

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, class-agnostic, and programmer friendly through a flexible and parsimonious syntax. It is well integrated with base R, 'dplyr' / (grouped) 'tibble', 'data.table', 'sf', 'plm' (panel-series and data frames), and non-destructively handles other matrix or data frame based classes (like 'ts', 'xts' / 'zoo', 'tsibble', ...)

--- 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, data object conversions, and memory efficient R programming.
- (2) Advanced aggregation: Fast and easy multi-data-type, multi-function, weighted and parallelized data aggregation.
- (3) Advanced transformations: Fast row/column arithmetic, (grouped) replacing and sweeping out of statistics (by reference), (grouped, weighted) scaling/standardizing, (higher-dimensional) between (averaging) and (quasi-)within (demeaning) transformations, linear prediction, model fitting and testing exclusion restrictions.
- (4) Advanced time-computations: Fast and flexible indexed time series and panel data classes. Fast (sequences of) lags/leads, and (lagged/leaded, iterated, quasi-, log-) differences and (compounded) growth rates on (irregular) time series and panels. Multivariate auto-, partial- and cross-correlation functions for panel data. Panel data to (ts-)array conversions.
- (5) List processing: Recursive list search, splitting, extraction/subsetting, apply, and generalized row-binding / unlisting to data frame.
- (6) Advanced data exploration: Fast (grouped, weighted, panel-decomposed) summary statistics and descriptive tools.

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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Encoding UTF-8

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LinkingTo Rcpp

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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. Its 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*, *sf* and the *plm* approach to panel data, and non-destructively handles other classes such as *xts*.

Getting Started

See [Collapse Documentation & Overview](#) (the most up-to-date documentation for *collapse* 1.8), or read the [introductory vignette](#). All vignettes can be accessed on the [package website](#). A cheatsheet is available [here](#). A compact introduction for quick-starters is provided in the examples section below.

Details

collapse provides an integrated suite of statistical and data manipulation functions. These improve, complement and extend the capabilities of base R and packages like *dplyr*, *data.table*, *plm*, *matrixS-tats*, *Rfast* etc. In a nutshell, *collapse* provides:

- 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 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++. R code is strongly optimized and inputs are swiftly passed to compiled C/C++ code, where various efficient algorithms are implemented.

To facilitate efficient programming, core S3 methods, grouping and ordering functionality and some C-level helper functions can be accessed by the user.

Additional (hidden) S3 methods and C-level features enable broad based compatibility with *dplyr* (grouped tibble), *data.table*, *sf* and *plm* panel data classes. Functions and core methods also seek to preserve object attributes (including column attributes such as variable labels), ensuring flexibility and effective workflows with a very broad range of R objects (including most time-series classes).

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 13,000 unit tests for Base R equivalence, exempting some improvements (e.g. `fsum(NA, na.rm = TRUE)` evaluates to NA, not 0, similarly for `fmin` and `fmax`; no NaN values are generated from computations involving NA values). Generic functions provide some [security](#) against silent swallowing of 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.

The package is coded both in C and C++ and built with *Rcpp*, but also uses C/C++ functions from *data.table* (grouping, ordering, subsetting, row-binding), *kit* (hash-based grouping), *fixest* (centering on multiple factors), *weights* (weighted pairwise correlations), *stats* (ACF and PACF) and *RcppArmadillo* / *RcppEigen* (fast linear fitting methods).

Author(s)

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Other contributors from packages *collapse* utilizes:

- Matt Dowle, Arun Srinivasan and contributors worldwide (*data.table*)
- Dirk Eddelbuettel and contributors worldwide (*Rcpp*, *RcppArmadillo*, *RcppEigen*)
- Morgan Jacob (*kit*)
- Laurent Berge (*fixest*)
- Josh Pasek (*weights*)
- R Core Team and contributors worldwide (*stats*)

I thank Ralf Stubner, Joseph Wood and Dirk Eddelbuettel and a host of other quant people from diverse fields 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, Kevin Tappe and Grant McDermott for feature requests and helpful suggestions.

Developing / 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 to the 'development' branch of the repository, or e-mail me.
- Please report issues at <https://github.com/SebKrantz/collapse/issues>.

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*fbetween(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(fhdbetween(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)) # Group scaling (if sd's not needed: fsd(mtcars, f2, TRA = "/"))

# All functions above perserve 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(mrml(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, 61 years, 5 series (columns 9-13)

# 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 %>% head # fgroup_by is faster than dplyr::group_by

rm(wlddev) # .. but only works with collapse functions

## Now lets start putting things together
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:POP) %>%
  fgroup_by(region, income) %>% fmean(POP) # Weighted group means

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

wlddev %>% na_omit(cols = "POP") %>% fgroup_by(region, income) %>%
  fselect(PCGDP:POP) %>% fnth(0.75, POP) # Weighted group third quartile

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

```

```

wlddev %>% na_omit(cols = "POP") %>% fgroup_by(country) %>%
  fselect(country, year, PCGDP:POP) %>%
  ftransform(fselect(., -country, -year) %>%
    fnth(0.25, POP, "replace_fill")) %>% head

wlddev %>% fgroup_by(country) %>% fselect(PCGDP:ODA) %>% fscale %>% head # Standardizing
wlddev %>% fgroup_by(country) %>% fselect(PCGDP:POP) %>%
  fscale(POP) %>% head # Weigted..

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

# 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
  } %>% head

# 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"))

# On a groped data frame it is also possible to grouped transform certain columns
# but perform aggregate operatins on others:
wlddev %>% fgroup_by(region, income) %>%
  ftransform(gmedian_GDP = fmedian(PCGDP, GRP(.), TRA = "replace"),
            omedian_GDP = fmedian(PCGDP, TRA = "replace"), # "replace" preserves NA's
            omedian_GDP_fill = fmedian(PCGDP)) %>% tail

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))

# taking weighted mean and weighted mode:
head(collap(wlddev, ~ country + decade, fmean, fmode, w = ~ POP, 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")) %>% head

## 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 indexed data classes:
wldi <- findindex_by(wlddev, country, year)
head(W(wldi$PCGDP)) # Country-demeaning
head(W(wldi, cols = 9:12))

```

```

head(W(wldi$PCGDP, effect = 2))           # Time-demeaning
head(W(wldi, effect = 2, cols = 9:12))
head(HDW(wldi$PCGDP))                   # Country- and time-demeaning
head(HDW(wldi, cols = 9:12))
head(STD(wldi$PCGDP))                   # Standardizing by country
head(STD(wldi, cols = 9:12))
head(L(wldi$PCGDP, -1:3))                # Panel-lags
head(L(wldi, -1:3, 9:12))
head(G(wldi$PCGDP))                     # Panel-Growth rates
head(G(wldi, 1, 1, 9:12))

lm(Dlog(PCGDP) ~ L(Dlog(LIFEEX), 0:3), wldi) # Panel data regression
rm(wldi)

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

```

across

Apply Functions Across Multiple Columns

Description

`across()` can be used inside `fmutate` and `fsummarise` to apply one or more functions to a selection of columns. It is overall very similar to `dplyr::across`, but does not support some `rlang` features, has some additional features (arguments), and is optimized to work with *collapse*'s, `.FAST_FUN`, yielding much faster computations.

Usage

```

across(.cols = NULL, .fns, ..., .names = NULL,
       .apply = "auto", .transpose = "auto")

# acr(...) can be used to abbreviate across(...)

```

Arguments

<code>.cols</code>	select columns using column names and expressions (e.g. <code>a:b</code> or <code>c(a, b, c:f)</code>), column indices, logical vectors, or functions yielding a logical value e.g. <code>is.numeric</code> . <code>NULL</code> applies functions to all columns except for grouping columns.
<code>.fns</code>	A function, character vector of functions or list of functions. Vectors / lists can be named to yield alternative names in the result (see <code>.names</code>). This argument is evaluated inside <code>substitute()</code> , and the content (not the names of vectors/lists) is checked against <code>.FAST_FUN</code> and <code>.OPERATOR_FUN</code> . Matching functions receive vectorized execution, other functions are applied to the data in a standard way.
<code>...</code>	further arguments to <code>.fns</code> . Arguments are evaluated in the data environment and split by groups as well (for non-vectorized functions, if of the same length as the data).

<code>.names</code>	controls the naming of computed columns. <code>NULL</code> generates names of the form <code>col_i_funj</code> if multiple functions are used. <code>.names = TRUE</code> enables this for a single function, <code>.names = FALSE</code> disables it for multiple functions (sensible for functions such as <code>.OPERATOR_FUN</code> that rename columns (if <code>.apply = FALSE</code>)). It is also possible to supply a function with two arguments for column and function names e.g. <code>function(c, f) paste0(f, "_", c)</code> . Finally, you can supply a custom vector of names which must match <code>length(.cols) * length(.fns)</code> .
<code>.apply</code>	controls whether functions are applied column-by-column (<code>TRUE</code>) or to multiple columns at once (<code>FALSE</code>). The default, <code>"auto"</code> , does the latter for vectorized functions, which have an efficient data frame method. It can also be sensible to use <code>.apply = FALSE</code> for non-vectorized functions, especially multivariate functions like <code>lm</code> or <code>pwcor</code> , or functions renaming the data. See Examples.
<code>.transpose</code>	with multiple <code>.fns</code> , <code>.transpose</code> controls whether the result is ordered first by column, then by function (<code>TRUE</code>), or vice-versa (<code>FALSE</code>). <code>"auto"</code> does the former if all functions yield results of the same dimensions (dimensions may differ if <code>.apply = FALSE</code>). See Examples.

Note

`across` does not support *purrr*-style lambdas, and does not support *dplyr*-style predicate functions e.g. `across(where(is.numeric), sum)`, simply use `across(is.numeric, sum)`. In contrast to `dplyr`, you can also compute on grouping columns.

See Also

[fsummarise](#), [fmutate](#), [Fast Data Manipulation](#), [Collapse Overview](#)

Examples

```
# Basic (Weighted) Summaries
fsummarise(wlddev, across(PCGDP:GINI, fmean, w = POP))

library(magrittr) # Note: Used because |> is not available on older R versions
wlddev %>% fgroup_by(region, income) %>%
  fsummarise(across(PCGDP:GINI, fmean, w = POP))

# Note that for these we don't actually need across...
fselect(wlddev, PCGDP:GINI) %>% fmean(w = wlddev$POP, drop = FALSE)
wlddev %>% fgroup_by(region, income) %>%
  fselect(PCGDP:GINI, POP) %>% fmean(POP, keep.w = FALSE)
collap(wlddev, PCGDP + LIFEEEX + GINI ~ region + income, w = ~ POP, keep.w = FALSE)

# But if we want to use some base R function that requires argument splitting...
wlddev %>% na_omit(cols = "POP") %>% fgroup_by(region, income) %>%
  fsummarise(across(PCGDP:GINI, weighted.mean, w = POP, na.rm = TRUE))

# Or if we want to apply different functions...
wlddev %>% fgroup_by(region, income) %>%
  fsummarise(across(PCGDP:GINI, list(mu = fmean, sd = fsd), w = POP),
    POP_sum = fsum(POP), OECD = fmean(OECD))
```

```

# Note that the above still detects fmean as a fast function, the names of the list
# are irrelevant, but the function name must be typed or passed as a character vector,
# Otherwise functions will be executed by groups e.g. function(x) fmean(x) won't vectorize

# Or we want to do more advanced things..
# Such as nesting data frames..
qTBL(wlddev) %>% fgroup_by(region, income) %>%
  fsummarise(across(c(PCGDP, LIFEEEX, ODA),
    function(x) list(Nest = list(x)),
    .apply = FALSE))
# Or linear models..
qTBL(wlddev) %>% fgroup_by(region, income) %>%
  fsummarise(across(c(PCGDP, LIFEEEX, ODA),
    function(x) list(Mods = list(lm(PCGDP ~., x))),
    .apply = FALSE))
# Or computing grouped correlation matrices
qTBL(wlddev) %>% fgroup_by(region, income) %>%
  fsummarise(across(c(PCGDP, LIFEEEX, ODA),
    function(x) qDF(pwcor(x), "Variable"), .apply = FALSE))

# Here calculating 1- and 10-year lags and growth rates of these variables
qTBL(wlddev) %>% fgroup_by(country) %>%
  fmutate(across(c(PCGDP, LIFEEEX, ODA), list(L, G),
    n = c(1, 10), t = year, .names = FALSE))

# Same but variables in different order
qTBL(wlddev) %>% fgroup_by(country) %>%
  fmutate(across(c(PCGDP, LIFEEEX, ODA), list(L, G), n = c(1, 10),
    t = year, .names = FALSE, .transpose = FALSE))

```

arithmetic

Fast Row/Column Arithmetic for Matrix-Like Objects

Description

Fast operators to perform row- or column-wise replacing and sweeping operations of vectors on matrices, data frames, lists. See also [setop](#) for math by reference and [setTRA](#) for sweeping by reference.

Usage

```
## Perform the operation with v and each row of X
```

```

X %rr% v    # Replace rows of X with v
X %r+% v    # Add v to each row of X
X %r-% v    # Subtract v from each row of X
X %r*v% v   # Multiply each row of X with v

```

```

X %r/% v    # Divide each row of X by v

## Perform a column-wise operation between V and X

X %cr% V    # Replace columns of X with V
X %c+% V    # Add V to columns of X
X %c-% V    # Subtract V from columns of X
X %c*% V    # Multiply columns of X with V
X %c/% V    # Divide columns of X by V

```

Arguments

X	a vector, matrix, data frame or list like object (with rows (r) columns (c) matching v / V).
v	for row operations: an atomic vector of matching NCOL(X). If X is a data frame, v can also be a list of scalar atomic elements. It is also possible to sweep lists of vectors v out of lists of matrices or data frames X.
V	for column operations: a suitable scalar, vector, or matrix / data frame matching NROW(X). X can also be a list of vectors / matrices in which case V can be a scalar / vector / matrix or matching list of scalars / vectors / matrices.

Details

With a matrix or data frame X, the default behavior of R when calling X op v (such as multiplication X * v) is to perform the operation of v with each column of X. The equivalent operation is performed by X %cop% V, with the difference that it computes significantly faster if X/V is a data frame / list. A more complex but frequently required task is to perform an operation with v on each row of X. This is provided based on efficient C++ code by the %rop% set of functions, e.g. X %r*% v efficiently multiplies v to each row of X.

Value

X where the operation with v / V was performed on each row or column. All attributes of X are preserved.

Note

Computations and Output: These functions are all quite simple, they only work with X on the LHS i.e. v %op% X will likely fail. The row operations are simple wrappers around [TRA](#) which provides more operations including grouped replacing and sweeping (where v would be a matrix or data frame with less rows than X being mapped to the rows of X by grouping vectors). One consequence is that just like [TRA](#), row-wise mathematical operations (+, -, *, /) always yield numeric output, even if both X and v may be integer. This is different for column- operations which depend on base R and may also preserve integer data.

Rules of Arithmetic: Since these operators are defined as simple infix functions, the normal rules of arithmetic are not respected. So a %c+% b %c*% c evaluates as (a %c+% b) %c*% c. As with all chained infix operations, they are just evaluated sequentially from left to right.

Performance Notes: The function `setup` and a related set of `%op=%` operators as well as the `setTRA` function can be used to perform these operations by reference, and are faster if copies of the output are not required!! Furthermore, for Fast Statistical Functions, using `fmedian(X, TRA = "-")` will be a tiny bit faster than `X %r-% fmedian(X)`. Also use `fwithin(X)` for fast centering using the mean, and `fscale(X)` for fast scaling and centering or mean-preserving scaling.

See Also

[setup](#), [TRA](#), [dapply](#), [Efficient Programming](#), [Data Transformations](#), [Collapse Overview](#)

Examples

```
## Using data frame's / lists
v <- mtcars$cyl
mtcars %cr% v
mtcars %c-% v
mtcars %r-% seq_col(mtcars)
mtcars %r-% lapply(mtcars, quantile, 0.28)

mtcars %c*% 5      # Significantly faster than mtcars * 5
mtcars %c*% mtcars # Significantly faster than mtcars * mtcars

## Using matrices
X <- qM(mtcars)
X %cr% v
X %c-% v
X %r-% dapply(X, quantile, 0.28)

## Chained Operations
library(magrittr) # Note: Used because |> is not available on older R versions
mtcars %>% fwithin() %r-% rnorm(11) %c*% 5 %>%
  tfm(mpg = fsum(mpg)) %>% qsu()
```

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, reorder = 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, reorder = 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, reorder = 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, ..., reorder = TRUE, keep.group_vars = TRUE, use.g.names = FALSE)

```

Arguments

<code>x</code>	a vector, matrix, data frame or alike object.
<code>g</code>	a GRP object, or a factor / atomic vector / list of atomic vectors (internally converted to a GRP object) used to group <code>x</code> .
<code>FUN</code>	a function, can be scalar- or vector-valued. For vector valued functions see also <code>reorder</code> and <code>expand.wide</code> .
<code>...</code>	further arguments to <code>FUN</code> , or to <code>BY.data.frame</code> for the <code>'grouped_df'</code> method.
<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). For vector-valued functions (row-)names are only generated if the function itself creates names for the statistics e.g. <code>quantile()</code> adds names, <code>range()</code> or <code>log()</code> don't. No row-names are generated on <i>data.table</i> 's.
<code>sort</code>	logical. Sort the groups? Internally passed to GRP , and only effective if <code>g</code> is not already a factor or GRP object.
<code>reorder</code>	logical. If a vector-valued function is passed that preserves the data length, <code>TRUE</code> will reorder the result such that the elements/rows match the original data. <code>FALSE</code> just combines the data in order of the groups (i.e. all elements of the first group in first-appearance order followed by all elements in the second group etc..). <i>Note</i> that if <code>reorder = FALSE</code> , grouping variables, names or rownames are only retained if the grouping is on sorted data, see GRP .
<code>expand.wide</code>	logical. If <code>FUN</code> 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).
<code>parallel</code>	logical. <code>TRUE</code> implements simple parallel execution by internally calling mclapply instead of lapply . Parallelism is across columns, except for the default method.
<code>mc.cores</code>	integer. Argument to mclapply indicating the number of cores to use for parallel execution. Can use detectCores() to select all available cores.

`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 if the underlying data type is the same, 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. See also the Note.

Details

BY is a frugal re-implementation of the Split-Apply-Combine computing paradigm. It is faster than [tapply](#), [by](#), [aggregate](#) and *(d)plyr*, and preserves data attributes just like [dapply](#).

It is principally a wrapper around `lapply(gsplit(x, g), FUN, ...)`, that uses `gsplit` for optimized splitting and also strongly optimizes on the internal code 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). The function is intended for simple cases involving flexible computation of statistics across groups using a single function e.g. `iris |> gby(Species) |> BY(IQR)` is simpler than `iris |> gby(Species) |> smr(acr(.fns = IQR))` etc..

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$Sepal.Length # A numeric vector
g <- GRP(iris$Species) # A grouping

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

## matrix method
m <- qM(num_vars(iris))
BY(m, g, sum) # Also return as matrix
BY(m, g, sum, return = "data.frame") # Return as data.frame.. also works for computations below
head(BY(m, g, scale))
BY(m, g, quantile)
BY(m, g, quantile, expand.wide = TRUE)
m1 <- BY(m, g, quantile, expand.wide = TRUE, # Return as list of matrices
        return = "list")
m1
```

```

# Unlisting to Data Frame
unlist2d(ml, idcols = "Variable", row.names = "Species")

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

## grouped data frame method
library(magrittr) # Note: Used because |> is not available on older R versions
giris <- fgroup_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, 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, return.order = sort,
       method = "auto", parallel = FALSE, mc.cores = 2L,
       return = c("wide", "list", "long", "long_dupl"), give.names = "auto", ...)

```

```
# 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, return.order = sort,
        method = "auto", parallel = FALSE, mc.cores = 2L,
        return = c("wide", "list", "long", "long_dupl"), give.names = "auto", ...)

# 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 = 2L,
        return = c("wide", "list", "long", "long_dupl"), give.names = "auto", ...)
```

Arguments

X	a data frame, or an object coercible to data frame using qDF .
by	for collap: 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 GRP object used to group X. For collapv: names or indices of grouping columns, or a logical vector or selector function such as is_categorical 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 (is_categorical).
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 collap or column name / index etc. i.e. <code>"weightvar"</code> in collapv. collapg 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 collap to aggregate columns 1-6 of X using the mean, columns 7-9 using the standard deviation etc. <i>Notes</i> : custom lets collap ignore any inputs passed to FUN, catFUN or cols. Since v1.6.0 you can also rename columns e.g. <code>custom = list(fmean = c(newname = "col1", "col2"), fmode = c(newname = 3))</code> .
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).

<code>keep.w</code>	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).
<code>keep.col.order</code>	logical. Retain original column order post-aggregation.
<code>sort, decreasing, na.last, return.order, method</code>	logical / character. Arguments passed to <code>GRP.default</code> and affecting the row-order in the aggregated data frame and the grouping algorithm.
<code>parallel</code>	logical. Use <code>mclapply</code> instead of <code>lapply</code> to parallelize the computation at the column level. Not available for Windows.
<code>mc.cores</code>	integer. Argument to <code>mclapply</code> setting the number of cores to use, default is 2.
<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.var'. 'auto' will automatically create such prefixes whenever multiple functions are applied to a column.
<code>...</code>	additional arguments passed to all functions supplied to FUN, catFUN, wFUN or custom. The behavior of Fast Statistical Functions is regulated by option("collapse_unused_arg_acti") 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 setting `parallel = TRUE` on a non-windows computer, aggregations will efficiently be parallelized at the column level using `mclapply` utilizing `mc.cores` cores.

Value

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

Note

- (1) Additional arguments passed are not split by groups. Weighted aggregations with user defined functions should be done with `fsummarise`, or using the `data.table` package.
- (2) When the `w` argument is used, the weights are passed to all [Fast Statistical Functions](#). This may be undesirable in settings like `collapse::collap(data, ~ id, custom = list(fsum = ... ,`

fmean = ...), w = ~ weights) where we wish to aggregate some columns using the weighted mean, and others using a simple sum or another unweighted statistic. Therefore it is possible to append [Fast Statistical Functions](#) by `_uw` to yield an unweighted computation. So for the above example we can write: `collapse::collap(data, ~ id, custom = list(fsum_uw = ..., fmean = ...), w = ~ weights)` to get the weighted mean and the simple sum. *Note* that the `_uw` functions are not available for use outside `collap`. Thus one also needs to quote them when passing to the `FUN` or `catFUN` arguments, e.g. use `collap(data, ~ id, fmean, "fmode_uw", w = ~ weights)`. *Note* also that it is never necessary for functions passed to `wFUN` to be appended like this, as the weights are never used to aggregate themselves.

(3) The dispatch between using optimized [Fast Statistical 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`. It is sufficient to write `collapse::collap(data, ~ id, "fmedian")` to get the desired result when the `collapse` namespace is not attached.

See Also

[fsummarise](#), [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)

## 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 = 9:13))           # Only the 5 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 -----
# We aggregate to region level using population weights
head(collap(wlddev, ~ region + year, w = ~ POP))             # Takes weighted mean for numeric..
# ..and weighted mode for categorical data. The weight vector is aggregated using fsum

head(collap(wlddev, ~ region + year, w = ~ POP,              # Aggregating weights using sum
  wFUN = list(fsum, fmax)))                                  # and max (corresponding to mode)

## Multi-Function Aggregation -----
head(collap(wlddev, ~ country + decade, list(fmean, fnobs),  # Saving mean and Nobs
  cols = 9:13))

head(collap(wlddev, ~ country + decade,                      # Same using base R -> slower
  list(mean = mean,
        Nobs = function(x, ...) sum(!is.na(x))),
  cols = 9:13, na.rm = TRUE))

lapply(collap(wlddev, ~ country + decade,                   # List output format
  list(fmean, fnobs), cols = 9:13, return = "list"), head)

head(collap(wlddev, ~ country + decade,                     # Long output format
  list(fmean, fnobs), cols = 9:13, 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 = 9:13, 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 = ~ POP,
  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 = ~ POP,
  wFUN = list(fsum, fmax),
  parallel = TRUE, mc.cores = 1L, keep.col.order = FALSE))

## Piped Use -----
library(magrittr) # Note: Used because |> is not available on older R versions
iris %>% fgroup_by(Species) %>% collapg()
wlddev %>% fgroup_by(country, decade) %>% collapg() %>% head()
wlddev %>% fgroup_by(region, year) %>% collapg(w = POP) %>% head()
wlddev %>% fgroup_by(country, decade) %>% collapg(fmedian, flast) %>% head()
wlddev %>% fgroup_by(country, decade) %>%
  collapg(custom = list(fmean = 9:12, fmode = 5:7, flast = 3)) %>% head()

```

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

Topic

[Fast Statistical Functions](#)

Main Features / Keywords

Fast (grouped and weighted) statistical functions for vector, matrix, data frame and gro

Fast Grouping and Ordering	Fast (ordered) groupings from vectors, data frames, lists. 'GRP' objects are efficient in
Fast Data Manipulation	Fast and flexible select, subset, summarise, mutate/transform, sort/reorder, rename and
Quick Data Conversion	Quick conversions: data.frame <> data.table <> tibble <> matrix (row- or column-wise)
Advanced Data Aggregation	Fast and easy (weighted and parallelized) aggregation of multi-type data, with differen
Data Transformations	Fast row- and column- arithmetic and (object preserving) apply functionality for vecto
Linear Models	Fast (weighted) linear model fitting with 6 different solvers and a fast F-test to test exc
Time Series and Panel Series List Processing Summary Statistics	Fast and class-agnostic indexed time series and panel data objects, check for irregularit (Recursive) list search and checks, extraction of list-elements / list-subsetting, fast (rec Fast (grouped and weighted) summary statistics for cross-sectional and panel data. Fas
Recode and Replace Values	Recode multiple values (exact or regex matching) and replace NaN/Inf/-Inf and outli
(Memory) Efficient Programming	Efficient comparisons of a vector/matrix with a value, and replacing values/rows in vec
Small (Helper) Functions	Multiple-assignment, non-standard concatenation, set and extract variable labels and c
Data and Global Macros	Groningen Growth and Development Centre 10-Sector Database, World Bank World D

Package Options

- `options("collapse_unused_arg_action")` sets the action taken by generic statistical functions when unknown arguments are passed to a method. The default is "warning".
- `options("collapse_mask")` can be used to export copies of functions starting with "f" when loading the package, removing the leading "f" (e.g. also exporting subset as a clone to

fsubset). This will mask like-named base R or *dplyr* functions.

- `options("collapse_F_to_FALSE")` can also be called before loading the package to set the lead operator F in the package to FALSE, to avoid problems with `base::F`.

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)

Maintainer: Sebastian Krantz <sebastian.krantz@graduateinstitute.ch>

See Also

[collapse-package](#)

collapse-options

collapse *Package Options*

Description

- `option("collapse_unused_arg_action")` 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.
- `option("collapse_mask")` can be used to create additional functions in the *collapse* namespace when loading the package, which will mask some existing base R and *dplyr* functions. In particular, *collapse* provides a large number of functions that start with 'f' e.g. `fsubset`, `ftransform`, `fdroplevels` etc.. Specifying `options(collapse_mask = c("fsubset", "ftransform", "fdroplevels"))` before loading the package will make additional functions `subset`, `transform`, and `droplevels` available to the user, and mask the corresponding base R functions when the package is attached. In general, all functions starting with 'f' can be passed to the option. There are also a couple of keywords that you can specify to add groups of functions, and 2 special functions:
 - "manip" adds data manipulation functions: `fsubset`, `ftransform`, `ftransform<-`, `ftransformv`, `fcompute`, `fcomputev`, `fselect`, `fselect<-`, `fgroup_by`, `fgroup_vars`, `fungroup`, `fsummarise`, `fmutate`, `frename`, `findex_by`, `findex`
 - "helper" adds the functions: `fdroplevels`, `finteraction`, `funique`, `fnunique`, `frange`, `fnlevels`, `fnrow` and `fncol`.
 - "fast-fun" adds the functions contained in the macro: `.FAST_FUN`.
 - "fast-stat-fun" adds the functions contained in the macro: `.FAST_STAT_FUN`.
 - "fast-trfm-fun" adds the functions contained in: `setdiff(.FAST_FUN, .FAST_STAT_FUN)`.

- "all" turns on all of the above, and additionally exports a function `n()` for use in `summarise` and `mutate`, and masks `base::table()` by the much faster `qtab()` function.
- Since v1.8.8 it is also possible to pass "n" and "qtab" directly to the option.

Note that none of these options will impact internal *collapse* code, but they may change the way your programs run. "manip" is probably the safest option to start with. Specifying "fast-fun", "fast-stat-fun", "fast-trfm-fun" or "all" are ambitious as they replace basic R functions like `sum` and `max`, introducing *collapse*'s `na.rm = TRUE` default and different behavior for matrices and data frames. These options also change some internal macros so that base R functions like `sum` or `max` called inside `fsummarise`, `fmutate` or `collap` will also receive vectorized execution. In other words, if you put `options(collapse_mask = "all")` before loading the package, and you have a *collapse*-compatible line of *dplyr* code like `wlddev |> group_by(region, income) |> summarise(across(PCGDP:POP, sum))`, this will now receive fully optimized execution. Note however that because of *collapse*'s `na.rm = TRUE` default, the result will be different unless you add `na.rm = FALSE`.

In General, this option is for your convenience, if you want to write visually more appealing code or you want to translate existing *dplyr* codes to *collapse*. Use with care! **Note** that the option takes effect upon loading the package (code is in the `.onLoad` function), so it needs to be set before any function from the package is accessed in any way by any code you run. A safe way to enable it is by using a [.Rprofile](#) file in your user or project directory (see also [here](#), the user-level file is located at `file.path(Sys.getenv("HOME"), ".Rprofile")`) and can be edited using `file.edit(Sys.getenv("HOME"), ".Rprofile")`, or by using a [.fastverse](#) configuration file in the project directory.

- `option("collapse_F_to_FALSE")`, if set to `TRUE`, replaces the lead operator `F` in the package with a value `FALSE` when loading the package, which solves issues arising from the use of `F` as a shortcut for `FALSE` in R codes when *collapse* is attached. Note that `F` is just a value in the *base* package namespace, and it should NOT be used in production codes, precisely because users can overwrite it by assignment. An alternative solution to invoking this option would also just be assigning a value `F <- FALSE` in your global environment.

See Also

[Collapse Overview](#), [collapse-package](#)

collapse-renamed

Renamed Functions

Description

These functions were renamed moving from *collapse* 1.5.3 to 1.6.0 to make the namespace more consistent. With *collapse* 1.7.0 I have deprecated all methods to `fNobs`, `fNdistinct`, `fHDbetween` and `fHDwithin`. The S3 generics and the other functions will be deprecated in 2023 for the earliest. These all now give a message reminding you not to use them in fresh code.

Renaming

```

fNobs -> fnobs
fNdistinct -> fndistinct
pwNobs -> pwnobs
fHDwithin -> fhwithin
fHDbetween -> fhdbetween
as.factor_GRP -> as_factor_GRP
as.factor_qG -> as_factor_qG
is.GRP -> is_GRP
is.qG -> is_qG
is.unlistable -> is_unlistable
is.categorical -> is_categorical
is.Date -> is_date
as.numeric_factor -> as_numeric_factor
as.character_factor -> as_character_factor
Date_vars -> date_vars
`Date_vars<-` -> `date_vars<-`

```

colorder

Fast Reordering of Data Frame Columns

Description

Efficiently reorder columns in a data frame. To do this fully by reference see also `data.table::setcolorder`.

Usage

```

colorder(.X, ..., pos = "front")

colorder(X, neworder = radixorder(names(X)),
         pos = "front", regex = FALSE, ...)

```

Arguments

<code>.X, X</code>	a data frame or list.
<code>...</code>	for <code>colorder</code> : Column names of <code>.X</code> in the new order (can also use sequences i.e. <code>col1:coln</code> , <code>newname = colk, ...</code>). For <code>colorder</code> : Further arguments to <code>grep</code> if <code>regex = TRUE</code> .
<code>neworder</code>	a vector of column names, positive indices, a suitable logical vector, a function such as <code>is.numeric</code> , or a vector of regular expressions matching column names (if <code>regex = TRUE</code>).
<code>pos</code>	integer or character. Different options regarding column arrangement if <code>...length() < ncol(.X)</code> (or <code>length(neworder) < ncol(X)</code>).

<i>Int.</i>	<i>String</i>	<i>Description</i>
1	"front"	move specified columns to the front (the default).

- | | | |
|---|------------|---------------------------------------------------------------------------------------------|
| 2 | "end" | move specified columns to the end. |
| 3 | "exchange" | just exchange the positions of selected columns, other columns remain in the same position. |
| 4 | "after" | place all further selected columns behind the first selected column. |

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/X with columns reordered (no deep copies).

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:hp, am, pos = "after"))
head(colorder(mtcars, vs, cyl, pos = "exchange"))
head(colorder(mtcars, vs, cyl:hp, new = am)) # renaming

## 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, 2:4, 9), pos = "after"))
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>mclapply</code> instead of <code>lapply</code> .
mc.cores	integer. Argument to <code>mclapply</code> indicating the number of cores to use for parallel execution. Can use <code>detectCores()</code> to select all available cores.
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, drop = TRUE 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 `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(cbind, X)` and also convert to list of rows using `mrtl`.
- Call `lapply` or `mclapply` on these plain lists (which is faster than calling `lapply` on an object with attributes).
- depending on the requested output type, use `matrix`, `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 `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 based 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")

```

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 efficient **Split-Apply-Combine computing**, similar to **dapply**.

- A set of arithmetic operators facilitates **row-wise** `%rr%`, `%r+%`, `%r-%`, `%r*%`, `%r/%` and **column-wise** `%cr%`, `%c+%`, `%c-%`, `%c*%`, `%c/%` **replacing and sweeping operations** involving a vector and a matrix or data frame / list. Since v1.7, the operators `%+=%`, `%-=%`, `%*=%` and `%/=%` do column- and element- wise math by reference, and the function `setop` can also perform sweeping out rows by reference.
- `(set)TRA` is a more advanced S3 generic to efficiently perform **(groupwise) replacing and sweeping out of statistics**, either by creating a copy of the data or by reference. Supported operations are:

<i>Integer-id</i>	<i>String-id</i>	<i>Description</i>
0	"replace_NA"	replace missing values
1	"replace_fill"	replace everything
2	"replace"	replace data 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 `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** (also a lot faster than `ave`).
- `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 and interactions). In other words, `fhdwithin/HDW` efficiently computes **residuals** from linear models. Similarly `fhdbetween/HDB`, shorthand for 'higher-dimensional between transformation', computes the corresponding means or **fitted values**.
- `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. `fcumsum` flexibly computes (grouped, ordered) cumulative sums. 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

Function / S3 Generic`dapply``BY``%(r/c)(r/+/-/*//)%``(set)TRA``fscale/STD``fwithin/W``fbetween/B``fhdwithin/HDW``fhdbetween/HDB``flag/L/F, fdiff/D/Dlog, fgrowth/G, fcumsum`*Methods*

No methods, works with matrices and data frames

default, matrix, data.frame, grouped_df

No methods, works with matrices and data frames / lists

default, matrix, data.frame, grouped_df

default, matrix, data.frame, pseries, pdata.frame, grouped_df

default, matrix, data.frame, pseries, pdata.frame, grouped_df

default, matrix, data.frame, pseries, pdata.frame, grouped_df

default, matrix, data.frame, pseries, pdata.frame

default, matrix, data.frame, pseries, pdata.frame

default, matrix, data.frame, pseries, pdata.frame, grouped_df

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

`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 also computes frequency tables for categorical variables, and quantiles and the number of distinct values for numeric variables.

Usage

```
descr(X, Ndistinct = TRUE, higher = TRUE, table = TRUE, sort.table = "freq",
      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'
x[...]
```

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

```
## S3 method for class 'descr'
print(x, n = 14, perc = TRUE, digits = 2, t.table = TRUE,
      summary = TRUE, reverse = FALSE, stepwise = FALSE, ...)
```

Arguments

<code>X</code>	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 <code>qDF</code> .
<code>Ndistinct</code>	logical. TRUE (default) computes the number of distinct values on all variables using <code>fndistinct</code> .
<code>higher</code>	logical. Argument is passed down to <code>qsu</code> : TRUE (default) computes the skewness and the kurtosis.
<code>table</code>	logical. TRUE (default) computes a (sorted) frequency table for all categorical variables (excluding <code>Date</code> variables).
<code>sort.table</code>	an integer or character string specifying how the frequency table should be presented:

<i>Int.</i>	<i>String</i>	<i>Description</i>
1	"value"	sort table by values.
2	"freq"	sort table by frequencies.
3	"none"	return table in first-appearance order of values, or levels for factors (most efficient).

<code>Qprobs</code>	double. Probabilities for quantiles to compute on numeric variables, passed down to <code>quantile</code> . If something non-numeric is passed (i.e. NULL, FALSE, NA, "" etc.), no quantiles are computed.
<code>cols</code>	select columns to describe using column names, indices, a logical vector or a function (e.g. <code>is.numeric</code>).
<code>label.attr</code>	character. The name of a label attribute to display for each variable (if variables are labeled).
<code>...</code>	for <code>descr</code> : other arguments passed to <code>qsu.default</code> . For <code> [.descr</code> : variable names or indices passed to <code> [.list</code> . The argument is unused in the <code>print</code> and <code>as.data.frame</code> methods.
<code>x</code>	an object of class 'descr'.
<code>n</code>	integer. The maximum number of table elements to print for categorical variables. If the number of distinct elements is $\leq n$, the whole table is printed. Otherwise the remaining items are grouped into an '... %s Others' category.
<code>perc</code>	logical. TRUE (default) adds percentages to the frequencies in the table for categorical variables.
<code>digits</code>	integer. The number of decimals to print in statistics and percentage tables.
<code>t.table</code>	logical. TRUE (default) prints a transposed table.
<code>summary</code>	logical. TRUE (default) computes and displays a summary of the frequencies, if the size of the table for a categorical variable exceeds <code>n</code> .
<code>reverse</code>	logical. TRUE prints contents in reverse order, starting with the last column, so that the dataset can be analyzed by scrolling up the console after calling <code>descr</code> .
<code>stepwise</code>	logical. TRUE prints one variable at a time. The user needs to press [enter] to see the printout for the next variable.

Details

descr was heavily inspired by `Hmisc::describe`, but computes about 10x faster. The performance is comparable to [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)

# Some useful print options (also try stepwise argument)
print(descr(GGDC10S), reverse = TRUE, t.table = FALSE)

# Generating a data frame
as.data.frame(descr(wlddev, table = FALSE))

## Passing Arguments down to qsu.default: 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)
```

Description

A small set of functions to addresses some common inefficiencies in R, such as the creation of logical vectors to compare quantities, unnecessary copies of objects in elementary mathematical or subsetting operations, obtaining information about objects (esp. data frames), or dealing with missing values.

Usage

```

anyv(x, value)           # Faster than any(x == value). See also kit::panyv()
allv(x, value)          # Faster than all(x == value). See also kit::pallv()
allNA(x)                # Faster than all(is.na(x)). See also kit::pallNA()
whichv(x, value,
      invert = FALSE)   # Faster than which(x == value)
                        # or which(x != value). See also Note (3)
whichNA(x, invert = FALSE) # Faster than which(!(is.na(x)))
x %==% value            # Infix for whichv(v, value, FALSE), use e.g. in fsubset()
x %!=% value           # Infix for whichv(v, value, TRUE). See also Note (3)
alloc(value, n)         # Faster than rep_len(value, n)
copyv(X, v, R, ..., invert = FALSE, vind1 = FALSE, # Fast replace(X, v, R), replace(X, X (!/=) v, R) or
xlist = FALSE)         # replace(X, (!)v, R[(!)v]). See Details and Note (4).
                        # For multi-replacement see also kit::vswitch()
setv(X, v, R, ..., invert = FALSE, vind1 = FALSE, # Same for X[v] <- r, X[x (!/=) v] <- r or
xlist = FALSE)         # x[(!)v] <- r[(!)v]. Modifies X by reference, fastest.
                        # X/R/V can also be lists/DFs. See Details and Examples.
setop(X, op, V, ...,   # Faster than X <- X +\-\*\ / V (modifies by reference)
      rowwise = FALSE) # optionally can also add v to rows of a matrix or list
X %+=% V               # Infix for setop(X, "+", V). See also Note (2)
X %-=% V               # Infix for setop(X, "-", V). See also Note (2)
X %*=% V               # Infix for setop(X, "*", V). See also Note (2)
X %/=% V               # Infix for setop(X, "/", V). See also Note (2)
na_rm(x)               # Fast: if(anyNA(x)) x[!is.na(x)] else x,
                        # also removes NULL / empty elements from list
na_omit(X, cols = NULL, # Faster na.omit for matrices and data frames,
      na.attr = FALSE, ...) # can use selected columns and attach indices
na_insert(X, prop = 0.1, # Insert missing values at random
      value = NA)
missing_cases(X,       # The opposite of complete.cases(), faster for
      cols = NULL)    # data frames. See also kit::panyNA() and kit::pallNA()
vlengths(X, use.names=TRUE) # Faster version of lengths() (in C, no method dispatch)
vtypes(X, use.names = TRUE) # Get data storage types (faster vapply(X, typeof, ...))
vgcd(x)                # Greatest common divisor of positive integers or doubles
frange(x, na.rm = TRUE) # Much faster base::range, for integer and double objects
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)
seq_row(X)       # Fast integer sequences along rows of X
seq_col(X)       # Fast integer sequences along columns of X
cinv(x)          # Choleski (fast) inverse of symmetric PD matrix, e.g. X'X

```

Arguments

`X, V, R` a vector, matrix or data frame.

`x, v` a (atomic) vector or matrix (`na_rm` also supports lists).

`value` a single value of any (atomic) vector type. For `whichv` it can also be a `length(x)` vector.

`invert` logical. TRUE considers elements `x != value`.

`vind1` logical. If `length(v) == 1L`, setting `vind1 = TRUE` will interpret `v` as an index, rather than a value to search and replace.

`xlist` logical. If `X` is a list, the default is to treat it like a data frame and replace rows. Setting `xlist = TRUE` will treat `X` and its replacement `R` like 1-dimensional list vectors.

`op` an integer or character string indicating the operation to perform.

<i>Int.</i>	<i>String</i>	<i>Description</i>
1	"+"	add V
2	"-"	subtract V
3	"*"	multiply by V
4	"/"	divide by V

`rowwise` logical. TRUE performs the operation between `V` and each row of `X`.

`cols` select columns to check for missing values using column names, indices, a logical vector or a function (e.g. `is.numeric`). The default is to check all columns, which could be inefficient.

`n` integer. The length of the vector to allocate with `value`.

`na.attr` logical. TRUE adds an attribute containing the removed cases. For compatibility reasons this is exactly the same format as `na.omit` i.e. the attribute is called "na.action" and of class "omit".

`prop` double. Specify the proportion of observations randomly replaced with NA.

`use.names` logical. Preserve names if `X` is a list.

`na.rm` logical. TRUE omits missing values by skipping them in the computation. FALSE terminates the computation once a missing value is encountered and returns 2 missing values.

... for `na_omit`: further arguments passed to `[]` for vectors and matrices. With indexed data it is also possible to specify the `drop.index.levels` argument, see [indexing](#). For `copyv`, `setv` and `setop`, the argument is unused, and serves as a placeholder for possible future arguments.

Details

`copyv` and `setv` are designed to optimize operations that require replacing data in objects in the broadest sense. The only difference between them is that `copyv` first deep-copies `X` before doing replacements whereas `setv` modifies `X` in place and returns the result invisibly. There are 3 ways these functions can be used:

1. To replace a single value, `setv(X, v, R)` is an efficient alternative to `X[X == v] <- R`, and `copyv(X, v, R)` is more efficient than `replace(X, X == v, R)`. This can be inverted using `setv(X, v, R, invert = TRUE)`, equivalent to `X[X != v] <- R`.
2. To do standard replacement with integer or logical indices i.e. `X[v] <- R` is more efficient using `setv(X, v, R)`, and, if `v` is logical, `setv(X, v, R, invert = TRUE)` is efficient for `X[!v] <- R`. To distinguish this from use case (1) when `length(v) == 1`, the argument `vind1 = TRUE` can be set to ensure that `v` is always interpreted as an index.
3. To copy values from objects of equal size i.e. `setv(X, v, R)` is faster than `X[v] <- R[v]`, and `setv(X, v, R, invert = TRUE)` is faster than `X[!v] <- R[!v]`.

Both `X` and `R` can be atomic or data frames / lists. If `X` is a list, the default behavior is to interpret it like a data frame, and apply `setv/copyv` to each element/column of `X`. If `R` is also a list, this is done using `apply`. Thus `setv/copyv` can also be used to replace elements or rows in data frames, or copy rows from equally sized frames. Note that for replacing subsets in data frames `set` from `data.table` provides a more convenient interface (and there is also `copy` if you just want to deep-copy an object without any modifications to it).

If `X` should not be interpreted like a data frame, setting `xlist = TRUE` will interpret it like a 1D list-vector analogous to atomic vectors, except that use case (1) is not permitted i.e. no value comparisons on list elements.

Note

1. None of these functions currently support complex vectors.
2. `setop` and the operators `%+=%`, `%-=%`, `%*=%` and `%/=%` also work with integer data, but do not perform any integer related checks. R's integers are bounded between `+2,147,483,647` and `NA_integer_` is stored as the value `-2,147,483,648`. Thus computations resulting in values exceeding `+2,147,483,647` will result in integer overflows, and `NA_integer_` should not occur on either side of a `setop` call. These are programmers functions and meant to provide the most efficient math possible to responsible users.
3. It is possible to compare factors by the levels (e.g. `iris$Species %==% "setosa"`) or using integers (`iris$Species %==% 1L`). The latter is slightly more efficient. Nothing special is implemented for other objects apart from basic types, e.g. for dates (which are stored as doubles) you need to generate a date object i.e. `wlddev$date %==% as.Date("2019-01-01")`. Using `wlddev$date %==% "2019-01-01"` will give `integer(0)`.
4. `setv/copyv` only allow positive integer indices being passed to `v`, and, for efficiency reasons, they only check the first and the last index. Thus if there are indices in the middle that fall outside of the data range it will terminate R.

See Also

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

Examples

```

## Which value
whichNA(wlddev$PCGDP)           # Same as which(is.na(wlddev$PCGDP))
whichNA(wlddev$PCGDP, invert = TRUE) # Same as which(!is.na(wlddev$PCGDP))
whichv(wlddev$country, "Chad")   # Same as which(wlddev$country == "Chad")
wlddev$country %==% "Chad"       # Same thing
whichv(wlddev$country, "Chad", TRUE) # Same as which(wlddev$country != "Chad")
wlddev$country %!=% "Chad"       # Same thing
lvec <- wlddev$country == "Chad"  # If we already have a logical vector...
whichv(lvec, FALSE)              # is faster than which(!lvec)
rm(lvec)

# Using the %==% operator can yield tangible performance gains
fsubset(wlddev, iso3c %==% "DEU") # 3x faster than:
fsubset(wlddev, iso3c == "DEU")

## Math by reference: permissible types of operations
x <- alloc(1.0, 1e5) # Vector
x %+=% 1
x %+=% 1:1e5
xm <- matrix(alloc(1.0, 1e5), ncol = 100) # Matrix
xm %+=% 1
xm %+=% 1:1e3
setop(xm, "+", 1:100, rowwise = TRUE)
xm %+=% xm
xm %+=% 1:1e5
xd <- qDF(replicate(100, alloc(1.0, 1e3), simplify = FALSE)) # Data Frame
xd %+=% 1
xd %+=% 1:1e3
setop(xd, "+", 1:100, rowwise = TRUE)
xd %+=% xd
rm(x, xm, xd)

## setv() and copyv()
x <- rnorm(100)
y <- sample.int(10, 100, replace = TRUE)
setv(y, 5, 0)           # Faster than y[y == 5] <- 0
setv(y, 4, x)           # Faster than y[y == 4] <- x[y == 4]
setv(y, 20:30, y[40:50]) # Faster than y[20:30] <- y[40:50]
setv(y, 20:30, x)       # Faster than y[20:30] <- x[20:30]
rm(x, y)

# Working with data frames, here returning copies of the frame
copyv(mtcars, 20:30, ss(mtcars, 10:20))
copyv(mtcars, 20:30, fscale(mtcars))
ftransform(mtcars, new = copyv(cyl, 4, vs))
# Column-wise:
copyv(mtcars, 2:3, fscale(mtcars), xlist = TRUE)
copyv(mtcars, 2:3, mtcars[4:5], xlist = TRUE)

## Missing values

```

```

mtc_na <- na_insert(mtcars, 0.15) # Set 15% of values missing at random
fnobs(mtc_na) # See observation count
missing_cases(mtc_na) # Fast equivalent to !complete.cases(mtc_na)
missing_cases(mtc_na, cols = 3:4) # Missing cases on certain columns?
# to see all missing cases use kit::pallNA(mtc_na)
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)

```

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 [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]`.
- [fsummarise](#) is a much faster version of `dplyr::summarise` when used together with the [Fast Statistical Functions](#) and [fgroup_by](#), with whom it also supports super fast weighted aggregation.
- [fmutate](#) is a much faster version of `dplyr::mutate` when used together with the [Fast Statistical Functions](#) as well as fast [Data Transformation Functions](#) and [fgroup_by](#).
- [ftransform](#) is a much faster version of [transform](#), which also supports list input and nested pipelines. [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. `relabel` and `setrelabel` do the same thing for variable labels (see also `vlabels`).

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](#)
[fsummarise](#)
[fmutate](#), [\(f/set\)ftransform\(<-\)](#)
[fcompute\(v\)](#)
[roworder\(v\)](#)
[colorder\(v\)](#)
[\(f/set\)rename](#), [\(set\)relabel](#)

See Also

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

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 `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`.
- `group` provides fast grouping in first-appearance order of rows, based on a hashing algorithm in C. Objects have class 'qG', see below.
- `GRP` creates `collapse` grouping objects of class 'GRP' based on `radixorder_v` or `group`. '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.

- `fgroup_by` provides a fast replacement for `dplyr::group_by`, creating a grouped data frame (or `data.table` / `tibble` etc.) with a 'GRP' object attached. This grouped frame can be used for grouped operations using `collapse`'s 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. `funique` efficiently calculates the number of unique values/rows.
- `qF`, shorthand for 'quick-factor' implements very fast factor generation from atomic vectors using either radix ordering method = "radix" or 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 `droplevels`.
- `finteraction` is a fast alternative to `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 regular 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.
- `timeid` is a specialized function to convert integer or double vectors representing time (such as 'Date', 'POSIXct' etc.) to factor or 'qG' object based on the greatest common divisor of elements (thus preserving gaps in time intervals).

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 incl. <code>pdata.frame</code>	Row sorting/reordering
<code>group</code>	No methods, for data frames and vectors	Hash-based grouping
<code>GRP</code>	default, GRP, factor, qG, grouped_df, pseries, pdata.frame	Fast grouping and a flexible object
<code>fgroup_by</code>	No methods, for data frames	Fast grouped data frame
<code>funique, funique</code>	default, data.frame, sf, pseries, pdata.frame, list	Fast (number of) unique values
<code>qF</code>	No methods, for vectors	Quick factor generation
<code>qG</code>	No methods, for vectors	Quick grouping of vectors
<code>fdroplevels</code>	factor, data.frame, list	Fast removal of unused levels
<code>finteraction</code>	No methods, for data frames and vectors	Fast interactions
<code>groupid</code>	No methods, for vectors	Run-length type group-id

<code>seqid</code>	No methods, for integer vectors	Run-length type integer
<code>timeid</code>	No methods, for integer or double vectors	Integer-id from time/date

See Also

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

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`, `fnoobs` 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 vectors, matrices and data frames, with special support for grouped data frames / tibbles (*dplyr*) 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, [nthreads = 1L,] ...)
```

```
## S3 method for class 'matrix'
FUN(x, g = NULL, [w = NULL,] TRA = NULL, [na.rm = TRUE,]
     use.g.names = TRUE, drop = TRUE, [nthreads = 1L,] ...)
```

```
## S3 method for class 'data.frame'
FUN(x, g = NULL, [w = NULL,] TRA = NULL, [na.rm = TRUE,]
     use.g.names = TRUE, drop = TRUE, [nthreads = 1L,] ...)
```

```
## 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,] [nthreads = 1L,] ...)
```

Arguments

x	a vector, matrix, data frame or grouped data frame (class 'grouped_df').
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 .
TRA	an integer or quoted operator indicating the transformation to perform: 0 - "replace_NA" 1 - "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
nthreads	integer. The number of threads to utilize. Supported by fsum , fmean , fmedian , fmode and fndistinct
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. If TRA is used, passing set = TRUE will transform da

Details

Please see the documentation of individual functions.

Value

x suitably aggregated or transformed. Data frame column-attributes and overall attributes are generally preserved if the output is of the same data type.

Related Functionality

- Panel-decomposed (i.e. between and within) statistics as well as grouped and weighted skewness and kurtosis are implemented in [qsu](#).
- Function [frange](#) efficiently computes the minimum and maximum on atomic vectors.
- The vector-valued functions and operators [fcumsum](#), [fscale/STD](#), [fbetween/B](#), [fhdbetween/HDB](#), [fwithin/W](#), [fhdwithin/HDW](#), [flag/L/F](#), [fdiff/D/Dlog](#) and [fgrowth/G](#) are grouped under [Data Transformations](#) and [Time Series and Panel Series](#). These functions also support [indexed data \(plm\)](#).

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) # ..
\donttest{
## method for grouped data frames - created with dplyr::group_by or fgroup_by
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](#)

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 indexed data / 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 grouped data frame / 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, 'indexed_series' ('pseries'), 'indexed_frame' ('pdata.frame') or grouped data frame ('grouped_df').
g	a factor, GRP object, or atomic vector / list of vectors (internally grouped with <code>group</code>) 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. <code>~ group1</code> or <code>var1 + var2 ~ group1 + group2</code> . See Examples.
w	a numeric vector of (non-negative) weights. B/W data frame and <code>pdata.frame</code> methods also allow a one-sided formula i.e. <code>~ weightcol</code> . The <code>grouped_df</code> (<i>dplyr</i>) method supports lazy-evaluation. See Examples.
cols	<i>B/W (p)data.frame methods</i> : Select columns to scale using a function, column names, indices or a logical vector. Default: All numeric columns. <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 <code>na.rm = FALSE</code> 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 <code>index</code> , 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 <code>mean = "overall.mean"</code> . 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. $x - \theta * x_i$. 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	<i>B and W data.frame, pdata.frame and grouped_df methods</i> : 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`: $B(x, g) + W(x, g) = xi. + x - xi. = x$. 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 $\alpha_i \neq \alpha = const.$ (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 fhwithin/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 = 9:13)) # Center the 5 series in this dataset by country
head(cbind(get_vars(wlddev,"iso3c"), # Same thing done manually using fwithin..
  add_stub(fwithin(get_vars(wlddev,9:13), 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) ~ W(carb), data = iby(mtcars, id = finteraction(cyl, vs, am)))
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")
```

fcumsum

Fast (Grouped, Ordered) Cumulative Sum for Matrix-Like Objects

Description

fcumsum is a generic function that computes the (column-wise) cumulative sum of x , (optionally) grouped by g and/or ordered by o . Several options to deal with missing values are provided.

Usage

```
fcumsum(x, ...)

## Default S3 method:
fcumsum(x, g = NULL, o = NULL, na.rm = TRUE, fill = FALSE, check.o = TRUE, ...)

## S3 method for class 'matrix'
fcumsum(x, g = NULL, o = NULL, na.rm = TRUE, fill = FALSE, check.o = TRUE, ...)

## S3 method for class 'data.frame'
fcumsum(x, g = NULL, o = NULL, na.rm = TRUE, fill = FALSE, check.o = TRUE, ...)

# Methods for indexed data / compatibility with plm:

## S3 method for class 'pseries'
fcumsum(x, na.rm = TRUE, fill = FALSE, shift = "time", ...)

## S3 method for class 'pdata.frame'
fcumsum(x, na.rm = TRUE, fill = FALSE, shift = "time", ...)

# Methods for grouped data frame / compatibility with dplyr:

## S3 method for class 'grouped_df'
fcumsum(x, o = NULL, na.rm = TRUE, fill = FALSE, check.o = TRUE, keep.ids = TRUE, ...)
```

Arguments

x	a numeric vector / time series, (time series) matrix, data frame, 'indexed_series' ('pseries'), 'indexed_frame' ('pdata.frame') or grouped data frame ('grouped_df').
g	a factor, GRP object, or atomic vector / list of vectors (internally grouped with group) used to group x .
o	a vector or list of vectors providing the order in which the elements of x are cumulatively summed. Will be passed to radixorderv unless <code>check.o = FALSE</code> .

<code>na.rm</code>	logical. Skip missing values in <code>x</code> . Defaults to <code>TRUE</code> and implemented at very little computational cost.
<code>fill</code>	if <code>na.rm = TRUE</code> , setting <code>fill = TRUE</code> will overwrite missing values with the previous value of the cumulative sum, starting from 0.
<code>check.o</code>	logical. Programmers option: <code>FALSE</code> prevents passing <code>o</code> to <code>radixorder</code> , requiring <code>o</code> to be a valid ordering vector that is integer typed with each element in the range <code>[1, length(x)]</code> . This gives some extra speed, but will terminate R if any element of <code>o</code> is too large or too small.
<code>shift</code>	<i>pseries / pdata.frame methods</i> : character. "time" or "row". See flag for details. The argument here does not control 'shifting' of data but rather the order in which elements are summed.
<code>keep.ids</code>	<i>pdata.frame / grouped_df methods</i> : Logical. Drop all identifiers from the output (which includes all grouping variables and variables passed too). <i>Note</i> : For grouped / panel data frames identifiers are dropped, but the "groups" / "index" attributes are kept.
<code>...</code>	arguments to be passed to or from other methods.

Details

If `na.rm = FALSE`, `fcumsum` works like `cumsum` and propagates missing values. The default `na.rm = TRUE` skips missing values and computes the cumulative sum on the non-missing values. Missing values are kept. If `fill = TRUE`, missing values are replaced with the previous value of the cumulative sum (starting from 0), computed on the non-missing values.

By default the cumulative sum is computed in the order in which elements appear in `x`. If `o` is provided, the cumulative sum is computed in the order given by `radixorder(o)`, without the need to first sort `x`. This applies as well if groups are used (`g`), in which case the cumulative sum is computed separately in each group.

The *pseries* and *pdata.frame* methods assume that the last factor in the `index` is the time-variable and the rest are grouping variables. The time-variable is passed to `radixorder` and used for ordered computation, so that cumulative sums are accurately computed regardless of whether the panel-data is ordered or balanced.

`fcumsum` explicitly supports integers. Integers in R are bounded at bounded at $\pm 2,147,483,647$, and an integer overflow error will be provided if the cumulative sum (within any group) exceeds $\pm 2,147,483,647$. In that case data should be converted to double beforehand.

Value

the cumulative sum of values in `x`, (optionally) grouped by `g` and/or ordered by `o`. See Details and Examples.

See Also

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

Examples

```
## Non-grouped
fcumsum(AirPassengers)
head(fcumsum(EuStockMarkets))
fcumsum(mtcars)

# Non-grouped but ordered
o <- order(rnorm(nrow(EuStockMarkets)))
all.equal(copyAttrib(fcumsum(EuStockMarkets[o, ], o = o)[order(o), ], EuStockMarkets),
          fcumsum(EuStockMarkets))

## Grouped
head(with(wlddev, fcumsum(PCGDP, iso3c)))

## Grouped and ordered
head(with(wlddev, fcumsum(PCGDP, iso3c, year)))
head(with(wlddev, fcumsum(PCGDP, iso3c, year, fill = TRUE)))
```

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 or (quasi-)log-differences. The difference and log-difference operators D and Dlog also exists as parsimonious wrappers around fdiff, providing 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 indexed data / compatibility with plm:

## S3 method for class 'pseries'
fdiff(x, n = 1, diff = 1, fill = NA, log = FALSE, rho = 1,
      stubs = length(n) + length(diff) > 2L, shift = "time", ...)
## S3 method for class 'pseries'
D(x, n = 1, diff = 1, fill = NA, rho = 1, stubs = TRUE, shift = "time", ...)
## S3 method for class 'pseries'
Dlog(x, n = 1, diff = 1, fill = NA, rho = 1, stubs = TRUE, shift = "time", ...)

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

# Methods for grouped data frame / 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, 'indexed_series' ('pseries'), 'indexed_frame' ('pdata.frame') or grouped data frame ('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, or atomic vector / list of vectors (internally grouped with <code>group</code>) used to group x.
by	<i>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.
t	a time vector or list of vectors. See <code>flag</code> .
cols	<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> : cols is ignored if a two-sided formula is passed to by.
fill	value to insert when vectors are shifted. Default is NA.
log	logical. TRUE computes log-differences. See Details.
rho	double. Autocorrelation parameter. Set to a value between 0 and 1 for quasi-differencing. Any numeric value can be supplied.
stubs	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.
shift	<i>pseries / pdata.frame methods</i> : character. "time" or "row". See <code>flag</code> for details.
keep.ids	<i>data.frame / pdata.frame / grouped_df methods</i> : Logical. Drop all identifiers from the output (which includes all variables passed to by or t). <i>Note</i> : For 'grouped_df' / 'pdata.frame' identifiers are dropped, but the "groups" / "index" attributes are kept.
...	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 $\log(x[i]) - \rho * \log(x[i-n])$ for `diff = 1` and $\text{repeat}(\text{diff}-1) x[i] - \rho * x[i-n]$ is used to compute subsequent differences (usually `diff = 1` for log-differencing). 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. 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 $\text{ncol}(x) \times \text{length}(n) \times \text{length}(\text{diff})$ columns ordered first by column name, then by lag, then by difference.

For further computational details and efficiency considerations see the help page of [flag](#).

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,
  rho = pwcov(AirPassengers, L(AirPassengers))) # Quasi-difference, see a better example below

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
pwcov(r, L(r)) # Residual Autocorrelation
ffttest(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))

## Indexed computations:
wldi <- findindex_by(wlddev, iso3c, year)

# Dynamic Panel Data Models:
summary(lm(D(PCGDP) ~ L(PCGDP) + D(LIFEEEX), data = wldi)) # Simple case
summary(lm(Dlog(PCGDP) ~ L(log(PCGDP)) + Dlog(LIFEEEX), data = wldi)) # In log-differneces
# Adding a lagged difference...
summary(lm(D(PCGDP) ~ L(D(PCGDP, 0:1)) + L(D(LIFEEEX), 0:1), data = wldi))
summary(lm(Dlog(PCGDP) ~ L(Dlog(PCGDP, 0:1)) + L(Dlog(LIFEEEX), 0:1), data = wldi))
# Same thing:
summary(lm(D1.PCGDP ~., data = L(D(wldi,0:1,1,9:10),0:1,keep.ids = FALSE)[-1]))

## Grouped data
library(magrittr)
wlddev %>% fgroup_by(country) %>%
  fselect(PCGDP,LIFEEEX) %>% fdiff(0:1,1:2) # Adding a first and second difference
wlddev %>% fgroup_by(country) %>%
  fselect(year,PCGDP,LIFEEEX) %>% D(0:1,1:2,year) # Also using t (safer)
wlddev %>% fgroup_by(country) %>%
  fselect(year,PCGDP,LIFEEEX) %>% 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

`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` with unused factor levels removed.

Note

If `x` is malformed e.g. has too few levels, this function can cause a segmentation fault terminating the R session, 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	<i>Fast (Grouped) First and Last Value for Matrix-Like Objects</i>
--------------	--------------------------------------------------------------------

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 data frame (class 'grouped_df').
<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> .

TRA	an integer or quoted operator indicating the transformation to perform: 0 - "replace_NA" 1 - "replace_fill" 2 - "replace" 3 - "-" 4 - "-+" 5 - "/" 6 - "%" 7 - "+" 8 - "*" 9 - "%%" 10 - "-%%" . See TRA .
na.rm	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..
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. If TRA is used, passing set = TRUE will transform data by reference and return the result invisibly.

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, ...

Note

Both functions are significantly faster if na.rm = FALSE, particularly ffirst which can take direct advantage of the 'group.starts' elements in [GRP](#) objects.

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 data frames - created with dplyr::group_by or fgroup_by
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 (Weighted) 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. There is also an efficient 2-part formula method.

Usage

```
fFtest(...) # Internal method dispatch: formula if is.call(..1) || is.call(..2)

## Default S3 method:
fFtest(y, exc, X = NULL, w = NULL, full.df = TRUE, ...)

## S3 method for class 'formula'
fFtest(formula, data = NULL, weights = NULL, ...)
```

Arguments

<code>y</code>	a numeric vector: the dependent variable.
<code>exc</code>	a numeric vector, factor, numeric matrix or list / data frame of numeric vectors and/or factors: variables to test / exclude.
<code>X</code>	a numeric vector, factor, numeric matrix or list / data frame of numeric vectors and/or factors: covariates to include in both the restricted (without <code>exc</code>) and unrestricted model. If left empty (<code>X = NULL</code>), the test amounts to the F-test of the regression of <code>y</code> on <code>exc</code> .
<code>w</code>	numeric. A vector of (frequency) weights.
<code>formula</code>	a 2-part formula: $y \sim exc \mid X$, where both <code>exc</code> and <code>X</code> are expressions connected with <code>+</code> , and <code>X</code> can be omitted. <i>Note</i> that other operators (<code>:</code> , <code>*</code> , <code>^</code> , <code>-</code> , etc.) are not supported, you can interact variables using standard functions like <code>finteraction/itn</code> or <code>magrittr::multiply_by</code> inside the formula e.g. <code>log(y) ~ x1 + itn(x2, x3) x4</code> or <code>log(y) ~ x1 + multiply_by(x2, x3) x4</code> .
<code>data</code>	a named list or data frame.
<code>weights</code>	a weights vector or expression that results in a vector when evaluated in the data environment.

`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 `fFtest.default` or to `fhdwithin`. Sensible options might be the `lm.method` argument or further control parameters to `fixest::demean`, the workhorse function underlying `fhdwithin` for higher-order centering tasks.

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 (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.

Note that an intercept is always added by `fhdwithin`, so it is not necessary to include an intercept in data supplied to `exc / X`.

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 = NULL`, only a vector of the same 5 statistics testing the model ($y \sim exc$) is shown.

See Also

[flm](#), [fhdwithin](#), [Data Transformations](#), [Collapse Overview](#)

Examples

```
## We could use fFtest as a simple 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(mpg ~ cyl + vs | hp + carb, mtcars)
fFtest(mtcars$mpg, mtcars[c("cyl", "vs")], mtcars[c("hp", "carb")])

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

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

## Testing the significance of country-FE in regression of GDP on life expectancy
fFtest(log(PCGDP) ~ iso3c | LIFEEEX, wlddev)
fFtest(log(wlddev$PCGDP), wlddev$iso3c, wlddev$LIFEEEX)

## Ok, country-FE are significant, what about adding time-FE
fFtest(log(PCGDP) ~ qF(year) | iso3c + LIFEEEX, wlddev)
fFtest(log(wlddev$PCGDP), qF(wlddev$year), wlddev[c("iso3c", "LIFEEEX")])

# Same test done using lm:
data <- na_omit(get_vars(wlddev, c("iso3c", "year", "PCGDP", "LIFEEEX")))
full <- lm(PCGDP ~ LIFEEEX + iso3c + qF(year), data)
rest <- lm(PCGDP ~ LIFEEEX + 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, iterated and compounded growth rates, obtained with via the exact method of computation or 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 indexed data / compatibility with plm:

## S3 method for class 'pseries'
fgrowth(x, n = 1, diff = 1, fill = NA, logdiff = FALSE, scale = 100,
        power = 1, stubs = length(n) + length(diff) > 2L, shift = "time", ...)
## S3 method for class 'pseries'
G(x, n = 1, diff = 1, fill = NA, logdiff = FALSE, scale = 100,
  power = 1, stubs = TRUE, shift = "time", ...)

## 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, shift = "time", ...)
## 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, shift = "time", keep.ids = TRUE, ...)

# Methods for grouped data frame / 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 / time series, (time series) matrix, data frame, 'indexed_series' ('pseries'), 'indexed_frame' ('pdata.frame') or grouped data frame ('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, or atomic vector / list of vectors (internally grouped with group) 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	a time vector or list of vectors. See flag .
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. fgrowth(AirPassengers, 12, power = 1/12) is equivalent to ((AirPassengers/flag(AirPassengers, 12))^(1/12)-1)*100.
stubs	logical. TRUE will rename all computed columns by adding a prefix "LnGdiff." / "FnGdiff.", or "LnDlogdiff." / "FnDlogdiff." if logdiff = TRUE.
shift	<i>pseries / pdata.frame methods</i> : character. "time" or "row". See flag for details.
keep.ids	<i>data.frame / pdata.frame / grouped_df methods</i> : Logical. Drop all identifiers from the output (which includes all variables passed to by or t). <i>Note</i> : For 'grouped_df' / 'pdata.frame' identifiers are dropped, but the "groups" / "index" 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`, so for `diff > 1` it computes growth rate of growth rates. If `logdiff = TRUE`, approximate growth rates are computed using `log(x[i]/x[i-n])*scale` for `diff = 1` and `repeat(diff-1) x[i] - x[i-n]` thereafter (usually `diff = 1` for log-differencing). For further details see the help pages of [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
summary(lm(L260G1.DAX ~ ., G(EuStockMarkets,260))) # Annual growth rate of DAX regressed on the
# growth rates of the other indicators

## World Development Panel Data
head(fgrowth(num_vars(wlddev), 1, 1, # Computes growth rates of numeric variables
wlddev$country, wlddev$year)) # fgrowth requires external inputs..
head(G(wlddev, 1, 1, ~country, ~year)) # Growth of numeric variables, id's attached
head(G(wlddev, 1, 1, ~country)) # Without t: Works because data is ordered
head(G(wlddev, 1, 1, PCGDP + LIFEEX ~ country, ~year)) # Growth of GDP per Capita & Life Expectancy
head(G(wlddev, 0:1, 1, ~ country, ~year, cols = 9:10)) # Same, also retaining original series
head(G(wlddev, 0:1, 1, ~ country, ~year, 9:10, # Dropping id columns
keep.ids = FALSE))
```

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, lm.method = "qr", ...)
## Default S3 method:
fhdwithin(x, fl, w = NULL, na.rm = TRUE, fill = FALSE, lm.method = "qr", ...)
## Default S3 method:
HDB(x, fl, w = NULL, na.rm = TRUE, fill = FALSE, lm.method = "qr", ...)
## Default S3 method:
HDW(x, fl, w = NULL, na.rm = TRUE, fill = FALSE, lm.method = "qr", ...)

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

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

# Methods for indexed data / compatibility with plm:

## S3 method for class 'pseries'
fhdbetween(x, effect = "all", w = NULL, na.rm = TRUE, fill = TRUE, ...)
## S3 method for class 'pseries'
fhdwithin(x, effect = "all", w = NULL, na.rm = TRUE, fill = TRUE, ...)
## S3 method for class 'pseries'
HDB(x, effect = "all", w = NULL, na.rm = TRUE, fill = TRUE, ...)
## S3 method for class 'pseries'
HDW(x, effect = "all", w = NULL, na.rm = TRUE, fill = TRUE, ...)

## S3 method for class 'pdata.frame'
fhdbetween(x, effect = "all", w = NULL, na.rm = TRUE, fill = TRUE,
           variable.wise = TRUE, ...)
## S3 method for class 'pdata.frame'
fhdwithin(x, effect = "all", w = NULL, na.rm = TRUE, fill = TRUE,
)
```

```

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

```

Arguments

x	a numeric vector, matrix, data frame, 'indexed_series' ('pseries') or 'indexed_frame' ('pdata.frame').
f1	a numeric vector, factor, matrix, data frame or list (which may or may not contain factors). In the HDW/HDB data frame method f1 can also be a one- or two-sided <code>lm()</code> formula with variables contained in x. Interactions (<code>:</code>) and full interactions (<code>*</code>) are supported. See Examples and the Note.
w	a vector of (non-negative) weights.
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 <code>NULL</code> , all columns are selected.
na.rm	remove missing values from both x and f1. by default rows with missing values in x or f1 are removed. In that case an attribute "na.rm" is attached containing the rows removed.
fill	If <code>na.rm = TRUE</code> , <code>fill = TRUE</code> will not remove rows with missing values in x or f1, but fill them with NA's.
variable.wise	<i>(p)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 f1 (f1 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.
effect	<i>plm methods</i> : Select which panel identifiers should be used for centering. 1L takes the first variable in the <code>index</code> , 2L the second etc.. Index variables can also be called by name using a character vector. The keyword "all" uses all identifiers.
stub	a prefix or stub to rename all transformed columns. <code>FALSE</code> will not rename columns.
lm.method	character. The linear fitting method. Supported are "chol" and "qr". See <code>flm</code> .
...	further arguments passed to <code>fixest::demean</code> (other than <code>notes</code> and <code>im_confident</code>) and <code>chol / qr</code> . Possible choices are <code>tol</code> to set a uniform numerical tolerance for the entire fitting process, or <code>nthreads</code> and <code>iter</code> to govern the higher-order centering process.

Details

fhdbetween/HDB and fhdwithin/HDW are powerful functions for high-dimensional linear prediction problems involving large factors and datasets, but can just as well handle ordinary regression problems. They are implemented as efficient wrappers around `fbetween / fwithin`, `flm` and some

C++ code from the `fixest` package that is imported for higher-order centering tasks (thus `fixest` needs to be installed for problems involving more than one factor).

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 `(g)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 either `fbetween / fwithin` for a single factor or `fixest` C++ code for multiple factors. 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 `model.matrix` and expanded to matrices of dummies but projected out beforehand.

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 + 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 `'indexed_series'` (`plm::pseries`) and `'indexed_frame'`'s (`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

On the differences between `fhdwithin/HDW...` and `fwithin/W...`:

- `fhdwithin/HDW` can center data on multiple factors and also partial out continuous variables and factor-continuous interactions 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 fl. 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](#), [flm](#), [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 + LIFEEX ~ iso3c + qF(year))) # Partialling out 2 fixed effects
head(HDW(wlddev, PCGDP + LIFEEX ~ iso3c + qF(year), variable.wise = TRUE)) # Variable-wise
head(HDW(wlddev, PCGDP + LIFEEX ~ iso3c + qF(year) + ODA)) # Adding ODA as a continuous regressor
head(HDW(wlddev, PCGDP + LIFEEX ~ iso3c:qF(decade) + qF(year) + ODA)) # Country-decade and year FE's

head(HDW(wlddev, PCGDP + LIFEEX ~ iso3c*year)) # Country specific time trends
head(HDW(wlddev, PCGDP + LIFEEX ~ iso3c*poly(year, 3))) # Country specific cubic trends

# More complex examples
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)
```

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.

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 indexed data / compatibility with plm:

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

## S3 method for class 'pdata.frame'
flag(x, n = 1, fill = NA, stubs = length(n) > 1L, shift = "time", ...)
## S3 method for class 'pdata.frame'
L(x, n = 1, cols = is.numeric, fill = NA, stubs = TRUE,
```

```

  shift = "time", keep.ids = TRUE, ...)
## S3 method for class 'pdata.frame'
F(x, n = 1, cols = is.numeric, fill = NA, stubs = TRUE,
  shift = "time", keep.ids = TRUE, ...)

# Methods for grouped data frame / 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, 'indexed_series' ('pseries'), 'indexed_frame' ('pdata.frame') or grouped data frame ('grouped_df'). Data must not be numeric.
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, or atomic vector / list of vectors (internally grouped with group) 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	a time vector or list of vectors. Data frame methods also allows one-sided formula i.e. ~time. grouped_df method supports lazy-evaluation i.e. time (no quotes). Either support wrapping a transformation function e.g. ~timeid(time), qG(time) etc.. See also Details on how t is processed.
cols	<i>data.frame method</i> : Select columns to lag 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.
stubs	logical. TRUE will rename all lagged / leaded columns by adding a stub or prefix "Ln." / "Fn.".
shift	<i>pseries / pdata.frame methods</i> : character. "time" performs a fully identified time-lag (if the index contains a time variable), whereas "row" performs a simple (group) lag, where observations are shifted based on the present order of rows (in each group). The latter is significantly faster, but requires time series / panels to be regularly spaced and sorted by time within each group.
keep.ids	<i>data.frame / pdata.frame / grouped_df methods</i> : Logical. Drop all identifiers from the output (which includes all variables passed to by or t). <i>Note</i> : For 'grouped_df' / 'pdata.frame' identifiers are dropped, but the "groups" / "index" attributes are kept.
...	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 are alphabetically ordered. If a time-variable is supplied to `t` (or a list of time-variables uniquely identifying the time-dimension), the series / panel is fully identified and lags / leads can be securely computed even if the data is unordered / irregular.

Note that the `t` argument is processed as follows: If `is.factor(t) || (is.numeric(t) && !is.object(t))` (i.e. `t` is a factor or plain numeric vector), it is assumed to represent unit timesteps (e.g. a 'year' variable in a typical dataset), and thus coerced to integer using `as.integer(t)` and directly passed to C++ without further checks or transformations at the R-level. Otherwise, if `is.object(t) && is.numeric(unclass(t))` (i.e. `t` is a numeric time object, most likely 'Date' or 'POSIXct'), this object is passed through `timeid` before going to C++. Else (e.g. `t` is character), it is passed through `qG` which performs ordered grouping. If `t` is a list of multiple variables, it is passed through `finteraction`. You can customize this behavior by calling any of these functions (including `unclass/as.integer`) on your time variable beforehand.

At the C++ level, if both `g/by` and `t` are supplied, `flag` works as follows: Use two initial passes to create an ordering through which the data are accessed. First-pass: Calculate minimum and maximum time-value for each individual. Second-pass: Generate an internal ordering vector (`o`) 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 an integer/factor variable. For irregular time/panel series, `length(o) > length(x)`, and `o` represents the unobserved 'complete series'. If `length(o) > 1e7 && length(o) > 3*length(x)`, a warning is issued to make you aware of potential performance implications of the oversized ordering vector.

The 'indexed_series' ('pseries') and 'indexed_frame' ('pdata.frame') methods automatically utilize the identifiers attached to these objects, which are already factors, thus lagging is quite efficient. However, the internal ordering vector still needs to be computed, thus if data are known to be ordered and regularly spaced, using `shift = "row"` to toggle a simple group-lag (same as utilizing `g` but not `t` in other methods) can yield a significant performance gain.

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 its 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))

# Regressing GDP on its lags and life-Expectancy and its lags
summary(lm(PCGDP ~ ., L(wlddev, 0:2, ~iso3c, ~year, 9:10, keep.ids = FALSE)))

## Indexing the data: facilitates time-based computations
wldi <- findex_by(wlddev, iso3c, year)
head(L(wldi, 0:2, cols = 9:10)) # Again 2 lags of GDP and LIFEEEX
head(L(wldi$PCGDP))           # Lagging an indexed series
summary(lm(PCGDP ~ L(PCGDP,1:2) + L(LIFEEEX,0:2), wldi)) # Running the lm again
summary(lm(PCGDP ~ ., L(wldi, 0:2, 9:10, keep.ids = FALSE))) # Same thing

## Using grouped data:
library(magrittr)
wlddev %>% fgroup_by(iso3c) %>% fselect(PCGDP, LIFEEEX) %>% flag(0:2)
wlddev %>% fgroup_by(iso3c) %>% fselect(year, PCGDP, LIFEEEX) %>% flag(0:2, year) # Also using t (safer)
```

flm

*Fast (Weighted) Linear Model Fitting***Description**

flm is a fast linear model command that (by default) only returns a coefficient matrix. 6 different efficient fitting methods are implemented: 4 using base R linear algebra, and 2 utilizing the *RcppAr*-

madillo 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(...) # Internal method dispatch: default if is.atomic(..1)

## Default S3 method:
flm(y, X, w = NULL, add.icpt = FALSE, return.raw = FALSE,
     method = c("lm", "solve", "qr", "arma", "chol", "eigen"),
     eigen.method = 3L, ...)

## S3 method for class 'formula'
flm(formula, data = NULL, weights = NULL, add.icpt = TRUE, ...)
```

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.

formula a `lm` formula, without factors, interaction terms or other operators (`:`, `*`, `^`, `-`, etc.), may include regular transformations e.g. `log(var)`, `cbind(y1, y2)`, `magrittr::multiply_by(var1, var2)`, `magrittr::raise_to_power(var, 2)`.

data a named list or data frame.

weights a weights vector or expression that results in a vector when evaluated in the data environment.

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), y)</code> .
4	"arma"	uses <code>RcppArmadillo::fastLmPure</code> .
5	"chol"	<code>chol2inv(chol(crossprod(X))) %*% crossprod(X, y)</code> (quite fast, requires <code>crossprod(X)</code> to be positive definite).
6	"eigen"	uses <code>RcppEigen::fastLmPure</code> (very fast but, depending on the method, also unstable if multicollinear).

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. For the formula method further arguments passed to the default method. Additional arguments can also be passed to the default method e.g. `tol = value` to set 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 the LINPACK 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, "dgMatrix")` instead of just X .

See Also

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

Examples

```
# Simple usage
coef <- flm(mpg ~ hp + carb, mtcars, w = wt)

# Same thing in programming usage
flm(mtcars$mpg, qM(mtcars[c("hp", "carb")] ), mtcars$wt, add.icpt = TRUE)

# Check this is correct
lmcoef <- coef(lm(mpg ~ hp + carb, weights = wt, mtcars))
all.equal(drop(coef), lmcoef)

# Multi-dependent variable (only some methods)
flm(cbind(mpg, qsec) ~ hp + carb, mtcars, w = wt)

# Returning raw results from solver: different for different methods
flm(mpg ~ hp + carb, mtcars, return.raw = TRUE)
```

```
f1m(mpg ~ hp + carb, mtcars, method = "qr", return.raw = TRUE)

# Test that all methods give the same result
all_obj_equal(lapply(1:6, function(i)
  f1m(mpg ~ hp + carb, mtcars, w = wt, 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, nthreads = 1L, ...)
```

S3 method for class 'matrix'

```
fmean(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = TRUE, drop = TRUE, nthreads = 1L, ...)
```

S3 method for class 'data.frame'

```
fmean(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = TRUE, drop = TRUE, nthreads = 1L, ...)
```

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, nthreads = 1L, ...)
```

Arguments

x	a numeric vector, matrix, data frame or grouped data frame (class '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: 0 - "replace_NA" 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.
nthreads	integer. The number of threads to utilize. See Details of fsum .
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. If TRA is used, passing set = TRUE will transform data by reference and return the result invisibly.

Details

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 $x[\text{complete.cases}(x, w)]$ and $w[\text{complete.cases}(x, w)]$.

For further computational details see [fsum](#), which works equivalently.

Value

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

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 data frames - created with dplyr::group_by or fgroup_by
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, nthreads = 1L, ...)

## S3 method for class 'matrix'
fmedian(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
        use.g.names = TRUE, drop = TRUE, nthreads = 1L, ...)

## S3 method for class 'data.frame'
fmedian(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
        use.g.names = TRUE, drop = TRUE, nthreads = 1L, ...)

## 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,
        nthreads = 1L, ...)

```

Arguments

x	a numeric vector, matrix, data frame or grouped data frame (class '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, but only if x is also missing.
TRA	an integer or quoted operator indicating the transformation to perform: 0 - "replace_NA" 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.
nthreads	integer. The number of threads to utilize. Parallelism is across groups for grouped computations and at the column-level otherwise. No parallelism is available for weighted computations.
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. If TRA is used, passing set = TRUE will transform data by reference and return the result invisibly.

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. 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 (grouped, weighted) median.

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

x a numeric vector, matrix, data frame or grouped data frame (class '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.

TRA	an integer or quoted operator indicating the transformation to perform: 0 - "replace_NA" 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.
...	arguments to be passed to or from other methods. If TRA is used, passing set = TRUE will transform data by reference and return the result invisibly.

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 `max` and `min` which just run through without any checks).

For further computational details see [fsum](#).

Value

`fmax` returns the maximum value of x, grouped by g, or (if [TRA](#) is used) x transformed by its (grouped) maximum value. 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 data frames - created with dplyr::group_by or fgroup_by
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, (default) first or last 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", nthreads = 1L, ...)
```

S3 method for class 'matrix'

```
fmode(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
      use.g.names = TRUE, drop = TRUE, ties = "first", nthreads = 1L, ...)
```

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", nthreads = 1L, ...)
```

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", nthreads = 1L, ...)
```

Arguments

<code>x</code>	a vector, matrix, data frame or grouped data frame (class 'grouped_df').
<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: 0 - "replace_NA" 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> , NA is treated as any other 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>ties</code>	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.
4	"last"	take the last occurring mode.

Note: "min"/"max" don't work with character data. See also Details.

<code>nthreads</code>	integer. The number of threads to utilize. Parallelism is across groups for grouped computations and at the column-level otherwise.
<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. If <code>TRA</code> is used, passing <code>set = TRUE</code> will transform data by reference and return the result invisibly.

Details

`fmode` implements a pretty fast C-level hashing algorithm inspired by the *kit* package to find the statistical mode.

If `na.rm = FALSE`, NA is not removed but treated as any other value (i.e. its 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 (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. `ties = "last"` on the other hand gives 1. 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"` 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. `fmode` also implements a fast method for logical values which does not support the options "first"/"last" i.e. `TRUE` is returned unless `ties = "min"`.

`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), `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 (grouped, weighed) mode.

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 = "last")
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, LIFEX)) # 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, nthreads = 1L, ...)

## S3 method for class 'matrix'
fndistinct(x, g = NULL, TRA = NULL, na.rm = TRUE,
           use.g.names = TRUE, drop = TRUE, nthreads = 1L, ...)

## S3 method for class 'data.frame'
fndistinct(x, g = NULL, TRA = NULL, na.rm = TRUE,
           use.g.names = TRUE, drop = TRUE, nthreads = 1L, ...)

## S3 method for class 'grouped_df'
fndistinct(x, TRA = NULL, na.rm = TRUE,
           use.g.names = FALSE, keep.group_vars = TRUE, nthreads = 1L, ...)

```

Arguments

<code>x</code>	a vector, matrix, data frame or grouped data frame (class 'grouped_df').
<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: 0 - "replace_NA" 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>nthreads</code>	integer. The number of threads to utilize. Parallelism is across groups for grouped computations and at the column-level otherwise.
<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. If <code>TRA</code> is used, passing <code>set = TRUE</code> will transform data by reference and return the result invisibly.

Details

`fndistinct` implements a pretty fast C-level hashing algorithm inspired by the *kit* package to find the number of distinct values.

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.

`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

[fnunique](#), [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 data frames - created with dplyr::group_by or fgroup_by
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 data frame (class '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.
TRA	an integer or quoted operator indicating the transformation to perform: 0 - "replace_NA" 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. If TRA is used, passing set = TRUE will transform data by reference and return the result invisibly.

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 data frames - created with dplyr::group_by or fgroup_by
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", nthreads = 1L, ...)
```

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", nthreads = 1L, ...)
```

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", nthreads = 1L, ...)
```

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", nthreads = 1L, ...)
```

Arguments

x	a numeric vector, matrix, data frame or grouped data frame (class 'grouped_df').
n	the element to return using a single integer index such that $1 < n < NROW(x)$, or a probability $0 < n < 1$. See Details.
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.

<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: 0 - "replace_NA" 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>nthreads</code>	integer. The number of threads to utilize. Parallelism is across groups for grouped computations and at the column-level otherwise. No parallelism is available for weighted computations.												
<code>ties</code>	an integer or character string specifying the method to resolve ties between adjacent qualifying elements: <table data-bbox="406 777 1218 924"> <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. If <code>TRA</code> is used, passing <code>set = TRUE</code> will transform data by reference and return the result invisibly.												

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`L'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 $n = \text{NROW}(x)$ 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 $p = (n-1)/(\text{NROW}(x)/\text{ng}-1)$ (where `ng` contains the number of unique groups in `g`) and `ties = "min"` 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 (grouped, weighted) n 'th element.

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 data frame (class 'grouped_df').
<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: 0 - "replace_NA" 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>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 product of weighting variable after computation (if contained in <code>grouped_df</code>).
<code>...</code>	arguments to be passed to or from other methods. If <code>TRA</code> is used, passing <code>set = TRUE</code> will transform data by reference and return the result invisibly.

Details

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

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)]`.

For further computational details see [fsum](#), which works equivalently.

Value

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

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 data frames - created with dplyr::group_by or fgroup_by
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()
```

frename

Fast Renaming and Relabelling Objects

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. `relabel` and `setrelabel` do that same for labels attached to list elements / data frame columns.

Usage

```
frename(.x, ..., cols = NULL)
rnm(.x, ..., cols = NULL) # Shorthand for frename()

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

```
relabel(.x, ..., cols = NULL, attrn = "label")
```

```
setrelabel(.x, ..., cols = NULL, attrn = "label")
```

Arguments

<code>.x</code>	for (f/set)rename: an R object with a "names" attribute. For (set)relabel: a named list.
<code>...</code>	either tagged vector expressions of the form <code>name = newname / name = newlabel</code> , or a single function (+ optional arguments to the function) applied to all names/labels (of columns/elements selected in <code>cols</code>).
<code>cols</code>	If <code>...</code> is a function, select a subset of columns/elements to rename/relabel using names, indices, a logical vector or a function applied to the columns if <code>.x</code> is a list (e.g. <code>is.numeric</code>).
<code>attrn</code>	character. Name of attribute to store labels or retrieve labels from.

Value

`.x` renamed / relabelled. `setrename` and `setrelabel` return `.x` invisibly.

Note

Note that both `relabel` and `setrelabel` modify `.x` by reference. This is because labels are attached to columns themselves, making it impossible to avoid permanent modification by taking a shallow copy of the encompassing list / data.frame. On the other hand `frename` makes a shallow copy whereas `setrename` also modifies by reference.

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)
```

```
## Relabelling (by reference)
# namlab(relabel(wlddev, PCGDP = "GDP per Capita", LIFEEX = "Life Expectancy"))
# namlab(relabel(wlddev, toupper))
```

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.

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 indexed data / 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 grouped data frame / 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, 'indexed_series' ('pseries'), 'indexed_frame' ('pdata.frame') or grouped data frame ('grouped_df').
g	a factor, GRP object, or atomic vector / list of vectors (internally grouped with group) 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>STD (p)data.frame method</i> : Select columns to scale using a function, column names, indices or a logical vector. Default: All numeric columns. <i>Note</i> : cols is ignored if a two-sided formula is passed to by.
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. 1L takes the first variable in the index , 2L 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. FALSE will not rename columns.
mean	the mean to center on (default is 0). If mean = FALSE, no centering will be performed. In that case the scaling is mean-preserving. A numeric value different from 0 (i.e. mean = 5) 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 mean = "overall.mean". 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. sd = 3) will scale the data to have a standard deviation of 3. A special option when performing grouped scaling is sd = "within.sd". 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. The result is that all columns in `x` will have a (weighted) mean 0 and (weighted) 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.

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](#).

See Also

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

Examples

```
## Simple Scaling & Centering / Standardizing
head(fscales(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(fscales(get_vars(wlddev,9:12), wlddev$iso3c)) # Standardizing 4 series within each country
head(STD(wlddev, ~iso3c, cols = 9:12))           # Same thing using STD, id's added
pwcors(fscales(get_vars(wlddev,9:12), wlddev$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$iso3c)) # This calculates the within standard deviations
head(qsu(fscales(get_vars(wlddev, 9:12),
  wlddev$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

## Indexed data
wldi <- findindex_by(wlddev, iso3c, year)
head(STD(wldi)) # Standardizing all numeric variables by country
head(STD(wldi, effect = 2L)) # Standardizing all numeric variables by year

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

# Grouped data
library(magrittr)
wlddev %>% fgroup_by(iso3c) %>% fselect(PCGDP,LIFEEX) %>% STD()
wlddev %>% fgroup_by(iso3c) %>% fselect(PCGDP,LIFEEX) %>% STD(weights) # weighted standardizing
wlddev %>% fgroup_by(iso3c) %>% fselect(PCGDP,LIFEEX,POP) %>% STD(POP) # weighting by POP ->
# ..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, analgous to dplyr::select but significantly faster
fselect(.x, ..., return = "data")
fselect(x, ...) <- value
slt(.x, ..., return = "data") # Shorthand for fselect
slt(x, ...) <- value          # Shorthand 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", ...) # Shorthand for get_vars
  gvr(x, vars, return = "data", ...) # Shorthand for get_vars(..., regex = TRUE)

get_vars(x, vars, regex = FALSE, ...) <- value
  gv(x, vars, ...) <- value          # Shorthand for get_vars<-
  gvr(x, vars, ...) <- value        # Shorthand 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")          # Shorthand for add_vars
  av(x, pos = "end") <- value      # Shorthand for add_vars<-

## Select and replace columns by data type

num_vars(x, return = "data")
num_vars(x) <- value
  nv(x, return = "data")          # Shorthand for num_vars
  nv(x) <- value                  # Shorthand 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, .x a data frame or list.

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 `NROW(value) == nrow(x)`.

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 e.g. `fselect(mtcars, newname = mpg, hp, carb:vs)`. 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 (ab-

strating 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 (except for 'sf' and 'data.table' which are handled internally).

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.

All functions introduced here perform their operations class-independent. They all basically work like this: (1) save the attributes of `x`, (2) `unclass x`, (3) subset, replace or append `x` as a list, (4) modify the "names" component of the attributes of `x` accordingly and (5) efficiently attach the attributes again to the result from step (3). Thus they can freely be applied to `data.table`'s, grouped tibbles, panel data frames and other classes and will return an object of exactly the same class and the same attributes.

Note

The functions here only check the length of the first column, which is one of the reasons why they are so fast. When lists of unequal-length columns are offered as replacements this yields a malformed data frame (which will also print a warning in the console i.e. you will notice that).

See Also

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

Examples

```
## World Development Data
head(fselect(wlddev, Country = country, Year = year, ODA)) # Fast dplyr-like selecting
head(fselect(wlddev, -country, -year, -PCGDP))
head(fselect(wlddev, country, year, PCGDP:ODA))
head(fselect(wlddev, -(PCGDP:ODA)))
fselect(wlddev, country, year, PCGDP:ODA) <- NULL           # Efficient deleting
head(wlddev)
rm(wlddev)

head(num_vars(wlddev))                                     # Select numeric variables
head(cat_vars(wlddev))                                    # Select categorical (non-numeric) vars
head(get_vars(wlddev, is_categorical))                    # Same thing

num_vars(wlddev) <- num_vars(wlddev)                       # Replace Numeric Variables by themselves
get_vars(wlddev, is.numeric) <- get_vars(wlddev, is.numeric) # Same thing
```

```

head(get_vars(wlddev, 9:12))          # Select columns 9 through 12, 2x faster
head(get_vars(wlddev, -(9:12)))      # All except columns 9 through 12
head(get_vars(wlddev, c("PCGDP", "LIFEEX", "GINI", "ODA"))) # Select using column names
head(get_vars(wlddev, "[[:upper:]]", regex = TRUE)) # Same thing: match upper-case var. names
head(gvr(wlddev, "[[:upper:]]"))     # Same thing

get_vars(wlddev, 9:12) <- get_vars(wlddev, 9:12) # 9x faster wlddev[9:12] <- wlddev[9:12]
add_vars(wlddev) <- STD(gv(wlddev,9:12), wlddev$iso3c) # Add Standardized columns 9 through 12
head(wlddev) # gv and av are shortcuts

get_vars(wlddev, 14:17) <- NULL # Efficient Deleting added columns again
av(wlddev, "front") <- STD(gv(wlddev,9:12), wlddev$iso3c) # Again adding in Front
head(wlddev)
get_vars(wlddev, 1:4) <- NULL # Deleting
av(wlddev,c(10,12,14,16)) <- W(wlddev,~iso3c, cols = 9:12, # Adding next to original variables
keep.by = FALSE)
head(wlddev)
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. The methods also provide enhanced functionality compared to [subset](#). The function `ss` provides an (internal generic) programmers alternative to `[` that does not drop dimensions and is significantly faster than `[` for data frames.

Usage

```

fsubset(.x, ...)
sbt(.x, ...) # Shorthand 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, ...)

# Methods for indexed data / compatibility with plm:

## S3 method for class 'pseries'

```

```
fsubset(.x, subset, ..., drop.index.levels = "id")

## S3 method for class 'pdata.frame'
fsubset(.x, subset, ..., drop.index.levels = "id")

# Fast subsetting (replaces `[` with drop = FALSE, programmers choice)
ss(x, i, j)
```

Arguments

.x	object to be subsetted according to different methods.
x	a data frame / list, matrix or vector/array (only i).
subset	logical expression indicating elements or rows to keep: missing values are taken as FALSE. The default, matrix and pseries 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 [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> .
drop.index.levels	character. Either "id", "time", "all" or "none". See indexing .

Details

fsubset is a generic function, with methods supplied for vectors, matrices, and data frames (including lists). It represents an improvement over [subset](#) in terms of both speed and functionality. The function `ss` is an improvement of `[` to subset (vectors) matrices and data frames without dropping dimensions. It is significantly faster than `[.data.frame`.

For ordinary vectors, subset can be integer or logical, subsetting is done in C and more efficient than `[` for large vectors.

For matrices the implementation is all base-R but slightly more efficient and more versatile than [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`, and new column names may be assigned e.g. `fsubset(data, col1 > 20, newname = col2, col3:col6)` (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 is implemented in C, hence it is significantly faster than `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 `fdroplevels` to drop all unused levels from a data frame.

Value

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

Note

`ss` offers no support for indexed data. Use `fsubset` with indices instead.

No replacement method `fsubset<-` or `ss<-` is offered in *collapse*. For efficient subset replacement (without copying) use `data.table::set`, which can also be used with data frames and tibbles. To search and replace certain elements without copying, and to efficiently copy elements / rows from an equally sized vector / data frame, see `setv`.

For subsetting columns alone, please also see [selecting and replacing columns](#).

Note that the use of `%==%` can yield significant performance gains on large data.

See Also

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

Examples

```
fsubset(airquality, Temp > 90, Ozone, Temp)
fsubset(airquality, Temp > 90, OZ = Ozone, Temp) # With renaming
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)
fsubset(airquality, Day %==% 1, -Temp) # Faster for big data, as %==% directly returns indices

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
```

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, fill = FALSE, nthreads = 1L, ...)
```

```
## S3 method for class 'matrix'
fsum(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
     use.g.names = TRUE, drop = TRUE, fill = FALSE, nthreads = 1L, ...)
```

```
## S3 method for class 'data.frame'
fsum(x, g = NULL, w = NULL, TRA = NULL, na.rm = TRUE,
     use.g.names = TRUE, drop = TRUE, fill = FALSE, nthreads = 1L, ...)
```

```
## 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, fill = FALSE, nthreads = 1L, ...)
```

Arguments

x	a numeric vector, matrix, data frame or grouped data frame (class '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: 0 - "replace_NA" 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.
fill	logical. Initialize result with 0 instead of NA when na.rm = TRUE e.g. fsum(NA, fill = TRUE) returns 0 instead of NA.
nthreads	integer. The number of threads to utilize. See Details .
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. If TRA is used, passing set = TRUE will transform data by reference and return the result invisibly.

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 `sum` which just runs through without any checks).

The weighted sum (e.g. survey total) is computed as `sum(x * w)`, but in one pass and about twice as efficient. 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 are therefore extremely fast. See [Benchmark](#) and [Examples](#) below.

When applied to data frames with groups or `drop = FALSE`, `fsum` preserves all column attributes. The attributes of the data frame itself are also preserved.

Since v1.6.0 `fsum` explicitly supports integers. Integers are summed using the long long type in C which is bounded at $\pm 9,223,372,036,854,775,807$ (so ~ 4.3 billion times greater than the minimum/maximum R integer bounded at $\pm 2,147,483,647$). If the value of the sum is outside $\pm 2,147,483,647$, a double containing the result is returned, otherwise an integer is returned. With groups, an integer overflow error is provided if the sum in any group is outside $\pm 2,147,483,647$. Data should be coerced to double beforehand in such cases.

Multithreading, added in v1.8.0, applies at the column-level unless `g = NULL` and `nthreads > NCOL(x)`. Parallelism over groups is not available because sums are computed simultaneously within each group. `nthreads = 1L` uses a serial version of the code, not parallel code running on one thread. This serial code is always used with less than 100,000 obs (`length(x) < 100000` for vectors and matrices), because parallel execution itself has some overhead.

Value

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

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 data frames - created with dplyr::group_by or fgroup_by
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 1.000000 100 a

```

fsummarise

Fast Summarise

Description

fsummarize is a much faster version of `dplyr::summarise`, when used together with the [Fast Statistical Functions](#).

Usage

```

fsummarise(.data, ..., keep.group_vars = TRUE)
smr(.data, ..., keep.group_vars = TRUE)      # Shorthand

```

Arguments

<code>.data</code>	a (grouped) data frame or named list of columns. Grouped data can be created with fgroup_by or <code>dplyr::group_by</code> .
<code>...</code>	name-value pairs of summary functions, or across statements. For fast performance use the Fast Statistical Functions .
<code>keep.group_vars</code>	logical. FALSE removes grouping variables after computation.

Value

If `.data` is grouped by [fgroup_by](#) or `dplyr::group_by`, the result is a data frame of the same class and attributes with rows reduced to the number of groups. If `.data` is not grouped, the result is a data frame of the same class and attributes with 1 row.

Note

Since v1.7, `fsummarise` is fully featured, allowing expressions using functions and columns of the data as well as external scalar values (just like `dplyr::summarise`). **NOTE** however that once a [Fast Statistical Function](#) is used, the execution will be vectorized instead of split-apply-combine computing over groups. Please see the first Example.

See Also

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

Examples

```

library(magrittr) # Note: Used because |> is not available on older R versions
## Since v1.7, fsummarise supports arbitrary expressions, and expressions
## containing fast statistical functions receive vectorized execution:

# (a) This is an expression using base R functions which is executed by groups
mtcars %>% fgroup_by(cyl) %>% fsummarise(res = mean(mpg) + min(qsec))

# (b) Here, the use of fmean causes the whole expression to be executed
# in a vectorized way i.e. the expression is translated to something like
# fmean(mpg, g = cyl) + min(mpg) and executed, thus the result is different
# from (a), because the minimum is calculated over the entire sample
mtcars %>% fgroup_by(cyl) %>% fsummarise(mpg = fmean(mpg) + min(qsec))

# (c) For fully vectorized execution, use fmin. This yields the same as (a)
mtcars %>% fgroup_by(cyl) %>% fsummarise(mpg = fmean(mpg) + fmin(qsec))

# In across() statements it is fine to mix different functions, each will
# be executed on its own terms (i.e. vectorized for fmean and standard for sum)
mtcars %>% fgroup_by(cyl) %>% fsummarise(across(mpg:hp, list(fmean, sum)))

# Note that this still detects fmean as a fast function, the names of the list
# are irrelevant, but the function name must be typed or passed as a character vector,
# Otherwise functions will be executed by groups e.g. function(x) fmean(x) won't vectorize
mtcars %>% fgroup_by(cyl) %>% fsummarise(across(mpg:hp, list(mu = fmean, sum = sum)))

# We can force none-vectorized execution by setting .apply = TRUE
mtcars %>% fgroup_by(cyl) %>% fsummarise(across(mpg:hp, list(mu = fmean, sum = sum), .apply = TRUE))

# Another argument of across(): Order the result first by function, then by column
mtcars %>% fgroup_by(cyl) %>%
  fsummarise(across(mpg:hp, list(mu = fmean, sum = sum), .transpose = FALSE))

#-----
# Examples that also work for pre 1.7 versions

# Simple use
fsummarise(mtcars, mean_mpg = fmean(mpg),
           sd_mpg = fsd(mpg))

# Using base functions (not a big difference without groups)
fsummarise(mtcars, mean_mpg = mean(mpg),
           sd_mpg = sd(mpg))

# Grouped use
mtcars %>% fgroup_by(cyl) %>%
  fsummarise(mean_mpg = fmean(mpg),
            sd_mpg = fsd(mpg))

# This is still efficient but quite a bit slower on large data (many groups)
mtcars %>% fgroup_by(cyl) %>%

```

```

    fsummarise(mean_mpg = mean(mpg),
               sd_mpg = sd(mpg))

# Weighted aggregation
mtcars %>% fgroup_by(cyl) %>%
  fsummarise(w_mean_mpg = fmean(mpg, wt),
             w_sd_mpg = fsd(mpg, wt))

## Can also group with dplyr::group_by, but at a conversion cost, see ?GRP
library(dplyr)
mtcars %>% group_by(cyl) %>%
  fsummarise(mean_mpg = fmean(mpg),
             sd_mpg = fsd(mpg))

# Again less efficient...
mtcars %>% group_by(cyl) %>%
  fsummarise(mean_mpg = mean(mpg),
             sd_mpg = sd(mpg))

```

ftransform

Fast Transform and Compute Columns on a Data Frame

Description

ftransform is a much faster version of [transform](#) 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. [fcompute](#) computes and returns new columns. These functions evaluate all arguments simultaneously, allow list-input (nested pipelines) and disregard grouped data.

Catering to the *tidyverse* user, v1.7.0 introduced [fmutate](#), providing familiar functionality i.e. arguments are evaluated sequentially, computation on grouped data is done by groups, and functions can be applied to multiple columns using [across](#). See also the [Details](#).

Usage

```

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

# Modify data frame by reference
settransform(.data, ...)
settransformv(.data, ...) # Same arguments as ftransformv
settfm(.data, ...) # Shorthand for settransform
settfmv(.data, ...)

```

```

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

# Compute columns, returned as a new data frame
fcompute(.data, ..., keep = NULL)
fcomputev(.data, vars, FUN, ..., apply = TRUE, keep = NULL)

# New: dplyr-style mutate (sequential evaluation + across() feature)
fmutate(.data, ..., .keep = "all")
mtt(.data, ..., .keep = "all") # Shorthand for fmutate

```

Arguments

<code>.data</code>	a data frame or named list of columns.
<code>...</code>	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> and <code>fcomputev</code> , <code>...</code> can be used to pass further arguments to <code>FUN</code> . <i>Note:</i> The ellipsis (<code>...</code>) is always evaluated within the data frame (<code>.data</code>) environment. See Examples. <code>fmutate</code> supports across statements, and evaluates tagged vector expressions sequentially.
<code>vars</code>	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>). Since v1.7 <code>vars</code> is evaluated within the <code>.data</code> environment, permitting expressions on columns e.g. <code>c(col1, col3:coln)</code> .
<code>FUN</code>	a single function yielding a result of length <code>NROW(.data)</code> or 1. See also <code>apply</code> .
<code>apply</code>	logical. <code>TRUE</code> (default) will apply <code>FUN</code> to each column selected in <code>vars</code> ; <code>FALSE</code> will apply <code>FUN</code> to the subsetting data frame i.e. <code>FUN(get_vars(.data, vars), ...)</code> . The latter is useful for <i>collapse</i> functions with data frame or grouped / panel data frame methods, yielding performance gains and enabling grouped transformations. See Examples.
<code>value</code>	a named list of replacements, it will be treated like an evaluated list of <code>column = value</code> arguments.
<code>keep</code>	select columns to preserve using column names, indices or a function (e.g. <code>is.numeric</code>). By default computed columns are added after the preserved ones, unless they are assigned the same name in which case the preserved columns will be replaced in order.
<code>.keep</code>	Either one of <code>"all"</code> , <code>"used"</code> , <code>"unused"</code> or <code>"none"</code> (see mutate), or column names/indices/function as <code>keep</code> .

Details

The `...` arguments to `ftransform` are tagged vector expressions, which are evaluated in the data frame `.data`. The tags are matched against `names(.data)`, and for those that match, the values replace the corresponding variable in `.data`, whereas the others are appended to `.data`. 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(.data)` 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` (without the grouping feature) 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(v)` works just like `ftransform(v)`, but returns only the changed / computed columns without modifying or appending the data in `.data`. See Examples.

The function `fmutate` added in v1.7.0, provides functionality familiar from *dplyr* 1.0.0 and higher. It evaluates tagged vector expressions sequentially and does operations by groups on a grouped frame (thus it is slower than `ftransform` if you have many tagged expressions or a grouped data frame). *Note* however that *collapse* does not depend on *rlang*, so things like lambda expressions are not available. *Note also* that `fmutate` operates differently on grouped data whether you use `.FAST_FUN` or base R functions / functions from other packages. With `.FAST_FUN` (including `.OPERATOR_FUN`, excluding `fhdbetween` / `fhdwithin` / `HDW` / `HDB`), `fmutate` performs an efficient vectorized execution, i.e. the grouping object from the grouped data frame is passed to the `g` argument of these functions, and for `.FAST_STAT_FUN` also `TRA = "replace_fill"` is set (if not overwritten by the user), yielding internal grouped computation by these functions without the need for splitting the data by groups. For base R and other functions, `fmutate` performs classical split-apply-combine computing i.e. the relevant columns of the data are selected and split into groups, the expression is evaluated for each group, and the result is recombined and suitably expanded to match the original data frame. **Note** that it is not possible to mix vectorized and standard execution in the same expression!! Vectorized execution is performed if **any** `.FAST_FUN` or `.OPERATOR_FUN` is part of the expression, thus a code like `mtcars |> gby(cyl) |> fmutate(new = fmin(mpg) / min(mpg))` will be expanded to something like `mtcars %>% gby(cyl) %>% ftransform(new = fmin(mpg, g = GRP(.), TRA = "replace_fill") / min(mpg))` and then executed, i.e. `fmin(mpg)` will be executed in a vectorized way, and `min(mpg)` will not be executed by groups at all.

Value

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

Note

`ftransform` ignores grouped data. This is on purpose as it allows non-grouped transformation inside a pipeline on grouped data, and affords greater flexibility and performance in programming with the `.FAST_FUN`. In particular, you can run a nested pipeline inside `ftransform`, and decide

which expressions should be grouped, and you can use the ad-hoc grouping functionality of the `.FAST_FUN`, allowing operations where different groupings are applied simultaneously in an expression. See Examples or the answer provided [here](#).

`fmutate` on the other hand supports grouped operations just like `dplyr::mutate`, but works in two different ways depending on whether you use `.FAST_FUN` in an expression or other functions. See the Examples section of [fsummarise](#) for an illustration.

See Also

[across](#), [fsummarise](#), [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 multiple 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 grouped modification of single columns in a grouped dataset, we can use GRP():
airquality %>% fgroup_by(Month) %>%
  ftransform(W_Ozone = fwithin(Ozone, GRP(.)), # Grouped centering
             sd_Ozone_m = fsd(Ozone, GRP(.), TRA = "replace"), # In-Month standard deviation
             sd_Ozone = fsd(Ozone, TRA = "replace"), # Overall standard deviation
             sd_Ozone2 = fsd(Ozone, TRA = "replace_fill"), # Same, overwriting NA's
             sd_Ozone3 = fsd(Ozone)) %>% head # Same thing (calling alloc())

rm(airquality)

## 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 data frame (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))

# Can preserve existing columns, computed ones are added to the right if names are different
head(fcompute(airquality, new = -Ozone, new2 = 1, keep = 1:3))

# If given same name as preserved columns, preserved columns are replaced in order...
head(fcompute(airquality, Ozone = -Ozone, new = 1, keep = 1:3))

# Same holds for fcomputev
head(fcomputev(iris, is.numeric, log)) # Same as:
iris %>% get_vars(is.numeric) %>% dapply(log) %>% head()

head(fcomputev(iris, is.numeric, log, keep = "Species")) # Adds in front
head(fcomputev(iris, is.numeric, log, keep = names(iris))) # Preserve order

# Keep a subset of the data, add standardized columns
head(fcomputev(iris, 3:4, STD, apply = FALSE, keep = names(iris)[3:5]))

```

funique

Fast Unique Elements / Rows

Description

funique is an efficient alternative to `unique` (or `unique.data.table`, `kit::funique`, `dplyr::distinct`).

fnunique is an alternative to `NROW(unique(x))` (or `data.table::uniqueN`, `kit::uniqLen`, `dplyr::n_distinct`).

The *collapse* versions are versatile and highly competitive.

Usage

```

funique(x, ...)

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

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

## S3 method for class 'sf'
funique(x, cols = NULL, sort = FALSE, method = "auto", ...)

# Methods for indexed data / compatibility with plm:

```

```
## S3 method for class 'pseries'
funique(x, sort = FALSE, method = "auto", drop.index.levels = "id", ...)

## S3 method for class 'pdata.frame'
funique(x, cols = NULL, sort = FALSE, method = "auto", drop.index.levels = "id", ...)

fnunique(x) # Fast NROW(unique(x))
```

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.

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 if sort = FALSE else radix.
2	"radix"	use radix ordering to determine unique values. Supports sort = FALSE but only for character data.
3	"hash"	use index hashing to determine unique values. Supports sort = TRUE but only for atomic vectors (default).

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 (e.g. `is.character`). *Note:* All columns are returned.

... arguments passed to [radixorder](#), e.g. `decreasing` or `na.last`. Only applicable if `method = "radix"`.

drop.index.levels character. Either "id", "time", "all" or "none". See [indexing](#).

Details

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

The `sf` method simply ignores the geometry column when determining unique values.

Methods for indexed data also subset the index accordingly.

Value

`x` with duplicate elements/rows removed.

Note

No matrix method is provided. Please see `kit::funique` for a fast alternative with a matrix method.

See Also

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

Examples

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

<code>x</code>	a numeric vector, matrix, data frame or grouped data frame (class 'grouped_df').
<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: 0 - "replace_NA" 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>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 summed weighting variable after computation (if contained in <code>grouped_df</code>).
<code>stable.algo</code>	logical. TRUE (default) use Welford's numerically stable online algorithm. FALSE implements a faster but numerically unstable one-pass method. See Details.
<code>...</code>	arguments to be passed to or from other methods. If <code>TRA</code> is used, passing <code>set = TRUE</code> will transform data by reference and return the result invisibly.

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[complete.cases(x, w)]` and `w[complete.cases(x, w)]`.

For further computational detail see [fsum](#).

Value

fvar returns the (w weighted) variance of x, grouped by g, or (if TRA is used) x transformed by its (grouped, weighted) variance. 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 data frames - created with dplyr::group_by or fgroup_by
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

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. `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, exact element names or indices applied to all final objects. `has_elem` checks for the existence of an 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 / subset list tree
get_elem(l, elem, recursive = TRUE, DF.as.list = FALSE, keep.tree = FALSE,
         keep.class = FALSE, regex = FALSE, ...)

## Check for the existence of elements
has_elem(l, elem, recursive = TRUE, DF.as.list = FALSE, regex = FALSE, ...)
```

Arguments

<code>l</code>	a list.
<code>value</code>	a list of the same length as the extracted subset of <code>l</code> .
<code>elem</code>	a function returning TRUE or FALSE when applied to elements of <code>l</code> , or a character vector of element names or regular expressions (if <code>regex = TRUE</code>). <code>get_elem</code> also supports a vector or indices which will be used to subset all final objects.
<code>return</code>	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 list (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, names are replaced together with the data.

<code>recursive</code>	logical. Should the list search be recursive (i.e. go though all the elements), or just at the top-level?
<code>DF.as.list</code>	logical. TRUE treats data frames like (sub-)lists; FALSE like atomic elements.
<code>keep.tree</code>	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.
<code>keep.class</code>	logical. For objects: should the class be retained?
<code>regex</code>	logical. Should regular expression search be used on the list names, or only exact matches?
<code>...</code>	further arguments to <code>grep</code> (if <code>regex = TRUE</code>).

Details

For a lack of better terminology, *collapse* defines 'regular' R objects as objects that are either atomic or a list. `reg_elem` with `recursive = TRUE` 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`. 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 as far as 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")

```

GGDC10S

Groningen Growth and Development Centre 10-Sector Database

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

[wlddev](#), [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("#00FF66FF", "#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")

```

group

Fast Hash-Based Grouping

Description

`group()` scans the rows of a data frame (or atomic vector / list of atomic vectors), assigning to each unique row an integer id - starting with 1 and proceeding in first-appearance order of the rows. The function is written in C and optimized for R's data structures. It is the workhorse behind functions like [GRP](#) / [fgroup_by](#), [collap](#), [qF](#), [qG](#), [finteraction](#) and [funique](#), when called with argument `sort = FALSE`.

Usage

```
group(x, starts = FALSE, group.sizes = FALSE)
```

Arguments

<code>x</code>	an atomic vector or data frame / list of equal-length atomic vectors.
<code>starts</code>	logical. If TRUE, an additional attribute "starts" is attached giving a vector of group starts (= index of first-occurrence of unique rows).
<code>group.sizes</code>	logical. If TRUE, an additional attribute "group.sizes" is attached giving the size of each group.

Details

A data frame is grouped on a column-by-column basis, starting from the leftmost column. For each new column the grouping vector obtained after the previous column is also fed back into the hash function so that unique values are determined on a running basis. The algorithm terminates as soon as the number of unique rows reaches the size of the data frame. Missing values are also grouped just like any other values. Invoking arguments `starts` and/or `group.sizes` requires an additional pass through the final grouping vector.

Value

An object is of class 'qG' see [qG](#).

Author(s)

The Hash Function and inspiration was taken from the excellent *kit* package by Morgan Jacob, the algorithm was developed by Sebastian Krantz.

See Also

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

Examples

```
# Let's replicate what funique does
g <- group(wlddev, starts = TRUE)
if(attr(g, "N.groups") == fnrow(wlddev)) wlddev else
  ss(wlddev, attr(g, "starts"))
```

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.
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](#), [timeid](#), [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)))
```

Description

GRP performs fast, ordered and unordered, groupings of vectors and data frames (or lists of vectors) using [radixorderv](#) or [group](#). 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 and operators (see macros `.FAST_FUN` and `.OPERATOR_FUN`), as well as to [collap.BY](#) and [TRA](#).

`fgroup_by` is similar to `dplyr::group_by` but faster and class-agnostic. It creates a grouped data frame with a 'GRP' object attached - for fast dplyr-like programming with *collapse*'s fast functions.

There are also several conversion methods 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`.

`gsplit` efficiently splits a vector based on a 'GRP' object, and `greorder` helps to recombine the results. These are the workhorses behind functions like `BY`, and `collap`, `fsummarise` and `fmutate` when evaluated with base R and user-defined functions.

Usage

```
GRP(X, ...)

## Default S3 method:
GRP(X, by = NULL, sort = TRUE, decreasing = FALSE, na.last = TRUE,
     return.groups = TRUE, return.order = sort, method = "auto",
     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 'GRP' objects
is_GRP(x)

## S3 method for class 'GRP'
length(x)                # Length of data being grouped
GRPN(x, expand = TRUE, ...) # Group sizes (default: expanded to match data length)
GRPnames(x, force.char = TRUE, sep = ".") # Group names
as_factor_GRP(x, ordered = FALSE) # 'GRP'-object to (ordered) factor conversion

# Efficiently split a vector using a 'GRP' object
gsplit(x, g, use.g.names = FALSE, ...)

# Efficiently reorder y = unlist(gsplit(x, g)) such that identical(greorder(y, g), x)
greorder(x, g, ...)
```

```

# Fast, class-agnostic pendant to dplyr::group_by for use with fast functions, see details
fgroup_by(.X, ..., sort = TRUE, decreasing = FALSE, na.last = TRUE,
          return.groups = TRUE, return.order = sort, method = "auto")
# Shorthand for fgroup_by
gby(.X, ..., sort = TRUE, decreasing = FALSE, na.last = TRUE,
    return.groups = TRUE, return.order = sort, method = "auto")

# 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

<code>X</code>	a vector, list of columns or data frame (default method), or a suitable object (conversion / extractor methods).
<code>.X</code>	a data frame or list.
<code>x, g</code>	a 'GRP' object. For <code>gsplit/greorder</code> , <code>x</code> can be a vector of any type, or NULL to return the integer indices of the groups. <code>gsplit/greorder/GRPN</code> also support vectors or data frames to be passed to <code>g/x</code> .
<code>by</code>	if <code>X</code> is a data frame or list, <code>by</code> 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> .
<code>sort</code>	logical. If FALSE, groups are not ordered but simply grouped in the order of first appearance of unique elements / rows. This often provides a performance gain if the data was not sorted beforehand. See also <code>method</code> .
<code>ordered</code>	logical. TRUE adds a class 'ordered' i.e. generates an ordered factor.
<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 / by</code> (argument passed to radixorderv).
<code>na.last</code>	logical. If missing values are encountered in grouping vector/columns, assign them to the last group (argument passed to radixorderv).
<code>return.groups</code>	logical. Include the unique groups in the created GRP object.
<code>return.order</code>	logical. If <code>sort = TRUE</code> , include the output from radixorderv in the created GRP object. This brings performance improvements in <code>gsplit</code> (and thus also benefits grouped execution of base R functions).
<code>method</code>	character. The algorithm to use for grouping: either "radix", "hash" or "auto". "auto" will chose "radix" when <code>sort = TRUE</code> , yielding ordered grouping via

`radixorder`, and "hash"-based grouping in first-appearance order via `group` otherwise. It is possible to put `method = "radix"` and `sort = FALSE`, which will group character data in first appearance order but sort numeric data (a good hybrid option). `method = "hash"` currently does not support any sorting, thus putting `sort = TRUE` will simply be ignored.

<code>group.sizes</code>	logical. TRUE tabulates factor levels using <code>tabulate</code> to create a vector of group sizes; FALSE leaves that slot empty when converting from factors.																								
<code>drop</code>	logical. TRUE efficiently drops unused factor levels beforehand using <code>fdroplevels</code> .																								
<code>call</code>	logical. TRUE calls <code>match.call</code> and saves it in the final slot of the GRP object.																								
<code>expand</code>	logical. TRUE returns a vector the same length as the data. FALSE returns the group sizes (computed in first-appearance-order of groups if <code>x</code> is not already a 'GRP' object).																								
<code>force.char</code>	logical. Always output group names as character vector, even if a single numeric vector was passed to <code>GRP.default</code> .																								
<code>sep</code>	character. The separator passed to <code>paste</code> when creating group names from multiple grouping variables by pasting them together.																								
<code>effect</code>	<i>plm</i> / indexed data methods: Select which panel identifier should be used as grouping variable. 1L takes the first variable in the <code>index</code> , 2L the second etc., identifiers can also be passed as a character string. More than one variable can be supplied.																								
<code>return</code>	an integer or string specifying what <code>fgroup_vars</code> should 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>"data"</td> <td>full grouping columns (default)</td> </tr> <tr> <td>2</td> <td>"unique"</td> <td>unique rows of grouping columns</td> </tr> <tr> <td>3</td> <td>"names"</td> <td>names of grouping columns</td> </tr> <tr> <td>4</td> <td>"indices"</td> <td>integer indices of grouping columns</td> </tr> <tr> <td>5</td> <td>"named_indices"</td> <td>named integer indices of grouping columns</td> </tr> <tr> <td>6</td> <td>"logical"</td> <td>logical selection vector of grouping columns</td> </tr> <tr> <td>7</td> <td>"named_logical"</td> <td>named logical selection vector of grouping columns</td> </tr> </tbody> </table>	<i>Int.</i>	<i>String</i>	<i>Description</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
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<code>use.g.names</code>	logical. TRUE returns a named list, like <code>split</code> . FALSE is slightly more efficient.																								
<code>n</code>	integer. Number of groups to print out.																								
<code>breaks</code>	integer. Number of breaks in the histogram of group-sizes.																								
<code>type</code>	linetype for plot.																								
<code>horizontal</code>	logical. TRUE arranges plots next to each other, instead of above each other.																								
<code>...</code>	for <code>fgroup_by</code> : unquoted comma-separated column names, sequences of columns, expressions involving columns, and column names, indices, logical vectors or selector functions. See Examples. For <code>gsplit</code> , <code>greorder</code> and <code>GRPN</code> : further arguments passed to <code>GRP</code> (if <code>g/x</code> is not already a 'GRP' object). For example the <code>by</code> argument could be used if a data frame is passed.																								

Details

GRP is a central function in the *collapse* package because it provides, in the form of integer vectors, some key pieces of information to efficiently perform grouped operations at the C/C++ level.

Most statistical function require 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, *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 functionality of `GRP.default` lets groups receive different integer-id's depending on whether the groups are sorted `sort = TRUE` (`FALSE` gives first-appearance order), and in which order (argument decreasing). This affects the order of values/rows in the output whenever an aggregation is performed.

Other elements in the object provide information about whether the data was sorted by the variables defining the grouping (6) and the ordering vector (7). These also feed into optimizations in `gsplit/greorder` that benefit the execution of base R functions across groups.

Complimentary to GRP, the function `fgroup_by` is a significantly faster and class-agnostic alternative to `dplyr::group_by` for programming with *collapse*. It creates a grouped data frame with a 'GRP' object attached in a "groups" attribute. This data frame has classes 'GRP_df', ..., 'grouped_df' and 'data.frame', where ... stands for any other classes the input frame inherits such as 'data.table', 'sf', 'tbl_df', 'indexed_frame' etc.. *collapse* functions with a 'grouped_df' method respond to 'grouped_df' objects created with either `fgroup_by` or `dplyr::group_by`. The method `GRP.grouped_df` takes the "groups" attribute from a 'grouped_df' and converts it to a 'GRP' object if created with `dplyr::group_by`.

The 'GRP_df' class in front responds to `print.GRP_df` which first calls `print(fungroup(x), ...)` and prints one line below the object indicating the grouping variables, followed, in square brackets, by some statistics on the group sizes: `[N | Mean (SD) Min-Max]`. The mean is rounded to a full number and the standard deviation (SD) to one digit. Minimum and maximum are only displayed if the SD is non-zero. There also exist a method `[.GRP_df` which calls `NextMethod` but makes sure that the grouping information is preserved or dropped depending on the dimensions of the result (subsetting rows or aggregation with *data.table* drops the grouping object).

`GRP.default` supports vector and list input and will also return 'GRP' objects if passed. There is also a hidden method `GRP.GRP` which simply returns grouping objects (no re-grouping functionality is offered).

Apart from `GRP.grouped_df` there are several further 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. Finally, a sortedness check `!is.unsorted(id)` is run on the group-id to check if the data represented by the factor was sorted (6). `GRP.qG` works similarly (see also `qG`), and the 'pseries' and 'pdata.frame' methods simply group one or more factors in the `index` (selected using the `effect` argument).

Creating a factor from a 'GRP' object using `as_factor_GRP` does not involve any computations, but may involve interacting multiple grouping columns using the `paste` function to produce unique factor levels.

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 and data grouped is sorted or not, the ordering vector used to perform the ordering and the group start positions. 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, except for fgr
[[5]]	group.vars	character	The names of the grouping variables
[[6]]	ordered	logical(2)	[1] Whether the groups are ordered: equal to the so
[[7]]	order	integer(NROW(X)) or NULL	Ordering vector from radixorder (with "starts"
[[8]]	group.starts	integer(N.groups) or NULL	The first-occurrence positions/rows of the groups. U
[[9]]	call	match.call() or NULL	The GRP() call, obtained from match.call(), or NU

See Also

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

Examples

```
## default method
GRP(mtcars$cyl)
GRP(mtcars, ~ cyl + vs + am)      # Or GRP(mtcars, c("cyl", "vs", "am")) or GRP(mtcars, c(2,8:9))
g <- GRP(mtcars, ~ cyl + vs + am) # Saving the object
print(g)                          # Printing it
plot(g)                            # Plotting it
GRPnames(g)                        # Retain group names
fsum(mtcars, g)                    # Compute the sum of mtcars, grouped by variables cyl, vs and am
gsplit(mtcars$mpg, g)              # Use the object to split a vector
gsplit(NULL, g)                   # The indices of the groups
identical(mtcars$mpg,             # greorder and unlist undo the effect of gsplit
           greorder(unlist(gsplit(mtcars$mpg, g)), g))

## 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 for grouped data frame

library(magrittr)
## Adding a column of group sizes.
mtcars %>% fgroup_by(cyl,vs,am) %>% fsummarise(Sizes = GRPN())
mtcars %>% fgroup_by(cyl,vs,am) %>% fmutate(Sizes = GRPN())
# Note: can also use n <- GRPN, or set options(collapse_mask = "all") to use n()
# Other options:
mtcars %>% fgroup_by(cyl,vs,am) %>% ftransform(Sizes = GRPN())
mtcars %>% ftransform(Sizes = GRPN(list(cyl,vs,am))) # Same thing, slightly more efficient

## Various options for programming and interactive use
fgroup_by(GGDC10S, Variable, Decade = floor(Year / 10) * 10) %>% head(3)
fgroup_by(GGDC10S, 1:3, 5) %>% head(3)
fgroup_by(GGDC10S, c("Variable", "Country")) %>% head(3)
fgroup_by(GGDC10S, is.character) %>% head(3)
fgroup_by(GGDC10S, Country:Variable, Year) %>% head(3)
fgroup_by(GGDC10S, Country:Region, Var = Variable, Year) %>% head(3)

## Note that you can create a grouped data frame without materializing the unique grouping columns
fgroup_by(GGDC10S, Variable, Country, return.groups = FALSE) %>% fmutate(across(AGR:SUM, fscale))
fgroup_by(GGDC10S, Variable, Country, return.groups = FALSE) %>% fselect(AGR:SUM) %>% fmean()

## Note also that setting sort = FALSE on unsorted data can be much faster... if not required...
library(microbenchmark)
microbenchmark(gby(GGDC10S, Variable, Country), gby(GGDC10S, Variable, Country, sort = FALSE))

```

indexing

Fast Indexed Time Series and Panels

Description

A fast and flexible indexed time series and panel data class that inherits from *plm*'s 'pseries' and 'pdata.frame', but is more rigorous, natively handles irregularity, can be superimposed on any data.frame/list, matrix or vector, and supports ad-hoc computations inside data masking functions and model formulas.

Usage

```

## Create an 'indexed_frame' containing 'indexed_series'
findex_by(.X, ..., single = "auto", interact.ids = TRUE)
iby(.X, ..., single = "auto", interact.ids = TRUE) # Shorthand

## Retrieve the index ('index_df') from an 'indexed_frame' or 'indexed_series'

```

```

findex(x)
ix(x)      # Shorthand

## Remove index from 'indexed_frame' or 'indexed_series' (i.e. get .X back)
unindex(x)

## Reindex 'indexed_frame' or 'indexed_series' (or index vectors / matrices)
reindex(x, index = findex(x), single = "auto")

## Check if 'indexed_frame', 'indexed_series', index or time vector is irregular
is_irregular(x, any_id = TRUE)

## Convert 'indexed_frame'/'indexed_series' to normal 'pdata.frame'/'pseries'
to_plm(x, row.names = FALSE)

# Subsetting & replacement methods: [(<-) methods call NextMethod().
# Also methods for fsubset, funique and roworder(v), na_omit (internal).

## S3 method for class 'indexed_series'
x[i, ..., drop.index.levels = "id"]

## S3 method for class 'indexed_frame'
x[i, ..., drop.index.levels = "id"]

## S3 replacement method for class 'indexed_frame'
x[i, j] <- value

## S3 method for class 'indexed_frame'
x$name

## S3 replacement method for class 'indexed_frame'
x$name <- value

## S3 method for class 'indexed_frame'
x[[i, ...]]

## S3 replacement method for class 'indexed_frame'
x[[i]] <- value

# Index subsetting and printing: optimized using ss()

## S3 method for class 'index_df'
x[i, j, drop = FALSE, drop.index.levels = "id"]

## S3 method for class 'index_df'
print(x, topn = 5, ...)

```

Arguments

<code>.X</code>	a data frame or list-like object of equal-length columns.
<code>x</code>	an 'indexed_frame' or 'indexed_series'. <code>findex</code> also works with 'pseries' and 'pdata.frame's created with <i>plm</i> . For <code>is_irregular</code> <code>x</code> can also be an index (inherits 'pindex') or a vector representing time.
<code>...</code>	for <code>findex_by</code> : variables identifying the individual (id) and/or time dimensions of the data. Passed either as unquoted comma-separated column names or (tagged) expressions involving columns, or as a vector of column names, indices, a logical vector or a selector function. The time variable must enter last. See Examples. Otherwise: further arguments passed to <code>NextMethod()</code> .
<code>single</code>	character. If only one indexing variable is supplied, this can be declared as "id" or "time" variable. "auto" chooses "id" if the variable has <code>anyDuplicated</code> values.
<code>interact.ids</code>	logical. If <code>n > 2</code> indexing variables are passed, TRUE calls <code>finteraction</code> on the first <code>n-1</code> of them (<code>n</code> 'th variable must be time). FALSE keeps all variables in the index. The latter slows down computations of lags / differences etc. because ad-hoc interactions need to be computed, but gives more flexibility for scaling / centering / summarising over different data dimensions.
<code>index</code>	and index (inherits 'pindex'), or an atomic vector or list of factors matching the data dimensions. Atomic vectors or lists with 1 factor will must be declared, see <code>single</code> . Atomic vectors will additionally be grouped / turned into time-factors. See Details.
<code>drop.index.levels</code>	character. Subset methods also subset the index (= a data.frame of factors), and this argument regulates which factor levels should be dropped: either "all", "id", "time" or "none". The default "id" only drops levels from id's. "all" or "time" should be used with caution because time-factors may contain levels for missing time periods (gaps in irregular sequences, or periods within a sequence removed through subsetting), and dropping those levels would create a variable that is ordinal but no longer represents time. The benefit of dropping levels is that it can speed-up subsequent computations by reducing the size of intermediate vectors created in C++.
<code>any_id</code>	logical. For panel series: FALSE returns the irregularity check performed for each id, TRUE calls <code>any</code> on those checks.
<code>row.names</code>	logical. TRUE creates descriptive row-names (or names for pseries) as in <i>plm</i> . This can be expensive and is usually not required for <i>plm</i> models to work.
<code>topn</code>	integer. The number of first and last rows to print.
<code>i, j, name, drop, value</code>	Arguments passed to <code>NextMethod</code> , or as in the <code>data.frame methods</code> . Note that for index subsetting to work, <code>i</code> needs to be integer or logical (or an expression evaluation to integer or logical if <code>x</code> is a <i>data.table</i>).

Details

The first thing to note about these new 'indexed_frame', 'indexed_series' and 'index_df' classes is that they inherit *plm*'s 'pdata.frame', 'pseries' and 'pindex' classes, respectively. Hence they

are sub-classes that add, improve, and, in some cases, remove functionality provided in *plm*, with the aim of striking an optimal balance of flexibility and performance. The inheritance means that all 'pseries' and 'pdata.frame' methods in *collapse*, and also some methods in *plm*, apply to them. Where compatibility or performance considerations allow for it, *collapse* will continue to create methods for *plm*'s classes instead of the sub-classes.

The use of these sub-classes does not require much knowledge of *plm*, but as a basic background: A 'pdata.frame' is a data.frame with an index attribute: a data.frame of 2 factors identifying the individual and time-dimension of the data. When pulling a variable out of the pdata.frame using a method like \$.pdata.frame or [[.pdata.frame (defined in *plm*), a 'pseries' is created by transferring the index attribute to the vector. Methods defined for functions like `lag / flag` etc. use the index for correct computations on this panel data, also inside *plm*'s estimation commands.

Main Features and Enhancements

The 'indexed_frame' and 'indexed_series' classes extend and enhance 'pdata.frame' and 'pseries' in a number of critical dimensions. Most notably they:

- Support **both time series and panel data**, by allowing indexation of data with one, two or more variables.
- Are **class-agnostic**: any data.frame/list (such as data.table, tibble, tsibble, sf etc.) can become an 'indexed_frame' and continue to function as usual for most use cases. Similarly, any vector or matrix (such as ts, mts, xts) can become an 'indexed_series'. This also allows for transient workflows e.g. `some_df |> findex_by(...) |> 'do something using collapse functions' |> unindex() |> 'continue working with some_df'`.
- Have a comprehensive and efficient set of **methods for subsetting and manipulation**, including methods for `fsubset`, `funique`, `roworder(v)` (internal) and `na_omit` (internal, `na.omit` also works but is slower). It is also possible to group indexed data with `fgroup_by` for transformations e.g. using `fmutate`, but aggregation requires `unindex()`ing.
- **Natively handle irregularity**: time objects (such as 'Date', 'POSIXct' etc.) are passed to `timeid`, which efficiently determines the temporal structure by finding the greatest common divisor (GCD), and creates a time-factor with levels corresponding to a complete time-sequence. The latter is also done with plain numeric vectors, which are assumed to represent unit time steps ($GDC = 1$) and coerced to integer (but can also be passed through `timeid` if non-unitary). Character time variables are converted to factor, which might also capture irregular gaps in panel series. Using this time-factor in the index, *collapse*'s functions efficiently perform correct computations on irregular sequences and panels without the need to 'expand' the data / fill gaps. `is_irregular` can be used to check for irregularity in the entire sequence / panel or separately for each individual in panel data.
- Support computations inside **data-masking functions and formulas**, by virtue of "**deep indexation**": Each variable inside an 'indexed_frame' is an 'indexed_series' which contains in its 'index_df' attribute an external pointer to the 'index_df' attribute of the frame. Functions operating on 'indexed_series' stored inside the frame (such as `with(data, flag(column))`) can fetch the index from this pointer. This allows worry-free application inside arbitrary data masking environments (`with`, `%%`, `attach`, etc..) and estimation commands (`glm`, `feols`, `lmrob` etc..) without duplication of the index in memory. A limitation is that external pointers are only valid during the present R session, thus when saving an 'indexed_frame' and loading it again, you need to call `data = reindex(data)` before computing on it.

Indexed series also have simple `Math` and `Ops` methods, which apply the operation to the unindexed series and shallow copy the attributes of the original object to the result, unless the result

it is a logical vector (from operations like `!`, `==` etc.). For `Ops` methods, if the LHS object is an `'indexed_series'` its attributes are taken, otherwise the attributes of the RHS object are taken.

Limits to plm Compatibility

In contrast to `'pseries'` and `'pdata.frame'`s, `'indexed_series'` and `'indexed_frames'` do not have descriptive `"names"` or `"row.names"` attributes attached to them, mainly for efficiency reasons.

Furthermore, the index is stored in an attribute named `'index_df'` (same as the class name), not `'index'` as in *plm*, mainly to make these classes work with *data.table*, *tsibble* and *xts*, which also utilize `'index'` attributes. This for the most part poses no problem to *plm* compatibility because *plm* source code fetches the index using `attr(x, "index")`, and `attr` by default performs partial matching.

A much greater obstacle in working with *plm* is that some internal *plm* code is hinged on there being no `['.pseries` method, and the existence of `['.indexed_series` limits the use of these sub-classes in most *plm* estimation commands. Therefore the `to_plm` function is provided to efficiently coerce the sub-classes to ordinary *plm* objects before estimation. See Examples.

Overall these classes don't really benefit *plm*, especially given that *collapse*'s *plm* methods also support native *plm* objects. However, they work very well inside other models and software, including *stats* models, *fixest / lfe*, and a whole bunch of time series and ML models. See Examples.

Performance Considerations

When indexing long time-series or panels with a single variable, setting `single = "id"` or `"time"` avoids a potentially expensive call to `anyDuplicated`. Note also that when panel-data are regular and sorted, omitting the time variable in the index can bring $\geq 2x$ performance improvements in operations like lagging and differencing (alternatively use `shift = "row"` argument to `flag`, `fdiff` etc.) .

When dealing with long Date or POSIXct time sequences, it may also be that the internal processing by `timeid` is slow simply because calling `strftime` on these sequences to create factor levels is slow. In this case you may choose to generate an index factor with integer levels by passing `timeid(t)` to `findex_by` or `reindex` (which by default generates a `'qG'` object which is internally converted to factor using `as_factor_qG`. The lazy evaluation of expressions like `as.character(seq_len(nlev))` in modern R makes this extremely efficient).

Print Method

The print methods for `'indexed_frame'` and `'indexed_series'` first call `print(unindex(x), ...)`, followed by the index variables with the number of categories (index factor levels) in square brackets. If the time factor contains unused levels (= irregularity in the sequence), the square brackets indicate the number of used levels (periods), followed by the total number of levels (periods in the sequence) in parentheses.

See Also

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

Examples

```
# Indexing panel data -----
wldi <- findex_by(wlddev, iso3c, year)
wldi
```

```

wldi[1:100,1]          # Works like a data frame
POP <- wldi$POP        # indexed_series
qsu(POP)              # Summary statistics
G(POP)                # Population growth
STD(G(POP, c(1, 10))) # Within-standardized 1 and 10-year growth rates
psmat(POP)           # Panel-Series Matrix
plot(psmat(log10(POP)))

POP[30:5000]          # Subsetting indexed_series
Dlog(POP[30:5000])    # Log-difference of subset
psacf(identity(POP[30:5000])) # ACF of subset
L(Dlog(POP[30:5000]), c(1, 10)), -1:1) # Multiple computations on subset

library(magrittr)
# Fast Statistical Functions don't have dedicated methods
# Thus for aggregation we need to unindex beforehand ...
fmean(unindex(POP))
wldi %>% unindex() %>%
  fgroup_by(iso3c) %>% num_vars() %>% fmean()

# ... or unindex after taking group identifiers from the index
fmean(unindex(fgrowth(POP)), ix(POP)$iso3c)
wldi %>% num_vars() %>%
  fgroup_by(iso3c = ix(.)$iso3c) %>%
  unindex() %>% fmean()

# With matrix methods it is easier as most attributes are dropped upon aggregation.
G(POP, c(1, 10)) %>% fmean(ix(.)$iso3c)

# Example of index with multiple ids
GGDC10S %>% findex_by(Variable, Country, Year) %>% head() # default is interact.ids = TRUE
GGDCi <- GGDC10S %>% findex_by(Variable, Country, Year, interact.ids = FALSE)
head(GGDCi)
findex(GGDCi)
# The benefit is increased flexibility for summary statistics and data transformation
qsu(GGDCi, effect = "Country")
STD(GGDCi$SUM, effect = "Variable")          # Standardizing by variable
STD(GGDCi$SUM, effect = c("Variable", "Year")) # ... by variable and year
# But time-based operations are a bit more expensive because of the necessary interactions
D(GGDCi$SUM)

# Panel-Data modelling -----

# Linear model of 5-year annualized growth rates of GDP on Life Expectancy + 5y lag
lm(G(PCGDP, 5, p = 1/5) ~ L(G(LIFEEX, 5, p = 1/5), c(0, 5)), wldi) # p abbreviates "power"

# Same, adding time fixed effects via plm package: need to utilize to_plm function
plm::plm(G(PCGDP, 5, p = 1/5) ~ L(G(LIFEEX, 5, p = 1/5), c(0, 5)), to_plm(wldi), effect = "time")

# With country and time fixed effects via fixest
fixest::feols(G(PCGDP, 5, p=1/5) ~ L(G(LIFEEX, 5, p=1/5), c(0, 5)), wldi, fixef = .c(iso3c, year))
## Not run:
# Running a robust MM regression without fixed effects

```

```

robustbase::lmrob(G(PCGDP, 5, p = 1/5) ~ L(G(LIFEEX, 5, p = 1/5), c(0, 5)), wldi)

# Running a robust MM regression with country and time fixed effects
wldi %>% fselect(PCGDP, LIFEEX) %>%
  fgrowth(5, power = 1/5) %>% ftransform(LIFEEX_L5 = L(LIFEEX, 5)) %>%
  # drop abbreviates drop.index.levels (not strictly needed here but more consistent)
  na_omit(drop = "all") %>% fhwithin(na.rm = FALSE) %>% # For TFE use fwithin(effect = "year")
  unindex() %>% robustbase::lmrob(formula = PCGDP ~.) # using lm() gives same result as fixest

# Using a random forest model without fixed effects
# ranger does not support these kinds of formulas, thus we need some preprocessing...
wldi %>% fselect(PCGDP, LIFEEX) %>%
  fgrowth(5, power = 1/5) %>% ftransform(LIFEEX_L5 = L(LIFEEX, 5)) %>%
  unindex() %>% na_omit() %>% ranger::ranger(formula = PCGDP ~.)

## End(Not run)

# Indexing other data frame based classes -----

library(tibble)
wlditbl <- qTBL(wlddev) %>% findindex_by(iso3c, year)
wlditbl[,2] # Works like a tibble...
wlditbl[[2]]
wlditbl[1:1000, 10]
head(wlditbl)

library(data.table)
wldidt <- qDT(wlddev) %>% findindex_by(iso3c, year)
wldidt[1:1000] # Works like a data.table...
wldidt[year > 2000]
wldidt[, .(sum_PCGDP = sum(PCGDP, na.rm = TRUE)), by = country] # Aggregation unindexes the result
wldidt[, lapply(.SD, sum, na.rm = TRUE), by = country, .SDcols = .c(PCGDP, LIFEEX)]
# This also works but is a bit inefficient since the index is subset and then dropped
# -> better unindex beforehand
wldidt[year > 2000, .(sum_PCGDP = sum(PCGDP, na.rm = TRUE)), by = country]
wldidt[, PCGDP_gr_5Y := G(PCGDP, 5, power = 1/5)] # Can add Variables by reference
# Note that .SD is a data.table of indexed_series, not an indexed_frame, so this is WRONG!
wldidt[, .c(PCGDP_gr_5Y, LIFEEX_gr_5Y) := G(slt(.SD, PCGDP, LIFEEX), 5, power = 1/5)]
# This gives the correct outcome
wldidt[, .c(PCGDP_gr_5Y, LIFEEX_gr_5Y) := lapply(slt(.SD, PCGDP, LIFEEX), G, 5, power = 1/5)]

## Not run:
library(sf)
nc <- st_read(system.file("shape/nc.shp", package = "sf"), quiet = TRUE)
nci <- findindex_by(nc, SID74)
nci[1:10, "AREA"]
st_centroid(nci) # The geometry column is never indexed, thus sf computations work normally
st_coordinates(nci)
fmean(st_area(nci))

library(tsibble)
pedi <- findindex_by(pedestrian, Sensor, Date_Time)
pedi[1:5, ]

```

```

findex(pedi) # Time factor with 17k levels from POSIXct
# Now here is a case where integer levels in the index can really speed things up
ix(iby(pedestrian, Sensor, timeid(Date_Time)))
library(microbenchmark)
microbenchmark(descriptive_levels = findex_by(pedestrian, Sensor, Date_Time),
               integer_levels = findex_by(pedestrian, Sensor, timeid(Date_Time)))
# Data has irregularity
is_irregular(pedi)
is_irregular(pedi, any_id = FALSE) # irregularity in all sequences
# Manipulation such as lagging with tsibble/dplyr requires expanding rows and grouping
# Collapse can just compute correct lag on indexed series or frames
library(dplyr)
microbenchmark(
  dplyr = fill_gaps(pedestrian) %>% group_by_key() %>% mutate(Lag_Count = lag(Count)),
  collapse = fmutate(pedi, Lag_Count = flag(Count)), times = 10)

## End(Not run)

# Indexing Atomic objects -----

## ts
print(AirPassengers)
AirPassengers[-(20:30)] # Ts class does not support irregularity, subsetting drops class
G(AirPassengers[-(20:30)], 12) # Annual Growth Rate: Wrong!
# Now indexing AirPassengers (identity() is a trick so that the index is named time(AirPassengers))
iAP <- reindex(AirPassengers, identity(time(AirPassengers)))
iAP
findex(iAP) # See the index
iAP[-(20:30)] # Subsetting
G(iAP[-(20:30)], 12) # Annual Growth Rate: Correct!
L(G(iAP[-(20:30)], c(0,1,12)), 0:1) # Lagged level, period and annual growth rates...

## xts
library(xts)
library(zoo) # Needed for as.yearmon() and index() functions
X <- wlddev %>% fsubset(iso3c == "DEU", date, PCGDP:POP) %>% {
  xts(num_vars(.), order.by = as.yearmon(.$date))
} %>% ss(-(30:40)) %>% reindex(identity(index(.))) # Introducing a gap
# plot(G(unindex(X)))
diff(unindex(X)) # diff.xts gives wrong result
fdiff(X) # fdiff gives right result

# But xts range-based subsets do not work...
## Not run:
X["1980/"]

## End(Not run)
# Thus a better way is not to index and perform ad-hoc computations on the xts index
X <- unindex(X)
X["1980/"] %>% fdiff(t = index(.)) # xts index is internally processed by timeid()

## Of course you can also index plain vectors / matrices...

```

is_unlistable	<i>Unlistable Lists</i>
---------------	-------------------------

Description

A (nested) list with atomic objects in all final nodes of the list-tree is unlistable - checked with `is_unlistable`.

Usage

```
is_unlistable(l, DF.as.list = FALSE)
```

Arguments

`l` a list.
`DF.as.list` logical. TRUE treats data frames like (sub-)lists; FALSE like atomic elements.

Details

`is_unlistable` with `DF.as.list = TRUE` is defined as `all(rapply(l, is.atomic))`, whereas `DF.as.list = FALSE` yields checking using `all(unlist(rapply2d(l, function(x) is.atomic(x) || is.list(x)), use.names = FALSE))`, assuming that data frames are lists composed of atomic elements. If `l` contains data frames, the latter 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

```
l <- list(1, 2, list(3, 4, "b", FALSE))
is_unlistable(l)
l <- list(1, 2, list(3, 4, "b", FALSE, e ~ b))
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 = FALSE)
```

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 model 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 = FALSE**, 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)
```

Description

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

- **Search and Identification**

- `is_unlistable` checks whether a (nested) list is composed of atomic objects in all final nodes, and thus unlistable to an atomic vector using `unlist`.
- `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 and Transposition**

- `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.
- `t_list` efficiently transposes nested lists of lists, such as those obtained from splitting a data frame by multiple variables using `rsplit`.

- **Apply Functions**

- `rapply2d` is a recursive version of `lapply` with two key differences to `rapply` to apply a function to nested lists of data frames or other list-based objects.

- **Unlisting / Row-Binding**

- `unlist2d` efficiently unlists unlistable lists in 2-dimensions and creates a data frame (or *data.table*) representation of the list. This is done by recursively flattening and row-binding R objects in the list 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_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>t_list</code>	Transpose lists of 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](#)

pad

Pad Matrix-Like Objects with a Value

Description

The `pad` function inserts elements / rows filled with `value` into a vector matrix or data frame `X` at positions given by `i`. It is particularly useful to expand objects returned by statistical procedures which remove missing values to the original data dimensions.

Usage

```
pad(X, i, value = NA, method = c("auto", "xpos", "vpos"))
```

Arguments

`X` a vector, matrix, data frame or list of equal-length columns.

`i` either an integer (positive or negative) or logical vector giving positions / rows of `X` into which `value`'s should be inserted, or, alternatively, a positive integer vector with `length(i) == NROW(X)`, but with some gaps in the indices into which

value's can be inserted, or a logical vector with `sum(i) == NROW(X)` such that value's can be inserted for FALSE values in the logical vector. See also method and Examples.

value a scalar value to be replicated and inserted into X at positions / rows given by i. Default is NA.

method an integer or string specifying the use of i. The options are:

<i>Int.</i>	<i>String</i>	<i>Description</i>
1	"auto"	automatic method selection: If i is positive integer and <code>length(i) == NROW(X)</code> or if i is logical and <code>sum(i) == NROW(X)</code>
1	"xpos"	i is a vector of positive integers or a logical vector giving the positions of the the elements / rows of X.
2	"vpos"	i is a vector of positive / negative integers or a logical vector giving the positions at which values's / rows of X are inserted.

Value

X with elements / rows filled with value inserted at positions given by i.

See Also

[append, Recode and Replace Values, Small \(Helper\) Functions, Collapse Overview](#)

Examples

```
v <- 1:3

pad(v, 1:2)      # Automatic selection of method "vpos"
pad(v, -(1:2))  # Same thing
pad(v, c(TRUE, TRUE, FALSE, FALSE, FALSE)) # Same thing

pad(v, c(1, 3:4)) # Automatic selection of method "xpos"
pad(v, c(TRUE, FALSE, TRUE, TRUE, FALSE)) # Same thing

head(pad(wlddev, 1:3)) # Insert 3 missing rows at the beginning of the data
head(pad(wlddev, 2:4)) # ... at rows positions 2-4

# pad() is mostly useful for statistical models which only use the complete cases:
mod <- lm(LIFEEX ~ PCGDP, wlddev)
# Generating a residual column in the original data (automatic selection of method "vpos")
settfm(wlddev, resid = pad(resid(mod), mod$na.action))
# Another way to do it:
r <- resid(mod)
i <- as.integer(names(r))
resid2 <- pad(r, i)      # automatic selection of method "xpos"
# here we need to add some elements as flast(i) < nrow(wlddev)
resid2 <- c(resid2, rep(NA, nrow(wlddev)-length(resid2)))
# See that these are identical:
identical(unattrib(wlddev$resid), resid2)
```

```
# Can also easily get a model matrix at the dimensions of the original data
mm <- pad(model.matrix(mod), mod$na.action)
```

psacf	<i>Auto- and Cross- Covariance and Correlation Function Estimation for Panel Series</i>
-------	-----------------------------------------------------------------------------------------

Description

psacf, pspacf and pscacf compute (and by default plot) estimates of the auto-, partial auto- and cross- correlation or covariance functions for panel series. They are analogues to [acf](#), [pacf](#) and [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 '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, ...)

# Methods for indexed data / compatibility with plm:

## 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 '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, 'indexed_series' ('pseries'), data frame or 'indexed_frame' ('pdata.frame').
<code>g</code>	a factor, GRP object, or atomic vector / list of vectors (internally grouped with group) used to group <code>x</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>	a time vector or list of vectors. See flag .
<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 $2 \cdot \sqrt{\text{length}(x) / \text{ng}}$ 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</code> , <code>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 plot.acf .

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 [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 [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 [pacf](#).

Value

An object of class 'acf', see [acf](#). The result is returned invisibly if `plot = TRUE`.

See Also

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

Examples

```

## World Development Panel Data
head(wlddev) # See also help(wlddev)
psacf(wlddev$PCGDP, wlddev$country, wlddev$year) # ACF of GDP per Capita
psacf(wlddev, PCGDP ~ country, ~year) # Same using data.frame method
psacf(wlddev$PCGDP, wlddev$country) # The Data is sorted, can omit t
pspacf(wlddev$PCGDP, wlddev$country) # Partial ACF
psccf(wlddev$PCGDP, wlddev$LIFEEX, wlddev$country) # CCF with Life-Expectancy at Birth

psacf(wlddev, PCGDP + LIFEEX + ODA ~ country, ~year) # ACF and CCF of GDP, LIFEEX and ODA
psacf(wlddev, ~ country, ~year, c(9:10,12)) # Same, using cols argument
pspacf(wlddev, ~ country, ~year, c(9:10,12)) # Partial ACF

## Using indexed data:
wldi <- findex_by(wlddev, iso3c, year) # Creating a indexed frame
PCGDP <- wldi$PCGDP # Indexed Series of GDP per Capita
LIFEEX <- wldi$LIFEEX # Indexed Series of Life Expectancy
psacf(PCGDP) # Same as above, more parsimonious
pspacf(PCGDP)
psccf(PCGDP, LIFEEX)
psacf(wldi[c(9:10,12)])
pspacf(wldi[c(9:10,12)])

```

psmat

*Matrix / Array from Panel Series***Description**

psmat efficiently expands a panel-vector or 'indexed_series' ('pseries') into a matrix. If a data frame or 'indexed_frame' ('pdata.frame') is passed, psmat returns 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 'data.frame'
psmat(x, by, t = NULL, cols = NULL, transpose = FALSE, array = TRUE, ...)

# Methods for indexed data / compatibility with plm:

## S3 method for class 'pseries'
psmat(x, transpose = FALSE, drop.index.levels = "none", ...)

## S3 method for class 'pdata.frame'

```

```
psmat(x, cols = NULL, transpose = FALSE, array = TRUE, drop.index.levels = "none", ...)
```

```
## S3 method for class 'psmat'
plot(x, legend = FALSE, colours = legend, labs = NULL, grid = FALSE, ...)
```

Arguments

x	a vector, indexed series 'indexed_series' ('pseries'), data frame or 'indexed_frame' ('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. If the panel is balanced an integer indicating the number of groups can also be supplied. See Examples.
by	<i>data.frame method</i> : Same input as g, but also allows one- or two-sided formulas using the variables in x, i.e. \sim idvar or $\text{var1} + \text{var2} \sim \text{idvar1} + \text{idvar2}$.
t	same inputs as g/by, to indicate the time-variable(s) or second identifier(s). g and t together should fully identify the panel. If t = NULL, the data is assumed sorted and seq_col is used to generate rownames for the output matrix.
cols	<i>data.frame method</i> : Select columns 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.
transpose	logical. TRUE generates the matrix such that g/by \rightarrow columns, t \rightarrow rows. Default is g/by \rightarrow rows, t \rightarrow columns.
array	<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.
drop.index.levels	character. Either "id", "time", "all" or "none". See indexing .
...	arguments to be passed to or from other methods, or for the plot method additional arguments passed to ts.plot .
legend	logical. Automatically create a legend of panel-groups.
colours	either TRUE to automatically colour by panel-groups using rainbow or a character vector of colours matching the number of panel-groups (series).
labs	character. Provide a character-vector of variable labels / series titles when plotting an array.
grid	logical. Calls grid to draw gridlines on the plot.

Details

If $n > 2$ index variables are attached to an indexed series or frame, the first $n-1$ variables in the index are 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 subsetted objects of class `'pdata.frame'`. A list of `'pseries'` 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) # Sumarizing data
str(psmat(wlddev$PCGDP, wlddev$iso3c, wlddev$year)) # Generating matrix of GDP
r <- psmat(wlddev, PCGDP ~ iso3c, ~ year) # Same thing using data.frame method
plot(r, main = vlabels(wlddev)[9], xlab = "Year") # Plot the matrix
str(r) # See sstructure
str(psmat(wlddev$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

## Indexing simplifies things
wldi <- findex_by(wlddev, iso3c, year) # Creating an indexed frame
PCGDP <- wldi$PCGDP # An indexed_series of GDP per Capita
head(psmat(PCGDP), 2) # Same as above, more parsimonious
plot(psmat(PCGDP))
plot(psmat(wldi[9:12]))
plot(psmat(G(wldi[9:12]))) # Here plotting panel-growth rates
```

pwcov-pwcor-pwnobs *(Pairwise, Weighted) Correlations, Covariances and Observation Counts*

Description

Computes (pairwise, weighted) Pearsons 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 `pwcor` offer an elaborate print method.

Usage

```

pwcov(X, ..., w = NULL, N = FALSE, P = FALSE, array = TRUE, use = "pairwise.complete.obs")

pwcov(X, ..., w = NULL, 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, return = FALSE, ...)

## S3 method for class 'pwcov'
print(x, digits = 2L, sig.level = 0.05, show = c("all", "lower.tri", "upper.tri"),
      spacing = 1L, return = FALSE, ...)

```

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'.
w	numeric. A vector of (frequency) weights.
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.
return	logical. TRUE returns the formatted object from the print method for exporting. The default is to return x invisibly.
...	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.

Note

`weights::wtd.cors` is imported for weighted pairwise correlations (written in C for speed). For weighted correlations with bootstrap SE's see `weights::wtd.cor` (bootstrap can be slow). Weighted correlations for complex surveys are implemented in `jtools::svycor`. An equivalent and faster implementation of `pwcor` (without weights) is provided in `Hmisc::rcorr` (written in Fortran).

See Also

[qsu](#), [Summary Statistics](#), [Collapse Overview](#)

Examples

```
mna <- na_insert(mtcars)
pwcor(mna)
pwcov(mna)
pwnobs(mna)
pwcor(mna, N = TRUE)
pwcor(mna, P = TRUE)
pwcor(mna, N = TRUE, P = TRUE)
aperm(pwcor(mna, N = TRUE, P = TRUE))
print(pwcor(mna, N = TRUE, P = TRUE), digits = 3, sig.level = 0.01, show = "lower.tri")
pwcor(mna, N = TRUE, P = TRUE, array = FALSE)
print(pwcor(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 factor generation from atomic vectors using either radix ordering or index hashing followed by sorting.

`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 (which can have large performance implications). Objects have a class 'qG'.

`finteraction` generates a factor or 'qG' object by interacting multiple vectors or factors. In that process missing values are always replaced with a level and unused levels/combinations are always dropped.

`collapse` internally makes optimal use of factors and 'qG' objects when passed as grouping vectors to statistical functions (`g/by`, or `t` arguments) i.e. typically no further grouping or ordering is performed and objects are used directly by statistical C/C++ code.

Usage

```
qF(x, ordered = FALSE, na.exclude = TRUE, sort = TRUE, drop = FALSE,
    keep.attr = TRUE, method = "auto")
```

```
qG(x, ordered = FALSE, na.exclude = TRUE, sort = TRUE,
    return.groups = FALSE, method = "auto")
```

```
is_qG(x)
```

```
as_factor_qG(x, ordered = FALSE, na.exclude = TRUE)
```

```
finteraction(..., factor = TRUE, ordered = FALSE, sort = factor,
             method = "auto")
```

```
itn(...) # Shorthand for finteraction
```

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). FALSE attaches an additional class "na.included" which is used to skip missing value checks performed before sending objects to C/C++. See Details.
sort	logical. TRUE sorts the levels in ascending order (like factor); FALSE provides the levels in order of first appearance, which can be significantly faster. Note that if a factor is passed as input, only <code>sort = FALSE</code> takes effect and unused levels will be dropped (as factors usually have sorted levels and checking sortedness can be expensive).
drop	logical. If x is a factor, TRUE efficiently drops unused factor levels beforehand using fdroplevels .
keep.attr	logical. If TRUE and x has additional attributes apart from 'levels' and 'class', these are preserved 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: <code>if(is.double(x) && sort) "radix" else if(sort && length(x) < 1e5) "</code>
2	"radix"	use radix ordering to generate factors. Supports <code>sort = FALSE</code> only for character vectors. See Details
3	"hash"	use hashing to generate factors. Since v1.8.3 this is a fast hybrid implementation using group and
4	"rcpp_hash"	the previous "hash" algorithm prior to v1.8.3: uses <code>Rcpp::sugar::sort_unique</code> and <code>Rcpp::sugar</code>

Note that for `finteraction`, `method = "hash"` is always unsorted and `method = "rcpp_hash"` is not available.

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.
factor	logical. TRUE returns an factor, FALSE returns a 'qG' object.

... multiple atomic vectors or factors, or a single list of equal-length vectors or factors. See Details.

Details

Whenever a vector is passed to a [Fast Statistical Function](#) such as `fmean(mtcars, mtcars$cyl)`, is grouped using qF, or qG if use `g.names = FALSE`.

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 first-appearance order (unless `method = "radix"` and `x` is numeric, in which case the levels are always sorted). This often gives a noticeable speed improvement.

There are 3 internal methods of computation: radix ordering, hashing, and Rcpp sugar hashing. Radix ordering is done by combining the functions `radixorder` and `groupid`. It is generally faster than hashing for large numeric data and pre-sorted data (although there are exceptions). Hashing uses `group`, followed by `radixorder` on the unique elements if `sort = TRUE`. It is generally fastest for character data. Rcpp hashing uses `Rcpp::sugar::sort_unique` and `Rcpp::sugar::match`. This is often less efficient than the former on large data, but the sorting properties (relying on `std::sort`) may be superior in borderline cases where `radixorder` fails to deliver exact lexicographic ordering of factor levels.

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' class `'qG'` consisting of only an integer grouping vector and an attribute providing the number of groups. It is slightly faster and more memory efficient than `GRP` for grouping atomic vectors, and also convenient as it can be stored in a data frame column, which are the main reasons for its existence.

`finteraction` is simply a wrapper around `as_factor_GRP(GRP.default(X))`, where `X` is replaced by the arguments in `'...'` combined in a list (so its not really an interaction function but just a multivariate grouping converted to factor, 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 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. `finteraction` can return either.

Note

An efficient alternative for character vectors with multithreading support is provided by `kit::charToFact`.

qG(x, sort = FALSE, na.exclude = FALSE, method = "hash") internally calls `group(x)` which can also be used directly and also supports multivariate groupings where x can be a list of vectors.

Neither qF nor qG reorder groups / factor levels. An exception was added in v1.7, when calling qF(f, sort = FALSE) on a factor f, the levels are recast in first appearance order. These objects can however be converted into one another using qF/qG or the direct method `as_factor_qG` (called inside qF). It is also possible to add a class 'ordered' (ordered = TRUE) and to create an extra level / integer for missing values (na.exclude = FALSE) if factors or 'qG' objects are passed to qF or qG.

See Also

[group](#), [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..

finteraction(mtcars$cyl, mtcars$vs, factor = FALSE) # Returns 'qG', by default unsorted
group(mtcars[c("cyl", "vs")]) # Same thing. Use whatever syntax is more convenient
```

 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, stable.algo = TRUE, ...)

## S3 method for class 'matrix'
qsu(x, g = NULL, pid = NULL, w = NULL, higher = FALSE,
     array = TRUE, stable.algo = TRUE, ...)

## S3 method for class 'data.frame'
qsu(x, by = NULL, pid = NULL, w = NULL, cols = NULL, higher = FALSE,
     array = TRUE, vlabels = FALSE, stable.algo = TRUE, ...)

# Methods for indexed data / compatibility with plm:

## S3 method for class 'pseries'
qsu(x, g = NULL, w = NULL, effect = 1L, higher = FALSE,
     array = TRUE, stable.algo = TRUE, ...)

## S3 method for class 'pdata.frame'
qsu(x, by = NULL, w = NULL, cols = NULL, effect = 1L, higher = FALSE,
     array = TRUE, vlabels = FALSE, stable.algo = TRUE, ...)

# Methods for compatibility with sf:

## S3 method for class 'sf'
qsu(x, by = NULL, pid = NULL, w = NULL, cols = NULL, higher = FALSE,
     array = TRUE, vlabels = FALSE, stable.algo = TRUE, ...)

## S3 method for class 'qsu'
as.data.frame(x, ..., gid = "Group", stringsAsFactors = TRUE)

## 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, 'indexed_series' ('pseries') or 'indexed_frame' ('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. ~ group1 + group2 or var1 + var2 ~ group1 + group2. See Examples.

pid	same input as <code>g/by</code> : 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 <code>g/by</code> (grouped statistics are computed on the transformed data if <code>g/by</code> is also used). However, passing any LHS variables to <code>pid</code> will overwrite any LHS variables passed to <code>by</code> .
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 <code>pid</code> is used.
cols	select columns to summarize using column names, indices, a logical vector or a function (e.g. <code>is.numeric</code>). Two-sided formulas passed to <code>by</code> or <code>pid</code> overwrite <code>cols</code> .
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) TRUE returns an array, while FALSE returns a (nested) list of matrices.
stable.algo	logical. FALSE uses a faster but less stable method to calculate the standard deviation (see Details of <code>fsd</code>). Only available if <code>w = NULL</code> and <code>higher = FALSE</code> .
vlabels	logical TRUE or a function: to display variable labels in the summary. See Details.
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>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.
gid	character. Name assigned to the group-id column, when summarising variables by groups.
stringsAsFactors	logical. Make factors from dimension names of 'qsu' array. Same as option to <code>as.data.frame.table</code> .
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 \mathbf{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 $\mathbf{x}_{N.}$ 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 $\mathbf{x}_{N.}$, 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 \mathbf{x} can be slightly different than the 'Between' mean computed on $\mathbf{x}_{N.}$, and the variance decomposition is not exact). If groups are supplied to `g/by`, $\mathbf{x}_{N.}$ is expanded to the vector $\mathbf{x}_{i.}$ (length $N \times T$) by replacing each value x_{it} in \mathbf{x} with $x_{i.}$, while preserving missing values in \mathbf{x} . Grouped Between-statistics are then computed on $\mathbf{x}_{i.}$, 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 '). See Examples.

'Within' statistics are always computed on the vector $\mathbf{x} - \mathbf{x}_{i.} + \mathbf{x}_{..}$, where $\mathbf{x}_{..}$ is simply the 'Overall' mean computed from \mathbf{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(s) ' 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'. See Examples.

For data frame methods, if `vlabels = TRUE`, `qsu` uses `function(x) paste(names(x), setv(vlabels(x), NA, ""), sep = ": ")` to combine variable names and labels for display. Alternatively, the user can pass a custom function which will be applied to the data frame, e.g. using `vlabels = vlabels` just displays the labels. See also [vlabels](#).

`qsu` comes with its 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, an apostrophe (') is placed after the 6th digit to designate the millions. Missing values are printed using '-'

The `sf` method simply ignores the geometry column.

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

In weighted summaries, observations with missing or zero weights are skipped, and thus do not affect any of the calculated statistics, including the observation count. This also implies that a logical vector passed to `w` can be used to efficiently summarize a subset of the data.

Note

If weights `w` are used together with `pid`, transformed data is computed using weighted individual means i.e. weighted \bar{x}_i and weighted $\bar{x} \dots$. 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](#), [Summary Statistics](#), [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 + LIFEEX ~ 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, LIFEEX and GINI vary more between-countries, but ODA received varies more within
# countries over time.

# Let's do this manually for PCGDP:
x <- wlddev$PCGDP
g <- wlddev$iso3c

# This is the exact variance decomposition
all.equal(fvar(x), fvar(B(x, g)) + fvar(W(x, g)))

# What qsu does is calculate
```

```

r <- rbind(Overall = qsu(x),
          Between = qsu(fmean(x, g)), # Aggregation instead of between-transform
          Within = qsu(fwithin(x, g, mean = "overall.mean"))) # Same as qsu(W(x, g) + fmean(x))
r[3, 1] <- r[1, 1] / r[2, 1]
print.qsu(r)
# Proof:
qsu(x, pid = g)

# Using indexed data:
wldi <- findex_by(wlddev, iso3c, year) # Creating a Indexed Data Frame frame from this data
qsu(wldi) # Summary for pdata.frame -> qsu(wlddev, pid = ~ iso3c)
qsu(wldi$PCGDP) # Default summary for Panel Series
qsu(G(wldi$PCGDP)) # Summarizing GDP growth, see also ?G

# Grouped Panel Data Summaries -----
qsu(wlddev, ~ region, ~ iso3c, cols = 9:12) # Panel-Statistics by region
psr <- qsu(wldi, ~ region, cols = 9:12) # Same on indexed data
psr # -> Gives a 4D array
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..
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..

# Again let's do this manually for PDGCP:
d <- cbind(Overall = x,
          Between = fbetween(x, g),
          Within = fwithin(x, g, mean = "overall.mean"))

r <- qsu(d, g = wlddev$region)
r[, "N", "Between"] <- fndistinct(g[!is.na(x)], wlddev$region[!is.na(x)])
r[, "N", "Within"] <- r[, "N", "Overall"] / r[, "N", "Between"]
r

# Proof:
qsu(wlddev, PCGDP ~ region, ~ iso3c)

# 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 manner

# Alternative Output Formats -----
# Simple case
as.data.frame(qsu(mtcars))
# For matrices can also use qDF/qDT/qTBL to assign custom name and get a character-id

```

```

qDF(qsu(mtcars), "car")
# DF from 3D array: do not combine with aperm(), might introduce wrong column labels
as.data.frame(stats, gid = "Region_Income")
# DF from 4D array: also no aperm()
as.data.frame(qsu(wlddev, ~ income, ~ iso3c, cols = 9:10), gid = "Region")

# Output as nested list
psrl <- qsu(wlddev, ~ income, ~ iso3c, cols = 9:10, array = FALSE)
psrl

# We can now use unlist2d to create a tidy data frame
unlist2d(psrl, c("Variable", "Trans"), row.names = "Income")

```

qtab

Fast (Weighted) Cross Tabulation

Description

A versatile and computationally more efficient replacement for `table`. Notably, it also supports tabulations with frequency weights, and computation of a statistic over combinations of variables.

Usage

```

qtab(..., w = NULL, wFUN = NULL, wFUN.args = NULL,
      dnn = "auto", sort = TRUE, na.exclude = TRUE,
      drop = FALSE, method = "auto")

```

```

qtable(...) # Long-form: to facilitate replacement of table()

```

Arguments

- | | |
|-----------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ... | atomic vectors or factors spanning the table dimensions, (optionally) with tags for the dimension names, or a data frame / list of these. See Examples. |
| w | a single vector to aggregate over the table dimensions e.g. a vector of frequency weights. |
| wFUN | a function used to aggregate w over the table dimensions. The default NULL computes the sum of the non-missing weights via an optimized internal algorithm. Fast Statistical Functions also receive vectorized execution. |
| wFUN.args | a list of (optional) further arguments passed to wFUN. See Examples. |
| dnn | the names of the table dimensions. Either passed directly as a character vector or list (internally <code>unlist</code> 'ed), a function applied to the ... list (e.g. <code>names</code> , or <code>vlabels</code>), or one of the following options: <ul style="list-style-type: none"> "auto" constructs names based on the ... arguments, or calls <code>names</code> if a single list is passed as input. "namlab" does the same as "auto", but also calls <code>vlabels</code> on the list and appends the names by the variable labels. |

dnn = NULL will return a table without dimension names.
 sort, na.exclude, drop, method

arguments passed down to `qF`:

- `sort = FALSE` orders table dimensions in first-appearance order of items in the data (can be more efficient if vectors are not factors already). Note that for factors this option will both recast levels in first-appearance order and drop unused levels.
- `na.exclude = FALSE` includes NA's in the table (equivalent to `table`'s `useNA = "ifany"`).
- `drop = TRUE` removes any unused factor levels (= zero frequency rows or columns).
- `method` `in` `c("radix", "hash")` provides additional control over the algorithm used to convert atomic vectors to factors.

Value

An array of class 'qtab' that inherits from 'table'. Thus all 'table' methods apply to it.

See Also

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

Examples

```
## Basic use
qtab(iris$Species)
with(mtcars, qtab(vs, am))
qtab(mtcars[.c(vs, am)])

library(magrittr)
iris %>% qtab(Sepal.Length > mean(Sepal.Length), Species)
iris %>% qtab(AMSL = Sepal.Length > mean(Sepal.Length), Species)

## World after 2015
wlda15 <- wlddev %>% fsubset(year >= 2015) %>% collap(~ iso3c)

# Regions and income levels (country frequency)
wlda15 %>% qtab(region, income)
wlda15 %>% qtab(region, income, dnn = vlabels)
wlda15 %>% qtab(region, income, dnn = "namlab")

# Population (millions)
wlda15 %>% qtab(region, income, w = POP) %>% divide_by(1e6)

# Life expectancy (years)
wlda15 %>% qtab(region, income, w = LIFEEX, wFUN = fmean)

# Life expectancy (years), weighted by population
wlda15 %>% qtab(region, income, w = LIFEEX, wFUN = fmean,
  wFUN.args = list(w = POP))
```

```

# GDP per capita (constant 2010 US$): median
wlda15 %$$ qtab(region, income, w = PCGDP, wFUN = fmedian,
               wFUN.args = list(na.rm = TRUE))

# GDP per capita (constant 2010 US$): median, weighted by population
wlda15 %$$ qtab(region, income, w = PCGDP, wFUN = fmedian,
               wFUN.args = list(w = POP))

# Including OECD membership
tab <- wlda15 %$$ qtab(region, income, OECD)
tab

# Various 'table' methods
tab %>% addmargins()
tab %>% marginSums(margin = c("region", "income"))
tab %>% proportions()
tab %>% proportions(margin = "income")
as.data.frame(tab) %>% head(10)
ftable(tab, row.vars = c("region", "OECD"))

# Other options
tab %>% fsum(TRA = "%")      # Percentage table (on a matrix use fsum.default)
tab %/=% (sum(tab)/100)     # Another way (division by reference, preserves integers)
tab

rm(tab, wlda15)

```

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/qDT/qTBL`, `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 character or numeric (by converting the levels).

Usage

```
# Converting between matrices, data frames / tables / tibbles

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, class = c("tbl_df", "tbl", "data.frame"))
qM(X,
    keep.attr = FALSE, class = NULL)

# Programmer functions: matrix rows or columns to list / DF / DT - fully in C++

mctl(X, names = FALSE, return = "list")
mrtl(X, names = FALSE, return = "list")

# Converting factors or factor columns

as_numeric_factor(X, keep.attr = TRUE)
as_character_factor(X, keep.attr = TRUE)
```

Arguments

X a vector, factor, matrix, higher-dimensional array, data frame or list. `mctl` and `mrtl` only accept matrices, `as_numeric_factor` and `as_character_factor` only accept factors, data frames or lists.

row.names.col should a column capturing names or `row.names` be added? e.g. when converting atomic objects to data frame or data frame to *data.table*. Can be logical `TRUE`, which will add a column "row.names" in front, or can supply a name for the column e.g. "variable".

keep.attr logical. `FALSE` (default) yields a *hard / thorough* object conversion: All unnecessary attributes are removed from the object yielding a plain matrix / data.frame / *data.table*. `FALSE` yields a *soft / minimal* 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:

<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. Its 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)` evaluates to TRUE.)

The default `keep.attr = FALSE` ensures *hard* conversions so that all unnecessary attributes are dropped. Furthermore in `qDF/qDT/qTBL` the default classes were explicitly assigned. This is to ensure that the default methods apply, 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

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(mr1(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)))

```

radixorder

Fast Radix-Based Ordering

Description

A slight modification of `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). `radixorder` is a programmers version directly supporting vector and list input.

Usage

```
radixorder(..., na.last = TRUE, decreasing = FALSE, starts = FALSE,
           group.sizes = FALSE, sort = TRUE)
```

```
radixorder(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>...</code> / <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.

`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. See also [group](#).

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.

Author(s)

The C code was taken - with slight modifications - from [base R source code](#), and is originally due to *data.table* authors Matt Dowle and Arun Srinivasan.

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)
```

Description

rapply2d is a recursive version of lapply with three differences to [rapply](#):

1. data frames (or other list-based objects specified in `classes`) are considered as atomic, not as (sub-)lists
2. FUN is applied to all 'atomic' objects in the nested list
3. the result is not simplified / unlisted.

Usage

```
rapply2d(l, FUN, ..., classes = "data.frame")
```

Arguments

<code>l</code>	a list.
<code>FUN</code>	a function that can be applied to all 'atomic' elements in <code>l</code> .
<code>...</code>	additional elements passed to <code>FUN</code> .
<code>classes</code>	character. Classes of list-based objects inside <code>l</code> that should be considered as atomic.

Value

A list of the same structure as `l`, where `FUN` was applied to all atomic elements and list-based objects of a class included in `classes`.

Note

The main reason `rapply2d` exists is to have a recursive function that out-of-the-box applies a function to a nested list of data frames.

For most other purposes [rapply](#), or by extension the excellent [rrapply](#) function / package, provide more advanced functionality and greater performance.

See Also

[rsplit](#), [unlist2d](#), [List Processing](#), [Collapse Overview](#)

Examples

```
l <- list(mtcars, list(mtcars, as.matrix(mtcars)))
rapply2d(l, fmean)
unlist2d(rapply2d(l, fmean))
```

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 (default is `∅L`). data can be multi-typed, in which case appropriate columns can be selected through the `cols` argument. For numeric data a more versatile alternative is provided by `data.table::nafill` and `data.table::setnafill`.
- `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 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, set = FALSE)
```

```
recode_char(X, ..., default = NULL, missing = NULL, regex = FALSE,
            ignore.case = FALSE, fixed = FALSE, set = FALSE)
```

```
replace_NA(X, value = ∅L, cols = NULL, set = FALSE)
```

```
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` = ∅, Secondary = "SEC"</code> etc.. <code>recode_char</code> with <code>regex = TRUE</code> also supports regular expressions i.e. <code>``^S D\$`` = "STD"</code> etc.
<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!
set	logical. TRUE does (some) replacements by reference (i.e. in-place modification of the data). For <code>replace_NA</code> this feature is mature, and the result will be returned invisibly. For <code>recode_num</code> and <code>recode_char</code> , replacement by reference is still partial, so you need to assign the result to an object to materialize all changes.
regex	logical. If TRUE, all recode-argument names are (sequentially) passed to <code>grepl</code> as a pattern to search X. All matches are replaced. <i>Note</i> that NA's are also matched as strings by <code>grepl</code> .
value	a single (scalar) value to replace matching elements with.
cols	select columns to replace missing values in using a function, column names, indices or logical vector.
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 on standardized data. 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).
ignore.case, fixed	logical. Passed to <code>grepl</code> and only applicable if <code>regex = TRUE</code> .

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.

Simple replacing tasks on a vector can also effectively be handled by, `setv` / `copyv`. Fast vectorized switches are offered by package `kit` (functions `iif`, `nif`, `vswitch`, `nswitch`) as well as `data.table::fcase` and `data.table::fifelse`.

See Also

[pad](#), [Efficient Programming](#), [Collapse Overview](#)

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

```

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 = "front")

```

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 radixorder).

decreasing	logical. Should the sort order be increasing or decreasing? Can also be a vector of length equal to the number of arguments in cols (argument passed to radixorder).
neworder	an ordering vector, can be $< nrow(X)$. if <code>pos = "front"</code> or <code>pos = "end"</code> , a logical vector can also be supplied. This argument overwrites cols.
pos	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 neworder to the front (top) of X (the default).
2	"end"	move rows in neworder to the end (bottom) of X.
3	"exchange"	just exchange the order of rows in neworder, other rows remain in the same position.
4	"after"	place all further selected rows behind the first selected row.

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).

`roworder(v)` has internal facilities to deal with [indexed data](#).

See Also

[colororder](#), [Data Frame Manipulation](#), [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 and returns a (nested) list. If `flatten = TRUE`, the list is flattened yielding the same result as `split`. rsplit is implemented as a wrapper around `gsplit`, and significantly faster than `split`.

Usage

```
rsplit(x, ...)

## Default S3 method:
rsplit(x, f1, drop = TRUE, flatten = FALSE, use.names = TRUE, ...)

## S3 method for class 'data.frame'
rsplit(x, by, drop = TRUE, flatten = FALSE, cols = NULL,
       keep.by = FALSE, simplify = TRUE, use.names = TRUE, ...)
```

Arguments

x	a vector, data.frame or list.
f1	a GRP object, or a (list of) vector(s) / factor(s) (internally converted to a GRP object(s)) 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 GRP on the list, creating a single grouping used for splitting; FALSE yields recursive splitting.
use.names	logical. TRUE returns a named list (like <code>split</code>); FALSE returns a plain list.
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 GRP . Sensible choices would be <code>sort = FALSE</code> , <code>decreasing = TRUE</code> or <code>na.last = FALSE</code> . Note that these options only apply if f1 is not already a (list of) factor(s).

Value

a (nested) list containing the subsets of x.

See Also

[gsplit](#), [rapply2d](#), [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)

# Split this sectoral data, first by Variable (Employment and Value Added), then by Country
GGDCspl <- rsplit(GGDC10S, ~ Variable + Country, cols = 6:16)
str(GGDCspl)

# The nested list can be reassembled using unlist2d()
head(unlist2d(GGDCspl, idcols = .c(Variable, Country)))
rm(GGDCspl)

# Another example with mtcars (not as clean because of row.names)
nl <- rsplit(mtcars, mpg + hp ~ cyl + vs + am)
str(nl)
unlist2d(nl, idcols = .c(cyl, vs, am), row.names = "car")
rm(nl)
```

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

x	a factor or integer vector. Numeric vectors will be converted to integer i.e. rounded downwards.
o	an (optional) integer ordering vector specifying the order by which to pass through x.
del	integer. The integer delimiting two consecutive points in a sequence. del = 1 lets seqid track sequences of the form c(1, 2, 3, ...), del = 2 tracks sequences c(1, 3, 5, ...) etc.
start	integer. The starting value of the resulting sequence id. Default is starting from 1.
na.skip	logical. TRUE skips missing values in the sequence. The default behavior is skipping such that seqid(c(1, NA, 2)) is regarded as one sequence and coded as c(1, NA, 1).
skip.seq	logical. If na.skip = TRUE, this changes the behavior such that missing values are viewed as part of the sequence, i.e. seqid(c(1, NA, 3)) is regarded as one sequence and coded as c(1, NA, 1).
check.o	logical. Programmers option: FALSE prevents checking that each element of o is in the range [1, length(x)], 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.

Details

seqid was created primarily as a workaround to deal with problems of computing lagged values, differences and growth rates on irregularly spaced time series and panels before *collapse* version 1.5.0 (#26). Now flag, fdiff and fgrowth natively support irregular data so this workaround is superfluous, except for iterated differencing which is not yet supported with irregular data.

The theory of the workaround was to express an irregular time series or panel series as a regular panel series with a group-id created such that the time-periods within each group are consecutive. seqid makes this very easy: For an irregular panel with some 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.

In general, for any regularly spaced panel the identity given by `identical(groupid(id, order(id, time)), seqid(time, order(id, time)))` should hold.

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

[timeid](#), [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

## This gave a gaps in time error previous to collapse 1.5.0
L(data, 1, value ~ id, ~time)

## 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 this way
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)
```

small-helpers

Small (Helper) Functions

Description

Convenience functions in the *collapse* package that help to deal with object attributes such as variable names and labels, matching and object checking, metaprogramming, and that improve the workflow.

Usage

```
.c(...)          # Non-standard concatenation i.e. .c(a, b) == c("a", "b")
nam %=% values   # Multiple-assignment e.g. .c(x, y) %=% c(1, 2),
massign(nam, values, # can also assign to different environment.
        envir = parent.frame())
vlabels(X, attrn = "label", # Get labels of variables in X, in attr(X[[i]], attrn)
        use.names = TRUE)
vlabels(X, attrn = "label") <- value # Set labels of variables in X (by reference)
setLabels(X, value, attrn = "label", # Set labels of variables in X (by reference)
```

```

        cols = NULL)                # and return X
vclasses(X, use.names = TRUE) # Get classes of variables in X
namlab(X, class = FALSE,      # Return data frame of names and labels,
      attrn = "label", N = FALSE, # and (optionally) classes, number of observations
      Ndistinct = FALSE)        # and number of non-missing distinct values
add_stub(X, stub, pre = TRUE, # Add a stub (i.e. prefix or postfix) to column names
      cols = NULL)
rm_stub(X, stub, pre = TRUE, # Remove stub from column names, also supports general
      regex = FALSE,        # regex matching and removing of characters
      cols = NULL, ...)
x %!in% table                    # The opposite of %in%
ckmatch(x, table,               # Check-match: throws an informative error if non-matched
      e = "Unknown columns:")
all_identical(...)             # Check exact equality of multiple objects or list-elements
all_obj_equal(...)            # Check near equality of multiple objects or list-elements
all_funs(expr)                 # Find all functions called in an R language expression
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.
expr	an expression of type "language" e.g. quote(x / sum(x)).
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.
N, Ndistinct	logical. Options to display the number of observations or number of distinct non-missing values.
value	for whichv and alloc: a single value of any vector type. For vlabels<- and setLabels: a matching character vector or list of variable labels.
use.names	logical. Preserve names if X is a list.

cols	integer. (optional) indices of columns to apply the operation to. Note that for these small functions this needs to be integer, whereas for other functions in the package this argument is more flexible.
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.
regex	logical. Match pattern anywhere in names using a regular expression and remove it with gsub .
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.
e	the error message thrown by <code>ckmatch</code> for non-matched elements. The message is followed by the comma-separated non-matched elements.
nam	character. A vector of object names.
values	a matching atomic vector or list of objects.
envir	the environment to assign into.
...	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. For <code>rm_stub</code> : further arguments passed to gsub .

Details

`all_funs` is the opposite of [all.vars](#), to return the functions called rather than the variables in an expression. See Examples.

`copyAttrib` and `copyMostAttrib` take a shallow copy of the attribute list, i.e. they don't duplicate in memory the attributes themselves. They also, along with `setAttrib`, take a shallow copy of lists passed to the `to` argument, so that lists are not modified by reference. Atomic `to` arguments are however modified by reference.

`copyMostAttrib` copies all attributes except for "names", "dim" and "dimnames" (like the corresponding C-API function), and further only copies the "row.names" attribute of data frames if known to be valid. Thus it is a suitable choice if objects should be of the same type but are not of equal dimensions.

See Also

[Efficient Programming, Collapse Overview](#)

Examples

```

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

## Multiple assignment
.c(a, b) %=% list(1, 2)
.c(T, N) %=% dim(EuStockMarkets)
names(iris) %=% iris
list2env(iris)          # Same thing
rm(list = c("a", "b", "T", "N", names(iris)))

## Variable labels
namlab(wlddev)
namlab(wlddev, class = TRUE, N = TRUE, Ndistinct = 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)

## Function names from expressions
ex = quote(sum(x) + mean(y) / z)
all.names(ex)
all.vars(ex)
all_funs(ex)
rm(ex)

```

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).
- [qtab](#), shorthand for quick-table, is a faster and more versatile alternative to [table](#). Notably, it also supports tabulations with frequency weights, as well as computing a statistic over combinations of variables. `'qtab'`'s inherit the `'table'` class, allowing for seamless application of `'table'` methods.
- [descr](#) computes a concise and detailed description of a data frame, including (sorted) frequency tables for categorical variables and various statistics and quantiles for numeric variables. It is inspired by `Hmisc::describe`, but about 10x faster.
- [pwcov](#), [pwnobs](#) and [pwwcor](#) compute (weighted) 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. The elaborate print method displays 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). A variable is variant if it has at least 2 distinct non-missing data points.

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)
qtab	No methods, for data frames or vectors	Fast (weighted) cross-tabulation
descr	No methods, for data frames or lists of vectors	Detailed statistical description
pwwcor	No methods, for matrices or data frames	Pairwise (weighted) correlations
pwwcov	No methods, for matrices or data frames	Pairwise (weighted) covariances
pwnobs	No methods, for matrices or data frames	Pairwise observation counts
varying	default, matrix, data.frame, pseries, pdata.frame, grouped_df	Fast variation check

See Also

[Collapse Overview, Fast Statistical Functions](#)

time-series-panel-series

Time Series and Panel Series

Description

collapse provides a flexible and powerful set of functions and classes to work with time-dependent data:

- `findex_by/iby` creates an 'indexed_frame': a flexible structure that can be imposed upon any data-frame like object and facilitates **indexed (time-aware) computations on time series and panel data**. Indexed frames are composed of 'indexed_series', which can also be created from vector and matrix-based objects using the `reindex` function. Further functions `findex/ix`, `unindex`, `is_irregular` and `to_plm` help operate these classes, check for irregularity, and ensure *plm* compatibility. Methods are defined for various time series, data transformation and data manipulation functions in *collapse*.
- `timeid` efficiently converts numeric time sequences, such as 'Date' or 'POSIXct' vectors, to a **time-factor / integer id**, where a unit-step represents the greatest common divisor of the underlying sequence.
- `flag`, and the lag- and lead- operators `L` and `F` are S3 generics to efficiently compute sequences of **lags and leads** on regular or irregular / unbalanced time series and panel data.
- Similarly, `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**. `fdiff/D/Dlog` can also compute **quasi-differences** of the form $x_t - \rho x_{t-1}$.
- `fcumsum` is an S3 generic to efficiently compute **cumulative sums** on time series and panel data. In contrast to `cumsum`, it can handle missing values and supports both grouped and indexed / ordered computations.
- `psmat` is an S3 generic to efficiently convert panel-vectors / 'indexed_series' and data frames / 'indexed_frame's to **panel series matrices and 3D arrays**, respectively (where time, individuals and variables receive different dimensions, allowing for fast indexation, visualization, and computations).
- `psacf`, `pspacf` and `psccf` are S3 generics to compute estimates of the **auto-, partial auto- and cross- correlation or covariance functions** for panel-vectors / 'indexed_series', and multivariate versions for data frames / 'indexed_frame's.

Table of Functions

S3 Generic

`findex_by/iby`, `findex/ix`, `reindex`, `unindex`, `is_irregular`, `to_plm`
`timeid`
`flag/L/F`
`fdiff/D/Dlog`
`fgrowth/G`
`fcumsum`
`psmat`
`psacf`
`pspacf`
`psccf`

Methods

For vectors, matrices and data frames / lists.
 For time sequences represented by integer or d
 default, matrix, data.frame, pseries, p
 default, pseries, data.frame, pdata.fra
 default, pseries, data.frame, pdata.fra
 default, pseries, data.frame, pdata.fra
 default, pseries, data.frame, pdata.fra

See Also

[Collapse Overview, Data Transformations](#)

timeid	<i>Generate Integer-Id From Time/Date Sequences</i>
--------	-----------------------------------------------------

Description

timeid groups time vectors in a way that preserves the temporal structure. It generate an integer id where unit steps represent the greatest common divisor in the original sequence e.g `c(4, 6, 10) -> c(1, 2, 4)` or `c(0.25, 0.75, 1) -> c(1, 3, 4)`.

Usage

```
timeid(x, factor = FALSE, ordered = factor, extra = FALSE)
```

Arguments

x	a numeric time object such as a Date, POSIXct or other integer or double vector representing time.
factor	logical. TRUE returns an (ordered) factor with levels corresponding to the full sequence (without irregular gaps) of time. This is useful for inclusion in the index but might be computationally expensive for long sequences, see Details. FALSE returns a simpler object of class 'qG'.
ordered	logical. TRUE adds a class 'ordered'.
extra	logical. TRUE attaches a set of 4 diagnostic items as attributes to the result: <ul style="list-style-type: none"> • "unique_ints": <code>unique(unattrib(timeid(x)))</code> - the unique integer time steps in first-appearance order. This can be useful to check the size of gaps in the sequence. • "sort_unique_x": <code>sort(unique(x))</code>. • "range_x": <code>range(x)</code>. • "step_x": <code>vgcd(sort(unique(diff(sort(unique(x))))))</code> - the greatest common divisor.

Note that returning these attributes does not incur additional computations.

Details

Let `range_x` and `step_x` be the like-named attributes returned when `extra = TRUE`, then, if `factor = TRUE`, a complete sequence of levels is generated as `seq(range_x[1], range_x[2], by = step_x) |> copyMostAttrib(x) |> as.character()`. If `factor = FALSE`, the number of timesteps recorded in the "N.groups" attribute is computed as $(\text{range_x}[2] - \text{range_x}[1]) / \text{step_x} + 1$, which is equal to the number of factor levels. In both cases the underlying integer id is the same and preserves gaps in time. Large gaps (strong irregularity) can result in many unused factor levels, the generation of which can become expensive. Using `factor = FALSE` (the default) is thus more efficient.

Value

A factor or 'qG' object, optionally with additional attributes attached.

See Also

[seqid](#), [Indexing](#), [Time Series and Panel Series](#), [Collapse Overview](#)

Examples

```
oldopts <- options(max.print = 30)

# A normal use case
timeid(wlddev$decade)
timeid(wlddev$decade, factor = TRUE)
timeid(wlddev$decade, extra = TRUE)

# Here a large number of levels is generated, which is expensive
timeid(wlddev$date, factor = TRUE)
tid <- timeid(wlddev$date, extra = TRUE) # Much faster
str(tid)

# The reason for step = 1 are leap years with 366 days every 4 years
diff(attr(tid, "unique"))

# So in this case simple factor generation gives a better result
qF(wlddev$date, ordered = TRUE, na.exclude = FALSE)

# The best way to deal with this data would be to convert it
# to zoo::yearmon and then use timeid:
timeid(zoo::as.yearmon(wlddev$date), factor = TRUE, extra = TRUE)

options(oldopts)
rm(oldopts, tid)
```

 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 operations and data transformation by reference, and is thus a generalization of [sweep](#).

Usage

```
TRA(x, STATS, FUN = "-", ...)
setTRA(x, STATS, FUN = "-", ...) # Shorthand for invisible(TRA(..., set = TRUE))
```

```
## Default S3 method:
TRA(x, STATS, FUN = "-", g = NULL, set = FALSE, ...)

## S3 method for class 'matrix'
TRA(x, STATS, FUN = "-", g = NULL, set = FALSE, ...)

## S3 method for class 'data.frame'
TRA(x, STATS, FUN = "-", g = NULL, set = FALSE, ...)

## S3 method for class 'grouped_df'
TRA(x, STATS, FUN = "-", keep.group_vars = TRUE, set = FALSE, ...)
```

Arguments

x a atomic vector, matrix, data frame or grouped data frame (class '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 11 supported operations:

<i>Int.</i>	<i>String</i>	<i>Description</i>
0	"replace_NA"	replace missing values in x
1	"replace_fill"	replace data and missing values in x
2	"replace"	replace data 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. make data divisible 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.

set logical. TRUE transforms data by reference i.e. performs in-place modification of the data without creating a copy.

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 ($g = \text{NULL}$), TRA is little more than a column based version of [sweep](#), albeit many times more efficient. In this case all methods support an atomic vector of statistics of length $\text{NCOL}(x)$ 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, -2.90)` [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`, thus together with these functions, `TRA` can also safely be used with atomic- or list-groups (as long as all functions apply sorted grouping, which is the default in `collapse`).

If `x` is a grouped data frame (`'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 `fungroup()` or `dplyr::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 statistics 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), # Also the same thing done manually !!
        fmean(m), "+"))

# Grouped data method
library(magrittr)
iris %>% fgroup_by(Species) %>% TRA(fmean())
iris %>% fgroup_by(Species) %>% fmean(TRA = "-") # Same thing
iris %>% fgroup_by(Species) %>% TRA(fmean(.)[c(2,4)]) # Only transforming 2 columns
iris %>% fgroup_by(Species) %>% TRA(fmean(.)[c(2,4)], # Dropping species column
        keep.group_vars = FALSE)

```

t_list

Efficient List Transpose

Description

t_list turns a list of lists inside-out. The performance is quite efficient regardless of the size of the list.

Usage

```
t_list(l)
```

Arguments

1 a list of lists. Elements inside the sublists can be heterogeneous, including further lists.

Value

l transposed such that the second layer of the list becomes the top layer and the top layer the second layer. See Examples.

Note

To transpose a data frame / list of atomic vectors see `data.table::transpose()`.

See Also

[rsplit](#), [List Processing](#), [Collapse Overview](#)

Examples

```
# Homogenous list of lists
l <- list(a = list(c = 1, d = 2), b = list(c = 3, d = 4))
str(l)
str(t_list(l))

# Heterogenous case
l2 <- list(a = list(c = 1, d = letters), b = list(c = 3:10, d = list(4, e = 5)))
attr(l2, "bla") <- "abc" # Attributes other than names are preserved
str(l2)
str(t_list(l2))

rm(l, l2)
```

unlist2d

*Recursive Row-Binding / Unlisting in 2D - to Data Frame***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](#), and best understood as a recursive generalization of `do.call(rbind, ...)`.

It 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 = "variable"</code> can be supplied. For plain matrices in <code>l</code> , integer row names are generated.

recursive	logical. if FALSE, only process the lowest (deepest) level of 1. See Details.
id.factor	if TRUE and !isFALSE(idcols), create id columns as factors instead of character or integer vectors. Alternatively it is possible to specify id.factor = "ordered" to generate ordered factor id's. This is useful if id's are used for further analysis e.g. as inputs to ggplot2.
DT	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 (atomic) 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 !isFALSE(idcols), create id-columns on the left, filled with the object names or indices (if the (sub-)list is unnamed). If !isFALSE(row.names), store rownames 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 rownames of the objects (if !isFALSE(row.names)), followed by the data columns, matched at each level of recursion. Optimal results are 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(1, use.names = TRUE, fill = TRUE, idcol = ".id")` however for lists of lists `unlist2d` does not produce the same output as `data.table::rbindlist` because `unlist2d` is a recursive function.

See Also

[rsplit](#), [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 <- rsplit(GGDC10S, ~ Variable + Country, cols = 6:16)

# 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

# List of panel-series matrices
psml <- psmat(fsubset(GGDC10S, Variable == "VA"), ~Country, ~Year, cols = 6:16, array = FALSE)

# Recombining with unlist2d() (effectively like reshaping the data)
head(unlist2d(psml, idcols = "Sector", row.names = "Country"))

rm(l, dat, sdat, psml)

```

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 indexed data / 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 grouped data frame / compatibility with dplyr:

## S3 method for class 'grouped_df'
varying(x, any_group = TRUE, use.g.names = FALSE, drop = TRUE,
        keep.group_vars = TRUE, ...)

# Methods for grouped data frame / compatibility with sf:

## S3 method for class 'sf'
varying(x, by = NULL, cols = NULL, any_group = TRUE, use.g.names = TRUE, drop = TRUE, ...)
```

Arguments

<code>x</code>	a vector, matrix, data frame, 'indexed_series' ('pseries'), 'indexed_frame' ('pdata.frame') or grouped data frame ('grouped_df'). 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> , <code>FALSE</code> will check and report variation in all groups, whereas the default <code>TRUE</code> only checks if there is variation within any group. See Examples.
<code>cols</code>	select columns using column names, indices or a function (e.g. <code>is.numeric</code>). Two-sided formulas passed to by 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. <code>TRUE</code> 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 index , 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. <code>FALSE</code> 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.

The *sf* method simply ignores the geometry column.

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 5 indicators from the World Bank's World Development Indicators (WDI) database: (1) GDP per capita, (2) Life expectancy at birth, (3) GINI index, (4) Net ODA and official aid received and (5) Population. The panel data is balanced and covers 216 present and historic countries from 1960-2020 (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 13176 observations on the following 13 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 int Year
decade int 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$)
LIFEEX num Life expectancy at birth, total (years)
GINI num GINI index (World Bank estimate)
ODA num Net official development assistance and official aid received (constant 2018 US$)
POP num Population, total
```

Source

<https://data.worldbank.org/>, accessed via the WDI package. The codes for the series are `c("NY.GDP.PCAP.KD", "SP.DYN.LE00.IN", "SI.POV.GINI", "DT.ODA.ALLD.KD", "SP.POP.TOTL")`.

See Also

[GGDC10S, Collapse Overview](#)

Examples

```
data(wlddev)

# Panel-summarizing the 5 series
qsu(wlddev, pid = ~iso3c, cols = 9:13, vlabels = TRUE)

# By Region
qsu(wlddev, by = ~region, cols = 9:13, vlabels = TRUE)

# Panel-summary by region
qsu(wlddev, by = ~region, pid = ~iso3c, cols = 9:13, vlabels = TRUE)

# Pairwise correlations: Overall
print(pwcor(get_vars(wlddev, 9:13), N = TRUE, P = TRUE), show = "lower.tri")

# Pairwise correlations: Between Countries
print(pwcor(fmean(get_vars(wlddev, 9:13), wlddev$iso3c), N = TRUE, P = TRUE), show = "lower.tri")

# Pairwise correlations: Within Countries
print(pwcor(fwithin(get_vars(wlddev, 9:13), wlddev$iso3c), N = TRUE, P = TRUE), show = "lower.tri")
```

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