

Package ‘collapse’

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Title Advanced and Fast Data Transformation

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Description A C/C++ based package for advanced data transformation and statistical computing in R that is extremely fast, flexible and parsimonious to code with, class-agnostic and programmer friendly. It is well integrated with base R, 'dplyr' / (grouped) 'tibble', 'data.table' and 'plm' (panel-series and data frames), and non-destructively handles other matrix or data frame based classes (such as 'ts', 'xts' / 'zoo', 'timeSeries', 'tsibble', 'sf' data frames etc.)

--- Key Features: ---

- (1) Advanced statistical programming: A full set of fast statistical functions supporting grouped and weighted computations on vectors, matrices and data frames. Fast and programmable grouping, ordering, unique values / rows, factor generation and interactions. Fast and flexible functions for data manipulation and data object conversions.
- (2) Advanced aggregation: Fast and easy multi-data-type, multi-function, weighted, parallelized and fully customized data aggregation.
- (3) Advanced transformations: Fast (grouped) replacing and sweeping out of statistics, and (grouped, weighted) scaling / standardizing, between (averaging) and (quasi-)within (centering / demeaning) transformations, higher-dimensional centering (i.e. multiple fixed effects transformations), linear prediction / partialling-out, linear model fitting and testing.
- (4) Advanced time-computations: Fast (sequences of) lags / leads, and (lagged / leaded, iterated, quasi-, log-) differences and (compounded) growth rates on (unordered) time series and panel data. Multivariate auto-, partial- and cross-correlation functions for panel data. Panel data to (ts-)array conversions.
- (5) List processing: (Recursive) list search / identification, splitting, extraction / subsetting, data-apply, and generalized recursive row-binding / unlisting in 2D.
- (6) Advanced data exploration: Fast (grouped, weighted, panel-decomposed) summary statistics for complex multilevel / panel data.

URL <https://sebkrantz.github.io/collapse/>,
<https://github.com/SebKrantz/collapse>,

https://twitter.com/collapse_R

BugReports <https://github.com/SebKrantz/collapse/issues>

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collapse-package *Advanced and Fast Data Transformation*

Description

collapse is a C/C++ based package for data transformation and statistical computing in R. It's aims are:

- To facilitate complex data transformation, exploration and computing tasks in R.
- To help make R code fast, flexible, parsimonious and programmer friendly.

It is made compatible with *dplyr*, *data.table* and the *plm* approach to panel data, and non-destructively handles other classes.

Getting Started

Please see [Collapse Documentation & Overview](#), or the introductory vignette. The documentation and vignettes can also comfortably be read on the [package website](#). A cheatsheet is available at [Rstudio](#). A compact introduction for quick-starters is provided in the examples below.

Details

collapse provides an integrated suite of statistical and data manipulation functions (see [Collapse Overview](#)). These improve, complement and significantly extend the capabilities of base R and packages like *dplyr*, *data.table*, *plm*, *matrixStats*, *Rfast* etc.. Key improvements and extensions are:

- Fast C/C++ based (grouped, weighted) computations embedded in highly optimized R code.
- More complex statistical, time series / panel data and recursive (list-processing) operations.
- A flexible and generic approach supporting and preserving many R objects.
- Optimized programming in standard and non-standard evaluation.

The statistical and data transformation functions in *collapse* are S3 generic with core methods for vectors, matrices and data frames, and internally support grouped and weighted computations carried out in C/C++. Thus functions need only be called once for column-wise and/or grouped computations, providing a lot of extra speed and full support for sampling weights. Furthermore the R code is strongly optimized and inputs are swiftly passed to compiled C/C++ code, with further checks run at C/C++ level. Various efficient algorithms are implemented in C/C++.

Core S3 methods and efficient grouping and ordering functionality can be accessed by the user. For example `GRP()` creates grouping objects directly passed to C++ by statistical functions. `fgroup_by()` attaches these objects to a data frame, yielding efficient chained calls when combined with *magrittr* pipes, [fast manipulation functions](#) and [fast statistical functions](#). Performance gains are also realized when grouping with factors, or computing on grouped (*dplyr*) or panel data (*plm*) frames.

Additional (hidden) S3 methods provide broad based compatibility and support for *dplyr* (grouped tibble), *data.table* and *plm* panel data classes. Non-generic functions and core methods also seek to preserve object attributes (including column attributes such as variable labels), ensuring flexibility and non-destructive workflows.

Missing values are efficiently skipped at C/C++ level. The package default is `na.rm = TRUE`, whereas `na.rm = FALSE` also yields efficient checking and early termination. Missing weights are supported. Core functionality and all statistical functions / computations are tested with 7700 unit tests for Base R equivalence, exempting some improvements (e.g. `fsum(NA, na.rm = TRUE)` evaluates to NA, not 0 like `sum(NA, na.rm = TRUE)`; similarly for `fmin` and `fmax`; no NaN values are generated from computations involving NA values etc...). Generic functions provide [security](#) against silent swallowing of unknown / misspelled arguments.

collapse installs with a built-in hierarchical [documentation](#) facilitating the use of the package. The vignettes are complimentary and also follow a more structured approach.

Apart from general performance considerations, *collapse* excels at applications involving fast panel data transformations and techniques, fast weighted computations (e.g. weighted aggregation), fast programming and aggregation with categorical and mixed-type data, fast programming with (multivariate) time series, and programming with lists of data objects.

collapse is mainly coded in C++ and built with Rcpp, but also uses C functions from *data.table* (grouping, ordering, subsetting, row-binding), *lfe* (centering on multiple factors) and *stats* (ACF and PACF). For the moment *collapse* does not use low-level parallelism (such as OpenMP).

Author(s)

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Other contributors from packages *collapse* utilizes:

- Matt Dowle, Arun Srinivasan and contributors worldwide (*data.table*)
- Simen Gaure (*lfe*)
- Dirk Eddelbuettel and contributors worldwide (Rcpp)
- R Core Team and contributors worldwide (*stats*)

I thank Ralf Stubner, Joseph Wood and Dirk Eddelbuettel for helpful answers on Stackoverflow, Joris Meys for encouraging me and helping to set up the [Github repository](#) for *collapse*, Matthieu Stigler, Patrice Kiener, Zhiyi Xu and Kevin Tappe for feature requests and helpful suggestions.

Developing / Feature Requests / Bug Reporting

- If you are interested in extending or optimizing this package, see the source code at <https://github.com/SebKrantz/collapse/tree/master>, fork and send pull-requests, or e-mail me.
- Please send feature requests via e-mail.
- Please report issues at <https://github.com/SebKrantz/collapse/issues> or e-mail me.

Examples

```

## Let's start with some statistical programming
v <- iris$Sepal.Length
d <- num_vars(iris) # Saving numeric variables
f <- iris$Species   # Factor

# Simple statistics
fmean(v)           # vector
fmean(qM(d))       # matrix (qM is a faster as.matrix)
fmean(d)           # data.frame

# Preserving data structure
fmean(qM(d), drop = FALSE) # Still a matrix
fmean(d, drop = FALSE)    # Still a data.frame

# Weighted statistics, supported by most functions...
w <- abs(rnorm(fnrow(iris)))
fmean(d, w = w)

# Grouped statistics...
fmean(d, f)

# Groupwise-weighted statistics...
fmean(d, f, w)

# Simple Transformations...
head(fmode(d, TRA = "replace")) # Replacing values with the mode
head(fmedian(d, TRA = "-"))     # Subtracting the median
head(fsum(d, TRA = "%"))        # Computing percentages
head(fsd(d, TRA = "/"))         # Dividing by the standard-deviation (scaling), etc...

# Weighted Transformations...
head(fnth(d, 0.75, w = w, TRA = "replace")) # Replacing by the weighted 3rd quartile

# Grouped Transformations...
head(fvar(d, f, TRA = "replace")) # Replacing values with the group variance
head(fsd(d, f, TRA = "/"))        # Grouped scaling
head(fmin(d, f, TRA = "-"))       # Setting the minimum value in each species to 0
head(fsum(d, f, TRA = "/"))       # Dividing by the sum (proportions)
head(fmedian(d, f, TRA = "-"))    # Groupwise de-median
head(ffirst(d, f, TRA = "%"))     # Taking modulus of first group-value, etc. ...

# Grouped and weighted transformations...
head(fsd(d, f, w, "/"), 3)        # weighted scaling
head(fmedian(d, f, w, "-"), 3)    # subtracting the weighted group-median
head(fmode(d, f, w, "replace"), 3) # replace with weighted statistical mode

## Some more advanced transformations...
head(fbetween(d))                 # Averaging (faster t.: fmean(d, TRA = "replace"))
head(fwithin(d))                  # Centering (faster than: fmean(d, TRA = "-"))
head(fwithin(d, f, w))            # Grouped and weighted (same as fmean(d, f, w, "-"))
head(fwithin(d, f, w, mean = 5))  # Setting a custom mean

```

```

head(fwithin(d, f, w, theta = 0.76))      # Quasi-centering i.e. d - theta*f between(d, f, w)
head(fwithin(d, f, w, mean = "overall.mean")) # Preserving the overall mean of the data
head(fscale(d))                          # Scaling and centering
head(fscale(d, mean = 5, sd = 3))        # Custom scaling and centering
head(fscale(d, mean = FALSE, sd = 3))    # Mean preserving scaling
head(fscale(d, f, w))                    # Grouped and weighted scaling and centering
head(fscale(d, f, w, mean = 5, sd = 3))  # Custom grouped and weighted scaling and centering
head(fscale(d, f, w, mean = FALSE,      # Preserving group means
      sd = "within.sd"))                # and setting group-sd to fsd(fwithin(d, f, w), w = w)
head(fscale(d, f, w, mean = "overall.mean", # Full harmonization of group means and variances,
      sd = "within.sd"))                # while preserving the level and scale of the data.

head(get_vars(iris, 1:2))                 # Use get_vars for fast selecting, gv is shortcut
head(fHDbetween(gv(iris, 1:2), gv(iris, 3:5))) # Linear prediction with factors and covariates
head(fHDwithin(gv(iris, 1:2), gv(iris, 3:5))) # Linear partialling out factors and covariates
ss(iris, 1:10, 1:2)                       # Similarly fsubset/ss for fast subsetting rows

# Simple Time-Computations..
head(flag(AirPassengers, -1:3))           # One lead and three lags
head(fdiff(EuStockMarkets,              # Suitably lagged first and second differences
  c(1, frequency(EuStockMarkets)), diff = 1:2))
head(fdiff(EuStockMarkets, rho = 0.87))  # Quasi-differences (x_t - rho*x_t-1)
head(fdiff(EuStockMarkets, log = TRUE))  # Log-differences
head(fgrowth(EuStockMarkets))           # Exact growth rates (percentage change)
head(fgrowth(EuStockMarkets, logdiff = TRUE)) # Log-difference growth rates (percentage change)

# Note that it is not necessary to use factors for grouping.
fmean(gv(mtcars, -c(2,8:9)), mtcars$cyl) # Can also use vector (internally converted using qF())
fmean(gv(mtcars, -c(2,8:9)),
  gv(mtcars, c(2,8:9)))                  # or a list of vector (internally grouped using GRP())
g <- GRP(mtcars, ~ cyl + vs + am)        # It is also possible to create grouping objects
print(g)                                 # These are instructive to learn about the grouping,
plot(g)                                  # and are directly handed down to C++ code
fmean(gv(mtcars, -c(2,8:9)), g)         # This can speed up multiple computations over same groups
fsd(gv(mtcars, -c(2,8:9)), g)

# Factors can efficiently be created using qF()
f1 <- qF(mtcars$cyl)                     # Unlike GRP objects, factors are checked for NA's
f2 <- qF(mtcars$cyl, na.exclude = FALSE) # This can however be avoided through this option
class(f2)                                # Note the added class
library(microbenchmark)
microbenchmark(fmean(mtcars, f1), fmean(mtcars, f2)) # A minor difference, larger on larger data

with(mtcars, finteraction(cyl, vs, am))  # Efficient interactions of vectors and/or factors
finteraction(gv(mtcars, c(2,8:9)))       # .. or lists of vectors/factors

# Simple row- or column-wise computations on matrices or data frames with dapply()
dapply(mtcars, quantile)                 # column quantiles
dapply(mtcars, quantile, MARGIN = 1)     # Row-quantiles
# dapply preserves the data structure of any matrices / data frames passed
# Some fast matrix row/column functions are also provided by the matrixStats package
# Similarly, BY performs grouped computations
BY(mtcars, f2, quantile)

```

```

BY(mtcars, f2, quantile, expand.wide = TRUE)
# For efficient (grouped) replacing and sweeping out computed statistics, use TRA()
sds <- fsd(mtcars)
head(TRA(mtcars, sds, "/")) # Simple scaling (if sd's not needed, use fsd(mtcars, TRA = "/"))
microbenchmark(TRA(mtcars, sds, "/"), sweep(mtcars, 2, sds, "/")) # A remarkable performance gain.
sds <- fsd(mtcars, f2)
head(TRA(mtcars, sds, "/", f2)) # Groupd scaling (if sd's not needed: fsd(mtcars, f2, TRA = "/"))

# All functions above preserve the structure of matrices / data frames
# If conversions are required, use these efficient functions:
mtcarsM <- qM(mtcars) # Matrix from data.frame
head(qDF(mtcarsM)) # data.frame from matrix columns
head(mrt1(mtcarsM, TRUE, "data.frame")) # data.frame from matrix rows, etc..
head(qDT(mtcarsM, "cars")) # Saving row.names when converting matrix to data.table
head(qDT(mtcars, "cars")) # Same use a data.frame

## Now let's get some real data and see how we can use this power for data manipulation
library(magrittr)
head(wlddev) # World Bank World Development Data: 216 countries, 59 years, 4 series (columns 9-12)

# Starting with some discriptive tools...
namlab(wlddev, class = TRUE) # Show variable names, labels and classes
fNobs(wlddev) # Observation count
pwNobs(wlddev) # Pairwise observation count
head(fNobs(wlddev, wlddev$country)) # Grouped observation count
fNdistinct(wlddev) # Distinct values
descr(wlddev) # Describe data
varying(wlddev, ~ country) # Show which variables vary within countries
qsu(wlddev, pid = ~ country, cols = 9:12, vlabels = TRUE) # Panel-summarize columns 9 though 12 of this data
# (between and within countries)
qsu(wlddev, ~ region, ~ country, cols = 9:12, higher = TRUE) # Do all of that by region and also compute higher moments
# -> returns a 4D array
qsu(wlddev, ~ region, ~ country, cols = 9:12, higher = TRUE, array = FALSE) %>% # Return as a list of matrices..
unlist2d(c("Variable", "Trans"), row.names = "Region") %>% head # and turn into a tidy data.frame
pwcov(num_vars(wlddev), P = TRUE) # Pairwise correlations with p-value
pwcov(fmean(num_vars(wlddev), wlddev$country), P = TRUE) # Correlating country means
pwcov(fwithin(num_vars(wlddev), wlddev$country), P = TRUE) # Within-country correlations
psacf(wlddev, ~country, ~year, cols = 9:12) # Panel-data Autocorrelation function
pspacf(wlddev, ~country, ~year, cols = 9:12) # Partial panel-autocorrelations
psmat(wlddev, ~iso3c, ~year, cols = 9:12) %>% plot # Convert panel to 3D array and plot

## collapse offers a few very efficient functions for data manipulation:
# Fast selecting and replacing columns
series <- get_vars(wlddev, 9:12) # Same as wlddev[9:12] but 2x faster
series <- fselect(wlddev, PCGDP:ODA) # Same thing: > 100x faster than dplyr::select
get_vars(wlddev, 9:12) <- series # Replace, 8x faster wlddev[9:12] <- series + replaces names
fselect(wlddev, PCGDP:ODA) <- series # Same thing

# Fast subsetting
head(fsubset(wlddev, country == "Ireland", -country, -iso3c))
head(fsubset(wlddev, country == "Ireland" & year > 1990, year, PCGDP:ODA))

```



```

ss(wlddev, 1:10, 1:10) # This is an order of magnitude faster than wlddev[1:10, 1:10]

# Fast transforming
head(ftransform(wlddev, ODA_GDP = ODA / PCGDP, ODA_LIFEEX = sqrt(ODA) / LIFEEX))
settransform(wlddev, ODA_GDP = ODA / PCGDP, ODA_LIFEEX = sqrt(ODA) / LIFEEX) # by reference
head(ftransform(wlddev, PCGDP = NULL, ODA = NULL, GINI_sum = fsum(GINI)))
head(ftransformv(wlddev, 9:12, log)) # Can also transform with lists of columns
head(ftransformv(wlddev, 9:12, fscale, apply = FALSE)) # apply = FALSE invokes fscale.data.frame
settransformv(wlddev, 9:12, fscale, apply = FALSE) # Changing the data by reference
ftransform(wlddev) <- fscale(gv(wlddev, 9:12)) # Same thing (using replacement method)
wlddev %<>% ftransformv(9:12, fscale, apply = FALSE) # Same thing, using magrittr
wlddev %>% ftransform(gv(., 9:12) %>% # With compound pipes: Scaling and lagging
  fscale %>% flag(0:2, iso3c, year)) %>% head

# Fast reordering
head(roworder(wlddev, -country, year))
head(colorder(wlddev, country, year))

# Fast renaming
head(frename(wlddev, country = Ctry, year = Yr))
setrename(wlddev, country = Ctry, year = Yr) # By reference
head(frename(wlddev, tolower, cols = 9:12))

# Fast grouping
fgroup_by(wlddev, Ctry, decade) %>% fgroup_vars # fgroup_by is a lot faster than dplyr::group_by
rm(wlddev) # .. but only works with collapse functions

## Now lets start putting things together
wlddev[["weights"]] <- abs(rnorm(fnrow(wlddev))) # Adding some weights

wlddev %>% fsubset(year > 1990, region, income, PCGDP:ODA) %>%
  fgroup_by(region, income) %>% fmean # Fast aggregation using the mean

# Same thing using dplyr manipulation verbs
library(dplyr)
wlddev %>% filter(year > 1990) %>% select(region, income, PCGDP:ODA) %>%
  group_by(region, income) %>% fmean # This is already a lot faster than summarize_all(mean)

wlddev %>% fsubset(year > 1990, region, income, PCGDP:weights) %>%
  fgroup_by(region, income) %>% fmean(weights) # Weighted group means

wlddev %>% fsubset(year > 1990, region, income, PCGDP:weights) %>%
  fgroup_by(region, income) %>% fsd(weights) # Weighted group standard deviations

wlddev %>% fgroup_by(region, income) %>% fselect(PCGDP:weights) %>%
  fnth(0.75, weights) # Weighted group third quartile

wlddev %>% fgroup_by(country) %>% fselect(PCGDP:ODA) %>%
  fwithin # Within transformation
wlddev %>% fgroup_by(country) %>% fselect(PCGDP:ODA) %>%
  fmedian(TRA = "-") # Grouped centering using the median
# Replacing data points by the weighted first quartile:
wlddev %>% fgroup_by(country) %>% fselect(country, year, PCGDP:weights) %>%

```

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  ftransform(fselect(., -country, -year) %>% fnth(0.25, weights, "replace_fill"))

wlddev %>% fgroup_by(country) %>% fselect(PCGDP:ODA) %>% fscale           # Standardizing
wlddev %>% fgroup_by(country) %>% fselect(PCGDP:weights) %>% fscale(weights) # Weighted..

wlddev %>% fselect(country, year, PCGDP:ODA) %>% # Adding 1 lead and 2 lags of each variable
  fgroup_by(country) %>% flag(-1:2, year)
wlddev %>% fselect(country, year, PCGDP:ODA) %>% # Adding 1 lead and 10-year growth rates
  fgroup_by(country) %>% fgrowth(c(0:1,10), 1, year)

# etc...

# Aggregation with multiple functions
wlddev %>% fsubset(year > 1990, region, income, PCGDP:ODA) %>%
  fgroup_by(region, income) %>% {
    add_vars(fgroup_vars(., "unique"),
             fmedian(., keep.group_vars = FALSE) %>% add_stub("median_"),
             fmean(., keep.group_vars = FALSE) %>% add_stub("mean_"),
             fsd(., keep.group_vars = FALSE) %>% add_stub("sd_"))
  } %>% head

# Transformation with multiple functions
wlddev %>% fselect(country, year, PCGDP:ODA) %>%
  fgroup_by(country) %>% {
    add_vars(fdiff(., c(1,10), 1, year) %>% flag(0:2, year), # Sequence of lagged differences
             ftransform(., fselect(., PCGDP:ODA) %>% fwithin %>% add_stub("W.")) %>%
             flag(0:2, year, keep.ids = FALSE))           # Sequence of lagged demeaned vars
  }

# With ftransform, can also easily do one or more grouped mutations on the fly..
settransform(wlddev, median_ODA = fmedian(ODA, list(region, income), TRA = "replace_fill"))

settransform(wlddev, sd_ODA = fsd(ODA, list(region, income), TRA = "replace_fill"),
             mean_GDP = fmean(PCGDP, country, TRA = "replace_fill"))

wlddev %<>% ftransform(fmedian(list(median_ODA = ODA, median_GDP = PCGDP),
                             list(region, income), TRA = "replace_fill"))
rm(wlddev)

## For multi-type data aggregation, the function collap offers ease and flexibility
# Aggregate this data by country and decade: Numeric columns with mean, categorical with mode
head(collap(wlddev, ~ country + decade, fmean, fmode))

wlddev[["weights"]] <- abs(rnorm(fnrow(wlddev))) # Adding some weights
# taking weighted mean and weighted mode:
head(collap(wlddev, ~ country + decade, fmean, fmode, w = ~ weights, wFUN = fsum))

# Multi-function aggregation of certain columns
head(collap(wlddev, ~ country + decade,
           list(fmean, fmedian, fsd),
           list(ffirst, flast), cols = c(3,9:12)))

# Customized Aggregation: Assign columns to functions

```

```

head(collap(wlddev, ~ country + decade,
           custom = list(fmean = 9:10, fsd = 9:12, flast = 3, ffirst = 6:8)))

# For grouped data frames use collapg
wlddev %>% fsubset(year > 1990, country, region, income, PCGDP:ODA) %>%
  fgroup_by(country) %>% collapg(fmean, ffirst) %>%
  ftransform(AMGDP = PCGDP > fmedian(PCGDP, list(region, income), TRA = "replace_fill"),
            AMODA = ODA > fmedian(ODA, income, TRA = "replace_fill"))

## Additional flexibility for data transformation tasks is offered by tidy transformation operators
# Within-transformation (centering on overall mean)
head(W(wlddev, ~ country, cols = 9:12, mean = "overall.mean"))
# Partialling out country and year fixed effects
head(HDW(wlddev, PCGDP + LIFEEEX ~ qF(country) + qF(year)))
# Same, adding ODA as continuous regressor
head(HDW(wlddev, PCGDP + LIFEEEX ~ qF(country) + qF(year) + ODA))
# Standardizing (scaling and centering) by country
head(STD(wlddev, ~ country, cols = 9:12))
# Computing 1 lead and 3 lags of the 4 series
head(L(wlddev, -1:3, ~ country, ~year, cols = 9:12))
# Computing the 1- and 10-year first differences
head(D(wlddev, c(1,10), 1, ~ country, ~year, cols = 9:12))
head(D(wlddev, c(1,10), 1:2, ~ country, ~year, cols = 9:12)) # ..first and second differences
# Computing the 1- and 10-year growth rates
head(G(wlddev, c(1,10), 1, ~ country, ~year, cols = 9:12))
# Adding growth rate variables to dataset
add_vars(wlddev) <- G(wlddev, c(1, 10), 1, ~ country, ~year, cols = 9:12, keep.ids = FALSE)
get_vars(wlddev, "G1.", regex = TRUE) <- NULL # Deleting again

# These operators can conveniently be used in regression formulas:
# Using a Mundlak (1978) procedure to estimate the effect of OECD on LIFEEEX, controlling for PCGDP
lm(LIFEEEX ~ log(PCGDP) + OECD + B(log(PCGDP), country),
   wlddev %>% fselect(country, OECD, PCGDP, LIFEEEX) %>% na_omit)

# Adding 10-year lagged life-expectancy to allow for some convergence effects (dynamic panel model)
lm(LIFEEEX ~ L(LIFEEEX, 10, country) + log(PCGDP) + OECD + B(log(PCGDP), country),
   wlddev %>% fselect(country, OECD, PCGDP, LIFEEEX) %>% na_omit)

# Transformation functions and operators also support plm panel data classes:
library(plm)
pwlddev <- pdata.frame(wlddev, index = c("country", "year"))
head(W(pwlddev$PCGDP)) # Country-demeaning
head(W(pwlddev, cols = 9:12))
head(W(pwlddev$PCGDP, effect = 2)) # Time-demeaning
head(W(pwlddev, effect = 2, cols = 9:12))
head(HDW(pwlddev$PCGDP)) # Country- and time-demeaning
head(HDW(pwlddev, cols = 9:12))
head(STD(pwlddev$PCGDP)) # Standardizing by country
head(STD(pwlddev, cols = 9:12))
head(L(pwlddev$PCGDP, -1:3)) # Panel-lags
head(L(pwlddev, -1:3, 9:12))
head(G(pwlddev$PCGDP)) # Panel-Growth rates
head(G(pwlddev, 1, 1, 9:12))

```

```
# Remove all objects used in this example section
rm(v, d, w, f, f1, f2, g, mtcarsM, pwllddev, sds, series, wlddev)
```

A0-collapse-documentation

Collapse Documentation & Overview

Description

The following table fully summarizes the contents of *collapse*. The documentation is structured hierarchically: This is the main overview page, linking to topical overview pages and associated function pages (unless functions are documented on the topic page).

Topics and Functions

<i>Topic</i>	<i>Main Features / Keywords</i>
Fast Statistical Functions	Fast (grouped and weighted) statistical functions for vector, matrix, data frame and grouped
Fast Grouping and Ordering	Fast (ordered) groupings from vectors, data frames, lists. 'GRP' objects are extremely efficient
Fast Data Manipulation	Fast and flexible select, subset, transform, sort/reorder and rename data, including modifying
Quick Data Conversion	Quick conversions: data.frame <> data.table <> tibble matrix <> list, data.frame, data.table
Advanced Data Aggregation	Fast and easy (weighted and parallelized) aggregation of multi-type data, with (multiple) fun
Data Transformations	Efficient row- and column- apply to data objects (preserving data structure) and Split-Apply
Time Series and Panel Series	Fast (sequences of) lags / leads and (lagged / leaded and iterated) differences, quasi-differen
List Processing	(Recursive) list search and identification, search and extract list-elements / list-subsetting, s
Summary Statistics	Fast (grouped and weighted), summary statistics for cross-sectional and complex multilevel
Recode and Replace Values	Recode multiple values (exact or regex matching) and replace NaN/Inf/-Inf and outliers (
Small (Helper) Functions	Fast missing value insertion and removal, faster nlevels for factors, fast nrow, ncol, dim (for

Data and Global Macros
[Package Options](#)

Groningen Growth and Development Centre 10-Sector Database, World Bank World Development Indicators
 Set the action taken by generic functions encountering unknown arguments. The default is

Details

The added top-level documentation infrastructure in *collapse* allows you to effectively navigate the package. Calling `?FUN` brings up the documentation page documenting the function, which contains links to associated topic pages and closely related functions. You can also call topical documentation pages directly from the console. The links to these pages are contained in the global macro `.COLLAPSE_TOPICS` (e.g. calling `help(.COLLAPSE_TOPICS[1])` brings up this page).

Author(s)

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See Also

[collapse-package](#)

A1-fast-statistical-functions

Fast (Grouped, Weighted) Statistical Functions for Matrix-Like Objects

Description

With `fsum`, `fprod`, `fmean`, `fmedian`, `fmode`, `fvar`, `fsd`, `fmin`, `fmax`, `fnth`, `ffirst`, `flast`, `fNobs` and `fNdistinct`, *collapse* presents a coherent set of extremely fast and flexible statistical functions (S3 generics) to perform column-wise, grouped and weighted computations on atomic vectors, matrices and data frames, with special support for *dplyr* grouped tibbles and `data.table`'s.

Usage

```
## All functions (FUN) follow a common syntax in 4 methods:
FUN(x, ...)

## Default S3 method:
FUN(x, g = NULL, [w = NULL,] TRA = NULL, [na.rm = TRUE,]
     use.g.names = TRUE, ...)

## S3 method for class 'matrix'
FUN(x, g = NULL, [w = NULL,] TRA = NULL, [na.rm = TRUE,]
     use.g.names = TRUE, drop = TRUE, ...)
```

```
## S3 method for class 'data.frame'
FUN(x, g = NULL, [w = NULL,] TRA = NULL, [na.rm = TRUE,]
     use.g.names = TRUE, drop = TRUE, ...)

## S3 method for class 'grouped_df'
FUN(x, [w = NULL,] TRA = NULL, [na.rm = TRUE,]
     use.g.names = FALSE, keep.group_vars = TRUE, [keep.w = TRUE,] ...)
```

Arguments

x	a vector, matrix, data frame or grouped tibble (<code>dplyr::grouped_df</code>).
g	a factor, GRP object, atomic vector (internally converted to factor) or a list of vectors / factors (internal
w	a numeric vector of (non-negative) weights, may contain missing values. Supported by fsum , fprod , t
TRA	an integer or quoted operator indicating the transformation to perform: 1 - "replace_fill" 2 - "replace"
na.rm	logical. Skip missing values in x. Defaults to TRUE in all functions and implemented at very little com
use.g.names	logical. Make group-names and add to the result as names (default method) or row-names (matrix and
drop	<i>matrix and data.frame methods</i> : Logical. TRUE drops dimensions and returns an atomic vector if g = N
keep.group_vars	<i>grouped_df method</i> : Logical. FALSE removes grouping variables after computation. By default groupi
keep.w	<i>grouped_df method</i> : Logical. TRUE (default) also aggregates weights and saves them in a column, FAL
...	arguments to be passed to or from other methods, and extra arguments to some functions, i.e. the algo

Details

Please see the documentation of individual functions.

Value

x suitably aggregated or transformed. Data frame column-attributes and overall attributes are preserved.

Notes

- Panel-decomposed (i.e. between and within) statistics as well as grouped and weighted skewness and kurtosis are implemented in [qsu](#).
- The vector-valued functions and operators [fscale/STD](#), [fbetween/B](#), [fHDbetween/HDB](#), [fwithin/W](#), [fHDwithin/HDW](#), [flag/L/F](#), [fdiff/D/Dlog](#) and [fgrowth/G](#) are documented under [Data Transformations](#) and [Time Series and Panel Series](#). These functions also support `plm::pseries` and `plm::pdata.frame`'s.

Examples

```
## default vector method
mpg <- mtcars$mpg
fsum(mpg)                               # Simple sum
```

```

fsum(mpg, TRA = "/")          # Simple transformation: divide all values by the sum
fsum(mpg, mtcars$cyl)         # Grouped sum
fmean(mpg, mtcars$cyl)       # Grouped mean
fmean(mpg, w = mtcars$hp)    # Weighted mean, weighted by hp
fmean(mpg, mtcars$cyl, mtcars$hp) # Grouped mean, weighted by hp
fsum(mpg, mtcars$cyl, TRA = "/") # Proportions / division by group sums
fmean(mpg, mtcars$cyl, mtcars$hp, # Subtract weighted group means, see also ?fwithin
      TRA = "-")

## data.frame method
fsum(mtcars)
fsum(mtcars, TRA = "%")      # This computes percentages
fsum(mtcars, mtcars[c(2,8:9)]) # Grouped column sum
g <- GRP(mtcars, ~ cyl + vs + am) # Here precomputing the groups!
fsum(mtcars, g)              # Faster !!
fmean(mtcars, g, mtcars$hp)
fmean(mtcars, g, mtcars$hp, "-") # Demeaning by weighted group means..
fmean(fgroup_by(mtcars, cyl, vs, am), hp, "-") # Another way of doing it..

fmode(wlddev, drop = FALSE)  # Compute statistical modes of variables in this data
fmode(wlddev, wlddev$income) # Grouped statistical modes ..

## matrix method
m <- qM(mtcars)
fsum(m)
fsum(m, g) # ..

## method for grouped tibbles - for use with dplyr
library(dplyr)
mtcars %>% group_by(cyl,vs,am) %>% select(mpg,carb) %>% fsum
mtcars %>% fgroup_by(cyl,vs,am) %>% fselect(mpg,carb) %>% fsum # equivalent and faster !!
mtcars %>% fgroup_by(cyl,vs,am) %>% fsum(TRA = "%")
mtcars %>% fgroup_by(cyl,vs,am) %>% fmean(hp) # weighted grouped mean, save sum of weights
mtcars %>% fgroup_by(cyl,vs,am) %>% fmean(hp, keep.group_vars = FALSE)

```

Benchmark

```

## This compares fsum with data.table (2 threads) and base::rowsum
# Starting with small data
mtcDT <- qDT(mtcars)
f <- qF(mtcars$cyl)

library(microbenchmark)
microbenchmark(mtcDT[, lapply(.SD, sum), by = f],
               rowsum(mtcDT, f, reorder = FALSE),
               fsum(mtcDT, f, na.rm = FALSE), unit = "relative")

          expr      min       lq     mean   median      uq     max neval cld

```

```

mtcDT[, lapply(.SD, sum), by = f] 145.436928 123.542134 88.681111 98.336378 71.880479 85.217726 100
rowsum(mtcDT, f, reorder = FALSE) 2.833333 2.798203 2.489064 2.937889 2.425724 2.181173 100 b
  fsum(mtcDT, f, na.rm = FALSE) 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 100 a

# Now larger data
tdata <- qDT(replicate(100, rnorm(1e5), simplify = FALSE)) # 100 columns with 100.000 obs
f <- qF(sample.int(1e4, 1e5, TRUE)) # A factor with 10.000 groups

microbenchmark(tdata[, lapply(.SD, sum), by = f],
               rowsum(tdata, f, reorder = FALSE),
               fsum(tdata, f, na.rm = FALSE), unit = "relative")

      expr      min       lq     mean  median      uq      max neval  cld
tdata[, lapply(.SD, sum), by = f] 2.646992 2.975489 2.834771 3.081313 3.120070 1.2766475 100 c
rowsum(tdata, f, reorder = FALSE) 1.747567 1.753313 1.629036 1.758043 1.839348 0.2720937 100 b
  fsum(tdata, f, na.rm = FALSE) 1.000000 1.000000 1.000000 1.000000 1.000000 1.0000000 100 a

```

See Also

[Collapse Overview](#), [Data Transformations](#), [Time Series and Panel Series](#)

A2-fast-grouping-ordering

Fast Grouping and Ordering

Description

collapse provides the following functions to efficiently group and order data:

- [radixorder](#), provides fast radix-ordering through direct access to the method base::`order(..., method = "radix")`, as well as the possibility to return some attributes very useful for grouping data and finding unique elements. [radixorder_v](#) exists as a programmers alternative. The function [roworder\(v\)](#) efficiently reorders a data frame based on an ordering computed by [radixorder_v](#).
- [GRP](#) creates *collapse* grouping objects of class 'GRP' based on [radixorder_v](#). 'GRP' objects form the central building block for grouped operations and programming in *collapse* and are very efficient inputs to all *collapse* functions supporting grouped operations. A 'GRP' object provides information about (1) the number of groups, (2) which rows belong to which group, (3) the group sizes, (4) the unique groups, (5) the variables used for grouping, (6) whether the grouping and initial inputs were ordered and (7) (optionally) the output from [radixorder](#) containing the ordering vector with group starts and maximum group size attributes.
- [fgroup_by](#) provides a fast replacement for `dplyr::group_by`, creating a grouped data frame with a 'GRP' object attached. This grouped data frame can however only be used for grouped operations using *collapse* fast functions.
- [funique](#) is a faster version of [unique](#). The data frame method also allows selecting unique rows according to a subset of the columns.

- **qF**, shorthand for 'quick-factor' implements very fast (ordered) factor generation from atomic vectors using either radix ordering method = "radix" or index hashing method = "hash". Factors can also be used for efficient grouped programming with *collapse* functions, especially if they are generated using `qF(x, na.exclude = FALSE)` which assigns a level to missing values and attaches a class 'na.included' ensuring that no additional missing value checks are executed by *collapse* functions.
- **qG**, shorthand for 'quick-group', generates a kind of factor-light without the levels attribute but instead an attribute providing the number of levels. Optionally the levels / groups can be attached, but without converting them to character. Objects have a class 'qG', which is also recognized in the *collapse* ecosystem.
- **fdroplevels** is a substantially faster replacement for `base::droplevels`.
- **finteraction** is a fast alternative to `base::interaction` implemented as a wrapper around `as.factor_GRP(GRP(...))`. It can be used to generate a factor from multiple vectors, factors or a list of vectors / factors. Unused factor levels are always dropped.
- **groupid** is a generalization of `data.table::rleid` providing a run-length type group-id from atomic vectors. It is generalization as it also supports passing an ordering vector and skipping missing values. For example **qF** and **qG** with method = "radix" are essentially implemented using `groupid(x, radixorder(x))`.
- **seqid** is a specialized function which creates a group-id from sequences of integer values. For any ordinary panel dataset `groupid(id, order(id, time))` and `seqid(time, order(id, time))` provide the same id variable. **seqid** is especially useful for identifying discontinuities in time-sequences and helps to perform operations such as lags or differences on irregularly spaced time series and panels.

Table of Functions

<i>Function / S3 Generic</i>	<i>Methods</i>	<i>Description</i>
<code>radixorder(v)</code>	No methods, for data frames and vectors	Radix-based ordering -
<code>roworder(v)</code>	No methods, for data frames	Row sorting/reordering
<code>GRP</code>	<code>default</code> , <code>GRP</code> , <code>factor</code> , <code>qG</code> , <code>grouped_df</code> , <code>pseries</code> , <code>pdata.frame</code>	Fast grouping and a fle
<code>fgroup_by</code>	No methods, for data frames	Fast grouped data fram
<code>funique</code>	<code>default</code> , <code>data.frame</code>	Fast unique values/row
<code>qF</code>	No methods, for vectors	Quick factor generation
<code>qG</code>	No methods, for vectors	Quick grouping of vect
<code>fdroplevels</code>	<code>factor</code> , <code>data.frame</code> , <code>list</code>	Fast removal of unusec
<code>finteraction</code>	No methods, for data frames and vectors	Fast interactions
<code>groupid</code>	No methods, for vectors	Run-length type group
<code>seqid</code>	No methods, for vectors	Run-length type intege

See Also

[Collapse Overview](#), [Data Frame Manipulation](#), [Fast Statistical Functions](#)

A3-fast-data-manipulation

Fast Data Manipulation

Description

collapse provides the following functions for fast manipulation of (mostly) data frames.

- `fselect` is a much faster alternative to `dplyr::select` to select columns using expressions involving column names. `get_vars` is a more versatile and programmer friendly function to efficiently select and replace columns by names, indices, logical vectors, regular expressions or using functions to identify columns.
- The functions `num_vars`, `cat_vars`, `char_vars`, `fact_vars`, `logi_vars` and `Date_vars` are convenience functions to efficiently select and replace columns by data type.
- `add_vars` efficiently adds new columns at any position within a data frame (default at the end). This can be done via replacement (i.e. `add_vars(data) <- newdata`) or returning the appended data (i.e. `add_vars(data, newdata1, newdata2, ...)`). Because of the latter, `add_vars` is also a more efficient alternative to `cbind.data.frame`.
- `fsubset` is a much faster version of `base::subset` to efficiently subset vectors, matrices and data frames. If the non-standard evaluation offered by `fsubset` is not needed, the function `ss` is a much faster and also more secure alternative to `[.data.frame`.
- `ftransform` is a much faster version of `base::transform`, to modify and delete existing columns or append a data frame with new computed columns. `settransform` does all of that by reference, i.e. it modifies the data frame in the global environment. `fcompute` is similar to `ftransform` but only returns modified and computed columns in a new data frame.
- `roworder` is a fast substitute for `dplyr::arrange`, but the syntax is inspired by `data.table::setorder`.
- `colorder` efficiently reorders columns in a data frame, see also `data.table::setcolorder`.
- `frename` is a fast substitute for `dplyr::rename`, to efficiently rename various objects. `setrename` renames objects by reference.

Table of Functions

Function / S3 Generic

```
fselect(<-)
get_vars(<-), num_vars(<-), cat_vars(<-), char_vars(<-), fact_vars(<-), logi_vars(<-), Date_vars(<-)
add_vars(<-)
fsubset
ss
(f/set)ftransform(<-)
fcompute
roworder(v)
colorder(v)
(f/set)rename
```

See Also

[Collapse Overview](#), [Quick Data Conversion](#), [Recode and Replace Values](#)

A4-quick-conversion *Quick Data Conversion*

Description

Fast, flexible and precise conversion of common data objects, without method dispatch and extensive checks:

- `qDF`, `qDT` and `qTBL` convert vectors, matrices, higher-dimensional arrays and suitable lists to data frame, *data.table* and *tibble*, respectively.
- `qM` converts vectors, higher-dimensional arrays, data frames and suitable lists to matrix.
- `mctl` and `mrtl` column- or row-wise convert a matrix to list, data frame or *data.table*. They are used internally by `qDF` and `qDT`, [dapply](#), [BY](#), etc...
- `qF` converts atomic vectors to factor (documented on a separate page).
- `as.numeric_factor` and `as.character_factor` convert factors, or all factor columns in a data frame / list, to numeric or character (by converting the levels).

Usage

```
qDF(X, row.names.col = FALSE, keep.attr = FALSE, class = "data.frame")
qDT(X, row.names.col = FALSE, keep.attr = FALSE, class = c("data.table", "data.frame"))
qTBL(X, row.names.col = FALSE, keep.attr = FALSE)
qM(X, keep.attr = FALSE, class = NULL)
as.numeric_factor(X, keep.attr = TRUE)
as.character_factor(X, keep.attr = TRUE)

# Programmer functions: matrix rows or columns to list - fully in C++
mctl(X, names = FALSE, return = "list")
mrtl(X, names = FALSE, return = "list")
```

Arguments

<code>X</code>	a vector, factor, matrix, higher-dimensional array, data frame or list. <code>mctl</code> and <code>mrtl</code> only accept matrices, <code>as.numeric_factor</code> and <code>as.character_factor</code> only accept factors, data frames or lists.
<code>row.names.col</code>	should a column capturing names or <code>row.names</code> be added? i.e. when converting atomic objects to data frame or data frame to <i>data.table</i> . Can be logical <code>TRUE</code> , which will add a column "row.names" in front, or can supply a name for the column i.e. "column1".

keep.attr	logical. FALSE (default) yields a <i>hard / thorough</i> object conversion: All unnecessary attributes are removed from the object yielding a plain matrix / data.frame / data.table. FALSE yields a <i>soft / minimal</i> object conversion: Only the attributes 'names', 'row.names', 'dim', 'dimnames' and 'levels' are modified in the conversion. Other attributes are preserved. See also class.												
class	if a vector of classes is passed here, the converted object will be assigned these classes. If NULL is passed, the default classes are assigned: qM assigns no class, qDF a class "data.frame", and qDT a class c("data.table", "data.frame"). If keep.attr = TRUE and class = NULL and the object already inherits the default classes, further inherited classes are preserved. See Details and the Example.												
names	logical. Should the list be named using row/column names from the matrix?												
return	an integer or string specifying what to return. The options are:												
	<table> <thead> <tr> <th><i>Int.</i></th> <th><i>String</i></th> <th><i>Description</i></th> </tr> </thead> <tbody> <tr> <td>1</td> <td>"list"</td> <td>returns a plain list</td> </tr> <tr> <td>2</td> <td>"data.frame"</td> <td>returns a plain data.frame</td> </tr> <tr> <td>3</td> <td>"data.table"</td> <td>returns a plain <i>data.table</i></td> </tr> </tbody> </table>	<i>Int.</i>	<i>String</i>	<i>Description</i>	1	"list"	returns a plain list	2	"data.frame"	returns a plain data.frame	3	"data.table"	returns a plain <i>data.table</i>
<i>Int.</i>	<i>String</i>	<i>Description</i>											
1	"list"	returns a plain list											
2	"data.frame"	returns a plain data.frame											
3	"data.table"	returns a plain <i>data.table</i>											

Details

Object conversions using these functions are maximally efficient and involve 3 consecutive steps: (1) Converting the storage mode / dimensions / data of the object, (2) converting / modifying the attributes and (3) modifying the class of the object:

(1) is determined by the choice of function and the optional row.names.col argument to qDF and qDT. Higher-dimensional arrays are converted by expanding the second dimension (adding columns, same as as.matrix, as.data.frame, as.data.table).

(2) is determined by the keep.attr argument: keep.attr = TRUE seeks to preserve the attributes of the object. It's effect is like copying attributes(converted) <- attributes(original), and then modifying the "dim", "dimnames", "names", "row.names" and "levels" attributes as necessitated by the conversion task. keep.attr = FALSE only converts / assigns / removes these attributes and drops all others.

(3) is determined by the class argument: Setting class = "myclass" will yield a converted object of class "myclass", with any other / prior classes being removed by this replacement. Setting class = NULL does NOT mean that a class NULL is assigned (which would remove the class attribute), but rather that the default classes are assigned: qM assigns no class, qDF a class "data.frame", and qDT a class c("data.table", "data.frame"). At this point there is an interaction with keep.attr: If keep.attr = TRUE and class = NULL and the object converted already inherits the respective default classes, then any other inherited classes will also be preserved (with qM(x, keep.attr = TRUE, class = NULL) any class will be preserved if is.matrix(x) evaluated to TRUE.)

The default keep.attr = FALSE ensures *hard* conversions so that all unnecessary attributes are dropped. Furthermore in qDF and qDT the default classes were explicitly assigned, thus any other classes (like 'tbl_df', 'tbl', 'pdata.frame', 'sf', 'tsibble' etc.) will be removed when these objects are passed, regardless of the keep.attr setting. This is to ensure that the default methods for 'data.frame' and 'data.table' can be assumed to work, even if the user chooses to preserve further

attributes. For `qM` a more lenient default setup was chosen to enable the full preservation of time series matrices with `keep.attr = TRUE`. If the user wants to keep attributes attached to a matrix but make sure that all default methods work properly, either one of `qM(x, keep.attr = TRUE, class = "matrix")` or `unclass(qM(x, keep.attr = TRUE))` should be employed.

Value

`qDF` - returns a `data.frame`
`qDT` - returns a `data.table`
`qTBL` - returns a `tibble`
`qM` - returns a matrix
`mctl`, `mrtl` - return a list, data frame or *data.table*
`qF` - returns a factor
`as.numeric_factor` - returns `X` with factors converted to numeric variables
`as.character_factor` - returns `X` with factors converted to character variables

Note

`qTBL` is a simple wrapper around `qDT` assigning different classes, i.e. `qTBL(x)` is equivalent to `qDT(x, class = c("tbl_df", "tbl", "data.frame"))`. Similar converters for other data frame based classes are easily created from `qDF` and `qDT`. The principle difference between them is that `qDF` preserves rownames whereas `qDT` always assigns integer rownames.

See Also

[qF, Collapse Overview](#)

Examples

```
## Basic Examples
mtcarsM <- qM(mtcars)           # Matrix from data.frame
mtcarsDT <- qDT(mtcarsM)       # data.table from matrix columns
mtcarsTBL <- qTBL(mtcarsM)     # tibble from matrix columns
head(mrtl(mtcarsM, TRUE, "data.frame")) # data.frame from matrix rows, etc..
head(qDF(mtcarsM, "cars"))     # Adding a row.names column when converting from matrix
head(qDT(mtcars, "cars"))      # Saving row.names when converting data frame to data.table

cylF <- qF(mtcars$cyl)         # Factor from atomic vector
cylF

# Factor to numeric conversions
identical(mtcars, as.numeric_factor(dapply(mtcars, qF)))
```

A6-data-transformations

Data Transformations

Description

collapse provides an ensemble of functions to perform common data transformations efficiently and user friendly:

- **dapply** applies functions to **rows or columns** of matrices and data frames, preserving the data format.
- **BY** is an S3 generic for **Split-Apply-Combine computing** and can perform aggregation as well as grouped transformations (for aggregation please also see [collap](#) and the [Fast Statistical Functions](#)).
- **TRA** is an S3 generic to efficiently perform (groupwise) **replacement and sweeping out of statistics**. Supported operations are:

<i>Integer-id</i>	<i>String-id</i>	<i>Description</i>
1	"replace_fill"	replace and overwrite missing values
2	"replace"	replace but preserve missing values
3	"-"	subtract
4	"-+"	subtract group-statistics but add group-frequency weighted average of group statistics
5	"/"	divide
6	"%"	compute percentages
7	"+"	add
8	"*"	multiply
9	"%%"	modulus
10	"-%%"	subtract modulus

All of *collapse*'s [Fast Statistical Functions](#) have a built-in TRA argument for faster access (i.e. you can compute (groupwise) statistics and use them to transform your data with a single function call).

- **fscale/STD** is an S3 generic to perform (groupwise and / or weighted) **scaling / standardizing** of data and is orders of magnitude faster than `base::scale`.
- **fwithin/W** is an S3 generic to efficiently perform (groupwise and / or weighted) **within-transformations / demeaning / centering** of data. Similarly **fbetween/B** computes (groupwise and / or weighted) **between-transformations / averages**.
- **fHDwithin/HDW**, shorthand for 'higher-dimensional within transform', is an S3 generic to efficiently **center data on multiple groups** and partial-out linear models (possibly involving many levels of fixed effects). In other words, **fHDwithin/HDW** efficiently computes **residuals** from (potentially complex) linear models. Similarly **fHDbetween/HDB**, shorthand for 'higher-dimensional between transformation', computes the corresponding means or **fitted values**.
- **flm** is an efficient function for bare-bones (weighted) **linear model fitting**. It supports 6 different fitting methods, 4 from base R, and 2 utilizing the *RcppArmadillo* or *RcppEigen* packages.

- `flag/L/F`, `fdiff/D/Dlog` and `fgrowth/G` are S3 generics to compute sequences of **lags / leads** and suitably lagged and iterated (quasi-, log-) **differences** and **growth rates** on time series and panel data. More in [Time Series and Panel Series](#).
- `STD`, `W`, `B`, `HDW`, `HDB`, `L`, `D`, `Dlog` and `G` are parsimonious wrappers around the f- functions above representing the corresponding transformation 'operators'. They have additional capabilities when applied to data-frames (i.e. variable selection, formula input, auto-renaming and id-variable preservation), and are easier to employ in regression formulas, but are otherwise identical in functionality.

Table of Functions

<i>Function / S3 Generic</i>	<i>Methods</i>	<i>Description</i>
<code>dapply</code>	No methods, works with matrices and data frames	Apply functions to
<code>BY</code>	default, matrix, data.frame, grouped_df	Split-Apply-Comb
<code>TRA</code>	default, matrix, data.frame, grouped_df	Replace and sweep
<code>fscale/STD</code>	default, matrix, data.frame, pseries, pdata.frame, grouped_df	Scale / standardize
<code>fwithin/W</code>	default, matrix, data.frame, pseries, pdata.frame, grouped_df	Demean / center d
<code>fbetween/B</code>	default, matrix, data.frame, pseries, pdata.frame, grouped_df	Compute means /
<code>fHDwithin/HDW</code>	default, matrix, data.frame, pseries, pdata.frame	High-dimensional
<code>fHDbetween/HDB</code>	default, matrix, data.frame, pseries, pdata.frame	High-dimensional
<code>flm</code>	No methods, for matrices	Linear model fitting
<code>flag/L/F</code>	default, matrix, data.frame, pseries, pdata.frame, grouped_df	(Sequences of) lag
<code>fdiff/D/Dlog</code>	default, matrix, data.frame, pseries, pdata.frame, grouped_df	(Sequences of) lag
<code>fgrowth/G</code>	default, matrix, data.frame, pseries, pdata.frame, grouped_df	(Sequences of) lag

See Also

[Collapse Overview](#), [Fast Statistical Functions](#), [Time Series and Panel Series](#)

A7-time-series-panel-series

Time Series and Panel Series

Description

collapse provides the following functions to work with time-dependent data:

- `flag`, and the lag- and lead- operators `L` and `F` are S3 generics to efficiently compute sequences of **lags and leads** on ordered or unordered time series and panel data.
- `fdiff`, `fgrowth`, and the operators `D`, `Dlog` and `G` are S3 generics to efficiently compute sequences of suitably lagged / leaded and iterated **differences, log-differences and growth rates** on ordered or unordered time series and panel data. `fdiff/D/Dlog` can also compute **quasi-differences** of the form $x_t - \rho x_{t-1}$ or $\log(x_t) - \rho \log(x_{t-1})$ for log-differences.

- `psmat` is an S3 generic to efficiently convert panel-vectors or `plm::pseries` and data frames or `plm::pdata.frame`'s to **panel series matrices and 3D arrays**, respectively.
- `psacf`, `pspacf` and `psccf` are S3 generics to compute estimates of the **auto-, partial auto- and cross- correlation or covariance functions** for panel-vectors or `plm::pseries`, and multivariate versions for data frames or `plm::pdata.frame`'s.

Table of Functions

<i>S3 Generic</i>	<i>Methods</i>	<i>Description</i>
<code>flag/L/F</code>	default, matrix, data.frame, pseries, pdata.frame, grouped_df	Compute (sequences of) la
<code>fdiff/D/Dlog</code>	default, matrix, data.frame, pseries, pdata.frame, grouped_df	Compute (sequences of) la
<code>fgrowth/G</code>	default, matrix, data.frame, pseries, pdata.frame, grouped_df	Compute (sequences of) la
<code>psmat</code>	default, pseries, data.frame, pdata.frame	Convert panel data to matr
<code>psacf</code>	default, pseries, data.frame, pdata.frame	Compute ACF on panel da
<code>pspacf</code>	default, pseries, data.frame, pdata.frame	Compute PACF on panel c
<code>psccf</code>	default, pseries, data.frame, pdata.frame	Compute CCF on panel da

See Also

[Collapse Overview, Data Transformations](#)

A8-list-processing *List Processing*

Description

`collapse` provides the following set of functions to work with lists of R objects:

- **Search and Identification**

- `is.regular` checks whether an R object is either atomic or a list. A (nested) list composed of regular objects at each level of the list-tree is unlistable to an atomic vector - checked by `is.unlistable`.
- `ldepth` determines the level of nesting of the list (i.e. the maximum number of nodes of the list-tree).
- `has_elem` searches elements in a list using element names, regular expressions applied to element names, or a function applied to the elements, and returns TRUE if any matches were found.

- **Subsetting**

- `atomic_elem` examines the top-level of a list and returns a sublist with the atomic elements. Conversely `list_elem` returns the sublist of elements which are themselves lists or list-like objects.

- `reg_elem` and `irreg_elem` are recursive versions of the former. `reg_elem` extracts the regular part of the list-tree (leading to atomic elements in the final nodes), while `irreg_elem` extracts the 'irregular' part of the list tree leading to non-atomic elements in the final nodes. (*Tip*: try calling both on an `lm` object). Naturally for all lists `l`, `is.unlistable(reg_elem(l))` evaluates to `TRUE`...
 - `get_elem` extracts elements from a list using element names, regular expressions applied to element names, a function applied to the elements, or element-indices used to subset the lowest-level sub-lists. by default the result is presented as a simplified list containing all matching elements. With the `keep.tree` option however `get_elem` can also be used to subset lists i.e. maintain the full tree but cut off non-matching branches.
- **Splitting**
 - `rsplit` recursively splits a vector or data frame into subsets according to combinations of (multiple) vectors / factors - by default returning a (nested) list. If `flatten = TRUE`, the list is flattened yielding the same result as `split`. `rsplit` is also faster than `split`, particularly for data frames.
 - **Apply Functions**
 - `rapply2d` is a recursive version of `base::lapply` with two key differences to `base::rapply`: (1) Data frames are considered as atomic objects, not as (sub-)lists, and (2) the result is not simplified.
 - **Unlisting / Row-Binding**
 - `unlist2d` efficiently unlists unlistable lists in 2-dimensions and creates a data frame (or *data.table*) representation of the list (unlike `base::unlist` which returns an atomic vector). This is done by recursively flattening and row-binding R objects in the list (using `data.table::rbindlist`) while creating identifier columns for each level of the list-tree and (optionally) saving the row-names of the objects in a separate column. `unlist2d` can thus also be understood as a recursive generalization of `do.call(rbind, l)`, for lists of vectors, data frames, arrays or heterogeneous objects.

Table of Functions

<i>Function</i>	<i>Description</i>
<code>is.regular</code>	<code>function(x) is.atomic(x) is.list(x)</code>
<code>is.unlistable</code>	Checks if list is unlistable
<code>ldepth</code>	Level of nesting / maximum depth of list-tree
<code>has_elem</code>	Checks if list contains a certain element
<code>get_elem</code>	Subset list / extract certain elements
<code>atomic_elem</code>	Top-level subset atomic elements
<code>list_elem</code>	Top-level subset list/list-like elements
<code>reg_elem</code>	Recursive version of <code>atomic_elem</code> : Subset / extract regular part of list
<code>irreg_elem</code>	Subset / extract non-regular part of list
<code>rsplit</code>	Recursively split vectors or data frames / lists
<code>rapply2d</code>	Recursively apply functions to lists of data objects
<code>unlist2d</code>	Recursively unlist/row-bind lists of data objects in 2D, to data frame or <i>data.table</i>

See Also

[Collapse Overview](#)

A9-summary-statistics *Summary Statistics*

Description

collapse provides the following functions to efficiently summarize and examine data:

- [qsu](#), shorthand for quick-summary, is an extremely fast summary command inspired by the (xt)summarize command in the STATA statistical software. It computes a set of 7 statistics (nobs, mean, sd, min, max, skewness and kurtosis) using a numerically stable one-pass method. Statistics can be computed weighted, by groups, and also within-and between entities (for multilevel / panel data).
- [descr](#) computes a concise and detailed description of a data frame, including frequency tables for categorical variables and various statistics and quantiles for numeric variables. It is inspired by `Hmisc::describe`, but about 10x faster.
- [pwcov](#), [pwcov](#) and [pwNobs](#) compute pairwise correlations, covariances and observation counts on matrices and data frames. Pairwise correlations and covariances can be computed together with observation counts and p-values, and output as 3D array (default) or list of matrices. A major feature of `pwcov` and `pwcov` is the print method displaying all of these statistics in a single correlation table.
- [varying](#) very efficiently checks for the presence of any variation in data (optionally) within groups (such as panel-identifiers).
- [fftest](#) is a fast implementation of the R-Squared based F-test, to test **exclusion restrictions** in linear models potentially involving multiple large factors (fixed effects). It internally utilizes [fHDwithin](#) to project out factors while counting the degrees of freedom.

Table of Functions

<i>Function / S3 Generic</i>	<i>Methods</i>	<i>Description</i>
qsu	default, matrix, data.frame, pseries, pdata.frame	Fast (grouped, weighted)
descr	No methods, for data frames or lists of vectors	Detailed statistical
pwcov	No methods, for matrices or data frames	Pairwise correlation
pwcov	No methods, for matrices or data frames	Pairwise covariance
pwNobs	No methods, for matrices or data frames	Pairwise observation
varying	default, matrix, data.frame, pseries, pdata.frame, grouped_df	Fast variation check
fftest	No methods, it's a standalone test to which data needs to be supplied.	Fast F-test of exclusion

See Also

[Collapse Overview, Fast Statistical Functions](#)

AA1-recode-replace *Recode and Replace Values in Matrix-Like Objects*

Description

A small suite of functions to efficiently perform common recoding and replacing tasks in matrix-like objects (vectors, matrices, arrays, data frames, lists of atomic objects):

- `recode_num` and `recode_char` can be used to efficiently recode multiple numeric or character values, respectively. The syntax is inspired by `dplyr::recode`, but the functionality is enhanced in the following respects: (1) they are faster than `dplyr::recode`, (2) when passed a data frame / list, all appropriately typed columns will be recoded. (3) They preserve the attributes of the data object and of columns in a data frame / list, and (4) `recode_char` also supports regular expression matching using [grepl](#).
- `replace_NA` efficiently replaces NA/NaN with a value. data frames can be multi-typed.
- `replace_Inf` replaces Inf/-Inf (or optionally NaN/Inf/-Inf) with a value (default is NA). `replace_Inf` skips non-numeric columns in a data frame.
- `replace_outliers` replaces values falling outside a 1- or 2-sided numeric threshold or outside a certain number of column- standard deviations with a value (default is NA). `replace_outliers` skips non-numeric columns in a data frame.

Usage

```
recode_num(X, ..., default = NULL, missing = NULL)

recode_char(X, ..., default = NULL, missing = NULL, regex = FALSE)

replace_NA(X, value)

replace_Inf(X, value = NA, replace.nan = FALSE)

replace_outliers(X, limits, value = NA,
                 single.limit = c("SDs", "min", "max", "overall_SDs"))
```

Arguments

<code>X</code>	a vector, matrix, array, data frame or list of atomic objects.
<code>...</code>	comma-separated recode arguments of the form: <code>value = replacement, `2` = 0, Secondary = "SEC" etc..</code> <code>recode_char</code> with <code>regex = TRUE</code> also supports regular expressions i.e. <code>``^S D\$`` = "STD" etc.</code>
<code>default</code>	optional argument to specify a scalar value to replace non-matched elements with.

missing	optional argument to specify a scalar value to replace missing elements with. <i>Note</i> that to increase efficiency this is done before the rest of the recoding i.e. the recoding is performed on data where missing values are filled!
regex	logical. If TRUE, all recode-argument names are (sequentially) passed to <code>grep1</code> as a pattern to search X. All matches are replaced. <i>Note</i> that NA's are also matched as strings by <code>grep1</code> .
value	a single (scalar) value to replace matching elements with.
replace.nan	logical. TRUE replaces NaN/Inf/-Inf. FALSE (default) replaces only Inf/-Inf.
limits	either a vector of two-numeric values <code>c(minval,maxval)</code> constituting a two-sided outlier threshold, or a single numeric value constituting either a factor of standard deviations (default), or the minimum or maximum of a one-sided outlier threshold. See also <code>single.limit</code> .
single.limit	a character or integer (argument only applies if <code>length(limits) == 1</code>): <ul style="list-style-type: none"> • 1 - "SDs" specifies that <code>limits</code> will be interpreted as a (two-sided) threshold in column standard-deviations. The underlying code is equivalent to <code>X[abs(fscale(X)) > limits] <-value</code> but faster. Since <code>fscale</code> is S3 generic with methods for <code>grouped_df</code>, <code>pseries</code> and <code>pdata.frame</code>, the standardizing will be grouped if such objects are passed (i.e. the outlier threshold is then measured in within-group standard deviations). • 2 - "min" specifies that <code>limits</code> will be interpreted as a (one-sided) minimum threshold. The underlying code is equivalent to <code>X[X < limits] <-value</code>. • 3 - "max" specifies that <code>limits</code> will be interpreted as a (one-sided) maximum threshold. The underlying code is equivalent to <code>X[X > limits] <-value</code>. • 4 - "overall_SDs" is equivalent to "SDs" but ignores groups when a <code>grouped_df</code>, <code>pseries</code> or <code>pdata.frame</code> is passed (i.e. standardizing and determination of outliers is by the overall column standard deviation).

Note

These functions are not generic and do not offer support for factors or date(-time) objects. see `dplyr::recode_factor`, `forcats` and other appropriate packages for dealing with these classes.

See Also

[Collapse Overview, Small \(Helper\) Functions](#)

Examples

```
recode_char(c("a","b","c"), a = "b", b = "c")
recode_char(month.name, ber = NA, regex = TRUE)
mtcr <- recode_num(mtcars, `0` = 2, `4` = Inf, `1` = NaN)
replace_Inf(mtcr)
replace_Inf(mtcr, replace.nan = TRUE)
replace_outliers(mtcars, c(2, 100))           # Replace all values below 2 and above 100 w. NA
replace_outliers(mtcars, 2, single.limit = "min") # Replace all value smaller than 2 with NA
replace_outliers(mtcars, 100, single.limit = "max") # Replace all value larger than 100 with NA
replace_outliers(mtcars, 2)                   # Replace all values above or below 2 column-
                                              # standard-deviations from the column-mean w. NA
```

```
replace_outliers(fgroup_by(iris, Species), 2) # Passing a grouped_df, pseries or pdata.frame
# allows to remove outliers according to
# in-group standard-deviation. see ?fscale
```

AA2-small-helpers *Small (Helper) Functions*

Description

Convenience functions in the *collapse* package that help to deal with attributes such as variable names and labels, missing values, matching and object checking etc.. Some functions are performance improved replacements for base R functions.

Usage

```
.c(...) # Non-standard concatenation i.e. .c(a, b) == c("a", "b")
vlabels(X, attrn = "label") # Get labels of variables in X, in attr(X[[i]], attrn)
vlabels(X, attrn = "label") <- value # Set labels of variables in X
vclasses(X) # Get classes of variables in X
vtypes(X) # Get data storage types of variables in X (calling typeof)
namlab(X, class = FALSE, # Return data frame of names, labels and classes
      attrn = "label")
add_stub(X, stub, pre = TRUE) # Add a stub (i.e. prefix or postfix) to column names
rm_stub(X, stub, pre = TRUE) # Remove stub from column names
x %!in% table # The opposite of %in%
ckmatch(x, table, # Check-match: throws an informative error if non-matched
      e = "Unknown columns:")
fnlevels(x) # Faster version of nlevels(x) (for factors)
fnrow(X) # Faster nrow for data frames (not faster for matrices)
fncol(X) # Faster ncol for data frames (not faster for matrices)
fdim(X) # Faster dim for data frames (not faster for matrices)
na_rm(x) # Remove missing values from vector and return vector
na_omit(X, cols = NULL, # Faster na.omit for matrices and data frames
      na.attr = FALSE)
na_insert(X, prop = 0.1) # Insert missing values at random in vectors, matrices DF's
cinv(X) # Choleski (fast) inverse of symmetric, positive def. matrix
all_identical(...) # Check exact equality of multiple objects or list-elements
all_obj_equal(...) # Check near equality of multiple objects or list-elements
seq_row(X) # Fast integer sequences along rows of X
seq_col(X) # Fast integer sequences along columns of X
setRownames(object,
  nm = if(is.atomic(object)) # Set rownames of object and return object
  seq_row(object) else NULL)
setColnames(object, nm) # Set colnames of object and return object
setDimnames(object, dn,
  which = NULL) # Set dimension names of object and return object
unattrib(object) # Remove all attributes from object
```

```

setAttrib(object, a)      # Replace all attributes with list of attributes 'a'
copyAttrib(to, from)     # Copy all attributes from object 'from' to object 'to'
copyMostAttrib(to, from) # Copy most attributes from object 'from' to object 'to'
is.categorical(x)        # The opposite of is.numeric
is.Date(x)              # Check if object is of class "Date", "POSIXlt" or "POSIXct"

```

Arguments

X	a matrix or data frame (some functions also support vectors and arrays although that is less common).
x, table	a atomic vector.
object, to, from	a suitable R object.
a	a suitable list of attributes.
attrn	character. Name of attribute to store labels or retrieve labels from.
value	a matching character vector of variable labels.
class	logical. Also show the classes of variables in X in a column?
stub	a single character stub, i.e. "log.", which by default will be pre-applied to all variables or column names in X.
pre	logical. FALSE will post-apply stub.
cols	only removes rows with missing values on these columns. Columns can be selected using column names, indices, a logical vector or a selector function (i.e. <code>is.numeric</code>).
na.attr	logical. TRUE adds an attribute containing the removed cases. For compatibility reasons this is exactly the same format as <code>na.omit</code> i.e. the attribute is called "na.action" and of class "omit".
nm	a suitable vector of row- or column-names.
dn	a suitable vector or list of names for dimension(s).
which	integer. If NULL, dn has to be a list fully specifying the dimension names of the object. Alternatively, a vector or list of names for dimensions which can be supplied. See Examples.
prop	double. Specify the proportion of observations randomly replaced with NA.
e	the error message thrown by <code>ckmatch</code> for non-matched elements. The message is followed by the comma-separated non-matched elements.
...	for <code>.c</code> : Comma-separated expressions. For <code>all_identical</code> / <code>all_obj_equal</code> : Either multiple comma-separated objects or a single list of objects in which all elements will be checked for exact / numeric equality.

See Also

[Collapse Overview](#)

Examples

```
## Non-standard concatenation
.c(a, b, "c d", e == f)

## Variable labels
namlab(wlddev, class = TRUE)
vlabels(wlddev)
vlabels(wlddev) <- vlabels(wlddev)

## Stub-renaming
log_mtc <- add_stub(log(mtcars), "log.")
head(log_mtc)
head(rm_stub(log_mtc, "log."))
rm(log_mtc)

## Setting dimension names of an object
head(setRownames(mtcars))
ar <- array(1:9, c(3,3,3))
setRownames(ar)
setColnames(ar, c("a","b","c"))
setDimnames(ar, c("a","b","c"), which = 3)
setDimnames(ar, list(c("d","e","f"), c("a","b","c")), which = 2:3)
setDimnames(ar, list(c("g","h","i"), c("d","e","f"), c("a","b","c")))

## Checking exact equality of multiple objects
all_identical(iris, iris, iris, iris)
l <- replicate(100, fmean(num_vars(iris), iris$Species), simplify = FALSE)
all_identical(l)
rm(l)

## Missing values
mtc_na <- na_insert(mtcars, 0.15) # Set 15% of values missing at random
fNobs(mtc_na) # See observation count
na_omit(mtc_na) # 12x faster than na.omit(mtc_na)
na_omit(mtc_na, na.attr = TRUE) # Adds attribute with removed cases, like na.omit
na_omit(mtc_na, cols = c("vs","am")) # Removes only cases missing vs or am
na_omit(qM(mtc_na)) # Also works for matrices
na_omit(mtc_na$vs, na.attr = TRUE) # Also works with vectors
na_rm(mtc_na$vs) # For vectors na_rm is faster ...
rm(mtc_na)
```

Description

BY is an S3 generic that efficiently applies functions over vectors or matrix- and data frame columns by groups. Similar to [dapply](#) it seeks to retain the structure and attributes of the data, but can also output to various standard formats. A simple parallelism is also available.

Usage

```

BY(x, ...)

## Default S3 method:
BY(x, g, FUN, ..., use.g.names = TRUE, sort = TRUE,
   expand.wide = FALSE, parallel = FALSE, mc.cores = 1L,
   return = c("same", "vector", "list"))

## S3 method for class 'matrix'
BY(x, g, FUN, ..., use.g.names = TRUE, sort = TRUE,
   expand.wide = FALSE, parallel = FALSE, mc.cores = 1L,
   return = c("same", "matrix", "data.frame", "list"))

## S3 method for class 'data.frame'
BY(x, g, FUN, ..., use.g.names = TRUE, sort = TRUE,
   expand.wide = FALSE, parallel = FALSE, mc.cores = 1L,
   return = c("same", "matrix", "data.frame", "list"))

## S3 method for class 'grouped_df'
BY(x, FUN, ..., use.g.names = FALSE, keep.group_vars = TRUE,
   expand.wide = FALSE, parallel = FALSE, mc.cores = 1L,
   return = c("same", "matrix", "data.frame", "list"))

```

Arguments

x	a atomic vector, matrix, data frame or alike object.
g	a factor, GRP object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a GRP object) used to group x.
FUN	a function, can be scalar- or vector-valued.
...	further arguments to FUN.
use.g.names	logical. Make group-names and add to the result as names (default method) or row-names (matrix and data frame methods). No row-names are generated for <i>data.table</i> 's.
sort	logical. Sort the groups? Internally passed to GRP or qF , and only effective if g is not already a factor or GRP object.
expand.wide	logical. If FUN is a vector-valued function returning a vector of fixed length > 1 (such as the quantile function), <code>expand.wide</code> can be used to return the result in a wider format (instead of stacking the resulting vectors of fixed length above each other in each output column).
parallel	logical. TRUE implements simple parallel execution by internally calling <code>parallel::mclapply</code> instead of <code>base::lapply</code> .
mc.cores	integer. Argument to <code>parallel::mclapply</code> indicating the number of cores to use for parallel execution. Can use <code>parallel::detectCores()</code> to select all available cores. See also <code>?parallel::mclapply</code> .
return	an integer or string indicating the type of object to return. The default 1 - "same" returns the same object type (i.e. class and other attributes are retained, just

the names for the dimensions are adjusted). 2 -"matrix" always returns the output as matrix, 3 -"data.frame" always returns a data frame and 4 -"list" returns the raw (uncombined) output. *Note:* 4 -"list" works together with `expand.wide` to return a list of matrices.

`keep.group_vars`

grouped_df method: Logical. FALSE removes grouping variables after computation.

Details

BY is a frugal re-implementation of the Split-Apply-Combine computing paradigm. It is generally faster than `base::tapply`, `base::by`, `base::aggregate` and `plyr`, and preserves data attributes just like `dapply`.

It is however principally a wrapper around `lapply(split(x,g),FUN,...)`, that strongly optimizes on attribute checking compared to *base* R functions. For more details look at the documentation for `dapply` which works very similar (apart from the splitting performed in BY). For larger tasks requiring split-apply-combine computing on data frames use *dplyr*, *data.table*, or try to work with the [Fast Statistical Functions](#).

BY is used internally in `collap` for functions that are not [Fast Statistical Functions](#).

Value

X where FUN was applied to every column split by g.

See Also

[dapply](#), [collap](#), [Fast Statistical Functions](#), [Data Transformations](#), [Collapse Overview](#)

Examples

```
v <- iris$Sepal.Length # A numeric vector
f <- iris$Species      # A factor. Vectors/lists will internally be converted to factor

## default vector method
BY(v, f, sum)          # Sum by species
head(BY(v, f, scale)) # Scale by species (please use fscale instead)
head(BY(v, f, scale, use.g.names = FALSE)) # Omitting auto-generated names
BY(v, f, quantile)    # Species quantiles: by default stacked
BY(v, f, quantile, expand.wide = TRUE)     # Wide format

## matrix method
m <- qM(num_vars(iris))
BY(m, f, sum)         # Also return as matrix
BY(m, f, sum, return = "data.frame") # Return as data.frame.. also works for computations below
head(BY(m, f, scale))
head(BY(m, f, scale, use.g.names = FALSE))
BY(m, f, quantile)
BY(m, f, quantile, expand.wide = TRUE)
BY(m, f, quantile, expand.wide = TRUE, # Return as list of matrices
  return = "list")
```

```
## data.frame method
BY(num_vars(iris), f, sum)          # Also returns a data.frame
BY(num_vars(iris), f, sum, return = 2) # Return as matrix.. also works for computations below
head(BY(num_vars(iris), f, scale))
head(BY(num_vars(iris), f, scale, use.g.names = FALSE))
BY(num_vars(iris), f, quantile)
BY(num_vars(iris), f, quantile, expand.wide = TRUE)
BY(num_vars(iris), f, quantile,      # Return as list of matrices
   expand.wide = TRUE, return = "list")

## grouped data frame method (faster than dplyr only for small data)
library(dplyr)
giris <- group_by(iris, Species)
giris %>% BY(sum)                # Compute sum
giris %>% BY(sum, use.g.names = TRUE, # Use row.names and
             keep.group_vars = FALSE) # remove 'Species' and groups attribute
giris %>% BY(sum, return = "matrix") # Return matrix
giris %>% BY(sum, return = "matrix", # Matrix with row.names
             use.g.names = TRUE)
giris %>% BY(quantile)           # Compute quantiles (output is stacked)
giris %>% BY(quantile,          # Much better, also keeps 'Species'
             expand.wide = TRUE)
```

collap

Advanced Data Aggregation

Description

collap is a fast and easy to use multi-purpose data aggregation command.

It performs simple aggregations, multi-type data aggregations applying different functions to numeric and categorical data, weighted aggregations (including weighted multi-type aggregations), multi-function aggregations applying multiple functions to each column, and fully customized aggregations where the user passes a list mapping functions to columns.

collap works with *collapse*'s [Fast Statistical Functions](#), providing extremely fast conventional and weighted aggregation. It also works with other functions but this does not deliver high speeds on large data and does not support weighted aggregations.

Usage

```
# Main function: allows formula and data input to `by` and `w` arguments
collap(X, by, FUN = fmean, catFUN = fmode, cols = NULL, w = NULL, wFUN = fsum,
       custom = NULL, keep.by = TRUE, keep.w = TRUE, keep.col.order = TRUE,
       sort = TRUE, decreasing = FALSE, na.last = TRUE, parallel = FALSE, mc.cores = 1L,
       return = c("wide", "list", "long", "long_dupl"), give.names = "auto", sort.row, ...)

# Programmer function: allows column names and indices input to `by` and `w` arguments
collapv(X, by, FUN = fmean, catFUN = fmode, cols = NULL, w = NULL, wFUN = fsum,
```

```

custom = NULL, keep.by = TRUE, keep.w = TRUE, keep.col.order = TRUE,
sort = TRUE, decreasing = FALSE, na.last = TRUE, parallel = FALSE, mc.cores = 1L,
return = c("wide", "list", "long", "long_dupl"), give.names = "auto", sort.row, ...)

```

```

# Auxiliary function: for grouped data ('grouped_df') input + non-standard evaluation
collapg(X, FUN = fmean, catFUN = fmode, cols = NULL, w = NULL, wFUN = fsum, custom = NULL,
keep.group_vars = TRUE, keep.w = TRUE, keep.col.order = TRUE,
parallel = FALSE, mc.cores = 1L,
return = c("wide", "list", "long", "long_dupl"), give.names = "auto", sort.row, ...)

```

Arguments

X	a data frame, or an object coercible to data frame using <code>qDF</code> .
by	for <code>collap</code> : a one-or two sided formula, i.e. <code>~ group1</code> or <code>var1 + var2 ~ group1 + group2</code> , or a atomic vector, list of vectors or <code>GRP</code> object used to group X. For <code>collapv</code> : names or indices of grouping columns, or a logical vector or selector function such as <code>is.categorical</code> selecting grouping columns.
FUN	a function, list of functions (i.e. <code>list(fsum, fmean, fsd)</code> or <code>list(myfun1 = function(x) . . , sd = sd)</code>), or a character vector of function names, which are automatically applied only to numeric variables.
catFUN	same as FUN, but applied only to categorical (non-numeric) typed columns (<code>is.categorical</code>).
cols	select columns to aggregate using a function, column names, indices or logical vector. <i>Note</i> : cols is ignored if a two-sided formula is passed to by.
w	weights. Can be passed as numeric vector or alternatively as formula i.e. <code>~ weightvar</code> in <code>collap</code> or column name / index etc. i.e. <code>"weightvar"</code> in <code>collapv</code> . <code>collapg</code> supports non-standard evaluations so <code>weightvar</code> can be indicated without quotes if found in X.
wFUN	same as FUN: Function(s) to aggregate weight variable if <code>keep.w = TRUE</code> . By default the sum of the weights is computed in each group.
custom	a named list specifying a fully customized aggregation task. The names of the list are function names and the content columns to aggregate using this function (same input as cols). For example <code>custom = list(fmean = 1:6, fsd = 7:9, fmode = 10:11)</code> tells <code>collap</code> to aggregate columns 1-6 of X using the mean, columns 7-9 using the standard deviation etc. <i>Note</i> : custom lets <code>collap</code> ignore any inputs passed to FUN, catFUN or cols.
keep.by, keep.group_vars	logical. FALSE will omit grouping variables from the output. TRUE keeps the variables, even if passed externally in a list or vector (unlike other <i>collapse</i> functions).
keep.w	logical. FALSE will omit weight variable from the output i.e. no aggregation of the weights. TRUE aggregates and adds weights, even if passed externally as a vector (unlike other <i>collapse</i> functions).
keep.col.order	logical. Retain original column order post-aggregation.
sort, decreasing, na.last	logical. Arguments passed to <code>GRP.default</code> and affecting the row-order in the aggregated data frame.

<code>parallel</code>	logical. Use <code>parallel::mclapply</code> instead of <code>lapply</code> for multi-function or custom aggregation.
<code>mc.cores</code>	integer. Argument to <code>parallel::mclapply</code> setting the number of cores to use.
<code>return</code>	character. Control the output format when aggregating with multiple functions or performing custom aggregation. "wide" (default) returns a wider data frame with added columns for each additional function. "list" returns a list of data frames - one for each function. "long" adds a column "Function" and row-binds the results from different functions using <code>data.table::rbindlist</code> . "long.dupl" is a special option for aggregating multi-type data using multiple FUN but only one catFUN or vice-versa. In that case the format is long and data aggregated using only one function is duplicated. See Examples.
<code>give.names</code>	logical. Create unique names of aggregated columns by adding a prefix 'FUN.'. 'auto' will automatically create such prefixes whenever multiple functions are applied to a column or custom is used.
<code>sort.row</code>	deprecated, renamed to <code>sort</code> .
<code>...</code>	additional arguments passed to all functions supplied to FUN, catFUN, wFUN or custom. The behavior of Fast Statistical Functions is regulated by <code>option("collapse_unused_arg_acti</code> and defaults to "warning".

Details

`collap` automatically checks each function passed to it whether it is a [Fast Statistical Function](#) (i.e. whether the function name is contained in `.FAST_STAT_FUN`). If the function is a fast statistical function, `collap` only does the grouping and then calls the function to carry out the grouped computations. If the function is not one of `.FAST_STAT_FUN`, `BY` is called internally to perform the computation. The resulting computations from each function are put into a list and recombined to produce the desired output format as controlled by the `return` argument. When multiple functions are used with `collap`, setting `parallel = TRUE` and the number of cores with `mc.cores` will instruct `collap` to execute these function calls in parallel using `parallel::mclapply`. If only a single function is used which is not a `.FAST_STAT_FUN`, the `parallel` and `mc.cores` arguments are handed down to `BY`. See Examples.

Value

X aggregated. If X is not a data frame it is coerced to one using `qDF` and then aggregated.

Note

Since `BY` does not check and split additional arguments passed to it, it is presently not possible to create a weighted function in R and apply it to data by groups with `collap`. Weighted aggregations only work with [Fast Statistical Functions](#) supporting weights. User written weighted functions can be applied using the `data.table` package.

The dispatch between using optimized collapse functions performing grouped computations internally or calling `BY` to perform split-apply-combine computing is done by matching the function name against `.FAST_STAT_FUN`. Thus code like `collapse::collap(data, ~ id, collapse::fmedian)` does not yield an optimized computation, as `"collapse::fmedian" %!in% .FAST_STAT_FUN`. If you want to perform optimized computations with `collap` without loading the package, load the

functions beforehand as well, e.g. `fmedian <- collapse::fmedian; data, ~ id, fmedian)`. Alternatively it is of course also possible to use `collapse::fmedian(collapse::fgroup_by(data, id))`, or something similar...

See Also

[BY, Fast Statistical Functions, Collapse Overview](#)

Examples

```
## A Simple Introduction -----
head(iris)
collap(iris, ~ Species) # Default: FUN = fmean for numeric
collapv(iris, 5) # Same using collapv
collap(iris, ~ Species, fmedian) # Using the median
collap(iris, ~ Species, fmedian, keep.col.order = FALSE) # Groups in-front
collap(iris, Sepal.Width + Petal.Width ~ Species, fmedian) # Only '.Width' columns
collapv(iris, 5, cols = c(2, 4)) # Same using collapv
collap(iris, ~ Species, list(fmean, fmedian)) # Two functions
collap(iris, ~ Species, list(fmean, fmedian), return = "long") # Long format
collapv(iris, 5, custom = list(fmean = 1:2, fmedian = 3:4)) # Custom aggregation
collapv(iris, 5, custom = list(fmean = 1:2, fmedian = 3:4), # Raw output, no column reordering
  return = "list")
collapv(iris, 5, custom = list(fmean = 1:2, fmedian = 3:4), # A strange choice..
  return = "long")
collap(iris, ~ Species, w = ~ Sepal.Length) # Using Sepal.Length as weights, ..
weights <- abs(rnorm(fnrow(iris)))
collap(iris, ~ Species, w = weights) # Some random weights..
collap(iris, iris$Species, w = weights) # Note this behavior..
collap(iris, iris$Species, w = weights,
  keep.by = FALSE, keep.w = FALSE)
library(dplyr) # Needed for "%>%"
iris %>% fgroup_by(Species) %>% collapg # dplyr style, but faster

## Multi-Type Aggregation -----
head(wlddev) # World Development Panel Data
head(collap(wlddev, ~ country + decade)) # Aggregate by country and decade
head(collap(wlddev, ~ country + decade, fmedian, ffirst)) # Different functions
head(collap(wlddev, ~ country + decade, cols = is.numeric)) # Aggregate only numeric columns
head(collap(wlddev, ~ country + decade, cols = 9:12)) # Only the 4 series
head(collap(wlddev, PCGDP + LIFEEX ~ country + decade)) # Only GDP and life-expectancy
head(collap(wlddev, PCGDP + LIFEEX ~ country + decade, fsum)) # Using the sum instead
head(collap(wlddev, PCGDP + LIFEEX ~ country + decade, sum, # Same using base::sum -> slower!
  na.rm = TRUE))
head(collap(wlddev, wlddev[c("country", "decade")], fsum, # Same, exploring different inputs
  cols = 9:10))
head(collap(wlddev[9:10], wlddev[c("country", "decade")], fsum))
head(collapv(wlddev, c("country", "decade"), fsum)) # ..names/indices with collapv
head(collapv(wlddev, c(1,5), fsum))

g <- GRP(wlddev, ~ country + decade) # Precomputing the grouping
head(collap(wlddev, g, keep.by = FALSE)) # This is slightly faster now
```

```

# Aggregate categorical data using not the mode but the last element
head(collap(wlddev, ~ country + decade, fmean, flast))
head(collap(wlddev, ~ country + decade, catFUN = flast,      # Aggregate only categorical data
           cols = is.categorical))

## Weighted Aggregation -----
weights <- abs(rnorm(fnrow(wlddev)))                # Random weight vector
head(collap(wlddev, ~ country + decade, w = weights))  # Takes weighted mean for numeric..
# ..and weighted mode for categorical data. The weight vector is aggregated using fsum
wlddev$weights <- weights                            # Adding to data
head(collap(wlddev, ~ country + decade, w = ~ weights)) # Keeps column order
head(collap(wlddev, ~ country + decade, w = ~ weights,    # Aggregating weights using sum
           wFUN = list(fsum, fmax)))                  # and max (corresponding to mode)
wlddev$weights <- NULL

## Multi-Function Aggregation -----
head(collap(wlddev, ~ country + decade, list(fmean, fNobs), # Saving mean and Nobs
           cols = 9:12))

head(collap(wlddev, ~ country + decade,                    # Same using base R -> slower
           list(mean = mean,
                 Nobs = function(x, ...) sum(!is.na(x))),
           cols = 9:12, na.rm = TRUE))

lapply(collap(wlddev, ~ country + decade,                  # List output format
             list(fmean, fNobs), cols = 9:12, return = "list"), head)

head(collap(wlddev, ~ country + decade,                    # Long output format
           list(fmean, fNobs), cols = 9:12, return = "long"))

head(collap(wlddev, ~ country + decade,                    # Also aggregating categorical data,
           list(fmean, fNobs), return = "long_dupl"))      # and duplicating it 2 times

head(collap(wlddev, ~ country + decade,                    # Now also using 2 functions on
           list(fmean, fNobs), list(fmode, flast),         # categorical data
           keep.col.order = FALSE))

head(collap(wlddev, ~ country + decade,                    # More functions, string input,
           c("fmean", "fsum", "fNobs", "fsd", "fvar"),    # parallelized execution
           c("fmode", "ffirst", "flast", "fNdistinct"),  # (choose more than 1 cores,
           parallel = TRUE, mc.cores = 1L,                # depending on your machine)
           keep.col.order = FALSE))

## Custom Aggregation -----
head(collap(wlddev, ~ country + decade,                    # Custom aggregation
           custom = list(fmean = 9:12, fsd = 9:10, fmode = 7:8)))

head(collap(wlddev, ~ country + decade,                    # Using column names
           custom = list(fmean = "PCGDP", fsd = c("LIFEEX", "GINI"),
                         flast = "date")))

```

```

head(collap(wlddev, ~ country + decade,                                # Weighted parallelized custom
          custom = list(fmean = 9:12, fsd = 9:10,                      # aggregation
                        fmode = 7:8), w = weights,
          wFUN = list(fsum, fmax),
          parallel = TRUE, mc.cores = 1L))

head(collap(wlddev, ~ country + decade,                                # No column reordering
          custom = list(fmean = 9:12, fsd = 9:10,
                        fmode = 7:8), w = weights,
          wFUN = list(fsum, fmax),
          parallel = TRUE, mc.cores = 1L, keep.col.order = FALSE))

## Piped Use -----
wlddev %>% fgroup_by(country, decade) %>% collapg
wlddev %>% fgroup_by(country, decade) %>% collapg(w = ODA)
wlddev %>% fgroup_by(country, decade) %>% collapg(fmedian, flast)
wlddev %>% fgroup_by(country, decade) %>%
  collapg(custom = list(fmean = 9:12, fmode = 5:7, flast = 3))

```

collapse-depreciated *Deprecated collapse Functions*

Description

The functions `Recode` and `replace_non_finite` available until *collapse* v1.1.0 will be removed soon. Since v1.2.0, `Recode` is replaced by `recode_num` and `recode_char` and `replace_non_finite` is replaced by `replace_Inf`.

The function `as.factor.GRP` was renamed to `as.factor_GRP` to make it clear that this is not a method, and `group_names.GRP` was renamed to `GRPnames` for the same reason and to increase parsimony.

Usage

```
Recode(X, ..., copy = FALSE, reserve.na.nan = TRUE, regex = FALSE)
```

```
replace_non_finite(X, value = NA, replace.nan = TRUE)
```

Arguments

<code>X</code>	a vector, matrix or data frame.
<code>...</code>	comma-separated recode arguments of the form: <code>name = newname</code> , <code>`2` = 0</code> , <code>`NaN` = 0</code> , <code>`NA` = 0</code> , <code>`Inf` = NA</code> , <code>`-Inf` = NA</code> , etc...
<code>value</code>	a single (scalar) value to replace matching elements with. Default is <code>NA</code> .

copy	logical. For reciprocal or sequential replacements of the form $a = b, b = c$ make a copy of X to prevent a being replaced with b and then all b -values being replaced with c again. In general <code>Recode</code> does the replacements one-after the other, starting with the first.
reserve.na.nan	logical. TRUE identifies NA and NaN as special numeric values and does the correct replacement. FALSE will treat NA/NaN as strings, and thus not match numeric NA/NaN. <i>Note</i> : This is not an issue for $Inf/-Inf$, which are matched in both numeric and character variables.
regex	logical. If TRUE, all recode-argument names are (sequentially) passed to <code>grep</code> as a pattern to search X . All matches are replaced.
replace.nan	logical. TRUE (default) replaces $NaN/Inf/-Inf$. FALSE replaces only $Inf/-Inf$.

Note

`Recode` is not suitable for recoding factors or other classed objects / columns, it simply does $X[X == \text{value}] \leftarrow \text{replacement}$ in a more efficient way. For classed objects, see for example `dplyr::recode`.

See Also

[Recode and Replace Values, Collapse Overview](#)

Examples

```
## Not run:
Recode(c("a", "b", "c"), a = "b", b = "c")
Recode(c("a", "b", "c"), a = "b", b = "c", copy = TRUE)
Recode(c("a", "b", "c"), a = "b", b = "a", copy = TRUE)
Recode(month.name, ber = NA, regex = TRUE)
mtcr <- Recode(mtcars, `0` = 2, `4` = Inf, `1` = NaN)
replace_non_finite(mtcr)
replace_non_finite(mtcr, replace.nan = FALSE)

## End(Not run)
```

collapse-options
collapse *Package Options*

Description

`collapse` provides `option("collapse_unused_arg_action")`, which regulates how generic functions (such as the [Fast Statistical Functions](#)) in the package react when an unknown argument is passed to a method. The default action is "warning" which issues a warning. Other options are "error", "message" or "none", whereby the latter enables silent swallowing of such arguments.

Description

Efficiently reorder columns in a data frame (no copies). To do this by reference see also `data.table::setcolorder`.

Usage

```
colorder(X, ..., pos = c("front", "end", "exchange"))
```

```
colorderv(X, neworder = radixorder(names(X)), pos = c("front", "end", "exchange"),
          regex = FALSE, ...)
```

Arguments

`X` a data frame or list.

`...` for `colorder`: Column names of `X` in the new order (can also use sequences i.e. `col1:coln, colk, ...`). For `colorderv`: Further arguments to `grep` if `regex = TRUE`.

`neworder` a vector of column names, positive indices, a suitable logical vector, a function such as `is.numeric`, or a vector of regular expressions matching column names (if `regex = TRUE`).

`pos` integer or character. Different options regarding column arrangement if `...length() < ncol(X)` (or `length(neworder) < ncol(X)`).

<i>Int.</i>	<i>String</i>	<i>Description</i>
1	"front"	move specified columns to the front of <code>X</code> (the default).
2	"end"	move specified columns to the end of <code>X</code> .
3	"exchange"	just exchange the positions of selected columns in <code>X</code> , other columns remain in the same position.

`regex` logical. `TRUE` will do regular expression search on the column names of `X` using a (vector of) regular expression(s) passed to `neworder`. Matching is done using `grep`. *Note* that multiple regular expressions will be matched in the order they are passed, and `funique` will be applied to the resulting set of indices.

Value

`X` with columns re-ordered (no deep copy).

See Also

[roworder](#), [Data Frame Manipulation](#), [Collapse Overview](#)

Examples

```

head(colorder(mtcars, vs, cyl:hp, am))
head(colorder(mtcars, vs, cyl:hp, am, pos = "end"))
head(colorder(mtcars, vs, cyl, pos = "exchange"))

## Same in standard evaluation
head(colorder(mtcars, c(8, 2:4, 9)))
head(colorder(mtcars, c(8, 2:4, 9), pos = "end"))
head(colorder(mtcars, c(8, 2), pos = "exchange"))

```

dapply*Data Apply*

Description

dapply efficiently applies functions to columns or rows of matrix-like objects and by default returns an object of the same type and with the same attributes. Alternatively it is possible to return the result in a plain matrix or data.frame. A simple parallelism is also available.

Usage

```

dapply(X, FUN, ..., MARGIN = 2, parallel = FALSE, mc.cores = 1L,
       return = c("same", "matrix", "data.frame"), drop = TRUE)

```

Arguments

X	a matrix, data frame or alike object.
FUN	a function, can be scalar- or vector-valued.
...	further arguments to FUN.
MARGIN	integer. The margin which FUN will be applied over. Default 2 indicates columns while 1 indicates rows. See also Details.
parallel	logical. TRUE implements simple parallel execution by internally calling <code>parallel::mclapply</code> instead of <code>base::lapply</code> .
mc.cores	integer. Argument to <code>parallel::mclapply</code> indicating the number of cores to use for parallel execution. Can use <code>parallel::detectCores()</code> to select all available cores. See also <code>?parallel::mclapply</code> .
return	an integer or string indicating the type of object to return. The default 1 - "same" returns the same object type (i.e. class and other attributes are retained, just the names for the dimensions are adjusted). 2 - "matrix" always returns the output as matrix and 3 - "data.frame" always returns a data frame.
drop	logical. If the result has only one row or one column, <code>drop = TRUE</code> will drop dimensions and return a (named) atomic vector.

Details

dapply is an efficient command to apply functions to rows or columns of data without losing information (attributes) about the data or changing the classes or format of the data. It is principally an efficient wrapper around `base::lapply` and works as follows:

- Save the attributes of X.
- If `MARGIN = 2` (columns), convert matrices to plain lists of columns using `mctl` and remove all attributes from data frames.
- If `MARGIN = 1` (rows), convert matrices to plain lists of rows using `mrtl`. For data frames remove all attributes, efficiently convert to matrix using `do.call(rbind, X)` and also convert to list of rows using `mrtl`.
- Call `base::lapply` or `parallel::mclapply` on these plain lists (which is faster than calling `lapply` on an object with attributes).
- depending on the requested output type, use `base::matrix`, `base::unlist` or `do.call(cbind, ...)` to convert the result back to a matrix or list of columns.
- modify the relevant attributes accordingly and efficiently attach to the object again (no further checks).

The performance gain from working with plain lists makes dapply not much slower than calling `lapply` itself on a data frame. Because of the conversions involved, row-operations require some memory, but are still faster than `base::apply`.

Value

X where FUN was applied to every row or column.

See Also

[BY](#), [collap](#), [Fast Statistical Functions](#), [Data Transformations](#), [Collapse Overview](#)

Examples

```
head(dapply(mtcars, log))                # Take natural log of each variable
head(dapply(mtcars, log, return = "matrix")) # Return as matrix
m <- as.matrix(mtcars)
head(dapply(m, log))                    # Same thing
head(dapply(m, log, return = "data.frame")) # Return data frame from matrix
dapply(mtcars, sum); dapply(m, sum)      # Computing sum of each column, return as vector
dapply(mtcars, sum, drop = FALSE)       # This returns a data frame of 1 row
dapply(mtcars, sum, MARGIN = 1)          # Compute row-sum of each column, return as vector
dapply(m, sum, MARGIN = 1)               # Same thing for matrices, faster t. apply(m, 1, sum)
head(dapply(m, sum, MARGIN = 1, drop = FALSE)) # Gives matrix with one column
head(dapply(m, quantile, MARGIN = 1))     # Compute row-quantiles
dapply(m, quantile)                      # Column-quantiles
head(dapply(mtcars, quantile, MARGIN = 1)) # Same for data frames, output is also a data.frame
dapply(mtcars, quantile)

# With classed objects, we have to be a bit careful
## Not run:
```

```
dapply(EuStockMarkets, quantile) # This gives an error because the tsp attribute is misspecified

## End(Not run)
dapply(EuStockMarkets, quantile, return = "matrix") # These both work fine..
dapply(EuStockMarkets, quantile, return = "data.frame")

# Similarly for grouped tibbles and other data frame classes
library(dplyr)
gmtcars <- group_by(mtcars, cyl, vs, am)
head(dapply(gmtcars, log)) # Still gives a grouped tibble back
dapply(gmtcars, quantile, MARGIN = 1) # Here it makes sense to keep the groups attribute
dapply(gmtcars, quantile) # This does not make much sense, ...
dapply(gmtcars, quantile, # better convert to plain data.frame:
       return = "data.frame")
```

 descr

Detailed Statistical Description of Data Frame

Description

descr offers a concise description of each variable in a data frame. It is built as a wrapper around [qsu](#), but by default also computes frequency tables with percentages for categorical variables, and quantiles and the number of distinct values for numeric variables (next to the mean, sd, min, max, skewness and kurtosis computed by [qsu](#)).

Usage

```
descr(X, Ndistinct = TRUE, higher = TRUE, table = TRUE,
      Qprobs = c(0.01, 0.05, 0.25, 0.5, 0.75, 0.95, 0.99),
      cols = NULL, label.attr = "label", ...)

## S3 method for class 'descr'
print(x, n = 7, perc = TRUE, digits = 2, t.table = TRUE, summary = TRUE, ...)

## S3 method for class 'descr'
as.data.frame(x, ...)
```

Arguments

X	a data frame or list of atomic vectors. Atomic vectors, matrices or arrays can be passed but will first be coerced to data frame using qDF .
Ndistinct	logical. TRUE (default) computes the number of distinct values on all variables using fNdistinct .
higher	logical. Argument is passed down to qsu : TRUE (default) computes the skewness and the kurtosis.
table	logical. TRUE (default) calls table on all categorical variables (excluding Date variables).

Qprobs	double. Probabilities for quantiles to compute on numeric variables, passed down to quantile . If something non-numeric is passed (i.e. NULL, FALSE, NA, "" etc.), no quantiles are computed.
cols	select columns to describe using column names, indices, a logical vector or a function (i.e. <code>is.numeric</code>).
label.attr	character. The name of a label attribute to display for each variable (if variables are labeled).
...	other arguments passed to qsu.default .
x	an object of class 'descr'.
n	integer. The number of first and last entries to display of the table computed for categorical variables. If the number of distinct elements is $< 2*n$, the whole table is printed.
perc	logical. TRUE (default) adds percentages to the frequencies in the table for categorical variables.
digits	integer. The number of decimals to print in statistics and percentage tables.
t.table	logical. TRUE (default) prints a transposed table.
summary	logical. TRUE (default) computes and displays a summary of the frequencies if the size of the table for a categorical variables exceeds $2*n$.

Details

`descr` was heavily inspired by `Hmisc::describe`, but computes about 10x faster. The performance is comparable to `base::summary`. `descr` was built as a wrapper around [qsu](#), to enrich the set of statistics computed by [qsu](#) for both numeric and categorical variables.

[qsu](#) itself is yet about 10x faster than `descr`, and is optimized for grouped, panel data and weighted statistics. It is possible to also compute grouped, panel data and/or weighted statistics with `descr` by passing group-ids to `g`, panel-ids to `pid` or a weight vector to `w`. These arguments are handed down to [qsu.default](#) and only affect the statistics natively computed by `qsu`, i.e. passing a weight vector produces a weighted mean, sd, skewness and kurtosis but not weighted quantiles.

The list-object returned from `descr` can be converted to a tidy data frame using `as.data.frame`. This representation will not include frequency tables computed for categorical variables, and the method cannot handle arrays of statistics (applicable when `g` or `pid` arguments are passed to `descr`, in that case `as.data.frame.descr` will throw an appropriate error).

Value

A 2-level nested list, the top-level containing the statistics computed for each variable, which are themselves stored in a list containing the class, the label, the basic statistics and quantiles / tables computed for the variable. The object is given a class 'descr' and also has the number of observations in the dataset attached as an 'N' attribute, as well as an attribute 'arstat' indicating whether the object contains arrays of statistics, and an attribute 'table' indicating whether `table = TRUE` (i.e. the object could contain tables for categorical variables).

See Also

[qsu](#), [pwcov](#), [Summary Statistics](#), [Fast Statistical Functions](#), [Collapse Overview](#)

Examples

```
## Standard Use
descr(iris)
descr(wlddev)
descr(GGDC10S)

as.data.frame(descr(wlddev))

## Passing Arguments down to qsu: For Panel Data Statistics
descr(iris, pid = iris$Species)
descr(wlddev, pid = wlddev$iso3c)

## Grouped Statistics
descr(iris, g = iris$Species)
descr(GGDC10S, g = GGDC10S$Region)
```

fbetween, fwithin	<i>Fast Between (Averaging) and (Quasi-)Within (Centering) Transformations</i>
-------------------	--

Description

fbetween and fwithin are S3 generics to efficiently obtain between-transformed (averaged) or (quasi-)within-transformed (demeaned) data. These operations can be performed groupwise and/or weighted. B and W are wrappers around fbetween and fwithin representing the 'between-operator' and the 'within-operator'.

(B / W provide more flexibility than fbetween / fwithin when applied to data frames (i.e. column subsetting, formula input, auto-renaming and id-variable-preservation capabilities...), but are otherwise identical.)

Usage

```
fbetween(x, ...)
fwithin(x, ...)
  B(x, ...)
  W(x, ...)

## Default S3 method:
fbetween(x, g = NULL, w = NULL, na.rm = TRUE, fill = FALSE, ...)
## Default S3 method:
fwithin(x, g = NULL, w = NULL, na.rm = TRUE, mean = 0, theta = 1, ...)
## Default S3 method:
B(x, g = NULL, w = NULL, na.rm = TRUE, fill = FALSE, ...)
## Default S3 method:
W(x, g = NULL, w = NULL, na.rm = TRUE, mean = 0, theta = 1, ...)

## S3 method for class 'matrix'
```

```

fbetween(x, g = NULL, w = NULL, na.rm = TRUE, fill = FALSE, ...)
## S3 method for class 'matrix'
fwithin(x, g = NULL, w = NULL, na.rm = TRUE, mean = 0, theta = 1, ...)
## S3 method for class 'matrix'
B(x, g = NULL, w = NULL, na.rm = TRUE, fill = FALSE, stub = "B.", ...)
## S3 method for class 'matrix'
W(x, g = NULL, w = NULL, na.rm = TRUE, mean = 0, theta = 1, stub = "W.", ...)

## S3 method for class 'data.frame'
fbetween(x, g = NULL, w = NULL, na.rm = TRUE, fill = FALSE, ...)
## S3 method for class 'data.frame'
fwithin(x, g = NULL, w = NULL, na.rm = TRUE, mean = 0, theta = 1, ...)
## S3 method for class 'data.frame'
B(x, by = NULL, w = NULL, cols = is.numeric, na.rm = TRUE,
  fill = FALSE, stub = "B.", keep.by = TRUE, keep.w = TRUE, ...)
## S3 method for class 'data.frame'
W(x, by = NULL, w = NULL, cols = is.numeric, na.rm = TRUE,
  mean = 0, theta = 1, stub = "W.", keep.by = TRUE, keep.w = TRUE, ...)

# Methods for compatibility with plm:

## S3 method for class 'pseries'
fbetween(x, effect = 1L, w = NULL, na.rm = TRUE, fill = FALSE, ...)
## S3 method for class 'pseries'
fwithin(x, effect = 1L, w = NULL, na.rm = TRUE, mean = 0, theta = 1, ...)
## S3 method for class 'pseries'
B(x, effect = 1L, w = NULL, na.rm = TRUE, fill = FALSE, ...)
## S3 method for class 'pseries'
W(x, effect = 1L, w = NULL, na.rm = TRUE, mean = 0, theta = 1, ...)

## S3 method for class 'pdata.frame'
fbetween(x, effect = 1L, w = NULL, na.rm = TRUE, fill = FALSE, ...)
## S3 method for class 'pdata.frame'
fwithin(x, effect = 1L, w = NULL, na.rm = TRUE, mean = 0, theta = 1, ...)
## S3 method for class 'pdata.frame'
B(x, effect = 1L, w = NULL, cols = is.numeric, na.rm = TRUE,
  fill = FALSE, stub = "B.", keep.ids = TRUE, keep.w = TRUE, ...)
## S3 method for class 'pdata.frame'
W(x, effect = 1L, w = NULL, cols = is.numeric, na.rm = TRUE,
  mean = 0, theta = 1, stub = "W.", keep.ids = TRUE, keep.w = TRUE, ...)

# Methods for compatibility with dplyr:

## S3 method for class 'grouped_df'
fbetween(x, w = NULL, na.rm = TRUE, fill = FALSE,
  keep.group_vars = TRUE, keep.w = TRUE, ...)
## S3 method for class 'grouped_df'
fwithin(x, w = NULL, na.rm = TRUE, mean = 0, theta = 1,

```

```

      keep.group_vars = TRUE, keep.w = TRUE, ...)
## S3 method for class 'grouped_df'
B(x, w = NULL, na.rm = TRUE, fill = FALSE,
  stub = "B.", keep.group_vars = TRUE, keep.w = TRUE, ...)
## S3 method for class 'grouped_df'
W(x, w = NULL, na.rm = TRUE, mean = 0, theta = 1,
  stub = "W.", keep.group_vars = TRUE, keep.w = TRUE, ...)

```

Arguments

x	a numeric vector, matrix, data frame, panel series (class pseries of package plm), panel data frame (plm::pdata.frame) or grouped tibble (dplyr::grouped_df).
g	a factor, GRP object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a GRP object) used to group x.
by	<i>B and W data.frame method</i> : Same as g, but also allows one- or two-sided formulas i.e. ~ group1 or var1 + var2 ~ group1 + group2. See Examples.
w	a numeric vector of (non-negative) weights. B/W data frame and pdata.frame methods also allow a one-sided formula i.e. ~ weightcol. The grouped_df (dplyr) method supports lazy-evaluation. See Examples.
cols	<i>data.frame method</i> : Select columns to center/average using a function, column names, indices or a logical vector. Default: All numeric variables. <i>Note</i> : cols is ignored if a two-sided formula is passed to by.
na.rm	logical. Skip missing values in x and w when computing averages. If na.rm = FALSE and a NA or NaN is encountered, the average for that group will be NA, and all data points belonging to that group in the output vector will also be NA.
effect	<i>plm methods</i> : Select which panel identifier should be used as grouping variable. 1L takes the first variable in the plm::index, 2L the second etc. Index variables can also be called by name using a character string. If more than one variable is supplied, the corresponding index-factors are interacted.
stub	a prefix or stub to rename all transformed columns. FALSE will not rename columns.
fill	<i>option to fbetween/B</i> : Logical. TRUE will overwrite missing values in x with the respective average. By default missing values in x are preserved.
mean	<i>option to fwithin/W</i> : The mean to center on, default is 0, but a different mean can be supplied and will be added to the data after the centering is performed. A special option when performing grouped centering is mean = "overall.mean". In that case the overall mean of the data will be added after subtracting out group means.
theta	<i>option to fwithin/W</i> : Double. An optional scalar parameter for quasi-demeaning i.e. $x - \theta * xi$. This is useful for variance components ('random-effects') estimators. see Details.
keep.by, keep.ids, keep.group_vars	<i>B and W data.frame, pdata.frame and grouped_df methods</i> : Logical. Retain grouping / panel-identifier columns in the output. For data frames this only works if grouping variables were passed in a formula.

keep.w *B and W data.frame, pdata.frame and grouped_df methods*: Logical. Retain column containing the weights in the output. Only works if w is passed as formula / lazy-expression.

... arguments to be passed to or from other methods.

Details

Without groups, `fbetween/B` replaces all data points in `x` with their mean or weighted mean (if `w` is supplied). Similarly `fwithin/W` subtracts the (weighted) mean from all data points i.e. centers the data on the mean.

With groups supplied to `g`, the replacement / centering performed by `fbetween/B` | `fwithin/W` becomes groupwise. In terms of panel data notation: If `x` is a vector in such a panel dataset, `xit` denotes a single data-point belonging to group `i` in time-period `t` (`t` need not be a time-period). Then `xi.` denotes `x`, averaged over `t`. `fbetween/B` now returns `xi.` and `fwithin/W` returns `x - xi.`. Thus for any data `x` and any grouping vector `g`: $B(x, g) + W(x, g) = x_{i.} + x - x_{i.} = x$. In terms of variance, `fbetween/B` only retains the variance between group averages, while `fwithin/W`, by subtracting out group means, only retains the variance within those groups.

The data replacement performed by `fbetween/B` can keep (default) or overwrite missing values (option `fill = TRUE`) in `x`. `fwithin/W` can center data simply (default), or add back a mean after centering (option `mean = value`), or add the overall mean in groupwise computations (option `mean = "overall.mean"`). Let `x.` denote the overall mean of `x`, then `fwithin/W` with `mean = "overall.mean"` returns `x - xi. + x.` instead of `x - xi.`. This is useful to get rid of group-differences but preserve the overall level of the data. In regression analysis, centering with `mean = "overall.mean"` will only change the constant term. See Examples.

If `theta != 1`, `fwithin/W` performs quasi-demeaning `x - theta * xi.`. If `mean = "overall.mean"`, `x - theta * xi. + theta * x.` is returned, so that the mean of the partially demeaned data is still equal to the overall data mean `x.`. A numeric value passed to `mean` will simply be added back to the quasi-demeaned data i.e. `x - theta * xi. + mean`.

Now in the case of a linear panel model $y_{it} = \beta_0 + \beta_1 X_{it} + u_{it}$ with $u_{it} = \alpha_i + \epsilon_{it}$. If $\alpha_i \neq \alpha = \text{const.}$ (there exists individual heterogeneity), then pooled OLS is at least inefficient and inference on β_1 is invalid. If $E[\alpha_i | X_{it}] = 0$ (mean independence of individual heterogeneity α_i), the variance components or 'random-effects' estimator provides an asymptotically efficient FGLS solution by estimating a transformed model $y_{it} - \theta y_{i.} = \beta_0 + \beta_1 (X_{it} - \theta X_{i.}) + (u_{it} - \theta u_{i.})$, where $\theta = 1 - \frac{\sigma_\alpha}{\sqrt{\sigma_\alpha^2 + T\sigma_\epsilon^2}}$. An estimate of θ can be obtained from the an estimate of \hat{u}_{it} (the residuals from the pooled model). If $E[\alpha_i | X_{it}] \neq 0$, pooled OLS is biased and inconsistent, and taking $\theta = 1$ gives an unbiased and consistent fixed-effects estimator of β_1 . See Examples.

Value

`fbetween/B` returns `x` with every element replaced by its (groupwise) mean (`xi.`). Missing values are preserved if `fill = FALSE` (the default). `fwithin/W` returns `x` where every element was subtracted its (groupwise) mean (`x - theta * xi. + mean` or, if `mean = "overall.mean"`, `x - theta * xi. + theta * x.`). See Details.

References

Mundlak, Yair. 1978. On the Pooling of Time Series and Cross Section Data. *Econometrica* 46 (1): 69-85.

See Also

[fHDbetween/HDB](#) and [fHDwithin/HDW](#), [fscale/STD](#), [TRA](#), [Data Transformations](#), [Collapse Overview](#)

Examples

```
## Simple centering and averaging
head(fbetween(mtcars))
head(B(mtcars))
head(fwithin(mtcars))
head(W(mtcars))
all.equal(fbetween(mtcars) + fwithin(mtcars), mtcars)

## Groupwise centering and averaging
head(fbetween(mtcars, mtcars$cyl))
head(fwithin(mtcars, mtcars$cyl))
all.equal(fbetween(mtcars, mtcars$cyl) + fwithin(mtcars, mtcars$cyl), mtcars)

head(W(wlddev, ~ iso3c, cols = 9:12)) # Center the 4 series in this dataset by country
head(cbind(get_vars(wlddev,"iso3c"), # Same thing done manually using fwithin..
          add_stub(fwithin(get_vars(wlddev,9:12), wlddev$iso3c), "W.")))

## Using B() and W() for fixed-effects regressions:

# Several ways of running the same regression with cyl-fixed effects
lm(W(mpg,cyl) ~ W(carb,cyl), data = mtcars) # Centering each individually
lm(mpg ~ carb, data = W(mtcars, ~ cyl, stub = FALSE)) # Centering the entire data
lm(mpg ~ carb, data = W(mtcars, ~ cyl, stub = FALSE, # Here only the intercept changes
                        mean = "overall.mean"))
lm(mpg ~ carb + B(carb,cyl), data = mtcars) # Procedure suggested by
# ..Mundlak (1978) - partialling out group averages amounts to the same as demeaning the data

plm::plm(mpg ~ carb, mtcars, index = "cyl", model = "within") # "Proof"..

# This takes the interaction of cyl, vs and am as fixed effects
lm(W(mpg,list(cyl,vs,am)) ~ W(carb,list(cyl,vs,am)), data = mtcars)
lm(mpg ~ carb, data = W(mtcars, ~ cyl + vs + am, stub = FALSE))
lm(mpg ~ carb + B(carb,list(cyl,vs,am)), data = mtcars)

# Now with cyl fixed effects weighted by hp:
lm(W(mpg,cyl,hp) ~ W(carb,cyl,hp), data = mtcars)
lm(mpg ~ carb, data = W(mtcars, ~ cyl, ~ hp, stub = FALSE))
lm(mpg ~ carb + B(carb,cyl,hp), data = mtcars) # WRONG ! Gives a different coefficient!!

## Manual variance components (random-effects) estimation
res <- HDW(mtcars, mpg ~ carb)[[1]] # Get residuals from pooled OLS
sig2_u <- fvar(res)
sig2_e <- fvar(fwithin(res, mtcars$cyl))
```

```

T <- length(res) / fNdistinct(mtcars$cyl)
sig2_alpha <- sig2_u - sig2_e
theta <- 1 - sqrt(sig2_alpha) / sqrt(sig2_alpha + T * sig2_e)
lm(mpg ~ carb, data = W(mtcars, ~ cyl, theta = theta, mean = "overall.mean", stub = FALSE))

# A slightly different method to obtain theta...
plm::plm(mpg ~ carb, mtcars, index = "cyl", model = "random")

```

fdiff

*Fast (Quasi-, Log-) Differences for Time Series and Panel Data***Description**

fdiff is a S3 generic to compute (sequences of) suitably lagged / leaded and iterated differences, quasi-differences, log-differences or quasi-log-differences. The difference and log-difference operators D and Dlog also exists as parsimonious wrappers around fdiff. Apart from being more parsimonious, they provide more flexibility than fdiff when applied to data frames.

Usage

```

fdiff(x, n = 1, diff = 1, ...)
  D(x, n = 1, diff = 1, ...)
  Dlog(x, n = 1, diff = 1, ...)

## Default S3 method:
fdiff(x, n = 1, diff = 1, g = NULL, t = NULL, fill = NA, log = FALSE, rho = 1,
      stubs = TRUE, ...)
## Default S3 method:
D(x, n = 1, diff = 1, g = NULL, t = NULL, fill = NA, rho = 1,
  stubs = TRUE, ...)
## Default S3 method:
Dlog(x, n = 1, diff = 1, g = NULL, t = NULL, fill = NA, rho = 1, stubs = TRUE, ...)

## S3 method for class 'matrix'
fdiff(x, n = 1, diff = 1, g = NULL, t = NULL, fill = NA, log = FALSE, rho = 1,
      stubs = length(n) + length(diff) > 2L, ...)
## S3 method for class 'matrix'
D(x, n = 1, diff = 1, g = NULL, t = NULL, fill = NA, rho = 1,
  stubs = TRUE, ...)
## S3 method for class 'matrix'
Dlog(x, n = 1, diff = 1, g = NULL, t = NULL, fill = NA, rho = 1, stubs = TRUE, ...)

## S3 method for class 'data.frame'
fdiff(x, n = 1, diff = 1, g = NULL, t = NULL, fill = NA, log = FALSE, rho = 1,
      stubs = length(n) + length(diff) > 2L, ...)
## S3 method for class 'data.frame'
D(x, n = 1, diff = 1, by = NULL, t = NULL, cols = is.numeric,

```

```

    fill = NA, rho = 1, stubs = TRUE, keep.ids = TRUE, ...)
## S3 method for class 'data.frame'
Dlog(x, n = 1, diff = 1, by = NULL, t = NULL, cols = is.numeric,
     fill = NA, rho = 1, stubs = TRUE, keep.ids = TRUE, ...)

# Methods for compatibility with plm:

## S3 method for class 'pseries'
fdiff(x, n = 1, diff = 1, fill = NA, log = FALSE, rho = 1, stubs = TRUE, ...)
## S3 method for class 'pseries'
D(x, n = 1, diff = 1, fill = NA, rho = 1, stubs = TRUE, ...)
## S3 method for class 'pseries'
Dlog(x, n = 1, diff = 1, fill = NA, rho = 1, stubs = TRUE, ...)

## S3 method for class 'pdata.frame'
fdiff(x, n = 1, diff = 1, fill = NA, log = FALSE, rho = 1,
     stubs = length(n) + length(diff) > 2L, ...)
## S3 method for class 'pdata.frame'
D(x, n = 1, diff = 1, cols = is.numeric, fill = NA, rho = 1, stubs = TRUE,
  keep.ids = TRUE, ...)
## S3 method for class 'pdata.frame'
Dlog(x, n = 1, diff = 1, cols = is.numeric, fill = NA, rho = 1, stubs = TRUE,
     keep.ids = TRUE, ...)

# Methods for compatibility with dplyr:

## S3 method for class 'grouped_df'
fdiff(x, n = 1, diff = 1, t = NULL, fill = NA, log = FALSE, rho = 1,
     stubs = length(n) + length(diff) > 2L, keep.ids = TRUE, ...)
## S3 method for class 'grouped_df'
D(x, n = 1, diff = 1, t = NULL, fill = NA, rho = 1, stubs = TRUE,
  keep.ids = TRUE, ...)
## S3 method for class 'grouped_df'
Dlog(x, n = 1, diff = 1, t = NULL, fill = NA, rho = 1, stubs = TRUE,
     keep.ids = TRUE, ...)

```

Arguments

x	a numeric vector / time series, (time series) matrix, data frame, panel series (plm::pseries), panel data frame (plm::pdata.frame) or grouped tibble (dplyr::grouped_df).
n	integer. A vector indicating the number of lags or leads.
diff	integer. A vector of integers > 1 indicating the order of differencing / log-differencing.
g	a factor, GRP object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a GRP object) used to group x.
by	<i>data.frame method</i> : Same as g, but also allows one- or two-sided formulas i.e. ~ group1 or var1 + var2 ~ group1 + group2. See Examples.

<code>t</code>	same input as <code>g/by</code> , to indicate the time-variable. For safe computation of differences on unordered time series and panels. Data Frame method also allows one-sided formula i.e. <code>~time</code> . <code>grouped_df</code> method supports lazy-evaluation i.e. <code>time</code> (no quotes).
<code>cols</code>	<i>data.frame method</i> : Select columns to difference using a function, column names, indices or a logical vector. Default: All numeric variables. <i>Note</i> : <code>cols</code> is ignored if a two-sided formula is passed to <code>by</code> .
<code>fill</code>	value to insert when vectors are shifted. Default is NA.
<code>log</code>	logical. TRUE Computes log-differences instead. See Details.
<code>rho</code>	double. Autocorrelation parameter. Set to a value between 0 and 1 for quasi-differencing. However any numeric value can be supplied.
<code>stubs</code>	logical. TRUE will rename all differenced columns by adding prefixes "LnDdiff." / "FnDdiff." for differences "LnDlogdiff." / "FnDlogdiff." for log-differences and replacing "D" / "Dlog" with "QD" / "QDlog" for quasi-differences.
<code>keep.ids</code>	<i>data.frame / pdata.frame / grouped_df methods</i> : Logical. Drop all panel-identifiers from the output (which includes all variables passed to <code>by</code> or <code>t</code>). <i>Note</i> : For panel data frames and grouped tibbles identifiers are dropped, but the 'index' / 'groups' attributes are kept.
<code>...</code>	arguments to be passed to or from other methods.

Details

By default, `fdiff/D/Dlog` return `x` with all columns differenced / log-differenced. Differences are computed as $\text{repeat}(\text{diff}) x[i] - \rho * x[i-n]$, and log-differences as $\text{repeat}(\text{diff}) \log(x[i]) - \rho * \log(x[i-n])$. If $\rho < 1$, this becomes quasi- (or partial) differencing, which is a technique suggested by Cochrane and Orcutt (1949) to deal with serial correlation in regression models, where ρ is typically estimated by running a regression of the model residuals on the lagged residuals. Setting `diff = 2` returns differences of differences etc. . . and setting `n = 2` returns simple differences computed by subtracting twice-lagged `x` from `x`. It is also possible to compute forward differences by passing negative `n` values. `n` also supports arbitrary vectors of integers (lags), and `diff` supports positive sequences of integers (differences):

If more than one value is passed to `n` and/or `diff`, the data is expanded-wide as follows: If `x` is an atomic vector or time series, a (time series) matrix is returned with columns ordered first by lag, then by difference. If `x` is a matrix or data frame, each column is expanded in like manor such that the output has $\text{ncol}(x) * \text{length}(n) * \text{length}(\text{diff})$ columns ordered first by column name, then by lag, then by difference.

With groups/panel-identifiers supplied to `g/by`, `fdiff/D/Dlog` efficiently compute panel-differences. If `t` is left empty, the data needs to be ordered such that all values belonging to a group are consecutive and in the right order. It is not necessary that the groups themselves occur in the right order. If time-variable(s) are supplied to `t`, the panel is fully identified and differences can be securely computed even if the data is completely unordered.

`fdiff/D/Dlog` supports balanced panels and unbalanced panels where various individuals are observed for different time-sequences (both start, end and duration of observation can differ for each individual), but does not natively support irregularly spaced time series and panels. For computational details and efficiency considerations see the help page for [flag](#). A work-around for differencing irregular panels is easily achieved with the help of [seqid](#).

It is also possible to compute differences on unordered vectors / time series (thus utilizing `t` but leaving `g/by` empty).

The methods applying to *plm* objects (panel series and panel data frames) automatically utilize the panel-identifiers attached to these objects and thus securely compute fully identified panel-differences. If these objects have > 2 panel-identifiers attached to them, the last identifier is assumed to be the time-variable, and the others are taken as grouping-variables and interacted.

Value

`x` differenced `diff` times using lags `n` of itself. Quasi and log-differences are toggled by the `rho` and `log` arguments or the `Dlog` operator. Computations can be grouped by `g/by` and/or ordered by `t`. See Details and Examples.

References

Cochrane, D.; Orcutt, G. H. (1949). Application of Least Squares Regression to Relationships Containing Auto-Correlated Error Terms. *Journal of the American Statistical Association*. 44 (245): 32-61.

Prais, S. J. & Winsten, C. B. (1954). Trend Estimators and Serial Correlation. *Cowles Commission Discussion Paper No. 383*. Chicago.

See Also

[flag/L/F, fgrowth/G, Time Series and Panel Series, Collapse Overview](#)

Examples

```
## Simple Time Series: AirPassengers
D(AirPassengers)           # 1st difference, same as fdiff(AirPassengers)
D(AirPassengers, -1)      # Forward difference
Dlog(AirPassengers)       # Log-difference
D(AirPassengers, 1, 2)    # Second difference
Dlog(AirPassengers, 1, 2) # Second log-difference
D(AirPassengers, 12)      # Seasonal difference (data is monthly)
D(AirPassengers,         # Quasi-difference, see a better example below
  rho = pwcov(AirPassengers, L(AirPassengers)))

head(D(AirPassengers, -2:2, 1:3)) # Sequence of leaded/lagged and iterated differences

# let's do some visual analysis
plot(AirPassengers)         # Plot the series - seasonal pattern is evident
plot(stl(AirPassengers, "periodic")) # Seasonal decomposition
plot(D(AirPassengers,c(1,12),1:2)) # Plotting ordinary and seasonal first and second differences
plot(stl(window(D(AirPassengers,12), # Taking seasonal differences removes most seasonal variation
  1950), "periodic"))

## Time Series Matrix of 4 EU Stock Market Indicators, recorded 260 days per year
plot(D(EuStockMarkets, c(0, 260))) # Plot series and annual differences
mod <- lm(DAX ~., L(EuStockMarkets, c(0, 260))) # Regressing the DAX on its annual lag
summary(mod) # and the levels and annual lags others
```

```

r <- residuals(mod) # Obtain residuals
pvcor(r, L(r)) # Residual Autocorrelation
fFtest(r, L(r)) # F-test of residual autocorrelation
# (better use lmtest::bgtest)

modCO <- lm(QD1.DAX ~., D(L(EuStockMarkets, c(0, 260))), # Cochrane-Orcutt (1949) estimation
rho = pvcor(r, L(r)))

summary(modCO)
rCO <- residuals(modCO)
fFtest(rCO, L(rCO)) # No more autocorrelation

## World Development Panel Data
head(fdiff(num_vars(wlddev), 1, 1, # Computes differences of numeric variables
wlddev$country, wlddev$year)) # fdiff requires external inputs..
head(D(wlddev, 1, 1, ~country, ~year)) # Differences of numeric variables
head(D(wlddev, 1, 1, ~country)) # Without t: Works because data is ordered
head(D(wlddev, 1, 1, PCGDP + LIFEEEX ~ country, ~year)) # Difference of GDP & Life Expectancy
head(D(wlddev, 0:1, 1, ~ country, ~year, cols = 9:10)) # Same, also retaining original series
head(D(wlddev, 0:1, 1, ~ country, ~year, 9:10, # Dropping id columns
keep.ids = FALSE))

# Dynamic Panel Data Models:
summary(lm(D(PCGDP,1,1,iso3c,year) ~ # Diff. GDP regressed on it's lagged level
L(PCGDP,1,iso3c,year) + # and the difference of Life Expanctancy
D(LIFEEEX,1,1,iso3c,year), data = wlddev))

g = qF(wlddev$country) # Omitting t and precomputing g allows for
summary(lm(D(PCGDP,1,1,g) ~ L(PCGDP,1,g) + # a bit more parsimonious specification
D(LIFEEEX,1,1,g), wlddev))

summary(lm(D1.PCGDP ~., # Now adding level and lagged level of
L(D(wlddev,0:1,1, ~ country, ~year,9:10),0:1, # LIFEEEX and lagged differences rates
~ country, ~year, keep.ids = FALSE)[-1]))

## Using plm can make things easier, but avoid attaching or 'with' calls:
pwldev <- plm::pdata.frame(wlddev, index = c("country","year"))
head(D(pwldev, 0:1, 1, 9:10)) # Again differences of LIFEEEX and PCGDP
PCGDP <- pwldev$PCGDP # A panel-Series of GDP per Capita
head(D(PCGDP)) # Differencing the panel series
summary(lm(D1.PCGDP ~., # Running the dynamic model again ->
data = L(D(pwldev,0:1,1,9:10),0:1, # code becomes a bit simpler
keep.ids = FALSE)[-1]))

# One could be tempted to also do something like this, but THIS DOES NOT WORK!!:
# -> a pseries is only created when subsetting the pdata.frame using $ or [[
summary(lm(D(PCGDP) ~ L(D(PCGDP,0:1)) + L(D(LIFEEEX,0:1),0:1), pwldev))

# To make it work, one needs to create pseries
LIFEEEX <- pwldev$LIFEEEX
summary(lm(D(PCGDP) ~ L(D(PCGDP,0:1)) + L(D(LIFEEEX,0:1),0:1))) # THIS WORKS !

## Using dplyr:
library(dplyr)
wlddev %>% group_by(country) %>%

```

```

      select(PCGDP,LIFEEX) %>% fdiff(0:1,1:2)      # Adding a first and second difference
wlddev %>% group_by(country) %>%
      select(year,PCGDP,LIFEEX) %>% D(0:1,1:2,year) # Also using t (safer)
wlddev %>% group_by(country) %>%
      select(year,PCGDP,LIFEEX) %>% D(0:1,1:2,year, keep.ids = FALSE)

```

 fdroplevels

Fast Removal of Unused Factor Levels

Description

A substantially faster replacement for [droplevels](#).

Usage

```

fdroplevels(x, ...)

## S3 method for class 'factor'
fdroplevels(x, ...)

## S3 method for class 'data.frame'
fdroplevels(x, ...)

```

Arguments

`x` a factor, or data frame / list containing one or more factors.
`...` not used.

Details

`base::droplevels` passes a factor from which levels are to be dropped to [factor](#), which first calls [unique](#) and then [match](#) to drop unused levels. Both functions internally use a hash table, which is highly inefficient. `fdroplevels` does not require mapping values at all, but uses a super fast boolean vector method to determine which levels are unused and remove those levels. In addition, if no unused levels are found, `x` is simply returned. Any missing values found in `x` are efficiently skipped in the process of checking and replacing levels. All other attributes of `x` are preserved.

Value

`x` will any unused factor levels removed.

Note

If `x` is malformed i.e. has too few levels, this function can cause a segmentation fault, thus only use with ordinary / proper factors.

See Also

[qF](#), [funique](#), [Fast Grouping and Ordering](#), [Collapse Overview](#)

Examples

```
f <- iris$Species[1:100]
fdroplevels(f)
identical(fdroplevels(f), droplevels(f))

fNA <- na_insert(f)
fdroplevels(fNA)
identical(fdroplevels(fNA), droplevels(fNA))

identical(fdroplevels(ss(iris, 1:100)), droplevels(ss(iris, 1:100)))
```

ffirst, flast

Fast (Grouped) First and Last Value for Matrix-Like Objects

Description

ffirst and flast are S3 generic functions that (column-wise) returns the first and last values in x, (optionally) grouped by g. The [TRA](#) argument can further be used to transform x using its (groupwise) first and last values.

Usage

```
ffirst(x, ...)
flast(x, ...)

## Default S3 method:
ffirst(x, g = NULL, TRA = NULL, na.rm = TRUE,
       use.g.names = TRUE, ...)
## Default S3 method:
flast(x, g = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = TRUE, ...)

## S3 method for class 'matrix'
ffirst(x, g = NULL, TRA = NULL, na.rm = TRUE,
       use.g.names = TRUE, drop = TRUE, ...)
## S3 method for class 'matrix'
flast(x, g = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = TRUE, drop = TRUE, ...)

## S3 method for class 'data.frame'
ffirst(x, g = NULL, TRA = NULL, na.rm = TRUE,
       use.g.names = TRUE, drop = TRUE, ...)
## S3 method for class 'data.frame'
```

```

flast(x, g = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = TRUE, drop = TRUE, ...)

## S3 method for class 'grouped_df'
ffirst(x, TRA = NULL, na.rm = TRUE,
       use.g.names = FALSE, keep.group_vars = TRUE, ...)
## S3 method for class 'grouped_df'
flast(x, TRA = NULL, na.rm = TRUE,
      use.g.names = FALSE, keep.group_vars = TRUE, ...)

```

Arguments

<code>x</code>	a vector, matrix, data frame or grouped tibble (<code>dplyr::grouped_df</code>).
<code>g</code>	a factor, GRP object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a GRP object) used to group <code>x</code> .
<code>TRA</code>	an integer or quoted operator indicating the transformation to perform: 1 - "replace_fill" 2 - "replace" 3 - "-" 4 - "-+" 5 - "/" 6 - "%" 7 - "+" 8 - "*" 9 - "%%" 10 - "-%%" . See TRA .
<code>na.rm</code>	logical. TRUE skips missing values and returns the first / last non-missing value i.e. if the first (1) / last (n) value is NA, take the second (2) / second-to-last (n-1) value etc..
<code>use.g.names</code>	logical. Make group-names and add to the result as names (default method) or row-names (matrix and data frame methods). No row-names are generated for <i>data.table</i> 's.
<code>drop</code>	<i>matrix and data.frame method</i> : Logical. TRUE drops dimensions and returns an atomic vector if <code>g = NULL</code> and <code>TRA = NULL</code> .
<code>keep.group_vars</code>	<i>grouped_df method</i> : Logical. FALSE removes grouping variables after computation.
<code>...</code>	arguments to be passed to or from other methods.

Value

`ffirst` returns the first value in `x`, grouped by `g`, or (if [TRA](#) is used) `x` transformed by its first value, grouped by `g`. Similarly `flast` returns the last value in `x`, ...

See Also

[Fast Statistical Functions, Collapse Overview](#)

Examples

```

## default vector method
ffirst(airquality$Ozone) # Simple first value
ffirst(airquality$Ozone, airquality$Month) # Grouped first value
ffirst(airquality$Ozone, airquality$Month,
      na.rm = FALSE) # Grouped first, but without skipping initial NA's

```

```
## data.frame method
ffirst(airquality)
ffirst(airquality, airquality$Month)
ffirst(airquality, airquality$Month, na.rm = FALSE) # Again first Ozone measurement in month 6 is NA

## matrix method
aqm <- qM(airquality)
ffirst(aqm)
ffirst(aqm, airquality$Month) # etc..

## method for grouped tibbles - for use with dplyr
library(dplyr)
airquality %>% group_by(Month) %>% ffirst
airquality %>% group_by(Month) %>% select(Ozone) %>% ffirst(na.rm = FALSE)

# Note: All examples generalize to flast.
```

fFtest

Fast F-test for Linear Models (with Factors)

Description

fFtest computes an R-squared based F-test for the exclusion of the variables in exc, where the full (unrestricted) model is defined by variables supplied to both exc and X. The test is efficient and designed for cases where both exc and X may contain multiple factors and continuous variables.

Usage

```
fFtest(y, exc, X = NULL, full.df = TRUE, ...)
```

Arguments

y	a numeric vector: The dependent variable.
exc	a numeric vector, factor, numeric matrix or list / data frame of numeric vectors and/or factors: Variables to test / exclude.
X	a numeric vector, factor, numeric matrix or list / data frame of numeric vectors and/or factors: Covariates to include in both the restricted (without exc) and unrestricted model. If left empty (X = NULL), the test amounts to the F-test of the regression of y on exc.
full.df	logical. If TRUE (default), the degrees of freedom are calculated as if both restricted and unrestricted models were estimated using lm() (i.e. as if factors were expanded to matrices of dummies). FALSE only uses one degree of freedom per factor.
...	other arguments passed to lfe::demeanlist, the workhorse function underlying fHDwithin.

Details

Factors and continuous regressors are efficiently projected out using `fHDwithin`, and the option `full.df` regulates whether a degree of freedom is subtracted for each used factor level (equivalent to dummy-variable estimator / expanding factors), or only one degree of freedom per factor (fixed-effects estimation / treating factors as variables). The test automatically removes missing values and considers only the complete cases of y , exc and X . Unused factor levels in exc and X are dropped.

Value

A 5 x 3 numeric matrix of statistics. The columns contain statistics:

1. the R-squared of the model
2. the numerator degrees of freedom i.e. the number of variables (k) and used factor levels if `full.df = TRUE`
3. the denominator degrees of freedom: $N - k - 1$.
4. the F-statistic
5. the corresponding P-value

The rows show these statistics for:

1. the Full (unrestricted) Model ($y \sim exc + X$)
2. the Restricted Model ($y \sim X$)
3. the Exclusion Restriction of exc . The R-squared shown is simply the difference of the full and restricted R-Squared's, not the R-Squared of the model $y \sim exc$.

If $X = \text{NULL}$, only a vector of the same 5 statistics testing the model ($y \sim exc$) is shown.

See Also

[fHDwithin](#), [Summary Statistics](#), [Data Transformations](#), [Collapse Overview](#)

Examples

```
## We could use fFtest as a seasonality test:
fFtest(AirPassengers, qF(cycle(AirPassengers)))           # Testing for level-seasonality
fFtest(AirPassengers, qF(cycle(AirPassengers)),          # Seasonality test around a cubic trend
      poly(seq_along(AirPassengers), 3))
fFtest(fdiff(AirPassengers), qF(cycle(AirPassengers)))  # Seasonality in first-difference

## A more classical example with only continuous variables
fFtest(mtcars$mpg, mtcars[c("cyl", "vs")], mtcars[c("hp", "carb")])

## Now encoding cyl and vs as factors
fFtest(mtcars$mpg, dapply(mtcars[c("cyl", "vs")], qF), mtcars[c("hp", "carb")])

## Using iris data: A factor and a continuous variable excluded
fFtest(iris$Sepal.Length, iris[4:5], iris[2:3])

## Testing the significance of country-FE in regression of GDP on life expectancy
fFtest(wlddev$PCGDP, wlddev$iso3c, wlddev$LIFEEX)
```

```
## Ok, country-FE are significant, what about adding time-FE
fFtest(wlddev$PCGDP, qF(wlddev$year), wlddev[c("iso3c","LIFEEX")])

# Same test done using lm:
data <- na_omit(get_vars(wlddev, c("iso3c","year","PCGDP","LIFEEX")))
full <- lm(PCGDP ~ LIFEEX + iso3c + qF(year), data)
rest <- lm(PCGDP ~ LIFEEX + iso3c, data)
anova(rest, full)
```

fgrowth

Fast Growth Rates for Time Series and Panel Data

Description

fgrowth is a S3 generic to compute (sequences of) suitably lagged / leaded and iterated growth rates, obtained with via the exact method of computation of through log differencing. By default growth rates are provided in percentage terms, but any scale factor can be applied. The growth operator G is a parsimonious wrapper around fgrowth, and also provides more flexibility when applied to data frames.

Usage

```
fgrowth(x, n = 1, diff = 1, ...)
```

```
G(x, n = 1, diff = 1, ...)
```

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

```
fgrowth(x, n = 1, diff = 1, g = NULL, t = NULL, fill = NA,
        logdiff = FALSE, scale = 100, power = 1, stubs = TRUE, ...)
```

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

```
G(x, n = 1, diff = 1, g = NULL, t = NULL, fill = NA, logdiff = FALSE,
  scale = 100, power = 1, stubs = TRUE, ...)
```

```
## S3 method for class 'matrix'
```

```
fgrowth(x, n = 1, diff = 1, g = NULL, t = NULL, fill = NA,
        logdiff = FALSE, scale = 100, power = 1,
        stubs = length(n) + length(diff) > 2L, ...)
```

```
## S3 method for class 'matrix'
```

```
G(x, n = 1, diff = 1, g = NULL, t = NULL, fill = NA, logdiff = FALSE,
  scale = 100, power = 1, stubs = TRUE, ...)
```

```
## S3 method for class 'data.frame'
```

```
fgrowth(x, n = 1, diff = 1, g = NULL, t = NULL, fill = NA,
        logdiff = FALSE, scale = 100, power = 1,
        stubs = length(n) + length(diff) > 2L, ...)
```

```
## S3 method for class 'data.frame'
```

```

G(x, n = 1, diff = 1, by = NULL, t = NULL, cols = is.numeric,
  fill = NA, logdiff = FALSE, scale = 100, power = 1, stubs = TRUE,
  keep.ids = TRUE, ...)

# Methods for compatibility with plm:

## S3 method for class 'pseries'
fgrowth(x, n = 1, diff = 1, fill = NA, logdiff = FALSE, scale = 100,
  power = 1, stubs = TRUE, ...)
## S3 method for class 'pseries'
G(x, n = 1, diff = 1, fill = NA, logdiff = FALSE, scale = 100,
  power = 1, stubs = TRUE, ...)

## S3 method for class 'pdata.frame'
fgrowth(x, n = 1, diff = 1, fill = NA, logdiff = FALSE, scale = 100,
  power = 1, stubs = length(n) + length(diff) > 2L, ...)
## S3 method for class 'pdata.frame'
G(x, n = 1, diff = 1, cols = is.numeric, fill = NA, logdiff = FALSE,
  scale = 100, power = 1, stubs = TRUE, keep.ids = TRUE, ...)

# Methods for compatibility with dplyr:

## S3 method for class 'grouped_df'
fgrowth(x, n = 1, diff = 1, t = NULL, fill = NA, logdiff = FALSE,
  scale = 100, power = 1, stubs = length(n) + length(diff) > 2L,
  keep.ids = TRUE, ...)
## S3 method for class 'grouped_df'
G(x, n = 1, diff = 1, t = NULL, fill = NA, logdiff = FALSE,
  scale = 100, power = 1, stubs = TRUE, keep.ids = TRUE, ...)

```

Arguments

x	a numeric vector, matrix, data frame, panel series (plm::pseries), panel data frame (plm::pdata.frame) or grouped tibble (dplyr::grouped_df).
n	integer. A vector indicating the number of lags or leads.
diff	integer. A vector of integers > 1 indicating the order of taking growth rates, e.g. diff = 2 means computing the growth rate of the growth rate.
g	a factor, GRP object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a GRP object) used to group x.
by	<i>data.frame method</i> : Same as g, but also allows one- or two-sided formulas i.e. ~group1 or var1 + var2 ~ group1 + group2. See Examples.
t	same input as g/by, to indicate the time-variable. For safe computation of growth rates on unordered time series and panels. Data Frame method also allows one-sided formula i.e. ~time. grouped_df method supports lazy-evaluation i.e. time (no quotes).
cols	<i>data.frame method</i> : Select columns to compute growth rates using a function, column names, indices or a logical vector. Default: All numeric variables. <i>Note</i> : cols is ignored if a two-sided formula is passed to by.

fill	value to insert when vectors are shifted. Default is NA.
logdiff	logical. Compute log-difference growth rates instead of exact growth rates. See Details.
scale	logical. Scale factor post-applied to growth rates, default is 100 which gives growth rates in percentage terms. See Details.
power	numeric. Apply a power to annualize or compound growth rates e.g. <code>fgrowth(AirPassengers, 12, power = 1/12)</code> is equivalent to <code>((AirPassengers/flag(AirPassengers, 12))^(1/12)-1)*100</code> .
stubs	logical. TRUE will rename all computed columns by adding a prefix "LnGdiff." / "FnGdiff.", or "LnDlogdiff." / "FnDlogdiff." if <code>logdiff = TRUE</code> .
keep.ids	<i>data.frame / pdata.frame / grouped_df methods</i> : Logical. Drop all panel-identifiers from the output (which includes all variables passed to <code>by</code> or <code>t</code>). <i>Note</i> : For panel data frames and grouped tibbles identifiers are dropped, but the 'index' / 'groups' attributes are kept.
...	arguments to be passed to or from other methods.

Details

`fgrowth/G` by default computes exact growth rates using `repeat(diff) ((x[i]/x[i-n])^power - 1)*scale`, and, if `logdiff = TRUE` approximate growth rates using `repeat(diff) log(x[i]/x[i-n])*scale`. So for `diff > 1` it computes growth rate of growth rates etc.. For further details see the help pages for [fdiff](#) and [flag](#).

Value

`x` where the growth rate was taken `diff` times using lags `n` of itself, scaled by `scale`. Computations can be grouped by `g/by` and/or ordered by `t`. See Details and Examples.

See Also

[flag/L/F](#), [fdiff/D/Dlog](#), [Time Series and Panel Series](#), [Collapse Overview](#)

Examples

```
## Simple Time Series: AirPassengers
G(AirPassengers)           # Growth rate, same as fgrowth(AirPassengers)
G(AirPassengers, logdiff = TRUE) # Log-difference
G(AirPassengers, 1, 2)     # Growth rate of growth rate
G(AirPassengers, 12)      # Seasonal growth rate (data is monthly)

head(G(AirPassengers, -2:2, 1:3)) # Sequence of leaded/lagged and iterated growth rates

# let's do some visual analysis
plot(G(AirPassengers, c(0, 1, 12)))
plot(stl(window(G(AirPassengers, 12), # Taking seasonal growth rate removes most seasonal variation
              1950), "periodic"))

## Time Series Matrix of 4 EU Stock Market Indicators, recorded 260 days per year
plot(G(EuStockMarkets, c(0, 260))) # Plot series and annual growth rates
```

fHDbetween, fHDwithin *Higher-Dimensional Centering and Linear Prediction*

Description

fHDbetween is a generalization of fbetween to efficiently predict with multiple factors and linear models (i.e. predict with vectors/factors, matrices, or data frames/lists where the latter may contain multiple factor variables). Similarly fHDwithin is a generalization of fwithin to center on multiple factors and partial-out linear models.

The corresponding operators HDB and HDW additionally allow to predict / partial out full lm() formulas with interactions between variables.

Usage

```
fHDbetween(x, ...)
fHDwithin(x, ...)
  HDB(x, ...)
  HDW(x, ...)

## Default S3 method:
fHDbetween(x, fl, w = NULL, na.rm = TRUE, fill = FALSE, ...)
## Default S3 method:
fHDwithin(x, fl, w = NULL, na.rm = TRUE, fill = FALSE, ...)
## Default S3 method:
HDB(x, fl, w = NULL, na.rm = TRUE, fill = FALSE, ...)
## Default S3 method:
HDW(x, fl, w = NULL, na.rm = TRUE, fill = FALSE, ...)

## S3 method for class 'matrix'
fHDbetween(x, fl, w = NULL, na.rm = TRUE, fill = FALSE, ...)
## S3 method for class 'matrix'
fHDwithin(x, fl, w = NULL, na.rm = TRUE, fill = FALSE, ...)
## S3 method for class 'matrix'
HDB(x, fl, w = NULL, na.rm = TRUE, fill = FALSE, stub = "HDB.", ...)
## S3 method for class 'matrix'
HDW(x, fl, w = NULL, na.rm = TRUE, fill = FALSE, stub = "HDW.", ...)

## S3 method for class 'data.frame'
fHDbetween(x, fl, w = NULL, na.rm = TRUE, fill = FALSE,
  variable.wise = FALSE, ...)
## S3 method for class 'data.frame'
fHDwithin(x, fl, w = NULL, na.rm = TRUE, fill = FALSE,
  variable.wise = FALSE, ...)
## S3 method for class 'data.frame'
HDB(x, fl, w = NULL, cols = is.numeric, na.rm = TRUE, fill = FALSE,
  variable.wise = FALSE, stub = "HDB.", ...)
```

```

## S3 method for class 'data.frame'
HDW(x, fl, w = NULL, cols = is.numeric, na.rm = TRUE, fill = FALSE,
     variable.wise = FALSE, stub = "HDW.", ...)

# Methods for compatibility with plm:

## S3 method for class 'pseries'
fHDbetween(x, w = NULL, na.rm = TRUE, fill = TRUE, ...)
## S3 method for class 'pseries'
fHDwithin(x, w = NULL, na.rm = TRUE, fill = TRUE, ...)
## S3 method for class 'pseries'
HDB(x, w = NULL, na.rm = TRUE, fill = TRUE, ...)
## S3 method for class 'pseries'
HDW(x, w = NULL, na.rm = TRUE, fill = TRUE, ...)

## S3 method for class 'pdata.frame'
fHDbetween(x, w = NULL, na.rm = TRUE, fill = TRUE,
           variable.wise = TRUE, ...)
## S3 method for class 'pdata.frame'
fHDwithin(x, w = NULL, na.rm = TRUE, fill = TRUE,
          variable.wise = TRUE, ...)
## S3 method for class 'pdata.frame'
HDB(x, w = NULL, cols = is.numeric, na.rm = TRUE, fill = TRUE,
    variable.wise = TRUE, stub = "HDB.", ...)
## S3 method for class 'pdata.frame'
HDW(x, w = NULL, cols = is.numeric, na.rm = TRUE, fill = TRUE,
    variable.wise = TRUE, stub = "HDW.", ...)

```

Arguments

x	a numeric vector, matrix, data frame, panel series (plm::pseries) or panel data frame (plm::pdata.frame).
fl	a numeric vector, factor, matrix, data frame or list (which may or may not contain factors). In the data frame method fl can also be a one- or two-sided lm() formula with variables contained in x. Interactions (:) and full interactions (*) are supported. See Examples and the Note.
w	a vector of (non-negative) weights. Currently only weighted centering/averaging is supported, not weighted linear models.
cols	<i>data.frame methods</i> : Select columns to center (partial-out) or predict using column names, indices, a logical vector or a function. Unless specified otherwise all numeric columns are selected. If NULL, all variables are selected.
na.rm	remove missing values from both x and fl. by default rows with missing values in x or fl are removed. In that case an attribute "na.rm" is attached containing the rows removed.
fill	If na.rm = TRUE, fill = TRUE will not remove rows with missing values in x or fl, but fill them with NA's.

variable.wise	<i>data.frame methods:</i> Setting <code>variable.wise = TRUE</code> will process each column individually i.e. use all non-missing cases in each column and in <code>f1</code> (<code>f1</code> is only checked for missing values if <code>na.rm = TRUE</code>). This is a lot less efficient but uses all data available in each column.
stub	a prefix / stub to rename all transformed columns. <code>FALSE</code> will not rename columns.
...	further arguments passed to <code>lfe::demeanlist</code> (if <code>f1</code> contains factors), or to / from other methods.

Details

fHDbetween/HDB and fHDwithin/HDW can be understood as generalizations of `lfe::demeanlist` to continuous-data and formula input, and more choices dealing with missing values. They are powerful tools for high-dimensional linear prediction problems involving large factors and datasets, but can just as well handle ordinary regression problems. Intended areas of use are to efficiently obtain residuals and predicted values from data, and to prepare data for complex linear models involving multiple levels of fixed effects. Such models can now be fitted using `lm()` on data prepared with fHDwithin / HDW (relying on bootstrapped SE's for inference, or implementing the appropriate corrections). See Examples.

If `f1` is a vector or matrix, the result are identical to `lm` i.e. fHDbetween / HDB returns `fitted(lm(x ~ f1))` and fHDwithin / HDW `residuals(lm(x ~ f1))`. If `f1` is a list containing factors, all variables in `x` and non-factor variables in `f1` are centered on these factors using the method of alternating projections implemented by `lfe::demeanlist`. Afterwards the centered data is regressed on the centered predictors. If `f1` is just a list of factors, fHDwithin/HDW returns the centered data and fHDbetween/HDB the corresponding means. Take as a most general example a list `f1 = list(fct1, fct2, ..., var1, var2, ...)` where `fcti` are factors and `vari` are continuous variables. The output of fHDwithin/HDW | fHDbetween/HDB will then be identical to calling `resid | fitted` on `lm(x ~ fct1 + fct2 + ... + var1 + var2 + ...)`. The computations performed by fHDwithin/HDW and fHDbetween/HDB are however much faster and more memory efficient than `lm` because factors are not passed to `stats::model.matrix` and expanded to matrices of dummies but projected out using `lfe::demeanlist`.

The formula interface to the `data.frame` method (only supported by the operators HDW | HDB) provides ease of use and allows for additional modeling complexity. For example it is possible to project out formulas like `HDW(data, ~ fct1*var1 + fct2:fct3 + var2:fct2:fct3 + var1:var2:var3 + poly(var5, 3)*fct5)` containing simple (`:`) or full (`*`) interactions of factors with continuous variables or polynomials of continuous variables, and two-or three-way interactions of factors and continuous variables. If the formula is one-sided as in the example above (the space left of (`~`) is left empty), the formula is applied to all variables selected through `cols`. The specification provided in `cols` (default: all numeric variables not used in the formula) can be overridden by supplying one-or more dependent variables. For example `HDW(data, var1 + var2 ~ fct1 + fct2)` will return a `data.frame` with `var1` and `var2` centered on `fct1` and `fct2`.

The special methods for `plm::pseries` and `plm::pdata.frame` center a panel series or variables in a panel data frame on all panel-identifiers. By default in these methods `fill = TRUE` and `variable.wise = TRUE`, so missing values are kept. This change in the default arguments was done to ensure a coherent framework of functions and operators applied to *plm* panel data classes.

Value

HDB returns fitted values of regressing x on $f1$. HDW returns residuals. See Details and Examples.

Note

Weights are currently only supported for centering / averaging, not for linear regression.

Caution with full (*) and factor-continuous variable interactions:: In general full interactions specified with (*) can be very slow on large data, and `lfe::demeanlist` is also not very speedy on interaction between factors and continuous variables, so these structures should be used with caution (don't just specify an interaction like that on a large dataset, start with smaller data and see how long computations take. Upon further updates of `lfe::demeanlist`, performance might improve).

On the differences between fHDwithin/HDW...and fwithin/W...::

- `fHDwithin/HDW` can center data on multiple factors and also partial out continuous variables while `fwithin/W` only centers on one factor or the interaction of a set of factors, and does that very efficiently...
- `HDW(data, ~ qF(group1) + qF(group2))` simultaneously centers numeric variables in data on `group1` and `group2`, while `W(data, ~ group1 + group2)` centers data on the interaction of `group1` and `group2`. The equivalent operation in HDW would be: `HDW(data, ~ qF(group1):qF(group2))`.
- `W` always does computations on the variable-wise complete observations (in both matrices and data frames), whereas by default HDW removes all cases missing in either x or $f1$. In short, `W(data, ~ group1 + group2)` is actually equivalent to `HDW(data, ~ qF(group1):qF(group2), variable.wise = TRUE)`. `HDW(data, ~ qF(group1):qF(group2))` would remove any missing cases.
- `fbetween/B` and `fwithin/W` have options to fill missing cases using group-averages and to add the overall mean back to group-demeaned data. These options are not available in `fHDbetween/HDB` and `fHDwithin/HDW`. Since `HDB` and `HDW` by default remove missing cases, they also don't have options to keep grouping-columns as in `B` and `W`.

See Also

[fbetween](#), [fwithin](#), [fscale](#), [TRA](#), [fFtest](#), [Data Transformations](#), [Collapse Overview](#)

Examples

```
HDW(mtcars$mpg, mtcars$carb) # Simple regression problems..
HDW(mtcars$mpg, mtcars[-1])
HDW(mtcars$mpg, qM(mtcars[-1]))
head(HDW(qM(mtcars[3:4]), mtcars[1:2]))
head(HDW(iris[1:2], iris[3:4])) # Partialling columns 3 and 4 out of columns 1 and 2
head(HDW(iris[1:2], iris[3:5])) # Adding the Species factor -> fixed effect
head(HDW(wlddev, PCGDP + LIFEEEX ~ iso3c + qF(year))) # Partialling out 2 fixed effects
head(HDW(wlddev, PCGDP + LIFEEEX ~ iso3c + qF(year), variable.wise = TRUE)) # Variable-wise
head(HDW(wlddev, PCGDP + LIFEEEX ~ iso3c + qF(year) + ODA)) # Adding ODA as a continuous regressor
head(HDW(wlddev, PCGDP + LIFEEEX ~ iso3c:qF(decade) + qF(year) + ODA)) # Country-decade and year FE's

# More complex examples (Currently only recommended for smaller data)
lm(HDW.mpg ~ HDW.hp, data = HDW(mtcars, ~ factor(cyl)*carb + vs + wt:gear + wt:gear:carb))
lm(mpg ~ hp + factor(cyl)*carb + vs + wt:gear + wt:gear:carb, data = mtcars)
```

```
lm(HDW.mpg ~ HDW.hp, data = HDW(mtcars, ~ factor(cyl)*carb + vs + wt:gear))
lm(mpg ~ hp + factor(cyl)*carb + vs + wt:gear, data = mtcars)

lm(HDW.mpg ~ HDW.hp, data = HDW(mtcars, ~ cyl*carb + vs + wt:gear))
lm(mpg ~ hp + cyl*carb + vs + wt:gear, data = mtcars)

lm(HDW.mpg ~ HDW.hp, data = HDW(mtcars, mpg + hp ~ cyl*carb + factor(cyl)*poly(drat,2)))
lm(mpg ~ hp + cyl*carb + factor(cyl)*poly(drat,2), data = mtcars)
```

flag

Fast Lags and Leads for Time Series and Panel Data

Description

flag is an S3 generic to compute (sequences of) lags and leads. L and F are wrappers around flag representing the lag- and lead-operators, such that $L(x, -1) = F(x, 1) = F(x)$ and $L(x, -3:3) = F(x, 3:-3)$. L and F provide more flexibility than flag when applied to data frames (i.e. column subsetting, formula input and id-variable-preservation capabilities...), but are otherwise identical.

(flag is more of a programmers function in style of the [Fast Statistical Functions](#) while L and F are more practical to use in regression formulas or for computations on data frames.)

Usage

```
flag(x, n = 1, ...)
  L(x, n = 1, ...)
  F(x, n = 1, ...)

## Default S3 method:
flag(x, n = 1, g = NULL, t = NULL, fill = NA, stubs = TRUE, ...)
## Default S3 method:
L(x, n = 1, g = NULL, t = NULL, fill = NA, stubs = TRUE, ...)
## Default S3 method:
F(x, n = 1, g = NULL, t = NULL, fill = NA, stubs = TRUE, ...)

## S3 method for class 'matrix'
flag(x, n = 1, g = NULL, t = NULL, fill = NA, stubs = length(n) > 1L, ...)
## S3 method for class 'matrix'
L(x, n = 1, g = NULL, t = NULL, fill = NA, stubs = TRUE, ...)
## S3 method for class 'matrix'
F(x, n = 1, g = NULL, t = NULL, fill = NA, stubs = TRUE, ...)

## S3 method for class 'data.frame'
flag(x, n = 1, g = NULL, t = NULL, fill = NA, stubs = length(n) > 1L, ...)
## S3 method for class 'data.frame'
L(x, n = 1, by = NULL, t = NULL, cols = is.numeric,
  fill = NA, stubs = TRUE, keep.ids = TRUE, ...)
```

```

## S3 method for class 'data.frame'
F(x, n = 1, by = NULL, t = NULL, cols = is.numeric,
  fill = NA, stubs = TRUE, keep.ids = TRUE, ...)

# Methods for compatibility with plm:

## S3 method for class 'pseries'
flag(x, n = 1, fill = NA, stubs = TRUE, ...)
## S3 method for class 'pseries'
L(x, n = 1, fill = NA, stubs = TRUE, ...)
## S3 method for class 'pseries'
F(x, n = 1, fill = NA, stubs = TRUE, ...)

## S3 method for class 'pdata.frame'
flag(x, n = 1, fill = NA, stubs = length(n) > 1L, ...)
## S3 method for class 'pdata.frame'
L(x, n = 1, cols = is.numeric, fill = NA, stubs = TRUE,
  keep.ids = TRUE, ...)
## S3 method for class 'pdata.frame'
F(x, n = 1, cols = is.numeric, fill = NA, stubs = TRUE,
  keep.ids = TRUE, ...)

# Methods for compatibility with dplyr:

## S3 method for class 'grouped_df'
flag(x, n = 1, t = NULL, fill = NA, stubs = length(n) > 1L, keep.ids = TRUE, ...)
## S3 method for class 'grouped_df'
L(x, n = 1, t = NULL, fill = NA, stubs = TRUE, keep.ids = TRUE, ...)
## S3 method for class 'grouped_df'
F(x, n = 1, t = NULL, fill = NA, stubs = TRUE, keep.ids = TRUE, ...)

```

Arguments

x	a vector / time series, (time series) matrix, data frame, panel series (plm: :pseries), panel data frame (plm: :pdata.frame) or grouped tibble (dplyr: :grouped_df). Data must not be numeric i.e you can also lag a date variable, character data etc...
n	integer. A vector indicating the lags / leads to compute (passing negative integers to flag or L computes leads, passing negative integers to F computes lags).
g	a factor, GRP object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a GRP object) used to group x.
by	<i>data.frame method</i> : Same as g, but also allows one- or two-sided formulas i.e. ~ group1 or var1 + var2 ~ group1 + group2. See Examples.
t	same input as g/by, to indicate the time-variable. For safe computation of differences on unordered time series and panels. Data Frame method also allows one-sided formula i.e. ~time. grouped_df method supports lazy-evaluation i.e. time (no quotes).

<code>cols</code>	<i>data.frame method</i> : Select columns to difference using a function, column names, indices or a logical vector. Default: All numeric variables. <i>Note</i> : <code>cols</code> is ignored if a two-sided formula is passed to <code>by</code> .
<code>fill</code>	value to insert when vectors are shifted. Default is NA.
<code>stubs</code>	logical. TRUE will rename all lagged / leaded columns by adding a stub or prefix "Ln." / "Fn.".
<code>keep.ids</code>	<i>data.frame / pdata.frame / grouped_df methods</i> : Logical. Drop all panel-identifiers from the output (which includes all variables passed to <code>by</code> or <code>t</code>). <i>Note</i> : For panel data frames and grouped tibbles identifiers are dropped, but the 'index' / 'groups' attributes are kept.
<code>...</code>	arguments to be passed to or from other methods.

Details

If a single integer is passed to `n`, and `g/by` and `t` are left empty, `flag/L/F` just returns `x` with all columns lagged / leaded by `n`. If `length(n)>1`, and `x` is an atomic vector (time series), `flag/L/F` returns a (time series) matrix with lags / leads computed in the same order as passed to `n`. If instead `x` is a matrix / data frame, a matrix / data frame with `ncol(x)*length(n)` columns is returned where columns are sorted first by variable and then by lag (so all lags computed on a variable are grouped together). `x` can be of any standard data type.

With groups/panel-identifiers supplied to `g/by`, `flag/L/F` efficiently computes a panel-lag/lead by shifting the entire vector(s) but inserting `fill` elements in the right places. If `t` is left empty, the data needs to be ordered such that all values belonging to a group are consecutive and in the right order. It is not necessary that the groups themselves occur in the right order. If a time-variable is supplied to `t` (or a list of time-variables uniquely identifying the time-dimension), the panel is fully identified and lags / leads can be securely computed even if the data is completely unordered.

`flag/L/F` supports balanced panels and unbalanced panels where various individuals are observed for different time-sequences (both start, end and duration of observation can differ for each individual). `flag/L/F` does not natively support irregularly spaced time series and panels, that is situations where there are either gaps in time and/or repeated observations in the same time-period for some individual (see also computational details below). For such cases the function `seqid` can be used to generate an appropriate panel-identifier (i.e. splitting individuals with an irregular time-sequence into multiple individuals with regular time-sequences before applying `flag/L/F`).

It is also possible to compute lags / leads on unordered time series (thus utilizing `t` but leaving `g/by` empty), although this is probably more rare to encounter than unordered panels. Irregularly spaced time series can also be lagged using a panel- identifier generated with `seqid`.

Computationally, if both `g/by` and `t` are supplied, `flag/L/F` uses two initial passes to create an ordering through which the data are accessed. First-pass: Calculate group sizes and the minimum time-value for each individual. Second-pass: Generate the ordering by placing the current element index into the vector slot obtained by adding the cumulative group size and the current time-value subtracted its individual-minimum together. This method of computation is faster than any sort-based method and delivers optimal performance if the panel-id supplied to `g/by` is already a factor variable, and if `t` is either an integer or factor variable. If `g/by` is not factor or `t` is not factor or integer, `qG` or `GRP` will be called to group the respective identifier and this can be expensive, so for optimal performance prepare the data (or use `plm` classes). A caveat of not using sort-based methods is that gaps or repeated values in time are only recognized towards the end of the second

pass where they cannot be rectified anymore, and thus `flag/L/F` does not natively support irregular panels but throws an error.

The methods applying to *plm* objects (panel series and panel data frames) automatically utilize the factor panel-identifiers attached to these objects and thus securely and efficiently compute fully identified panel-lags. If these objects have > 2 panel-identifiers attached to them, the last identifier is assumed to be the time-variable, and the others are taken as grouping-variables and interacted. Note that `flag/L/F` is significantly faster than `plm::lag/plm::lead` since the latter is written in R and based on a Split-Apply-Combine logic.

Value

x lagged / leaded n-times, grouped by g/by, ordered by t. See Details and Examples.

See Also

[fdiff](#), [fgrowth](#), [Time Series and Panel Series](#), [Collapse Overview](#)

Examples

```
## Simple Time Series: AirPassengers
L(AirPassengers)          # 1 lag
F(AirPassengers)          # 1 lead

all_identical(L(AirPassengers),      # 3 identical ways of computing 1 lag
              flag(AirPassengers),
              F(AirPassengers, -1))

head(L(AirPassengers, -1:3))          # 1 lead and 3 lags - output as matrix

## Time Series Matrix of 4 EU Stock Market Indicators, 1991-1998
tsp(EuStockMarkets)              # Data is recorded on 260 days per year
freq <- frequency(EuStockMarkets)
plot(stl(EuStockMarkets[, "DAX"], freq))      # There is some obvious seasonality
head(L(EuStockMarkets, -1:3 * freq))          # 1 annual lead and 3 annual lags
summary(lm(DAX ~ ., data = L(EuStockMarkets, -1:3*freq))) # DAX regressed on it's own annual lead,
                                                    # lags and the lead/lags of the other series

## World Development Panel Data
head(flag(wlddev, 1, wlddev$iso3c, wlddev$year))      # This lags all variables,
head(L(wlddev, 1, ~iso3c, ~year))                    # This lags all numeric variables
head(L(wlddev, 1, ~iso3c))                          # Without t: Works because data is ordered
head(L(wlddev, 1, PCGDP + LIFEEEX ~ iso3c, ~year))    # This lags GDP per Capita & Life Expectancy
head(L(wlddev, 0:2, ~ iso3c, ~year, cols = 9:10))    # Same, also retaining original series
head(L(wlddev, 1:2, PCGDP + LIFEEEX ~ iso3c, ~year,   # Two lags, dropping id columns
      keep.ids = FALSE))

# Different ways of regressing GDP on its lags and life-Expectancy and it's lags
summary(lm(PCGDP ~ ., L(wlddev, 0:2, ~iso3c, ~year, 9:10, keep.ids = FALSE))) # 1 - Precomputing
summary(lm(PCGDP ~ L(PCGDP, 1:2, iso3c, year) + L(LIFEEEX, 0:2, iso3c, year), wlddev)) # 2 - Ad-hoc
summary(lm(PCGDP ~ L(PCGDP, 1:2, iso3c) + L(LIFEEEX, 0:2, iso3c), wlddev))      # 3 - same no year
g = qF(wlddev$iso3c); t = qF(wlddev$year)                                       # 4- Precomputing
summary(lm(PCGDP ~ L(PCGDP, 1:2, g, t) + L(LIFEEEX, 0:2, g, t), wlddev))      # panel-id's
```



```
## Using plm:
pwlddev <- plm::pdata.frame(wlddev, index = c("iso3c","year"))
head(L(pwlddev, 0:2, 9:10)) # Again 2 lags of GDP and LIFEEEX
PCGDP <- pwlddev$PCGDP # A panel-Series of GDP per Capita
head(L(PCGDP)) # Lagging the panel series
summary(lm(PCGDP ~ ., L(pwlddev, 0:2, 9:10, keep.ids = FALSE))) # Running the lm again
# THIS DOES NOT WORK: -> a pseries is only created when subsetting the pdata.frame using $ or []
summary(lm(PCGDP ~ L(PCGDP,1:2) + L(LIFEEEX,0:2), pwlddev)) # ..so L.default is used here..
LIFEEEX <- pwlddev$LIFEEEX # To make it work, create pseries
summary(lm(PCGDP ~ L(PCGDP,1:2) + L(LIFEEEX,0:2))) # THIS WORKS !

## Using dplyr:
library(dplyr)
wlddev %>% group_by(iso3c) %>% select(PCGDP,LIFEEEX) %>% L(0:2)
wlddev %>% group_by(iso3c) %>% select(year,PCGDP,LIFEEEX) %>% L(0:2,year) # Also using t (safer)
```

flm

Fast (Weighted) Linear Model Fitting

Description

flm is a fast linear model command that takes matrices as input and (by default) only returns a coefficient matrix. 6 different efficient fitting methods are implemented: 4 using base R linear algebra, and 2 utilizing the *RcppArmadillo* and *RcppEigen* packages. The function itself only has an overhead of 5-10 microseconds, and is thus well suited as a bootstrap workhorse.

Usage

```
flm(y, X, w = NULL, add.icpt = FALSE, return.raw = FALSE,
    method = c("lm", "solve", "qr", "arma", "chol", "eigen"),
    eigen.method = 3L, ...)
```

Arguments

y	a response vector or matrix. Multiple dependent variables are only supported by methods "lm", "solve", "qr" and "chol".
X	a matrix of regressors.
w	a weight vector.
add.icpt	logical. TRUE adds an intercept column named '(Intercept)' to X.
return.raw	logical. TRUE returns the original output from the different methods. For 'lm', 'arma' and 'eigen', this includes additional statistics such as residuals, fitted values or standard errors. The other methods just return coefficients but in different formats.

method an integer or character string specifying the method of computation:

<i>Int.</i>	<i>String</i>	<i>Description</i>
1	"lm"	uses <code>.lm.fit</code> .
2	"solve"	<code>solve(crossprod(X), crossprod(X, y))</code> .
3	"qr"	<code>qr.coef(qr(X, LAPACK = TRUE), y)</code> .
4	"arma"	uses <code>RcppArmadillo::fastLmPure</code> .
5	"chol"	<code>chol2inv(chol(crossprod(X))) %% crossprod(X, y)</code> (quite fast but requires <code>crossprod(X)</code> to be
6	"eigen"	uses <code>RcppEigen::fastLmPure</code> (very fast but potentially unstable, depending on the method).

eigen.method integer. Select the method of computation used by `RcppEigen::fastLmPure`:

<i>Int.</i>	<i>Description</i>
0	column-pivoted QR decomposition.
1	unpivoted QR decomposition.
2	LLT Cholesky.
3	LDLT Cholesky.
4	Jacobi singular value decomposition (SVD).
5	method based on the eigenvalue-eigenvector decomposition of $X'X$.

See `vignette("RcppEigen-Introduction", package = "RcppEigen")` for details on these methods and benchmark results. Run `source(system.file("examples", "lmBenchmark.R", package = "RcppEigen"))` to re-run the benchmark on your machine.

... further arguments passed to other methods. Sensible choices are `tol = value` - a numerical tolerance for the solution - applicable with methods "lm", "solve" and "qr" (default is $1e-7$), or `LAPACK = TRUE` with method "qr" to use LAPACK routines to for the qr decomposition (typically faster than LINPACK (the default)).

Value

If `return.raw = FALSE`, a matrix of coefficients with the rows corresponding to the columns of X , otherwise the raw results from the various methods are returned.

Note

Method "qr" supports sparse matrices, so for an X matrix with many dummy variables consider method "qr" passing `as(X, "dgCMatrix")` instead of just X .

See Also

[fHDwithin/HDW](#), [fftest](#), [Data Transformations](#), [Collapse Overview](#)

Examples

```
coef <- flm(mtcars$mpg, qM(mtcars[c("hp", "carb")]),
           mtcars$wt, add.icpt = TRUE)
coef
```

```
lmcoef <- coef(lm(mpg ~ hp + carb, weights = wt, mtcars))
lmcoef

all.equal(drop(coef), lmcoef)

all_obj_equal(lapply(1:6, function(i)
  flm(mtcars$mpg, qM(mtcars[c("hp", "carb")]),
    mtcars$wt, add.icpt = TRUE, method = i)))
```

fmean

*Fast (Grouped, Weighted) Mean for Matrix-Like Objects***Description**

fmean is a generic function that computes the (column-wise) mean of x , (optionally) grouped by g and/or weighted by w . The [TRA](#) argument can further be used to transform x using its (grouped, weighted) mean.

Usage

```
fmean(x, ...)
```

Default S3 method:

```
fmean(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = TRUE, ...)
```

S3 method for class 'matrix'

```
fmean(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = TRUE, drop = TRUE, ...)
```

S3 method for class 'data.frame'

```
fmean(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = TRUE, drop = TRUE, ...)
```

S3 method for class 'grouped_df'

```
fmean(x, w = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = FALSE, keep.group_vars = TRUE, keep.w = TRUE, ...)
```

Arguments

x a numeric vector, matrix, data frame or grouped tibble (`dplyr::grouped_df`).

g a factor, [GRP](#) object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a [GRP](#) object) used to group x .

w a numeric vector of (non-negative) weights, may contain missing values.

TRA	an integer or quoted operator indicating the transformation to perform: 1 - "replace_fill" 2 - "replace" 3 - "-" 4 - "+ " 5 - "/" 6 - "%" 7 - "+" 8 - "*" 9 - "%%" 10 - "-%%" . See TRA .
na.rm	logical. Skip missing values in x. Defaults to TRUE and implemented at very little computational cost. If na.rm = FALSE a NA is returned when encountered.
use.g.names	logical. Make group-names and add to the result as names (default method) or row-names (matrix and data frame methods). No row-names are generated for <i>data.table</i> 's.
drop	<i>matrix and data.frame method</i> : Logical. TRUE drops dimensions and returns an atomic vector if g = NULL and TRA = NULL.
keep.group_vars	<i>grouped_df method</i> : Logical. FALSE removes grouping variables after computation.
keep.w	<i>grouped_df method</i> : Logical. Retain summed weighting variable after computation (if contained in grouped_df).
...	arguments to be passed to or from other methods.

Details

Missing-value removal as controlled by the `na.rm` argument is done very efficiently by simply skipping them in the computation (thus setting `na.rm = FALSE` on data with no missing values doesn't give extra speed). Large performance gains can nevertheless be achieved in the presence of missing values if `na.rm = FALSE`, since then the corresponding computation is terminated once a NA is encountered and NA is returned (unlike `base::mean` which just runs through without any checks).

The weighted mean is computed as $\text{sum}(x * w) / \text{sum}(w)$. If `na.rm = TRUE`, missing values will be removed from both x and w i.e. utilizing only `x[complete.cases(x,w)]` and `w[complete.cases(x,w)]`.

This all seamlessly generalizes to grouped computations, which are performed in a single pass (without splitting the data) and therefore extremely fast.

When applied to data frames with groups or `drop = FALSE`, `fmean` preserves all column attributes (such as variable labels) but does not distinguish between classed and unclassed object (thus applying `fmean` to a factor column will give a 'malformed factor' error). The attributes of the data frame itself are also preserved.

Value

The (w weighted) mean of x, grouped by g, or (if [TRA](#) is used) x transformed by its mean, grouped by g.

See Also

[fmedian](#), [fmode](#), [Fast Statistical Functions](#), [Collapse Overview](#)

Examples

```
## default vector method
mpg <- mtcars$mpg
fmean(mpg)                                # Simple mean
```

```

fmean(mpg, w = mtcars$hp)           # Weighted mean: Weighted by hp
fmean(mpg, TRA = "-")              # Simple transformation: demeaning (See also ?W)
fmean(mpg, mtcars$cyl)             # Grouped mean
fmean(mpg, mtcars[8:9])           # another grouped mean.
g <- GRP(mtcars[c(2,8:9)])
fmean(mpg, g)                      # Pre-computing groups speeds up the computation
fmean(mpg, g, mtcars$hp)          # Grouped weighted mean
fmean(mpg, g, TRA = "-")          # Demeaning by group
fmean(mpg, g, mtcars$hp, "-")     # Group-demeaning using weighted group means

## data.frame method
fmean(mtcars)
fmean(mtcars, g)
fmean(fgroup_by(mtcars, cyl, vs, am)) # Another way of doing it..
head(fmean(mtcars, g, TRA = "-"))    # etc..

## matrix method
m <- qM(mtcars)
fmean(m)
fmean(m, g)
head(fmean(m, g, TRA = "-")) # etc..

## method for grouped tibbles - for use with dplyr
library(dplyr)
mtcars %>% group_by(cyl,vs,am) %>% fmean           # Ordinary
mtcars %>% group_by(cyl,vs,am) %>% fmean(hp)      # Weighted
mtcars %>% group_by(cyl,vs,am) %>% fmean(hp, "-") # Weighted Transform
mtcars %>% group_by(cyl,vs,am) %>%
  select(mpg,hp) %>% fmean(hp, "-")             # Only mpg

mtcars %>% fgroup_by(cyl,vs,am) %>%
  fselect(mpg,hp) %>% fmean(hp, "-")           # Equivalent and faster !

```

fmedian

Fast (Grouped, Weighted) Median Value for Matrix-Like Objects

Description

fmedian is a generic function that computes the (column-wise) median value of all values in x, (optionally) grouped by g and/or weighted by w. The [TRA](#) argument can further be used to transform x using its (grouped, weighted) median value.

Usage

```
fmedian(x, ...)
```

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

```
fmedian(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
        use.g.names = TRUE, ...)
```

```
## S3 method for class 'matrix'
fmedian(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
        use.g.names = TRUE, drop = TRUE, ...)

## S3 method for class 'data.frame'
fmedian(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
        use.g.names = TRUE, drop = TRUE, ...)

## S3 method for class 'grouped_df'
fmedian(x, w = NULL, TRA = NULL, na.rm = TRUE,
        use.g.names = FALSE, keep.group_vars = TRUE, keep.w = TRUE, ...)
```

Arguments

<code>x</code>	a numeric vector, matrix, data frame or grouped tibble (<code>dplyr::grouped_df</code>).
<code>g</code>	a factor, GRP object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a GRP object) used to group <code>x</code> .
<code>w</code>	a numeric vector of (non-negative) weights, may contain missing values, but only if <code>x</code> is also missing.
<code>TRA</code>	an integer or quoted operator indicating the transformation to perform: 1 - "replace_fill" 2 - "replace" 3 - "-" 4 - "+-" 5 - "/" 6 - "%" 7 - "+" 8 - "*" 9 - "%%" 10 - "-%%" . See TRA .
<code>na.rm</code>	logical. Skip missing values in <code>x</code> . Defaults to <code>TRUE</code> and implemented at very little computational cost. If <code>na.rm = FALSE</code> a NA is returned when encountered.
<code>use.g.names</code>	logical. Make group-names and add to the result as names (default method) or row-names (matrix and data frame methods). No row-names are generated for <i>data.table</i> 's.
<code>drop</code>	<i>matrix and data.frame method</i> : Logical. <code>TRUE</code> drops dimensions and returns an atomic vector if <code>g = NULL</code> and <code>TRA = NULL</code> .
<code>keep.group_vars</code>	<i>grouped_df method</i> : Logical. <code>FALSE</code> removes grouping variables after computation.
<code>keep.w</code>	<i>grouped_df method</i> : Logical. Retain summed weighting variable after computation (if contained in <code>grouped_df</code>).
<code>...</code>	arguments to be passed to or from other methods.

Details

Median value estimation is done using `std::nth_element` in C++, which is an efficient partial sorting algorithm. A downside of this is that vectors need to be copied first and then partially sorted, thus `fmedian` currently requires additional memory equal to the size of the vector (`x` or a column of `x`).

Grouped computations are currently performed by mapping the data to a sparse-array and then partially sorting each row (group) of that array. Because of compiler optimizations this requires less memory than a full deep copy done with no groups.

The weighted median is defined as the element k from a set of sorted elements, such that the sum of weights of all elements larger and all elements smaller than k is $\leq \text{sum}(w)/2$. If the half-sum of weights ($\text{sum}(w)/2$) is reached exactly for some element k , then (summing from the lower end) both k and $k+1$ would qualify as the weighted median (and some possible additional elements with zero weights following k would also qualify). `fmedian` solves these ties by taking a simple arithmetic mean of all elements qualifying as the weighted median.

The weighted median is computed using `radixorder` to first obtain an ordering of all elements, so it is considerably more computationally expensive than the unweighted version. With groups, the entire vector is also ordered, and the weighted median is computed in a single ordered pass through the data (after group-summing the weights, skipping weights for which x is missing).

If x is a matrix or data frame, these computations are performed independently for each column. When applied to data frames with groups or `drop = FALSE`, `fmedian` preserves all column attributes (such as variable labels) but does not distinguish between classed and unclassed objects. The attributes of the data frame itself are also preserved.

Value

The (w weighted) median value of x , grouped by g , or (if `TRA` is used) x transformed by its median, grouped by g .

See Also

[fnth](#), [fmean](#), [fmode](#), [Fast Statistical Functions](#), [Collapse Overview](#)

Examples

```
## default vector method
mpg <- mtcars$mpg
fmedian(mpg) # Simple median value
fmedian(mpg, w = mtcars$hp) # Weighted median: Weighted by hp
fmedian(mpg, TRA = "-") # Simple transformation: Subtract median value
fmedian(mpg, mtcars$cyl) # Grouped median value
fmedian(mpg, mtcars[c(2,8:9)]) # More groups..
g <- GRP(mtcars, ~ cyl + vs + am) # Precomputing groups gives more speed !
fmedian(mpg, g)
fmedian(mpg, g, mtcars$hp) # Grouped weighted median
fmedian(mpg, g, TRA = "-") # Groupwise subtract median value
fmedian(mpg, g, mtcars$hp, "-") # Groupwise subtract weighted median value

## data.frame method
fmedian(mtcars)
head(fmedian(mtcars, TRA = "-"))
fmedian(mtcars, g)
fmedian(fgroup_by(mtcars, cyl, vs, am)) # Another way of doing it..
fmedian(mtcars, g, use.g.names = FALSE) # No row-names generated

## matrix method
m <- qM(mtcars)
fmedian(m)
head(fmedian(m, TRA = "-"))
fmedian(m, g) # etc..
```

```

library(dplyr)
# grouped_df method
mtcars %>% group_by(cyl,vs,am) %>% fmedian
mtcars %>% group_by(cyl,vs,am) %>% fmedian(hp)           # Weighted
mtcars %>% fgroup_by(cyl,vs,am) %>% fmedian             # Faster grouping!
mtcars %>% fgroup_by(cyl,vs,am) %>% fmedian(TRA = "-")  # De-median
mtcars %>% fgroup_by(cyl,vs,am) %>% fselect(mpg, hp) %>% # Faster selecting
  fmedian(hp, "-") # Weighted de-median mpg, using hp as weights

```

fmin, fmax

Fast (Grouped) Maxima and Minima for Matrix-Like Objects

Description

fmax and fmin are generic functions that compute the (column-wise) maximum and minimum value of all values in x, (optionally) grouped by g. The `TRA` argument can further be used to transform x using its (grouped) maximum or minimum value.

Usage

```

fmax(x, ...)
fmin(x, ...)

## Default S3 method:
fmax(x, g = NULL, TRA = NULL, na.rm = TRUE,
     use.g.names = TRUE, ...)
## Default S3 method:
fmin(x, g = NULL, TRA = NULL, na.rm = TRUE,
     use.g.names = TRUE, ...)

## S3 method for class 'matrix'
fmax(x, g = NULL, TRA = NULL, na.rm = TRUE,
     use.g.names = TRUE, drop = TRUE, ...)
## S3 method for class 'matrix'
fmin(x, g = NULL, TRA = NULL, na.rm = TRUE,
     use.g.names = TRUE, drop = TRUE, ...)

## S3 method for class 'data.frame'
fmax(x, g = NULL, TRA = NULL, na.rm = TRUE,
     use.g.names = TRUE, drop = TRUE, ...)
## S3 method for class 'data.frame'
fmin(x, g = NULL, TRA = NULL, na.rm = TRUE,
     use.g.names = TRUE, drop = TRUE, ...)

## S3 method for class 'grouped_df'
fmax(x, TRA = NULL, na.rm = TRUE,
     use.g.names = FALSE, keep.group_vars = TRUE, ...)

```



```
## S3 method for class 'grouped_df'
fmin(x, TRA = NULL, na.rm = TRUE,
     use.g.names = FALSE, keep.group_vars = TRUE, ...)
```

Arguments

<code>x</code>	a numeric vector, matrix, data frame or grouped tibble (<code>dplyr::grouped_df</code>).
<code>g</code>	a factor, GRP object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a GRP object) used to group <code>x</code> .
<code>TRA</code>	an integer or quoted operator indicating the transformation to perform: 1 - "replace_fill" 2 - "replace" 3 - "-" 4 - "-+" 5 - "/" 6 - "%" 7 - "+" 8 - "*" 9 - "%%" 10 - "-%%". See TRA .
<code>na.rm</code>	logical. Skip missing values in <code>x</code> . Defaults to <code>TRUE</code> and implemented at very little computational cost. If <code>na.rm = FALSE</code> a <code>NA</code> is returned when encountered.
<code>use.g.names</code>	logical. Make group-names and add to the result as names (default method) or row-names (matrix and data frame methods). No row-names are generated for <i>data.table</i> 's.
<code>drop</code>	<i>matrix and data.frame method:</i> Logical. <code>TRUE</code> drops dimensions and returns an atomic vector if <code>g = NULL</code> and <code>TRA = NULL</code> .
<code>keep.group_vars</code>	<i>grouped_df method:</i> Logical. <code>FALSE</code> removes grouping variables after computation.
<code>...</code>	arguments to be passed to or from other methods.

Details

Missing-value removal as controlled by the `na.rm` argument is done at no extra cost since in C++ any logical comparison involving `NA` or `NaN` evaluates to `FALSE`. Large performance gains can nevertheless be achieved in the presence of missing values if `na.rm = FALSE`, since then the corresponding computation is terminated once a `NA` is encountered and `NA` is returned (unlike `base::max` and `base::min` which just run through without any checks).

This all seamlessly generalizes to grouped computations, which are performed in a single pass (without splitting the data) and therefore extremely fast.

When applied to data frames with groups or `drop = FALSE`, `fmax` and `fmin` preserve all column attributes (such as variable labels) but do not distinguish between classed and unclassed objects. The attributes of the data frame itself are also preserved.

Value

`fmax` returns the maximum value of `x`, grouped by `g`, or (if [TRA](#) is used) `x` transformed by its maximum value, grouped by `g`. Analogous, `fmin` returns the minimum value ...

See Also

[Fast Statistical Functions](#), [Collapse Overview](#)

Examples

```
## default vector method
mpg <- mtcars$mpg
fmax(mpg) # Maximum value
fmin(mpg) # Minimum value (all examples below use fmax but apply to fmin)
fmax(mpg, TRA = "%") # Simple transformation: Take percentage of maximum value
fmax(mpg, mtcars$cyl) # Grouped maximum value
fmax(mpg, mtcars[c(2,8:9)]) # More groups..
g <- GRP(mtcars, ~ cyl + vs + am) # Precomputing groups gives more speed !
fmax(mpg, g)
fmax(mpg, g, TRA = "%") # Groupwise percentage of maximum value
fmax(mpg, g, TRA = "replace") # Groupwise replace by maximum value

## data.frame method
fmax(mtcars)
head(fmax(mtcars, TRA = "%"))
fmax(mtcars, g)
fmax(mtcars, g, use.g.names = FALSE) # No row-names generated

## matrix method
m <- qM(mtcars)
fmax(m)
head(fmax(m, TRA = "%"))
fmax(m, g) # etc..

## method for grouped tibbles - for use with dplyr
library(dplyr)
mtcars %>% group_by(cyl,vs,am) %>% fmax
mtcars %>% group_by(cyl,vs,am) %>% fmax("%")
mtcars %>% group_by(cyl,vs,am) %>% select(mpg) %>% fmax
```

fmode

Fast (Grouped, Weighted) Statistical Mode for Matrix-Like Objects

Description

fmode is a generic function and returns the (column-wise) statistical mode i.e. the most frequent value of x, (optionally) grouped by g and/or weighted by w. The *TRA* argument can further be used to transform x using its (grouped, weighted) mode. Ties between multiple possible modes can be resolved by taking the minimum, maximum or (default) first occurring mode.

Usage

```
fmode(x, ...)
```

Default S3 method:

```
fmode(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = TRUE, ties = "first", ...)
```

```
## S3 method for class 'matrix'
fmode(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = TRUE, drop = TRUE, ties = "first", ...)

## S3 method for class 'data.frame'
fmode(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = TRUE, drop = TRUE, ties = "first", ...)

## S3 method for class 'grouped_df'
fmode(x, w = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = FALSE, keep.group_vars = TRUE, keep.w = TRUE,
      ties = "first", ...)
```

Arguments

x a vector, matrix, data frame or grouped tibble (`dplyr::grouped_df`).

g a factor, [GRP](#) object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a [GRP](#) object) used to group `x`.

w a numeric vector of (non-negative) weights, may contain missing values.

TRA an integer or quoted operator indicating the transformation to perform: 1 - "replace_fill" | 2 - "replace" | 3 - "-" | 4 - "--" | 5 - "/" | 6 - "%" | 7 - "+" | 8 - "*" | 9 - "%%" | 10 - "-%". See [TRA](#).

na.rm logical. Skip missing values in `x`. Defaults to `TRUE` and implemented at very little computational cost. If `na.rm = FALSE`, `NA` is treated as any other value.

use.g.names logical. Make group-names and add to the result as names (default method) or row-names (matrix and data frame methods). No row-names are generated for *data.table*'s.

ties an integer or character string specifying the method to resolve ties between multiple possible modes i.e. multiple values with the maximum frequency or sum of weights:

<i>Int.</i>	<i>String</i>	<i>Description</i>
1	"first"	take the first occurring mode.
2	"min"	take the smallest of the possible modes.
3	"max"	take the largest of the possible modes.

drop *matrix and data.frame method:* Logical. `TRUE` drops dimensions and returns an atomic vector if `g = NULL` and `TRA = NULL`.

keep.group_vars *grouped_df method:* Logical. `FALSE` removes grouping variables after computation.

keep.w *grouped_df method:* Logical. Retain sum of weighting variable after computation (if contained in `grouped_df`).

... arguments to be passed to or from other methods.

Details

fmode implements a pretty fast algorithm to find the statistical mode utilizing index- hashing implemented in the `Rcpp::sugar::IndexHash` class.

If `na.rm = FALSE`, NA is not removed but treated as any other value (i.e. it's frequency is counted). If all values are NA, NA is always returned.

The weighted mode is computed by summing up the weights for all distinct values and choosing the value with the largest sum. If `na.rm = TRUE`, missing values will be removed from both `x` and `w` i.e. utilizing only `x[complete.cases(x,w)]` and `w[complete.cases(x,w)]`.

It is possible that multiple values have the same mode that is the maximum frequency or sum of weights. Typical cases are simply when all values are either all the same or all distinct. In such cases, the default option `ties = "first"` returns the first occurring value in the data reaching the maximum frequency count or sum of weights. For example in a sample `x = c(1, 3, 2, 2, 4, 4, 1, 7)`, the first mode is 2 as fmode goes through the data from left to right. It is also possible to take the minimum or maximum mode, i.e. `fmode(x, ties = "min")` returns 1, and `fmode(x, ties = "max")` returns 4. It should be noted that options `ties = "min"` and `ties = "max"` work well for numeric/integer/factor data as well as date/time variables, but give unintuitive results for character data (no strict alphabetic sorting, similar to using `<` and `>` to compare character values in R). These options are also best avoided if missing values are counted (`na.rm = FALSE`) since no proper logical comparison with missing values is possible: With numeric data it depends, since in C++ any comparison with `NA_real_` evaluates to `FALSE`, `NA_real_` is chosen as the min or max mode only if it is also the first mode, and never otherwise. For integer data, `NA_integer_` is stored as the smallest integer in C++, so it will always be chosen as the min mode and never as the max mode. For character data, `NA_character_` is stored as the string "NA" in C++ and thus the behavior depends on the other character content.

This all seamlessly generalizes to grouped computations, which are performed by mapping the data to a sparse-array and then going group-by group.

fmode preserves all the attributes of the objects it is applied to (apart from names or row-names which are adjusted as necessary in grouped operations). If a data frame is passed to fmode and `drop = TRUE` (the default), `base::unlist` will be called on the result, which might not be sensible depending on the data at hand.

Value

The (`w` weighted) statistical mode of `x`, grouped by `g`, or (if [TRA](#) is used) `x` transformed by its mode, grouped by `g`. See also [Details](#).

See Also

[fmean](#), [fmedian](#), [Fast Statistical Functions](#), [Collapse Overview](#)

Examples

```
x <- c(1, 3, 2, 2, 4, 4, 1, 7, NA, NA, NA)
fmode(x) # Default is ties = "first"
fmode(x, ties = "min")
fmode(x, ties = "max")
fmode(x, na.rm = FALSE) # Here NA is the mode, regardless of ties option
```

```

fmode(x[-length(x)], na.rm = FALSE) # Not anymore..

## World Development Data
attach(wlddev)
## default vector method
fmode(PCGDP) # Numeric mode
head(fmode(PCGDP, iso3c)) # Grouped numeric mode
head(fmode(PCGDP, iso3c, LIFEEX)) # Grouped and weighted numeric mode
fmode(region) # Factor mode
fmode(date) # Date mode (defaults to first value since panel is balanced)
fmode(country) # Character mode (also defaults to first value)
fmode(OECD) # Logical mode
# ..all the above can also be performed grouped and weighted

## matrix method
m <- qM(airquality)
fmode(m)
fmode(m, na.rm = FALSE) # NA frequency is also counted
fmode(m, airquality$Month) # Groupwise
fmode(m, w = airquality$Day) # Weighted: Later days in the month are given more weight
fmode(m>50, airquality$Month) # Groupwise logical mode
# etc..

## data.frame method
fmode(wlddev) # Calling unlist -> coerce to character vector
fmode(wlddev, drop = FALSE) # Gives one row
head(fmode(wlddev, iso3c)) # Grouped mode
head(fmode(wlddev, iso3c, LIFEEX)) # Grouped and weighted mode

detach(wlddev)

```

fNdistinct

Fast (Grouped) Distinct Value Count for Matrix-Like Objects

Description

fNdistinct is a generic function that (column-wise) computes the number of distinct values in x, (optionally) grouped by g. It is significantly faster than length(unique(x)). The [TRA](#) argument can further be used to transform x using its (grouped) distinct value count.

Usage

```

fNdistinct(x, ...)

## Default S3 method:
fNdistinct(x, g = NULL, TRA = NULL, na.rm = TRUE,
           use.g.names = TRUE, ...)

## S3 method for class 'matrix'
fNdistinct(x, g = NULL, TRA = NULL, na.rm = TRUE,
           use.g.names = TRUE, drop = TRUE, ...)

```

```
## S3 method for class 'data.frame'
fNdistinct(x, g = NULL, TRA = NULL, na.rm = TRUE,
           use.g.names = TRUE, drop = TRUE, ...)

## S3 method for class 'grouped_df'
fNdistinct(x, TRA = NULL, na.rm = TRUE,
           use.g.names = FALSE, keep.group_vars = TRUE, ...)
```

Arguments

<code>x</code>	a vector, matrix, data frame or grouped tibble (<code>dplyr::grouped_df</code>).
<code>g</code>	a factor, GRP object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a GRP object) used to group <code>x</code> .
<code>TRA</code>	an integer or quoted operator indicating the transformation to perform: 1 - "replace_fill" 2 - "replace" 3 - "-" 4 - "-+" 5 - "/" 6 - "%" 7 - "+" 8 - "*" 9 - "%%" 10 - "-%%" . See TRA .
<code>na.rm</code>	logical. TRUE: Skip missing values in <code>x</code> (faster computation). FALSE: Also consider 'NA' as one distinct value.
<code>use.g.names</code>	logical. Make group-names and add to the result as names (default method) or row-names (matrix and data frame methods). No row-names are generated for <i>data.table</i> 's.
<code>drop</code>	<i>matrix and data.frame method</i> : Logical. TRUE drops dimensions and returns an atomic vector if <code>g = NULL</code> and <code>TRA = NULL</code> .
<code>keep.group_vars</code>	<i>grouped_df method</i> : Logical. FALSE removes grouping variables after computation.
<code>...</code>	arguments to be passed to or from other methods.

Details

`fNdistinct` implements a fast algorithm to find the number of distinct values utilizing index- hashing implemented in the `Rcpp::sugar::IndexHash` class.

If `na.rm = TRUE` (the default), missing values will be skipped yielding substantial performance gains in data with many missing values. If `na.rm = FALSE`, missing values will simply be treated as any other value and read into the hash-map. Thus with the former, a numeric vector `c(1.25, NaN, 3.56, NA)` will have a distinct value count of 2, whereas the latter will return a distinct value count of 4.

Grouped computations are performed by mapping the data to a sparse-array and then hash-mapping each group. This is often not much slower than using a larger hash-map for the entire data when `g = NULL`.

`fNdistinct` preserves all attributes of non-classed vectors / columns, and only the 'label' attribute (if available) of classed vectors / columns (i.e. dates or factors). When applied to data frames and matrices, the row-names are adjusted as necessary.

Value

Integer. The number of distinct values in *x*, grouped by *g*, or (if [TRA](#) is used) *x* transformed by its distinct value count, grouped by *g*.

See Also

[fNobs](#), [Fast Statistical Functions](#), [Collapse Overview](#)

Examples

```
## default vector method
fNdistinct(airquality$Solar.R)           # Simple distinct value count
fNdistinct(airquality$Solar.R, airquality$Month) # Grouped distinct value count

## data.frame method
fNdistinct(airquality)
fNdistinct(airquality, airquality$Month)
fNdistinct(wlddev)                       # Works with data of all types!
head(fNdistinct(wlddev, wlddev$iso3c))

## matrix method
aqm <- qM(airquality)
fNdistinct(aqm)                          # Also works for character or logical matrices
fNdistinct(aqm, airquality$Month)

## method for grouped tibbles - for use with dplyr:
library(dplyr)
airquality %>% group_by(Month) %>% fNdistinct
wlddev %>% group_by(country) %>%
  select(PCGDP,LIFEEX,GINI,ODA) %>% fNdistinct
```

fNobs

Fast (Grouped) Observation Count for Matrix-Like Objects

Description

`fNobs` is a generic function that (column-wise) computes the number of non-missing values in *x*, (optionally) grouped by *g*. It is much faster than `sum(!is.na(x))`. The [TRA](#) argument can further be used to transform *x* using its (grouped) observation count.

Usage

```
fNobs(x, ...)
```

Default S3 method:

```
fNobs(x, g = NULL, TRA = NULL, use.g.names = TRUE, ...)
```

```
## S3 method for class 'matrix'
fNobs(x, g = NULL, TRA = NULL, use.g.names = TRUE, drop = TRUE, ...)

## S3 method for class 'data.frame'
fNobs(x, g = NULL, TRA = NULL, use.g.names = TRUE, drop = TRUE, ...)

## S3 method for class 'grouped_df'
fNobs(x, TRA = NULL, use.g.names = FALSE, keep.group_vars = TRUE, ...)
```

Arguments

x	a vector, matrix, data frame or grouped tibble (<code>dplyr::grouped_df</code>).
g	a factor, GRP object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a GRP object) used to group x.
TRA	an integer or quoted operator indicating the transformation to perform: 1 - "replace_fill" 2 - "replace" 3 - "-" 4 - "-+" 5 - "/" 6 - "%" 7 - "+" 8 - "*" 9 - "%%" 10 - "-%%" . See TRA .
use.g.names	logical. Make group-names and add to the result as names (default method) or row-names (matrix and data frame methods). No row-names are generated for <i>data.table</i> 's.
drop	<i>matrix and data.frame method</i> : Logical. TRUE drops dimensions and returns an atomic vector if g = NULL and TRA = NULL.
keep.group_vars	<i>grouped_df method</i> : Logical. FALSE removes grouping variables after computation.
...	arguments to be passed to or from other methods.

Details

fNobs preserves all attributes of non-classed vectors / columns, and only the 'label' attribute (if available) of classed vectors / columns (i.e. dates or factors). When applied to data frames and matrices, the row-names are adjusted as necessary.

Value

Integer. The number of non-missing observations in x, grouped by g, or (if [TRA](#) is used) x transformed by its number of non-missing observations, grouped by g.

See Also

[fNdistinct](#), [Fast Statistical Functions](#), [Collapse Overview](#)

Examples

```
## default vector method
fNobs(airquality$Solar.R) # Simple Nobs
fNobs(airquality$Solar.R, airquality$Month) # Grouped Nobs
```



```

## data.frame method
fNobs(airquality)
fNobs(airquality, airquality$Month)
fNobs(wlddev) # Works with data of all types!
head(fNobs(wlddev, wlddev$iso3c))

## matrix method
aqm <- qM(airquality)
fNobs(aqm) # Also works for character or logical matrices
fNobs(aqm, airquality$Month)

## method for grouped tibbles - for use with dplyr
library(dplyr)
airquality %>% group_by(Month) %>% fNobs
wlddev %>% group_by(country) %>%
  select(PCGDP, LIFEEX, GINI, ODA) %>% fNobs

```

fnth	<i>Fast (Grouped, Weighted) N'th Element/Quantile for Matrix-Like Objects</i>
------	---

Description

fnth (column-wise) returns the n'th smallest element from a set of unsorted elements x corresponding to an integer index (n), or to a probability between 0 and 1. If n is passed as a probability, ties can be resolved using the lower, upper, or (default) average of the possible elements. These are discontinuous and fast methods to estimate a sample quantile.

Usage

```

fnth(x, n = 0.5, ...)

## Default S3 method:
fnth(x, n = 0.5, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
     use.g.names = TRUE, ties = "mean", ...)

## S3 method for class 'matrix'
fnth(x, n = 0.5, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
     use.g.names = TRUE, drop = TRUE, ties = "mean", ...)

## S3 method for class 'data.frame'
fnth(x, n = 0.5, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
     use.g.names = TRUE, drop = TRUE, ties = "mean", ...)

## S3 method for class 'grouped_df'
fnth(x, n = 0.5, w = NULL, TRA = NULL, na.rm = TRUE,
     use.g.names = FALSE, keep.group_vars = TRUE, keep.w = TRUE,
     ties = "mean", ...)

```

Arguments

<code>x</code>	a numeric vector, matrix, data frame or grouped tibble (<code>dplyr::grouped_df</code>).												
<code>n</code>	the element to return using a single integer index such that $1 < n < \text{NROW}(x)$, or a probability $0 < n < 1$. See Details.												
<code>g</code>	a factor, GRP object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a GRP object) used to group <code>x</code> .												
<code>w</code>	a numeric vector of (non-negative) weights, may contain missing values.												
<code>TRA</code>	an integer or quoted operator indicating the transformation to perform: 1 - "replace_fill" 2 - "replace" 3 - "-" 4 - "-+" 5 - "/" 6 - "%" 7 - "+" 8 - "*" 9 - "%%" 10 - "-%". See TRA .												
<code>na.rm</code>	logical. Skip missing values in <code>x</code> . Defaults to TRUE and implemented at very little computational cost. If <code>na.rm = FALSE</code> a NA is returned when encountered.												
<code>use.g.names</code>	logical. Make group-names and add to the result as names (default method) or row-names (matrix and data frame methods). No row-names are generated for <i>data.table</i> 's.												
<code>ties</code>	an integer or character string specifying the method to resolve ties between adjacent qualifying elements: <table> <thead> <tr> <th><i>Int.</i></th> <th><i>String</i></th> <th><i>Description</i></th> </tr> </thead> <tbody> <tr> <td>1</td> <td>"mean"</td> <td>take the arithmetic mean of all qualifying elements.</td> </tr> <tr> <td>2</td> <td>"min"</td> <td>take the smallest of the elements.</td> </tr> <tr> <td>3</td> <td>"max"</td> <td>take the largest of the elements.</td> </tr> </tbody> </table>	<i>Int.</i>	<i>String</i>	<i>Description</i>	1	"mean"	take the arithmetic mean of all qualifying elements.	2	"min"	take the smallest of the elements.	3	"max"	take the largest of the elements.
<i>Int.</i>	<i>String</i>	<i>Description</i>											
1	"mean"	take the arithmetic mean of all qualifying elements.											
2	"min"	take the smallest of the elements.											
3	"max"	take the largest of the elements.											
<code>drop</code>	<i>matrix and data.frame method:</i> Logical. TRUE drops dimensions and returns an atomic vector if <code>g = NULL</code> and <code>TRA = NULL</code> .												
<code>keep.group_vars</code>	<i>grouped_df method:</i> Logical. FALSE removes grouping variables after computation.												
<code>keep.w</code>	<i>grouped_df method:</i> Logical. Retain sum of weighting variable after computation (if contained in <code>grouped_df</code>).												
<code>...</code>	arguments to be passed to or from other methods.												

Details

This is an R port to `std::nth_element`, an efficient partial sorting algorithm in C++. It is also used to calculate the median (in fact the default `fnth(x, n = 0.5)` is identical to `fmedian(x)`, so see also the details for [fmedian](#)).

`fnth` generalizes the principles of median value calculation to find arbitrary elements. It offers considerable flexibility by providing both simple order statistics and simple discontinuous quantile estimation. Regarding the former, setting `n` to an index between 1 and `NROW(x)` will return the `n`'th smallest element of `x`, about $2x$ faster than `sort(x, partial = n)[n]`. As to the latter, setting `n` to a probability between 0 and 1 will return the corresponding element of `x`, and resolve ties between multiple qualifying elements (such as when `n = 0.5` and `x` is even) using the arithmetic average `ties = "mean"`, or the smallest ties = `"min"` or largest ties = `"max"` of those elements.

If $n > 1$ is used and x contains missing values (and `na.rm = TRUE`, otherwise NA is returned), n is internally converted to a probability using $p = (n-1)/(NROW(x)-1)$, and that probability is applied to the set of complete elements (of each column if x is a matrix or data frame) to find the `as.integer(p*(fNobs(x)-1))+1`'th element (which corresponds to option `ties = "min"`). Note that it is necessary to subtract and add 1 so that $n = 1$ corresponds to $p = 0$ and $n = NROW(x)$ to $p = 1$.

When using grouped computations (supplying a vector or list to `g` subdividing x) and $n > 1$ is used, it is transformed to a probability $p = (n-1)/(NROW(x)/ng-1)$ (where `ng` contains the number of unique groups in `g`) and `ties = "lower"` is used to sort out clashes. This could be useful for example to return the n 'th smallest element of each group in a balanced panel, but with unequal group sizes it more intuitive to pass a probability to `n`.

If weights are used, the same principles apply as for weighted median calculation: A target partial sum of weights $p*\text{sum}(w)$ is calculated, and the weighted n 'th element is the element k such that all elements smaller than k have a sum of weights $\leq p*\text{sum}(w)$, and all elements larger than k have a sum of weights $\leq (1-p)*\text{sum}(w)$. If the partial-sum of weights ($p*\text{sum}(w)$) is reached exactly for some element k , then (summing from the lower end) both k and $k+1$ would qualify as the weighted n 'th element (and some possible additional elements with zero weights following k would also qualify). If $n > 1$, the lowest of those elements is chosen (congruent with the unweighted behavior), but if $0 < n < 1$, the `ties` option regulates how to resolve such conflicts, yielding lower-weighted, upper-weighted or (default) average weighted n 'th elements.

The weighted n 'th element is computed using `radixorder` to first obtain an ordering of all elements, so it is considerably more computationally expensive than the unweighted version. With groups, the entire vector is also ordered, and the weighted n 'th element is computed in a single ordered pass through the data (after calculating partial-group sums of the weights, skipping weights for which x is missing).

If x is a matrix or data frame, these computations are performed independently for each column. Column-attributes and overall attributes of a data frame are preserved (if `g` is used or `drop = FALSE`).

Value

The (w weighted) n 'th element of x , grouped by `g`, or (if `TRA` is used) x transformed by its n 'th element, grouped by `g`.

See Also

[fmean](#), [fmedian](#), [fmode](#), [Fast Statistical Functions](#), [Collapse Overview](#)

Examples

```
## default vector method
mpg <- mtcars$mpg
fnth(mpg)                # Simple nth element: Median (same as fmedian(mpg))
fnth(mpg, 5)            # 5th smallest element
sort(mpg, partial = 5)[5] # Same using base R, fnth is 2x faster.
fnth(mpg, 0.75)         # Third quartile
fnth(mpg, 0.75, w = mtcars$hp) # Weighted third quartile: Weighted by hp
fnth(mpg, 0.75, TRA = "-") # Simple transformation: Subtract third quartile
fnth(mpg, 0.75, mtcars$cyl) # Grouped third quartile
fnth(mpg, 0.75, mtcars[c(2,8:9)]) # More groups..
```

```

g <- GRP(mtcars, ~ cyl + vs + am) # Precomputing groups gives more speed !
fnth(mpg, 0.75, g)
fnth(mpg, 0.75, g, mtcars$hp) # Grouped weighted third quartile
fnth(mpg, 0.75, g, TRA = "-") # Groupwise subtract third quartile
fnth(mpg, 0.75, g, mtcars$hp, "-") # Groupwise subtract weighted third quartile

## data.frame method
fnth(mtcars, 0.75)
head(fnth(mtcars, 0.75, TRA = "-"))
fnth(mtcars, 0.75, g)
fnth(fgroup_by(mtcars, cyl, vs, am), 0.75) # Another way of doing it..
fnth(mtcars, 0.75, g, use.g.names = FALSE) # No row-names generated

## matrix method
m <- qM(mtcars)
fnth(m, 0.75)
head(fnth(m, 0.75, TRA = "-"))
fnth(m, 0.75, g) # etc..

library(dplyr)
## grouped_df method
mtcars %>% group_by(cyl,vs,am) %>% fnth(0.75)
mtcars %>% group_by(cyl,vs,am) %>% fnth(0.75, hp) # Weighted
mtcars %>% fgroup_by(cyl,vs,am) %>% fnth(0.75) # Faster grouping!
mtcars %>% fgroup_by(cyl,vs,am) %>% fnth(0.75, TRA = "/") # Divide by third quartile
mtcars %>% fgroup_by(cyl,vs,am) %>% fselect(mpg, hp) %>% # Faster selecting
  fnth(0.75, hp, "/") # Divide mpg by its third weighted group-quartile, using hp as weights

```

fprod

Fast (Grouped, Weighted) Product for Matrix-Like Objects

Description

fprod is a generic function that computes the (column-wise) product of all values in x, (optionally) grouped by g and/or weighted by w. The TRA argument can further be used to transform x using its (grouped, weighted) product.

Usage

```

fprod(x, ...)

## Default S3 method:
fprod(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = TRUE, ...)

## S3 method for class 'matrix'
fprod(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = TRUE, drop = TRUE, ...)

```

```
## S3 method for class 'data.frame'
fprod(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = TRUE, drop = TRUE, ...)

## S3 method for class 'grouped_df'
fprod(x, w = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = FALSE, keep.group_vars = TRUE, keep.w = TRUE, ...)
```

Arguments

<code>x</code>	a numeric vector, matrix, data frame or grouped tibble (<code>dplyr::grouped_df</code>).
<code>g</code>	a factor, GRP object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a GRP object) used to group <code>x</code> .
<code>w</code>	a numeric vector of (non-negative) weights, may contain missing values.
<code>TRA</code>	an integer or quoted operator indicating the transformation to perform: 1 - "replace_fill" 2 - "replace" 3 - "-" 4 - "--" 5 - "/" 6 - "%" 7 - "+" 8 - "*" 9 - "%%" 10 - "-%%" . See TRA .
<code>na.rm</code>	logical. Skip missing values in <code>x</code> . Defaults to <code>TRUE</code> and implemented at very little computational cost. If <code>na.rm = FALSE</code> a NA is returned when encountered.
<code>use.g.names</code>	logical. Make group-names and add to the result as names (default method) or row-names (matrix and data frame methods). No row-names are generated for <i>data.table</i> 's.
<code>drop</code>	<i>matrix and data.frame method</i> : Logical. <code>TRUE</code> drops dimensions and returns an atomic vector if <code>g = NULL</code> and <code>TRA = NULL</code> .
<code>keep.group_vars</code>	<i>grouped_df method</i> : Logical. <code>FALSE</code> removes grouping variables after computation.
<code>keep.w</code>	<i>grouped_df method</i> : Logical. Retain product of weighting variable after computation (if contained in <code>grouped_df</code>).
<code>...</code>	arguments to be passed to or from other methods.

Details

Non-grouped product computations internally utilize long-doubles in C++, for additional numeric precision.

Missing-value removal as controlled by the `na.rm` argument is done very efficiently by simply skipping them in the computation (thus setting `na.rm = FALSE` on data with no missing values doesn't give extra speed). Large performance gains can nevertheless be achieved in the presence of missing values if `na.rm = FALSE`, since then the corresponding computation is terminated once a NA is encountered and NA is returned (unlike `base::prod` which just runs through without any checks).

This all seamlessly generalizes to grouped computations, which are performed in a single pass (without splitting the data) and therefore extremely fast.

The weighted product is computed as `prod(x * w)`. If `na.rm = TRUE`, missing values will be removed from both `x` and `w` i.e. utilizing only `x[complete.cases(x, w)]` and `w[complete.cases(x, w)]`.

When applied to data frames with groups or `drop = FALSE`, `fprod` preserves all column attributes (such as variable labels) but does not distinguish between classed and unclassed objects. The attributes of the data frame itself are also preserved.

Value

The (w weighted) product of x, grouped by g, or (if `TRA` is used) x transformed by its product, grouped by g.

See Also

[fsum](#), [Fast Statistical Functions](#), [Collapse Overview](#)

Examples

```
## default vector method
mpg <- mtcars$mpg
fprod(mpg) # Simple product
fprod(mpg, w = mtcars$hp) # Weighted product
fprod(mpg, TRA = "/") # Simple transformation: Divide by product
fprod(mpg, mtcars$cyl) # Grouped product
fprod(mpg, mtcars$cyl, mtcars$hp) # Weighted grouped product
fprod(mpg, mtcars[c(2,8:9)]) # More groups..
g <- GRP(mtcars, ~ cyl + vs + am) # Precomputing groups gives more speed !
fprod(mpg, g)
fprod(mpg, g, TRA = "/") # Groupwise divide by product

## data.frame method
fprod(mtcars)
head(fprod(mtcars, TRA = "/"))
fprod(mtcars, g)
fprod(mtcars, g, use.g.names = FALSE) # No row-names generated

## matrix method
m <- qM(mtcars)
fprod(m)
head(fprod(m, TRA = "/"))
fprod(m, g) # etc..

## method for grouped tibbles - for use with dplyr
library(dplyr)
mtcars %>% group_by(cyl,vs,am) %>% fprod(hp) # Weighted grouped product
mtcars %>% fgroup_by(cyl,vs,am) %>% fprod(hp) # Equivalent and faster
mtcars %>% fgroup_by(cyl,vs,am) %>% fprod(TRA = "/")
mtcars %>% fgroup_by(cyl,vs,am) %>% fselect(mpg) %>% fprod
```

Description

A fast substitute for `dplyr::rename`. `setrename` renames objects by reference. These functions also work with objects other than data frames that have a 'names' attribute.

Usage

```
frename(x, ..., cols = NULL)
setrename(x, ..., cols = NULL)
```

Arguments

x	an R object with a 'names' attribute.
...	either tagged vector expressions of the form name = newname, or a single function (+ optional arguments to the function) applied to all names (of columns/elements selected in cols).
cols	If ... is a function, select a subset of columns/elements to rename using names, indices, a logical vector or a function applied to the columns if x is a data frame (i.e. is.numeric).

Value

x renamed.

See Also

[Data Frame Manipulation, Collapse Overview](#)

Examples

```
## Using tagged expressions
head(frename(iris, Sepal.Length = SL, Sepal.Width = SW,
             Petal.Length = PL, Petal.Width = PW))
head(frename(iris, Sepal.Length = "S L", Sepal.Width = "S W",
             Petal.Length = "P L", Petal.Width = "P W"))

## Using a function
head(frename(iris, tolower))
head(frename(iris, tolower, cols = 1:2))
head(frename(iris, tolower, cols = is.numeric))
head(frename(iris, paste, "new", sep = "_", cols = 1:2))

## Renaming by reference
setrename(iris, tolower)
head(iris)
rm(iris)
```

fscale	<i>Fast (Grouped, Weighted) Scaling and Centering of Matrix-like Objects</i>
--------	--

Description

fscale is a generic function to efficiently standardize (scale and center) data. STD is a wrapper around fscale representing the 'standardization operator', with more options than fscale when applied to matrices and data frames. Standardization can be simple or groupwise, ordinary or weighted. Arbitrary target means and standard deviations can be set, with special options for grouped scaling and centering. It is also possible to scale data without centering i.e. perform mean-preserving scaling.

Note: For centering without scaling see [fwithin/W](#). For simple not mean-preserving scaling use [fsd\(..., TRA = "/"\)](#). To sweep pre-computed means and scale-factors out of data see [TRA](#).

Usage

```
fscale(x, ...)
  STD(x, ...)

## Default S3 method:
fscale(x, g = NULL, w = NULL, na.rm = TRUE, mean = 0, sd = 1, ...)
## Default S3 method:
STD(x, g = NULL, w = NULL, na.rm = TRUE, mean = 0, sd = 1, ...)

## S3 method for class 'matrix'
fscale(x, g = NULL, w = NULL, na.rm = TRUE, mean = 0, sd = 1, ...)
## S3 method for class 'matrix'
STD(x, g = NULL, w = NULL, na.rm = TRUE, mean = 0, sd = 1,
    stub = "STD.", ...)

## S3 method for class 'data.frame'
fscale(x, g = NULL, w = NULL, na.rm = TRUE, mean = 0, sd = 1, ...)
## S3 method for class 'data.frame'
STD(x, by = NULL, w = NULL, cols = is.numeric, na.rm = TRUE,
    mean = 0, sd = 1, stub = "STD.", keep.by = TRUE, keep.w = TRUE, ...)

# Methods for compatibility with plm:

## S3 method for class 'pseries'
fscale(x, effect = 1L, w = NULL, na.rm = TRUE, mean = 0, sd = 1, ...)
## S3 method for class 'pseries'
STD(x, effect = 1L, w = NULL, na.rm = TRUE, mean = 0, sd = 1, ...)

## S3 method for class 'pdata.frame'
fscale(x, effect = 1L, w = NULL, na.rm = TRUE, mean = 0, sd = 1, ...)
```



```
## S3 method for class 'pdata.frame'
STD(x, effect = 1L, w = NULL, cols = is.numeric, na.rm = TRUE,
     mean = 0, sd = 1, stub = "STD.", keep.ids = TRUE, keep.w = TRUE, ...)

# Methods for compatibility with dplyr:

## S3 method for class 'grouped_df'
fscale(x, w = NULL, na.rm = TRUE, mean = 0, sd = 1,
       keep.group_vars = TRUE, keep.w = TRUE, ...)
## S3 method for class 'grouped_df'
STD(x, w = NULL, na.rm = TRUE, mean = 0, sd = 1,
     stub = "STD.", keep.group_vars = TRUE, keep.w = TRUE, ...)
```

Arguments

x	a numeric vector, matrix, data frame, panel series (<code>plm::pseries</code>), panel data frame (<code>plm::pdata.frame</code>) or grouped tibble (<code>dplyr::grouped_df</code>).
g	a factor, GRP object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a GRP object) used to group x.
by	<i>STD data.frame method</i> : Same as g, but also allows one- or two-sided formulas i.e. <code>~ group1</code> or <code>var1 + var2 ~ group1 + group2</code> . See Examples.
cols	<i>data.frame method</i> : Select columns to scale using a function, column names, indices or a logical vector. Default: All numeric variables. <i>Note</i> : <code>cols</code> is ignored if a two-sided formula is passed to <code>by</code> .
w	a numeric vector of (non-negative) weights. <i>STD data frame and pdata.frame methods</i> also allow a one-sided formula i.e. <code>~ weightcol</code> . The <i>grouped_df (dplyr)</i> method supports lazy-evaluation. See Examples.
na.rm	logical. Skip missing values in x or w when computing means and sd's.
effect	<i>plm methods</i> : Select which panel identifier should be used as group-id. <code>1L</code> takes the first variable in the <code>plm::index</code> , <code>2L</code> the second etc.. Index variables can also be called by name using a character string. More than one variable can be supplied.
stub	a prefix or stub to rename all transformed columns. <code>FALSE</code> will not rename columns.
mean	the mean to center on (default is 0). If <code>mean = FALSE</code> , no centering will be performed. In that case the scaling is mean-preserving. A numeric value different from 0 (i.e. <code>mean = 5</code>) will be added to the data after subtracting out the mean(s), such that the data will have a mean of 5. A special option when performing grouped scaling and centering is <code>mean = "overall.mean"</code> . In that case the overall mean of the data will be added after subtracting out group means.
sd	the standard deviation to scale the data to (default is 1). A numeric value different from 0 (i.e. <code>sd = 3</code>) will scale the data to have a standard deviation of 3. A special option when performing grouped scaling is <code>sd = "within.sd"</code> . In that case the within standard deviation (= the standard deviation of the group-centered series) will be calculated and applied to each group. The results is that the variance of the data within each group is harmonized without forcing a certain variance (such as 1).

keep.by, keep.ids, keep.group_vars
data.frame, pdata.frame and grouped_df methods: Logical. Retain grouping / panel-identifier columns in the output. For `STD.data.frame` this only works if grouping variables were passed in a formula.

keep.w
data.frame, pdata.frame and grouped_df methods: Logical. Retain column containing the weights in the output. Only works if `w` is passed as formula / lazy-expression.

... arguments to be passed to or from other methods.

Details

If `g = NULL`, `fscale` by default (column-wise) subtracts the mean or weighted mean (if `w` is supplied) from all data points in `x`, and then divides this difference by the standard deviation or frequency-weighted standard deviation (if `w` is supplied). The result is that all columns in `x` will have mean 0 and standard deviation 1. Alternatively, data can be scaled to have a mean of `mean` and a standard deviation of `sd`. If `mean = FALSE` the data is only scaled (not centered) such that the mean of the data is preserved.

Means and standard deviations are computed using Welford's numerically stable online algorithm.

With groups supplied to `g`, this standardizing becomes groupwise, so that in each group (in each column) the data points will have mean `mean` and standard deviation `sd`. Naturally if `mean = FALSE` then each group is just scaled and the mean is preserved. For centering without scaling see `fwithin`.

If `na.rm = FALSE` and a NA or NaN is encountered, the mean and sd for that group will be NA, and all data points belonging to that group will also be NA in the output.

If `na.rm = TRUE`, means and sd's are computed (column-wise) on the available data points, and also the weight vector can have missing values. In that case, the weighted mean and sd are computed on (column-wise) `complete.cases(x, w)`, and `x` is scaled using these statistics. *Note* that `fscale` will not insert a missing value in `x` if the weight for that value is missing, rather, that value will be scaled using a weighted mean and standard-deviated computed without itself! (The intention here is that a few (randomly) missing weights shouldn't break the computation when `na.rm = TRUE`, but it is not meant for weight vectors with many missing values. If you don't like this behavior, you should prepare your data using `x[is.na(w),] <- NA`, or impute your weight vector for non-missing `x`).

Special options for grouped scaling are `mean = "overall.mean"` and `sd = "within.sd"`. The former group-centers vectors on the overall mean of the data (see `fwithin` for more details) and the latter scales the data in each group to have the within-group standard deviation (= the standard deviation of the group-centered data). Thus scaling a grouped vector with options `mean = "overall.mean"` and `sd = "within.sd"` amounts to removing all differences in the mean and standard deviations between these groups. In weighted computations, `mean = "overall.mean"` will subtract weighted group-means from the data and add the overall weighted mean of the data, whereas `sd = "within.sd"` will compute the weighted within- standard deviation and apply it to each group.

Value

`x` standardized (mean = `mean`, standard deviation = `sd`), grouped by `g/by`, weighted with `w`. See Details.

See Also

[fwithin](#), [fsd](#), [TRA](#), [Fast Statistical Functions](#), [Data Transformations](#), [Collapse Overview](#)

Examples

```
## Simple Scaling & Centering / Standardizing
head(fscale(mtcars))           # Doesn't rename columns
head(STD(mtcars))             # By default adds a prefix
qsu(STD(mtcars))              # See that it works
qsu(STD(mtcars, mean = 5, sd = 3)) # Assigning a mean of 5 and a standard deviation of 3
qsu(STD(mtcars, mean = FALSE))  # No centering: Scaling is mean-preserving

## Panel Data
head(fscale(get_vars(wlddev,9:12), wlddev$iso3c)) # Standardizing 4 series within each country
head(STD(wlddev, ~iso3c, cols = 9:12))           # Same thing using STD, id's added
pwcov(fscale(get_vars(wlddev,9:12), wlddev$iso3c)) # Correlating panel series after standardizing

fmean(get_vars(wlddev, 9:12))                    # This calculates the overall means
fsd(fwithin(get_vars(wlddev, 9:12), wlddev$iso3c)) # This calculates the within standard deviations
head(qsu(fscale(get_vars(wlddev, 9:12),
  wlddev$iso3c,
  mean = "overall.mean", sd = "within.sd"),
  by = wlddev$iso3c)) # This group-centers on the overall mean and
# group-scales to the within standard deviation
# -> data harmonized in the first 2 moments

## Using plm
pwlddev <- plm::pdata.frame(wlddev, index = c("iso3c","year"))
head(STD(pwlddev)) # Standardizing all numeric variables by country
head(STD(pwlddev, effect = 2L)) # Standardizing all numeric variables by year

## Weighted Standardizing
weights = abs(rnorm(nrow(wlddev)))
head(fscale(get_vars(wlddev,9:12), wlddev$iso3c, weights))
head(STD(wlddev, ~iso3c, weights, 9:12))

# Using dplyr
library(dplyr)
wlddev %>% group_by(iso3c) %>% select(PCGDP,LIFEEX) %>% STD
wlddev %>% group_by(iso3c) %>% select(PCGDP,LIFEEX) %>% STD(weights) # weighted standardizing
wlddev %>% group_by(iso3c) %>% select(PCGDP,LIFEEX,ODA) %>% STD(ODA) # weighting by ODA ->
# ..keeps the weight column unless keep.w = FALSE
```

fselect, get_vars, add_vars

Fast Select, Replace or Add Data Frame Columns

Description

Efficiently select and replace (or add) a subset of columns from (to) a data frame. This can be done by data type, or using expressions, column names, indices, logical vectors, selector functions or regular expressions matching column names.

Usage

```

## Select and replace variables, analogous to dplyr::select but significantly faster
fselect(x, ..., return = "data")
fselect(x, ...) <- value
slt(x, ..., return = "data") # Shortcut for fselect
slt(x, ...) <- value        # Shortcut for fselect<-

## Select and replace columns by names, indices, logical vectors,
## regular expressions or using functions to identify columns

get_vars(x, vars, return = "data", regex = FALSE, ...)
  gv(x, vars, return = "data", ...) # Shortcut for get_vars
  gvr(x, vars, return = "data", ...) # Shortcut for get_vars(..., regex = TRUE)

get_vars(x, vars, regex = FALSE, ...) <- value
  gv(x, vars, ...) <- value          # Shortcut for get_vars<-
  gvr(x, vars, ...) <- value        # Shortcut for get_vars<-(..., regex = TRUE)

## Add columns at any position within a data.frame

add_vars(x, ..., pos = "end")
add_vars(x, pos = "end") <- value
  av(x, ..., pos = "end")          # Shortcut for add_vars
  av(x, pos = "end") <- value      # Shortcut for add_vars<-

## Select and replace columns by data type

num_vars(x, return = "data")
num_vars(x) <- value
  nv(x, return = "data")          # Shortcut for num_vars
  nv(x) <- value                  # Shortcut for num_vars<-
cat_vars(x, return = "data")     # Categorical variables, see is.categorical
cat_vars(x) <- value
char_vars(x, return = "data")
char_vars(x) <- value
fact_vars(x, return = "data")
fact_vars(x) <- value
logi_vars(x, return = "data")
logi_vars(x) <- value
Date_vars(x, return = "data")    # See is.Date
Date_vars(x) <- value

```

Arguments

x	a data frame.
value	a data frame or list of columns whose dimensions exactly match those of the extracted subset of x. If only 1 variable is in the subset of x, value can also be an atomic vector or matrix, provided that <code>NROW(value) == nrow(x)</code> .

vars a vector of column names, indices (can be negative), a suitable logical vector, or a vector of regular expressions matching column names (if `regex = TRUE`). It is also possible to pass a function returning `TRUE` or `FALSE` when applied to the columns of `x`.

return an integer or string specifying what the selector function should return. The options are:

<i>Int.</i>	<i>String</i>	<i>Description</i>
1	"data"	subset of data frame (default)
2	"names"	column names
3	"indices"	column indices
4	"named_indices"	named column indices
5	"logical"	logical selection vector
6	"named_logical"	named logical vector

Note: replacement functions only replace data, However column names are replaced together with the data (if available).

regex logical. `TRUE` will do regular expression search on the column names of `x` using a (vector of) regular expression(s) passed to `vars`. Matching is done using `grep`.

pos the position where columns are added in the data frame. "end" (default) will append the data frame at the end (right) side. "front" will add columns in front (left). Alternatively one can pass a vector of positions (matching `length(value)` if `value` is a list). In that case the other columns will be shifted around the new ones while maintaining their order.

... for `fselect`: column names and expressions. for `get_vars`: further arguments passed to `grep`, if `regex = TRUE`. For `add_vars`: Same as `value`, a single argument passed may also be a vector or matrix, multiple arguments must each be a list (they are combined using `c(...)`).

Details

`get_vars(<-)` is around 2x faster than ``[.data.frame`` and 8x faster than ``[<-.data.frame``, so the common operation `data[cols] <-someFUN(data[cols])` can be made 10x more efficient (abstracting from computations performed by `someFUN`) using `get_vars(data, cols) <-someFUN(get_vars(data, cols))` or the shorthand `gv(data, cols) <-someFUN(gv(data, cols))`.

Similarly type-wise operations like `data[sapply(data, is.numeric)]` or `data[sapply(data, is.numeric)] <-value` are facilitated and more efficient using `num_vars(data)` and `num_vars(data) <-value` or the shortcuts `nv` and `nv<-` etc.

`fselect` provides an efficient alternative to `dplyr::select`, allowing the selection of variables based on expressions evaluated within the data frame, see Examples. It is about 100x faster than `dplyr::select` but also more simple as it does not provide special methods for grouped tibbles.

Finally, `add_vars(data1, data2, data3, ...)` is a lot faster than `cbind(data1, data2, data3, ...)`, and preserves the attributes of `data1` (i.e. it is like adding columns to `data1`). The replacement function `add_vars(data) <-someFUN(get_vars(data, cols))` efficiently appends data with computed columns. The `pos` argument allows adding columns at positions other than the end (right) of the data frame, see Examples.


```
get_vars(wlddev, c(10,12,14,16)) <- NULL # Deleting
```

fsubset

Fast Subsetting Matrix-Like Objects

Description

fsubset returns subsets of vectors, matrices or data frames which meet conditions. It is programmed very efficiently and uses C source code from the *data.table* package. Especially for data frames it is significantly (4-5 times) faster than `base::subset` or `dplyr::filter`. The methods also provide enhanced functionality compared to `base::subset`. The function `ss` provides a significantly faster alternative to `[.data.frame]`.

Usage

```
fsubset(x, ...)
sbt(x, ...) # Shortcut for fsubset

## Default S3 method:
fsubset(x, subset, ...)

## S3 method for class 'matrix'
fsubset(x, subset, ..., drop = FALSE)

## S3 method for class 'data.frame'
fsubset(x, subset, ...)

# Fast subsetting data frames (replaces `[`)
ss(x, i, j)
```

Arguments

x	object to be subsetted.
subset	logical expression indicating elements or rows to keep: missing values are taken as FALSE. The default and matrix methods only support logical vectors or row-indices (or a character vector of rownames if the matrix has rownames; the data frame method also supports logical vectors or row-indices).
...	For the matrix or data frame method: multiple comma-separated expressions indicating columns to select. Otherwise: further arguments to be passed to or from other methods.
drop	passed on to <code>[</code> indexing operator. Only available for the matrix method.
i	positive or negative row-indices or a logical vector to subset the rows of x.
j	a vector of column names, positive or negative indices or a suitable logical vector to subset the columns of x. <i>Note:</i> Negative indices are converted to positive ones using <code>j <- seq_along(x)[j]</code> .

Details

fsubset is a generic function, with methods supplied for vectors, matrices, and data frames (including lists). It represents an improvement in both speed and functionality over `base::subset`. The non-generic function `ss` is an improvement of `[.data.frame]`. For subsetting columns alone, please see [selecting and replacing columns](#).

For ordinary vectors, the result is `.Call(C_subsetVector, x, subset)`, where `C_subsetVector` is an internal function in the *data.table* package. The `subset` can be integer or logical. Appropriate errors are delivered for wrong use.

For matrices the implementation is all base-R but slightly more efficient and more versatile than `base::subset.matrix`. Thus it is possible to subset matrix rows using logical or integer vectors, or character vectors matching rownames. The `drop` argument is passed on to the indexing method for matrices.

For both matrices and data frames, the `...` argument can be used to subset columns, and is evaluated in a non-standard way. Thus it can support vectors of column names, indices or logical vectors, but also multiple comma separated column names passed without quotes, each of which may also be replaced by a sequence of columns i.e. `col1:coln` (see examples).

For data frames, the `subset` argument is also evaluated in a non-standard way. Thus next to vector of row-indices or logical vectors, it supports logical expressions of the form `col2 > 5 & col2 < col3` etc. (see examples). The data frame method uses `C_subsetDT`, an internal C function from the *data.table* package to subset data frames, hence it is significantly faster than `base::subset.data.frame`. If fast data frame subsetting is required but no non-standard evaluation, the function `ss` is slightly simpler and faster.

Factors may have empty levels after subsetting; unused levels are not automatically removed. See [droplevels](#) for a way to drop all unused levels from a data frame.

Value

An object similar to `x` containing just the selected elements (for a vector), rows and columns (for a matrix or data frame).

See Also

[fselect](#), [get_vars](#), [ftransform](#), [Data Frame Manipulation](#), [Collapse Overview](#)

Examples

```
fsubset(airquality, Temp > 90, Ozone, Temp)
fsubset(airquality, Day == 1, -Temp)
fsubset(airquality, Day == 1, -(Day:Temp))
fsubset(airquality, Day == 1, Ozone:Wind)
fsubset(airquality, Day == 1 & !is.na(Ozone), Ozone:Wind, Month)

ss(airquality, 1:10, 2:3)      # Significantly faster than airquality[1:10, 2:3]
fsubset(airquality, 1:10, 2:3) # This is possible but not advised
```


fsum

*Fast (Grouped, Weighted) Sum for Matrix-Like Objects***Description**

fsum is a generic function that computes the (column-wise) sum of all values in x, (optionally) grouped by g and/or weighted by w (e.g. to calculate survey totals). The [TRA](#) argument can further be used to transform x using its (grouped, weighted) sum.

Usage

```
fsum(x, ...)
```

```
## Default S3 method:
fsum(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = TRUE, ...)
```

```
## S3 method for class 'matrix'
fsum(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = TRUE, drop = TRUE, ...)
```

```
## S3 method for class 'data.frame'
fsum(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = TRUE, drop = TRUE, ...)
```

```
## S3 method for class 'grouped_df'
fsum(x, w = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = FALSE, keep.group_vars = TRUE, keep.w = TRUE, ...)
```

Arguments

x	a numeric vector, matrix, data frame or grouped tibble (<code>dplyr::grouped_df</code>).
g	a factor, GRP object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a GRP object) used to group x.
w	a numeric vector of (non-negative) weights, may contain missing values.
TRA	an integer or quoted operator indicating the transformation to perform: 1 - "replace_fill" 2 - "replace" 3 - "-" 4 - "--" 5 - "/" 6 - "%" 7 - "+" 8 - "*" 9 - "%%" 10 - "-%". See TRA .
na.rm	logical. Skip missing values in x. Defaults to TRUE and implemented at very little computational cost. If <code>na.rm = FALSE</code> a NA is returned when encountered.
use.g.names	logical. Make group-names and add to the result as names (default method) or row-names (matrix and data frame methods). No row-names are generated for <i>data.table</i> 's.
drop	<i>matrix and data.frame method:</i> Logical. TRUE drops dimensions and returns an atomic vector if <code>g = NULL</code> and <code>TRA = NULL</code> .

```

keep.group_vars      grouped_df method: Logical. FALSE removes grouping variables after computation.
keep.w               grouped_df method: Logical. Retain summed weighting variable after computation (if contained in grouped_df).
...                  arguments to be passed to or from other methods.

```

Details

Missing-value removal as controlled by the `na.rm` argument is done very efficiently by simply skipping them in the computation (thus setting `na.rm = FALSE` on data with no missing values doesn't give extra speed). Large performance gains can nevertheless be achieved in the presence of missing values if `na.rm = FALSE`, since then the corresponding computation is terminated once a NA is encountered and NA is returned (unlike `base::sum` which just runs through without any checks).

The weighted sum (i.e. survey total) is computed as `sum(x * w)`. If `na.rm = TRUE`, missing values will be removed from both `x` and `w` i.e. utilizing only `x[complete.cases(x, w)]` and `w[complete.cases(x, w)]`.

This all seamlessly generalizes to grouped computations, which are performed in a single pass (without splitting the data) and therefore extremely fast. See Benchmark and Examples below.

When applied to data frames with `groups` or `drop = FALSE`, `fsum` preserves all column attributes (such as variable labels) but does not distinguish between classed and unclassed objects. The attributes of the data frame itself are also preserved.

Value

The (`w` weighted) sum of `x`, grouped by `g`, or (if `TRA` is used) `x` transformed by its sum, grouped by `g`.

See Also

[fprod](#), [fmean](#), [Fast Statistical Functions](#), [Collapse Overview](#)

Examples

```

## default vector method
mpg <- mtcars$mpg
fsum(mpg)                # Simple sum
fsum(mpg, w = mtcars$hp) # Weighted sum (total): Weighted by hp
fsum(mpg, TRA = "%")    # Simple transformation: obtain percentages of mpg
fsum(mpg, mtcars$cyl)   # Grouped sum
fsum(mpg, mtcars$cyl, mtcars$hp) # Weighted grouped sum (total)
fsum(mpg, mtcars[c(2,8:9)]) # More groups..
g <- GRP(mtcars, ~ cyl + vs + am) # Precomputing groups gives more speed !
fsum(mpg, g)
fmean(mpg, g) == fsum(mpg, g) / fNobs(mpg, g)
fsum(mpg, g, TRA = "%") # Percentages by group

## data.frame method
fsum(mtcars)

```

```

fsum(mtcars, TRA = "%")
fsum(mtcars, g)
fsum(mtcars, g, TRA = "%")

## matrix method
m <- qM(mtcars)
fsum(m)
fsum(m, TRA = "%")
fsum(m, g)
fsum(m, g, TRA = "%")

## method for grouped tibbles - for use with dplyr
library(dplyr)
mtcars %>% group_by(cyl,vs,am) %>% fsum(hp) # Weighted grouped sum (total)
mtcars %>% fgroup_by(cyl,vs,am) %>% fsum(hp) # Equivalent and faster !!
mtcars %>% fgroup_by(cyl,vs,am) %>% fsum(TRA = "%")
mtcars %>% fgroup_by(cyl,vs,am) %>% fselect(mpg) %>% fsum

```

Benchmark

```

## This compares fsum with data.table (2 threads) and base::rowsum
# Starting with small data
mtcDT <- qDT(mtcars)
f <- qF(mtcars$cyl)

library(microbenchmark)
microbenchmark(mtcDT[, lapply(.SD, sum), by = f],
               rowsum(mtcDT, f, reorder = FALSE),
               fsum(mtcDT, f, na.rm = FALSE), unit = "relative")

      expr      min       lq     mean  median      uq      max neval cld
mtcDT[, lapply(.SD, sum), by = f] 145.436928 123.542134 88.681111 98.336378 71.880479 85.217726 100
rowsum(mtcDT, f, reorder = FALSE)  2.833333  2.798203  2.489064  2.937889  2.425724  2.181173 100 b
fsum(mtcDT, f, na.rm = FALSE)      1.000000  1.000000  1.000000  1.000000  1.000000  1.000000 100 a

# Now larger data
tdata <- qDT(replicate(100, rnorm(1e5), simplify = FALSE)) # 100 columns with 100.000 obs
f <- qF(sample.int(1e4, 1e5, TRUE)) # A factor with 10.000 groups

microbenchmark(tdata[, lapply(.SD, sum), by = f],
               rowsum(tdata, f, reorder = FALSE),
               fsum(tdata, f, na.rm = FALSE), unit = "relative")

      expr      min       lq     mean  median      uq      max neval cld
tdata[, lapply(.SD, sum), by = f] 2.646992 2.975489 2.834771 3.081313 3.120070 1.2766475 100 c
rowsum(tdata, f, reorder = FALSE) 1.747567 1.753313 1.629036 1.758043 1.839348 0.2720937 100 b
fsum(tdata, f, na.rm = FALSE)      1.000000  1.000000  1.000000  1.000000  1.000000  1.0000000 100 a

```

ftransform

*Fast Transform and Compute Columns on a Data Frame***Description**

ftransform is a much faster version of `base::transform` and `dplyr::mutate` for data frames. It returns the data frame with new columns computed and/or existing columns modified or deleted. `settransform` does all of that by reference i.e. it modifies the data frame in the global environment. `fcompute` can be used to compute new columns from the columns in a data frame and returns only the computed columns.

Usage

```
# Modify and return data frame
ftransform(X, ...)
ftransformv(X, vars, FUN, ..., apply = TRUE)
tfm(X, ...)           # Shortcut for ftransform
tfmv(X, vars, FUN, ..., apply = TRUE)

# Modify data frame by reference
settransform(X, ...)
settransformv(X, vars, FUN, ..., apply = TRUE)
settfm(X, ...)       # Shortcut for settransform
settfmv(X, vars, FUN, ..., apply = TRUE)

# Replace/add modified columns in/to a data frame
ftransform(X) <- value
tfm(X) <- value      # Shortcut for ftransform<-

# Compute columns, returned as a new data frame
fcompute(X, ...)
```

Arguments

X	a data frame or named list of columns.
...	further arguments of the form <code>column = value</code> . The value can be a combination of other columns, a scalar value, or <code>NULL</code> , which deletes column. Alternatively it is also possible to place a single list here, which will be treated like a list of <code>column = value</code> arguments. For <code>ftransformv</code> , ... can be used to pass further arguments to <code>FUN</code> . <i>Note:</i> The ellipsis (...) is always evaluated within the data frame (X) environment. See Examples.
vars	variables to be transformed by applying <code>FUN</code> to them: select using names, indices, a logical vector or a selector function (e.g. <code>is.numeric</code>).
FUN	a single function yielding a result of length <code>NROW(X)</code> or 1. See also <code>apply</code> .

apply	logical. TRUE (default) will apply FUN to each column selected in vars; FALSE will apply FUN to the subsetted data frame i.e. FUN(get_vars(X, vars), ...). The latter is useful for <i>collapse</i> functions with data frame or grouped tibble / panel-data frame methods, yielding performance gains and enabling grouped transformations. See Examples.
value	a named list of replacements, it will be treated like an evaluated list of column = value arguments.

Details

The ... arguments to ftransform are tagged vector expressions, which are evaluated in the data frame X. The tags are matched against names(X), and for those that match, the values replace the corresponding variable in X, whereas the others are appended to X. It is also possible to delete columns by assigning NULL to them, i.e. ftransform(data, colk = NULL) removes colk from the data. *Note* that names(X) and the names of the ... arguments are checked for uniqueness beforehand, yielding an error if this is not the case.

Since *collapse* v1.3.0, it is also possible to pass a single named list to ..., i.e. ftransform(data, newdata). This list will be treated like a list of tagged vector expressions. *Note* the different behavior: ftransform(data, list(newcol = col1)) is the same as ftransform(data, newcol = col1), whereas ftransform(data, newcol = as.list(col1)) creates a list column. Something like ftransform(data, as.list(col1)) gives an error because the list is not named. See Examples.

The function ftransformv added in v1.3.2 provides a fast replacement for the functions dplyr::mutate_at and dplyr::mutate_if facilitating mutations of groups of columns (dplyr::mutate_all is already accounted for by dapply). See Examples.

The function settransform does all of that by reference, but uses base-R's copy-on modify semantics, which is equivalent to replacing the data with <- (thus it is still memory efficient but the data will have a different memory address afterwards).

The function fcompute works just like ftransform, but returns only the changed / computed columns without modifying or appending the data in X.

Value

The modified data frame X, or, for fcompute, a new data frame with the columns computed on X. All attributes of X are preserved.

See Also

[with](#), [within](#), [add_vars](#), [Data Frame Manipulation](#), [Collapse Overview](#)

Examples

```
## ftransform modifies and returns a data.frame
head(ftransform(airquality, Ozone = -Ozone))
head(ftransform(airquality, new = -Ozone, Temp = (Temp-32)/1.8))
head(ftransform(airquality, new = -Ozone, new2 = 1, Temp = NULL)) # Deleting Temp
head(ftransform(airquality, Ozone = NULL, Temp = NULL))           # Deleting columns

# With collapse's grouped and weighted functions, complex operations are done on the fly
```

```

head(ftransform(airquality, # Grouped operations by month:
                Ozone_Month_median = fmedian(Ozone, Month, TRA = "replace_fill"),
                Ozone_Month_sd = fsd(Ozone, Month, TRA = "replace"),
                Ozone_Month_centered = fwithin(Ozone, Month)))

# Grouping by month and above/below average temperature in each month
head(ftransform(airquality, Ozone_Month_high_median =
                fmedian(Ozone, list(Month, Temp > fbetween(Temp, Month)), TRA = "replace_fill"))))

## ftransformv can be used to modify multiply columns using a function
head(ftransformv(airquality, 1:3, log))
head(`[<-`(airquality, 1:3, value = lapply(airquality[1:3], log))) # Same thing in base R

head(ftransformv(airquality, 1:3, log, apply = FALSE))
head(`[<-`(airquality, 1:3, value = log(airquality[1:3]))) # Same thing in base R

# Using apply = FALSE yields meaningful performance gains with collapse functions
# This calls fwithin.default, and repeats the grouping by month 3 times:
head(ftransformv(airquality, 1:3, fwithin, Month))

# This calls fwithin.data.frame, and only groups one time -> 5x faster!
head(ftransformv(airquality, 1:3, fwithin, Month, apply = FALSE))

library(magrittr) # Pipe operators
# This also works for grouped and panel data frames (calling fwithin.grouped_df)
airquality %>% fgroup_by(Month) %>%
  ftransformv(1:3, fwithin, apply = FALSE) %>% head

# But this gives the WRONG result (calling fwithin.default). Need option apply = FALSE!!
airquality %>% fgroup_by(Month) %>%
  ftransformv(1:3, fwithin) %>% head

## For more complex mutations we can use ftransform with compound pipes
airquality %>% fgroup_by(Month) %>%
  ftransform(get_vars(., 1:3) %>% fwithin %>% flag(0:2)) %>% head

airquality %>% ftransform(STD(., cols = 1:3) %>% replace_NA(0)) %>% head

# The list argument feature also allows flexible operations creating multiple new columns
airquality %>% # The variance of Wind and Ozone, by month, weighted by temperature:
  ftransform(fvar(list(Wind_var = Wind, Ozone_var = Ozone), Month, Temp, "replace")) %>% head

# Same as above using a grouped tibble (a bit more complex)
airquality %>% fgroup_by(Month) %>%
  ftransform(fselect(., Wind, Ozone) %>% fvar(Temp, "replace") %>% add_stub("_var", FALSE)) %>%
  fungroup %>% head

# This performs 2 different multi-column grouped operations (need c() to make it one list)
ftransform(airquality, c(fmedian(list(Wind_Day_median = Wind,
                                     Ozone_Day_median = Ozone), Day, TRA = "replace"),
                      fsd(list(Wind_Month_sd = Wind,
                               Ozone_Month_sd = Ozone), Month, TRA = "replace"))) %>% head

```

```

## settransform(v) works like ftransform(v) but modifies a data frame in the global environment..
settransform(airquality, Ratio = Ozone / Temp, Ozone = NULL, Temp = NULL)
head(airquality)
rm(airquality)

# Grouped and weighted centering
settransformv(airquality, 1:3, fwithin, Month, Temp, apply = FALSE)
head(airquality)
rm(airquality)

# Suitably lagged first-differences
settransform(airquality, get_vars(airquality, 1:3) %>% fdiff %>% flag(0:2))
head(airquality)
rm(airquality)

# Same as above using magrittr::`%<>%`
airquality %<>% ftransform(get_vars(., 1:3) %>% fdiff %>% flag(0:2))
head(airquality)
rm(airquality)

# It is also possible to achieve the same thing via a replacement method (if needed)
ftransform(airquality) <- get_vars(airquality, 1:3) %>% fdiff %>% flag(0:2)
head(airquality)
rm(airquality)

## fcompute only returns the modified / computed columns, ...
head(fcompute(airquality, Ozone = -Ozone))
head(fcompute(airquality, new = -Ozone, Temp = (Temp-32)/1.8))
head(fcompute(airquality, new = -Ozone, new2 = 1))

```

funique

Fast Unique Elements / Rows

Description

funique is a substantially faster alternative to [unique](#). It is generic with a default vector method and a data frame method.

Usage

```

funique(x, ...)

## Default S3 method:
funique(x, sort = FALSE, method = c("auto", "radix", "hash"), ...)

## S3 method for class 'data.frame'
funique(x, cols = NULL, sort = FALSE, ...)

```

Arguments

x		a atomic vector or data frame / list of equal-length columns.
sort		logical. TRUE orders the unique elements / rows. FALSE returns unique values in order of first occurrence, however numeric values are only provided in order of first occurrence when method = "hash" i.e. the radix method always sorts numeric data.
method		an integer or character string specifying the method of computation:
<i>Int.</i>	<i>String</i>	<i>Description</i>
1	"auto"	automatic selection: hash for character, logical or if <code>length(x) < 500</code> , else radix.
2	"radix"	use radix ordering to determine unique values.
3	"hash"	use index hashing to determine unique values.
cols		compute unique rows according to a subset of columns. Columns can be selected using column names, indices, a logical vector or a selector function (i.e. <code>is.character</code>). <i>Note:</i> All columns are returned.
...		arguments passed to <code>radixorder</code> , e.g. <code>decreasing</code> or <code>na.last</code> . Only applicable in <code>funique.default</code> if <code>method = "radix"</code> .

Details

If `x` is a data frame / list and all rows are already unique, then `x` is returned. Otherwise a copy of `x` with duplicate rows removed is returned. See [qf](#) for some additional computational details.

Value

`x` with duplicate elements/rows removed.

See Also

[qf](#), [Fast Grouping and Ordering](#), [Collapse Overview](#).

Examples

```
funique(mtcars$cyl)
funique(gv(mtcars, c(2,8,9)))
funique(mtcars, cols = c(2,8,9))
```

fvar, fsd

Fast (Grouped, Weighted) Variance and Standard Deviation for Matrix-Like Objects

Description

`fvar` and `fsd` are generic functions that compute the (column-wise) variance and standard deviation of `x`, (optionally) grouped by `g` and/or frequency-weighted by `w`. The [TRA](#) argument can further be used to transform `x` using its (grouped, weighted) variance/sd.

Usage

```

fvar(x, ...)
fsd(x, ...)

## Default S3 method:
fvar(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
     use.g.names = TRUE, stable.algo = TRUE, ...)
## Default S3 method:
fsd(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
     use.g.names = TRUE, stable.algo = TRUE, ...)

## S3 method for class 'matrix'
fvar(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
     use.g.names = TRUE, drop = TRUE, stable.algo = TRUE, ...)
## S3 method for class 'matrix'
fsd(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
     use.g.names = TRUE, drop = TRUE, stable.algo = TRUE, ...)

## S3 method for class 'data.frame'
fvar(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
     use.g.names = TRUE, drop = TRUE, stable.algo = TRUE, ...)
## S3 method for class 'data.frame'
fsd(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
     use.g.names = TRUE, drop = TRUE, stable.algo = TRUE, ...)

## S3 method for class 'grouped_df'
fvar(x, w = NULL, TRA = NULL, na.rm = TRUE,
     use.g.names = FALSE, keep.group_vars = TRUE, keep.w = TRUE,
     stable.algo = TRUE, ...)
## S3 method for class 'grouped_df'
fsd(x, w = NULL, TRA = NULL, na.rm = TRUE,
     use.g.names = FALSE, keep.group_vars = TRUE, keep.w = TRUE,
     stable.algo = TRUE, ...)

```

Arguments

x	a numeric vector, matrix, data frame or grouped tibble (<code>dplyr::grouped_df</code>).
g	a factor, GRP object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a GRP object) used to group x.
w	a numeric vector of (non-negative) weights, may contain missing values.
TRA	an integer or quoted operator indicating the transformation to perform: 1 - "replace_fill" 2 - "replace" 3 - "-" 4 - "--" 5 - "/" 6 - "%" 7 - "+" 8 - "*" 9 - "%%" 10 - "-%%". See TRA .
na.rm	logical. Skip missing values in x. Defaults to TRUE and implemented at very little computational cost. If <code>na.rm = FALSE</code> a NA is returned when encountered.
use.g.names	logical. Make group-names and add to the result as names (default method) or row-names (matrix and data frame methods). No row-names are generated for

	<i>data.table</i> 's and grouped tibbles.
drop	<i>matrix and data.frame method</i> : Logical. TRUE drops dimensions and returns an atomic vector if g = NULL and TRA = NULL.
keep.group_vars	<i>grouped_df method</i> : Logical. FALSE removes grouping variables after computation.
keep.w	<i>grouped_df method</i> : Logical. Retain summed weighting variable after computation (if contained in grouped_df).
stable.algo	logical. TRUE (default) use Welford's numerically stable online algorithm. FALSE implements a faster but numerically unstable one-pass method. See Details.
...	arguments to be passed to or from other methods.

Details

Welford's online algorithm used by default to compute the variance is well described [here](#) (the section *Weighted incremental algorithm* also shows how the weighted variance is obtained by this algorithm).

If `stable.algo = FALSE`, the variance is computed in one-pass as $(\text{sum}(x^2) - n \cdot \text{mean}(x)^2) / (n-1)$, where $\text{sum}(x^2)$ is the sum of squares from which the expected sum of squares $n \cdot \text{mean}(x)^2$ is subtracted, normalized by $n-1$ (Bessel's correction). This is numerically unstable if $\text{sum}(x^2)$ and $n \cdot \text{mean}(x)^2$ are large numbers very close together, which will be the case for large n , large x -values and small variances (catastrophic cancellation occurs, leading to a loss of numeric precision). Numeric precision is however still maximized through the internal use of long doubles in C++, and the fast algorithm can be up to 4-times faster compared to Welford's method.

The weighted variance is computed with frequency weights as $(\text{sum}(x^2 \cdot w) - \text{sum}(w) \cdot \text{weighted.mean}(x, w)^2) / (\text{sum}(w) - 1)$. If `na.rm = TRUE`, missing values will be removed from both x and w i.e. utilizing only $x[\text{complete.cases}(x, w)]$ and $w[\text{complete.cases}(x, w)]$.

Missing-value removal as controlled by the `na.rm` argument is done very efficiently by simply skipping the values (thus setting `na.rm = FALSE` on data with no missing values doesn't give extra speed). Large performance gains can nevertheless be achieved in the presence of missing values if `na.rm = FALSE`, since then the corresponding computation is terminated once a NA is encountered and NA is returned.

This all seamlessly generalizes to grouped computations, which are performed in a single pass (without splitting the data) and therefore extremely fast.

When applied to data frames with groups or `drop = FALSE`, `fvar/fsd` preserves all column attributes (such as variable labels) but does not distinguish between classed and unclassed object (thus applying `fvar/fsd` to a factor column will give a 'malformed factor' error). The attributes of the data frame itself are also preserved.

Value

`fvar` returns the variance of x , grouped by g , or (if `TRA` is used) x transformed by its variance, grouped by g . `fsd` computes the standard deviation of x in like manor.

References

Welford, B. P. (1962). Note on a method for calculating corrected sums of squares and products. *Technometrics*. 4 (3): 419-420. doi:10.2307/1266577.

See Also

[Fast Statistical Functions](#), [Collapse Overview](#)

Examples

```
## default vector method
fvar(mtcars$mpg)                # Simple variance (all examples also hold for fvar!)
fsd(mtcars$mpg)                 # Simple standard deviation
fsd(mtcars$mpg, w = mtcars$hp)  # Weighted sd: Weighted by hp
fsd(mtcars$mpg, TRA = "/")     # Simple transformation: scaling (See also ?fscale)
fsd(mtcars$mpg, mtcars$cyl)     # Grouped sd
fsd(mtcars$mpg, mtcars$cyl, mtcars$hp) # Grouped weighted sd
fsd(mtcars$mpg, mtcars$cyl, TRA = "/") # Scaling by group
fsd(mtcars$mpg, mtcars$cyl, mtcars$hp, "/") # Group-scaling using weighted group sds

## data.frame method
fsd(iris)                       # This works, although 'Species' is a factor variable
fsd(mtcars, drop = FALSE)       # This works, all columns are numeric variables
fsd(iris[-5], iris[5])         # By Species: iris[5] is still a list, and thus passed to GRP()
fsd(iris[-5], iris[[5]])       # Same thing much faster: fsd recognizes 'Species' is a factor
head(fsd(iris[-5], iris[[5]], TRA = "/")) # Data scaled by species (see also fscale)

## matrix method
m <- qM(mtcars)
fsd(m)
fsd(m, mtcars$cyl) # etc..

## method for grouped tibbles - for use with dplyr:
library(dplyr)
mtcars %>% group_by(cyl,vs,am) %>% fsd
mtcars %>% group_by(cyl,vs,am) %>% fsd(keep.group_vars = FALSE) # Remove grouping columns
mtcars %>% group_by(cyl,vs,am) %>% fsd(hp) # Weighted by hp
mtcars %>% group_by(cyl,vs,am) %>% fsd(hp, "/") # Weighted scaling transformation
```

Description

The GGDC 10-Sector Database provides a long-run internationally comparable dataset on sectoral productivity performance in Africa, Asia, and Latin America. Variables covered in the data set are annual series of value added (in local currency), and persons employed for 10 broad sectors.

Usage

```
data("GGDC10S")
```

Format

A data frame with 5027 observations on the following 16 variables.

Country *char*: Country (43 countries)

Regioncode *char*: ISO3 Region code

Region *char*: Region (6 World Regions)

Variable *char*: Variable (Value Added or Employment)

Year *num*: Year (67 Years, 1947-2013)

AGR *num*: Agriculture

MIN *num*: Mining

MAN *num*: Manufacturing

PU *num*: Utilities

CON *num*: Construction

WRT *num*: Trade, restaurants and hotels

TRA *num*: Transport, storage and communication

FIRE *num*: Finance, insurance, real estate and business services

GOV *num*: Government services

OTH *num*: Community, social and personal services

SUM *num*: Summation of sector GDP

Source

<https://www.rug.nl/ggdc/productivity/10-sector/>

References

Timmer, M. P., de Vries, G. J., & de Vries, K. (2015). "Patterns of Structural Change in Developing Countries." . In J. Weiss, & M. Tribe (Eds.), *Routledge Handbook of Industry and Development*. (pp. 65-83). Routledge.

See Also

[w1ddev](#), [Collapse Overview](#)

Examples

```

namlab(GGDC10S, class = TRUE)
# aperm(qsu(GGDC10S, ~ Variable, ~ Variable + Country, vlabels = TRUE))

library(data.table)
library(ggplot2)

## World Regions Structural Change Plot

dat <- GGDC10S
fselect(dat, AGR:OTH) <- replace_outliers(dapply(fselect(dat, AGR:OTH), `*`, 1 / dat$SUM),
                                          0, NA, "min")
dat$Variable <- recode_char(dat$Variable, VA = "Value Added Share", EMP = "Employment Share")
dat <- collap(dat, ~ Variable + Region + Year, cols = 6:15)
dat <- melt(qDT(dat), 1:3, variable.name = "Sector", na.rm = TRUE)

ggplot(aes(x = Year, y = value, fill = Sector), data = dat) +
  geom_area(position = "fill", alpha = 0.9) + labs(x = NULL, y = NULL) +
  theme_linedraw(base_size = 14) + facet_grid(Variable ~ Region, scales = "free_x") +
  scale_fill_manual(values = sub("#00FF66", "#00CC66", rainbow(10))) +
  scale_x_continuous(breaks = scales::pretty_breaks(n = 7), expand = c(0, 0)) +
  scale_y_continuous(breaks = scales::pretty_breaks(n = 10), expand = c(0, 0),
                    labels = scales::percent) +
  theme(axis.text.x = element_text(angle = 315, hjust = 0, margin = ggplot2::margin(t = 0)),
        strip.background = element_rect(colour = "grey30", fill = "grey30"))

# A function to plot the structural change of an arbitrary country

plotGGDC <- function(ctry) {
  dat <- fsubset(GGDC10S, Country == ctry, Variable, Year, AGR:SUM)
  fselect(dat, AGR:OTH) <- replace_outliers(dapply(fselect(dat, AGR:OTH), `*`, 1 / dat$SUM),
                                          0, NA, "min")

  dat$SUM <- NULL
  dat$Variable <- recode_char(dat$Variable, VA = "Value Added Share", EMP = "Employment Share")
  dat <- melt(qDT(dat), 1:2, variable.name = "Sector", na.rm = TRUE)

  ggplot(aes(x = Year, y = value, fill = Sector), data = dat) +
    geom_area(position = "fill", alpha = 0.9) + labs(x = NULL, y = NULL) +
    theme_linedraw(base_size = 14) + facet_wrap(~ Variable) +
    scale_fill_manual(values = sub("#00FF66", "#00CC66", rainbow(10))) +
    scale_x_continuous(breaks = scales::pretty_breaks(n = 7), expand = c(0, 0)) +
    scale_y_continuous(breaks = scales::pretty_breaks(n = 10), expand = c(0, 0),
                      labels = scales::percent) +
    theme(axis.text.x = element_text(angle = 315, hjust = 0, margin = ggplot2::margin(t = 0)),
          strip.background = element_rect(colour = "grey20", fill = "grey20"),
          strip.text = element_text(face = "bold"))
}

plotGGDC("BWA")

```

 groupid

Generate Run-Length Type Group-Id

Description

groupid is an enhanced version of `data.table::rleid` for atomic vectors. It generates a run-length type group-id where consecutive identical values are assigned the same integer. It is a generalization as it can be applied to unordered vectors, generate group id's starting from an arbitrary value, and skip missing values.

Usage

```
groupid(x, o = NULL, start = 1L, na.skip = FALSE, check.o = TRUE)
```

Arguments

x	an atomic vector of any type. Attributes are not considered.
o	an (optional) integer ordering vector specifying the order by which to pass through x.
start	integer. The starting value of the resulting group-id. Default is starting from 1. For C++ programmers, starting from 0 could be a better choice.
na.skip	logical. Skip missing values i.e. if TRUE something like <code>groupid(c("a", NA, "a"))</code> gives <code>c(1, NA, 1)</code> whereas FALSE gives <code>c(1, 2, 3)</code> .
check.o	logical. Programmers option: FALSE prevents checking that each element of o is in the range <code>[1, length(x)]</code> , it only checks the length of o. This gives some extra speed, but will terminate R if any element of o is too large or too small.

Value

An integer vector of class 'qG'. See [qG](#).

See Also

[seqid](#), [qG](#), [Fast Grouping and Ordering](#), [Collapse Overview](#)

Examples

```
groupid(airquality$Month)
groupid(airquality$Month, start = 0)
groupid(wlddev$country)[1:100]

## Same thing since country is alphabetically ordered: (groupid is faster..)
all.equal(groupid(wlddev$country), qG(wlddev$country, na.exclude = FALSE))

## When data is unordered, group-id can be generated through an ordering..
```

```
uo <- order(rnorm(fnrow(airquality)))
monthuo <- airquality$Month[uo]
o <- order(monthuo)
groupid(monthuo, o)
identical(groupid(monthuo, o)[o], unattrib(groupid(airquality$Month)))
```

GRP, fgroup_by

Fast Grouping / collapse Grouping Objects

Description

GRP performs fast, ordered and unordered, groupings of vectors and data frames (or lists of vectors) using [radixorderv](#). The output is a list-like object of class 'GRP' which can be printed, plotted and used as an efficient input to all of *collapse*'s fast statistical and transformation functions / operators, as well as to [collap](#), [BY](#) and [TRA](#).

`fgroup_by` is similar to `dplyr::group_by` but faster. It creates a grouped data frame with a 'GRP' object attached - for faster `dplyr`-like programming with *collapse*'s fast functions.

There are also several conversion methods to convert to and from 'GRP' objects. Notable among these is `GRP.grouped_df`, which returns a 'GRP' object from a grouped data frame created with `dplyr::group_by` (or `fgroup_by`), and the duo `GRP.factor` and `as.factor_GRP`.

Usage

```
GRP(X, ...)
```

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

```
GRP(X, by = NULL, sort = TRUE, decreasing = FALSE, na.last = TRUE,
     return.groups = TRUE, return.order = FALSE, call = TRUE, ...)
```

```
## S3 method for class 'factor'
```

```
GRP(X, ..., group.sizes = TRUE, drop = FALSE, return.groups = TRUE,
     call = TRUE)
```

```
## S3 method for class 'qG'
```

```
GRP(X, ..., group.sizes = TRUE, return.groups = TRUE, call = TRUE)
```

```
## S3 method for class 'pseries'
```

```
GRP(X, effect = 1L, ..., group.sizes = TRUE, return.groups = TRUE,
     call = TRUE)
```

```
## S3 method for class 'pdata.frame'
```

```
GRP(X, effect = 1L, ..., group.sizes = TRUE, return.groups = TRUE,
     call = TRUE)
```

```
## S3 method for class 'grouped_df'
```

```
GRP(X, ..., return.groups = TRUE, call = TRUE)
```

```

# Identify, get group names, and convert GRP object to factor
is.GRP(x)
GRPnames(x, force.char = TRUE)
as.factor_GRP(x, ordered = FALSE)

# Fast, class-agnostic version of dplyr::group_by for use with fast functions, see details
fgroup_by(X, ..., sort = TRUE, decreasing = FALSE, na.last = TRUE,
          return.order = FALSE)
gby(X, ..., sort = TRUE, decreasing = FALSE, na.last = TRUE,
    return.order = FALSE)

# Get grouping columns from a grouped data frame created with dplyr::group_by or fgroup_by
fgroup_vars(X, return = "data")

# Ungroup grouped data frame created with dplyr::group_by or fgroup_by
fungroup(X, ...)

## S3 method for class 'GRP'
print(x, n = 6, ...)

## S3 method for class 'GRP'
plot(x, breaks = "auto", type = "s", horizontal = FALSE, ...)

```

Arguments

X	a vector, list of columns or data frame (default method), or a classed object (conversion/extractor methods).
x	a GRP object.
by	if X is a data frame or list, by can indicate columns to use for the grouping (by default all columns are used). Columns must be passed using a vector of column names, indices, or using a one-sided formula i.e. <code>~ col1 + col2</code> .
sort	logical. This argument only affects character vectors / columns passed. If FALSE, these are not ordered but simply grouped in the order of first appearance of unique elements. This provides a slight performance gain if only grouping but not alphabetic ordering is required (argument passed to radixorder).
ordered	logical. TRUE adds a class 'ordered' i.e. generates an ordered factor.
decreasing	logical. Should the sort order be increasing or decreasing? Can be a vector of length equal to the number of arguments in X / by (argument passed to radixorder).
na.last	logical. If missing values are encountered in grouping vector/columns, assign them to the last group (argument passed to radixorder).
return.groups	logical. Include the unique groups in the created GRP object.
return.order	logical. Include the output from radixorder in the created GRP object.
group.sizes	logical. TRUE tabulates factor levels using tabulate to create a vector of group sizes; FALSE leaves that slot empty when converting from factors.
drop	logical. TRUE efficiently drops unused factor levels beforehand using fdroplevels .

call	logical.	TRUE calls <code>match.call</code> and saves it in the final slot of the GRP object.
force.char	logical.	Always output group names as character vector, even if a single numeric vector was passed to <code>GRP.default</code> .
effect	<i>plm</i> methods:	Select which panel identifier should be used as grouping variable. 1L takes the first variable in the <code>plm::index</code> , 2L the second etc., identifiers can also be passed as a character string. More than one variable can be supplied.
return	an integer or string	specifying what <code>fgroup_vars</code> should return. The options are:
	<i>Int.</i>	<i>String</i>
	1	"data" full grouping columns (default)
	2	"unique" unique rows of grouping columns
	3	"names" names of grouping columns
	4	"indices" integer indices of grouping columns
	5	"named_indices" named integer indices of grouping columns
	6	"logical" logical selection vector of grouping columns
	7	"named_logical" named logical selection vector of grouping columns
n	integer.	Number of groups to print out.
breaks	integer.	Number of breaks in the histogram of group-sizes.
type	linetype	for plot.
horizontal	logical.	TRUE arranges plots next to each other, instead of above each other.
...	for <code>fgroup_by</code> :	unquoted comma-separated column names of grouping columns. Otherwise: arguments to be passed to or from other methods.

Details

GRP is a central function in the *collapse* package because it provides the key inputs to facilitate easy and efficient groupwise-programming at the C/C++ level: Information about (1) the number of groups (2) an integer group-id indicating which values / rows belong to which group and (3) information about the size of each group. Provided with these informations, *collapse*'s [Fast Statistical Functions](#) pre-allocate intermediate and result vectors of the right sizes and (in most cases) perform grouped statistical computations in a single pass through the data.

The sorting and ordering functionality for GRP only affects (2), that is groups receive different integer-id's depending on whether the groups are sorted `sort = TRUE`, and in which order (argument decreasing). This in-turn changes the order of values/rows in the output of *collapse* functions. *Note* that `sort = FALSE` is only effective on character vectors, numeric grouping vectors will always produce ordered groupings.

Next to GRP, there is the function `fgroup_by` as a significantly faster alternative to `dplyr::group_by`. It creates a grouped data frame by attaching a 'GRP' object to a data frame. *collapse* functions with a `grouped_df` method applied to that data frame will yield grouped computations. Note that `fgroup_by` can only be used in combination with *collapse* functions, not with *dplyr* verbs such as `summarize` or `mutate`. The converse is not true, you can group data with `dplyr::group_by` and then apply *collapse* functions. Note also the `fgroup_by` is class-agnostic, i.e. the classes of the data frame or list passed are preserved, and all standard methods (like subsetting with ``[`` or `print`

methods) apply to the grouped object. Apart from the class 'grouped_df' which is added behind any classes the object might inherit (apart from 'data.frame'), a class 'GRP_df' is added in front. This class responds to print method and a subset (`[`) methods. Both first call corresponding method for the object and then print / attach the grouping information. `print.GRP_df` prints below the object print one line indicating the grouping variables, followed, in square brackets, by the following information: [number of groups | average group size (standard-deviation of group sizes)].

GRP is an S3 generic function with one default method supporting vector and list input and several conversion methods:

The conversion of factors to 'GRP' objects by `GRP.factor` involves obtaining the number of groups calling `ng <- fnlevels(f)` and then computing the count of each level using `tabulate(f, ng)`. The integer group-id (2) is already given by the factor itself after removing the levels and class attributes and replacing any missing values with `ng + 1L`. The levels are put in a list and moved to position (4) in the 'GRP' object, which is reserved for the unique groups. Going from factor to 'GRP' object thus only requires a tabulation of the levels, whereas creating a factor from a 'GRP' object using `as.factor_GRP` does not involve any computations, but may involve interactions if multiple grouping columns were used (which are then interacted to produce unique factor levels) or `as.character` conversions if the grouping column(s) were numeric (which are potentially expensive).

The method `GRP.grouped_df` takes the 'groups' attribute from a grouped data frame and converts it to a 'GRP' object. If the grouped data frame was generated using `fgroup_by`, all work is done already. If it was created using `dplyr::group_by`, a C++ routine is called to efficiently convert the grouping object.

Note: For faster factor generation and a factor-light class 'qG' which avoids the coercion of factor levels to character also see `qF` and `qG`.

Value

A list-like object of class 'GRP' containing information about the number of groups, the observations (rows) belonging to each group, the size of each group, the unique group names / definitions, whether the groups are ordered or not and (optionally) the ordering vector used to perform the ordering. The object is structured as follows:

<i>List-index</i>	<i>Element-name</i>	<i>Content type</i>	<i>Content description</i>
[[1]]	N.groups	integer(1)	Number of Groups
[[2]]	group.id	integer(NROW(X))	An integer group-identifier
[[3]]	group.sizes	integer(N.groups)	Vector of group sizes
[[4]]	groups	unique(X) or NULL	Unique groups (same format as input, sorted if <code>sort = TRUE</code>)
[[5]]	group.vars	character	The names of the grouping variables
[[6]]	ordered	logical(2)	[1]- TRUE if <code>sort = TRUE</code> , [2]- TRUE if X already sorted
[[7]]	order	integer(NROW(X)) or NULL	Ordering vector from <code>radixorder</code> or NULL if returned
[[8]]	call	call() or NULL	The <code>GRP()</code> call, obtained from <code>match.call()</code> , or NULL

See Also

[radixorder](#), [qF](#), [Fast Grouping and Ordering](#), [Collapse Overview](#)

Examples

```
## default method
GRP(mtcars$cyl)
GRP(mtcars, ~ cyl + vs + am) # Or GRP(mtcars, c("cyl","vs","am")) or GRP(mtcars, c(2,8:9))
g <- GRP(mtcars, ~ cyl + vs + am) # Saving the object
print(g) # Printing it
plot(g) # Plotting it
GRPnames(g) # Retain group names
fsum(mtcars, g) # Compute the sum of mtcars, grouped by variables cyl, vs and am

## Convert factor to GRP object and vice-versa
GRP(iris$Species)
as.factor_GRP(g)

## dplyr integration
library(dplyr)
mtcars %>% group_by(cyl,vs,am) %>% GRP # Get GRP object from a dplyr grouped tibble
mtcars %>% group_by(cyl,vs,am) %>% fmean # Grouped mean using dplyr grouping
mtcars %>% fgroup_by(cyl,vs,am) %>% fmean # Faster alternative with collapse grouping

mtcars %>% fgroup_by(cyl,vs,am) # Print method
```

has_elem, get_elem *Find and Extract / Subset List Elements*

Description

A suite of functions to subset or extract from (potentially complex) lists and list-like structures. Subsetting may occur according to certain data types, using identifier functions, element names or regular expressions to search the list for certain objects.

- `atomic_elem` and `list_elem` are non-recursive functions to extract and replace the atomic and sub-list elements at the top-level of the list tree.
- `reg_elem` is the recursive equivalent of `atomic_elem` and returns the 'regular' part of the list - with atomic elements in the final nodes. See [is.regular](#). `irreg_elem` returns all the non-regular elements (i.e. call and terms objects, formulas, etc...). See Examples.
- `get_elem` returns the part of the list responding to either an identifier function, regular expression or exact element names, or indices applied to all final objects. `has_elem` checks for the existence of the searched element and returns TRUE if a match is found. See Examples.

Usage

```
## Non-recursive (top-level) subsetting and replacing
atomic_elem(l, return = "sublist", keep.class = FALSE)
atomic_elem(l) <- value
list_elem(l, return = "sublist", keep.class = FALSE)
```

```
list_elem(l) <- value

## Recursive separation of regular (atomic) and irregular (non-atomic) parts
reg_elem(l, recursive = TRUE, keep.tree = FALSE, keep.class = FALSE)
irreg_elem(l, recursive = TRUE, keep.tree = FALSE, keep.class = FALSE)

## Extract elements using a function or regular expression
get_elem(l, elem, recursive = TRUE, DF.as.list = TRUE, keep.tree = FALSE,
         keep.class = FALSE, regex = FALSE, ...)

## Check for the existence of elements
has_elem(l, elem, recursive = TRUE, DF.as.list = TRUE, regex = FALSE, ...)
```

Arguments

l a list.

value a list of the same length as the extracted subset of **l**.

elem a function returning TRUE or FALSE when applied to elements of **l**, or a character vector of element names or regular expressions (if **regex = TRUE**). **get_elem** also supports a vector or indices which will be used to subset all final objects.

return an integer or string specifying what the selector function should return. The options are:

<i>Int.</i>	<i>String</i>	<i>Description</i>
1	"sublist"	subset of data frame (default)
2	"names"	column names
3	"indices"	column indices
4	"named_indices"	named column indices
5	"logical"	logical selection vector
6	"named_logical"	named logical vector

Note: replacement functions only replace data, However column names are replaced together with the data.

recursive logical. Should the list search be recursive (i.e. go through all the elements), or just at the top-level?

DF.as.list logical. TRUE treats data frames like (sub-)lists; FALSE like atomic elements.

keep.tree logical. TRUE always returns the entire list tree leading up to all matched results, while FALSE drops the top-level part of the tree if possible.

keep.class logical. For classed objects: Should the class be retained?

regex logical. Should regular expression search be used on the list names, or only exact matches?

... further arguments to **grep** (if **regex = TRUE**).

Details

A list is made up of regular and irregular elements. *collapse* defines regular elements as all elements that are either atomic or a list (see [is.regular](#)). `reg_elem` with `recursive = TRUE` therefore extracts the subset of the list tree leading up to atomic elements in the final nodes. This part of the list tree is unlistable - calling `is.unlistable(reg_elem(l))` will be `TRUE` for all lists `l`. Conversely, all elements left behind by `reg_elem` will be picked up by `irreg_elem` (if available). Thus `is.unlistable(irreg_elem(l))` is always `FALSE` for lists with irregular elements (otherwise `irreg_elem` returns an empty list).

If `keep.tree = TRUE`, `reg_elem`, `irreg_elem` and `get_elem` always return the entire list tree, but cut off all of the branches not leading to the desired result. If `keep.tree = FALSE`, top-level parts of the tree are omitted so far this is possible. For example in a nested list with three levels and one data-matrix in one of the final branches, `get_elem(l, is.matrix, keep.tree = TRUE)` will return a list (`lres`) of depth 3, from which the matrix can be accessed as `lres[[1]][[1]][[1]]`. This however does not make much sense. `get_elem(l, is.matrix, keep.tree = FALSE)` will therefore figure out that it can drop the entire tree and return just the matrix. `keep.tree = FALSE` makes additional optimizations if matching elements are at far-apart corners in a nested structure, by only preserving the hierarchy if elements are above each other on the same branch. Thus for a list `l <- list(list(2, list("a", 1)), list(1, list("b", 2)))` calling `get_elem(l, is.character)` will just return `list("a", "b")`.

See Also

[List Processing, Collapse Overview](#)

Examples

```
m <- qM(mtcars)
get_elem(list(list(list(m))), is.matrix)
get_elem(list(list(list(m))), is.matrix, keep.tree = TRUE)

l <- list(list(2, list("a", 1)), list(1, list("b", 2)))
has_elem(l, is.logical)
has_elem(l, is.numeric)
get_elem(l, is.character)
get_elem(l, is.character, keep.tree = TRUE)

l <- lm(mpg ~ cyl + vs, data = mtcars)
str(reg_elem(l))
str(irreg_elem(l))
get_elem(l, is.matrix)
get_elem(l, "residuals")
get_elem(l, "fit", regex = TRUE)
has_elem(l, "tol")
get_elem(l, "tol")
```

is.regular, is.unlistable

Regular Objects and Unlistable Lists

Description

In *collapse* a regular R object is defined as an R object that is either atomic or a list - checked with `is.regular`. A (nested) list composed of regular objects at each level is unlistable - checked with `is.unlistable`.

Usage

```
is.regular(x)
is.unlistable(l, DF.as.list = TRUE)
```

Arguments

<code>x</code>	an R object.
<code>l</code>	a list.
<code>DF.as.list</code>	logical. TRUE treats data frames like (sub-)lists; FALSE like atomic elements.

Details

`is.regular` is simply defined as `is.atomic(x) || is.list(x)`. `is.unlistable` is defined as `all(rapply(l, is.atomic))`. If `l` contains data frames, setting `DF.as.list = FALSE` yields checking using `all(unlist(rapply2d(l, is.regular)))`, which can be a lot faster than applying `is.atomic` to every data frame column.

Value

logical(1) - TRUE or FALSE.

See Also

[ldepth](#), [has_elem](#), [List Processing](#), [Collapse Overview](#)

Examples

```
is.regular(list(1,2))
is.regular(2)
is.regular(a ~ c)
l <- list(1, 2, list(3, 4, "b", FALSE))
is.regular(l)
is.unlistable(l)
l <- list(1, 2, list(3, 4, "b", FALSE, e ~ b))
is.regular(l)
is.unlistable(l)
```

`ldepth`*Determine the Depth / Level of Nesting of a List*

Description

`ldepth` provides the depth of a list or list-like structure.

Usage

```
ldepth(l, DF.as.list = TRUE)
```

Arguments

`l` a list.
`DF.as.list` logical. TRUE treats data frames like (sub-)lists; FALSE like atomic elements.

Details

The depth or level or nesting of a list or list-like structure (e.g. a classed object) is found by recursing down to the bottom of the list and adding an integer count of 1 for each level passed. For example the depth of a data frame is 1. If a data frame has list-columns, the depth is 2. However for reasons of efficiency, if `l` is not a data frame and `DF.as.list = TRUE`, data frames found inside `l` will not be checked for list column's but assumed to have a depth of 1.

Value

A single integer indicating the depth of the list.

See Also

[is.unlistable](#), [has_elem](#), [List Processing](#), [Collapse Overview](#)

Examples

```
l <- list(1, 2)
ldepth(l)
l <- list(1, 2, mtcars)
ldepth(l)
ldepth(l, DF.as.list = FALSE)
l <- list(1, 2, list(4, 5, list(6, mtcars)))
ldepth(l)
ldepth(l, DF.as.list = FALSE)
```

psacf

*Auto- and Cross- Covariance and Correlation Function Estimation for Panel Series***Description**

psacf, pspacf and pscf compute (and by default plot) estimates of the auto-, partial auto- and cross- correlation or covariance functions for panel-vectors and `plm::pseries`. They are analogues to `stats::acf`, `stats::pacf` and `stats::ccf`.

Usage

```
psacf(x, ...)
pspacf(x, ...)
psccf(x, y, ...)

## Default S3 method:
psacf(x, g, t = NULL, lag.max = NULL, type = c("correlation", "covariance", "partial"),
      plot = TRUE, gscale = TRUE, ...)
## Default S3 method:
pspacf(x, g, t = NULL, lag.max = NULL, plot = TRUE, gscale = TRUE, ...)
## Default S3 method:
psccf(x, y, g, t = NULL, lag.max = NULL, type = c("correlation", "covariance"),
      plot = TRUE, gscale = TRUE, ...)

## S3 method for class 'pseries'
psacf(x, lag.max = NULL, type = c("correlation", "covariance", "partial"),
      plot = TRUE, gscale = TRUE, ...)
## S3 method for class 'pseries'
pspacf(x, lag.max = NULL, plot = TRUE, gscale = TRUE, ...)
## S3 method for class 'pseries'
psccf(x, y, lag.max = NULL, type = c("correlation", "covariance"),
      plot = TRUE, gscale = TRUE, ...)

## S3 method for class 'data.frame'
psacf(x, by, t = NULL, cols = is.numeric, lag.max = NULL,
      type = c("correlation", "covariance", "partial"), plot = TRUE, gscale = TRUE, ...)
## S3 method for class 'data.frame'
pspacf(x, by, t = NULL, cols = is.numeric, lag.max = NULL,
      plot = TRUE, gscale = TRUE, ...)

## S3 method for class 'pdata.frame'
psacf(x, cols = is.numeric, lag.max = NULL,
      type = c("correlation", "covariance", "partial"), plot = TRUE, gscale = TRUE, ...)
## S3 method for class 'pdata.frame'
pspacf(x, cols = is.numeric, lag.max = NULL, plot = TRUE, gscale = TRUE, ...)
```


Arguments

<code>x, y</code>	a numeric vector, panel series (<code>plm::pseries</code>), data frame or panel data-frame (<code>plm::pdata.frame</code>).
<code>g</code>	a factor, GRP object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a GRP object) used to group <code>x, y</code> .
<code>by</code>	<i>data.frame method</i> : Same input as <code>g</code> , but also allows one- or two-sided formulas using the variables in <code>x</code> , i.e. <code>~ idvar</code> or <code>var1 + var2 ~ idvar1 + idvar2</code> .
<code>t</code>	same input as <code>g</code> , to indicate the time-variable. For secure computations on un-ordered panel-vectors. Data frame method also allows one-sided formula i.e. <code>~time</code> .
<code>cols</code>	<i>data.frame method</i> : Select columns using a function, column names, indices or a logical vector. <i>Note</i> : <code>cols</code> is ignored if a two-sided formula is passed to <code>by</code> .
<code>lag.max</code>	integer. Maximum lag at which to calculate the acf. Default is $2 \times \sqrt{\text{length}(x) / \text{ng}}$ where <code>ng</code> is the number of groups in the panel series / supplied to <code>g</code> .
<code>type</code>	character. String giving the type of acf to be computed. Allowed values are "correlation" (the default), "covariance" or "partial".
<code>plot</code>	logical. If TRUE (default) the acf is plotted.
<code>gscale</code>	logical. Do a groupwise scaling / standardization of <code>x, y</code> (using fscale and the groups supplied to <code>g</code>) before computing panel-autocovariances / correlations. See Details.
<code>...</code>	further arguments to be passed to <code>stats:::plot.acf</code> .

Details

If `gscale = TRUE` data are standardized within each group (using [fscale](#)) such that the group-mean is 0 and the group-standard deviation is 1. This is strongly recommended for most panels to get rid of individual-specific heterogeneity which would corrupt the ACF computations.

After scaling, `psacf`, `pspacf` and `psccf` compute the ACF/CCF by creating a matrix of panel-lags of the series using [flag](#) and then correlating this matrix with the series (`x, y`) using `stats::cor` and pairwise-complete observations. This may require a lot of memory on large data, but is done because passing a sequence of lags to [flag](#) and thus calling [flag](#) and `stats::cor` one time is much faster than calling them `lag.max` times. The partial ACF is computed from the ACF using a Yule-Walker decomposition, in the same way as in `stats::pacf`.

Value

An object of class 'acf', see `?stats::acf`. The result is returned invisibly if `plot = TRUE`.

Note

For `plm::pseries` and `plm::pdata.frame`, the first index variable is assumed to be the group-id and the second the time variable. If more than 2 index variables are attached to `plm::pseries`, the last one is taken as the time variable and the others are taken as group-id's and interacted.

The `pdata.frame` method only works for properly subsetted objects of class 'pdata.frame'. A list of 'pseries' will not work.

See Also

[Time Series and Panel Series, Collapse Overview](#)

Examples

```
## World Development Panel Data
head(wlddev)
psacf(wlddev$PCGDP, wlddev$country, wlddev$year)
psacf(wlddev, PCGDP ~ country, ~year)
psacf(wlddev$PCGDP, wlddev$country)
pspacf(wlddev$PCGDP, wlddev$country)
psccf(wlddev$PCGDP, wlddev$LIFEEX, wlddev$country)

psacf(wlddev, PCGDP + LIFEEX + ODA ~ country, ~year)
psacf(wlddev, ~ country, ~year, c(9:10,12))
pspacf(wlddev, ~ country, ~year, c(9:10,12))

## Using plm:
pwldev <- plm::pdata.frame(wlddev, index = c("country", "year")) # Creating a Panel Data Frame
PCGDP <- pwldev$PCGDP # Panel Series of GDP per Capita
LIFEEX <- pwldev$LIFEEX # Panel Series of Life Expectancy
psacf(PCGDP) # Same as above, more parsimonious
pspacf(PCGDP)
psccf(PCGDP, LIFEEX)
psacf(pwldev[c(9:10,12)])
pspacf(pwldev[c(9:10,12)])
```

psmat

Matrix / Array from Panel Series

Description

psmat efficiently expands a panel-vector or plm::pseries into a matrix. If a data frame or plm::pdata.frame is passed, psmat returns (default) a 3D array or a list of matrices.

Usage

```
psmat(x, ...)

## Default S3 method:
psmat(x, g, t = NULL, transpose = FALSE, ...)

## S3 method for class 'pseries'
psmat(x, transpose = FALSE, ...)

## S3 method for class 'data.frame'
psmat(x, by, t = NULL, cols = NULL, transpose = FALSE, array = TRUE, ...)
```

```
## S3 method for class 'pdata.frame'
psmat(x, cols = NULL, transpose = FALSE, array = TRUE, ...)

## S3 method for class 'psmat'
plot(x, legend = FALSE, colours = legend, labs = NULL, ...)
```

Arguments

<code>x</code>	a vector, panel series (<code>plm::pseries</code>), data frame or panel data frame (<code>plm::pdata.frame</code>).
<code>g</code>	a factor, GRP object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a GRP object) used to group <code>x</code> . If the panel is balanced an integer indicating the number of groups can also be supplied. See Examples.
<code>by</code>	<i>data.frame method</i> : Same input as <code>g</code> , but also allows one- or two-sided formulas using the variables in <code>x</code> , i.e. <code>~ idvar</code> or <code>var1 + var2 ~ idvar1 + idvar2</code> .
<code>t</code>	same inputs as <code>g</code> , to indicate the time-variable or second identifier(s). <code>g</code> and <code>t</code> together should fully identify the panel. If <code>t = NULL</code> , the data is assumed sorted and <code>seq_col</code> is used to generate rownames for the output matrix.
<code>cols</code>	<i>data.frame method</i> : Select columns using a function, column names, indices or a logical vector. <i>Note</i> : <code>cols</code> is ignored if a two-sided formula is passed to <code>by</code> .
<code>transpose</code>	logical. TRUE generates the matrix such that <code>g/by</code> -> columns, <code>t</code> -> rows. Default is <code>g/by</code> -> rows, <code>t</code> -> columns.
<code>array</code>	<i>data.frame / pdata.frame methods</i> : logical. TRUE returns a 3D array (if just one column is selected a matrix is returned). FALSE returns a list of matrices.
<code>...</code>	arguments to be passed to or from other methods, or for the plot method additional arguments passed to <code>ts.plot</code> .
<code>legend</code>	logical. Automatically create a legend of panel-groups.
<code>colours</code>	logical. Automatically colour by panel-groups.
<code>labs</code>	character. Provide a character-vector of variable labels / series titles when plotting an array.

Details

For `plm::pseries`, the first index variable is taken to be the group-id and the second the time variable. If more than 2 index variables are attached to `plm::pseries`, the last one is taken as the time variable and the others are taken as group-id's and interacted.

Value

A matrix or 3D array containing the data in `x`, where by default the rows constitute the groups-ids (`g/by`) and the columns the time variable or individual ids (`t`). 3D arrays contain the variables in the 3rd dimension. The objects have a class 'psmat', and also a 'transpose' attribute indicating whether `transpose = TRUE`.

Note

The `pdata.frame` method only works for properly subsetting objects of class `'pdata.frame'`. A list of `'series'` won't work. There also exist simple `aperm` and `[]` (subset) methods for `'psmat'` objects. These differ from the default methods only by keeping the class and the `'transpose'` attribute.

See Also

[Time Series and Panel Series, Collapse Overview](#)

Examples

```
## World Development Panel Data
head(wlddev) # View data
qsu(wlddev, pid = ~ iso3c, cols = 9:12, vlabels = TRUE) # Summarizing data
str(psmat(wlddev$PCGDP, wlddev$iso3c, wlddev$year)) # Generating matrix of GDP
r <- psmat(wlddev, PCGDP ~ iso3c, ~ year) # Same thing using data.frame method
plot(r, main = vlabels(wlddev)[9], xlab = "Year") # Plot the matrix
str(r) # See structure
str(psmat(wlddev$PCGDP, wlddev$iso3c)) # The Data is sorted, could omit t
str(psmat(wlddev$PCGDP, 216)) # This panel is also balanced, so
# ..indicating the number of groups would be sufficient to obtain a matrix

ar <- psmat(wlddev, ~ iso3c, ~ year, 9:12) # Get array of transposed matrices
str(ar)
plot(ar)
plot(ar, legend = TRUE)
plot(psmat(collap(wlddev, ~region+year, cols = 9:12), # More legible and fancy plot
         ~region, ~year), legend = TRUE,
      labs = vlabels(wlddev)[9:12])

psml <- psmat(wlddev, ~ iso3c, ~ year, 9:12, array = FALSE) # This gives list of ps-matrices
head(unlist2d(psml, "Variable", "Country", id.factor = TRUE), 2) # Using unlist2d, can generate DF

## Using plm simplifies things
pwlddev <- plm::pdata.frame(wlddev, index = c("iso3c", "year")) # Creating a Panel Data Frame
PCGDP <- pwlddev$PCGDP # A panel-Series of GDP per Capita
head(psmat(PCGDP), 2) # Same as above, more parsimonious
plot(psmat(PCGDP))
plot(psmat(pwlddev[9:12]))
plot(psmat(G(pwlddev[9:12]))) # Here plotting panel- growth rates
```

pwcov, pwcov, pwNobs *Pairwise Correlations, Covariances and Observation Count*

Description

Computes (pairwise) Pearson's correlations, covariances and observation counts. Pairwise correlations and covariances can be computed together with observation counts and p-values, and output

as 3D array (default) or list of matrices. pwcov and pwcov offer an elaborate print method. For an equivalent and faster implementation of pwcov see `Hmisc::rcorr` (written in Fortran), for weighted correlations see `weights::wtd.cors` (written in C).

Usage

```
pwcov(X, ..., N = FALSE, P = FALSE, array = TRUE, use = "pairwise.complete.obs")
```

```
pwcov(X, ..., N = FALSE, P = FALSE, array = TRUE, use = "pairwise.complete.obs")
```

```
pwNobs(X)
```

```
## S3 method for class 'pwcov'
print(x, digits = 2L, sig.level = 0.05, show = c("all", "lower.tri", "upper.tri"),
      spacing = 1L, ...)
```

```
## S3 method for class 'pwcov'
print(x, digits = 2L, sig.level = 0.05, show = c("all", "lower.tri", "upper.tri"),
      spacing = 1L, ...)
```

Arguments

X	a matrix or data.frame, for pwcov and pwcov all columns must be numeric. All functions are faster on matrices, so converting is advised for large data (see qM).
x	an object of class 'pwcov' / 'pwcov'.
N	logical. TRUE also computes pairwise observation counts.
P	logical. TRUE also computes pairwise p-values (same as cor.test and <code>Hmisc::rcorr</code>).
array	logical. If N = TRUE or P = TRUE, TRUE (default) returns output as 3D array whereas FALSE returns a list of matrices.
use	argument passed to cor / cov . If use != "pairwise.complete.obs", <code>sum(complete.cases(X))</code> is used for N, and p-values are computed accordingly.
digits	integer. The number of digits to round to in print.
sig.level	numeric. P-value threshold below which a '*' is displayed above significant coefficients if P = TRUE.
show	character. The part of the correlation / covariance matrix to display.
spacing	integer. Controls the spacing between different reported quantities in the print-out of the matrix: 0 - compressed, 1 - single space, 2 - double space.
...	other arguments passed to cor or cov . Only sensible if P = FALSE.

Value

a numeric matrix, 3D array or list of matrices with the computed statistics. For pwcov and pwcov the object has a class 'pwcov' and 'pwcov', respectively.

See Also

[qsu, Summary Statistics, Collapse Overview](#)

Examples

```
mna <- na_insert(mtcars)
pwcov(mna)
pwcov(mna)
pwNobs(mna)
pwcov(mna, N = TRUE)
pwcov(mna, P = TRUE)
pwcov(mna, N = TRUE, P = TRUE)
aperm(pwcov(mna, N = TRUE, P = TRUE))
print(pwcov(mna, N = TRUE, P = TRUE), digits = 3, sig.level = 0.01, show = "lower.tri")
pwcov(mna, N = TRUE, P = TRUE, array = FALSE)
print(pwcov(mna, N = TRUE, P = TRUE, array = FALSE), show = "lower.tri")
```

qF, qG, finteraction *Fast Factor Generation, Interactions and Vector Grouping*

Description

qF, shorthand for 'quick-factor' implements very fast (ordered) factor generation from atomic vectors using either radix ordering or index hashing.

qG, shorthand for 'quick-group', generates a kind of factor-light without the levels attribute but instead an attribute providing the number of levels. Optionally the levels / groups can be attached, but without converting them to character. Objects have a class 'qG'.

finteraction generates a factor by interacting multiple vectors or factors. In that process missing values are always replaced with a level and unused levels are always dropped.

Usage

```
qF(x, ordered = FALSE, na.exclude = TRUE, sort = TRUE, drop = FALSE,
    keep.attr = TRUE, method = c("auto", "radix", "hash"))
```

```
qG(x, ordered = FALSE, na.exclude = TRUE, sort = TRUE,
    return.groups = FALSE, method = c("auto", "radix", "hash"))
```

```
is.qG(x)
```

```
as.factor_qG(x, ordered = FALSE, na.exclude = TRUE)
```

```
finteraction(..., ordered = FALSE, sort = TRUE)
```

Arguments

x	a atomic vector, factor or quick-group.
ordered	logical. Adds a class 'ordered'.
na.exclude	logical. TRUE preserves missing values (i.e. no level is generated for NA).
sort	logical. TRUE sorts the levels in ascending order (like <code>factor</code>); FALSE provides the levels in an arbitrary order (determined by the hash map if method = "hash"), which can be slightly faster.
drop	logical. If x is a factor, TRUE efficiently drops unused factor levels beforehand using <code>fdroplevels</code> .
keep.attr	logical. If TRUE and x has additional attributes apart from 'levels' and 'class', these are preseved in the conversion to factor.
method	an integer or character string specifying the method of computation:

<i>Int.</i>	<i>String</i>	<i>Description</i>
1	"auto"	automatic selection: hash for character, logical or if <code>length(x) < 500</code> , else radix.
2	"radix"	use radix ordering to generate factors. See Details.
3	"hash"	use index hashing to generate factors. See Details.

return.groups	logical. TRUE returns the unique elements / groups / levels of x in an attribute called 'groups'. Unlike qF, they are not converted to character.
...	multiple atomic vectors or factors, or a single list of equal-length vectors or factors. See Details.

Details

These functions are quite important. Whenever a vector is passed to a *collapse* function such as `fmean(mtcars,mtcars$ cyl)`, is is grouped using qF or qG.

qF is a combination of `as.factor` and `factor`. Applying it to a vector i.e. `qF(x)` gives the same result as `as.factor(x)`. `qF(x, ordered = TRUE)` generates an ordered factor (same as `factor(x, ordered = TRUE)`), and `qF(x, na.exclude = FALSE)` generates a level for missing values (same as `factor(x, exclude = NULL)`). An important addition is that `qF(x, na.exclude = FALSE)` also adds a class 'na.included'. This prevents *collapse* functions from checking missing values in the factor, and is thus computationally more efficient. Therefore factors used in grouped operations should preferably be generated using `qF(x, na.exclude = FALSE)`. Setting `sort = FALSE` gathers the levels in a random order (unless `method = "radix"` and x is numeric, in which case the levels are always sorted). This can provide a speed improvement, particularly for character data.

There are two methods of computation: radix ordering and index hashing. Radix ordering is done through combining the functions `radixorder` and `groupid`. It is generally faster than index hashing for large numeric data (although there are exceptions). Index hashing is done using `Rcpp::sugar::sort_unique` and `Rcpp::sugar::match`. It is generally faster for character data. For logical data, a super fast one-pass method was written which is subsumed in the hash method. Regarding speed: In general qF is around 5x faster than `as.factor` on character data and about 30x faster on numeric data. Automatic method dispatch typically does a good job delivering optimal performance.

qG is in the first place a programmers function. It generates a factor-'light' consisting of only an integer grouping vector and an attribute providing the number of groups. It is faster and more memory efficient than [GRP](#) for grouping atomic vectors, which is the main reason it exists. The fact that it (optionally) returns the unique groups / levels without converting them to character is an added bonus (this also provides a small performance gain compared to qF).

finteraction is simply a wrapper around `as.factor_GRP(GRP.default(X, sort = TRUE))`, where X is replaced by the arguments in `'...'` combined in a list. See [GRP](#) for computational details. In general: All vectors, factors, or lists of vectors / factors passed can be interacted. Interactions always create a level for missing values and always drop any unused levels.

Value

qF returns an (ordered) factor. qG returns an object of class 'qG': an integer grouping vector with an attribute 'N.groups' indicating the number of groups, and, if `return.groups = TRUE`, an attribute 'groups' containing the vector of unique groups / elements in x corresponding to the integer-id.

Note

Neither qF nor qG can reorder groups / factor levels. These objects can however be converted into one another using qF/qG or the direct method `as.factor_qG`, and it is also possible to add a class 'ordered' (`ordered = TRUE`) and to create an extra level / integer for missing values (`na.exclude = FALSE`).

See Also

[groupid](#), [GRP](#), [Fast Grouping and Ordering](#), [Collapse Overview](#)

Examples

```
cylF <- qF(mtcars$cyl)      # Factor from atomic vector
cylG <- qG(mtcars$cyl)     # Quick-group from atomic vector
cylG                        # See the simple structure of this object

cf <- qF(wlddev$country)   # Bigger data
cf2 <- qF(wlddev$country, na.exclude = FALSE) # With na.included class
dat <- num_vars(wlddev)

# cf2 is faster in grouped operations because no missing value check is performed
library(microbenchmark)
microbenchmark(fmax(dat, cf), fmax(dat, cf2))

finteraction(mtcars$cyl, mtcars$vs) # Interacting two variables (can be factors)
head(finteraction(mtcars))        # A more crude example..
```

qsu *Fast (Grouped, Weighted) Summary Statistics for Cross-Sectional and Panel Data*

Description

qsu, shorthand for quick-summary, is an extremely fast summary command inspired by the (xt)summarize command in the STATA statistical software.

It computes a set of 7 statistics (nobs, mean, sd, min, max, skewness and kurtosis) using a numerically stable one-pass method generalized from Welford's Algorithm. Statistics can be computed weighted, by groups, and also within-and between entities (for panel data, see Details).

Usage

```
qsu(x, ...)

## Default S3 method:
qsu(x, g = NULL, pid = NULL, w = NULL, higher = FALSE, array = TRUE, ...)

## S3 method for class 'matrix'
qsu(x, g = NULL, pid = NULL, w = NULL, higher = FALSE, array = TRUE, ...)

## S3 method for class 'data.frame'
qsu(x, by = NULL, pid = NULL, w = NULL, cols = NULL,
    higher = FALSE, array = TRUE, vlabels = FALSE, ...)

# Methods for compatibility with plm:

## S3 method for class 'pseries'
qsu(x, g = NULL, w = NULL, effect = 1L, higher = FALSE, array = TRUE, ...)

## S3 method for class 'pdata.frame'
qsu(x, by = NULL, w = NULL, cols = NULL, effect = 1L,
    higher = FALSE, array = TRUE, vlabels = FALSE, ...)

## S3 method for class 'qsu'
print(x, digits = 4, nonsci.digits = 9, na.print = "-",
    return = FALSE, print.gap = 2, ...)
```

Arguments

- x a vector, matrix, data frame, panel series (plm::pseries) or panel data frame (plm::pdata.frame).
- g a factor, GRP object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a GRP object) used to group x.

by	<i>(p)data.frame method</i> : Same as g, but also allows one- or two-sided formulas i.e. \sim group1 + group2 or var1 + var2 \sim group1 + group2. See Examples.
pid	same input as g/by: Specify a panel-identifier to also compute statistics on between- and within- transformed data. Data frame method also supports one- or two-sided formulas. Transformations are taken independently from grouping with g/by (grouped statistics are computed on the transformed data if g/by is also used). However, passing any LHS variables to pid will overwrite any LHS variables passed to by.
w	a vector of (non-negative) weights. Adding weights will compute the weighted mean, sd, skewness and kurtosis, and transform the data using weighted individual means if pid is used.
cols	select columns to summarize using column names, indices, a logical vector or a function (i.e. <code>is.numeric</code>). Two-sided formulas passed to by or pid overwrite cols.
higher	logical. Add higher moments (skewness and kurtosis).
array	logical. If computations have more than 2 dimensions (up to a maximum of 4D: variables, statistics, groups and panel-decomposition) output to array, else output (nested) list of matrices.
vlabels	logical. Use variable labels in the summary. See vlabels .
effect	<i>plm</i> methods: Select which panel identifier should be used for between and within transformations of the data. 1L takes the first variable in the <code>plm::index</code> , 2L the second etc.. Index variables can also be called by name using a character string. More than one variable can be supplied.
...	arguments to be passed to or from other methods.
digits	the number of digits to print after the comma/dot.
nonsci.digits	the number of digits to print before resorting to scientific notation (default is to print out numbers with up to 9 digits and print larger numbers scientifically).
na.print	character string to substitute for missing values.
return	logical. Don't print but instead return the formatted object.
print.gap	integer. Spacing between printed columns. Passed to <code>print.default</code> .

Details

The algorithm used to compute statistics is well described [here](#) [see sections *Welford's online algorithm*, *Weighted incremental algorithm* and *Higher-order statistics*. Skewness and kurtosis are calculated as described in *Higher-order statistics* and are mathematically identical to those implemented in the *moments* package. Just note that `qsu` computes the kurtosis (like `moments::kurtosis`), not the excess-kurtosis (= kurtosis - 3) defined in *Higher-order statistics*. The *Weighted incremental algorithm* described can easily be generalized to higher-order statistics].

Grouped computations specified with `g/by` are carried out extremely efficiently as in `fsum` (in a single pass, without splitting the data).

If `pid` is used, `qsu` performs a panel-decomposition of each variable and computes 3 sets of statistics: Statistics computed on the 'Overall' (raw) data, statistics computed on the 'Between' - transformed (`pid` - averaged) data, and statistics computed on the 'Within' - transformed (`pid` - demeaned) data.

More formally, let x (bold) be a panel vector of data for N individuals indexed by i , recorded for T periods, indexed by t . x_{it} then denotes a single data-point belonging to individual i in time-period t (t/T must not represent time). Then $x_{i.}$ denotes the average of all values for individual i (averaged over t), and by extension $xN.$ is the vector (length N) of such averages for all individuals. If no groups are supplied to `g/by`, the 'Between' statistics are computed on $xN.$, the vector of individual averages. (This means that for a non-balanced panel or in the presence of missing values, the 'Overall' mean computed on x can be slightly different than the 'Between' mean computed on $xN.$). If groups are supplied to `g/by`, $xN.$ is expanded to the vector $x_{i.}$ (length $N \times T$) by replacing each value x_{it} in x with $x_{i.}$, while preserving missing values in x . Grouped Between-statistics are then computed on $x_{i.}$, with the only difference that the number of observations ('Between-N') reported for each group is the number of distinct non-missing values of $x_{i.}$ in each group (not the total number of non-missing values of $x_{i.}$ in each group, which is already reported in 'Overall-N'). 'Within' statistics are always computed on the vector $x - x_{i.} + x_{..}$, where $x_{..}$ is simply the 'Overall' mean computed from x , which is added back to preserve the level of the data. The 'Within' mean computed on this data will always be identical to the 'Overall' mean. In the summary output, `qsu` reports not 'N', which would be identical to the 'Overall-N', but 'T', the average number of time-periods of data available for each individual obtained as `'T' = 'Overall-N' / 'Between-N'`. See Examples.

Apart from 'N/T' and the extrema, the standard-deviations ('SD') computed on between- and within- transformed data are extremely valuable because they indicate how much of the variation in a panel-variable is between-individuals and how much of the variation is within-individuals (over time). At the extremes, variables that have common values across individuals (such as the time-variable 't' in a balanced panel), can readily be identified as individual-invariant because the 'Between-SD' on this variable is 0 and the 'Within-SD' is equal to the 'Overall-SD'. Analogous, time-invariant individual characteristics (such as the individual-id 'i') have a 0 'Within-SD' and a 'Between-SD' equal to the 'Overall-SD'.

`qsu` comes with it's own print method which by default writes out up to 9 digits at 4 decimal places. Larger numbers are printed in scientific format. for numbers between 7 and 9 digits, a comma ',' is placed after the 6th digit to designate the millions. Missing values are printed using '-'.

Value

A vector, matrix, array or list of matrices of summary statistics. All matrices and arrays have a class 'qsu' and a class 'table' attached.

Note

If weights w are used together with `pid`, transformed data is computed using weighted individual means i.e. weighted $x_{i.}$ and weighted $x_{..}$. Weighted statistics are subsequently computed on this weighted-transformed data.

References

Welford, B. P. (1962). Note on a method for calculating corrected sums of squares and products. *Technometrics*. 4 (3): 419-420. doi:10.2307/1266577.

See Also

[descr](#), [pwcov](#), [Fast Statistical Functions](#), [Collapse Overview](#)

Examples

```
## World Development Panel Data
# Simple Summaries -----
qsu(wlddev) # Simple summary
qsu(wlddev, vlabels = TRUE) # Display variable labels
qsu(wlddev, higher = TRUE) # Add skewness and kurtosis

# Grouped Summaries -----
qsu(wlddev, ~ region, vlabels = TRUE) # Statistics by World Bank Region
qsu(wlddev, PCGDP + LIFEEEX ~ income) # Summarize GDP per Capita and Life Expectancy by
stats <- qsu(wlddev, ~ region + income, # World Bank Income Level
            cols = 9:10, higher = TRUE) # Same variables, by both region and income
aperm(stats) # A different perspective on the same stats

# Panel Data Summaries -----
qsu(wlddev, pid = ~ iso3c, vlabels = TRUE) # Adding between and within countries statistics
# -> They show amongst other things that year and decade are individual-invariant,
# that we have GINI-data on only 161 countries, with only 8.42 observations per country on average,
# and that GDP, LIFEEEX and GINI vary more between-countries, but ODA received varies more within
# countries over time.

# Using plm:
pwldev <- plm::pdata.frame(wlddev, # Creating a Panel Data Frame from this data
                          index = c("iso3c", "year"))
qsu(pwldev) # Summary for pdata.frame -> qsu(wlddev, pid = ~ iso3c)
qsu(pwldev$PCGDP) # Default summary for Panel Series (class pseries)
qsu(G(pwldev$PCGDP)) # Summarizing GDP growth, see also ?G

# Grouped Panel Data Summaries -----
qsu(wlddev, ~ region, ~ iso3c, cols = 9:12) # Panel-Statistics by region
psr <- qsu(pwldev, ~ region, cols = 9:12) # Same on plm pdata.frame
psr # -> Gives a 4D array
print.qsu(psr[, "N/T", ,]) # Checking out the number of observations:
# In North America we only have 3 countries, for the GINI we only have 3.91 observations on average
# for 45 Sub-Saharan-African countries, etc..
print.qsu(psr[, "SD", ,]) # Considering only standard deviations
# -> In all regions variations in inequality (GINI) between countries are greater than variations
# in inequality within countries. The opposite is true for Life-Expectancy in all regions apart
# from Europe, etc..
psrl <- qsu(wlddev, ~ region, ~ iso3c, # Same, but output as nested list
            cols = 9:12, array = FALSE)
psrl # We can use unlist2d to create a tidy data.frame
head(unlist2d(psrl, c("Variable", "Trans"),
              row.names = "Region"))

# Weighted Summaries -----
n <- nrow(wlddev)
weights <- abs(rnorm(n)) # Generate random weights
qsu(wlddev, w = weights, higher = TRUE) # Computed weighted mean, SD, skewness and kurtosis
weightsNA <- weights # Weights may contain missing values.. inserting 1000
weightsNA[sample.int(n, 1000)] <- NA
```

```
qsu(wlddev, w = weightsNA, higher = TRUE) # But now these values are removed from all variables
# Grouped and panel-summaries can also be weighted in the same manor
```

radixorder *Fast Radix-Based Ordering*

Description

A slight modification of `base::order(..., method = "radix")` that is more programmer friendly and, importantly, provides features for ordered grouping of data (similar to `data.table::forderv` which has more or less the same source code). `radixorderv` is a programmers version directly supporting vector and list input.

Usage

```
radixorder(..., na.last = TRUE, decreasing = FALSE, starts = FALSE,
            group.sizes = FALSE, sort = TRUE)

radixorderv(x, na.last = TRUE, decreasing = FALSE, starts = FALSE,
            group.sizes = FALSE, sort = TRUE)
```

Arguments

<code>...</code>	comma-separated atomic vectors to order.
<code>x</code>	an atomic vector or list of atomic vectors such as a data frame.
<code>na.last</code>	logical. for controlling the treatment of NA's. If TRUE, missing values in the data are put last; if FALSE, they are put first; if NA, they are removed.
<code>decreasing</code>	logical. Should the sort order be increasing or decreasing? Can be a vector of length equal to the number of arguments in <code>... / x</code> .
<code>starts</code>	logical. TRUE returns an attribute 'starts' containing the first element of each new group i.e. the row denoting the start of each new group if the data were sorted using the computed ordering vector. See Examples.
<code>group.sizes</code>	logical. TRUE returns an attribute 'group.sizes' containing sizes of each group in the same order as groups are encountered if the data were sorted using the computed ordering vector. See Examples.
<code>sort</code>	logical. This argument only affects character vectors / columns passed. If FALSE, these are not ordered but simply grouped in the order of first appearance of unique elements. This provides a slight performance gain if only grouping but not alphabetic ordering is required.

Value

An integer ordering vector with attributes: Unless `na.last = NA` an attribute 'sorted' indicating whether the input data was already sorted is attached. If `starts = TRUE`, 'starts' giving a vector of group starts in the ordered data, and if `group.sizes = TRUE`, 'group.sizes' giving the vector of group sizes are attached. In either case an attribute 'maxgrpn' providing the size of the largest group is also attached.

See Also

[Fast Grouping and Ordering, Collapse Overview](#)

Examples

```
radixorder(mtcars$mpg)
head(mtcars[radixorder(mtcars$mpg), ])
radixorder(mtcars$cyl, mtcars$vs)

o <- radixorder(mtcars$cyl, mtcars$vs, starts = TRUE)
st <- attr(o, "starts")
head(mtcars[o, ])
mtcars[o[st], c("cyl", "vs")] # Unique groups

# Note that if attr(o, "sorted") == TRUE, then all(o[st] == st)
radixorder(rep(1:3, each = 3), starts = TRUE)

# Group sizes
radixorder(mtcars$cyl, mtcars$vs, group.sizes = TRUE)

# Both
radixorder(mtcars$cyl, mtcars$vs, starts = TRUE, group.sizes = TRUE)
```

rapply2d

Recursively Apply a Function to a List of Data Objects

Description

rapply2d is a recursive version of lapply with two key differences to [rapply](#): (1) Data frames are considered as final objects, not as (sub-)lists, and (2) the result is never simplified / unlisted.

Usage

```
rapply2d(l, FUN, ...)
```

Arguments

l	a list.
FUN	a function that can be applied to all elements in l.
...	additional elements passed to FUN.

Value

A list of the same structure as l, where FUN was applied to all elements.

See Also

[unlist2d, List Processing, Collapse Overview](#)

Examples

```
l <- list(mtcars, list(mtcars, as.matrix(mtcars)))
rapply2d(l, fmean)
unlist2d(rapply2d(l, fmean))
```

roworder

*Fast Reordering of Data Frame Rows***Description**

A fast substitute for `dplyr::arrange`. It returns a sorted copy of the data frame, unless the data is already sorted in which case no copy is made. In addition, rows can be manually re-ordered. Use `data.table::setorder` to sort a data frame without creating a copy.

Usage

```
roworder(X, ..., na.last = TRUE)
```

```
roworderv(X, cols = NULL, neworder = NULL, decreasing = FALSE,
          na.last = TRUE, pos = c("front", "end", "exchange"))
```

Arguments

<code>X</code>	a data frame or list of equal-length columns.
<code>...</code>	comma-separated columns of <code>X</code> to sort by e.g. <code>var1, var2</code> . Negatives i.e. <code>-var1, var2</code> can be used to sort in decreasing order of <code>var1</code> .
<code>cols</code>	select columns to sort by using a function, column names, indices or a logical vector. The default <code>NULL</code> sorts by all columns in order of occurrence (from left to right).
<code>na.last</code>	logical. If <code>TRUE</code> , missing values in the sorting columns are placed last; if <code>FALSE</code> , they are placed first; if <code>NA</code> they are removed (argument passed to <code>radixorder</code>).
<code>decreasing</code>	logical. Should the sort order be increasing or decreasing? Can also be a vector of length equal to the number of arguments in <code>cols</code> (argument passed to <code>radixorder</code>).
<code>neworder</code>	an ordering vector, can be <code>< nrow(X)</code> . if <code>pos = "front"</code> or <code>pos = "end"</code> , a logical vector can also be supplied. This argument overwrites <code>cols</code> .
<code>pos</code>	integer or character. Different arrangement options if <code>!is.null(neworder) && length(neworder) < nrow(X)</code> .

<i>Int.</i>	<i>String</i>	<i>Description</i>
1	"front"	move rows in <code>neworder</code> to the front (top) of <code>X</code> (the default).
2	"end"	move rows in <code>neworder</code> to the end (bottom) of <code>X</code> .
3	"exchange"	just exchange the order of rows in <code>neworder</code> , other rows remain in the same position.

Value

A copy of X with rows reordered. If X is already sorted, X is simply returned.

Note

If you don't require a copy of the data, use `data.table::setorder` (you can also use it in a piped call as it invisibly returns the data).

See Also

[colorder](#), [fsubset](#), [Fast Grouping and Ordering](#), [Collapse Overview](#).

Examples

```
head(roworder(airquality, Month, -Ozone))
head(roworder(airquality, Month, -Ozone, na.last = NA)) # Removes the missing values in Ozone

## Same in standard evaluation
head(roworder(airquality, c("Month", "Ozone"), decreasing = c(FALSE, TRUE)))
head(roworder(airquality, c("Month", "Ozone"), decreasing = c(FALSE, TRUE), na.last = NA))

## Custom reordering
head(roworder(mtcars, neworder = 3:4)) # Bring rows 3 and 4 to the front
head(roworder(mtcars, neworder = 3:4, pos = "end")) # Bring them to the end
head(roworder(mtcars, neworder = mtcars$vs == 1)) # Bring rows with vs == 1 to the top
```

rsplit

Recursive Splitting

Description

`rsplit` recursively splits a vector or data frame into subsets according to combinations of (multiple) vectors / factors - by default returning a (nested) list. If `flatten = TRUE`, the list is flattened yielding the same result as `split`. `rsplit` is also faster than `split`, particularly for data frames.

Usage

```
rsplit(x, ...)

## Default S3 method:
rsplit(x, fl, drop = TRUE, flatten = FALSE, ...)

## S3 method for class 'data.frame'
rsplit(x, by, drop = TRUE, flatten = FALSE, cols = NULL,
       keep.by = FALSE, simplify = TRUE, ...)
```


Arguments

x	a vector, data.frame or list.
f1	a vector, factor or list of vectors / factors used to split x.
by	<i>data.frame method</i> : Same as f1, but also allows one- or two-sided formulas i.e. <code>~ group1</code> or <code>var1 + var2 ~ group1 + group2</code> . See Examples.
drop	logical. TRUE removes unused levels or combinations of levels from factors before splitting; FALSE retains those combinations yielding empty list elements in the output.
flatten	logical. If f1 is a list of vectors / factors, TRUE calls finteraction on the list, creating a single factor used for splitting; FALSE yields recursive splitting.
cols	<i>data.frame method</i> : Select columns to split using a function, column names, indices or a logical vector. <i>Note</i> : cols is ignored if a two-sided formula is passed to by.
keep.by	logical. If a formula is passed to by, then TRUE preserves the splitting (right-hand-side) variables in the data frame.
simplify	<i>data.frame method</i> : Logical. TRUE calls <code>rsplit.default</code> if a single column is split e.g. <code>rsplit(data, col1 ~ group1)</code> becomes the same as <code>rsplit(data\$col1, data\$group1)</code> .
...	further arguments passed to split .

Value

a (nested) list containing the subsets of x.

See Also

[unlist2d](#), [List Processing](#), [Collapse Overview](#)

Examples

```
rsplit(mtcars$mpg, mtcars$cyl)
rsplit(mtcars, mtcars$cyl)

rsplit(mtcars, mtcars[.c(cyl, vs, am)])
rsplit(mtcars, ~ cyl + vs + am, keep.by = TRUE) # Same thing
rsplit(mtcars, ~ cyl + vs + am)

rsplit(mtcars, ~ cyl + vs + am, flatten = TRUE)

rsplit(mtcars, mpg ~ cyl)
rsplit(mtcars, mpg ~ cyl, simplify = FALSE)
rsplit(mtcars, mpg + hp ~ cyl + vs + am)
rsplit(mtcars, mpg + hp ~ cyl + vs + am, keep.by = TRUE)
```

seqid

*Generate Group-Id from Integer Sequences***Description**

seqid can be used to group sequences of integers in a vector, e.g. `seqid(c(1:3, 5:7))` becomes `c(rep(1, 3), rep(2, 3))`. It also supports increments > 1, unordered sequences, and missing values in the sequence.

Some applications are to facilitate identification of, and grouped operations on, (irregular) time series and panels.

Usage

```
seqid(x, o = NULL, del = 1L, start = 1L, na.skip = FALSE,
      skip.seq = FALSE, check.o = TRUE)
```

Arguments

<code>x</code>	a factor or integer vector. Numeric vectors will be converted to integer i.e. rounded downwards.
<code>o</code>	an (optional) integer ordering vector specifying the order by which to pass through <code>x</code> .
<code>del</code>	integer. The integer delimiting two consecutive points in a sequence. <code>del = 1</code> lets seqid track sequences of the form <code>c(1, 2, 3, ...)</code> , <code>del = 2</code> tracks sequences <code>c(1, 3, 5, ...)</code> etc.
<code>start</code>	integer. The starting value of the resulting sequence id. Default is starting from 1. For C++ programmers, starting from 0 could be a better choice.
<code>na.skip</code>	logical. Skip missing values in the sequence. The default behavior is skipping such that <code>seqid(c(1, NA, 2))</code> is regarded as one sequence and coded as <code>c(1, NA, 1)</code> .
<code>skip.seq</code>	logical. If <code>na.skip = TRUE</code> , this changes the behavior such that missing values are viewed as part of the sequence, i.e. <code>seqid(c(1, NA, 3))</code> is regarded as one sequence and coded as <code>c(1, NA, 1)</code> .
<code>check.o</code>	logical. Programmers option: <code>FALSE</code> prevents checking that each element of <code>o</code> is in the range <code>[1, length(x)]</code> , it only checks the length of <code>o</code> . This gives some extra speed, but will terminate R if any element of <code>o</code> is too large or too small.

Details

seqid was created primarily to deal with problems of computing lagged values, differences and growth rates on irregularly spaced time series and panels (#26). `flag`, `fdiff` and `fgrowth` do not natively support such panels because they do not pre-compute an ordering of the data but directly compute the ordering from the supplied id and time variables while providing errors for gaps and repeated time values. see [flag](#) for computational details.

Fortunately any irregular time series or panel series can be expressed as a regular panel series with a group-id created such that the time-periods within each group are consecutive.

A simple solution to applying existing functionality (`flag`, `fdiff` and `fgrowth`) to irregular time series and panels is thus to create a group-id that fully identifies the data together with the time variable. `seqid` makes this very easy: For an irregular panel with some arbitrary gaps or repeated values in the time variable, an appropriate id variable can be generated using `settransform(data, newid = seqid(time, radixorder(id, time)))`. Lags can then be computed using `L(data, 1, ~newid, ~time)` etc. This way *collapse* maintains a balance between offering very fast computations on regular time series and panels (which may be unbalanced but where observations for each entity are consecutive in time), and flexibility of application.

In general, for any regularly spaced panel the identity given by `identical(groupid(id, order(id, time)), seqid(time, order(id, time)))` should hold.

Regularly spaced panels with gaps in time (such as a panel-survey with measurements every 2 years) can be handled either by `seqid(..., del = gap)` or, in most cases, simply by converting the time variable to factor using `qF`, which will make observations consecutive.

There are potentially other more analytical applications for `seqid...`

For the opposite operation of creating a new time-variable that is consecutive in each group, see `data.table::rowid`.

Value

An integer vector of class 'qG'. See `qG`.

See Also

[groupid](#), [qG](#), [Fast Grouping and Ordering](#), [Collapse Overview](#)

Examples

```
## This creates an irregularly spaced panel, with a gap in time for id = 2
data <- data.frame(id = rep(1:3, each = 4),
                  time = c(1:4, 1:2, 4:5, 1:4),
                  value = rnorm(12))

data
## Not run:
## Gaps in time error
L(data, 1, value ~ id, ~time)

## End(Not run)
## Generating new id variable (here seqid(time) would suffice as data is sorted)
settransform(data, newid = seqid(time, order(id, time)))
data

## Lag the panel
L(data, 1, value ~ newid, ~time)

## A different possibility: Creating a consecutive time variable
settransform(data, newtime = data.table::rowid(id))
data
```

```
L(data, 1, value ~ id, ~newtime)

## With sorted data, the time variable can also just be omitted..
L(data, 1, value ~ id)
```

TRA

*Transform Data by (Grouped) Replacing or Sweeping out Statistics***Description**

TRA is an S3 generic that efficiently transforms data by either (column-wise) replacing data values with supplied statistics or sweeping the statistics out of the data. TRA supports grouped sweeping and replacing operations, and is thus a generalization of [sweep](#).

Usage

```
TRA(x, STATS, FUN = "-", ...)
```

Default S3 method:

```
TRA(x, STATS, FUN = "-", g = NULL, ...)
```

S3 method for class 'matrix'

```
TRA(x, STATS, FUN = "-", g = NULL, ...)
```

S3 method for class 'data.frame'

```
TRA(x, STATS, FUN = "-", g = NULL, ...)
```

S3 method for class 'grouped_df'

```
TRA(x, STATS, FUN = "-", keep.group_vars = TRUE, ...)
```

Arguments

x a atomic vector, matrix, data frame or grouped tibble (`dplyr::grouped_df`).

STATS a matching set of summary statistics. See [Details and Examples](#).

FUN an integer or character string indicating the operation to perform. There are 10 supported operations:

<i>Int.</i>	<i>String</i>	<i>Description</i>
1	"replace_fill"	replace and overwrite missing values in x
2	"replace"	replace but preserve missing values in x
3	"-"	subtract (i.e. center)
4	"-+"	subtract group-statistics but add group-frequency weighted average of group statistics (i.e. center)
5	"/"	divide (i.e. scale. For mean-preserving scaling see also fscale)
6	"%"	compute percentages (i.e. divide and multiply by 100)
7	"+"	add
8	"*"	multiply
9	"%%"	modulus (i.e. remainder from division by STATS)
10	"-%%"	subtract modulus (i.e. floor data by STATS)

- `g` a factor, [GRP](#) object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a [GRP](#) object) used to group `x`. Number of groups must match rows of `STATS`. See [Details](#).
- `keep.group_vars` *grouped_df method*: Logical. FALSE removes grouping variables after computation. See [Details](#) and [Examples](#).
- ... arguments to be passed to or from other methods.

Details

Without groups (`g = NULL`), `TRA` is nothing more than a column based version of [sweep](#), albeit 4-times more efficient on matrices and many times more efficient on data frames. In this case all methods support an atomic vector of statistics of length `NCOL(x)` passed to `STATS`. The matrix and data frame methods also support a 1-row matrix or 1-row data frame / list, respectively. `TRA` always preserves all attributes of `x`.

With groups passed to `g`, `STATS` needs to be of the same type as `x` and of appropriate dimensions [such that `NCOL(x) == NCOL(STATS)` and `NROW(STATS)` equals the number of groups (i.e. the number of levels if `g` is a factor)]. If this condition is satisfied, `TRA` will assume that the first row of `STATS` is the set of statistics computed on the first group/level of `g`, the second row on the second group/level etc. and do groupwise replacing or sweeping out accordingly.

For example Let `x = c(1.2, 4.6, 2.5, 9.1, 8.7, 3.3)`, `g` is an integer vector in 3 groups `g = c(1, 3, 3, 2, 1, 2)` and `STATS = fmean(x, g) = c(4.95, 6.20, 3.55)`. Then `out = TRA(x, STATS, "-", g) = c(-3.75, 1.05, -1.05, 2.90, 3.75, ...)` [same as `fmean(x, g, TRA = "-")`] does the equivalent of the following for-loop: `for(i in 1:6) out[i] = x[i] - STATS[g[i]]`.

Correct computation requires that `g` as used in `fmean` and `g` passed to `TRA` are exactly the same vector. Using `g = c(1, 3, 3, 2, 1, 2)` for `fmean` and `g = c(3, 1, 1, 2, 3, 2)` for `TRA` will not give the right result. The safest way of programming with `TRA` is thus to repeatedly employ the same factor or [GRP](#) object for all grouped computations. Atomic vectors passed to `g` will be converted to factors (see [qF](#)) and lists will be converted to [GRP](#) objects. This is also done by all [Fast Statistical Functions](#) and by default by [BY](#), thus together with these functions, `TRA` can also safely be used with atomic- or list-groups. Problems may arise if functions from other packages internally group atomic vectors or lists in a non-sorted way. [*Note*: `as.factor` conversions are ok as this also involves sorting.]

If `x` is a grouped tibble (`grouped_df`), `TRA` matches the columns of `x` and `STATS` and also checks for grouping columns in `x` and `STATS`. `TRA.grouped_df` will then only transform those columns in `x` for which matching counterparts were found in `STATS` (exempting grouping columns) and return `x` again (with columns in the same order). If `keep.group_vars = FALSE`, the grouping columns are dropped after computation, however the "groups" attribute is not dropped (it can be removed using `drop1yr::ungroup()`).

Value

`x` with columns replaced or swept out using `STATS`, (optionally) grouped by `g`.

Note

In most cases there is no need to call the `TRA()` function, because of the `TRA`-argument to all [Fast Statistical Functions](#) (ensuring that the exact same grouping vector is used for computing statis-

tics and subsequent transformation). In addition the functions `fbetween/B` and `fwithin/W` and `fscale/STD` provide optimized solutions for frequent scaling, centering and averaging tasks.

See Also

[sweep](#), [Fast Statistical Functions](#), [Data Transformations](#), [Collapse Overview](#)

Examples

```
v <- iris$Sepal.Length      # A numeric vector
f <- iris$Species          # A factor
dat <- num_vars(iris)      # Numeric columns
m <- qM(dat)               # Matrix of numeric data

head(TRA(v, fmean(v)))     # Simple centering [same as fmean(v, TRA = "--") or W(v)]
head(TRA(m, fmean(m)))     # [same as sweep(m, 2, fmean(m)), fmean(m, TRA = "--") or W(m)]
head(TRA(dat, fmean(dat))) # [same as fmean(dat, TRA = "--") or W(dat)]
head(TRA(v, fmean(v), "replace")) # Simple replacing [same as fmean(v, TRA = "replace") or B(v)]
head(TRA(m, fmean(m), "replace")) # [same as sweep(m, 2, fmean(m)), fmean(m, TRA = 1L) or B(m)]
head(TRA(dat, fmean(dat), "replace")) # [same as fmean(dat, TRA = "replace") or B(dat)]
head(TRA(m, fsd(m), "/" )) # Simple scaling...[same as fsd(m, TRA = "/" )]...

# Note: All grouped examples also apply for v and dat...
head(TRA(m, fmean(m, f), "--", f)) # Centering [same as fmean(m, f, TRA = "--") or W(m, f)]
head(TRA(m, fmean(m, f), "replace", f)) # Replacing [same fmean(m, f, TRA = "replace") or B(m, f)]
head(TRA(m, fsd(m, f), "/" , f)) # Scaling [same as fsd(m, f, TRA = "/" )]

head(TRA(m, fmean(m, f), "--+", f)) # Centering on the overall mean ...
# [same as fmean(m, f, TRA = "--+") or
# W(m, f, mean = "overall.mean")]

head(TRA(TRA(m, fmean(m, f), "--", f),
         fmean(m), "--")) # Also the same thing done manually !!

# grouped tibble method
library(dplyr)
iris %>% group_by(Species) %>% TRA(fmean(.))
iris %>% group_by(Species) %>% fmean(TRA = "--") # Same thing
iris %>% group_by(Species) %>% TRA(fmean(.)[c(2,4)]) # Only transforming 2 columns
iris %>% group_by(Species) %>% TRA(fmean(.)[c(2,4)], # Dropping species column
                                keep.group_vars = FALSE)
```

Description

`unlist2d` efficiently unlists lists of regular R objects (objects built up from atomic elements) and creates a data frame representation of the list through recursive flattening and intelligent row-binding operations. It is a full 2-dimensional generalization of `unlist`, but best understood as a recursive generalization of `do.call(rbind, ...)`. This function is a powerful tool to create a tidy

data frame representation from (nested) lists of vectors, data frames, matrices, arrays or heterogeneous objects.

Usage

```
unlist2d(l, idcols = ".id", row.names = FALSE, recursive = TRUE,
         id.factor = FALSE, DT = FALSE)
```

Arguments

<code>l</code>	a unlistable list (with atomic elements in all final nodes, see is.unlistable).
<code>idcols</code>	a character stub or a vector of names for id-columns automatically added - one for each level of nesting in <code>l</code> . By default the stub is <code>".id"</code> , so columns will be of the form <code>".id.1"</code> , <code>".id.2"</code> , etc... . if <code>idcols = TRUE</code> , the stub is also set to <code>".id"</code> . If <code>idcols = FALSE</code> , id-columns are omitted. The content of the id columns are the list names, or (if missing) integers for the list elements. Missing elements in asymmetric nested structures are filled up with NA. See Examples.
<code>row.names</code>	TRUE extracts row names from all the objects in <code>l</code> (where available) and adds them to the output in a column named <code>"row.names"</code> . Alternatively, a column name i.e. <code>row.names = "file"</code> can be supplied. For plain matrices in <code>l</code> , integer row names are generated.
<code>recursive</code>	logical. if FALSE, only process the lowest (deepest) level of <code>l</code> .
<code>id.factor</code>	if TRUE and <code>idcols != FALSE</code> , create id columns as factors instead of character or integer vectors. Alternatively it is possible to specify <code>id.factor = "ordered"</code> to generate ordered factor id's. This is useful if id's are used for further analysis e.g. as inputs to <code>ggplot2</code> .
<code>DT</code>	logical. TRUE returns a <i>data.table</i> , not a data.frame.

Details

The data frame representation created by `unlist2d` is built as follows:

- Recurse down to the lowest level of the list-tree, data frames are exempted and treated as a final elements.
- Identify the objects, if they are vectors, matrices or arrays convert them to data frame (in the case of atomic vectors each element becomes a column).
- Row-bind these data frames using *data.table*'s `rbindlist` function. Columns are matched by name. If the number of columns differ, fill empty spaces with NA's. If `idcols != FALSE`, create id-columns on the left, filled with the object names or indices (if the (sub-)list is unnamed). If `row.names != FALSE`, store row names of the objects (if available) in a separate column.
- Move up to the next higher level of the list-tree and repeat: Convert atomic objects to data frame and row-bind while matching all columns and filling unmatched ones with NA's. Create another id-column for each level of nesting passed through. If the list-tree is asymmetric, fill empty spaces in lower-level id columns with NA's.

The result of this iterative procedure is a single data frame containing on the left side id-columns for each level of nesting (from higher to lower level), followed by a column containing all the

row.names of the objects (if row.names != FALSE), followed by the object columns, matched at each level of recursion. Optimal results are of course obtained with symmetric lists of arrays, matrices or data frames, which unlist2d efficiently binds into a beautiful data frame ready for plotting or further analysis. See examples below.

Value

A data frame or (if DT = TRUE) a *data.table*.

Note

For lists of data frames unlist2d works just like `data.table::rbindlist(l, use.names = TRUE, fill = TRUE, idcol = ".id")` (also the same speed), however for lists of lists unlist2d does not produce the same output as `data.table::rbindlist`.

See Also

[rapply2d](#), [List Processing](#), [Collapse Overview](#)

Examples

```
## Basic Examples:
l <- list(mtcars, list(mtcars, mtcars))
tail(unlist2d(l))
unlist2d(rapply2d(l, fmean))
l = list(a = qM(mtcars[1:8]),
        b = list(c = mtcars[4:11], d = list(e = mtcars[2:10], f = mtcars)))
tail(unlist2d(l, row.names = TRUE))
unlist2d(rapply2d(l, fmean))
unlist2d(rapply2d(l, fmean), recursive = FALSE)

## Groningen Growth and Development Center 10-Sector Database
head(GGDC10S) # See ?GGDC10S
namlab(GGDC10S, class = TRUE)

# Panel-Summarize this data by Variable (Employment and Value Added)
l <- qsu(GGDC10S, by = ~ Variable, # Output as list (instead of 4D array)
        pid = ~ Variable + Country,
        cols = 6:16, array = FALSE)
str(l, give.attr = FALSE) # A list of 2-levels with matrices of statistics
head(unlist2d(l)) # Default output, missing the variables (row-names)
head(unlist2d(l, row.names = TRUE)) # Here we go, but this is still not very nice
head(unlist2d(l, idcols = c("Sector", "Trans"), # Now this is looking pretty good
        row.names = "Variable"))

dat <- unlist2d(l, c("Sector", "Trans"), # Id-columns can also be generated as factors
        "Variable", id.factor = TRUE)
str(dat)

# Split this sectoral data, first by Variable (Employment and Value Added), then by Country
sdat <- rapply2d(split(GGDC10S[c(1,6:16)], GGDC10S$Variable), function(x) split(x[-1],x[[1]]))
```



```
# Compute pairwise correlations between sectors and recombine:
dat <- unlist2d(rapply2d(sdat, pwcov,
  idcols = c("Variable", "Country"),
  row.names = "Sector")
head(dat)
plot(hclust(as.dist(1-pwcov(dat[-(1:3)])))) # Using corrs. as distance metric to cluster sectors

# Together with other functions like psmat, unlist2d can also effectively help reshape data:
head(unlist2d(psmat(subset(GGDC10S, Variable == "VA"), ~Country, ~Year, cols = 6:16, array = FALSE),
  idcols = "Sector", row.names = "Country"), 2)
```

varying

Fast Check of Variation in Data

Description

varying is a generic function that (column-wise) checks for variation in the values of x , (optionally) within the groups g (e.g. a panel-identifier).

Usage

```
varying(x, ...)

## Default S3 method:
varying(x, g = NULL, any_group = TRUE, use.g.names = TRUE, ...)

## S3 method for class 'matrix'
varying(x, g = NULL, any_group = TRUE, use.g.names = TRUE, drop = TRUE, ...)

## S3 method for class 'data.frame'
varying(x, by = NULL, cols = NULL, any_group = TRUE, use.g.names = TRUE, drop = TRUE, ...)

# Methods for compatibility with plm:

## S3 method for class 'pseries'
varying(x, effect = 1L, any_group = TRUE, use.g.names = TRUE, ...)

## S3 method for class 'pdata.frame'
varying(x, effect = 1L, cols = NULL, any_group = TRUE, use.g.names = TRUE,
  drop = TRUE, ...)

# Methods for compatibility with dplyr:

## S3 method for class 'grouped_df'
varying(x, any_group = TRUE, use.g.names = FALSE, drop = TRUE,
  keep.group_vars = TRUE, ...)
```

Arguments

<code>x</code>	a vector, matrix, data.frame, panel series (<code>plm::pseries</code>), panel data frame (<code>plm::pdata.frame</code>) or grouped tibble (<code>dplyr::grouped_df</code>). Data must not be numeric.
<code>g</code>	a factor, GRP object, atomic vector (internally converted to factor) or a list of vectors / factors (internally converted to a GRP object) used to group <code>x</code> .
<code>by</code>	same as <code>g</code> , but also allows one- or two-sided formulas i.e. <code>~ group1 + group2</code> or <code>var1 + var2 ~ group1 + group2</code> . See Examples
<code>any_group</code>	logical. If <code>!is.null(g)</code> , FALSE will check and report variation in all groups, whereas the default TRUE only checks if there is variation within any group. See Examples.
<code>cols</code>	select columns using column names, indices or a function (i.e. <code>is.numeric</code>). Two-sided formulas passed to <code>by</code> overwrite <code>cols</code> .
<code>use.g.names</code>	logical. Make group-names and add to the result as names (default method) or row-names (matrix and data frame methods). No row-names are generated for <i>data.table</i> 's.
<code>drop</code>	<i>matrix and data.frame methods</i> : Logical. TRUE drops dimensions and returns an atomic vector if the result is 1-dimensional.
<code>effect</code>	<i>plm methods</i> : Select the panel identifier by which variation in the data should be examined. 1L takes the first variable in the <code>plm::index</code> , 2L the second etc.. Index variables can also be called by name. More than one index variable can be supplied, which will be interacted.
<code>keep.group_vars</code>	<i>grouped_df method</i> : Logical. FALSE removes grouping variables after computation.
<code>...</code>	arguments to be passed to or from other methods.

Details

Without groups passed to `g`, `varying` simply checks if there is any variation in the columns of `x` and returns TRUE for each column where this is the case and FALSE otherwise. A set of data points is defined as varying if it contains at least 2 distinct non-missing values (such that a non-0 standard deviation can be computed on numeric data). `varying` checks for variation in both numeric and non-numeric data.

If groups are supplied to `g` (or alternatively a *grouped_df* to `x`), `varying` can operate in one of 2 modes:

- If `any_group = TRUE` (the default), `varying` checks each column for variation in any of the groups defined by `g`, and returns TRUE if such within-variation was detected and FALSE otherwise. Thus only one logical value is returned for each column and the computation on each column is terminated as soon as any variation within any group was found.
- If `any_group = FALSE`, `varying` runs through the entire data checking each group for variation and returns, for each column in `x`, a logical vector reporting the variation check for all groups. If a group contains only missing values, a NA is returned for that group.

Value

A logical vector or (if `!is.null(g)` and `any_group = FALSE`), a matrix or data frame of logical vectors indicating whether the data vary (over the dimension supplied by `g`).

See Also

[Summary Statistics](#), [Data Transformations](#), [Collapse Overview](#)

Examples

```
## Checks overall variation in all columns
varying(wlddev)

## Checks whether data are time-variant i.e. vary within country
varying(wlddev, ~ country)

## Same as above but done for each country individually, countries without data are coded NA
head(varying(wlddev, ~ country, any_group = FALSE))
```

wlddev

World Development Dataset

Description

This dataset contains 4 indicators from the World Bank's World Development Indicators (WDI) database: (1) GDP per capita, (2) Life expectancy at birth, (3) GINI index and (4) Net ODA received. The panel data is balanced and covers 216 present and historic countries from 1960-2018 (World Bank aggregates and regional entities are excluded).

Apart from the indicators the data contains a number of identifiers (character country name, factor ISO3 country code, World Bank region and income level, numeric year and decade) and 2 generated variables: A logical variable indicating whether the country is an OECD member, and a fictitious variable stating the date the data was recorded. These variables were added so that all common data-types are represented in this dataset, making it an ideal test-dataset for certain *collapse* functions.

Usage

```
data("wlddev")
```

Format

A data frame with 12744 observations on the following 12 variables. All variables are labeled e.g. have a 'label' attribute.

```
country chr Country Name
iso3c fct Country Code
date date Date Recorded (Fictitious)
year num Year
```

decade *num* Decade
 region *fct* World Bank Region
 income *fct* World Bank Income Level
 OECD *log* Is OECD Member Country?
 PCGDP *num* GDP per capita (constant 2010 US\$)
 LIFEEX *num* Life expectancy at birth, total (years)
 GINI *num* GINI index (World Bank estimate)
 ODA *num* Net ODA received (constant 2015 US\$)

Source

<https://data.worldbank.org/>. Search `vlabels(wlddev)[9:12]` to find the right series.

See Also

[GGDC10S, Collapse Overview](#)

Examples

```
data(wlddev)

# Panel-summarizing the 4 series
qsu(wlddev, pid = ~iso3c, cols = 9:12, vlabels = TRUE)

# By Region
qsu(wlddev, by = ~region, cols = 9:12, vlabels = TRUE)

# Panel-summary by region
qsu(wlddev, by = ~region, pid = ~iso3c, cols = 9:12, vlabels = TRUE)

# Pairwise correlations: Overall
print(pwcor(get_vars(wlddev, 9:12), N = TRUE, P = TRUE), show = "lower.tri")

# Pairwise correlations: Between Countries
print(pwcor(fmean(get_vars(wlddev, 9:12), wlddev$iso3c), N = TRUE, P = TRUE), show = "lower.tri")

# Pairwise correlations: Within Countries
print(pwcor(fwithin(get_vars(wlddev, 9:12), wlddev$iso3c), N = TRUE, P = TRUE), show = "lower.tri")
```

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