Package ‘lfe’

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Title Linear Group Fixed Effects
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Description Transforms away factors with many levels prior to doing an OLS.
Useful for estimating linear models with multiple group fixed effects, and for estimating linear models which uses factors with many levels as pure control variables. See Gaure (2013) <doi:10.1016/j.csda.2013.03.024>
Includes support for instrumental variables, conditional F statistics for weak instruments, robust and multi-way clustered standard errors, as well as limited mobility bias correction (Gaure 2014 <doi:10.1002/sta4.68>).
WARNING: This package is NOT under active development anymore, no further improvements are to be expected, and the package is at risk of being removed from CRAN.
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Overview. Linear Group Fixed Effects

Description

The package uses the Method of Alternating Projections to estimate linear models with multiple group fixed effects. A generalization of the within estimator. It supports IV-estimation with multiple endogenous variables via 2SLS, with conditional F statistics for detection of weak instruments. It is thread-parallelized and intended for large problems. A method for correcting limited mobility bias is also included.
Details

This package is intended for linear models with multiple group fixed effects, i.e. with 2 or more factors with a large number of levels. It performs similar functions as \texttt{stats::lm()}, but it uses a special method for projecting out multiple group fixed effects from the normal equations, hence it is faster. It is a generalization of the within estimator. This may be required if the groups have high cardinality (many levels), resulting in tens or hundreds of thousands of dummy variables. It is also useful if one only wants to control for the group effects, without actually estimating them. The package may optionally compute standard errors for the group effects by bootstrapping, but this is a very time- and memory-consuming process compared to finding the point estimates. If you only have a single huge factor, the package \texttt{plm} is probably better suited. If your factors don’t have thousands of levels, \texttt{stats::lm()} or other packages are probably better suited. \texttt{lfe} is designed to produce the same results as \texttt{stats::lm()} will do if run with the full set of dummies.

Projecting out interactions between continuous covariates and factors is supported. I.e. individual slopes, not only individual intercepts. Multiple left hand sides are supported.

The package does not support non-linear models. For GLMs with many dummies there is a package \texttt{alpaca} which uses similar methods to project them out.

The estimation is done in two steps. First the other coefficients are estimated with the function \texttt{felm()} by centering on all the group means, followed by an OLS (similar to \texttt{lm}). Then the group effects are extracted (if needed) with the function \texttt{getfe()}. This method is described by Gaure (2013), but also appears in Guimaraes and Portugal (2010), disguised as the Gauss-Seidel algorithm.

There’s also a function \texttt{demeanlist()} which just does the centering on an arbitrary matrix or data frame, and there’s a function \texttt{compfactor()} which computes the connected components which are used for interpreting the group effects when there are only two factors (see the Abowd et al references), they are also returned by \texttt{getfe()}.

For those who study the correlation between the fixed effects, like in Abowd et al. (1999), there are functions \texttt{bccorr()} and \texttt{fevcov()} for computing limited mobility bias corrected correlations and variances with the method described in Gaure (2014b).

Instrumental variable estimations are supported with 2SLS. Conditional F statistics for testing reduced rank weak instruments as in Sanderson and Windmeijer (2015) are available in \texttt{condfstat()}. Joint significance testing of coefficients is available in \texttt{waldtest()}.

The centering on the means is done with a tolerance which is set by \texttt{options(lfe.eps=1e-8)} (the default). This is a somewhat conservative tolerance, in many cases I’d guess \texttt{1e-6} may be sufficient. This may speed up the centering. In the other direction, setting \texttt{options(lfe.eps=0)} will provide maximum accuracy at the cost of computing time and warnings about convergence failure.

The package is threaded, that is, it may use more than one cpu. The number of threads is fetched upon loading the package from the environment variable \texttt{LFE_THREADS}, \texttt{OMP_THREAD_LIMIT}, \texttt{OMP_NUM_THREADS} or \texttt{NUMBER_OF_PROCESSORS} (for Windows), and stored by \texttt{options(lfe.threads=n)}. This option can be changed prior to calling \texttt{felm()}, if so desired. Note that, typically, \texttt{lfe} is limited by memory bandwidth, not cpu speed, thus fast memory and large cache is more important than clock frequency. It is therefore also not always true that running on all available cores is much better than running on half of them.

Threading is only done for the centering; the extraction of the group effects is not threaded. The default method for extracting the group coefficients is the iterative Kaczmarz-method, its tolerance is also the \texttt{lfe.eps} option. For some datasets the Kaczmarz-method is converging very slowly, in this case it may be replaced with a conjugate gradient method by setting the option
options(lfe.usecg=TRUE). Various time-consuming parts of lfe may print progress reports, the minimum interval in seconds is options(lfe.pint=1800).

The package has been tested on datasets with approx 20,000,000 observations with 15 covariates and approx 2,300,000 and 270,000 group levels (the felm() took about 50 minutes on 8 cpus, the getfe() takes 5 minutes). Though, beware that not only the size of the dataset matters, but also its structure, as demonstrated by Gaure (2014a).

The package will work with any number of grouping factors, but if more than two, their interpretation is in general not well understood, i.e. one should make sure that the group coefficients are estimable. A discussion of estimability, the algorithm used, and convergence rate are available in vignettes, as well as in the published papers in the citation list (citation('lfe')).

In the exec-directory there is a perl-script lfe.script which is used at the author’s site for automated creation of R-scripts from a simple specification file. The format is documented in doc/lfeguide.txt.

lfe is similar in function, though not in method, to the Stata modules a2reg and felsdvrreg. The method is very similar to the one in the Stata module reghdfe.

References


Examples

```r
oldopts <- options("lfe.threads")
options(lfe.threads = 2)
x <- rnorm(1000)
x2 <- rnorm(length(x))
id <- factor(sample(10, length(x), replace = TRUE))
firm <- factor(sample(3, length(x), replace = TRUE, prob = c(2, 1.5, 1)))
year <- factor(sample(10, length(x), replace = TRUE, prob = c(2, 1.5, rep(1, 8))))
id.eff <- rnorm(nlevels(id))
firm.eff <- rnorm(nlevels(firm))
year.eff <- rnorm(nlevels(year))
y <- x + 0.25 * x2 + id.eff[id] + firm.eff[firm] +
    year.eff[year] + rnorm(length(x))
est <- felm(y ~ x + x2 | id + firm + year)
summary(est)
getfe(est, se = TRUE)
# compare with an ordinary lm
summary(lm(y ~ x + x2 + id + firm + year - 1))
options(oldopts)
```

**bccorr**

*Compute limited mobility bias corrected correlation between fixed effects*

**Description**

With a model like $y = X\beta + D\theta + F\psi + \epsilon$, where $D$ and $F$ are matrices with dummy encoded factors, one application of *lfe* is to study the correlation $\text{cor}(D\theta, F\psi)$. However, if we use estimates for $\theta$ and $\psi$, the resulting correlation is biased. The function *bccorr* computes a bias corrected correlation as described in *Gaure (2014)*.

**Usage**

```r
bccorr(
est,
    alpha = getfe(est),
    corrfactors = 1L:2L,
    nocovar = (length(est$X) == 0) && length(est$fe) == 2,
    tol = 0.01,
    maxsamples = Inf,
    lhs = NULL
)
```
Arguments

- **est**: an object of class `'felm'`, the result of a call to `[felm](keepX=TRUE)`.
- **alpha**: a data frame, the result of a call to `getfe()`.
- **corrfactors**: integer or character vector of length 2. The factors to correlate. The default is fine if there are only two factors in the model.
- **nocovar**: logical. Assume no other covariates than the two factors are present, or that they are uncorrelated with them.
- **tol**: The absolute tolerance for the bias-corrected correlation.
- **maxsamples**: Maximum number of samples for the trace sample means estimates
- **lhs**: character. Name of left hand side if multiple left hand sides.

Details

The bias expressions from Andrews et al. are of the form $tr(AB^{-1}C)$ where $A$, $B$, and $C$ are matrices too large to be handled directly. `bccorr` estimates the trace by using the formula $tr(M) = E(x'^{t}Mx)$ where $x$ is a vector with coordinates drawn uniformly from the set $\{-1, 1\}$. More specifically, the expectation is estimated by sample means, i.e. in each sample a vector $x$ is drawn, the equation $Bv = Cx$ is solved by a conjugate gradient method, and the real number $x'^{t}Av$ is computed.

There are three bias corrections, for the variances of $D\theta$ ($vD$) and $F\psi$ ($vF$), and their covariance ($vDF$). The correlation is computed as $\rho \leftarrow \frac{vDF}{\sqrt{(vD)(vF)}}$. The variances are estimated to a relative tolerance specified by the argument `tol`. The covariance bias is estimated to an absolute tolerance in the correlation $\rho$ (conditional on the already bias corrected $vD$ and $vF$) specified by `tol`. The CG algorithm does not need to be exceedingly precise, it is terminated when the solution reaches a precision which is sufficient for the chosen precision in $vD$, $vF$, $vDF$.

If `est` is the result of a weighted `felm()` estimation, the variances and correlations are weighted too.

Value

`bccorr` returns a named integer vector with the following fields:

- **corr**: the bias corrected correlation.
- **v1**: the bias corrected variance for the first factor specified by `corrfactors`.
- **v2**: the bias corrected variance for the second factor.
- **cov**: the bias corrected covariance between the two factors.
- **d1**: the bias correction for the first factor.
- **d2**: the bias correction for the second factor.
- **d12**: the bias correction for covariance.

The bias corrections have been subtracted from the bias estimates. E.g. $v2 = v2' - d2$, where $v2'$ is the biased variance.
Note

Bias correction for IV-estimates are not supported as of now.

Note that if est is the result of a call to felm() with keepX=FALSE (the default), the correlation will be computed as if the covariates X are independent of the two factors. This will be faster (typically by a factor of approx. 4), and possibly wronger.

Note also that the computations performed by this function are non-trivial, they may take quite some time. It would be wise to start out with quite liberal tolerances, e.g. tol=0.1, to get an idea of the time requirements.

The algorithm used is not very well suited for small datasets with only a few thousand levels in the factors.

References


See Also

fevcov()

Examples

x <- rnorm(500)
x2 <- rnorm(length(x))

## create individual and firm
id <- factor(sample(40, length(x), replace = TRUE))
firm <- factor(sample(30, length(x), replace = TRUE, prob = c(2, rep(1, 29))))
foo <- factor(sample(20, length(x), replace = TRUE))

## effects
id.eff <- rnorm(nlevels(id))
firm.eff <- rnorm(nlevels(firm))
foo.eff <- rnorm(nlevels(foo))

## left hand side
y <- x + 0.25 * x2 + id.eff[id] + firm.eff[firm] + foo.eff[foo] + rnorm(length(x))

# make a data frame
fr <- data.frame(y, x, x2, id, firm, foo)

## estimate and print result
est <- felm(y ~ x + x2 | id + firm + foo, data = fr, keepX = TRUE)
# find bias corrections
bccorr(est)
**btrap**

*Bootstrap standard errors for the group fixed effects*

### Description

Bootstrap standard errors for the group fixed effects which were swept out during an estimation with `felm()`.

### Usage

```r
btrap(
    alpha, 
    obj, 
    N = 100, 
    ef = NULL, 
    eps = getOption("lfe.eps"), 
    threads = getOption("lfe.threads"), 
    robust = FALSE, 
    cluster = NULL, 
    lhs = NULL 
)
```

### Arguments

- **alpha**: data frame returned from `getfe()`
- **obj**: object of class "felm", usually, a result of a call to `felm()`
- **N**: integer. The number of bootstrap iterations
- **ef**: function. An estimable function such as in `getfe()`. The default is to use the one used on `alpha`
- **eps**: double. Tolerance for centering, as in `getfe`
- **threads**: integer. The number of threads to use
- **robust**: logical. Should heteroskedastic standard errors be estimated?
- **cluster**: logical or factor. Estimate clustered standard errors.
- **lhs**: character vector. Specify which left hand side if `obj` has multiple lhs.

### Details

The bootstrapping is done in parallel if `threads > 1`. `btrap()` is run automatically from `getfe()` if `se=TRUE` is specified. To save some overhead, the individual iterations are grouped together, the memory available for this grouping is fetched with `getOption('lfe.bootmem')`, which is initialized upon loading of `lfe` to options(lfe.bootmem=500) (MB).

If `robust=TRUE`, heteroskedastic robust standard errors are estimated. If `robust=FALSE` and `cluster=TRUE`, clustered standard errors with the cluster specified to `felm()` are estimated. If `cluster` is a factor, it is used for the cluster definition. `cluster` may also be a list of factors.
Value

A data-frame of the same size as alpha is returned, with standard errors filled in.

Examples

oldopts <- options("lfe.threads")
options(lfe.threads = 2)
## create covariates
x <- rnorm(3000)
x2 <- rnorm(length(x))
## create individual and firm
id <- factor(sample(700, length(x), replace = TRUE))
firm <- factor(sample(300, length(x), replace = TRUE))
## effects
id.eff <- rlnorm(nlevels(id))
firm.eff <- rexp(nlevels(firm))
## left hand side
y <- x + 0.25 * x2 + id.eff[id] + firm.eff[firm] + rnorm(length(x))
## estimate and print result
est <- felm(y ~ x + x2 | id + firm)
summary(est)
## extract the group effects
alpha <- getfe(est)
head(alpha)
## bootstrap standard errors
head(btrap(alpha, est))

## bootstrap some differences
ef <- function(v, addnames) {
  if (addnames) {
    names(w) <- c("id2-id1", "id3-id2", "id3-id1")
    attr(w, "extra") <- list(note = c("line1", "line2", "line3"))
  }
  w
}
# check that it's estimable
is.estimable(ef, est$fe)
head(btrap(alpha, est, ef = ef))
options(oldopts)

cgsolve

Solve a symmetric linear system with the conjugate gradient method
Description
cgsolve uses a conjugate gradient algorithm to solve the linear system \( Ax = b \) where \( A \) is a symmetric matrix. cgsolve is used internally in lfe in the routines fevcov() and bccorr(), but has been made public because it might be useful for other purposes as well.

Usage
cgsolve(A, b, eps = 0.001, init = NULL, symmtest = FALSE, name = "")

Arguments
- \( A \): matrix, Matrix or function.
- \( b \): vector or matrix of columns vectors.
- \( \epsilon \): numeric. Tolerance.
- \( \text{init} \): numeric. Initial guess.
- \( \text{symmtest} \): logical. Should the matrix be tested for symmetry?
- \( \text{name} \): character. Arbitrary name used in progress reports.

Details
The argument \( A \) can be a symmetric matrix or a symmetric sparse matrix inheriting from "Matrix" of the package Matrix. It can also be a function which performs the matrix-vector product. If so, the function must be able to take as input a matrix of column vectors.

If the matrix \( A \) is rank deficient, some solution is returned. If there is no solution, a vector is returned which may or may not be close to a solution. If symmtest is FALSE, no check is performed that \( A \) is symmetric. If not symmetric, cgsolve is likely to raise an error about divergence.

The tolerance \( \epsilon \) is a relative tolerance, i.e. \( ||x - x_0|| < \epsilon ||x_0|| \) where \( x_0 \) is the true solution and \( x \) is the solution returned by cgsolve. Use a negative \( \epsilon \) for absolute tolerance. The termination criterion for cgsolve is the one from Kaasschieter (1988), Algorithm 3.

Preconditioning is currently not supported.

If \( A \) is a function, the test for symmetry is performed by drawing two random vectors \( x, y \), and testing whether \( |(Ax, y) - (x, Ay)| < 10^{-6} \sqrt{(||Ax||^2 + ||Ay||^2)/N} \), where \( N \) is the vector length. Thus, the test is neither deterministic nor perfect.

Value
An solution \( x \) of the linear system \( Ax = b \) is returned.

References

See Also
kaczmarz()
Examples

```r
N <- 100000
# create some factors
f1 <- factor(sample(34000, N, replace = TRUE))
f2 <- factor(sample(25000, N, replace = TRUE))
# a matrix of dummies, which probably is rank deficient
B <- makeDmatrix(list(f1, f2))
dim(B)
# create a right hand side
b <- as.matrix(B %*% rnorm(ncol(B)))
# solve B B x = B b
sol <- cgsolve(crossprod(B), crossprod(B, b), eps = -1e-2)
# verify solution
sqrt(sum((B %*% sol - b)^2))
```

chainsubset

### Chain subset conditions

#### Description

Chain subset conditions

#### Usage

```r
chainsubset(..., out.vars)
```

#### Arguments

- `...` Logical conditions to be chained.
- `out.vars` character. Variables not in data.frame, only needed if you use variables which are not in the frame. If `out.vars` is not specified, it is assumed to match all variables starting with a dot (`.`).

#### Details

A set of logical conditions are chained, not and’ed. That is, each argument to `chainsubset` is used as a filter to create a smaller dataset. Each subsequent argument filters further. For independent conditions this will be the same as and’ing them. I.e. `chainsubset(x < 0, y < 0)` will yield the same subset as `(x < 0) & (y < 0)`. However, for aggregate filters like `chainsubset(x < mean(y), x > mean(y))` we first find all the observations with `x < mean(y)`, then among these we find the ones with `x > mean(y)`. The last `mean(y)` is now conditional on `x < mean(y)`.

#### Value

Expression that can be `eval`’ed to yield a logical subset mask.
Note

Some trickery is done to make this work directly in the subset argument of functions like `felm()` and `lm()`. It might possibly fail with an error message in some situations. If this happens, it should be done in two steps: `ss <- eval(chainsubset(...),data); lm(...,data=data, subset=ss)`. In particular, the arguments are taken literally, constructions like `function(...) {chainsubset(...)}` or `a <- quote(x < y); chainsubset(a)` do not work, but `do.call(chainsubset,list(a))` does.

Examples

```r
set.seed(48)
N <- 10000
dat <- data.frame(y = rnorm(N), x = rnorm(N))
# It's not the same as and'ing the conditions:
felm(y ~ x, data = dat, subset = chainsubset(x < mean(y), y < 2 * mean(x)))
felm(y ~ x, data = dat, subset = chainsubset(y < 2 * mean(x), x < mean(y)))
felm(y ~ x, data = dat, subset = (x < mean(y)) & (y < 2 * mean(x)))
lm(y ~ x, data = dat, subset = chainsubset(x < mean(y), x > mean(y)))
```

compfactor

Find the connected components

Description

'compfactor' computes the connected components of the dummy-part of the model.

Usage

`compfactor(f1, WW = FALSE)`

Arguments

- `f1`: a list of factors defining the dummies
- `WW`: logical. Use Weeks and Williams components

Details

If there are more than two factors and `WW=FALSE`, only the first two will be used. If `WW=TRUE` and `length(f1) > 2`, the component structure will be as in "A Note on the Determination of Connectedness in an N-Way Cross Classification" by D.L. Weeks and D.R. Williams, Technometrics, vol 6 no 3, August 1964. I.e. in each component, the coefficients within each factor are comparable, that is, their difference is estimable even if there are more than two factors. That is, one may use one reference in each factor in each component, and interpret the coefficients within a component as usual. This is not an exhaustion of all the estimable functions. There is somewhat more about this in one of the vignettes.
Value
A factor of the same length as the factors in the input argument. It defines the connected components. E.g. nlevels(compfactor(f1)) will yield the number of connected components.

Examples

```r
## create two factors
f1 <- factor(sample(300, 400, replace = TRUE))
f2 <- factor(sample(300, 400, replace = TRUE))

## find the components
cf <- compfactor(list(f1 = f1, f2 = f2))

## show the third largest component
fr <- data.frame(f1, f2, cf)
fr[cf == 3, ]
```

---

**condfstat**  
*Compute conditional F statistic for weak instruments in an IV-estimation with multiple endogenous variables*

Description
When using multiple instruments for multiple endogenous variables, the ordinary individual t-tests for the instruments in the first stage do not always reveal a weak set of instruments. Conditional F statistics can be used for such testing.

Usage
```
condfstat(object, type = "default", quantiles = 0, bN = 100L)
```

Arguments
- `object`  
  object of class "felm", a result of a call to `felm()`.
- `type`  
  character. Error structure. Passed to `waldtest()`. If NULL, both iid and robust Fs are returned.
- `quantiles`  
  numeric. Quantiles for bootstrap.
- `bN`  
  integer. Number of bootstrap samples.

Details
IV coefficient estimates are not normally distributed, in particular they do not have the right expectation. They follow a quite complicated distribution which is fairly close to normal if the instruments are good. The conditional F-statistic is a measure of how good the instruments are. If the F is large, the instruments are good, and any bias due to the instruments is small compared to the estimated
standard errors, and also small relative to the bias in OLS. See Sanderson and Windmeijer (2014) and Stock and Yogo (2004). If F is small, the bias can be large compared to the standard error.

If any(quantiles > 0.0), a bootstrap with bN samples will be performed to estimate quantiles of the endogenous parameters which includes the variance both from the 1st and 2nd stage. The result is returned in an array attribute quantiles of the value returned by condfstat. The argument quantiles can be a vector to estimate more than one quantile at once. If quantiles=NULL, the bootstrapped estimates themselves are returned. The bootstrap is normally much faster than running felm over and over again. This is so because all exogenous variables are projected out of the equations before doing the bootstrap.

Value

A p x k matrix, where k is the number of endogenous variables. Each row are the conditional F statistics on a residual equation as described in Sanderson and Windmeijer (2014), for a certain error structure. The default is to use iid, or cluster if a cluster was specified to felm(). The third choice is 'robust', for heteroskedastic errors. If type=NULL, iid and robust Fs are returned, and cluster, if that was specified to felm.

Note that for these F statistics it is not the p-value that matters, it is the F statistic itself which (coincidentally) pops up in the denominator for the asymptotic bias of the IV estimates, and thus a large F is beneficial.

Note

Please note that condfstat does not work with the old syntax for IV in [felm](...,iv=). The new multipart syntax must be used.

References


Examples

```r
z1 <- rnorm(4000)
z2 <- rnorm(length(z1))
u <- rnorm(length(z1))
# make x1, x2 correlated with errors u
x1 <- z1 + z2 + 0.2 * u + rnorm(length(z1))
x2 <- z1 + 0.94 * z2 - 0.3 * u + rnorm(length(z1))
y <- x1 + x2 + u
est <- felm(y - 1 | 0 | (x1 | x2 ~ z1 + z2))
summary(est)
## Not run:
```
demeanlist

Example usage:

```r
summary(est$stage1, lhs = "x1")
summary(est$stage1, lhs = "x2")
```

```r
## End(Not run)

# the joint significance of the instruments in both the first stages are ok:
t(sapply(est$stage1$lhs, function(lh) waldtest(est$stage1, ~ z1 | z2, lhs = lh)))
# everything above looks fine, t-tests for instruments,
# as well as F-tests for excluded instruments in the 1st stages.
# The conditional F-test reveals that the instruments are jointly weak
# (it's close to being only one instrument, z1+z2, for both x1 and x2)
condfstat(est, quantiles = c(0.05, 0.95))
```

demeanlist

Centre vectors on multiple groups

Description

Uses the method of alternating projections to centre a (model) matrix on multiple groups, as specified by a list of factors. This function is called by `felm()`, but it has been made available as standalone in case it’s needed. In particular, if one does not need transformations provided by R-formulas but have the covariates present as a matrix or a data.frame, a substantial amount of time can be saved in the centering.

Usage

```r
demeanlist(
  mtx,
  fl,
  icpt = 0L,
  eps = getOption("lfe.eps"),
  threads = getOption("lfe.threads"),
  progress = getOption("lfe.pint"),
  accel = getOption("lfe.accel"),
  randfact = TRUE,
  means = FALSE,
  weights = NULL,
  scale = TRUE,
  na.rm = FALSE,
  attrs = NULL
)
```

Arguments

- **mtx**: matrix whose columns form vectors to be group-centred. mtx can also be a list of vectors or matrices, such as a data frame.
- **fl**: list of factors defining the grouping structure.
icpt  the position of the intercept, this column is removed from the result matrix.
eps   a tolerance for the centering.
threads an integer specifying the number of threads to use.
progress integer. If positive, make progress reports (whenever a vector is centered, but
        not more often than every progress minutes).
accel  integer. Set to 1 if Gearhart-Koshy acceleration should be done.
randfact logical. Should the order of the factors be randomized? This may improve
        convergence.
means  logical. Should the means instead of the demeaned matrix be returned? Setting
        means=TRUE will return mtx - demeanlist(mtx,...), but without the extra
        copy.
weights numeric. For weighted demeaning.
scale  logical. Specify scaling for weighted demeaning.
na.rm  logical which indicates what should happen when the data contain NAs. If TRUE,
        rows in the input mtx are removed prior to centering. If FALSE, they are kept,
        leading to entire groups becoming NA in the output.
attrs  list. List of attributes which should be attached to the output. Used internally.

Details

For each column y in mtx, the equivalent of the following centering is performed, with cy as the
result.

cy <- y; oldy <- y-1
while(sqrt(sum((cy-oldy)**2)) >= eps) {
    oldy <- cy
    for(f in fl) cy <- cy - ave(cy,f)
}

Each factor in fl may contain an attribute ‘x’ which is a numeric vector of the same length as
the factor. The centering is then not done on the means of each group, but on the projection onto
the covariate in each group. That is, with a covariate x and a factor f, it is like projecting out the
interaction x:f. The ‘x’ attribute can also be a matrix of column vectors, in this case it can be
beneficial to orthogonalize the columns, either with a stabilized Gram-Schmidt method, or with the
simple method x \%\% solve(chol(crossprod(x))).

The weights argument is used if a weighted projection is computed. If W is the diagonal matrix
with weights on the diagonal, demeanlist computes $W^{-1}M_{WD}Wx$ where x is the input
vector, D is the matrix of dummies from fl and $M_{WD}$ is the projection on the orthogonal com-
plement of the range of the matrix WD. It is possible to implement the weighted projection with
the ‘x’ attribute mentioned above, but it is a separate argument for convenience. If scale=FALSE,
demeanlist computes $M_{WD}x$ without any W scaling. If length(scale) > 1, then scale[1]
specifies whether the input should be scaled by W, and scale[2] specifies whether the output
should be scaled by $W^{-1}$. This is just a convenience to save some memory copies in other func-
tions in the package.

Note that for certain large datasets the overhead in felm() is large compared to the time spent in
demeanlist. If the data are present directly without having to use the formula-interface to felm for
transformations etc, it is possible to run demeanlist directly on a matrix or "data.frame" and do the OLS "manually", e.g. with something like `cx <- demeanlist(x,...); beta <- solve(crossprod(cx), crossprod(cx,y))`

In some applications it is known that a single centering iteration is sufficient. In particular, if `length(fl)==1` and there is no interaction attribute `x`. In this case the centering algorithm is terminated after the first iteration. There may be other cases, e.g. if there is a single factor with a matrix `x` with orthogonal columns. If you have such prior knowledge, it is possible to force termination after the first iteration by adding an attribute `attr(fl, 'oneiter') <- TRUE`. Convergence will be reached in the second iteration anyway, but you save one iteration, i.e. you double the speed.

Value

If `mtx` is a matrix, a matrix of the same shape, possibly with column `icpt` deleted.

If `mtx` is a list of vectors and matrices, a list of the same length is returned, with the same vector and matrix-pattern, but the matrices have the column `icpt` deleted.

If `mtx` is a 'data.frame', a 'data.frame' with the same names is returned; the `icpt` argument is ignored.

If `na.rm` is specified, the return value has an attribute 'na.rm' with a vector of row numbers which has been removed. In case the input is a matrix or list, the same rows are removed from all of them. Note that removing NAs incurs a copy of the input, so if memory usage is an issue and many runs are done, one might consider removing NAs from the data set entirely.

Note


demeanlist will use an in place transform to save memory, provided the `mtx` argument is unnamed. Thus, as always in R, you shouldn't use temporary variables like `tmp <- fun(x[v,]); bar <- demeanlist(tmp,...); rm(tmp)`, it will be much better to do `bar <- demeanlist(fun(x[v,]),...).` However, demeanlist allows a construction like `bar <- demeanlist(unnamed(tmp),...)` which will use an in place transformation, i.e. `tmp` will be modified, quite contrary to the usual semantics of R.

Examples

```r
oldopts <- options("lfe.threads")
options(lfe.threads = 2)
## create a matrix
mtx <- data.frame(matrix(rnorm(999), ncol = 3))
# a list of factors
rgb <- c("red", "green", "blue")
fl <- replicate(4, factor(sample(rgb, nrow(mtx), replace = TRUE)), simplify = FALSE)
names(fl) <- paste("g", seq_along(fl), sep = "")
# centre on all means
mtx0 <- demeanlist(mtx, fl)
head(data.frame(mtx0, fl))
# verify that the group means for the columns are zero
lapply(fl, function(f) apply(mtx0, 2, tapply, f, mean))
options(oldopts)
```
Description

Creates an estimable function for a factor-structure.

Usage

```r
efactory(obj, opt = "ref", ...)
```

Arguments

- `obj`: object of class "felm", usually, a result of a call to `felm()`.
- `opt`: character. Which type of estimable function.
- `...`: various.

Details

There are several possibilities for the input parameter `opt`.

- "ref" yields an estimable function which is similar to the default one in `lm()`, one reference is forced to 0 in each connected component.
- "zm" Similar to "ref", but the factor which does not contain a reference is made to have zero mean, and an intercept is added.
- "zm2" Similar to "zm", but both factors are made to have zero mean.
- "ln" Least norm function. This will yield the raw coefficients from the Kaczmarz-method, i.e. the solution with smallest norm. This function is not estimable.

Note that in the case with more than two factors, it is not known how to analyze the factors to find the structure of the rank-deficiencies, i.e. the estimable functions. In this case, the factors beyond the first two are assumed not to contribute to the rank-deficiency beyond a single dimension in each. Both "ref" and "zm" keep one such reference at zero in each of these factors. This is the common method when using dummies.

In the case that interactions are specified in the model, i.e. with `x:f` in the second part of the formula, these terms are not analyzed to create an estimable function. Only the pure `f` terms are used for this purpose. It is assumed that the `x:f` terms are all identified. Note that in this case, all the levels of `f` are included.

Value

A function of two parameters `function(v, addnames)`. An estimable function (i.e. the result is the vector of some length N) of the input vector `v`. When `addnames=TRUE` the returned vector should have names, and optionally an attribute "extra" which is a list of vectors of length N which may be used to code additional information.
Note
The author is open to suggestions for other estimable functions, i.e. other useful normalizations of the solutions.
It is not strictly necessary that the obj argument is of class "felm", any list with entries "fe" and "cfactor" of the appropriate form will do. That is, list(fe=fl, cfactor=compfactor(fl)) where fl is the list of factors defining the component structure. I.e. if the model is y ~ ... | id + firm, we have fl=list(id=id, firm=firm).

Examples

oldopts <- options("lfe.threads")
options(lfe.threads = 2)
id <- factor(sample(5000, 50000, replace = TRUE))
firm <- factor(sample(3000, 50000, replace = TRUE))
fl <- list(id = id, firm = firm)
obj <- list(fe = fl, cfactor = compfactor(fl))
## the trivial least-norm transformation, which by the way is non-estimable
print(ef <- efactory(obj, "ln"))
is.estimable(ef, fl)
## then the default
print(ef <- efactory(obj, "ref"))
is.estimable(ef, fl)
# get the names of the coefficients, i.e. the nm-variable in the function
head(evalq(nm, environment(ef)))
options(oldopts)

felm Fit a linear model with multiple group fixed effects

Description
'felm' is used to fit linear models with multiple group fixed effects, similarly to lm. It uses the Method of Alternating projections to sweep out multiple group effects from the normal equations before estimating the remaining coefficients with OLS.

Usage
felm(
    formula,
data,
    exactDOF = FALSE,
    subset,
    na.action,
    contrasts = NULL,
    weights = NULL,
    ...
)
Arguments

- **formula**: an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted. Similarly to 'lm'. See Details.
- **data**: a data frame containing the variables of the model.
- **exactDOF**: logical. If more than two factors, the degrees of freedom used to scale the covariance matrix (and the standard errors) is normally estimated. Setting exactDOF=TRUE causes `felm` to attempt to compute it, but this may fail if there are too many levels in the factors. exactDOF='rM' will use the exact method in `Matrix::rankMatrix()`, but this is slower. If neither of these methods works, it is possible to specify exactDOF='mc', which utilizes a Monte-Carlo method to estimate the expectation E(x' P x) = tr(P), the trace of a certain projection, a method which may be more accurate than the default guess. If the degrees of freedom for some reason are known, they can be specified like exactDOF=342772.
- **subset**: an optional vector specifying a subset of observations to be used in the fitting process.
- **na.action**: a function which indicates what should happen when the data contain NAs. The default is set by the na.action setting of options, and is na.fail if that is unset. The 'factory-fresh' default is na.omit. Another possible value is NULL, no action. na.exclude is currently not supported.
- **contrasts**: an optional list. See the contrasts.arg of `model.matrix.default`.
- **weights**: an optional vector of weights to be used in the fitting process. Should be 'NULL' or a numeric vector. If non-NULL, weighted least squares is used with weights weights (that is, minimizing sum(w*e^2)); otherwise ordinary least squares is used.
- **...**: other arguments.
  - **cmethod**: character. Which clustering method to use. Known arguments are 'cgm' (the default), 'cgm2' (or 'reghdfe', its alias). These alternate methods will generally yield equivalent results, except in the case of multiway clustering with few clusters along at least one dimension.
  - **keepX**: logical. To include a copy of the expanded data matrix in the return value, as needed by `bccorr()` and `fevcov()` for proper limited mobility bias correction.
  - **keepCX**: logical. Keep a copy of the centred expanded data matrix in the return value. As list elements cX for the explanatory variables, and cY for the outcome.
  - **keepModel**: logical. Keep a copy of the model frame.
  - **nostats**: logical. Don't include covariance matrices in the output, just the estimated coefficients and various descriptive information. For IV, nostats can be a logical vector of length 2, with the last value being used for the 1st stages.
  - **psdef**: logical. In case of multiway clustering, the method of Cameron, Gelbach and Miller may yield a non-definite variance matrix. Ordinarily this is forced to be semidefinite by setting negative eigenvalues to zero. Setting psdef=FALSE will switch off this adjustment. Since the variance
estimator is asymptotically correct, this should only have an effect when the clustering factors have very few levels.

- `kclass` character. For use with instrumental variables. Use a k-class estimator rather than 2SLS/IV. Currently, the values 'nagar', 'b2sls', 'mb2sls', 'liml' are accepted, where the names are from Kolesar et al (2014), as well as a numeric value for the 'k' in k-class. With `kclass='liml'`, `felm` also accepts the argument `fuller=<numeric>`, for using a Fuller adjustment of the liml-estimator.

- `Nboot`, `bootexpr`, `bootcluster` Since `felm` has quite a bit of overhead in the creation of the model matrix, if one wants confidence intervals for some function of the estimated parameters, it is possible to bootstrap internally in `felm`. That is, the model matrix is resampled `Nboot` times and estimated, and the `bootexpr` is evaluated inside an `sapply`. The estimated coefficients and the left hand side(s) are available by name. Any right hand side variable `x` is available by the name `var.x`. The "`felm"-object for each estimation is available as `est`. If a `bootcluster` is specified as a factor, entire levels are resampled. `bootcluster` can also be a function with no arguments, it should return a vector of integers, the rows to use in the sample. It can also be the string 'model', in which case the cluster is taken from the model. `bootexpr` should be an expression, e.g. like `quote(x/x2 * abs(x3)/mean(y))`. It could be wise to specify `nostats=TRUE` when bootstrapping, unless the covariance matrices are needed in the bootstrap. If you need the covariance matrices in the full estimate, but not in the bootstrap, you can specify it in an attribute "boot" as `nostats=structure(FALSE, boot=TRUE).

- `iv`, `clustervar` deprecated. These arguments will be removed at a later time, but are still supported in this field. Users are STRONGLY encouraged to use multipart formulas instead. In particular, not all functionality is supported with the deprecated syntax; iv-estimations actually run a lot faster if multipart formulas are used, due to new algorithms which I didn’t bother to shoehorn in place for the deprecated syntax.

### Details

This function is intended for use with large datasets with multiple group effects of large cardinality. If dummy-encoding the group effects results in a manageable number of coefficients, you are probably better off by using `lm()`.

The formula specification is a response variable followed by a four part formula. The first part consists of ordinary covariates, the second part consists of factors to be projected out. The third part is an IVSpecification. The fourth part is a cluster specification for the standard errors. I.e. something like `y ~ x1 + x2 | f1 + f2 | (Q|W ~ x3+x4) | clu1 + clu2` where `y` is the response, `x1`, `x2` are ordinary covariates, `f1`, `f2` are factors to be projected out, `Q` and `W` are covariates which are instrumented by `x3` and `x4`, and `clu1`, `clu2` are factors to be used for computing cluster robust standard errors. Parts that are not used should be specified as 0, except if it's at the end of the formula, where they can be omitted. The parentheses are needed in the third part since `|` has higher precedence than `~`. Multiple left hand sides like `y|w|x ~ x1 + x2 | f1+f2|...` are allowed.

Interactions between a covariate `x` and a factor `f` can be projected out with the syntax `x:f`. The terms in the second and fourth parts are not treated as ordinary formulas, in particular it is not
possible with things like \( y \sim x_1 \mid x \cdot f \), rather one would specify \( y \sim x_1 + x \mid x : f + f \). Note that \( f : x \) also works, since R’s parser does not keep the order. This means that in interactions, the factor must be a factor, whereas a non-interacted factor will be coerced to a factor. I.e. in \( y \sim x_1 \mid x : f_1 + f_2 \), the \( f_1 \) must be a factor, whereas it will work as expected if \( f_2 \) is an integer vector.

In older versions of \texttt{lfe} the syntax was `felm(y \sim x_1 + x_2 + G(f1)`

- `G(f2), iv=list(Q \sim x3+x4, W \sim x3+x4), clustervar=c('clu1','clu2'))`. This syntax still works, but yields a warning. Users are strongly encouraged to change to the new multipart formula syntax. The old syntax will be removed at a later time.

The standard errors are adjusted for the reduced degrees of freedom coming from the dummies which are implicitly present. (An exception occurs in the case of clustered standard errors and, specifically, where clusters are nested within fixed effects; see here.) In the case of two factors, the exact number of implicit dummies is easy to compute. If there are more factors, the number of dummies is estimated by assuming there’s one reference-level for each factor, this may be a slight over-estimation, leading to slightly too large standard errors. Setting `exactDOF='rM'` computes the exact degrees of freedom with `rankMatrix()` in package \texttt{Matrix}.

For the iv-part of the formula, it is only necessary to include the instruments on the right hand side. The other explanatory covariates, from the first and second part of \texttt{formula}, are added automatically in the first stage regression. See the examples.

The \texttt{contrasts} argument is similar to the one in \texttt{lm()}, it is used for factors in the first part of the formula. The factors in the second part are analyzed as part of a possible subsequent \texttt{getfe()} call.

The \texttt{cmethod} argument may affect the clustered covariance matrix (and thus regressor standard errors), either directly or via adjustments to a degrees of freedom scaling factor. In particular, Cameron, Gelbach and Miller (CGM2011, sec. 2.3) describe two possible small cluster corrections that are relevant in the case of multiway clustering.

- The first approach adjusts each component of the cluster-robust variance estimator (CRVE) by its own \( c_i \) adjustment factor. For example, the first component (with \( G \) clusters) is adjusted by \( c_1 = \frac{G}{G-1} \frac{N-1}{N-K} \), the second component (with \( H \) clusters) is adjusted by \( c_2 = \frac{H}{H-1} \frac{N-1}{N-K} \), etc.
- The second approach applies the same adjustment to all CRVE components: \( c = \frac{J}{J-1} \frac{N-1}{N-K} \), where \( J = \min(G,H) \) in the case of two-way clustering, for example.

Any differences resulting from these two approaches are likely to be minor, and they will obviously yield exactly the same results when there is only one cluster dimension. Still, CGM2011 adopt the former approach in their own paper and simulations. This is also the default method that \texttt{felm} uses (i.e. \texttt{cmethod = 'cgm'}). However, the latter approach has since been adopted by several other packages that allow for robust inference with multiway clustering. This includes the popular Stata package \texttt{reghdfe}, as well as the \texttt{FixedEffectModels.jl} implementation in Julia. To match results from these packages exactly, use \texttt{cmethod = 'cgm2'} (or its alias, \texttt{cmethod = 'reghdfe'}). It is possible that some residual differences may still remain; see discussion here.

The old syntax with a single part formula with the \texttt{G()} syntax for the factors to transform away is still supported, as well as the \texttt{clustervar} and \texttt{iv} arguments, but users are encouraged to move to the new multi part formulas as described here. The \texttt{clustervar} and \texttt{iv} arguments have been moved to the \ldots argument list. They will be removed in some future update.
Value

felm returns an object of class "felm". It is quite similar to an "lm" object, but not entirely compatible.

The generic summary-method will yield a summary which may be print'ed. The object has some resemblance to an 'lm' object, and some postprocessing methods designed for lm may happen to work. It may however be necessary to coerce the object to succeed with this.

The "felm" object is a list containing the following fields:

coefficients a numerical vector. The estimated coefficients.
N an integer. The number of observations
p an integer. The total number of coefficients, including those projected out.
response a numerical vector. The response vector.
fitted.values a numerical vector. The fitted values.
residuals a numerical vector. The residuals of the full system, with dummies. For IV estimations, this is the residuals when the original endogenous variables are used, not their predictions from the 1st stage.
r.residuals a numerical vector. Reduced residuals, i.e. the residuals resulting from predicting without the dummies.
iv.residuals numerical vector. When using instrumental variables, residuals from 2. stage, i.e. when predicting with the predicted endogenous variables from the 1st stage.
weights numeric. The square root of the argument weights.
cfactor factor of length N. The factor describing the connected components of the two first terms in the second part of the model formula.
vcv a matrix. The variance-covariance matrix.
fe list of factors. A list of the terms in the second part of the model formula.
stage1 The 'felm' objects for the IV 1st stage, if used. The 1st stage has multiple left hand sides if there are more than one instrumented variable.
iv1fstat list of numerical vectors. For IV 1st stage, F-value for excluded instruments, the number of parameters in restricted model and in the unrestricted model.
X matrix. The expanded data matrix, i.e. from the first part of the formula. To save memory with large datasets, it is only included if felm(keepX=TRUE) is specified. Must be included if bccorr() or fevcov() is to be used for correcting limited mobility bias.
cX, cY matrix. The centred expanded data matrix. Only included if felm(keepCX=TRUE).
boot The result of a replicate applied to the bootexpr (if used).

Note

Side effect: If data is an object of class "pdata.frame" (from the plm package), the plm namespace is loaded if available, and data is coerced to a "data.frame" with as.data.frame which dispatches to a plm method. This ensures that transformations like diff and lag from plm works as expected, but it also incurs an additional copy of the data, and the plm namespace remains
loaded after `felm` returns. When working with "pdata.frame"s, this is what is usually wanted anyway.

For technical reasons, when running IV-estimations, the data frame supplied in the data argument to `felm`, should not contain variables with names ending in '(fit)'. Variables with such names are used internally by `felm`, and may then accidentally be looked up in the data frame instead of the local environment where they are defined.

References


See Also

`getfe()` `summary.felm()` `confstat()` `waldtest()`

Examples

```r
## Default is to use all cores. We'll limit it to 2 for this example.
opt <- options("lfe.threads")
options(lfe.threads = 2)

## Simulate data
set.seed(42)
n <- 1e3
d <- data.frame(
  # Covariates
  x1 = rnorm(n),
  x2 = rnorm(n),
  # Individuals and firms
  id = factor(sample(20, n, replace = TRUE)),
  firm = factor(sample(13, n, replace = TRUE)),
  # Noise
  u = rnorm(n)
)

# Effects for individuals and firms
id.eff <- rnorm(nlevels(d$id))
firm.eff <- rnorm(nlevels(d$firm))

# Left hand side
d$y <- d$x1 + 0.5 * d$x2 + id.eff[d$id] + firm.eff[d$firm] + d$u

## Estimate the model and print the results
est <- felm(y ~ x1 + x2 | id + firm, data = d)
summary(est)
```

# Compare with lm
summary(lm(y ~ x1 + x2 + id + firm - 1, data = d))

## Example with 'reverse causation' (IV regression)

# Q and W are instrumented by x3 and the factor x4.
d$x3 <- rnorm(n)
d$x4 <- sample(12, n, replace = TRUE)
d$Q <- 0.3 * d$x3 + d$x1 + 0.2 * d$x2 + id.eff[d$id] + 0.3 * log(d$x4) - 0.3 * d$y + rnorm(n, sd = 0.3)
d$W <- 0.7 * d$x3 - 2 * d$x1 + 0.1 * d$x2 - 0.7 * id.eff[d$id] + 0.8 * cos(d$x4) - 0.2 * d$y + rnorm(n, sd = 0.6)

# Add them to the outcome variable
d$y <- d$y + d$Q + d$W

## Estimate the IV model and report robust SEs
 ivest <- felm(y ~ x1 + x2 | id + firm | (Q | W ~ x3 + factor(x4)), data = d)
summary(ivest, robust = TRUE)
condfstat(ivest)

# Compare with the not instrumented fit:
summary(felm(y ~ x1 + x2 + Q + W | id + firm, data = d))

## Example with multiway clustering

# Create a large cluster group (500 clusters) and a small one (20 clusters)
d$cl1 <- factor(sample(rep(1:500, length.out = n)))
d$cl2 <- factor(sample(rep(1:20, length.out = n)))

# Function for adding clustered noise to our outcome variable
cl_noise <- function(cl) {
  obs_per_cluster <- n / nlevels(cl)
  unlist(replicate(nlevels(cl),
    rnorm(obs_per_cluster, mean = rnorm(1), sd = runif(1)),
    simplify = FALSE)
}

# New outcome variable
d$y_cl <- d$x1 + 0.5 * d$x2 + id.eff[d$id] + firm.eff[d$firm] +
  cl_noise(d$cl1) + cl_noise(d$cl2)

## Estimate and print the model with cluster-robust SEs (default)
est_cl <- felm(y_cl ~ x1 + x2 | id + firm | 0 | cl1 + cl2, data = d)
summary(est_cl)

# Print ordinary standard errors:
summary(est_cl, robust = FALSE)

# Match cluster-robust SEs from Stata's reghdfe package:
summary(felm(y_cl ~ x1 + x2 | id + firm | 0 | cl1 + cl2,
  data = d, cmethod = "reghdfe")
## fevcov

**Compute limited mobility bias corrected covariance matrix between fixed effects**

### Description

With a model like \( y = X\beta + D\theta + F\psi + \epsilon \), where \( D \) and \( F \) are matrices with dummy encoded factors, one application of \texttt{lfe} is to study the variances \( \text{var}(D\theta) \), \( \text{var}(F\psi) \) and covariances \( \text{cov}(D\theta, F\psi) \). However, if we use estimates for \( \theta \) and \( \psi \), the resulting variances are biased. The function \texttt{fevcov} computes a bias corrected covariance matrix as described in \textit{Gaure (2014)}.

### Usage

```r
fevcov(
  est,
  alpha = getfe(est),
  tol = 0.01,
  robust = !is.null(est$clustervar),
  maxsamples = Inf,
  lhs = NULL
)
```

### Arguments

- **est**: an object of class ”felm”, the result of a call to \texttt{[felm]}(keepX=TRUE).
- **alpha**: a data frame, the result of a call to \texttt{getfe()}.
- **tol**: numeric. The absolute tolerance for the bias-corrected correlation.
- **robust**: logical. Should robust (heteroskedastic or cluster) residuals be used, rather than i.i.d.
- **maxsamples**: integer. Maximum number of samples for expectation estimates.
- **lhs**: character. Name of left hand side if multiple left hand sides.

### Details

The \texttt{tol} argument specifies the tolerance. The tolerance is relative for the variances, i.e. the diagonal of the output. For the covariances, the tolerance is relative to the square root of the product of the variances, i.e. an absolute tolerance for the correlation. If a numeric of length 1, \texttt{tol} specifies the same tolerance for all variances/covariances. If it is of length 2, \texttt{tol[1]} specifies the variance tolerance, and \texttt{tol[2]} the covariance tolerance. \texttt{tol} can also be a square matrix of size \texttt{length(est$fe)}, in which case the tolerance for each variance and covariance is specified individually.
The function performs no checks for estimability. If the fixed effects are not estimable, the result of a call to `fevcov` is not usable. Moreover, there should be just a single connected component among the fixed effects.

alpha must contain a full set of coefficients, and contain columns 'fe' and 'effect' like the default estimable functions from `efactory()`.

In the case that the `felm()`-estimation has weights, it is the weighted variances and covariance which are bias corrected.

Value

`fevcov` returns a square matrix with the bias corrected covariances. An attribute 'bias' contains the biases. The bias corrections have been subtracted from the bias estimates. I.e. \( \text{vc} = \text{vc}' - b \), where \( \text{vc}' \) is the biased variance and \( b \) is the bias.

Note

Bias correction for IV-estimates are not supported as of now.

Note that if `est` is the result of a call to `felm()` with `keepX=FALSE` (the default), the biases will be computed as if the covariates \( X \) are independent of the factors. This will be faster (typically by a factor of approx. 4), and possibly wronger. Note also that the computations performed by this function are non-trivial, they may take quite some time. It would be wise to start out with quite liberal tolerances, e.g. `tol=0.1`, to get an idea of the time requirements.

If there are only two fixed effects, `fevcov` returns the same information as `bccorr()`, though in a slightly different format.

References


See Also

`varvars()` `bccorr()`

Examples

```r
x <- rnorm(5000)
x2 <- rnorm(length(x))

## create individual and firm
id <- factor(sample(40, length(x), replace = TRUE))
firm <- factor(sample(30, length(x), replace = TRUE, prob = c(2, rep(1, 29))))
foo <- factor(sample(20, length(x), replace = TRUE))

## effects
id.eff <- rnorm(nlevels(id))
firm.eff <- runif(nlevels(firm))
foo.eff <- rchisq(nlevels(foo), df = 1)

## left hand side
```
id.m <- id.eff[id]
firm.m <- firm.eff[firm]
foo.m <- foo.eff[foo]
# normalize them
id.m <- id.m / sd(id.m)
firm.m <- firm.m / sd(firm.m)
foo.m <- foo.m / sd(foo.m)
y <- x + 0.25 * x2 + id.m + firm.m + foo.m + rnorm(length(x), sd = 2)
z <- x + 0.5 * x2 + 0.7 * id.m + 0.5 * firm.m + 0.3 * foo.m + rnorm(length(x), sd = 2)
# make a data frame
fr <- data.frame(y, z, x, x2, id, firm, foo)
## estimate and print result
est <- felm(y | z ~ x + x2 | id + firm + foo, data = fr, keepX = TRUE)
# find bias corrections, there's little bias in this example
print(yv <- fevcov(est, lhs = "y"))
## Here's how to compute the unbiased correlation matrix:
cm <- cov2cor(yv)
structure(cm, bias = NULL)

---

getfe

Retrieve the group fixed effects

Description

Compute the group fixed effects, i.e. the dummy parameters, which were swept out during an estimation with felm().

Usage

getfe(
  obj,
  references = NULL,
  se = FALSE,
  method = "kaczmarz",
  ef = "ref",
  bN = 100,
  robust = FALSE,
  cluster = obj[["clustervar"]],
  lhs = NULL
)

Arguments

obj object of class "felm", usually, a result of a call to felm()
references a vector of strings. If there are more than two factors and you have prior knowledge of what the reference levels should be like references='id.23'. Not used with method='kaczmarz'
logical. Set to TRUE if standard errors for the group effects are wanted. This is very time-consuming for large problems, so leave it as FALSE unless absolutely needed.

character string. Either 'cholesky', 'cg', or the default 'kaczmarz'. The latter is often very fast and consumes little memory, it requires an estimable function to be specified, see efactory(). The 'cholesky' method is no longer maintained as the author sees no use for it.

function. A function of two variables, a vector of group fixed effects and a logical, i.e. function(v, addnames). This function should be estimable and is used to transform the raw-coefficients v from the kaczmarz-method. The second variable indicates whether the function must return a named vector (if this is FALSE, one may skip the names, saving memory allocations and time).

If a string is specified, it is fed to the efactory()-function. The default function is one which picks one reference in each component. Can be set to ef="ln" to yield the minimal-norm solution from the kaczmarz-method.

It can also be set to ef="zm" to get zero means (and intercept) in one of the factors, and a reference in the other.

integer. The number of bootstrap runs when standard errors are requested.

logical. Should heteroskedastic standard errors be estimated?

logical or factor. Estimate clustered standard errors.

classical vector. Specify which left hand side if obj has multiple lhs.

For the case with two factors (the terms in the second part of the formula supplied to felm()), one reference in each connected component is adequate when interpreting the results.

For three or more factors, no such easy method is known; for the "cholesky" method- reference levels are found by analyzing the pivoted Cholesky-decomposition of a slightly perturbed system. The "kaczmarz" method provides no rank-deficiency analysis, it is assumed that the factors beyond the two first contribute nothing to the rank-deficiency, so one reference in each is used.

If there are more than two factors, only the first two will be used to report connected components. In this case, it is not known which graph theoretic concept may be used to analyze the rank-deficiency.

The standard errors returned by the Kaczmarz-method are bootstrapped, keeping the other coefficients (from felm()) constant, i.e. they are from the variance when resampling the residuals. If robust=TRUE, heteroskedastic robust standard errors are estimated. If robust=FALSE and cluster=TRUE, clustered standard errors with the cluster specified to felm() are estimated. If cluster is a factor, it is used for the cluster definition.

The function getfe computes and returns a data frame containing the group fixed effects. It has the columns c('effect', 'se', 'obs', 'comp', 'fe', 'idx')

- effect is the estimated effect.
- se is the standard error.
• obs is the number of observations of this level.
• comp is the graph-theoretic component number, useful for interpreting the effects.
• fe is the name of factor.
• idx is the level of the factor.

With the Kaczmarz-method it’s possible to specify a different estimable function.

Examples

oldopts <- options("lfe.threads")
options(lfe.threads = 2)
## create covariates
x <- rnorm(4000)
x2 <- rnorm(length(x))

## create individual and firm
id <- factor(sample(500, length(x), replace = TRUE))
firm <- factor(sample(300, length(x), replace = TRUE))

## effects
id.eff <- rlnorm(nlevels(id))
firm.eff <- rexp(nlevels(firm))

## left hand side
y <- x + 0.25 * x2 + id.eff[id] + firm.eff[firm] + rnorm(length(x))

## estimate and print result
est <- felm(y ~ x + x2 | id + firm)
summary(est)

## extract the group effects
alpha <- getfe(est, se = TRUE)

## find some estimable functions, with standard errors, we don’t get
## names so we must precompute some numerical indices in ef
idx <- match(c("id.5", "id.6", "firm.11", "firm.12"), rownames(alpha))
alpha[idx, ]

ef <- function(v, addnames) {
w <- c(
  v[idx[[2]]] - v[idx[[1]]], v[idx[[4]]] + v[idx[[3]]],
  v[idx[[4]]] - v[idx[[3]]]
)
if (addnames) names(w) <- c("id6-id5", "f12+id5", "f12-f11")
w
}

getfe(est, ef = ef, se = TRUE)
options(oldopts)
## Not run:
summary(lm(y ~ x + x2 + id + firm - 1))

## End(Not run)
is.estimable

Verify estimability of function

**Description**

Verify that a function you have written for `getfe()` is indeed estimable.

**Usage**

```r
is.estimable(
  ef,
  fe,
  R = NULL,
  nowarn = FALSE,
  keepdiff = FALSE,
  threshold = 500 * getOption("lfe.eps")
)
```

**Arguments**

- `ef` function. The function to be verified.
- `fe` list of factors.
- `R` numeric. Vector of residuals, if NULL, a random one is created.
- `nowarn` logical. Set to TRUE if `is.estimable` should not throw a warning for non-estimable functions.
- `keepdiff` logical. Return differences between two different runs of the Kaczmarz method.
- `threshold` numeric. Threshold for determining estimability.

**Details**

When writing custom estimable functions for `getfe()`, the function `is.estimable` can be used to test it for estimability. `is.estimable()` solves the sparse residual system with the Kaczmarz method, using two different initial values. Then `ef()` is applied to the two solutions. If the value of `ef()` differs by more than `1e-5` in any coordinate, FALSE is returned, otherwise TRUE is returned. If `keepdiff=TRUE`, the vector of differences is attached as an attribute 'diff' to the returned logical value. If you have problems with estimability, it is a fair guess that those entries with a difference in absolute values smaller than, say, `1e-5` are estimable, whereas the others are not.

**Value**

Returns a logical.

**See Also**

- `getfe()`
Examples

oldopts <- options("lfe.threads")
options(lfe.threads = 2)
## create individual and firm
id <- factor(sample(5000, 50000, replace = TRUE))
firm <- factor(sample(3000, 50000, replace = TRUE))

## create some estimable functions. It's faster to
## use numerical indices in ef rather than strings, and the input v
## to ef has no names, we have to add them when requested
ef <- function(v, addnames) {
  w <- c(v[6] - v[5], v[7000] + v[5], v[7000] - v[6000])
  if (addnames) names(w) <- c("id6-id5", "f2k+id5", "f2k-f1k")
  w
}
is.estimable(ef, list(id = id, firm = firm))

## Then make an error; in the last coordinate, sum two firms
ef <- function(v, addnames) {
  w <- c(v[6] - v[5], v[7000] + v[5], v[7000] + v[6000])
  if (addnames) names(w) <- c("id6-id5", "f2k+id5", "f2k-f1k")
  w
}
is.estimable(ef, list(id = id, firm = firm), keepdiff = TRUE)
options(oldopts)

---

**kaczmarz**

*Solve a linear system defined by factors*

**Description**

Uses the Kaczmarz method to solve a system of the type \(Dx = R\), where \(D\) is the matrix of dummies created from a list of factors.

**Usage**

```r
kaczmarz(
  f1,
  R,
  eps = getOption("lfe.eps"),
  init = NULL,
  threads = getOption("lfe.threads")
)
```
Arguments

f1 A list of arbitrary factors of the same length
R numeric. A vector, matrix or list of such of the same length as the factors
eps a tolerance for the method
init numeric. A vector to use as initial value for the Kaczmarz iterations. The algo-
threads integer. The number of threads to use when R is more than one vector

Value

A vector x of length equal to the sum of the number of levels of the factors in f1, which solves
the system \( Dx = R \). If the system is inconsistent, the algorithm may not converge, it will give
a warning and return something which may or may not be close to a solution. By setting eps=0,
maximum accuracy (with convergence warning) will be achieved.

Note

This function is used by getfe(), it’s quite specialized, but it might be useful for other purposes
too.

In case of convergence problems, setting options(lfe.usecg=TRUE) will cause the kaczmarz() function to dispatch to the more general conjugate gradient method of cg solve(). This may or
may not be faster.

See Also

cg solve()

Examples

```r
## create factors
f1 <- factor(sample(24000, 100000, replace = TRUE))
f2 <- factor(sample(20000, length(f1), replace = TRUE))
f3 <- factor(sample(10000, length(f1), replace = TRUE))
f4 <- factor(sample(8000, length(f1), replace = TRUE))
## the matrix of dummies
D <- makeDmatrix(list(f1, f2, f3, f4))
dim(D)
## an x
truex <- runif(ncol(D))
## and the right hand side
R <- as.vector(D %*% truex)
## solve it
sol <- kaczmarz(list(f1, f2, f3, f4), R)
## verify that the solution solves the system Dx = R
sqrt(sum((D %*% sol - R)^2))
## but the solution is not equal to the true x, because the system is
## underdetermined
sqrt(sum((sol - truex)^2))
```
## moreover, the solution from kaczmarz has smaller norm
\[ \sqrt{\sum \text{sol}^2} < \sqrt{\sum \text{trux}^2} \]

---

**makeDmatrix**  
*Make sparse matrix of dummies from factor list*

### Description
Given a list of factors, return the matrix of dummies as a sparse matrix.

### Usage
```r
makeDmatrix(fl, weights = NULL)
```

### Arguments
- `fl`: list of factors.
- `weights`: numeric vector. Multiplied into the rows.

### Details
The function returns the model matrix for a list of factors. This matrix is not used internally by the package, but it’s used in some of the documentation for illustrative purposes.

### Value
Returns a sparse matrix.

### Examples
```r
fl <- lapply(1:3, function(i) factor(sample(3, 10, replace = TRUE)))
makeDmatrix(fl, weights = seq(0.1, 1, 0.1))
```
**mctrace**

Compute trace of a large matrix by sample means

**Description**

Some matrices are too large to be represented as a matrix, even as a sparse matrix. Nevertheless, it can be possible to compute the matrix vector product fairly easy, and this is utilized to estimate the trace of the matrix.

**Usage**

mctrace(mat, N, tol = 0.001, maxsamples = Inf, trname = "", init)

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>mat</td>
<td>square matrix, Matrix, function or list of factors.</td>
</tr>
<tr>
<td>N</td>
<td>integer. if mat is a function, the size of the matrix is specified here.</td>
</tr>
<tr>
<td>tol</td>
<td>numeric. Tolerance.</td>
</tr>
<tr>
<td>maxsamples</td>
<td>numeric. Maximum number of samples in the expectation estimation.</td>
</tr>
<tr>
<td>trname</td>
<td>character. Arbitrary name used in progress reports.</td>
</tr>
<tr>
<td>init</td>
<td>numeric. Initial guess for the trace.</td>
</tr>
</tbody>
</table>

**Details**

mctrace is used internally by `fevcov()` and `bccorr()`, but has been made public since it might be useful for other tasks as well.

For any matrix $A$, the trace equals the sum of the diagonal elements, or the sum of the eigenvalues. However, if the size of the matrix is very large, we may not have a matrix representation, so the diagonal is not immediately available. In that case we can use the formula $\text{tr}(A) = E(x^tAx)$ where $x$ is a random vector with zero expectation and $\text{Var}(x) = I$. We estimate the expectation with sample means. mctrace draws $x$ in $\{-1,1\}^N$, and evaluates mat on these vectors.

If mat is a function, it must be able to take a matrix of column vectors as input. Since $x^tAx = \langle Ax, x \rangle$ is evaluated, where $\langle \cdot, \cdot \rangle$ is the Euclidean inner product, the function mat can perform this inner product itself. In that case the function should have an attribute `attr(mat, 'IP') <- TRUE` to signal this.

If mat is a list of factors, the matrix for which to estimate the trace, is the projection matrix which projects out the factors. i.e. how many dimensions are left when the factors have been projected out. Thus, it is possible to estimate the degrees of freedom in an OLS where factors are projected out.

The tolerance tol is a relative tolerance. The iteration terminates when the normalized standard deviation of the sample mean (s.d. divided by absolute value of the current sample mean) goes below tol. Specify a negative tol to use the absolute standard deviation. The tolerance can also change during the iterations; you can specify `tol=function(current) {...}` and return a tolerance based on the current estimate of the trace (i.e. the current sample mean).
Value

An estimate of the trace of the matrix represented by `mat` is returned.

Examples

```r
A <- matrix(rnorm(25), 5)
fun <- function(x) A %*% x
sum(diag(A))
# mctrace is not really useful for small problems.
mctrace(fun, ncol(A), tol = 0.05)
# try a larger problem (3000x3000):
f1 <- factor(sample(1500, 3000, replace = TRUE))
f2 <- factor(sample(1500, 3000, replace = TRUE))
f1 <- list(f1, f2)
mctrace(f1, tol = -5)
# exact:
length(f1) - nlevels(f1) - nlevels(f2) + nlevels(compfactor(f1))
```

---

**nlexpect**  Compute expectation of a function of the coefficients.

**Description**

Use integration of the joint distribution of the coefficients to compute the expectation of some function of the coefficients. Can be used for non-linear inference tests.

**Usage**

```r
nlexpect(
  est,
  fun,
  coefs,
  ..., 
  tol =getOption("lfe.etol"),
  lhs = NULL,
  cv,
  istats = FALSE,
  flags = list(verbos = 0),
  max.eval = 200000L,
  method = c("hcubature", "pcubature", "cuhre", "suave", "vegas", "divonne"),
  vectorize = FALSE
)
```
Arguments

- **est**
  - object of class "felm" or "lm", a result of a call to felm() or lm.
- **fun**
  - function of coefficients to be integrated. Can also be a quoted expression.
- **coefs**
  - character. Names of coefficients to test. Only needed if fun is a function.
- **...**
  - other arguments passed to fun or the integration routine.
- **tol**
  - numeric. Tolerance for the computed integral.
- **lhs**
  - character. Name of the left hand side, if est has more than one.
- **cv**
  - Covariance matrix to use in place of vcov(est)
- **istats**
  - logical. Should convergence information from the integration routine be included as attributes?
- **flags**
  - list. Additional flags for the underlying integration routine. Not used after the package R2Cuba disappeared.
- **max.eval**
  - integer. Maximum number of integral evaluations.
- **method**
  - character. A method specification usable by cubature::cubintegrate. The documentation there says that "pcubature" is good for smooth integrands of low dimensions.
- **vectorize**
  - logical or numeric. Use vectorized function evaluation from package cubature. This can speed up integration significantly. If method is from the Cuba library (i.e. not pcubature or hcubature), vectorize should be specified as a numeric, a vectorization factor. The default is 128.

Details

The function nlexpect integrates the function fun(x) over the multivariate normal distribution specified by the point estimates and the covariance matrix vcov(est). This is the expectation of fun(beta) if we were to bootstrap the data (e.g. by drawing the residuals anew) and do repeated estimations.

The list of coefficients used by fun must be specified in coefs.

If the function is simple, it can be specified as a quoted expression like quote(a*b+log(abs(d))). In this case, if coefs is not specified, it will be set to the list of all the variables occurring in the expression which are also names of coefficients.

fun may return a vector of values, in which case a vector of expectations is computed, like quote(c(a*b, a^3-b)). However, if the expressions contain different variables, like quote(c(a*b, d*e)), a quite compute intensive 4-dimensional integral will be computed, compared to two cheap 2-dimensional integrals if you do them separately. There is nothing to gain from using vector-valued functions compared to multiple calls to nlexpect().

You may of course also integrate inequalities like quote(abs(x1-0.2) > 0.2) to simulate the probability from t-tests or Wald-tests. See the examples.

The function you provide will get an argument ... if it does not have one already. It will also be passed an argument .z which contains the actual coefficients in normalized coordinates, i.e. if ch is the Cholesky decomposition of the covariance matrix, and pt are the point estimates, the coefficients will be pt + ch \%*\% .z. The first argument is a vector with names corresponding to the coefficients.
If you specify `vectorized=TRUE`, your function will be passed a list with vectors in its first argument. The function must be able to handle a list, and must return a vector of the same length as the vectors in the list. If you pass an expression like `x < y`, each variable will be a vector. If your function is vector valued, it must return a matrix where each column is the values.

The `tol` argument specifies both the relative tolerance and the absolute tolerance. If these should not be the same, specify `tol` as a vector of length 2. The first value is the relative tolerance, the second is the absolute tolerance. Termination occurs when at least one of the tolerances is met.

The `...` can be used for passing other arguments to the integration routine `cubature::cubintegrate` and the function to be integrated.

**Value**

The function `nlexpect` computes and returns the expectation of the function `fun(beta)`, with `beta` a vector of coefficients. I.e., if the coefficients `beta` are bootstrapped a large number of times, `nlexpect(est, fun)` should be equal to `mean(fun(beta))`.

**Note**

An alternative to this method is to use the `bootexpr` argument with `felm()`, to do a Monte Carlo integration.

**See Also**

`waldtest()`

**Examples**

```r
N <- 100
x1 <- rnorm(N)
# make some correlation
x2 <- 0.1 * rnorm(N) + 0.1 * x1
y <- 0.1 * x1 + x2 + rnorm(N)
summary(est <- felm(y ~ x1 + x2))
pt1 <- coef(est)["x1"]
pt2 <- coef(est)["x2"]
# expected values of coefficients, should match the summary
# and variance, i.e. square of standard errors in the summary
nlexpect(est, quote(c(x1 = x1, x2 = x2, var = c((x1 - pt1)^2, (x2 - pt2)^2)))))

# the covariance matrix:
nlexpect(est, tcrossprod(as.matrix(c(x1 - pt1, x2 - pt2))))

# Wald test of single variable
waldtest(est, ~x1)["p.F"]
# the same with nlexpect, i.e. probability for observing abs(x1)>abs(pt1) conditional
# on E(x1) = 0.
nlexpect(est, (x1 - pt1)^2 > pt1^2, tol = 1e-7, vectorize = TRUE)
# which is the same as
2 * nlexpect(est, x1 * sign(pt1) < 0)
```
Here's a multivalued, vectorized example:
```
nlexpect(est, rbind(a = x1 * x2 < pt1, b = x1 * x2 > 0), vectorize = TRUE, method = "divonne")
```

# Non-linear test:

# A simple one, what's the probability that product x1*x2 is between 0 and |E(x1)|?
```
nlexpect(est, x1 * x2 > 0 & x1 * x2 < abs(pt1), vectorize = TRUE, method = "divonne")
```

# Then a more complicated one with the expected value of a polynomial in the coefficients
```
f <- function(x) c(poly = x[["x1"]][0] * (6 * x[["x1"]][0] * x[["x2"]][0]^2))
```

# This is the linearized test:
```
waldtest(est, f)["p.F"]
```

# In general, for a function f, the non-linear Wald test is something like
```
# the following:

# expected value of function
```
```
Ef <- nlexpect(est, f, coefs = c("x1", "x2"))
```

# point value of function
```
Pf <- f(c(pt1, pt2))
```

# similar to a Wald test, but non-linear:
```
nlexpect(est, function(x) (f(x) - Ef)^2 > Pf^2, c("x1", "x2"), vectorize = TRUE)
```

# one-sided
```
nlexpect(est, function(x) f(x) - Ef > abs(Pf), c("x1", "x2"), vectorize = TRUE)
```

# other sided
```
nlexpect(est, function(x) f(x) - Ef < -abs(Pf), c("x1", "x2"), vectorize = TRUE)
```

---

**sargan**

*Compute Sargan's S*

**Description**

Compute Sargan's S

**Usage**

```
sargan(object, ..., lhs = object$lhs[1])
```

**Arguments**

- `object` and object type "felm", the return value from `felm()`.
- `...` Not used at the moment.
- `lhs` in case of multiple left hand sides, specify the name of the left hand side for which you want to compute Sargan's S.

**Value**

`sargan` returns a numeric, the Sargan's S. The Basmann statistic is returned in the "basmann" attribute.
Description

summary method for class "felm".

Usage

```r
## S3 method for class 'felm'
summary(
  object,
  ...,
  robust = !is.null(object$clustervar) || getOption("lfe.robust"),
  lhs = NULL
)
```

Arguments

- `object`: an object of class "felm", a result of a call to `felm`.
- `...`: further arguments passed to or from other methods.
- `robust`: logical. Use robust standard errors. See notes.
- `lhs`: character. If multiple left hand sides, specify the name of the one to obtain a summary for.

Value

The function `summary.felm` returns an object of class "summary.felm". It is quite similar to an "summary.lm" object, but not entirely compatible.

The "summary.felm" object is a list containing the following fields:

- `residuals`: a numerical vector. The residuals of the full system, with dummies.
- `p`: an integer. The total number of coefficients, including those projected out.
- `Pp`: an integer. The number of coefficients, excluding those projected out.
- `coefficients`: a Pp x 4 matrix with columns for the estimated coefficients, their standard errors, t-statistic and corresponding (two-sided) p-value.
- `rse`: residual standard error.
- `r2`: R^2, the fraction of variance explained by the model.
- `r2adj`: Adjusted R^2.
- `fstat`: F-statistic.
- `pval`: P-values.
- `P.fstat`: Projected F-statistic. The result of a call to `waldtest()`.
- `fe`: list of factors. A list of the terms in the second part of the model.
lhs. character. If object is the result of an estimation with multiple left hand sides, the actual argument lhs will be copied to this field.

iv1fstat F-statistic for excluded instruments in 1. step IV, see felm().

iv1pval P-value for iv1fstat.

Note

The standard errors are adjusted for the reduced degrees of freedom coming from the dummies which are implicitly present. They are also small-sample corrected.

If the robust parameter is FALSE, the returned object will contain ordinary standard errors. If the robust parameter is TRUE, clustered standard errors are reported if a cluster was specified in the call to felm; if not, heteroskedastic robust standard errors are reported.

Several F-statistics reported. The P.fstat is for the projected system. I.e. a joint test on whether all the Pp coefficients in coefficients are zero. Then there are fstat and pval which is a test on all the coefficients including the ones projected out, except for an intercept. This statistic assumes i.i.d. errors and is not reliable for robust or clustered data.

For a 1st stage IV-regression, an F-statistic against the model with excluded instruments is also computed.

See Also

waldtest()
Details

With a model like \( y = X\beta + D\theta + F\psi + \epsilon \), where \( D \) and \( F \) are matrices with dummy encoded factors, one application of \texttt{if}e is to study the variances \( \text{var}(D\theta) \), \( \text{var}(F\psi) \) and covariances \( \text{cov}(D\theta, F\psi) \). The function \texttt{fevcov()} computes bias corrected variances and covariances. However, these variance estimates are still random variables for which \texttt{fevcov()} only estimate the expectation. The function \texttt{varvars} estimates the variance of these estimates.

This function returns valid results only for normally distributed residuals. Note that the estimates for the fixed effect variances from \texttt{fevcov()} are not normally distributed, but a sum of chi-square distributions which depends on the eigenvalues of certain large matrices. We do not compute that distribution. The variances returned by \texttt{varvars} can therefore not be used directly to estimate confidence intervals, other than through coarse methods like the Chebyshev inequality. These estimates only serve as a rough guideline as to how wrong the variance estimates from \texttt{fevcov()} might be.

Like the fixed effect variances themselves, their variances are also biased upwards. Correcting this bias can be costly, and is therefore by default switched off.

The variances tend to zero with increasing number of observations. Thus, for large datasets they will be quite small.

Value

\texttt{varvars} returns a vector with a variance estimate for each fixed effect variance. I.e. for the diagonal returned by \texttt{fevcov()}.

Note

The \texttt{tol} argument specifies the tolerance as in \texttt{fevcov()}. Note that if \texttt{est} is the result of a call to \texttt{felm()} with \texttt{keepX=FALSE} (the default), the variances will be estimated as if the covariates \( X \) are independent of the factors. There is currently no function available for estimating the variance of the covariance estimates from \texttt{fevcov()}.

The cited paper does not contain the expressions for the variances computed by \texttt{varvars} (there’s a 10 page limit in that journal), though they can be derived in the same fashion as in the paper, with the formula for the variance of a quadratic form.

References


See Also

\texttt{bccorr()} \texttt{fevcov()}

Examples

```r
x <- rnorm(500)
x2 <- rnorm(length(x))
## create individual and firm
```
id <- factor(sample(40, length(x), replace = TRUE))
firm <- factor(sample(30, length(x), replace = TRUE, prob = c(2, rep(1, 29))))
foo <- factor(sample(20, length(x), replace = TRUE))
### effects
id.eff <- rnorm(nlevels(id))
firm.eff <- rnorm(nlevels(firm))
foo.eff <- rnorm(nlevels(foo))
### left hand side
id.m <- id.eff[id]
firm.m <- 2 * firm.eff[firm]
foo.m <- 3 * foo.eff[foo]
y <- x + 0.25 * x2 + id.m + firm.m + foo.m + rnorm(length(x))

# make a data frame
fr <- data.frame(y, x, x2, id, firm, foo)
### estimate and print result
est <- felm(y ~ x + x2 | id + firm + foo, data = fr, keepX = TRUE)
alpha <- getfe(est)
# estimate the covariance matrix of the fixed effects
fevcov(est, alpha)
# estimate variances of the diagonal
varvars(est, alpha)

---

**waldtest**

*Compute Wald test for joint restrictions on coefficients*

**Description**

Compute a Wald test for a linear hypothesis on the coefficients. Also supports Delta-approximation for non-linear hypotheses.

**Usage**

```r
waldtest(
  object,
  R,
  r,
  type = c("default", "iid", "robust", "cluster"),
  lhs = NULL,
  df1,
  df2
)
```

**Arguments**

- **object**: object of class "felm", a result of a call to `felm()`.
- **R**: matrix, character, formula, function, integer or logical. Specification of which exclusions to test.
The function `waldtest` computes a Wald test for the \( H_0: R \beta = r \), where \( \beta \) is the estimated vector `coef(object)`. 

If \( R \) is a character, integer, or logical vector it is assumed to specify a matrix which merely picks out a subset of the coefficients for joint testing. If \( r \) is not specified, it is assumed to be a zero vector of the appropriate length.

\( R \) can also be a formula which is linear in the estimated coefficients, e.g. of the type \(~Q-2|x-2*z\) which will test the joint hypothesis \( Q=2 \) and \( x=2*z \).

If \( R \) is a function (of the coefficients), an approximate Wald test against \( H_0: R(\beta) == 0 \), using the Delta-method, is computed.

In case of an IV-estimation, the names for the endogenous variables in `coef(object)` are of the type "Q(fit)" which is a bit dull to type; if all the endogenous variables are to be tested they can be specified as "endovars". It is also possible to specify an endogenous variable simply as "Q", and `waldtest` will add the other syntactic sugar to obtain "Q(fit)".

The `type` argument works as follows. If `type=='default'` it is assumed that the residuals are i.i.d., unless a cluster structure was specified to `felm()`. If `type=='robust'`, a heteroscedastic structure is assumed, even if a cluster structure was specified in `felm()`.

**Value**

The function `waldtest` computes and returns a named numeric vector containing the following elements.

- `p` is the p-value for the \( \chi^2 \)-test
- `chi2` is the \( \chi^2 \)-distributed statistic.
- `df1` is the degrees of freedom for the \( \chi^2 \) statistic.
- `p.F` is the p-value for the F statistics
- `F` is the F-distributed statistic.
- `df2` is the additional degrees of freedom for the F statistic.

The return value has an attribute `formula` which encodes the restrictions.

**See Also**

`nlexpect()`
Examples

```r
x <- rnorm(10000)
x2 <- rnorm(length(x))
y <- x - 0.2 * x2 + rnorm(length(x))
# Also works for lm
summary(est <- lm(y ~ x + x2))
# We do not reject the true values
waldtest(est, ~ x - 1 | x2 + 0.2 | ~(Intercept))
# The Delta-method coincides when the function is linear:
waldtest(est, function(x) x - c(0, 1, -0.2))
```
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