Package 'broadcast'

February 8, 2025

Title Simple Broadcasted and Type-
Consistent Operations for Atomic and Recursive Arrays with Minimal Dependencies

Version 0.0.0.9

Description Implements simple broadcasted binding and binary operations,
for atomic and recursive arrays.
Besides linking to 'Rcpp',
'broadcast' does not depend on, vendor, link to, include, or otherwise use any external libraries;
'broadcast' was essentially made from scratch and can be installed out-of-the-box.
The broadcasted implementations include, but are not limited to, the following.
  1) A more efficient and broadcasted version of `abind()`, for binding arrays along an arbitrary dimension;
  2) Relational operations (like `==`, `!=`, `<`, `>`, `<=`, `>=`; can also take into account Machine precision);
  3) Arithmetic operations (like `+`, `-`, `*`, `/`, `^`, `pmin()`, `pmax()`, integer modulo);
  4) Boolean combiner operations (like `&`, `|`, `xor()`, ``nand");
  5) String distance, (in)equality, and concatenation operations;
  6) A Broadcasted implementation of `ifelse()`;
  7) A Broadcasted apply-like function;
The broadcasted implementations strive to minimize computation time and memory usage
(which is not just good for computer efficiency, but also for the environment).

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Encoding UTF-8

LinkingTo Rcpp

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.1

Depends R (>= 4.2.0)

Imports Rcpp (>= 1.0.11),
data.table

Suggests tinytest, roxygen2, altdoc, kableExtra

Contents

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Description

broadcast:
Simple Broadcasted Binding and Binary Operations for Atomic and Recursive Arrays with Minimal Dependencies.

Implements simple broadcasted binding and binary operations, for atomic and recursive arrays.

Besides linking to 'Rcpp', 'broadcast' does not depend on, vendor, link to, include, or otherwise use any external libraries; 'broadcast' was essentially made from scratch and can be installed out-of-the-box.

The broadcasted implementations include, but are not limited to, the following:

1. A more efficient and broadcasted version of abind(), for binding arrays along an arbitrary dimension;

2. Relational operations (like ==, !=, <, >, <=, >=; can also take into account Machine precision);

3. Arithmetic operations (like +, -, *, /, ^, pmin(), pmax(), integer modulo);

4. Boolean combiner operations (like &, |, xor(), "nand");

5. String distance, (in)equality, and concatenation operations;

6. A Broadcasted implementation of ifelse();

7. A Broadcasted apply-like function; The broadcasted implementations strive to minimize computation time and memory usage (which is not just good for computer efficiency, but also for the environment).

Getting Started

An introduction and overview of the package can be found on the website.

Methods and Functions

Type Specific Binary Operations

'broadcast' provides a set of functions for type-specific binary operations for broadcasted operations.

These functions use an API similar to the outer and sweep functions.

The following functions for type-specific binary operations are available:

- bc.d: numeric arithmetic and relational operations;

- bc.b: Boolean combiner operations;

- bc.cplx: complex arithmetic and equality operations;

- bc.str: string equality, concatenation, and distance operations;

- bc.list: apply any 'R' function to 2 recursive arrays with broadcasting.

General functions

'broadcast' also comes with 2 general broadcasted functions:

- bc_ifelse: Broadcasted version of ifelse.

- bcapply: Broadcasted apply-like function.

Binding Implementations

'broadcast' provides 3 binding implementations:
bind_mat, bind_array, and bind_dt.

Other functions

'broadcast' also provides type-casting functions, which preserve names and dimensions - convenient for arrays.

Author(s)

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References

The badges shown in the documentation of this R-package were made using the services of: https://shields.io/

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array_recycle   *Recycle Array Dimensions*

Description

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

The various broadcasting functions "recycle" an array virtually, meaning little to no additional memory is needed.
The `array_recycle()` function, however, physically recycles an array (and thus actually occupies memory space).

Usage

```
array_recycle(x, tdim)
```

Arguments

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

Value

Returns the recycled 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)

array_recycle(x, c(3,3,2)) # recycle to larger size
```

---

bc.b   *Broadcasted Boolean Operations*

Description

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

Usage

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

Arguments

x, y	conformable logical or numeric arrays.
op	a single string, giving the operator.
	Supported Boolean combiner operators: &, |, xor, nand.
	Supported relational operators: ==, !=, <, >, <=, >=.

Value

For the boolean combiner operators:
A logical array as a result of the broadcasted arithmetic operation.

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

Examples

```
x.dim <- c(10:8)
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(10,1,1))

bc.b(x, y, "&")
bc.b(x, y, "|")
bc.b(x, y, "xor")
bc.b(x, y, "nand")

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

---

bc.cplx	*Broadcasted Operations for Complex Number Arrays*

Description

The bc.cplx() function performs broadcasted operations on 2 complex arrays.

Note that bc.cplx() uses more strict NA checks than base 'R':
If for an element of either x or y, either the real or imaginary part is NA or NaN, than the result of the operation for that element is necessarily NA.

Usage

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

Arguments

x, y   conformable atomic arrays of typee `complex`.

op   a single string, giving the operator.
Supported arithmetic operators: +, -, *, /.
Supported relational operators: ==, !=.

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.

Examples

```
x.dim <- c(10:8)
x.len <- prod(x.dim)
gen <- function() sample(c(rnorm(10), NA, NA, NaN, NaN, Inf, Inf, -Inf, -Inf))
x <- array(gen() + gen() * -1i, x.dim)
y <- array(gen() + gen() * -1i, c(10,1,1))

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 <- gen() + gen() * -1i
y <- gen() + gen() * -1i
out <- bc.cplx(array(x), array(y), "*")
cbind(x, y, x*y, out)
```

---

bc.d   *Broadcasted Decimal Numeric Operations*

Description

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

Usage

```
bc.d(x, y, op, prec = sqrt(.Machine$double.eps))
```

Arguments

x, y	conformable logical or numeric arrays.
op	a single string, giving the operator. Supported arithmetic operators: +, -, *, /, ^, pmin, pmax. Supported relational operators: ==, !=, <, >, <=, >=, d==, d!=, d<, d>, d<=, d>=.
prec	a single number between 0 and 0.1, giving the machine precision to use. 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.

Examples

```
x.dim <- c(10:8)
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(10,1,1))

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   *Broadcasted Integer Numeric Operations*

Description

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

Usage

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

Arguments

x, y	conformable logical or numeric arrays.
op	a single string, giving the operator. Supported arithmetic operators: +, -, *, /, ^, pmin, pmax. Supported relational operators: ==, !=, <, >, <=, >=.

Value

For arithmetic operators:
A numeric array of whole numbers, as a result of the broadcasted arithmetic operation.
Base 'R' supports 53 bit integers, which thus range from approximately `-9` quadrillion to `+9` quadrillion.
Values outside of this range will be returned as `-Inf` or `Inf`.

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

Examples

```
x.dim <- c(10:8)
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(10,1,1))

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

---

bc.list   *Broadcasted Operations for Recursive Arrays*

Description

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

Usage

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

Arguments

x, y	conformable Recursive arrays (i.e. arrays of type `list`).
f	a function that takes in exactly **2** arguments, and **returns** a result that can be stored in a single element of a list.

Value

A recursive array.

Examples

```
x.dim <- c(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)c(length(x) == length(y), typeof(x) == typeof(y))
)
```

---

bc.str	*Broadcasted Operations for Character/String Arrays*

Description

The `bc.str()` function performs broadcasted operations on 2 character/string arrays.
`bc.chr()` is an alias for `bc.str()`.

Usage

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

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

Arguments

x, y	conformable atomic arrays of typee `character`.
op	a single string, giving the operator. Supported concatenation operators: +. Supported relational operators: ==, !=. Supported distance operators: levenshtein.

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 relational comparison.

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 distance (Levenshtein):
x <- array(month.name, c(12, 1))
y <- array(month.abb, c(1, 12))
out <- bc.str(x, y, "levenshtein")
dimnames(out) <- list(month.name, month.abb)
print(out)
```

---

bcapply   *Apply a Function to 2 Broadcasted Arrays*

Description

The bcapply() function applies a function to 2 arrays with broadcasting.

Usage

```
bcapply(x, y, f, v = "list")
```

Arguments

x, y   conformable atomic or recursive 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.

v   a single string, giving the scalar type for a single iteration.
                     If `NULL` or `"list"` (default), the result will be a recursive array.
                     If it is certain that, for every iteration, `f()` always results in a **single atomic**
                     scalar, 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.

Value

An atomic or recursive array with dimensions `bc_dim(x, y)`.

Examples

```
x.dim <- c(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))

f <- function(x, y) list(x, y)
bcapply(x, y, f)
```

---

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 array or matrix.

Value

Returns the recycled array.

Examples

```
x.dim <- c(10:8)
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(10,1,1))

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() S4 generic method performs a broadcasted form of ifelse.

Usage

```
bc_ifelse(cond, yes, no)
```

Arguments

cond	logical vector or array with the length equal to prod(bc_dim(yes, no)).
yes, no	conformable arrays of the same type. All atomic types (see atomic) are supported. Recursive arrays of type list are also supported. since bc_ifelse() is an S4 generic, it can be extended to support special array classes.

Value

The ouput, here referred to as out, will be an array of the same type as yes and no.
After broadcasting yes against no, given any element index i, the following will hold for the output:

- when cond[i] == TRUE, out[i] is yes[i];

- when cond[i] == FALSE, out[i] is no[i];

- when cond[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(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))

cond <- bc.list(
  x, y,
  \(x, y)c(length(x) == length(y) && typeof(x) == typeof(y))
) |> as_bool()

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

---

bind   *Dimensional Binding of Objects*

Description

The `bind_`implementations provide dimensional binding functionalities.

The following implementations are available:

- `bind_mat()` binds dimensionless (atomic/recursive) vectors and (atomic/recursive) matrices row- or column-wise.
  Allows for recycling.
- `bind_array()` binds (atomic/recursive) arrays and (atomic/recursive) matrices.
  Allows for broadcasting.
- `bind_dt()` binds data.tables and other data.frame-like objects.
  This function is only available if the 'data.table' package is installed.
  Returns a `data.table`.
  Faster than `do.call(cbind, ...)` or `do.call(rbind, ...)` for regular `data.frame` objects.

Note that the naming convention of the binding implementations here is "bind_" followed by the **resulting class** (abbreviated).
I.e. `bind_mat` **returns** a matrix, but can bind both matrices and vectors.
And `bind_array` **returns** an array, but can bind both arrays and matrices.
And `bind_dt` **returns** a data.table, but can bind not only data.tables, but also most other data.frame-like objects.

Usage

```
bind_mat(input, along, name_deparse = TRUE, comnames_from = 1L)

bind_array(
  input,
  along,
```

```
    revalong,
    max_bc = 1L,
    name_along = TRUE,
    comnames_from = 1L
)

bind_dt(input, along, ...)
```

Arguments

input	a list of only the appropriate objects. If input is named, its names will be used for the names of dimension along of the output, as far as possible.
along	a single integer, indicating the dimension along which to bind the dimensions. I.e. use along = 1 for row-binding, along = 2 for column-binding, etc. For arrays, additional flexibility is available:

  - Specifying along = 0 will bind the arrays on a new dimension before the first, making along the new first dimension.
  - Specifying along = N + 1, with N = max(lst.ndim(input)), will create an additional dimension (N + 1) and bind the arrays along that new dimension.

name_deparse	Boolean, for bind_mat(). Indicates if dimension along should be named. Uses the naming method from rbind/cbind itself.
comnames_from	either integer scalar or NULL, for bind_mat() and bind_array(). 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 comnames_from = 10 will then result in bind_array() using rownames(input[[10]]) for the rownames of the output.
revalong	for bind_array() only. Same as along, but counting backwards. I.e. revalong = 0 is equivalent to along = N+1, and revalong = N+1 is equivalent to along = 0; with N = max(lst.ndim(input)).
max_bc	integer, for bind_array only. Specify here the number of dimensions that are allowed to be broadcasted when binding arrays. If max_bc = 0L, **no** broadcasting will be allowed at all.
name_along	Boolean, for bind_array(). Indicates if dimension along should be named.
...	arguments to be passed to rbindlist.

Value

The bound object.

Empty inputs

If argument `input` has length `0`, or it contains exclusively objects where one or more dimensions are `0`, an error is returned.

If `input` has length 1, these functions simply return `input[[1L]]`.

Additional details for `bind_array()` **and** `bind_mat()`

Differences with `abind()`, `rbind()`/`cbind()`

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 the following ways:

- `bind_array()` differs from `abind::`abind in that it can handle recursive arrays properly (the `abind::`abind function would unlist everything to atomic arrays, ruining the structure).

- `bind_array()` allows for broadcasting, while `abind::`abind does not support broadcasting.

- `bind_array()` is generally faster than `abind::`abind, as `bind_array()` relies heavily on 'C' and 'C++' code.

- 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.

- `bind_array()` has more streamlined naming options, compared to `abind::`abind.

`bind_mat()` is a modified version of rbind/cbind.
`bind_mat()` differs from rbind/cbind in the following ways:

- it has more streamlined naming options/

- `bind_mat()` gives an error when fractional recycling is attempted (like binding `1:3` with `1:10`).

- `bind` The primary differences is that

Naming

...

References

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

Examples

```
# bind_array ====

# 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))
)
x <- matrix(x, 4, 3, byrow = TRUE)
dimnames(x) <- list(letters[1:4], LETTERS[1:3])
print(x)

y <- matrix(1:12, 4, 3)
print(y)

# binding the arrays
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
bind_array(input, along = 2L)
bind_array(input, along = 3L) # bind on new dimension after last


# binding, wwith 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


###############################################################################

# bind_mat ====

# here, atomic and recursive matrices are mixed,
# resulting in a recursive matrix

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))
)
x <- matrix(x, 4, 3, byrow = TRUE)
dimnames(x) <- list(letters[1:4], LETTERS[1:3])
print(x)

y <- matrix(1:12, 4, 3)
print(y)
```

```
bind_mat(list(x = x, y = y), 2L)



##############################################################################

# bind_dt ====


x <- data.frame(a = 1:12, b = month.abb) # data.frame
y <- data.table::data.table(a = 1:12, b = month.abb) # data.table

bind_dt(list(x = x, y = y), 2L) # column bind

bind_dt(list(x = x, y = y), 1L) # row bind
```

---

properties	*Small property functions*

Description

ndim() returns the number of dimensions of an object.
lst.ndim() returns the number of dimensions of every list-element.
lst.typeof() returns the (internal) type of every list-element.
len() is an alias for length.
lst.len() is an alias for lengths.

These functions were all designed to be efficient.

Usage

```
ndim(x)

lst.ndim(x)

lst.typeof(x)
```

Arguments

x   an object.
               For functions starting with lst., x must be a list (i.e. recursive vector or recur-
               sive array).

Value

An integer scalar

Examples

```
# bind_array ====

# 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))
)
x <- matrix(x, 4, 3, byrow = TRUE)
dimnames(x) <- list(letters[1:4], LETTERS[1:3])
print(x)

y <- matrix(1:12, 4, 3)
print(y)

# binding the arrays
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
bind_array(input, along = 2L)
bind_array(input, along = 3L) # bind on new dimension after last


# binding, wwith 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



################################################################################

# bind_mat ====

# here, atomic and recursive matrices are mixed,
# resulting in a recursive matrix

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))
)
x <- matrix(x, 4, 3, byrow = TRUE)
dimnames(x) <- list(letters[1:4], LETTERS[1:3])
print(x)

y <- matrix(1:12, 4, 3)
print(y)
```

```
bind_mat(list(x = x, y = y), 2L)


############################################################################

# bind_dt ====


x <- data.frame(a = 1:12, b = month.abb) # data.frame
y <- data.table::data.table(a = 1:12, b = month.abb) # data.table

bind_dt(list(x = x, y = y), 2L) # column bind

bind_dt(list(x = x, y = y), 1L) # row bind
```

---

typecast   *Atomic and List Type Casting With Names and Dimensions Preserved*

Description

Type casting usually strips away attributes of objects.
The functions provided here preserve dimensions, dimnames, and names, which may be more convenient for arrays and array-like objects.

The functions are as follows:

- `as_bool()`: 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_chr()`: converts object to atomic type `character`.
- `as_cplx()`: converts object to atomic type `complex`.
- `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()`.

See also typeof.

Usage

```
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_bool(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_bool(as_int(x) > 6)
as_int(x)
as_dbl(x)
as_chr(x)
as_cplx(x)
```

```
as_raw(x)
```

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