Package ‘plyr’

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**Title**  Tools for Splitting, Applying and Combining Data

**Version**  1.8.6

**Description**  A set of tools that solves a common set of problems: you need to break a big problem down into manageable pieces, operate on each piece and then put all the pieces back together. For example, you might want to fit a model to each spatial location or time point in your study, summarise data by panels or collapse high-dimensional arrays to simpler summary statistics. The development of `plyr` has been generously supported by 'Becton Dickinson'.

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Quote variables to create a list of unevaluated expressions for later evaluation.

Description

This function is similar to ~ in that it is used to capture the name of variables, not their current value. This is used throughout plyr to specify the names of variables (or more complicated expressions).

Usage

`.(..., .env = parent.frame())`

Arguments

... unevaluated expressions to be recorded. Specify names if you want the set the names of the resultant variables

.env environment in which unbound symbols in ... should be evaluated. Defaults to the environment in which . was executed.

Details

Similar tricks can be performed with substitute, but when functions can be called in multiple ways it becomes increasingly tricky to ensure that the values are extracted from the correct frame. Substitute tricks also make it difficult to program against the functions that use them, while the quoted class provides as.quoted.character to convert strings to the appropriate data structure.

Value

list of symbol and language primitives
Examples

(a, b, c)
(first = a, second = b, third = c)
(a ^ 2, b - d, log(c))
as.quoted(~ a + b + c)
as.quoted(a - b + c)
as.quoted(c("a", "b", "c"))

# Some examples using ddply - look at the column names
ddply(mtcars, "cyl", each(nrow, ncol))
ddply(mtcars, ~ cyl, each(nrow, ncol))
ddply(mtcars, .(cyl), each(nrow, ncol))
ddply(mtcars, .(log(cyl)), each(nrow, ncol))
ddply(mtcars, .(logcyl = log(cyl)), each(nrow, ncol))
ddply(mtcars, .(vs + am), each(nrow, ncol))
ddply(mtcars, .(vsam = vs + am), each(nrow, ncol))

aaply

Split array, apply function, and return results in an array.

Description

For each slice of an array, apply function, keeping results as an array.

Usage

aaply(
  .data,
  .margins,
  .fun = NULL,
  ..., 
  .expand = TRUE,
  .progress = "none",
  .inform = FALSE,
  .drop = TRUE,
  .parallel = FALSE,
  .paropts = NULL
)

Arguments

.data matrix, array or data frame to be processed
.margins a vector giving the subscripts to split up .data by. 1 splits up by rows, 2 by columns and c(1,2) by rows and columns, and so on for higher dimensions
.fun function to apply to each piece
... other arguments passed on to .fun
.expand if .data is a data frame, should output be 1d (expand = FALSE), with an element for each row; or nd (expand = TRUE), with a dimension for each variable.

.progress name of the progress bar to use, see create_progress_bar

.inform produce informative error messages? This is turned off by default because it substantially slows processing speed, but is very useful for debugging

.drop should extra dimensions of length 1 in the output be dropped, simplifying the output. Defaults to TRUE

.parallel if TRUE, apply function in parallel, using parallel backend provided by foreach

.paropts a list of additional options passed into the foreach function when parallel computation is enabled. This is important if (for example) your code relies on external data or packages: use the .export and .packages arguments to supply them so that all cluster nodes have the correct environment set up for computing.

Details

This function is very similar to apply, except that it will always return an array, and when the function returns >1 d data structures, those dimensions are added on to the highest dimensions, rather than the lowest dimensions. This makes aaply idempotent, so that aaply(input, X, identity) is equivalent to aperm(input, X).

Value

if results are atomic with same type and dimensionality, a vector, matrix or array; otherwise, a list-array (a list with dimensions)

Warning

Passing a data frame as first argument may lead to unexpected results, see https://github.com/hadley/plyr/issues/212.

Input

This function splits matrices, arrays and data frames by dimensions

Output

If there are no results, then this function will return a vector of length 0 (vector()).

References


See Also

Other array input: a_ply(), adply(), alply()
Other array output: daply(), laply(), maply()
Examples

```r
dim(ozone)
adply(ozone, 1, mean)
adply(ozone, 1, mean, .drop = FALSE)
adply(ozone, 3, mean)
adply(ozone, c(1,2), mean)

dim(adply(ozone, c(1,2), mean))
dim(adply(ozone, c(1,2), mean, .drop = FALSE))

adply(ozone, 1, each(min, max))
adply(ozone, 3, each(min, max))

standardise <- function(x) (x - min(x)) / (max(x) - min(x))
adply(ozone, 3, standardise)
adply(ozone, 1:2, standardise)

adply(ozone, 1:2, diff)
```

---

**adply**

Split array, apply function, and return results in a data frame.

Description

For each slice of an array, apply function then combine results into a data frame.

Usage

```r
adply(
  .data, .margins, .fun = NULL, ..., .expand = TRUE, .progress = "none", .inform = FALSE, .parallel = FALSE, .paropts = NULL, .id = NA
)
```

Arguments

- `.data` matrix, array or data frame to be processed
- `.margins` a vector giving the subscripts to split up data by. 1 splits up by rows, 2 by columns and c(1,2) by rows and columns, and so on for higher dimensions
- `.fun` function to apply to each piece
... other arguments passed on to .fun

.expand if .data is a data frame, should output be 1d (expand = FALSE), with an element for each row; or nd (expand = TRUE), with a dimension for each variable.

.progress name of the progress bar to use, see create_progress_bar

.inform produce informative error messages? This is turned off by default because it substantially slows processing speed, but is very useful for debugging

.parallel if TRUE, apply function in parallel, using parallel backend provided by foreach

.paropts a list of additional options passed into the foreach function when parallel computation is enabled. This is important if (for example) your code relies on external data or packages: use the .export and .packages arguments to supply them so that all cluster nodes have the correct environment set up for computing.

.id name(s) of the index column(s). Pass NULL to avoid creation of the index column(s). Omit or pass NA to use the default names "X1", "X2", .... Otherwise, this argument must have the same length as .margins.

Value

A data frame, as described in the output section.

Input

This function splits matrices, arrays and data frames by dimensions

Output

The most unambiguous behaviour is achieved when .fun returns a data frame - in that case pieces will be combined with rbind.fill. If .fun returns an atomic vector of fixed length, it will be rbinded together and converted to a data frame. Any other values will result in an error.

If there are no results, then this function will return a data frame with zero rows and columns (data.frame()).

References


See Also

Other array input: a_ply(), aaply(), alply()

Other data frame output: dply(), ldply(), mdply()
alply

Split array, apply function, and return results in a list.

Description

For each slice of an array, apply function then combine results into a list.

Usage

```r
alply(
  .data,
  .margins,
  .fun = NULL,
  ..., 
  .expand = TRUE,
  .progress = "none",
  .inform = FALSE,
  .parallel = FALSE,
  .paropts = NULL,
  .dims = FALSE
)
```

Arguments

- `.data` : matrix, array or data frame to be processed
- `.margins` : a vector giving the subscripts to split up data by. 1 splits up by rows, 2 by columns and c(1,2) by rows and columns, and so on for higher dimensions
- `.fun` : function to apply to each piece
- `...` : other arguments passed on to `.fun`
- `.expand` : if `.data` is a data frame, should output be 1d (expand = FALSE), with an element for each row; or nd (expand = TRUE), with a dimension for each variable.
- `.progress` : name of the progress bar to use, see `create_progress_bar`
- `.inform` : produce informative error messages? This is turned off by default because it substantially slows processing speed, but is very useful for debugging
- `.parallel` : if TRUE, apply function in parallel, using parallel backend provided by foreach
- `.paropts` : a list of additional options passed into the foreach function when parallel computation is enabled. This is important if (for example) your code relies on external data or packages: use the .export and .packages arguments to supply them so that all cluster nodes have the correct environment set up for computing.
- `.dims` : if TRUE, copy over dimensions and names from input.

Details

The list will have "dims" and "dimnames" corresponding to the margins given. For instance `alply(x, c(3, 2), ...)` where `x` has dims `c(4, 3, 2)` will give a result with dims `c(2, 3)`. `alply` is somewhat similar to `apply` for cases where the results are not atomic.
assemble

**Value**
- list of results

**Input**
- This function splits matrices, arrays and data frames by dimensions

**Output**
- If there are no results, then this function will return a list of length 0 (list()).

**References**

**See Also**
- Other array input: `a_ply()`, `aaply()`, `adply()`
- Other list output: `dlply()`, `llply()`, `mlply()`

**Examples**
```
alply(ozone, 3, quantile)
alply(ozone, 3, function(x) table(round(x)))
```

---

**arrange**  
Order a data frame by its columns.

**Description**
- This function completes the subsetting, transforming and ordering triad with a function that works in a similar way to `subset` and `transform` but for reordering a data frame by its columns. This saves a lot of typing!

**Usage**
```
arrange(df, ...)
```

**Arguments**
- `df` : data frame to reorder
- `...` : expressions evaluated in the context of `df` and then fed to `order`

**See Also**
- `order` for sorting function in the base package
Examples

# sort mtcars data by cylinder and displacement
mtcars[with(mtcars, order(cyl, disp)), ]
# Same result using arrange: no need to use with(), as the context is implicit
# NOTE: plyr functions do NOT preserve row.names
arrange(mtcars, cyl, disp)
# Let's keep the row.names in this example
myCars = cbind(vehicle=row.names(mtcars), mtcars)
arrange(myCars, cyl, disp)
# Sort with displacement in descending order
arrange(myCars, cyl, desc(disp))

as.data.frame.function

Make a function return a data frame.

Description

Create a new function that returns the existing function wrapped in a data.frame with a single column, value.

Usage

```r
## S3 method for class 'function'
as.data.frame(x, row.names, optional, ...)
```

Arguments

- `x` function to make return a data frame
- `row.names` necessary to match the generic, but not used
- `optional` necessary to match the generic, but not used
- `...` necessary to match the generic, but not used

Details

This is useful when calling *dply* functions with a function that returns a vector, and you want the output in rows, rather than columns. The value column is always created, even for empty inputs.
as.quoted

Convert input to quoted variables.

Description

Convert characters, formulas and calls to quoted .variables

Usage

as.quoted(x, env = parent.frame())

Arguments

x input to quote
env environment in which unbound symbols in expression should be evaluated. De-
faults to the environment in which as.quoted was executed.

Details

This method is called by default on all plyr functions that take a .variables argument, so that
equivalent forms can be used anywhere.

Currently conversions exist for character vectors, formulas and call objects.

Value

a list of quoted variables

See Also

.

Examples

as.quoted(c("a", "b", "log(d)"))
as.quoted(a - b + log(d))
a_ply

*Split array, apply function, and discard results.*

**Description**

For each slice of an array, apply function and discard results

**Usage**

```
a_ply(
  .data,
  .margins,
  .fun = NULL,
  ..., 
  .expand = TRUE,
  .progress = "none",
  .inform = FALSE,
  .print = FALSE,
  .parallel = FALSE,
  .paropts = NULL
)
```

**Arguments**

- `.data`: matrix, array or data frame to be processed
- `.margins`: a vector giving the subscripts to split up data by. 1 splits up by rows, 2 by columns and c(1,2) by rows and columns, and so on for higher dimensions
- `.fun`: function to apply to each piece
- `...`: other arguments passed on to `.fun`
- `.expand`: if `.data` is a data frame, should output be 1d (expand = FALSE), with an element for each row; or nd (expand = TRUE), with a dimension for each variable.
- `.progress`: name of the progress bar to use, see `create_progress_bar`
- `.inform`: produce informative error messages? This is turned off by default because it substantially slows processing speed, but is very useful for debugging
- `.print`: automatically print each result? (default: FALSE)
- `.parallel`: if TRUE, apply function in parallel, using parallel backend provided by foreach
- `.paropts`: a list of additional options passed into the `foreach` function when parallel computation is enabled. This is important if (for example) your code relies on external data or packages: use the `.export` and `.packages` arguments to supply them so that all cluster nodes have the correct environment set up for computing.

**Value**

Nothing
### Input
This function splits matrices, arrays and data frames by dimensions

### Output
All output is discarded. This is useful for functions that you are calling purely for their side effects like displaying plots or saving output.

### References

### See Also
Other array input: `aaply()`, `adply()`, `alply()`  
Other no output: `d_ply()`, `l_ply()`, `m_ply()`

---

**baseball**  
Yearly batting records for all major league baseball players

### Description
This data frame contains batting statistics for a subset of players collected from [http://www.baseball-databank.org/](http://www.baseball-databank.org/). There are a total of 21,699 records, covering 1,228 players from 1871 to 2007. Only players with more 15 seasons of play are included.

### Usage
```r
baseball
```

### Format
A 21699 x 22 data frame

### Variables
Variables:
- id, unique player id
- year, year of data
- stint
- team, team played for
- lg, league
- g, number of games
- ab, number of times at bat
• r, number of runs
• h, hits, times reached base because of a batted, fair ball without error by the defense
• X2b, hits on which the batter reached second base safely
• X3b, hits on which the batter reached third base safely
• hr, number of home runs
• rbi, runs batted in
• sb, stolen bases
• cs, caught stealing
• bb, base on balls (walk)
• so, strike outs
• ibb, intentional base on balls
• hbp, hits by pitch
• sh, sacrifice hits
• sf, sacrifice flies
• gidp, ground into double play

References

http://www.baseball-databank.org/

Examples

baberuth <- subset(baseball, id == "ruthba01")
baberuth$cyear <- baberuth$year - min(baberuth$year) + 1
calculate_cyear <- function(df) {
  mutate(df,
    cyear = year - min(year),
    cpercent = cyear / (max(year) - min(year))
  )
}
baseball <- ddply(baseball, .(id), calculate_cyear)
baseball <- subset(baseball, ab >= 25)

model <- function(df) {
  lm(rbi / ab ~ cyear, data=df)
}
model(baberuth)
models <- dplyr(baseball, .(id), model)
**colwise**

*Column-wise function.*

**Description**

Turn a function that operates on a vector into a function that operates column-wise on a data.frame.

**Usage**

```r
colwise(.fun, .cols = true, ...)  
catcolwise(.fun, ...)  
umcolwise(.fun, ...)
```

**Arguments**

- `.fun` function
- `.cols` either a function that tests columns for inclusion, or a quoted object giving which columns to process
- `...` other arguments passed on to `.fun`

**Details**

catcolwise and numcolwise provide version that only operate on discrete and numeric variables respectively.

**Examples**

```r
# Count number of missing values  
nmissing <- function(x) sum(is.na(x))

# Apply to every column in a data frame  
colwise(nmissing)(baseball)  
# This syntax looks a little different. It is shorthand for the  
# the following:  
f <- colwise(nmissing)  
f(baseball)  

# This is particularly useful in conjunction with dply  
ddply(baseball, .(year), colwise(nmissing))  

# To operate only on specified columns, supply them as the second  
# argument. Many different forms are accepted.  
ddply(baseball, .(year), colwise(nmissing, .(sb, cs, so)))  
ddply(baseball, .(year), colwise(nmissing, c("sb", "cs", "so")))  
ddply(baseball, .(year), colwise(nmissing, ~ sb + cs + so))
```
# Alternatively, you can specify a boolean function that determines
# whether or not a column should be included
ddply(baseball, .(year), colwise(nmissing, is.character))
ddply(baseball, .(year), colwise(nmissing, is.numeric))
ddply(baseball, .(year), colwise(nmissing, is.discrete))

# These last two cases are particularly common, so some shortcuts are
# provided:
ddply(baseball, .(year), numcolwise(nmissing))
ddply(baseball, .(year), catcolwise(nmissing))

# You can supply additional arguments to either colwise, or the function
# it generates:
numcolwise(mean)(baseball, na.rm = TRUE)
numcolwise(mean, na.rm = TRUE)(baseball)

---

**count**  

*Count the number of occurrences.*

**Description**

Equivalent to `as.data.frame(table(x))`, but does not include combinations with zero counts.

**Usage**

```r
count(df, vars = NULL, wt_var = NULL)
```

**Arguments**

- `df`  
  data frame to be processed
- `vars`  
  variables to count unique values of
- `wt_var`  
  optional variable to weight by - if this is non-NULL, count will sum up the value of this variable for each combination of id variables.

**Details**

Speed-wise count is competitive with `table` for single variables, but it really comes into its own when summarising multiple dimensions because it only counts combinations that actually occur in the data.

Compared to `table + as.data.frame`, count also preserves the type of the identifier variables, instead of converting them to characters/factors.

**Value**

a data frame with label and freq columns

**See Also**

`table` for related functionality in the base package
### Examples

# Count of each value of "id" in the first 100 cases
count(baseball[1:100,], vars = "id")
# Count of ids, weighted by their "g" loading
count(baseball[1:100,], vars = "id", wt_var = "g")
count(baseball, "id", "ab")
count(baseball, "lg")
# How many stints do players do?
count(baseball, "stint")
# Count of times each player appeared in each of the years they played
count(baseball[1:100,], c("id", "year"))
# Count of counts
count(count(baseball[1:100,], c("id", "year")), "id", "freq")
count(count(baseball, c("id", "year")), "freq")

### Description

Create progress bar object from text string.

### Usage

create_progress_bar(name = "none", ...)

### Arguments

- name: type of progress bar to create
- ...: other arguments passed onto progress bar function

### Details

Progress bars give feedback on how apply step is proceeding. This is mainly useful for long running functions, as for short functions, the time taken up by splitting and combining may be on the same order (or longer) as the apply step. Additionally, for short functions, the time needed to update the progress bar can significantly slow down the process. For the trivial examples below, using the tk progress bar slows things down by a factor of a thousand.

Note the that progress bar is approximate, and if the time taken by individual function applications is highly non-uniform it may not be very informative of the time left.

There are currently four types of progress bar: "none", "text", "tk", and "win". See the individual documentation for more details. In plyr functions, these can either be specified by name, or you can create the progress bar object yourself if you want more control over its appearance. See the examples.

### See Also

progress_none, progress_text, progress_tk, progress_win
Examples

# No progress bar
l_ply(1:100, identity, .progress = "none")
## Not run:
# Use the Tcl/Tk interface
l_ply(1:100, identity, .progress = "tk")
## End(Not run)
# Text-based progress (|======|)
l_ply(1:100, identity, .progress = "text")
# Choose a progress character, run a length of time you can see
l_ply(1:10000, identity, .progress = progress_text(char = "."))

daply

Split data frame, apply function, and return results in an array.

Description

For each subset of data frame, apply function then combine results into an array. daply with a function that operates column-wise is similar to aggregate. To apply a function for each row, use aapply with .margins set to 1.

Usage

daply(
  .data,
  .variables,
  .fun = NULL,
  ..., .progress = "none",
  .inform = FALSE,
  .drop_i = TRUE,
  .drop_o = TRUE,
  .parallel = FALSE,
  .paropts = NULL
)

Arguments

.data data frame to be processed
.variables variables to split data frame by, as quoted variables, a formula or character vector
.fun function to apply to each piece
... other arguments passed on to .fun
.progress name of the progress bar to use, see create_progress_bar
.inform produce informative error messages? This is turned off by default because it substantially slows processing speed, but is very useful for debugging
.drop_i should combinations of variables that do not appear in the input data be preserved (FALSE) or dropped (TRUE, default)

.drop_o should extra dimensions of length 1 in the output be dropped, simplifying the output. Defaults to TRUE

.parallel if TRUE, apply function in parallel, using parallel backend provided by foreach

.paropts a list of additional options passed into the foreach function when parallel computation is enabled. This is important if (for example) your code relies on external data or packages: use the .export and .packages arguments to supply them so that all cluster nodes have the correct environment set up for computing.

Value

if results are atomic with same type and dimensionality, a vector, matrix or array; otherwise, a list-array (a list with dimensions)

Input

This function splits data frames by variables.

Output

If there are no results, then this function will return a vector of length 0 (vector()).

References


See Also

Other array output: aaply(), laply(), maply()

Other data frame input: dply(), ddply(), dlply()

Examples

dply(baseball, .(year), nrow)

# Several different ways of summarising by variables that should not be # included in the summary
dply(baseball[, c(2, 6:9)], .(year), colwise(mean))
dply(baseball[, 6:9], .(baseball$year), colwise(mean))
dply(baseball, .(year), function(df) colwise(mean)(df[, 6:9]))
ddply

Split data frame, apply function, and return results in a data frame.

Description

For each subset of a data frame, apply function then combine results into a data frame. To apply a function for each row, use adply with .margins set to 1.

Usage

ddply(
  .data,
  .variables,
  .fun = NULL,
  ..., 
  .progress = "none",
  .inform = FALSE,
  .drop = TRUE,
  .parallel = FALSE,
  .paropts = NULL
)

Arguments

- **.data** data frame to be processed
- **.variables** variables to split data frame by, as as.quoted variables, a formula or character vector
- **.fun** function to apply to each piece
- **...** other arguments passed on to .fun
- **.progress** name of the progress bar to use, see create_progress_bar
- **.inform** produce informative error messages? This is turned off by default because it substantially slows processing speed, but is very useful for debugging
- **.drop** should combinations of variables that do not appear in the input data be preserved (FALSE) or dropped (TRUE, default)
- **.parallel** if TRUE, apply function in parallel, using parallel backend provided by foreach
- **.paropts** a list of additional options passed into the foreach function when parallel computation is enabled. This is important if (for example) your code relies on external data or packages: use the .export and .packages arguments to supply them so that all cluster nodes have the correct environment set up for computing.

Value

A data frame, as described in the output section.
**Input**

This function splits data frames by variables.

**Output**

The most unambiguous behaviour is achieved when `.fun` returns a data frame - in that case pieces will be combined with `rbind.fill`. If `.fun` returns an atomic vector of fixed length, it will be `rbind`ed together and converted to a data frame. Any other values will result in an error.

If there are no results, then this function will return a data frame with zero rows and columns (`data.frame()`).

**References**


**See Also**

tapply for similar functionality in the base package

Other data frame input: dply(), daply(), dlply()

Other data frame output: adply(), ldply(), mdply()

**Examples**

```r
# Summarize a dataset by two variables
defx <- data.frame(
    group = c(rep('A', 8), rep('B', 15), rep('C', 6)),
    sex = sample(c("M", "F"), size = 29, replace = TRUE),
    age = runif(n = 29, min = 18, max = 54)
)

# Note the use of the '. ' function to allow
# group and sex to be used without quoting
dply(df, .(group, sex), summarize,
    mean = round(mean(age), 2),
    sd = round(sd(age), 2))

# An example using a formula for .variables
dply(baseball[1:100,], ~ year, nrow)
# Applying two functions; nrow and ncol
dply(baseball, ~lg, c("nrow", "ncol"))

# Calculate mean runs batted in for each year
rbi <- dply(baseball, ~year, summarise,
    mean_rbi = mean(rbi, na.rm = TRUE))
# Plot a line chart of the result
plot(mean_rbi ~ year, type = "l", data = rbi)

# make new variable career_year based on the
# start year for each player (id)
```
base2 <- ddply(baseball, .(id), mutate,
  career_year = year - min(year) + 1
)

defaults(x, y)

Arguments

x      list of values
y      defaults

desc(x)

Arguments

x      vector to transform

Examples

desc(1:10)
desc(factor(letters))
first_day <- seq(as.Date("1910/1/1"), as.Date("1920/1/1"), "years")
desc(first_day)
dlply

Split data frame, apply function, and return results in a list.

Description

For each subset of a data frame, apply function then combine results into a list. \texttt{dlply} is similar to \texttt{by} except that the results are returned in a different format. To apply a function for each row, use \texttt{alply} with \texttt{.margins} set to 1.

Usage

\begin{verbatim}
dply(x, 
  .data, 
  .variables, 
  .fun = NULL, 
  ..., 
  .progress = "none", 
  .inform = FALSE, 
  .drop = TRUE, 
  .parallel = FALSE, 
  .paropts = NULL
)
\end{verbatim}

Arguments

- \texttt{.data} data frame to be processed
- \texttt{.variables} variables to split data frame by, as \texttt{as.quoted} variables, a formula or character vector
- \texttt{.fun} function to apply to each piece
- ... other arguments passed on to \texttt{.fun}
- \texttt{.progress} name of the progress bar to use, see \texttt{create_progress_bar}
- \texttt{.inform} produce informative error messages? This is turned off by default because it substantially slows processing speed, but is very useful for debugging
- \texttt{.drop} should combinations of variables that do not appear in the input data be preserved (FALSE) or dropped (TRUE, default)
- \texttt{.parallel} if TRUE, apply function in parallel, using parallel backend provided by \texttt{foreach}
- \texttt{.paropts} a list of additional options passed into the \texttt{foreach} function when parallel computation is enabled. This is important if (for example) your code relies on external data or packages: use the \texttt{.export} and \texttt{.packages} arguments to supply them so that all cluster nodes have the correct environment set up for computing.

Value

- list of results
Introduction

This function splits data frames by variables.

Output

If there are no results, then this function will return a list of length 0 (list()).

References


See Also

Other data frame input: dply(), daply(), ddply()
Other list output: alply(), llply(), mlply()

Examples

linmod <- function(df) {
  lm(rbi ~ year, data = mutate(df, year = year - min(year)))
}
models <- dlply(baseball, .(id), linmod)
models[[1]]

coef <- ldply(models, coef)
with(coef, plot("(Intercept)", year))
qual <- laply(models, function(mod) summary(mod)$r.squared)
hist(qual)

Dply

Split data frame, apply function, and discard results.

Description

For each subset of a data frame, apply function and discard results. To apply a function for each row, use a_ply with .margins set to 1.

Usage

d_ply(
  .data,
  .variables,
  .fun = NULL,
  ...,  
  .progress = "none",
  .inform = FALSE,
  .drop = TRUE,
  ...)


\[ \text{d_ply} \]

\begin{verbatim}
.data
.variables
.fun
.progress
.inform
.drop
.print
.parallel
.paropts
\)
\end{verbatim}

**Arguments**

- `.data` data frame to be processed
- `.variables` variables to split data frame by, as `as.quoted` variables, a formula or character vector
- `.fun` function to apply to each piece
- `...` other arguments passed on to `.fun`
- `.progress` name of the progress bar to use, see `create_progress_bar`
- `.inform` produce informative error messages? This is turned off by default because it substantially slows processing speed, but is very useful for debugging
- `.drop` should combinations of variables that do not appear in the input data be preserved (FALSE) or dropped (TRUE, default)
- `.print` automatically print each result? (default: FALSE)
- `.parallel` if TRUE, apply function in parallel, using parallel backend provided by foreach
- `.paropts` a list of additional options passed into the `foreach` function when parallel computation is enabled. This is important if (for example) your code relies on external data or packages: use the `.export` and `.packages` arguments to supply them so that all cluster nodes have the correct environment set up for computing.

**Value**

Nothing

**Input**

This function splits data frames by variables.

**Output**

All output is discarded. This is useful for functions that you are calling purely for their side effects like displaying plots or saving output.

**References**


**See Also**

Other data frame input: `daply()`, `ddply()`, `dlply()`
Other no output: `a_ply()`, `l_ply()`, `m_ply()`
### each

**Aggregate multiple functions into a single function.**

**Description**

Combine multiple functions into a single function returning a named vector of outputs. Note: you cannot supply additional parameters for the summary functions.

**Usage**

```r
each(...)```

**Arguments**

```r
...
```

functions to combine. each function should produce a single number as output.

**See Also**

`summarise` for applying summary functions to data

**Examples**

```r
# Call min() and max() on the vector 1:10
each(min, max)(1:10)
# This syntax looks a little different. It is shorthand for the
# the following:
f <- each(min, max)
f(1:10)
# Three equivalent ways to call min() and max() on the vector 1:10
each("min", "max")(1:10)
each(c("min", "max")(1:10)
each(c(min, max))(1:10)
# Call length(), min() and max() on a random normal vector
each(length, mean, var)(rnorm(100))
```

---

### failwith

**Fail with specified value.**

**Description**

Modify a function so that it returns a default value when there is an error.

**Usage**

```r
failwith(default = NULL, f, quiet = FALSE)```
Arguments

- `default` default value
- `f` function
- `quiet` all error messages be suppressed?

Value

- a function

See Also

- `try_default`

Examples

```r
f <- function(x) if (x == 1) stop("Error!") else 1
## Not run:
f(1)
f(2)
## End(Not run)
safef <- failwith(NULL, f)
safef(1)
safef(2)
```

Description

This function captures the current context, making it easier to use `ply` with functions that do special evaluation and need access to the environment where `ddply` was called from.

Usage

```r
here(f)
```

Arguments

- `f` a function that does non-standard evaluation

Author(s)

Peter Meilstrup, [https://github.com/crowding](https://github.com/crowding)
Examples

df <- data.frame(a = rep(c("a","b"), each = 10), b = 1:20)
f1 <- function(label) {
  ddply(df, "a", mutate, label = paste(label, b))
}
## Not run: f1("name:"
# Doesn't work because mutate can't find label in the current scope

f2 <- function(label) {
  ddply(df, "a", here(mutate), label = paste(label, b))
}
f2("name:"
# Works :)

### idata.frame

Construct an immutable data frame.

Description

An immutable data frame works like an ordinary data frame, except that when you subset it, it returns a reference to the original data frame, not a copy. This makes subsetting substantially faster and has a big impact when you are working with large datasets with many groups.

Usage

idata.frame(df)

Arguments

df a data frame

Details

This method is still a little experimental, so please let me know if you run into any problems.

Value

an immutable data frame

Examples

system.time(dlply(baseball, "id", nrow))
system.time(dlply(idata.frame(baseball), "id", nrow))
Join two data frames together.

**Description**

Join, like merge, is designed for the types of problems where you would use a sql join.

**Usage**

```r
join(x, y, by = NULL, type = "left", match = "all")
```

**Arguments**

- `x`: data frame
- `y`: data frame
- `by`: character vector of variable names to join by. If omitted, will match on all common variables.
- `type`: type of join: left (default), right, inner or full. See details for more information.
- `match`: how should duplicate ids be matched? Either match just the "first" matching row, or match "all" matching rows. Defaults to "all" for compatibility with merge, but "first" is significantly faster.

**Details**

The four join types return:

- **inner**: only rows with matching keys in both x and y
- **left**: all rows in x, adding matching columns from y
- **right**: all rows in y, adding matching columns from x
- **full**: all rows in x with matching columns in y, then the rows of y that don’t match x.

Note that from plyr 1.5, `join` will (by default) return all matches, not just the first match, as it did previously.

Unlike merge, preserves the order of x no matter what join type is used. If needed, rows from y will be added to the bottom. Join is often faster than merge, although it is somewhat less featureful - it currently offers no way to rename output or merge on different variables in the x and y data frames.

**Examples**

```r
first <- ddply(baseball, "id", summarise, first = min(year))
system.time(b2 <- merge(baseball, first, by = "id", all.x = TRUE))
system.time(b3 <- join(baseball, first, by = "id"))

b2 <- arrange(b2, id, year, stint)
b3 <- arrange(b3, id, year, stint)
stopifnot(all.equal(b2, b3))
```
join_all  

Recursively join a list of data frames.

Description

Recursively join a list of data frames.

Usage

join_all(dfs, by = NULL, type = "left", match = "all")

Arguments

dfs A list of data frames.
by character vector of variable names to join by. If omitted, will match on all common variables.
type type of join: left (default), right, inner or full. See details for more information.
match how should duplicate ids be matched? Either match just the "first" matching row, or match "all" matching rows. Defaults to "all" for compatibility with merge, but "first" is significantly faster.

Examples

dfs <- list(
a = data.frame(x = 1:10, a = runif(10)),
b = data.frame(x = 1:10, b = runif(10)),
c = data.frame(x = 1:10, c = runif(10))
)
join_all(dfs)
join_all(dfs, "x")

laply  

Split list, apply function, and return results in an array.

Description

For each element of a list, apply function then combine results into an array.
**Usage**

```r
laply(
  .data,
  .fun = NULL,
  ..., 
  .progress = "none",
  .inform = FALSE,
  .drop = TRUE,
  .parallel = FALSE,
  .paropts = NULL
)
```

**Arguments**

- `.data` list to be processed
- `.fun` function to apply to each piece
- `...` other arguments passed on to `.fun`
- `.progress` name of the progress bar to use, see `create_progress_bar`
- `.inform` produce informative error messages? This is turned off by default because it substantially slows processing speed, but is very useful for debugging
- `.drop` should extra dimensions of length 1 in the output be dropped, simplifying the output. Defaults to `TRUE`
- `.parallel` if `TRUE`, apply function in parallel, using parallel backend provided by `foreach`
- `.paropts` a list of additional options passed into the `foreach` function when parallel computation is enabled. This is important if (for example) your code relies on external data or packages: use the `.export` and `.packages` arguments to supply them so that all cluster nodes have the correct environment set up for computing.

**Details**

`laply` is similar in spirit to `sapply` except that it will always return an array, and the output is transposed with respect `sapply` - each element of the list corresponds to a row, not a column.

**Value**

if results are atomic with same type and dimensionality, a vector, matrix or array; otherwise, a list-array (a list with dimensions)

**Input**

This function splits lists by elements.

**Output**

If there are no results, then this function will return a vector of length 0 (`vector()`).
ldply

Description

For each element of a list, apply function then combine results into a data frame.

Usage

```r
ldply(
  .data,
  .fun = NULL,
  ..., 
  .progress = "none",
  .inform = FALSE,
  .parallel = FALSE,
  .paropts = NULL,
  .id = NA
)
```

Arguments

- `.data` list to be processed
- `.fun` function to apply to each piece
- `...` other arguments passed on to `.fun`
- `.progress` name of the progress bar to use, see `create_progress_bar`

Examples

```r
laply(baseball, is.factor)
  # cf
ldply(baseball, is.factor)
colwise(is.factor)(baseball)

laply(seq_len(10), identity)
laply(seq_len(10), rep, times = 4)
laply(seq_len(10), matrix, nrow = 2, ncol = 2)
```

See Also

Other list input: `l_ply()`, `ldply()`, `llply()`
Other array output: `aaply()`, `daply()`, `maply()`

References

produce informative error messages? This is turned off by default because it substantially slows processing speed, but is very useful for debugging.

- parallel: if TRUE, apply function in parallel, using parallel backend provided by foreach.
- paropts: a list of additional options passed into the foreach function when parallel computation is enabled. This is important if (for example) your code relies on external data or packages: use the .export and .packages arguments to supply them so that all cluster nodes have the correct environment set up for computing.
- id: name of the index column (used if .data is a named list). Pass NULL to avoid creation of the index column. For compatibility, omit this argument or pass NA to avoid converting the index column to a factor; in this case, ".id" is used as column name.

Value

A data frame, as described in the output section.

Input

This function splits lists by elements.

Output

The most unambiguous behaviour is achieved when .fun returns a data frame - in that case pieces will be combined with rbind.fill. If .fun returns an atomic vector of fixed length, it will be rbinded together and converted to a data frame. Any other values will result in an error.

If there are no results, then this function will return a data frame with zero rows and columns (data.frame()).

References


See Also

Other list input: lply(), laply(), llply()
Other data frame output: adply(), dply(), mdply()

Description

Because iterators do not have known length, lply starts by allocating an output list of length 50, and then doubles that length whenever it runs out of space. This gives O(n ln n) performance rather than the O(n^2) performance from the naive strategy of growing the list each time.
llply

Split list, apply function, and return results in a list.

Usage

llply(.iterator, .fun = NULL, ...)

Arguments

.iterator iterator object
.fun function to apply to each piece
... other arguments passed on to .fun

Warning

Deprecated, do not use in new code.

See Also

plyr-deprecated

Description

For each element of a list, apply function, keeping results as a list.

Usage

llply(  .data,  .fun = NULL,  ...,  .progress = "none",  .inform = FALSE,  .parallel = FALSE,  .paropts = NULL)

Arguments

.data list to be processed  .fun function to apply to each piece  ... other arguments passed on to .fun  .progress name of the progress bar to use, see create_progress_bar  .inform produce informative error messages? This is turned off by default because it substantially slows processing speed, but is very useful for debugging  .parallel if TRUE, apply function in parallel, using parallel backend provided by foreach
.paropts a list of additional options passed into the `foreach` function when parallel computation is enabled. This is important if (for example) your code relies on external data or packages: use the `.export` and `.packages` arguments to supply them so that all cluster nodes have the correct environment set up for computing.

Details

`llply` is equivalent to `lapply` except that it will preserve labels and can display a progress bar.

Value

list of results

Input

This function splits lists by elements.

Output

If there are no results, then this function will return a list of length 0 (`list()`).

References


See Also

Other list input: `lply()`, `laply()`, `ldply()`

Other list output: `alply()`, `dlply()`, `mlply()`

Examples

```r
llply(llply(mtcars, round), table)
llply(baseball, summary)
# Examples from ?lapply
x <- list(a = 1:10, beta = exp(-3:3), logic = c(TRUE, FALSE, FALSE, TRUE))
llply(x, mean)
llply(x, quantile, probs = 1:3/4)
```
l_ply

Split list, apply function, and discard results.

Description
For each element of a list, apply function and discard results

Usage
l_ply(
    .data,  
    .fun = NULL,  
    ...,  
    .progress = "none",  
    .inform = FALSE,  
    .print = FALSE,  
    .parallel = FALSE,  
    .paropts = NULL
)

Arguments
.data list to be processed
.fun function to apply to each piece
... other arguments passed on to .fun
.progress name of the progress bar to use, see create_progress_bar
.inform produce informative error messages? This is turned off by default because it substantially slows processing speed, but is very useful for debugging
.print automatically print each result? (default: FALSE)
.parallel if TRUE, apply function in parallel, using parallel backend provided by foreach
.paropts a list of additional options passed into the foreach function when parallel computation is enabled. This is important if (for example) your code relies on external data or packages: use the .export and .packages arguments to supply them so that all cluster nodes have the correct environment set up for computing.

Value
Nothing

Input
This function splits lists by elements.

Output
All output is discarded. This is useful for functions that you are calling purely for their side effects like displaying plots or saving output.
maply

References


See Also

Other list input: `laply()`, `ldply()`, `llply()`
Other no output: `a_ply()`, `d_ply()`, `m_ply()`

Examples

```r
l_ply(llply(mtcars, round), table, .print = TRUE)
l_ply(baseball, function(x) print(summary(x)))
```

maply

Call function with arguments in array or data frame, returning an array.

Description

Call a multi-argument function with values taken from columns of an data frame or array, and combine results into an array

Usage

```r
maply(
  .data,
  .fun = NULL,
  ...,
  .expand = TRUE,
  .progress = "none",
  .inform = FALSE,
  .drop = TRUE,
  .parallel = FALSE,
  .paropts = NULL
)
```

Arguments

- `.data` matrix or data frame to use as source of arguments
- `.fun` function to apply to each piece
- `...` other arguments passed on to `.fun`
- `.expand` should output be 1d (expand = FALSE), with an element for each row; or nd (expand = TRUE), with a dimension for each variable.
- `.progress` name of the progress bar to use, see `create_progress_bar`
.inform produce informative error messages? This is turned off by default because it substantially slows processing speed, but is very useful for debugging.
.drop should extra dimensions of length 1 in the output be dropped, simplifying the output. Defaults to TRUE.
.parallel if TRUE, apply function in parallel, using parallel backend provided by foreach
.paropts a list of additional options passed into the foreach function when parallel computation is enabled. This is important if (for example) your code relies on external data or packages: use the .export and .packages arguments to supply them so that all cluster nodes have the correct environment set up for computing.

Details
The m*ply functions are the plyr version of mapply, specialised according to the type of output they produce. These functions are just a convenient wrapper around a*ply with margins = 1 and .fun wrapped in splat.

Value
if results are atomic with same type and dimensionality, a vector, matrix or array; otherwise, a list-array (a list with dimensions)

Input
Call a multi-argument function with values taken from columns of an data frame or array

Output
If there are no results, then this function will return a vector of length 0 (vector()).

References

See Also
Other multiple arguments input: m_ply(), mdply(), mlply()
Other array output: aaply(), daply(), laply()

Examples
maply(cbind(mean = 1:5, sd = 1:5), rnorm, n = 5)
maply(expand.grid(mean = 1:5, sd = 1:5), rnorm, n = 5)
maply(cbind(1:5, 1:5), rnorm, n = 5)
mapvalues

Replace specified values with new values, in a vector or factor.

Description

Item in x that match items from will be replaced by items in to, matched by position. For example, items in x that match the first element in from will be replaced by the first element of to.

Usage

mapvalues(x, from, to, warn_missing = TRUE)

Arguments

x the factor or vector to modify
from a vector of the items to replace
to a vector of replacement values
warn_missing print a message if any of the old values are not actually present in x

Details

If x is a factor, the matching levels of the factor will be replaced with the new values.

The related revalue function works only on character vectors and factors, but this function works on vectors of any type and factors.

See Also

revalue to do the same thing but with a single named vector instead of two separate vectors.

Examples

x <- c("a", "b", "c")
mapvalues(x, c("a", "c"), c("A", "C"))

# Works on factors
y <- factor(c("a", "b", "c", "a"))
mapvalues(y, c("a", "c"), c("A", "C"))

# Works on numeric vectors
z <- c(1, 4, 5, 9)
mapvalues(z, from = c(1, 5, 9), to = c(10, 50, 90))
match_df

Extract matching rows of a data frame.

Description

Match works in the same way as join, but instead of return the combined dataset, it only returns the
matching rows from the first dataset. This is particularly useful when you’ve summarised the data
in some way and want to subset the original data by a characteristic of the subset.

Usage

match_df(x, y, on = NULL)

Arguments

x data frame to subset.
y data frame defining matching rows.
on variables to match on - by default will use all variables common to both data
frames.

Details

match_df shares the same semantics as join, not match:

• the match criterion is ==, not identical).
• it doesn’t work for columns that are not atomic vectors
• if there are no matches, the row will be omitted’

Value

a data frame

See Also

join to combine the columns from both x and y and match for the base function selecting matching
items

Examples

# count the occurrences of each id in the baseball dataframe, then get the subset with a freq > 25
longterm <- subset(count(baseball, "id"), freq > 25)
# longterm
#   id freq
# 30 ansonca01 27
# 48 baineha01 27
# ...
# Select only rows from these longterm players from the baseball dataframe
```r
# (match would default to match on shared column names, but here was explicitly set "id")
bb_longterm <- match_df(baseball, longterm, on="id")
bb_longterm[1:5,]
```

## `mdply`

`Call function with arguments in array or data frame, returning a data frame.`

### Description

Call a multi-argument function with values taken from columns of an data frame or array, and combine results into a data frame

### Usage

```r
mdply(
  .data,
  .fun = NULL,
  ...,
  .expand = TRUE,
  .progress = "none",
  .inform = FALSE,
  .parallel = FALSE,
  .paropts = NULL
)
```

### Arguments

- `.data`: matrix or data frame to use as source of arguments
- `.fun`: function to apply to each piece
- `...`: other arguments passed on to `.fun`
- `.expand`: should output be 1d (expand = FALSE), with an element for each row; or nd (expand = TRUE), with a dimension for each variable.
- `.progress`: name of the progress bar to use, see `create_progress_bar`
- `.inform`: produce informative error messages? This is turned off by default because it substantially slows processing speed, but is very useful for debugging
- `.parallel`: if TRUE, apply function in parallel, using parallel backend provided by `foreach`
- `.paropts`: a list of additional options passed into the `foreach` function when parallel computation is enabled. This is important if (for example) your code relies on external data or packages: use the `.export` and `.packages` arguments to supply them so that all cluster nodes have the correct environment set up for computing.

### Details

The `m*ply` functions are the `plyr` version of `mapply`, specialised according to the type of output they produce. These functions are just a convenient wrapper around `a*ply` with `margins = 1` and `.fun` wrapped in `splat`. 
mlply

Call function with arguments in array or data frame, returning a list.

Description
Call a multi-argument function with values taken from columns of an data frame or array, and combine results into a list.

Value
A data frame, as described in the output section.

Input
Call a multi-argument function with values taken from columns of an data frame or array

Output
The most unambiguous behaviour is achieved when .fun returns a data frame - in that case pieces will be combined with rbind.fill. If .fun returns an atomic vector of fixed length, it will be rbinded together and converted to a data frame. Any other values will result in an error.

If there are no results, then this function will return a data frame with zero rows and columns (data.frame()).

References

See Also
Other multiple arguments input: mply(), maply(), mlply()
Other data frame output: adply(), ddply(), ldply()

Examples
mlply(data.frame(mean = 1:5, sd = 1:5), rnorm, n = 2)
mlply(expand.grid(mean = 1:5, sd = 1:5), rnorm, n = 2)
mlply(cbind(mean = 1:5, sd = 1:5), rnorm, n = 5)
mlply(cbind(mean = 1:5, sd = 1:5), as.data.frame(rnorm), n = 5)
Usage

```r
mlply(
  .data,
  .fun = NULL,
  ..., 
  .expand = TRUE,
  .progress = "none",
  .inform = FALSE,
  .parallel = FALSE,
  .paropts = NULL
)
```

Arguments

- `.data` matrix or data frame to use as source of arguments
- `.fun` function to apply to each piece
- `...` other arguments passed on to `.fun`
- `.expand` should output be 1d (expand = FALSE), with an element for each row; or nd (expand = TRUE), with a dimension for each variable.
- `.progress` name of the progress bar to use, see `create_progress_bar`
- `.inform` produce informative error messages? This is turned off by default because it substantially slows processing speed, but is very useful for debugging
- `.parallel` if TRUE, apply function in parallel, using parallel backend provided by foreach
- `.paropts` a list of additional options passed into the `foreach` function when parallel computation is enabled. This is important if (for example) your code relies on external data or packages: use the `.export` and `.packages` arguments to supply them so that all cluster nodes have the correct environment set up for computing.

Details

The `m*ply` functions are the `plyr` version of `mapply`, specialised according to the type of output they produce. These functions are just a convenient wrapper around `a*ply` with `margins = 1` and `.fun` wrapped in `splat`.

Value

list of results

Input

Call a multi-argument function with values taken from columns of an data frame or array

Output

If there are no results, then this function will return a list of length 0 (list()).
mutate

Mutate a data frame by adding new or replacing existing columns.

Description

This function is very similar to `transform` but it executes the transformations iteratively so that later transformations can use the columns created by earlier transformations. Like transform, unnamed components are silently dropped.

Usage

`mutate(.data, ...)`

Arguments

- `.data` the data frame to transform
- `...` named parameters giving definitions of new columns.

Details

Mutate seems to be considerably faster than transform for large data frames.

See Also

`subset`, `summarise`, `arrange`. For another somewhat different approach to solving the same problem, see `within`.

References


See Also

Other multiple arguments input: `m_ply()`, `maply()`, `mdply()`

Other list output: `alply()`, `dlply()`, `llply()`

Examples

```r
mlply(cbind(1:4, 4:1), rep)
mlply(cbind(1:4, times = 4:1), rep)

mlply(cbind(1:4, 4:1), seq)
mlply(cbind(1:4, length = 4:1), seq)
mlply(cbind(1:4, by = 4:1), seq, to = 20)
```
Examples

# Examples from transform
mutate(airquality, Ozone = -Ozone)
mutate(airquality, new = -Ozone, Temp = (Temp - 32) / 1.8)

# Things transform can't do
mutate(airquality, Temp = (Temp - 32) / 1.8, OzT = Ozone / Temp)

# mutate is rather faster than transform
system.time(transform(baseball, avg_ab = ab / g))
system.time(mutate(baseball, avg_ab = ab / g))

---

m_ply

Call function with arguments in array or data frame, discarding results.

Description

Call a multi-argument function with values taken from columns of a data frame or array, and discard results into a list.

Usage

m_ply(
  .data,
  .fun = NULL,
  ...,
  .expand = TRUE,
  .progress = "none",
  .inform = FALSE,
  .print = FALSE,
  .parallel = FALSE,
  .paropts = NULL
)

Arguments

.data matrix or data frame to use as source of arguments
.fun function to apply to each piece
... other arguments passed on to .fun
.expand should output be 1d (expand = FALSE), with an element for each row; or nd (expand = TRUE), with a dimension for each variable.
.progress name of the progress bar to use, see create_progress_bar
.inform produce informative error messages? This is turned off by default because it substantially slows processing speed, but is very useful for debugging
.print automatically print each result? (default: FALSE)
.parallel
  if TRUE, apply function in parallel, using parallel backend provided by foreach
.paropts
  a list of additional options passed into the foreach function when parallel com-
  putation is enabled. This is important if (for example) your code relies on ex-
  ternal data or packages: use the .export and .packages arguments to supply
  them so that all cluster nodes have the correct environment set up for computing.

Details
The m*ply functions are the plyr version of mapply, specialised according to the type of output
they produce. These functions are just a convenient wrapper around a*ply with margins = 1 and
.fun wrapped in splat.

Value
Nothing

Input
Call a multi-argument function with values taken from columns of an data frame or array

Output
All output is discarded. This is useful for functions that you are calling purely for their side effects
like displaying plots or saving output.

References

See Also
Other multiple arguments input: maply(), mdply(), mply()
Other no output: a_ply(), d_ply(), l_ply()

name_rows
  Toggle row names between explicit and implicit.

Description
Plyr functions ignore row names, so this function provides a way to preserve them by convert-
ing them to an explicit column in the data frame. After the plyr operation, you can then apply
name_rows again to convert back from the explicit column to the implicit rownames.

Usage
name_rows(df)
Arguments

   df  a data.frame, with either rownames, or a column called .rownames.

Examples

   name_rows(mtcars)
   name_rows(name_rows(mtcars))

   df <- data.frame(a = sample(10))
   arrange(df, a)
   arrange(name_rows(df), a)
   name_rows(arrange(name_rows(df), a))

---

ozone  Monthly ozone measurements over Central America.

Description

   This data set is a subset of the data from the 2006 ASA Data expo challenge, http://stat-computing.org/dataexpo/2006/. The data are monthly ozone averages on a very coarse 24 by 24 grid covering Central America, from Jan 1995 to Dec 2000. The data is stored in a 3d array with the first two dimensions representing latitude and longitude, and the third representing time.

Usage

   ozone

Format

   A 24 x 24 x 72 numeric array

References

   http://stat-computing.org/dataexpo/2006/

Examples

   value <- ozone[1, 1, ]
   time <- 1:72
   month <- factor(rep(month.abbr, length = 72), levels = month.abbr)
   year <- rep(1:6, each = 12)
   deseasf <- function(value) lm(value ~ month - 1)
   models <- alply(ozone, 1:2, deseasf)
   coefs <- laply(models, coef)
   dimnames(coefs)[[3]] <- month.abbr
   names(dimnames(coefs))[3] <- "month"
deseas <- laply(models, resid)
dimnames(deseas)[[3]] <- 1:72
names(dimnames(deseas))[3] <- "time"

dim(coefs)
dim(deseas)

plyr

plyr: the split-apply-combine paradigm for R.

Description

The plyr package is a set of clean and consistent tools that implement the split-apply-combine
pattern in R. This is an extremely common pattern in data analysis: you solve a complex problem
by breaking it down into small pieces, doing something to each piece and then combining the results
back together again.

Details

The plyr functions are named according to what sort of data structure they split up and what sort of
data structure they return:

- a array
- l list
- d data.frame
- m multiple inputs
- r repeat multiple times
- _ nothing

So `ddply` takes a data frame as input and returns a data frame as output, and `lply` takes a list as
input and returns nothing as output.

Row names

By design, no plyr function will preserve row names - in general it is too hard to know what should
be done with them for many of the operations supported by plyr. If you want to preserve row
names, use `name_rows` to convert them into an explicit column in your data frame, perform the plyr
operations, and then use `name_rows` again to convert the column back into row names.

Helpers

Plyr also provides a set of helper functions for common data analysis problems:

- `arrange`: re-order the rows of a data frame by specifying the columns to order by
- `mutate`: add new columns or modifying existing columns, like `transform`, but new columns
can refer to other columns that you just created.
• **summarise**: like mutate but create a new data frame, not preserving any columns in the old data frame.

• **join**: an adaption of merge which is more similar to SQL, and has a much faster implementation if you only want to find the first match.

• **match_df**: a version of join that instead of returning the two tables combined together, only returns the rows in the first table that match the second.

• **colwise**: make any function work colwise on a data frame

• **rename**: easily rename columns in a data frame

• **round_any**: round a number to any degree of precision

• **count**: quickly count unique combinations and return return as a data frame.

---

**plyr-deprecated**

**Deprecated Functions in Package plyr**

**Description**

These functions are provided for compatibility with older versions of plyr only, and may be defunct as soon as the next release.

**Details**

- **liply**
- **isplit2**

---

**progress_text**

**Text progress bar.**

**Description**

A textual progress bar

**Usage**

`progress_text(style = 3, ...)`

**Arguments**

- **style**
  - style of text bar, see Details section of `txtProgressBar`

- **...**
  - other arguments passed on to `txtProgressBar`

**Details**

This progress bar displays a textual progress bar that works on all platforms. It is a thin wrapper around the built-in `setTxtProgressBar` and can be customised in the same way.
See Also

Other progress bars: `progress_none()`, `progress_time()`, `progress_tk()`, `progress_win()`

Examples

```r
l_ply(1:100, identity, .progress = "text")
l_ply(1:100, identity, .progress = progress_text(char = "-"))
```

---

**progress_time**

**Text progress bar with time.**

**Description**

A textual progress bar that estimates time remaining. It displays the estimated time remaining and, when finished, total duration.

**Usage**

```r
progress_time()
```

**See Also**

Other progress bars: `progress_none()`, `progress_text()`, `progress_tk()`, `progress_win()`

**Examples**

```r
l_ply(1:100, function(x) Sys.sleep(.01), .progress = "time")
```

---

**progress_tk**

**Graphical progress bar, powered by Tk.**

**Description**

A graphical progress bar displayed in a Tk window

**Usage**

```r
progress_tk(title = "plyr progress", label = "Working...", ...)
```

**Arguments**

- `title` window title
- `label` progress bar label (inside window)
- `...` other arguments passed on to `tkProgressBar`
progress_win

Details
This graphical progress will appear in a separate window.

See Also
 tkProgressBar for the function that powers this progress bar
Other progress bars: progress_none(), progress_text(), progress_time(), progress_win()

Examples
## Not run:
```
if(exists("winProgressBar")) {
  l_ply(1:100, identity, .progress = "win")
  l_ply(1:100, identity, .progress = progress_win(title="Working..."))
}
```

progress_win
Graphical progress bar, powered by Windows.

Description
A graphical progress bar displayed in a separate window

Usage
```
progress_win(title = "plyr progress", ...)
```

Arguments
title window title
...
other arguments passed on to winProgressBar

Details
This graphical progress only works on Windows.

See Also
 winProgressBar for the function that powers this progress bar
Other progress bars: progress_none(), progress_text(), progress_time(), progress_tk()

Examples
```
if(exists("winProgressBar")) {
  l_ply(1:100, identity, .progress = "win")
  l_ply(1:100, identity, .progress = progress_win(title="Working..."))
}
```
raply

Replicate expression and return results in a array.

Description
Evaluate expression n times then combine results into an array

Usage
raply(.n, .expr, .progress = "none", .drop = TRUE)

Arguments

.n number of times to evaluate the expression
.expr expression to evaluate
.progress name of the progress bar to use, see create_progress_bar
.drop should extra dimensions of length 1 be dropped, simplifying the output. Defaults to TRUE

Details
This function runs an expression multiple times, and combines the result into a data frame. If there are no results, then this function returns a vector of length 0 (vector(0)). This function is equivalent to replicate, but will always return results as a vector, matrix or array.

Value
if results are atomic with same type and dimensionality, a vector, matrix or array; otherwise, a list-array (a list with dimensions)

References

Examples
raply(100, mean(runif(100)))
raply(100, each(mean, var)(runif(100)))

raply(10, runif(4))
raply(10, matrix(runif(4), nrow=2))

# See the central limit theorem in action
hist(raply(1000, mean(rexp(10))))
hist(raply(1000, mean(rexp(100))))
hist(raply(1000, mean(rexp(1000))))
**rbind.fill**  
Combine data.frames by row, filling in missing columns.

**Description**

rbinds a list of data frames filling missing columns with NA.

**Usage**

```r
## S3 method for class 'fill'
rbind(...)
```

**Arguments**

... input data frames to row bind together. The first argument can be a list of data frames, in which case all other arguments are ignored. Any NULL inputs are silently dropped. If all inputs are NULL, the output is NULL.

**Details**

This is an enhancement to `rbind` that adds in columns that are not present in all inputs, accepts a list of data frames, and operates substantially faster.

Column names and types in the output will appear in the order in which they were encountered.

Unordered factor columns will have their levels unified and character data bound with factors will be converted to character. POSIXct data will be converted to be in the same time zone. Array and matrix columns must have identical dimensions after the row count. Aside from these there are no general checks that each column is of consistent data type.

**Value**

a single data frame

**See Also**

Other binding functions: `rbind.fill.matrix()`

**Examples**

```r
rbind.fill(mtcars[c("mpg", "wt")], mtcars[c("wt", "cyl")])
```
rbind.fill.matrix

Bind matrices by row, and fill missing columns with NA.

Description

The matrices are bound together using their column names or the column indices (in that order of precedence.) Numeric columns may be converted to character beforehand, e.g. using format. If a matrix doesn’t have colnames, the column number is used. Note that this means that a column with name "1" is merged with the first column of a matrix without name and so on. The returned matrix will always have column names.

Usage

## S3 method for class 'fill.matrix'
rbind(...)  

Arguments

...  

the matrices to rbind. The first argument can be a list of matrices, in which case all other arguments are ignored.

Details

Vectors are converted to 1-column matrices.

Matrices of factors are not supported. (They are anyways quite inconvenient.) You may convert them first to either numeric or character matrices. If a matrices of different types are merged, then normal conversion precedence will apply.

Row names are ignored.

Value

a matrix with column names

Author(s)

C. Beleites

See Also

rbind, cbind, rbind.fill

Other binding functions: rbind.fill()
Examples

```
A <- matrix(1:4, 2)
B <- matrix(6:11, 2)
A
B
rbind.fill.matrix(A, B)

colnames(A) <- c(3, 1)
A
rbind.fill.matrix(A, B)

rbind.fill.matrix(A, 99)
```

**rdply**  
*Replicate expression and return results in a data frame.*

**Description**

Evaluate expression n times then combine results into a data frame

**Usage**

```
rdply(.n, .expr, .progress = "none", .id = NA)
```

**Arguments**

- `.n` number of times to evaluate the expression
- `.expr` expression to evaluate
- `.progress` name of the progress bar to use, see `create_progress_bar`
- `.id` name of the index column. Pass NULL to avoid creation of the index column. For compatibility, omit this argument or pass NA to use ".n" as column name.

**Details**

This function runs an expression multiple times, and combines the result into a data frame. If there are no results, then this function returns a data frame with zero rows and columns (`data.frame()`). This function is equivalent to `replicate`, but will always return results as a data frame.

**Value**

a data frame

**References**

Examples

```r
dply(20, mean(runif(100)))
dply(20, each(mean, var)(runif(100)))
dply(20, data.frame(x = runif(2)))
```

rename

Modify names by name, not position.

Description

Modify names by name, not position.

Usage

```r
rename(x, replace, warn_missing = TRUE, warn_duplicated = TRUE)
```

Arguments

- `x`: named object to modify
- `replace`: named character vector, with new names as values, and old names as names.
- `warn_missing`: print a message if any of the old names are not actually present in `x`.
- `warn_duplicated`: print a message if any name appears more than once in `x` after the operation. Note: `x` is not altered: To save the result, you need to copy the returned data into a variable.

Examples

```r
x <- c("a" = 1, "b" = 2, d = 3, 4)
# Rename column d to "c", updating the variable "x" with the result
x <- rename(x, replace = c("d" = "c"))
x
# Rename column "disp" to "displacement"
rename(mtcars, c("disp" = "displacement"))
```

revalue

Replace specified values with new values, in a factor or character vector.

Description

If `x` is a factor, the named levels of the factor will be replaced with the new values.

Usage

```r
revalue(x, replace = NULL, warn_missing = TRUE)
```
Arguments

- `x`: factor or character vector to modify
- `replace`: named character vector, with new values as values, and old values as names.
- `warn_missing`: print a message if any of the old values are not actually present in `x`

Details

This function works only on character vectors and factors, but the related `mapvalues` function works on vectors of any type and factors, and instead of a named vector specifying the original and replacement values, it takes two separate vectors.

See Also

- `mapvalues` to replace values with vectors of any type

Examples

```r
x <- c("a", "b", "c")
revalue(x, c(a = "A", c = "C"))
revalue(x, c("a" = "A", "c" = "C"))

y <- factor(c("a", "b", "c", "a"))
revalue(y, c(a = "A", c = "C"))
```

---

**rlply**

*Replicate expression and return results in a list.*

Description

Evaluate expression n times then combine results into a list.

Usage

```r
rlply(.n, .expr, .progress = "none")
```

Arguments

- `.n`: number of times to evaluate the expression
- `.expr`: expression to evaluate
- `.progress`: name of the progress bar to use, see `create_progress_bar`

Details

This function runs an expression multiple times, and combines the result into a list. If there are no results, then this function will return a list of length 0 (`list()`). This function is equivalent to `replicate`, but will always return results as a list.
**Value**

list of results

**References**


**Examples**

```r
mods <- rlply(100, lm(y ~ x, data=data.frame(x=rnorm(100), y=rnorm(100))))
hist(lalply(mods, function(x) summary(x)$r.squared))
```

---

**round_any**  
**Round to multiple of any number.**

**Description**

Round to multiple of any number.

**Usage**

```r
round_any(x, accuracy, f = round)
```

**Arguments**

- `x` numeric or date-time (POSIXct) vector to round
- `accuracy` number to round to; for POSIXct objects, a number of seconds
- `f` rounding function: `floor`, `ceiling` or `round`

**Examples**

```r
round_any(135, 10)  
round_any(135, 100)  
round_any(135, 25)  
round_any(135, 10, floor)  
round_any(135, 100, floor)  
round_any(135, 25, floor)  
round_any(135, 10, ceiling)  
round_any(135, 100, ceiling)  
round_any(135, 25, ceiling)  
round_any(Sys.time() + 1:10, 5)  
round_any(Sys.time() + 1:10, 5, floor)  
round_any(Sys.time(), 3600)
```
**r_ply**

*Replicate expression and discard results.*

**Description**

Evaluate expression n times then discard results

**Usage**

```r
r_ply(.n, .expr, .progress = "none", .print = FALSE)
```

**Arguments**

- **.n**: number of times to evaluate the expression
- **.expr**: expression to evaluate
- **.progress**: name of the progress bar to use, see `create_progress_bar`
- **.print**: automatically print each result? (default: FALSE)

**Details**

This function runs an expression multiple times, discarding the results. This function is equivalent to `replicate`, but never returns anything

**References**


**Examples**

```r
r_ply(10, plot(runif(50)))
r_ply(25, hist(runif(1000)))
```

---

**splat**

*Splat* arguments to a function.

**Description**

Wraps a function in `do.call`, so instead of taking multiple arguments, it takes a single named list which will be interpreted as its arguments.

**Usage**

```r
splat(flat)
```
Arguments

flat function to splat

Details

This is useful when you want to pass a function a row of data frame or array, and don’t want to manually pull it apart in your function.

Value

a function

Examples

hp_per_cyl <- function(hp, cyl, ...) hp / cyl
splat(hp_per_cyl)(mtcars[1,])
splat(hp_per_cyl)(mtcars)

f <- function(mpg, wt, ...) data.frame(mw = mpg / wt)
ddply(mtcars, .(cyl), splat(f))

strip_splits

Remove splitting variables from a data frame.

Description

This is useful when you want to perform some operation to every column in the data frame, except the variables that you have used to split it. These variables will be automatically added back on to the result when combining all results together.

Usage

strip_splits(df)

Arguments

df data frame produced by dply.

Examples

dlply(mtcars, c("vs", "am"))
dlply(mtcars, c("vs", "am"), strip_splits)
summarise

Summarise a data frame.

Description

Summarise works in an analogous way to `mutate`, except instead of adding columns to an existing data frame, it creates a new data frame. This is particularly useful in conjunction with `ddply` as it makes it easy to perform group-wise summaries.

Usage

```
summarise(.data, ...)
```

Arguments

- `.data` the data frame to be summarised
- `...` further arguments of the form `var = value`

Note

Be careful when using existing variable names; the corresponding columns will be immediately updated with the new data and this can affect subsequent operations referring to those variables.

Examples

```
# Let's extract the number of teams and total period of time
# covered by the baseball dataframe
summarise(baseball,
    duration = max(year) - min(year),
    nteams = length(unique(team)) )

# Combine with ddply to do that for each separate id
ddply(baseball, "id", summarise, 
    duration = max(year) - min(year),
    nteams = length(unique(team)) )
```

take

Take a subset along an arbitrary dimension

Description

Take a subset along an arbitrary dimension

Usage

```
take(x, along, indices, drop = FALSE)
```

Arguments

- `x`: matrix or array to subset along dimension to subset along the indices to select should the dimensions of the array be simplified? Defaults to `FALSE` which is the opposite of the useful R default.

Examples

```r
x <- array(seq_len(3 * 4 * 5), c(3, 4, 5))
take(x, 3, 1)
take(x, 2, 1)
take(x, 1, 1)
take(x, 3, 1, drop = TRUE)
take(x, 2, 1, drop = TRUE)
take(x, 1, 1, drop = TRUE)
```

Description

This function is somewhat similar to `tapply`, but is designed for use in conjunction with `id`. It is simpler in that it only accepts a single grouping vector (use `id` if you have more) and uses `vapply` internally, using the `.default` value as the template.

Usage

```r
vaggregate(.value, .group, .fun, ..., .default = NULL, .n = nlevels(.group))
```

Arguments

- `.value`: vector of values to aggregate
- `.group`: grouping vector
- `.fun`: aggregation function
- `...`: other arguments passed on to `.fun`
- `.default`: default value used for missing groups. This argument is also used as the template for function output.
- `.n`: total number of groups

Details

`vaggregate` should be faster than `tapply` in most situations because it avoids making a copy of the data.
Examples

# Some examples of use borrowed from ?tapply
n <- 17; fac <- factor(rep(1:3, length.out = n), levels = 1:5)
table(fac)
vaggregate(1:n, fac, sum)
vaggregate(1:n, fac, sum, .default = NA_integer_)
vaggregate(1:n, fac, range)
vaggregate(1:n, fac, range, .default = c(NA, NA) + 0)
vaggregate(1:n, fac, quantile)

# Unlike tapply, vaggregate does not support multi-d output:
tapply(warpbreaks$breaks, warpbreaks[, -1], sum)
vaggregate(warpbreaks$breaks, id(warpbreaks[, -1]), sum)

# But it is about 10x faster
x <- rnorm(1e6)
y1 <- sample.int(10, 1e6, replace = TRUE)
system.time(tapply(x, y1, mean))
system.time(vaggregate(x, y1, mean))
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