_casting](#), [cast_hier2dim](#)

Examples

```
# Example 1: Basics ====
x <- list(
  group1 = list(
    class1 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    ),
    class2 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    )
  ),
  group2 = list(
    class1 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    ),
    class2 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    )
  )
)
```

```

)

# predict what dimensions `x` would have if casted as dimensional:
hier2dim(x)

x2 <- cast_hier2dim(x) # cast as dimensional

# since the original list uses the same names for all elements within the same depth,
# dimnames can be set easily:
dimnames(x2) <- hiernames2dimnames(x)

print(x2)

#####

# Example 2: Cast from outside to inside ====
x <- list(
  group1 = list(
    class1 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    ),
    class2 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    )
  ),
  group2 = list(
    class1 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    ),
    class2 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    )
  )
)

# by default, `in2out = TRUE`;
# for this example, `in2out = FALSE` is used

# predict what dimensions `x` would have if casted as dimensional:
hier2dim(x, in2out = FALSE)

x2 <- cast_hier2dim(x, in2out = FALSE) # cast as dimensional

```

```

# since the original list uses the same names for all elements within the same depth,
# dimnames can be set easily:
# because in2out = FALSE, go from the shallow names to the deeper names:
dimnames(x2) <- hiernames2dimnames(x, in2out = FALSE)

print(x2)

#####

# Example 3: padding ====

# For Example 3, take the same list as before, but remove x$group1$class2:

x <- list(
  group1 = list(
    class1 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    )
  ),
  group2 = list(
    class1 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    ),
    class2 = list(
      height = rnorm(10, 170),
      weight = rnorm(10, 80),
      sex = sample(c("M", "F", NA), 10, TRUE)
    )
  )
)

hier2dim(x) # as indicated here, dimension 2 (i.e. columns) will have padding

# casting this to a dimensional list will resulting in padding with `NULL`:
x2 <- cast_hier2dim(x)
print(x2)
# The `NULL` values are added for padding.
# This is because all slices of the same dimension need to have the same number of elements.
# For example, all rows need to have the same number of columns.

# one can also use custom padding:
x2 <- cast_hier2dim(x, padding = list(~ "this is padding"))
print(x2)

dimnames(x2) <- hiernames2dimnames(x)

```

```

print(x2)

# we can also use in2out = FALSE:
x2 <- cast_hier2dim(x, in2out = FALSE, padding = list(~ "this is padding"))
dimnames(x2) <- hiernames2dimnames(x, in2out = FALSE)
print(x2)

```

linear_algebra_stats *Simple Linear Algebra Functions for Statistics*

Description

'broadcast' provides some simple Linear Algebra Functions for Statistics:

```

cinv()
sd_lc()
ecumprob()

```

Usage

```

cinv(x)

sd_lc(X, vc, bad_rp = NaN)

ecumprob(y, sim, eps = 0)

```

Arguments

x	a real symmetric positive-definite square matrix.
X	a numeric (or logical) matrix of multipliers/constants
vc	the variance-covariance matrix for the (correlated) random variables.
bad_rp	if vc is not a Positive (semi-) Definite matrix, give here the value to replace bad standard deviations with.
y	values to estimate the cumulative probability for.
sim	a matrix (or data.frame) with at least 500 columns of simulated values. If sim is given as a dimensionless vector, it will be treated as a matrix with 1 row and length(sim) columns, and this will be noted with a message.

`eps` a non-negative numeric scalar smaller than 0.1, giving the cut-off value for probabilities.
 Probabilities smaller than `eps` will be replaced with `eps`, and probabilities larger than $1 - \text{eps}$ will be replaced with $1 - \text{eps}$.
 Set `eps = 0` to disable probability trimming.

Details

`cinv()`
`cinv()` computes the Choleski inverse of a real symmetric positive-definite square matrix.

`sd_lc()`
 Given the linear combination $X \%*\% b$, where:

- X is a matrix of multipliers/constants;
- b is a vector of (correlated) random variables;
- vc is the symmetric variance-covariance matrix for b ;

`sd_lc(X, vc)` computes the standard deviations for the linear combination $X \%*\% b$, without making needless copies.

`sd_lc(X, vc)` will use **much** less memory than a base 'R' approach.

`sd_lc(X, vc)` will *usually* be faster than a base 'R' approach (depending on the Linear Algebra Library used for base 'R').

`ecumprob()`
 The `ecumprod(y, sim)` function takes a matrix (or data.frame) of simulated values `sim`, and for each row i (after broadcasting), estimates the cumulative distribution function of `sim[i, ]`, and returns the cumulative probability for `y[i]`.

In terms of statistics, it is equivalent to the following operation for each index i :

`ecdf(sim[i, ])(y[i])`

However, `ecumprob()` is **much** faster, and supports NAs/NaNs.

In terms of linear algebra, it is equivalent to the following broadcasted operation:

`rowMeans(sim <= y)`

where y and `sim` are [broadcastable](#) arrays.

However, `ecumprob()` is **much more** memory-efficient, supports a data.frame for `sim`, and has statistical safety checks.

Value

For `cinv()`:

A matrix.

For `sd_lc()`:

A vector of standard deviations.

For `ecumprob()`:

A vector of cumulative probabilities.

If for any observation *i* (after broadcasting), `y[i]` is NA/NaN or any of `sim[i,]` is NA/NaN, the result for *i* will be NA.

If zero-length `y` or `sim` is given, a zero-length numeric vector is returned.

References

John A. Rice (2007), *Mathematical Statistics and Data Analysis* (6th Edition)

See Also

[chol](#), [chol2inv](#)

Examples

```
# variances ====
vc <- datasets::ability.cov$cov
X <- matrix(rnorm(100), 100, ncol(vc))

solve(vc)
cinv(vc) # faster than `solve()`, but only works on positive definite matrices
all(round(solve(vc), 6) == round(cinv(vc), 6)) # they're the same

sd_lc(X, vc)

# ecumprob() ====

sim <- rnbino(10 * 1e4, mu = 3, size = 2) |> matrix(10, 1e4)
y <- sample(0:9)

# vector:
pnbinom(y[1], mu = 3, size = 2) # real probability
ecumprob(y[1], sim[1, , drop = TRUE]) # approximation

# matrix:
cbind(
  real = pnbinom(y, mu = 3, size = 2), # real probability
  approx = ecumprob(y, sim) # approximation
)

# data.frame:
cbind(
  real = pnbinom(y, mu = 3, size = 2), # real probability
  approx = ecumprob(y, as.data.frame(sim)) # approximation
)
```

`ndim`*Get the Number of Dimensions of an Array*

Description

`ndim()` returns the number of dimensions of an object.

`lst.ndim()` returns the number of dimensions of every list-element.

Usage

```
ndim(x)
```

```
lst.ndim(x)
```

Arguments

`x` a vector or array (for `ndim()`), or a list of vectors/arrays (for `lst.ndim()`).

Value

For `ndim()`: an integer scalar.

For `lst.ndim()`: an integer vector, with the same length, names and dimensions as `x`.

Examples

```
x <- array(1:24, 2:4)
ndim(x)

x <- list(
  array(1:10, 10),
  array(1:10, c(2, 5)),
  array(c(letters, NA), c(3,3,3))
)
lst.ndim(x)

x <- list(
  1:10,
  array(1:10, 10),
  matrix(1:10, 2, 5),
  array(c(letters, NA), c(3,3,3))
)
```

```
dim(x) <- c(2,2)
dimnames(x) <- list(c("a", "b"), c("x", "y"))
l1st.ndim(x)
```

reorient_vector

*Change Orientation of An Oriented Vector and Make it a Broadcaster***Description**

The `lhs %orientbc<-% rhs` operator takes an oriented vector (`lhs`), and changes its orientation. It also makes `lhs` a broadcaster if it wasn't already.

The modification is done directly on `lhs` itself, using R's native semantics.

Usage

```
lhs %orientbc<-% rhs
```

Arguments

<code>lhs</code>	an atomic or recursive oriented vector.
<code>rhs</code>	an integer vector. The first value must be the new orientation, referred to as <code>orient</code> . The second value, optional, must be the number of dimensions, referred to as <code>ndim</code> . If no second value is given, it will be set at <code>max(ndim(lhs), rhs[1])</code> .

Details

In the context of broadcasting, an oriented vector `x` is a vector or array that satisfies the following conditions:

- It has `length > 1` and `<= (2^31 - 1)`;
- It has no dimensions, or one dimension is `length(x)` and all other dimensions are 1.

The orientation of an oriented vector is the index of the dimension with `size > 1`.

For example, if array `lhs` has dimensions `c(1, 10, 1)`, its orientation is 2L, since the second dimension has `size > 1`.

A vector with no dimensions has orientation 1L.

In the context of broadcasted operations, oriented vectors can be used to modify an array along

a dimension.
The examples section gives several examples of this.

Value

Nothing, but changes lhs directly.

See Also

[broadcast_casting](#)

Examples

```
# basic usage ====
x <- setNames(1:10, letters[1:10])
print(x)

x %orientbc<-% 2L
print(x)
x %orientbc<-% 3L
print(x)
x %orientbc<-% 1:2
print(x)
x %orientbc<-% c(1, 3)
print(x)

# modify an array along one specific dimension ====
x <- array(sample(0:9), c(3,3,3))
print(x)

# add 10 to second column, and 100 to third column:
v <- vector2array(c(0, 10, 100), 2, 2, TRUE)
x + v

# add 10 to second row, and 100 to third row:
v %orientbc<-% 1L
x + v

# add 10 to second layer, and 100 to third layer:
v %orientbc<-% 3L
x + v
```

`rep_dim`*Replicate Array Dimensions*

Description

The `rep_dim()` function replicates array dimensions until the specified dimension sizes are reached, and returns the array.

The various broadcasting functions recycle array dimensions virtually, meaning little to no additional memory is needed.

The `rep_dim()` function, however, physically replicates the dimensions of an array (and thus actually occupies additional memory space).

Usage

```
rep_dim(x, tdim)
```

Arguments

<code>x</code>	an atomic or recursive array or matrix.
<code>tdim</code>	an integer vector, giving the target dimension to reach.

Value

Returns the replicated array.

Examples

```
x <- matrix(1:9, 3,3)
colnames(x) <- LETTERS[1:3]
rownames(x) <- letters[1:3]
names(x) <- month.abb[1:9]
print(x)

rep_dim(x, c(3,3,2)) # replicate to larger size
```

Description

Type casting usually strips away attributes of objects.

The functions provided here preserve `dim`, `dimnames`, `names`, `comment`, and [broadcaster](#) attributes, which may be more convenient for arrays and array-like objects.

The functions are as follows:

- `as_lgl()`: converts object to atomic type logical (TRUE, FALSE, NA).
- `as_int()`: converts object to atomic type integer.
- `as_dbl()`: converts object to atomic type double (AKA numeric).
- `as_cplx()`: converts object to atomic type complex.
- `as_chr()`: converts object to atomic type character.
- `as_raw()`: converts object to atomic type raw.
- `as_list()`: converts object to recursive type list.

`as_num()` is an alias for `as_dbl()`.

`as_str()` is an alias for `as_chr()`.

`as_bool()` is an alias for `as_lgl()`.

See also [typeof](#).

Usage

```
as_lgl(x, ...)
```

```
as_bool(x, ...)
```

```
as_int(x, ...)
```

```
as_dbl(x, ...)
```

```
as_num(x, ...)
```

```
as_chr(x, ...)
```

```
as_str(x, ...)
```

```
as_cplx(x, ...)
```

```
as_raw(x, ...)
```

```
as_list(x, ...)
```

Arguments

`x` an R object.

`...` further arguments passed to or from other methods.

Value

The converted object.

Examples

```
# matrix example ====
x <- matrix(sample(-1:28), ncol = 5)
colnames(x) <- month.name[1:5]
rownames(x) <- month.abb[1:6]
names(x) <- c(letters[1:20], LETTERS[1:10])
print(x)

as_lgl(x)
as_int(x)
as_dbl(x)
as_chr(x)
as_cplx(x)
as_raw(x)

#####

# factor example ====
x <- factor(month.abb, levels = month.abb)
names(x) <- month.name
print(x)

as_lgl(as_int(x) > 6)
as_int(x)
as_dbl(x)
as_chr(x)
as_cplx(x)
as_raw(x)
```

vector2array

Turn Vector to Array and Vice-Versa

Description

vector2array() turns a vector into an array, with a specific vector orientation, and turning the names into dimnames, and keeping (or forcing) **broadcaster** attribute.

undim() returns a copy of an object, but with its dimensions removed, but still trying to keep the names if possible (it somewhat is like the dimensional version of unlist()).

undim() will also keep (or force) the **broadcaster** attribute

array2vector() is an alias for undim().

Usage

```
vector2array(x, orient, ndim = orient, broadcaster = NULL)
```

```
undim(x, broadcaster = NULL)
```

```
array2vector(x, broadcaster = NULL)
```

Arguments

- | | |
|-------------|---|
| x | an vector (for vector2array()) or an array (for undim()/array2vector()).
All atomic types, and the recursive type list, are supported. |
| orient | a positive integer scalar, giving the orientation of the vector.
In other words: give here which dimension should have size length(x) - all other dimensions will have size 1. |
| ndim | the number of dimensions in total.
It must be the case that ndim >= orient, and ndim <= 16L. |
| broadcaster | TRUE or FALSE, indicating if the result should be a broadcaster.
If NULL, broadcaster(x) will be used. |

Value

For vector2array():

If x is already an array, x is returned unchanged.

Otherwise, given out <- vector2array(x, orient, ndim), out will be an array with the following properties:

- ndim(out) == ndim;
- dim(out)[orient] == length(x), and all other dimensions will be 1;

- `dimnames(out)[[orient]] == names(x)`, and all other `dimnames` will be `NULL`.

For `undim()`:

If `x` is not an array, `x` is returned unchanged.

Otherwise, a copy of the original object, but without dimensions, but keeping names and **broadcaster** attribute as far as possible.

Examples

```
x <- setNames(1:27, c(letters, NA))
print(x)
y <- vector2array(x, 1L, 3L)
print(y)

undim(y)
```

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