Package ‘lavaSearch2’

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Type Package

Title Tools for Model Specification in the Latent Variable Framework

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BugReports https://github.com/bozenne/lavaSearch2/issues

Description Tools for model specification in the latent variable framework
(add-on to the 'lava' package). The package contains three main functionalities:
Wald tests/F-tests with improved control of the type 1 error in small samples,
adjustment for multiple comparisons when searching for local dependencies,
and adjustment for multiple comparisons when doing inference for multiple latent variable mod-
els.

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VignetteBuilder R.rsp

Depends R (>= 2.10), ggplot2, lava (>= 1.6.4)

Imports doParallel, MASS, Matrix, methods, multcomp, mvtnorm, nlme,
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lmerTest, numDeriv, pbapply, pbkrtest, R.rsp, riskRegression,
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LinkingTo Rcpp, RcppArmadillo

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Author Brice Ozenne [aut, cre](<https://orcid.org/0000-0001-9694-2956>)

Maintainer Brice Ozenne <brice.mh.ozenne@gmail.com>

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R topics documented:

addLink .................................................. 3
autoplot.intDensTri ................................. 4
autoplot_calibrateType1 ......................... 5
autplot-modelsearch2 ............................. 6
calcDistMax ........................................... 7
calcType1postSelection ......................... 9
calibrateType1 ....................................... 11
checkData ............................................. 14
clean ................................................... 15
coeByType ............................................. 16
coeType ............................................... 19
combineFormula ................................. 21
compare2 ............................................. 22
convFormulaCharacter ......................... 25
createContrast ..................................... 25
dfSigma ............................................... 28
dfSigmaRobust .................................... 28
effects2 ............................................... 29
estfun ................................................ 30
extractData .......................................... 31
findNewLink ......................................... 33
goingNewLink ....................................... 34
goingNewModel ................................... 35
getStep .............................................. 36
goingVarCov2 ..................................... 37
glht2 ................................................ 39
iid2 .................................................... 41
iidJack ............................................... 43
information2 ...................................... 45
initVarLink ......................................... 47
intDensTri .......................................... 48
lavaSearch2 ....................................... 50
leverage2 ........................................... 51
matrixPower ....................................... 53
modelsearch2 ...................................... 54
nStep ................................................ 57
residuals2 .......................................... 58
score2 ............................................... 59
sCorrect ............................................ 61
setLink .............................................. 64
summary_calibrateType1 ..................... 65
summary_modelsearch2 ....................... 66
summary2 ............................................ 66
tryWithWarnings .................................. 68
vcov2 .............................................. 69

Index .................................
addLink

Add a New Link Between Two Variables in a LVM

Description

Generic interface to add links to lvm objects.

Usage

addLink(object, ...)

## S3 method for class 'lvm'
addLink(object, var1, var2, covariance,
    all.vars = lava::vars(object), warnings = FALSE, ...)

## S3 method for class 'lvm.reduced'
addLink(object, ...)

Arguments

object
  a lvm object.

...  
  [internal] only used by the generic method and from addLink.lvm.reduced to
  addLink.lvm.

var1  
  [character or formula] the exogenous variable of the new link or a formula
describing the link to be added to the lvm.

var2  
  [character] the endogenous variable of the new link. Disregarded if the argument
  var1 is a formula.

covariance  
  [logical] is the link is bidirectional? Ignored if one of the variables non-stochastic
  (e.g. exogenous variables).

all.vars  
  [internal] a character vector containing all the variables of the lvm object.

warnings  
  [logical] Should a warning be displayed when no link is added?

Details

The argument all.vars is useful for lvm.reduce object where the command vars(object) does
not return all variables. The command vars(object,xlp = TRUE) must be used instead.
Arguments var1 and var2 are passed to initVarlink.

Examples

library(lava)
set.seed(10)

m <- lvm()
regression(m) <- c(y1,y2,y3)~u
regression(m) <- u~x1+x2
latent(m) <- ~u
m2 <- m

addLink(m, x1 ~ y1, covariance = FALSE)
addLink(m, y1 ~ x1, covariance = FALSE)
coef(addLink(m, y1 ~ y2, covariance = TRUE))

addLink(m2, "x1", "y1", covariance = FALSE)
addLink(m2, "y1", "x1", covariance = FALSE)
newM <- addLink(m, "y1", "y2", covariance = TRUE)
coef(newM)

### autoplot.intDensTri 2D-display of the Domain Used to Compute the Integral

**Description**

2D-display of the domain used to compute the integral.

**Usage**

```r
## S3 method for class 'intDensTri'
autoplot(object, coord.plot = c("x", "y1"), plot = TRUE, ...)
```

**Arguments**

- `object` output of the function `intDensTri`.
- `coord.plot` [character vector] the x and y coordinates. Can be "x", "y1" to "yd", "z" if `zmin` was specified when calling `intDensTri`.
- `plot` [logical] should the plot be displayed?
- `...` [internal] Only used by the generic method.

**Value**

A `ggplot` object.

**See Also**

`intDensTri`
Description

Graphical display of the bias or type 1 error for the output of `calibrateType1`.

Usage

```r
## S3 method for class 'calibrateType1'
autoplot(object, type = "bias", plot = TRUE, 
color.threshold = "red", type.bias = "absolute", alpha = 0.05,
nrow.legend = NULL, name2label = NULL, color = NULL, 
keep.method = NULL, ...)
```

Arguments

- `object`: output of `calibrateType1`.
- `type`: [character] if `type` equals "bias" the bias will be displayed. Otherwise if it equals "type1error" the type 1 error will be displayed.
- `plot`: [logical] should the plot be displayed?
- `color.threshold`: [character] the color for the line representing the expected value(s).
- `type.bias`: [character] if `type.bias` equals "absolute" the absolute bias will be used. Otherwise if it equals "relative" the relative bias will be used. Only relevant when `type` equals "bias".
- `alpha`: [numeric, 0-1] the significance threshold to consider. Only relevant when `type` equals "type1error".
- `nrow.legend`: [integer, >0] the number of rows for the legend. Only relevant when `type` equals "type1error".
- `name2label`: [named character vector] the label for the legend. The vector should contain the method names (see details). Only relevant when `type` equals "type1error".
- `color`: [character vector] a vector of colours to be used to color the lines. Only relevant when `type` equals "type1error".
- `keep.method`: [character vector] the methods names for which the type 1 error should be displayed. Only relevant when `type` equals "type1error".
- `...`: [internal] Only used by the generic method.

Details

Method names:

- `p.Ztest`
- p.Satt
- p.KR
- p.robustZtest
- p.robustSatt
- p.robustKR

Value
An list containing:
- plot: a ggplot object.
- data: the dataset used to generate the ggplot object.

Description
Display the value of a coefficient across the steps.

Usage
```r
## S3 method for class 'modelsearch2'
autoplot(object, param, ci = TRUE,
         step = 0:nStep(object), conf.level = 0.95, plot = TRUE,
         add.0 = TRUE, ...)
```

Arguments
- object: a modelsearch2 object.
- param: [character vector] the name of the coefficient(s) to be displayed.
- ci: [logical] should the confidence intervals of the coefficient(s) be displayed.
- step: [integer >0] the steps at which the coefficient value should be displayed.
- conf.level: [numeric, 0-1] confidence level of the interval.
- plot: [logical] should the graph be displayed?
- add.0: [logical] should an horizontal line representing no effect be displayed?
- ... [internal] only used by the generic method.

Value
A list containing
- plot: a ggplot object.
- data: the data used to generate the ggplot object.
Examples

```r
## Not run:
msim <- lvm(Y ~ G + X1 + X2 + X3 + X4 + X5)
addvar(msim) <- ~ Z1 + Z2

set.seed(10)
df.data <- lava::sim(msim, 1e2)

mBase <- lvm(Y ~ G)
addvar(mBase) <- ~ X1 + X2 + X3 + X4 + X5 + Z1 + Z2
e.lvm <- estimate(mBase, data = df.data)
res <- modelsearch2(e.lvm, method.p.adjust = "holm", alpha = 0.05)
autoplot(res, param = "Y ~ G")
autoplot(res, param = c("Y", "Y ~ G"))
## End(Not run)
```

calcDistMax

Adjust the p.values Using the Quantiles of the Max Statistic

Description

Adjust the p.values using the quantiles of the max statistic.

Usage

```r
calcDistMaxIntegral(statistic, iid, df, iid.previous = NULL,
quantile.previous = NULL, quantile.compute = lava.options()$search.calc.quantile.int,
alpha, cpus = 1, cl = NULL, trace)
calcDistMaxBootstrap(statistic, iid, iid.previous = NULL,
quantile.previous = NULL, method, alpha, cpus = 1, cl = NULL,
n.sim, trace, n.repmx = 100)
```

Arguments

- **statistic** [numeric vector] the observed Wald statistic. Each statistic correspond to a null hypothesis (i.e. a coefficient) that one wish to test.
- **iid** [matrix] zero-mean iid decomposition of the coefficient used to compute the statistic.
- **df** [numeric] the degree of freedom defining the multivariate Student's t distribution. If NULL the multivariate Gaussian distribution will be used instead.
- **iid.previous** [matrix, EXPERIMENTAL] zero-mean iid decomposition of previously tested coefficient.
quantile.previous
[numeric, EXPERIMENTAL] rejection quantiles of the previously tested hypotheses. If not NULL the values should correspond the variable in to the first column(s) of the argument iid.previous.

quantile.compute
[logical] should the rejection quantile be computed?

alpha
[numeric 0-1] the significance cutoff for the p-values. When the p-value is below, the corresponding link will be retained.

cpus
[integer >0] the number of processors to use. If greater than 1, the computation of the p-value relative to each test is performed in parallel.

cl
[cluster] a parallel socket cluster generated by parallel::makeCluster that has been registered using registerDoParallel.

trace
[logical] should the execution of the function be traced?

method
[character] the method used to compute the p-values. See the output of lava.options()$search.calcMaxDist for the possible values.

n.sim
[integer >0] the number of bootstrap simulations used to compute each p-values. Disregarded when the p-values are computed using numerical integration.

n.repmax
[integer >0] the maximum number of rejection for each bootstrap sample before switching to a new bootstrap sample. Only relevant when conditioning on a previous test. Disregarded when the p-values are computed using numerical integration.

Value
A list containing

- p.adjust: the adjusted p-values.
- z: the rejection threshold.
- Sigma: the correlation matrix between the test statistic.
- correctedLevel: the alpha level corrected for conditioning on previous tests.

Examples

library(mvtnorm)

set.seed(10)
n <- 100
p <- 4
link <- letters[1:p]
n.sim <- 1e3 # number of bootstrap simulations

#### test - not conditional ####
X.iid <- rmvnorm(n, mean = rep(0,p), sigma = diag(1,p))
colnames(X.iid) <- link
statistic <- setNames(1:p,link)
r1 <- calcDistMaxIntegral(statistic = statistic, iid = X.iid, 
                  trace = FALSE, alpha = 0.05, df = 1e6)

r3 <- calcDistMaxBootstrap(statistic = statistic, iid = X.iid, 
                  method = "residual", 
                  trace = FALSE, alpha = 0.05, n.sim = n.sim)

r4 <- calcDistMaxBootstrap(statistic = statistic, iid = X.iid, 
                  method = "wild", 
                  trace = FALSE, alpha = 0.05, n.sim = n.sim)

rbind(integration = c(r1$p.adjust, quantile = r1$z), 
       bootResidual = c(r3$p.adjust, quantile = r3$z), 
       bootWild = c(r4$p.adjust, quantile = r4$z))

### test - conditional ###
## Not run:
Z.iid <- rmvnorm(n, mean = rep(0,p+1), sigma = diag(1,p+1))
seqQuantile <- qmvnorm(p = 0.95, delta = rep(0,p+1), sigma = diag(1,p+1),
                        tail = "both.tails")$quantile

r1c <- calcDistMaxIntegral(statistic = statistic, iid = X.iid, 
                  iid.previous = Z.iid, quantile.previous = seqQuantile, 
                  trace = FALSE, alpha = 0.05, df = NULL)

r3c <- calcDistMaxBootstrap(statistic = statistic, iid = X.iid, 
                  iid.previous = Z.iid, quantile.previous = seqQuantile, method = "residual", 
                  trace = FALSE, alpha = 0.05, n.sim = n.sim)

r4c <- calcDistMaxBootstrap(statistic = statistic, iid = X.iid, 
                  iid.previous = Z.iid, quantile.previous = seqQuantile, method = "wild", 
                  trace = FALSE, alpha = 0.05, n.sim = n.sim)

rbind(integration = c(r1c$p.adjust, quantile = r1c$z), 
       bootResidual = c(r3c$p.adjust, quantile = r3c$z), 
       bootWild = c(r4c$p.adjust, quantile = r4c$z))

## End(Not run)

calcType1postSelection

Compute the Type 1 Error After Selection [EXPERIMENTAL]

Description

Compute the type 1 error after selection [EXPERIMENTAL].

Usage

calcType1postSelection(level, mu, Sigma, quantile.previous, distribution, 
df, n = 10, correct = TRUE, ...)

calcType1postSelection

Arguments

- **level** [numeric 0-1] expected coverage.
- **mu** [numeric vector] the expectation of the joint distribution of the test statistics
- **Sigma** [matrix] the variance-covariance of the joint distribution of the test statistics.
- **quantile.previous** [numeric] significance quantile used at the previous step.
- **distribution** [character] distribution of the test statistics. Can be “pmvnorm” (normal distribution) or “pvmt” (Student’s t distribution)
- **df** [integer > 0] the degree of freedom of the joint Student’s t distribution. Only used when distribution=“pvmt”.
- **n** [integer > 0] number of points for the numerical integration
- **correct** [logical] if true, correct the level to account for previous testings.
- ... arguments passed to `intDensTri`.

Details

The number of tests at the current step (i.e. after selection) is assumed to be one less than the number of tests at the previous step (i.e. before selection).

Arguments mu and Sigma must contain the moments for the vector of test statistics before and after selection (in that order).

Value

numeric the type 1 error.

Author(s)

Brice Ozenne

Examples

```r
library(mvtnorm)
n <- 350

#### only 2 tests
Sigma <- rbind(c(1,0,0),c(0,1,1),c(0,1,1))
z2 <- qmvnorm(0.95, mean = rep(0,2), sigma = Sigma[1:2,1:2], tail = "both.tails")$quantile

## no selection since strong effect
mu <- c(10,0,0)
calcType1postSelection(0.95, quantile.previous = z2, distribution = "gaussian",
                   mu = mu, Sigma = Sigma, correct = TRUE)

## strong selection
## Not run:
mu <- c(0,0,0)
levelC <- calcType1postSelection(0.95, quantile.previous = z2, distribution = "gaussian",
```
Perform a simulation study over one or several sample size to assess the bias of the estimate and the type 1 error of the Wald test and robust Wald test
n.bootstrap = 1000, checkType1 = FALSE, checkType2 = FALSE, 
dir.save = NULL, label.file = NULL, seed = NULL, cpus = 1, 
trace = 2, ...) 

## S3 method for class 'lvmfit'
calibrateType1(object, param, n.rep, correction = TRUE, 
F.test = FALSE, bootstrap = FALSE, n.bootstrap = 1000, 
seed = NULL, trace = 2, cpus = 1, ...) 

Arguments 

object a lvm object defining the model to be fitted. 
param [character vector] names of the coefficient whose value will be tested. 
n.rep [integer, >0] number of simulations per sample size. 
... [internal] Only used by the generic method. 
n [integer vector, >0] sample size(s) considered in the simulation study. 
correction [logical] should the type 1 error after correction be computed? 
warmup [list of lvm] a list of lvm objects that will be sequentially fitted with for starting values the parameter of the previous model in the list (if any). The parameters of the final model of the list are used to initialize the fit of the model of interest (i.e. object). 
null [numeric vector] vector of null hypotheses, one for each model coefficient. By default a vector of 0. 
F.test [logical] should a multivariate Wald test be perform testing simultaneously all the null hypotheses? 
cluster [integer vector] the grouping variable relative to which the observations are iid. Will be passed to lava::estimate. 
generative.object [lvm] object defining the statistical model generating the data. 
generative.coef [name numeric vector] values for the parameters of the generative model. Can also be NULL: in such a case the coefficients are set to default values decided by lava (usually 0 or 1). 
true.coef [name numeric vector] expected values for the parameters of the fitted model. 
n.true [integer, >0] sample size at which the estimated coefficients will be a reliable approximation of the true coefficients. 
round.true [integer, >0] the number of decimal places to be used for the true value of the coefficients. No rounding is done if NULL. 
bootstrap [logical] should bootstrap resampling be performed? 
n.bootstrap [integer, >0] the number of bootstrap sample to be used for each bootstrap. 
checkType1 [logical] returns an error if the coefficients associated to the null hypotheses do not equal 0. 
checkType2 [logical] returns an error if the coefficients associated to the null hypotheses equal 0.
calibrateType1

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>dir.save</td>
<td>[character] path to the directory were the results should be exported. Can also be NULL: in such a case the results are not exported.</td>
</tr>
<tr>
<td>label.file</td>
<td>[character] element to include in the file name.</td>
</tr>
<tr>
<td>seed</td>
<td>[integer, &gt;0] seed value that will be set at the beginning of the simulation to enable reproducibility of the results. Can also be NULL: in such a case no seed is set.</td>
</tr>
<tr>
<td>cpus</td>
<td>[integer &gt;0] the number of processors to use. If greater than 1, the simulations are performed in parallel.</td>
</tr>
<tr>
<td>trace</td>
<td>[integer] should the execution of the function be trace. Can be 0, 1 or 2.</td>
</tr>
</tbody>
</table>

Value

An object of class calibrateType1.

Author(s)

Brice Ozenne

See Also

link{autoplot.calibrateType1} for a graphical display of the bias or of the type 1 error.

Examples

```r
## Not run:

#### simulate data ####
m.Sim <- lvm(c(Y1~mu1:mu2:mu3:1*eta, 
Y2~mu2:mu3:1*eta, 
Y3~mu3:1*eta, 
eta~beta1*Group+beta2*Gender))
latent(m.Sim) <- ~eta
categorical(m.Sim, labels = c("M","F")) <- ~Gender
d <- lava::sim(m.Sim, 1e2)

#### calibrate type 1 error on the estimated model ####
m <- lvm(Y1~eta, 
Y2~eta, 
Y3~eta, 
eta~Group+Gender)
e <- lava::estimate(m, data = d)
res <- calibrateType1(e, param = "eta~Group", n.rep = 100)
res <- calibrateType1(e, param = c("eta~Group","Y1~eta"), F.test = TRUE, n.rep = 100)
res <- calibrateType1(e, param = "eta~Group", n.rep = 100, cpus = 4)
summary(res)

## End(Not run)
```
checkData  \hspace{1cm} \textit{Check that Validity of the Dataset}

\textbf{Description}

Check whether the dataset can be used to fit the \texttt{lvm} object.

\textbf{Usage}

\begin{verbatim}
checkData(object, data, trace)
## S3 method for class 'lvm'
checkData(object, data, trace = TRUE)
\end{verbatim}

\textbf{Arguments}

- \texttt{object} \hspace{1cm} a \texttt{lvm} object.
- \texttt{data} \hspace{1cm} \texttt{[data.frame]} the dataset used to obtain the object.
- \texttt{trace} \hspace{1cm} \texttt{[logical]} when \texttt{TRUE}, the outcome of the check will be displayed.

\textbf{Value}

Invisible \texttt{TRUE} or \texttt{FALSE}.

\textbf{Examples}

\begin{verbatim}
m <- lvm()
regression(m) <- c(y1,y2,y3)~u
regression(m) <- u~x
latent(m) <- ~u
d <- lava::sim(m,1e2)
try(checkData(m, data = d)) # return an error
checkData(m, data = d[,4])
try(checkData(m, data = d[,-(3:4)]) # return an error
\end{verbatim}
clean

Simplify a lvm object

Description

Remove variables with no link.

Usage

clean(x, ...)

## S3 method for class 'lvm'
clean(x, rm.exo = TRUE, rm.endo = TRUE,
       rm.latent = TRUE, ...)

Arguments

x  lvm-object

... additional arguments to lower level functions

rm.exo should exogenous variables with no links be removed from the object?

rm.endo should endogenous variables with no links be removed from the object?

rm.latent should latent variables with no links be removed from the object?

Examples

m <- lvm()
m <- regression(m, x=paste0("x",1:5),y="y1")
m <- regression(m, x=paste0("x",1:5),y="y2")
covariance(m) <- y1 ~ y2

cancel(m) <- y1 ~ x1
cancel(m) <- y2 ~ x1
clean(m)

m <- lvm(y1 ~ eta + x1, y2 ~ eta, y3 ~ eta + x2)
latent(m) <- ~eta

clean(m)

m
cancel(m) <- y1 ~ eta
cancel(m) <- y2 ~ eta
cancel(m) <- y3 ~ eta
clean(m)
Description

Extract specific types of coefficient from a `lvm` object: covariance coefficient(s) (`coefCov`), extra parameter(s) (`coefExtra`), position in the list of models for each coefficient (`coefIndexModel`), intercept coefficient(s) (`coefIntercept`), coefficient(s) that are used as reference (`coefRef`), regression coefficient(s) (`coefReg`), variance coefficient(s) (`coefVar`).

Usage

```r
coefCov(object, value, keep.var, ...)
```

### S3 method for class 'lvm'

```r
go coefCov(object, value = FALSE, keep.var = FALSE, ...)
```

### S3 method for class 'lvmfit'

```r
go coefCov(object, value = FALSE, keep.var = FALSE, ...)
```

### S3 method for class 'multigroup'

```r
go coefCov(object, value = FALSE, keep.var = FALSE, ...)
```

```r
go coefExtra(object, value, ...)
```

### S3 method for class 'lvm'

```r
go coefExtra(object, value = FALSE, ...)
```

### S3 method for class 'lvmfit'

```r
go coefExtra(object, value = FALSE, ...)
```

### S3 method for class 'multigroup'

```r
go coefExtra(object, value = FALSE, ...)
```

```r
go coefIndexModel(object, ...)
```

### S3 method for class 'lvm'

```r
go coefIndexModel(object, ...)
```

### S3 method for class 'lvmfit'

```r
go coefIndexModel(object, ...)
```

### S3 method for class 'multigroupfit'

```r
go coefIndexModel(object, ...)
```
coefByType

coefIndexModel(object, ...)

coefIntercept(object, value, ...)

## S3 method for class 'lvm'
coefIntercept(object, value = FALSE, ...)

## S3 method for class 'lvmfit'
coefIntercept(object, value = FALSE, ...)

## S3 method for class 'multigroup'
coefIntercept(object, value = FALSE, ...)

coefRef(object, value, ...)

## S3 method for class 'lvmfit'
coefRef(object, value = FALSE, ...)

coefReg(object, value, ...)

## S3 method for class 'lvm'
coefReg(object, value = FALSE, ...)

## S3 method for class 'lvmfit'
coefReg(object, value = FALSE, ...)

## S3 method for class 'multigroup'
coefReg(object, value = FALSE, ...)

coefVar(object, value, ...)

## S3 method for class 'lvm'
coefVar(object, value = FALSE, ...)

## S3 method for class 'lvmfit'
coefVar(object, value = FALSE, ...)

## S3 method for class 'multigroup'
coefVar(object, value = FALSE, ...)

Arguments

object a lvm model or a fitted lvm model
value should the name of the coefficient be returned? Else return the coefficients
keep.var should the variance coefficients be returned?
... arguments to be passed to
Value

A vector containing the names of the positions of the coefficients.

Examples

#### regression ####

```r
m <- lvm(Y~X1+X2)
e <- estimate(m, lava::sim(m, 1e2))
```

```r
c coefCov(m)
c coefCov(m, value = TRUE)
```

```r
c coefCov(m, keep.var = TRUE)
c coefCov(m, value = TRUE, keep.var = TRUE)
```

```r
c coefIndexModel(m)
c coefIndexModel(e)
```

```r
c coefIntercept(m)
c coefIntercept(m, value = TRUE)
```

```r
c coefReg(m)
c coefReg(m, value = TRUE)
```

#### LVM ####

```r
m <- lvm()
```

```r
regression(m) <- c(y1,y2,y3)~u
regression(m) <- u~x1+x2
latent(m) <- -u
covariance(m) <- y1~y2
```

```r
m.Sim <- m
categorical(m.Sim, labels = c("a","b","c")) <- -x2
e <- estimate(m, lava::sim(m.Sim, 1e2))
```

```r
c coefCov(m)
c coefCov(m, value = TRUE)
```

```r
c coefCov(m, keep.var = TRUE)
c coefCov(m, value = TRUE, keep.var = TRUE)
```

```r
c coefExtra(m)
c coefIndexModel(m)
c coefIndexModel(e)
```

## additional categorical variable

```r
categorical(m, labels = as.character(1:3)) <- "X1"
```

```r
c coefExtra(m)
c coefExtra(m, value = TRUE)
```
## additional categorical variable
categorical(m, labels = as.character(1:3)) <- "x1"

coeffIntercept(m)
coeffIntercept(m, value = TRUE)
coeffIntercept(e)

coeffReg(e, value = TRUE)

#### multigroup ####
m <- lvm(Y~X1+X2)
eG <- estimate(list(m,m), list(lava::sim(m, 1e2), lava::sim(m, 1e2)))
coefficientIndexModel(eG)

---

**coefType**

*Extract the Type of Each Coefficient*

### Description

Extract the type of each coefficient of a lvm object.

### Usage

```r
coeffType(object, as.lava, ...)
```

### S3 method for class 'lvm'
```r
coeffType(object, as.lava = TRUE, data = NULL, ...)
```

### S3 method for class 'lvmfit'
```r
coeffType(object, as.lava = TRUE, ...)
```

### S3 method for class 'multigroup'
```r
coeffType(object, as.lava = TRUE, ...)
```

### Arguments

- **object**: a lvm or lvmfit object.
- **as.lava**: [logical] export the type of coefficients mimicking lava:::coef.
- **...**: arguments to be passed to lava:::coef
- **data**: [data.frame, optional] the dataset. Help to identify the categorical variables.
Details

A lvm can be written as a measurement model:

\[ Y_i = \nu + \Lambda \eta_i + K X_i + \epsilon_i \]

and a structural model:

\[ \eta_i = \alpha + B \eta_i + \Gamma X_i + \zeta_i \]

where \( \Psi \) is the variance covariance matrix of the residuals \( \zeta \)
and \( \Sigma \) is the variance covariance matrix of the residuals \( \epsilon \).

coefType either returns the Latin/Greek letter corresponding to the coefficients or it groups them:

- **intercept**: \( \nu \) and \( \alpha \).
- **regression**: \( \Lambda \), \( K \), \( B \), and \( \Gamma \).
- **covariance**: extra-diagonal terms of \( \Sigma \) and \( \Psi \).
- **variance**: diagonal of \( \Sigma \) and \( \Psi \).

A link denotes a relationship between two variables. The coefficient are used to represent the strength of the association between two variable, i.e. the strength of a link. A coefficient may corresponds to the strength of one or several link.

Value

coefType returns a data.frame when \( \text{as.lava}=\text{FALSE} \):

- **name**: name of the link
- **Y**: outcome variable
- **X**: regression variable in the design matrix (could be a transformation of the original variables, e.g. dichotomization).
- **data**: original variable
- **type**: type of link
- **value**: if TRUE, the value of the link is set and not estimated.
- **marginal**: if TRUE, the value of the link does not impact the estimation.
- **detail**: a more detailed description of the type of link (see the details section)
- **lava**: name of the coefficient in lava

When \( \text{as.lava}=\text{TRUE} \), coefType returns a named vector containing the type of each coefficient.

Examples

```r
#### regression ####
m <- lvm(Y~X1+X2)
e <- estimate(m, lava::sim(m, 1e2))
coefType(m)
coefType(e)
```
### LVM ###
m <- lvm()
regression(m) <- c(y1, y2, y3) ~ u
regression(m) <- u ~ x1 + x2
latent(m) <- ~ u
covariance(m) <- y1 ~ y2

m.Sim <- m
categorical(m.Sim, labels = c("a", "b", "c")) <- ~ x2
e <- estimate(m, lava::sim(m.Sim, 1e2))

coefType(m)
coefType(e)

## additional categorical variables

categorical(m, labels = as.character(1:3)) <- "X1"

coefType(m, as.lava = FALSE)

### LVM with constrains ###
m <- lvm(c(Y1~0+1*eta1, Y2~0+1*eta1, Y3~0+1*eta1,
       Z1~0+1*eta2, Z2~0+1*eta2, Z3~0+1*eta2))
latent(m) <- ~ eta1 + eta2
e <- estimate(m, lava::sim(m, 1e2))

coefType(m)
coefType(e)

### multigroup ###
m <- lvm(Y~X1+X2)
eG <- estimate(list(m, m), list(lava::sim(m, 1e2), lava::sim(m, 1e2)))
coefType(eG)

---

**combineFormula**

*Combine formula*

**Description**

Combine formula by outcome

**Usage**

`combineFormula(ls.formula, as.formula = TRUE, as.unique = FALSE)`

**Arguments**

- `ls.formula`: a list of formula
- `as.formula`: should a list of formula be returned. Otherwise it will be a list of characters.
- `as.unique`: should regressors appears at most once in the formula
Examples

```r
combineFormula(list(Y~X1,Y~X3+X5,Y1~X2))
lava.options(symbols = c("-","\cdot","\Rightarrow"))
combineFormula(list("Y~X1","Y~X3+X5","Y1~X2"))
lava.options(symbols = c("\leftarrow","\leftrightarrow"))
combineFormula(list("Y\leftarrow X1","Y\leftarrow X3+X5","Y1\leftarrow X2"))
```

combineFormula(list(Y~X1,Y~X3+X1,Y1~X2))
combineFormula(list(Y~X1,Y~X3+X1,Y1~X2), as.formula = FALSE)
combineFormula(list(Y~X1,Y~X3+X1,Y1~X2), as.unique = TRUE)

```r
lava.options(symbols = c("-","\sim"))
combineFormula(list("Y\sim X1","Y\sim X3","Y1\sim X2"))
```

---

**compare2**

Test Linear Hypotheses with small sample correction

**Description**

Test Linear Hypotheses using a multivariate Wald statistic. Similar to `lava::compare` but with small sample correction.

**Usage**

```r
compare2(object, df, bias.correct, ...)
```

```r
## S3 method for class 'lm'
code2(object, df = TRUE, bias.correct = TRUE, ...)
```

```r
## S3 method for class 'gls'
code2(object, df = TRUE, bias.correct = TRUE, 
cluster = NULL, ...)
```

```r
## S3 method for class 'lme'
code2(object, df = TRUE, bias.correct = TRUE, 
cluster = NULL, ...)
```

```r
## S3 method for class 'lvmfit'
code2(object, df = TRUE, bias.correct = TRUE, 
cluster = NULL, ...)
```

```r
## S3 method for class 'lm2'
code2(object, ...)
```

```r
## S3 method for class 'gls2'
code2(object, ...)
```
compare2

## S3 method for class 'lme2'
compare2(object, ...)

## S3 method for class 'lvmfit2'
compare2(object, ...)

.compare2(object, par = NULL, contrast = NULL, null = NULL,
          rhs = NULL, robust = FALSE, cluster = NULL,
          df = object$sCorrect$args$df, as.lava = TRUE, F.test = TRUE,
          level = 0.95)

Arguments

object 
an object that inherits from lm/gls/lme/lvmfit.
df 
[logical] should the degree of freedoms of the Wald statistic be computed using the Satterthwaite correction? Otherwise the degree of freedoms are set to Inf, i.e. a normal distribution is used instead of a Student’s t distribution when computing the p-values.
bias.correct 
[logical] should the standard errors of the coefficients be corrected for small sample bias? Argument passed to sCorrect.
... 
[internal] only used by the generic method.
cluster 
[integer vector] the grouping variable relative to which the observations are iid.
par 
[vector of characters] expression defining the linear hypotheses to be tested. See the examples section.
contrast 
[matrix] a contrast matrix defining the left hand side of the linear hypotheses to be tested.
null, rhs 
[vector] the right hand side of the linear hypotheses to be tested.
robust 
[logical] should the robust standard errors be used instead of the model based standard errors?
as.lava 
[logical] should the output be similar to the one return by lava::compare?
F.test 
[logical] should a joint test be performed?
level 
[numeric 0-1] the confidence level of the confidence interval.

Details

The par argument or the arguments contrast and null (or equivalently rhs) specify the set of linear hypotheses to be tested. They can be written:

\[ \text{contrast} \times \theta = \text{null} \]

where \( \theta \) is the vector of the model coefficients.

The par argument must contain expression(s) involving the model coefficients. For example "beta = 0" or c("-5*beta + alpha = 3","-alpha") are valid expressions if alpha and beta belong to the set of model coefficients. A contrast matrix and the right hand side will be generated inside the function.
When directly specified, the contrast matrix must contain as many columns as there are coefficients in the model (mean and variance coefficients). Each hypothesis correspond to a row in the contrast matrix.

The null vector should contain as many elements as there are row in the contrast matrix.

Argument rhs and null are equivalent. This redondance enable compatibility between lava::compare, compare2, multcomp::glht, and glht2.

Value

If as.lava=TRUE an object of class htest. Otherwise a data.frame object.

See Also

createContrast to create contrast matrices.
sCorrect to pre-compute quantities for the small sample correction.

Examples

#### simulate data ####
set.seed(10)
mSim <- lvm(Y~0.1*X1+0.2*X2)
categorical(mSim, labels = c("a","b","c")) <- ~X1
transform(mSim, Id~Y) <- function(x){1:NROW(x)}
df.data <- lava::sim(mSim, 1e2)

#### with lm ####
## direct use of compare2
e.lm <- lm(Y~X1+X2, data = df.data)
anova(e.lm)
compare2(e.lm, par = c("X1b=0","X1c=0"))

## or first compute the derivative of the information matrix
sCorrect(e.lm) <- TRUE

## and define the contrast matrix
C <- createContrast(e.lm, par = c("X1b=0","X1c=0"), add.variance = TRUE)

## run compare2
compare2(e.lm, contrast = C$contrast, null = C$null)
compare2(e.lm, contrast = C$contrast, null = C$null, robust = TRUE)

#### with gls ####
library(nlme)
e.gls <- gls(Y~X1+X2, data = df.data, method = "ML")

## first compute the derivative of the information matrix
sCorrect(e.gls, cluster = 1:NROW(df.data)) <- TRUE

compare2(e.gls, par = c("5*X1b+2*X2 = 0","(Intercept) = 0"))
### with lvm ###
m <- lvm(Y~X1+X2)
e.lvm <- estimate(m, df.data)

compare2(e.lvm, par = c("-Y","Y-X1b+Y-X1c"))
compare2(e.lvm, par = c("-Y","Y-X1b+Y-X1c"), robust = TRUE)

---

**convFormulaCharacter**  *formula character conversion*

**Description**

Conversion of formula into character string or vice versa

**Usage**

```r
formula2character(f, type = "formula")
```

**Arguments**

- `f` a formula.
- `type` should the normal formula operator be used ("formula") or the one of lava.option ("symbols" or "symbol").

**Examples**

```r
formula2character(Y1~X1+X2)
formula2character(Y1~X1+X2, type = "symbols")
```

---

**createContrast**  *Create Contrast matrix*

**Description**

Returns a contrast matrix corresponding an object. The contrast matrix will contains the hypotheses in rows and the model coefficients in columns.
createContrast

Usage

createContrast(object, ...)  

## S3 method for class 'character'
createContrast(object, name.param,  
    diff.first = FALSE, add.rowname = TRUE, rowname.rhs = TRUE, ...)

## S3 method for class 'lm'
createContrast(object, par, add.variance, ...)

## S3 method for class 'gls'
createContrast(object, par, add.variance, ...)

## S3 method for class 'lme'
createContrast(object, par, add.variance, ...)

## S3 method for class 'lvmfit'
createContrast(object, par = NULL, var.test = NULL,  
    ...)

## S3 method for class 'list'
createContrast(object, par = NULL, add.variance = NULL,  
    var.test = NULL, ...)

## S3 method for class 'mmm'
createContrast(object, par = NULL, add.variance = NULL,  
    var.test = NULL, ...)

Arguments

object a lslvmfit object.

... [internal] Only used by the generic method.

name.param [internal] the names of all the model coefficients.

diff.first [logical] should the contrasts between the first and any of the other coefficients  
    define the null hypotheses.

add.rowname [internal] should a name be defined for each hypothesis.

rowname.rhs should the right hand side of the null hypothesis be added to the name.

par [vector of characters] expression defining the linear hypotheses to be tested. See  
    the examples section.

add.variance [logical] should the variance coefficients be considered as model coefficients?  
    Required for lm, gls, and lme models.

var.test [character] a regular expression that is used to identify the coefficients to be  
    tested using grep. Each coefficient will be tested in a separate hypothesis. When  
    this argument is used, the argument par is disregarded.
Details

One can initialize an empty contrast matrix setting the argument `par` to `character(0)`.

When using `multcomp::glht` one should set the argument `add.variance` to `FALSE`. When using `lavaSearch2::glht2` one should set the argument `add.variance` to `TRUE`.

Value

A list containing

- contrast [matrix] a contrast matrix corresponding to the left hand side of the linear hypotheses.
- null [vector] the right hand side of the linear hypotheses.
- Q [integer] the rank of the contrast matrix.
- ls.contrast [list, optional] the contrast matrix corresponding to each submodel. Only present when the argument `object` is a list of models.

Examples

```r
## Simulate data
mSim <- lvm(X ~ Age + Treatment,
            Y ~ Gender + Treatment,
            c(Z1,Z2,Z3) ~ eta, eta ~ treatment,
            Age[40:5]~1)
latent(mSim) <- ~eta
categorical(mSim, labels = c("placebo","SSRI")) <- ~Treatment
categorical(mSim, labels = c("male","female")) <- ~Gender
n <- 1e2
set.seed(10)
df.data <- lava::sim(mSim,n)

## Estimate separate models
lmX <- lava::estimate(lvm(X ~ -1 + Age + Treatment), data = df.data)
lmY <- lava::estimate(lvm(Y ~ -1 + Gender + Treatment), data = df.data)
lvmZ <- lava::estimate(lvm(c(Z1,Z2,Z3) ~ -1 + 1*eta, eta ~ -1 + Treatment),
                     data = df.data)

## Contrast matrix for a given model
createContrast(lmX, par = "X~Age")
createContrast(lmX, par = c("X~Age=0","X~Age+5*X~TreatmentSSRI=0"))
createContrast(lmX, par = character(0))

## Contrast matrix for the join model
ls.lvm <- list(X = lmX, Y = lmY, Z = lvmZ)
createContrast(ls.lvm, var.test = "Treatment", add.variance = FALSE)
createContrast(ls.lvm, par = character(0), add.variance = FALSE)

## Contrast for multigroup models
m <- lava::lvm(Y~Age+Treatment)
e <- lava::estimate(list(m,m), data = split(df.data, df.data$Gender))
```
print(coef(e))
createContrast(e, par = "Y~TreatmentSSRI@1 - Y~TreatmentSSRI@2 = 0")
createContrast(e, par = "Y~TreatmentSSRI@2 - Y~TreatmentSSRI@1 = 0")

---

**dfSigma**  
*Degree of Freedom for the Chi-Square Test*

**Description**

Computation of the degrees of freedom of the chi-squared distribution relative to the model-based variance

**Usage**

dfSigma(contrast, vcov, dVcov, keep.param)

**Arguments**

- **contrast**  
  [numeric vector] the linear combination of parameters to test
- **vcov**  
  [numeric matrix] the variance-covariance matrix of the parameters.
- **dVcov**  
  [numeric array] the first derivative of the variance-covariance matrix of the parameters.
- **keep.param**  
  [character vector] the name of the parameters with non-zero first derivative of their variance parameter.

---

**dfSigmaRobust**  
*Degree of Freedom for the Robust Chi-Square Test*

**Description**

Computation of the degrees of freedom of the chi-squared distribution relative to the robust-based variance

**Usage**

dfSigmaRobust(contrast, vcov, rvcov, score)

**Arguments**

- **contrast**  
  [numeric vector] the linear combination of parameters to test
- **vcov**  
  [numeric matrix] the variance-covariance matrix of the parameters.
- **rvcov**  
  [numeric matrix] the robust variance-covariance matrix of the parameters.
- **score**  
  [numeric matrix] the individual score for each parameter.
Details

When contrast is the identity matrix, this function compute the moments of the sandwich estimator and the degrees of freedom of the approximate t-test as described in (Pan, 2002) section 2 and 3.1.

References


effects2

Effects from a fitted model

Description

Test whether a path in the latent variable model correspond to a null effect. Similar to lava::effects but with small sample correction. So far it only work for paths composed of two edges.

Usage

effects2(object, link, ...)  
## S3 method for class 'lvmfit'  
effects2(object, link, df = TRUE, bias.correct = TRUE, ...)  
## S3 method for class 'lvmfit2'  
effects2(object, link, ...)  

Arguments

object an object that inherits from lvmfit.
link [character vector] The path for which the effect should be assessed (e.g. "A~B"), i.e. the effect of the right variable (B) on the left variable (A).
... [internal] only used by the generic method.
df [logical] should the degree of freedoms of the Wald statistic be computed using the Satterthwaite correction? Otherwise the degree of freedoms are set to Inf, i.e. a normal distribution is used instead of a Student’s t distribution when computing the p-values.
bias.correct [logical] should the standard errors of the coefficients be corrected for small sample bias? Argument passed to sCorrect.
estfun

Extract Empirical Estimating Functions (lvmfit Object)

Description

Extract the empirical estimating functions of a lvmfit object. This function is for internal use but need to be public to enable its use by multcomp::glht.

Usage

## S3 method for class 'lvmfit'
estfun(x, ...)

## S3 method for class 'gls'
estfun(x, ...)

## S3 method for class 'lme'
estfun(x, ...)

Arguments

x an lvmfit object.

... arguments passed to methods.

Details

This function enables to use the glht function with lvmfit object. Otherwise when calling multcomp:::vcov.mmm then sandwich::sandwich and then sandwich::meat, sandwich::meat will complain that estfun is not defined for lvmfit objects.

Examples

library(multcomp)

#### generative model ####
mSim <- lvm(X ~ Age + 0.5*Treatment,
Y ~ Gender + 0.25*Treatment,
c(Z1,Z2,Z3) ~ eta, eta ~ 0.75*treatment,
Age[40:5]-1)
latent(mSim) <- ~eta
categorical(mSim, labels = c("placebo","SSRI")) <- ~Treatment
categorical(mSim, labels = c("male","female")) <- ~Gender

#### simulate data ####
n <- 5e1
set.seed(10)
df.data <- lava::sim(mSim, n = n, latent = FALSE)
#### fit separate models ####

```r
lmX <- lm(X ~ Age + Treatment, data = df.data)
lvmY <- estimate(lvm(Y ~ Gender + Treatment), data = df.data)
lvmZ <- estimate(lvm(c(Z1,Z2,Z3) ~ eta, eta ~ Treatment),
                   data = df.data)
```

#### create mmm object ####

```r
e.mmm <- mmm(X = lmX, Y = lvmY, Z = lvmZ)
```

#### create contrast matrix ####

```r
resC <- createContrast(e.mmm, var.test = "Treatment", add.variance = FALSE)
```

#### adjust for multiple comparisons ####

```r
e.glht <- glht(e.mmm, linfct = resC$mlf)
summary(e.glht)
```

---

**extractData**

*Extract Data From a Model*

**Description**

Extract data from a model using `nlme::getData`, `riskRegression::coxDesign` or `model.frame`.. If it fails it will try to extract it by its name according to `model$call$data`.

**Usage**

```r
extractData(object, design.matrix, as.data.frame, envir)
```

- **S3 method for class 'lm'**
  ```r
  extractData(object, design.matrix = FALSE, 
              as.data.frame = TRUE, envir = environment())
  ```

- **S3 method for class 'coxph'**
  ```r
  extractData(object, design.matrix = FALSE, 
              as.data.frame = TRUE, envir = environment())
  ```

- **S3 method for class 'cph'**
  ```r
  extractData(object, design.matrix = FALSE, 
              as.data.frame = TRUE, envir = environment())
  ```

- **S3 method for class 'lvmfit'**
  ```r
  extractData(object, design.matrix = FALSE, 
              as.data.frame = TRUE, envir = environment())
  ```

- **S3 method for class 'gls'**
  ```r
  extractData(object, design.matrix = FALSE, 
              as.data.frame = TRUE, envir = environment())
  ```
## S3 method for class 'lme'
extractData(object, design.matrix = FALSE,
            as.data.frame = TRUE, envir = environment())

Arguments

- **object**: the fitted model.
- **design.matrix**: [logical] should the data be extracted after transformation (e.g. conversion of categorical variables to dummy variables)? Otherwise the original data will be returned.
- **as.data.frame**: [logical] should the output be converted into a data.frame object?
- **envir**: [environment] the environment from which to search the data.

Value

a dataset.

Examples

```r
set.seed(10)

n <- 101

#### linear regression ####
Y1 <- rnorm(n, mean = 0)
Y2 <- rnorm(n, mean = 0.3)
Id <- findInterval(runif(n), seq(0,1,0.1))
data.df <- rbind/data.frame(Y=Y1,G="1",Id = Id),
    data.frame(Y=Y2,G="2",Id = Id))
m.lm <- lm(Y ~ G, data = data.df)
a <- extractData(m.lm, design.matrix = TRUE)
b <- extractData(m.lm, design.matrix = FALSE)

library(nlme)
m.gls <- gls(Y ~ G, weights = varIdent(form = ~ 1|Id), data = data.df)
c <- extractData(m.gls)
m.lme <- lme(Y ~ G, random = ~ 1|Id, data = data.df)
d <- extractData(m.lme)

library(lava)
e.lvm <- estimate(lvm(Y ~ G), data = data.df)
e <- extractData(e.lvm)
e <- extractData(e.lvm, design.matrix = TRUE)

#### survival ####
library(survival)

## Not run:
library(riskRegression) ## needs version >=1.4.3
dt.surv <- sampleData(n, outcome = "survival")
m.cox <- coxph(Surv(time, event) ~ X1 + X2, data = dt.surv, x = TRUE, y = TRUE)
```

# Not run:

```r
library(riskRegression) ## needs version >=1.4.3
dt.surv <- sampleData(n, outcome = "survival")
m.cox <- coxph(Surv(time, event) ~ X1 + X2, data = dt.surv, x = TRUE, y = TRUE)
```
f <- extractData(m.cox, design.matrix = FALSE)
f <- extractData(m.cox, design.matrix = TRUE)
m.cox <- coxph(Surv(time, event) ~ strata(X1) + X2, data = dt.surv, x = TRUE, y = TRUE)
f <- extractData(m.cox, design.matrix = TRUE)

## End(Not run)

### nested fuuctions ###
fct1 <- function(m){
fct2(m)
}
fct2 <- function(m){
  extractData(m)
}
g <- fct1(m.gls)

---

### Find New Links Between Variables ###

**Description**

Find all new links between variables (adapted from lava::modelsearch).

**Usage**

```r
findNewLink(object, ...)
```

```r
## S3 method for class 'lvm'
findNewLink(object, data = NULL, type = "both",
  exclude.var = NULL, rm.latentlatent = FALSE, rm.endo_endo = FALSE,
  rm.latent_endo = FALSE, output = "names", ...)
```

**Arguments**

- `object` a lvm object.
- `...` [internal] only used by the generic method.
- `data` [optional] a dataset used to identify the categorical variables when not specified in the lvm object.
- `type` [character vector] the type of links to be considered: "regression", "covariance", or "both".
- `exclude.var` [character vector] all links related to these variables will be ignored.
- `rm.latent latent` [logical] should the links relating two latent variables be ignored?
- `rm. endo_endo` [logical] should the links relating two endogenous variables be ignored?
- `rm.latent_endo` [logical] should the links relating one endogenous variable and one latent variable be ignored?
- `output` [character] Specify "names" to return the names of the variables to link or specify "index" to return their position.
Value

A list containing:

- `M.links`: a matrix with two columns indicating (by name or position) the exogenous and endogenous variable corresponding to each link.
- `links`: the name of the additional possible links
- `directional`: a logical vector indicating for each link whether the link is unidirectional (`TRUE`, i.e. regression link) or bidirectional (`FALSE`, i.e. covariance link).

Examples

```r
library(lava)

m <- lvm()
regression(m) <- c(y1,y2,y3)~u
categorical(m,labels=c("M","F","MF")) <- ~X1
findNewLink(m, rm.endo = FALSE)
findNewLink(m, rm.endo = TRUE)
findNewLink(m, exclude.var = "X1")

regression(m) <- u~x1+x2
latent(m) <- ~u

findNewLink(m, rm.endo = FALSE)
findNewLink(m, rm.endo = TRUE)
findNewLink(m, rm.endo = TRUE, output = "index")
findNewLink(m, type = "covariance")
findNewLink(m, type = "regression")
```

getNewLink

Extract the Links that Have Been Found by the modelsearch2.

Description

Extract the links that have been found relevant by modelsearch2.

Usage

```r
getNewLink(object, step)
```
### Description

Extract the model that has been retained by `modelsearch2`.

### Usage

```r
getNewModel(object, step)
```

### Arguments

- `object`: A `modelsearch2` object.
- `step`: `[integer >=0]` the step at which the model should be extracted. 0 returns the initial model, i.e. before adding any links.

### Value

A `lvmfit` object.
Examples

### Not run:
```r
mSim <- lvm(Y~G+X1+X2)
addvar(mSim) <- ~Z1+Z2+Z3+Z4+Z5+Z6

set.seed(10)
df.data <- lava::sim(mSim, 1e2)

mBase <- lvm(Y~G)
addvar(mBase) <- ~X1+X2+Z1+Z2+Z3+Z4+Z5+Z6
e.lvm <- estimate(mBase, data = df.data)
res <- modelsearch2(e.lvm, method.p.adjust = "holm")
getNewModel(res)
```

## End(Not run)

---

getStep

### Extract one Step From the Sequential Procedure

#### Description
Extract one step from the sequential procedure.

#### Usage
```r
getStep(object, step, slot)
```

#### Arguments
- **object**: a `modelsearch2` object
- **step**: `[integer >0]` which test should be extracted?
- **slot**: `[character]` the element from the `modelsearch2` object that should be extracted.

#### Examples

### Not run:
```r
mSim <- lvm(Y~G+X1+X2)
addvar(mSim) <- ~Z1+Z2+Z3+Z4+Z5+Z6

df.data <- lava::sim(mSim, 1e2)

mBase <- lvm(Y~G)
addvar(mBase) <- ~X1+X2+Z1+Z2+Z3+Z4+Z5+Z6
e.lvm <- estimate(mBase, data = df.data)
res <- modelsearch2(e.lvm, method.p.adjust = "holm")
```

```r
getStep(res)
```
getVarCov2

Reconstruct the Conditional Variance Covariance Matrix

Description

Reconstruct the conditional variance covariance matrix from a nlme or lvm model. Only compatible with specific correlation and variance structure.

Usage

getVarCov2(object, ...)

## S3 method for class 'gls'
getVarCov2(object, data = NULL, cluster, ...)

## S3 method for class 'lme'
getVarCov2(object, data = NULL, cluster, ...)

## S3 method for class 'lvmfit'
getVarCov2(object, ...)

Arguments

object a gls or lme object
... [internal] only used by the generic method.
data [data.frame] the data set.
cluster [integer vector] the grouping variable relative to which the observations are iid.

Details

The compound symmetry variance-covariance matrix in a gls model is of the form:

\[
\Sigma = \begin{bmatrix}
\sigma^2 & \sigma^2 \rho & \sigma^2 \\
& \sigma^2 & \sigma^2 \rho \\
& & \sigma^2 \\
\end{bmatrix}
\]

The unstructured variance-covariance matrix in a gls model is of the form:

\[
\Sigma = \begin{bmatrix}
\sigma^2 & \sigma^2 \sigma_1 \sigma_2 & \sigma^2 \sigma_1 \sigma_3 \\
& \sigma^2 \sigma_2 & \sigma^2 \sigma_2 \sigma_3 \\
& & \sigma^2 \sigma_2 \sigma_3 \\
\end{bmatrix}
\]
\begin{align*}
\sigma_1^2 & = \ldots \\
\sigma_2^2 & = \ldots \\
\sigma_3^2 & = \ldots 
\end{align*}

\textbf{Value}

A list containing the residual variance-covariance matrix in the element Omega.

\textbf{Examples}

```r
## simulate data
library(nlme)
n <- 5e1
mSim <- lvm(c(Y1~1*eta,Y2~1*eta,Y3~1*eta,eta~G))
latent(mSim) <- -eta
transform(mSim,Id~Y1) <- function(x){1:NRW(x)}
set.seed(10)
dW <- lava::sim(mSim,n,latent = FALSE)
dW <- dW[order(dW$Id),,drop=FALSE]
dL <- reshape2::melt(dW,id.vars = c("G","Id"), variable.name = "time")
dL <- dL[order(dL$Id),,drop=FALSE]
dL$Z1 <- rnorm(NROW(dL))
dL$time.num <- as.numeric(as.factor(dL$time))

#### iid model ####
e1.gls <- nlme::gls(Y1 ~ G, data = dW, method = "ML")
getVarCov2(e1.gls, cluster = 1:n)$Omega

#### heteroscedasticity ####
dW$group <- rbinom(n, size = 1, prob = 1/2)
dW$repetition <- as.numeric(as.factor(dW$group))
e2a.gls <- nlme::gls(Y1 ~ G, data = dW, method = "ML",
                   weights = varIdent(form =~ repetition|group))
getVarCov2(e2a.gls, cluster = 1:n)$Omega

e2b.gls <- nlme::gls(value ~ 0+time + time:G,
                   weight = varIdent(form = ~ time.num|time),
                   data = dL, method = "ML")
getVarCov2(e2b.gls, cluster = "Id")$Omega

#### compound symmetry ####
e3.gls <- nlme::gls(value ~ time + G,
                   correlation = corCompSymm(form = ~1| Id),
                   data = dL, method = "ML")
getVarCov2(e3.gls)$Omega

#### unstructured ####
e4.gls <- nlme::gls(value ~ time,
                   correlation = corSymm(form = ~time.num| Id),
                   weight = varIdent(form = ~ 1|time),
                   data = dL, method = "ML")
getVarCov2(e4.gls)$Omega
```
### lvm model ###
m <- lvm(c(Y1~1*eta,Y2~1*eta,Y3~1*eta,eta~G))
latent(m) <- ~ eta
e <- estimate(m, Dm)
getVarCov2(e)

---

**glht2**

*General Linear Hypothesis*

**Description**

Test general linear hypotheses and across latent variable models with small sample corrections.

**Usage**

glht2(model, linfct, rhs, bias.correct, df, robust, cluster)

## S3 method for class 'lvmfit'

# S3 method for class 'lvmfit'

## S3 method for class 'mmm'

# S3 method for class 'mmm'

glht2(model, linfct, rhs = 0, bias.correct = TRUE,
      df = TRUE, robust = FALSE, cluster = NULL)

**Arguments**

- **model**: a lvmfit or mmm object. The mmm object can only contain lm/gls/lme/lvmfit objects.
- **linfct**: [matrix or vector of character] the linear hypotheses to be tested. Same as the argument par of createContrast.
- **rhs**: [vector] the right hand side of the linear hypotheses to be tested.
- **bias.correct**: [logical] should the standard errors of the coefficients be corrected for small sample bias?
- **df**: [logical] should the degree of freedoms of the Wald statistic be computed using the Satterthwaite correction?
- **robust**: [logical] should robust standard error be used? Otherwise rescale the influence function with the standard error obtained from the information matrix.
- **cluster**: [integer vector] the grouping variable relative to which the observations are iid.
Details

Whenever the argument linfct is not a matrix, it is passed to the function createContrast to generate the contrast matrix and, if not specified, rhs.

Since only one degree of freedom can be specify in a glht object and it must be an integer, the degree of freedom of the denominator of an F test simultaneously testing all hypotheses is retained, after rounding.

Argument rhs and null are equivalent. This redondance enable compatibility between lava::compare, compare2, multcomp::glht, and glht2.

Value

A glht object.

See Also

createContrast to create contrast matrices.
sCorrect to pre-compute quantities for the small sample correction.

Examples

library(multcomp)

## Simulate data
mSim <- lvm(c(Y1,Y2,Y3)~ beta * eta, Z1 ~ E, Z2 ~ E, Age[40:5]~-1)
latent(mSim) <- "eta"
set.seed(10)
n <- 1e2
df.data <- lava::sim(mSim, n, latent = FALSE, p = c(beta = 1))

#### Inference on a single model ####
e.lvm <- estimate(lvm(Y1~E), data = df.data)
summary(glht2(e.lvm, linfct = c("Y1+E + Y1","Y1")))

#### Inference on separate models ####
## fit separate models
lmX <- lm(Z1 ~ E, data = df.data)
lvmY <- estimate(lvm(Z2 ~ E + Age), data = df.data)
lvmZ <- estimate(lvm(c(Y1,Y2,Y3) ~ eta, eta ~ E),
  data = df.data)

#### create mmm object ####
e.mmm <- mmm(X = lmX, Y = lvmY, Z = lvmZ)

#### create contrast matrix ####
resC <- createContrast(e.mmm, var.test = "E", add.variance = TRUE)
### adjust for multiple comparisons ###

e.glht2 <- glht2(e.mmm, linfct = resC$contrast, df = FALSE)
summary(e.glht2)

---

**iid2**

*Extract corrected i.i.d. decomposition*

---

**Description**

Extract corrected i.i.d. decomposition from a gaussian linear model.

**Usage**

```r
iid2(object, ...) 
```

```r
## S3 method for class 'lm'

iid2(object, param = NULL, data = NULL, 
    bias.correct = TRUE, ...)

## S3 method for class 'gls'

iid2(object, cluster = NULL, param = NULL, data = NULL, 
    bias.correct = TRUE, ...)

## S3 method for class 'lme'

iid2(object, param = NULL, data = NULL, 
    bias.correct = TRUE, ...)

## S3 method for class 'lvmfit'

iid2(object, param = NULL, data = NULL, 
    bias.correct = TRUE, ...)

## S3 method for class 'lm2'

iid2(object, cluster = NULL, param = NULL, data = NULL, 
    robust = TRUE, ...)

## S3 method for class 'gls2'

iid2(object, cluster = NULL, param = NULL, 
    data = NULL, robust = TRUE, ...)

## S3 method for class 'lme2'

iid2(object, cluster = NULL, param = NULL, 
    data = NULL, robust = TRUE, ...)

## S3 method for class 'lvmfit2'

iid2(object, cluster = NULL, data = NULL, ...)
```
Arguments

- **object**: a linear model or a latent variable model
- **...**: arguments to be passed to `sCorrect`
- **param**: [named numeric vector] the fitted parameters
- **data**: [data.frame] the data set
- **bias.correct**: [logical] should the standard errors of the coefficients be corrected for small sample bias? Only relevant if the `sCorrect` function has not yet be applied to the object.
- **cluster**: [integer vector] the grouping variable relative to which the observations are iid.
- **robust**: [logical] if FALSE, the i.i.d. decomposition is rescaled such its the squared sum equals the model-based standard error (instead of the robust standard error).

Details

If argument p or data is not null, then the small sample size correction is recomputed to correct the influence function.

Value

A matrix containing the 1st order influence function relative to each sample (in rows) and each model coefficient (in columns).

See Also

`sCorrect` to obtain `lm2`, `gls2`, `lme2`, or `lvmfit2` objects.

Examples

```r
n <- 5e1
p <- 3
X.name <- paste0("X",1:p)
link.lvm <- paste0("Y"~X.name)
formula.lvm <- as.formula(paste0("Y~",paste0(X.name,collapse="+")))

m <- lvm(formula.lvm)
distribution(m,-Id) <- Sequence.lvm(0)
set.seed(10)
d <- sim(m,n)

## linear model
e.lm <- lm(formula.lvm,data=d)
IID.tempo <- iid2(e.lm, bias.correct = FALSE)
range(IID.tempo[,1:4]-IID(e.lm))

## latent variable model
e.lvm <- estimate(lvm(formula.lvm),data=d)
IID.tempo <- iid2(e.lvm, bias.correct = FALSE)
range(IID.tempo-iid(e.lvm))
```

## difference due to the use of the observed info matrix vs. the expected one.
## rescale i.i.d using model-based standard error

```r
iid.tempo <- iid2(e.lvm, robust = FALSE, bias.correct = FALSE)
diag(crossprod(iid.tempo)) - diag(vcov(e.lvm))
```

---

**iidJack**

*Jackknife iid Decomposition from Model Object*

### Description

Extract iid decomposition (i.e. influence function) from model object.

### Usage

```r
iidJack(object, ...)
```

### Arguments

- `object` a object containing the model.
- `...` [internal] only used by the generic method.
- `data` [data.frame] dataset used to perform the jackknife.
- `grouping` [vector] variable defining cluster of observations that will be simultaneously removed by the jackknife.
- `cpus` [integer >0] the number of processors to use. If greater than 1, the fit of the model and the computation of the influence function for each jackknife sample is performed in parallel.
- `keep.warnings` [logical] keep warning messages obtained when estimating the model with the jackknife samples.
- `keep.error` [logical] keep error messages obtained when estimating the model with the jackknife samples.
- `cl` [cluster] a parallel socket cluster generated by `parallel::makeCluster` that has been registered using `registerDoParallel`.
- `trace` [logical] should a progress bar be used to trace the execution of the function

### Value

A matrix with in row the samples and in columns the parameters.
Examples

```r
n <- 20

#### glm ####
set.seed(10)
m <- lvm(y~x+z)
distribution(m, ~y+z) <- binomial.lvm("logit")
d <- lava::sim(m,n)
g <- glm(y~x+z, data=d, family="binomial")
iid1 <- iidJack(g, cpus = 1)
iid2 <- lava::iid(g)
quantile(iid1-iid2)
vcov(g)
colSums(iid2^2)
colSums(iid1^2)

#### Cox model ####
## Not run:
library(survival)
data(Melanoma, package = "riskRegression")
m <- coxph(Surv(time,status==1)~ici+age, data = Melanoma, x = TRUE, y = TRUE)
## require riskRegression > 1.4.3
if(utils::packageVersion("riskRegression") > "1.4.3"){
  library(riskRegression)
iid1 <- iidJack(m)
iid2 <- iidCox(m)$IFbeta
apply(iid1,2,sd)
print(iid2)
apply(iid2,2,sd)
}
## End(Not run)

#### LVM ####
## Not run:
set.seed(10)

mSim <- lvm(c(Y1,Y2,Y3,Y4,Y5) ~ 1*eta)
latent(mSim) <- ~eta
categorical(mSim, K=2) <- ~G
transform(mSim, Id ~ eta) <- function(x){1:NROW(x)}
dW <- lava::sim(mSim, n, latent = FALSE)
dl <- reshape2::melt(dW, id.vars = c("G","Id"),
  variable.name = "time", value.name = "Y")
dl$time <- gsub("Y","",dl$time)
m1 <- lvm(c(Y1,Y2,Y3,Y4,Y5) ~ 1*eta)
latent(m1) <- ~eta
```
### information2

#### Extract The full Information Matrix

**Description**

Extract the full information matrix from a Gaussian linear model.

**Usage**

```r
information2(object, ...) 
```

## S3 method for class 'lm'
information2(object, ...)

## S3 method for class 'gls'
information2(object, ...)

## S3 method for class 'lme'
information2(object, ...)

## S3 method for class 'lvmfit'
information2(object, ...)

## S3 method for class 'lm2'
```
information2(object, ...)

## S3 method for class 'gls2'
information2(object, ...)

## S3 method for class 'lme2'
information2(object, ...)

## S3 method for class 'lvmfit2'
information2(object, ...)

Arguments

object a linear model or a latent variable model

... arguments to be passed to vcov2.

Value

A matrix.

See Also

scCorrect to obtain lm2, gls2, lme2, or lvmfit2 objects.

Examples

n <- 5e1
p <- 3
X.name <- paste0("X",1:p)
link.lvm <- paste0("Y-",X.name)
formula.lvm <- as.formula(paste0("Y~",paste0(X.name,collapse="+")))
m <- lvm(formula.lvm)
distribution(m,-1d) <- Sequence.lvm(0)
set.seed(10)
d <- lava::sim(m,n)

## linear model
e.lm <- lm(formula.lvm,data=d)
info.tempo <- vcov2(e.lm,bias.correct = TRUE)
info.tempo[names(coef(e.lm)),names(coef(e.lm))] - vcov(e.lm)

## latent variable model
e.lvm <- estimate(lvm(formula.lvm),data=d)
vcov.tempo <- vcov2(e.lvm, bias.correct = FALSE)
round(vcov.tempo %*% information(e.lvm), 5)
Normalize var1 and var2

Description

Convert var1 and var2 from formula or covariance to character.

Usage

```r
initVarLink(var1, var2, rep.var1 = FALSE, format = "list",
Slink = c(lava.options()$symbols[1], "~"),
Scov = lava.options()$symbols[2])

initVarLinks(var1, format = "list", ...)
```

Arguments

- **var1** [character or formula] the exogenous variable of the new link or a formula describing the link.
- **var2** [character] the endogenous variable of the new link. Disregarded if the argument var1 is a formula.
- **rep.var1** [logical] should var1 be duplicated to match var2 length. Only active if format = "list".
- **format** [character] should the name of the variable be returned (format = "list"), a vector of character formula (format = "txt.formula"), or a list of formula (format = "formula").
- **Slink** [character] the symbol for regression link.
- **Scov** [character] the symbol for covariance link.
- ... argument to be passed to initVarLink.

Value

See argument format.

Examples

```r
initVarLink(y ~ x1)
initVarLink("y ~ x1")
initVarLink(y ~ x1 + x2)
initVarLink("y ~ x1 + x2")
initVarLink(y ~ x1 + x2, rep.var1 = TRUE)
initVarLink(y ~ x1 + x2, rep.var1 = TRUE, format = "formula")
initVarLink(y ~ x1 + x2, rep.var1 = TRUE, format = "txt.formula")
initVarLink("y", "x1", format = "formula")

initVarLink("y - x1:0|1")
```
intDensTri(y ~ x1)
intVarLinks("y ~ x1")
intVarLinks(c("y ~ x1", "y ~ x2"))
intVarLinks(c(y ~ x1, y ~ x2))
intVarLinks(c("y ~ x1", "y ~ x2"), format = "formula")
intVarLinks(c(y ~ x1, y ~ x2), format = "formula")
intVarLinks(c("y ~ x1", "y ~ x2"), format = "txt.formula")
intVarLinks(c(y ~ x1, y ~ x2), format = "txt.formula")

---

**intDensTri**

*Integrate a Gaussian/Student Density over a Triangle*

**Description**

Consider a univariate random variable $X$, two multivariate random variables $Y$ and $Z$, and $t_1$ and $t_2$ two real numbers. This function can compute either $P[|X|>t_1,|X|>|Y_1|,...,|X|>|Y_p|]$ if $z_{min}$ is not specified, $P[|Z_1|<t_2,...,|Z_q|<t_2,|X|>|Y_1|,...,|X|>|Y_p|]$ if $z_{min}$ is specified.

**Usage**

```r
intDensTri(mu, Sigma, df, n, x.min, z.max = NULL, type = "double",
            proba.min = 1e-06, prune = NULL, distribution = "pmvnorm")
```

**Arguments**

- **mu**
  - [numeric vector] the expectation of the joint distribution.

- **Sigma**
  - [matrix] the variance-covariance of the joint distribution.

- **df**
  - [integer > 0] the degree of freedom of the joint Student’s t distribution. Only used when distribution="pvmt".

- **n**
  - [integer > 0] number of points for the numerical integration.

- **x.min**
  - [numeric] the minimum value along the x axis.

- **z.max**
  - [numeric vector, optional] the maximum value along the z axis. Define the dimension of $Z$.

- **type**
  - [character] the type of mesh to be used. Can be "raw", "double", or "fine".

- **proba.min**
  - [numeric 0-1] the probability used to find the maximum value along the x axis. Only used if prune is not specified.

- **prune**
  - [integer >0] number of standard deviations after which the domain ends along the x axis.

- **distribution**
  - [character] type of joint distribution. Can be "pmvnorm" (normal distribution) or "pvmt" (Student’s t distribution)
intDensTri

Details

Argument type:

- "raw": mesh with points inside the domain
- "double": mesh with points outside the domain
- "fine": mesh with points inside the domain plus additional rectangles trying to fill the missing domain.

Argument Sigma and mu: define the mean and variance-covariance of the random variables X, Y, Z (in this order). The length of the argument z.max is used to define the dimension of Z. The dimension of X is always 1.

Value

A numeric.

Examples

library(mvtnorm)

p <- 2
Sigma <- diag(p)
mu <- rep(0, p)

## bivariate normal distribution
z2 <- qmvt(0.975, mean = mu, sigma = Sigma, df = 1e3)$quantile

# compute integral
intDensTri(mu = mu, Sigma = Sigma, n=5, x.min=0, type = "fine")$value/2
intDensTri(mu = mu, Sigma = Sigma, n=30, x.min=0, type = "raw")$value/2
intDensTri(mu = mu, Sigma = Sigma, n=50, x.min=0, type = "raw")$value/2

intDensTri(mu = mu, Sigma = Sigma, df = 5, n=5, x.min=0, distribution = "pmvt")$value/2
res <- intDensTri(mu = mu, Sigma = Sigma, df = 5, n=10, x.min=0, distribution = "pmvt")
res$value/2

ggplot2::autoplot(res)

## trivariate normal distribution
## Not run:
p <- 3
Sigma <- diag(p)
mu <- rep(0, p)

res2 <- intDensTri(mu = mu, Sigma = Sigma, n=5, x.min = 0, z.max = 10)
ggplot2:: autoplot(res2)
ggplot2:: autoplot(res2, coord.plot = c("x","z1"))
res2

## End(Not run)

#### when the distribution is far from 0
## Not run:
eq1 <- intDensTri(mu = c(10,0), Sigma = diag(1,2),
                   x.min = 2, n=10)
eq1$value-1
ggplot2::autoplot(eq1)

eq2 <- intDensTri(mu = c(10,0,0), Sigma = diag(1,3),
                   x.min=2, z.max = 10, type = "raw",
                   n=10)
ggplot2::autoplot(eq2, coord.plot = c("y1","z1"))
eq2$value-1

## more variables
p <- 5
Sigma <- diag(p)
mu <- rep(0, p)
res2 <- intDensTri(mu = mu, Sigma = Sigma, n=5, x.min = 1, z.max = c(2,2))
res2$grid

## End(Not run)

---

**lavaSearch2**  
*Tools for Model Specification in the Latent Variable Framework*

### Description

The package contains three main functionalities:

- **compare2, summary2**: Wald tests/robust Wald tests/F-tests/robust F-tests with improved control of the type 1 error in small samples.
- **glht2**: adjustment for multiple comparisons when doing inference for multiple latent variable models.
- **modelsearch2**: searching for local dependencies with adjustment for multiple comparisons.

It contains other useful functions such as:

- **calibrateType1**: simulation study of the type 1 error of Wald tests.
- **createContrast**: user-friendly function generating a contrast matrix.
- **getVarCov2**: reconstruct the conditional variance covariance matrix.
- **iidJack**: extract the jackknife iid decomposition.
Details

The latent variable models (LVM) considered in this package can be written as a measurement model:

\[ Y_i = \nu + \eta_i \Lambda + X_i K + \epsilon_i \]

and a structural model:

\[ \eta_i = \alpha + \eta_i B + X_i \Gamma + \zeta_i \]

where \( \Sigma \) is the variance covariance matrix of the residuals \( \epsilon \), and \( \Psi \) is the variance covariance matrix of the residuals \( \zeta \).

The corresponding conditional mean is:

\[
\mu_i(\theta) = E[Y_i | X_i] = \nu + (\alpha + X_i \Gamma)(1 - B)^{-1}\Lambda + X_i K \\
\Omega(\theta) = Var[Y_i | X_i] = \Lambda^t (1 - B)^{-1} \Psi (1 - B)^{-1} \Lambda + \Sigma
\]

The package aims to provide tools for testing linear hypotheses on the model coefficients \( \nu, \Lambda, K, \Sigma, \alpha, B, \Gamma, \Psi \). Searching for local dependency enables to test whether the proposed model is too simplistic and if so identify which additional coefficients should be added to the model.

Limitations

' lavaSearch2' has been designed for Gaussian latent variable models. This means that it may not work or give valid results:

- in presence of censored or binary outcomes.
- with stratified models (i.e. object of class 'multigroup').

leverage2

Describe

Extract Leverage Values

Usage

leverage2(object, ...)  # S3 method for class 'lm'
leverage2(object, param = NULL, data = NULL, ...)

leverage2(object, param = NULL, data = NULL, ...)

leverage2(object, param = NULL, data = NULL, ...)

leverage2(object, param = NULL, data = NULL, ...)
## S3 method for class 'lvmfit'
leverage2(object, param = NULL, data = NULL, ...)

## S3 method for class 'lm2'
leverage2(object, param = NULL, data = NULL, ...)

## S3 method for class 'gls2'
leverage2(object, param = NULL, data = NULL, ...)

## S3 method for class 'lme2'
leverage2(object, param = NULL, data = NULL, ...)

## S3 method for class 'lvmfit2'
leverage2(object, param = NULL, data = NULL, ...)

### Arguments

- **object**: a lm2, gls2, lme2, or lvmfit2 object.
- **...**: arguments to be passed to sCorrect.
- **param**: [optional] the fitted parameters.
- **data**: [optional] the data set.

### Details

The leverage are defined as the partial derivative of the fitted values with respect to the observations.

\[
leverage_i = \frac{\partial \hat{Y}_i}{\partial Y_i}
\]

See Wei et al. (1998).

If argument `param` or `data` is not null, then the small sample size correction is recomputed to correct the residuals.

### Value

A matrix containing the leverage relative to each sample (in rows) and each endogenous variable (in column).

### References


### See Also

`sCorrect` to obtain lm2, gls2, lme2, or lvmfit2 objects.
Examples

```r
## simulate data
set.seed(10)
m <- lvm(Y1~eta,Y2~eta,Y3~eta)
latent(m) <- ~eta
d <- lava::sim(m,20, latent = FALSE)

## standard linear model
e.lm <- lm(Y1~Y2, data = d)
sCorrect(e.lm) <- TRUE
range(as.double(leverage2(e.lm)) - influence(e.lm)$hat)

## latent variable model
e.lvm <- estimate(m, data = d)
sCorrect(e.lvm) <- TRUE
leverage2(e.lvm)
```

---

**matrixPower**

*Power of a Matrix*

**Description**

Compute the power of a matrix.

**Usage**

```r
matrixPower(object, power, symmetric, tol = 1e-12,
            print.warning = TRUE)
```

**Arguments**

- `object` a matrix.
- `power` [numeric] power to be applied to the matrix.
- `symmetric` [logical] is the matrix symmetric? Argument passed to the function `eigen`.
- `tol` [numeric >0] the threshold under which the eigenvalues are set to 0.
- `print.warning` [logical] should a warning be print when some or the eigenvalues are not strictly positive.

**Value**

A matrix.
Examples

```r
## symmetric matrix
set.seed(10)
M <- matrix(rnorm(20*6),20,6)
Sigma <- var(M)
Sigma.half <- matrixPower(Sigma, power = 1/2, symmetric = TRUE)
round(Sigma.half %*% Sigma.half - Sigma,5)

iSigma <- matrixPower(Sigma, power = -1, symmetric = TRUE)
round(iSigma %*% Sigma,5)

iSigma.half <- matrixPower(Sigma, power = -1/2, symmetric = TRUE)
round(iSigma.half %*% iSigma.half - iSigma,5)

## non symmetric matrix
set.seed(10)
M <- matrix(abs(rnorm(9)), 3, 3) + diag(1,3,3)
M-t(M)
iM <- matrixPower(M, power = -1, symmetric = FALSE)
round(iM %*% M,5)
iM.half <- matrixPower(M, power = -1/2, symmetric = FALSE)
round(iM.half %*% iM.half %*% M,5)
```

modelsearch2

Data-driven Extension of a Latent Variable Model

Description

Procedure adding relationship between variables that are supported by the data.

Usage

```r
modelsearch2(object, link, data, method.p.adjust, type.information, alpha, 
nStep, na.omit, trace, cpus)
```

Arguments

- `object` a `lvmfit` object.
- `link` [character, optional for `lvmfit` objects] the name of the additional relationships to consider when expanding the model. Should be a vector containing strings like "Y~X". See the details section.
data [data.frame, optional] the dataset used to identify the model

method.p.adjust [character] the method used to adjust the p-values for multiple comparisons. Can be any method that is valid for the stats::p.adjust function (e.g. "fdr"). Can also be "max", "fastmax", or "gof".

type.information [character] the method used by lava::information to compute the information matrix.

alpha [numeric 0-1] the significance cutoff for the p-values. When the p-value is below, the corresponding link will be added to the model and the search will continue. Otherwise the search will stop.

nStep the maximum number of links that can be added to the model.

na.omit should tests leading to NA for the test statistic be ignored. Otherwise this will stop the selection process.

trace [logical] should the execution of the function be traced?

cpus the number of cpus that can be used for the computations.

Details

method.p.adjust = "max" computes the p-values based on the distribution of the max statistic. This max statistic is the max of the square root of the score statistic. The p-value are computed integrating the multivariate normal distribution.

method.p.adjust = "fastmax" only compute the p-value for the largest statistic. It is faster than "max" and lead to identical results.

method.p.adjust = "gof" keep adding links until the chi-squared test (of correct specification of the covariance matrix) is no longer significant.

Value

A list containing:

• sequenceTest: the sequence of test that has been performed.
• sequenceModel: the sequence of models that has been obtained.
• sequenceQuantile: the sequence of rejection threshold. Optional.
• sequenceIID: the influence functions relative to each test. Optional.
• sequenceSigma: the covariance matrix relative to each test. Optional.
• initialModel: the model before the sequential search.
• statistic: the argument statistic.
• alpha: [numeric 0-1] the significance cutoff for the p-values.
• cv: whether the procedure has converged.
Examples

```r
## simulate data
mSim <- lvm()
regression(mSim) <- c(y1,y2,y3,y4)~u
regression(mSim) <- u~x1+x2
categorical(mSim,labels=c("A","B","C")) <- "x2"
latent(mSim) <- ~u
covariance(mSim) <- y1~y2
transform(mSim, Id~u) <- function(x){1:NROW(x)}
df.data <- lava::sim(mSim, n = 1e2, latent = FALSE)

## only identifiable extensions
m <- lvm(c(y1,y2,y3,y4)~u)
latent(m) <- ~u
addvar(m) <- ~x1+x2
e <- estimate(m, df.data)

## Not run:
resSearch <- modelsearch(e)
resSearch
resSearch2 <- modelsearch2(e, nStep = 2)
resSearch2

## End(Not run)

## some extensions are not identifiable
m <- lvm(c(y1,y2,y3)~u)
latent(m) <- ~u
addvar(m) <- ~x1+x2
e <- estimate(m, df.data)

## Not run:
resSearch <- modelsearch(e)
resSearch
resSearch2 <- modelsearch2(e)
resSearch2

## End(Not run)

## for instance
mNI <- lvm(c(y1,y2,y3)~u)
latent(mNI) <- ~u
covariance(mNI) <- y1~y2
## estimate(mNI, data = df.data)
## does not converge
```
nStep

Find the Number of Steps Performed During the Sequential Testing

Description

Find the number of steps performed during the sequential testing.

Usage

nStep(object)

## S3 method for class 'modelsearch2'
nStep(object)

Arguments

object a modelsearch2 object.

Value

an integer.

Examples

## Not run:
mSim <- lvm(Y~G+X1+X2)
addvar(mSim) <- ~Z1+Z2+Z3+Z4+Z5+Z6
df.data <- lava::sim(mSim, 1e2)

mBase <- lvm(Y~G)
addvar(mBase) <- ~X1+X2+Z1+Z2+Z3+Z4+Z5+Z6
e.lvm <- estimate(mBase, data = df.data)
res <- modelsearch2(e.lvm, method.p.adjust = "holm")
nStep(res)

## End(Not run)
residuals2

Extract Corrected Residuals

Description

Extract correct residuals from a gaussian linear model.

Usage

residuals2(object, param, data, type)

## S3 method for class 'lm'
residuals2(object, param = NULL, data = NULL, 
type = "response")

## S3 method for class 'gls'
residuals2(object, param = NULL, data = NULL, 
type = "response")

## S3 method for class 'lme'
residuals2(object, param = NULL, data = NULL, 
type = "response")

## S3 method for class 'lvmfit'
residuals2(object, param = NULL, data = NULL, 
type = "response")

Arguments

object a lm, gls, lme, or lvmfit object.
par a numeric vector of the fitted parameters.
data [data.frame] the data set.
type [character] the type of residual to extract: "response" for raw residuals, "studentized" for studentized residuals, "normalized" for normalized residuals.

Details

If argument param or data is not null, then the small sample size correction is recomputed to correct the residuals.

The raw residuals are defined by observation minus the fitted value:

$$
\varepsilon = (Y_1 - \mu_1, \ldots, Y_m - \mu_m)
$$

The studentized residuals divided the raw residuals relative to each endogenous variable by the modeled variance of the endogenous variable.

$$
\varepsilon_{stud} = (\frac{Y_1 - \mu_1}{\sigma_1}, \ldots, \frac{Y_m - \mu_m}{\sigma_m})
$$
The normalized residuals multiply the raw residuals by the inverse of the square root of the modeled residual variance covariance matrix.

\[ \varepsilon_{\text{norm}} = \varepsilon \Omega^{-1/2} \]

**Value**

a matrix containing the residuals relative to each sample (in rows) and each endogenous variable (in column).

**See Also**

`sCorrect` to obtain lm2, gls2, lme2, or lvmfit2 objects.

**Examples**

```r
## simulate data
set.seed(10)
m <- lvm(Y1~eta,Y2~eta,Y3~eta)
latent(m) <- ~eta
d <- lava::sim(m,20, latent = FALSE)

## standard linear model
e.lm <- lm(Y1~Y2, data = d)
sCorrect(e.lm) <- TRUE

sigma(e.lm)^2
mean(residuals(e.lm)^2)
mean(residuals2(e.lm)^2)

## latent variable model
e.lvm <- estimate(m, data = d)
sCorrect(e.lvm) <- TRUE
mean(residuals2(e.lvm)^2)
```

**score2**

Extract the Individual Score

**Description**

Extract the individual score from a Gaussian linear model.

**Usage**

```r
score2(object, ...)
```

```r
## S3 method for class 'lm'
score2(object, param = NULL, data = NULL, bias.correct = TRUE, ...)
```
## S3 method for class 'gls'
score2(object, param = NULL, data = NULL,
       bias.correct = TRUE, ...)

## S3 method for class 'lme'
score2(object, param = NULL, data = NULL,
       bias.correct = TRUE, ...)

## S3 method for class 'lvmfit'
score2(object, param = NULL, data = NULL,
       bias.correct = TRUE, ...)

## S3 method for class 'lm2'
score2(object, param = NULL, data = NULL, ...)

## S3 method for class 'gls2'
score2(object, param = NULL, data = NULL, ...)

## S3 method for class 'lme2'
score2(object, param = NULL, data = NULL, ...)

## S3 method for class 'lvmfit2'
score2(object, param = NULL, data = NULL, ...)

### Arguments

- **object**: a linear model or a latent variable model
- **...**: arguments to be passed to sCorrect.
- **param**: [optional] the fitted parameters.
- **data**: [optional] the data set.
- **bias.correct**: [logical] should the standard errors of the coefficients be corrected for small sample bias? Only relevant if the sCorrect function has not yet be applied to the object.

### Details

If argument p or data is not null, then the small sample size correction is recomputed to correct the influence function.

### Value

A matrix containing the score relative to each sample (in rows) and each model coefficient (in columns).

### See Also

sCorrect to obtain lm2, gls2, lme2, or lvmfit2 objects.
Examples

\[
\begin{align*}
n &\leftarrow 5e1 \\
p &\leftarrow 3 \\
X.name &\leftarrow paste0("X",1:p) \\
link.lvm &\leftarrow paste0("Y~",X.name) \\
formula.lvm &\leftarrow as.formula(paste0("Y~",paste0(X.name,collapse="+"))) \\
\end{align*}
\]

\[
\begin{align*}
m &\leftarrow lvm(formula.lvm) \\
distribution(m,-Id) &\leftarrow Sequence.lvm(0) \\
set.seed(10) \\
d &\leftarrow lava::sim(m,n) \\
\end{align*}
\]

## linear model
\[
\begin{align*}
e.lm &\leftarrow lm(formula.lvm, data=d) \\
score.tempo &\leftarrow score2(e.lm, bias.correct = FALSE) \\
colMeans(score.tempo) \\
\end{align*}
\]

## latent variable model
\[
\begin{align*}
e.lvm &\leftarrow estimate(lvm(formula.lvm), data=d) \\
score.tempo &\leftarrow score2(e.lvm, bias.correct = FALSE) \\
range(score.tempo-score(e.lvm, indiv = TRUE)) \\
\end{align*}
\]

sCorrect  Satterthwaite Correction and Small Sample Correction

Description

Correct the bias of the ML estimate of the variance and compute the first derivative of the information matrix.

Usage

\[
sCorrect(object, adjust.Omega, adjust.n, df, numeric.derivative, param, data, tol, n.iter, trace, ...) \\
\]

## S3 method for class 'lm'
\[
sCorrect(object, adjust.Omega = TRUE, adjust.n = TRUE, \\
df = TRUE, numeric.derivative = FALSE, param = NULL, data = NULL, \\
tol = 1e-05, n.iter = 20, trace = 0, ...) \\
\]

## S3 method for class 'lm2'
\[
sCorrect(object, ...) \\
\]

## S3 method for class 'gls'
\[
sCorrect(object, adjust.Omega = TRUE, adjust.n = TRUE, \\
df = TRUE, numeric.derivative = FALSE, param = NULL, data = NULL, \\
tol = 1e-05, n.iter = 20, trace = 0, cluster, ...) \\
\]
## S3 method for class 'gls2'
sCorrect(object, ...)

## S3 method for class 'lme'
sCorrect(object, adjust.Omega = TRUE, adjust.n = TRUE,
          df = TRUE, numeric.derivative = FALSE, param = NULL, data = NULL,
          tol = 1e-05, n.iter = 20, trace = 0, cluster, ...)

## S3 method for class 'lme2'
sCorrect(object, ...)

## S3 method for class 'lvmfit'
sCorrect(object, adjust.Omega = TRUE, adjust.n = TRUE,
          df = TRUE, numeric.derivative = FALSE, param = NULL, data = NULL,
          tol = 1e-05, n.iter = 20, trace = 0, ...)

## S3 method for class 'lvmfit2'
sCorrect(object, ...)

sCorrect(x, ...) <- value

## S3 replacement method for class 'lm'
sCorrect(x, ...) <- value

## S3 replacement method for class 'lm2'
sCorrect(x, ...) <- value

## S3 replacement method for class 'gls'
sCorrect(x, ...) <- value

## S3 replacement method for class 'gls2'
sCorrect(x, ...) <- value

## S3 replacement method for class 'lme'
sCorrect(x, ...) <- value

## S3 replacement method for class 'lme2'
sCorrect(x, ...) <- value

## S3 replacement method for class 'lvmfit'
sCorrect(x, ...) <- value

## S3 replacement method for class 'lvmfit2'
sCorrect(x, ...) <- value

Arguments

object, x  a gls, lme, or lvm object.
adjust.Omega [logical] should the standard errors of the coefficients be corrected for small sample bias?

adjust.n [logical] should the correction for the degree of freedom be performed?

df [logical] should the degree of freedoms of the Wald statistic be computed using the Satterthwaite correction? Otherwise the degree of freedoms are set to Inf, i.e. a normal distribution is used instead of a Student’s t distribution when computing the p-values.

numeric.derivative [logical] should a numerical derivative be used to compute the first derivative of the information matrix? Otherwise an analytic formula is used.

param [numeric vector, optional] the values of the parameters at which to perform the correction.

data [data.frame, optional] the dataset relative to which the correction should be performed.

tol [numeric >0] the minimum absolute difference between two estimation of the small sample bias. Below this value, the algorithm used to estimate the bias stop.

n.iter [integer >0] the maximum number of iterations used to estimate the small sample bias of the residual variance-covariance matrix.

trace [logical] should the execution of the function be traced.

value [logical] value for the arguments adjust.Omega and adjust.n.

Details

The argument value is equivalent to the argument bias.correct of the function summary2.

Examples

```r
n <- 5e1
p <- 3
X.name <- paste0("X",1:p)
link.lvm <- paste0("Y","X.name")
formula.lvm <- as.formula(paste0("Y","paste0(X.name,collapse="+")))

m <- lvm(formula.lvm)
distribution(m,~Id) <- Sequence.lvm(0)
set.seed(10)
d <- lava::sim(m,n)

## linear model
e.lm <- lm(formula.lvm,data=d)
system.time(
sCorrect(e.lm) <- TRUE ## i.e. bias.correct = TRUE
)
```
## gls model
library(nlme)
e.gls <- gls(formula.lvm, data = d, method = "ML")
sCorrect(e.gls, cluster = 1:NROW(d)) <- TRUE ## i.e. bias.correct = TRUE
summary2(e.gls)

## latent variable model
e.lvm <- estimate(lvm(formula.lvm), data = d)
sCorrect(e.lvm) <- TRUE ## i.e. bias.correct = TRUE
summary2(e.lvm)

---

### setLink

**Set a Link to a Value**

**Description**
Generic interface to set a value to a link in a `lvm` object.

**Usage**
setLink(object, ...)

```
## S3 method for class 'lvm'
setLink(object, var1, var2, value, warnings = FALSE, ...)
```

**Arguments**
- `object`: a `lvm` object.
- `...`: [internal] only used by the generic method.
- `var1`: [character or formula] the exogenous variable of the new link or a formula describing the link to be added to the `lvm`.
- `var2`: [character] the endogenous variable of the new link. Disregarded if the argument `var1` is a formula.
- `value`: [numeric] the value at which the link should be set.
- `warnings`: [logical] should a warning be displayed if the link is not found in the `lvm` object.

**Examples**
library(lava)
set.seed(10)

```
m <- lvm()
regression(m) <- c(y1,y2,y3)~u
regression(m) <- u~x1+x2
latent(m) <- ~u
covariance(m) <- y1 ~ y2
```
m₁ <- setLink(m, y₃ ~ u, value = 1)
estimate(m₁, lava::sim(m, 1e2))
# m₁ <- setLink(m, u ~ y₃, value = 1)

m₂ <- setLink(m, y₁ ~ y₂, value = 0.5)
estimate(m₂, lava::sim(m, 1e2))

summary.calibrateType1

Display the Type 1 Error Rate

Description

Display the type 1 error rate from the simulation results.

Usage

## S3 method for class 'calibrateType1'
summary(object, robust = FALSE, type = "type1error", alpha = 0.05, log.transform = TRUE, digits = 5, print = TRUE, ...)

Arguments

object output of the calibrateType1 function.
robust [character] should the results be displayed for both model-based and robust standard errors (TRUE), only model-based standard error (FALSE), or only robust standard error ("only")?
type [character] should the type 1 error rate be displayed ("type1error") or the bias ("bias").
alpha [numeric, 0-1] the confidence levels.
log.transform [logical] should the confidence intervals be computed on the logit scale.
digits [integer >0] the number of decimal places to use when displaying the summary.
print should the summary be printed in the terminal.
... [internal] only used by the generic method.
**summary2**  

**summary2** Summary with Small Sample Correction

**Description**  
Summary with small sample correction.

**Usage**  

```r  
summary2(object, ...)  
```

## S3 method for class 'lm'  
summary2(object, df = TRUE, bias.correct = TRUE, ...)  

## S3 method for class 'gls'  
summary2(object, df = TRUE, bias.correct = TRUE,  
cluster = NULL, ...)  

## S3 method for class 'lme'  
summary2(object, df = TRUE, bias.correct = TRUE, ...)  
```
## S3 method for class 'lvmfit'
summary2(object, df = TRUE, bias.correct = TRUE, ...)

## S3 method for class 'lm2'
summary2(object, digit = max(3,getOption("digit")),
          robust = FALSE, df = TRUE, ...)

## S3 method for class 'gls2'
summary2(object, digit = max(3,getOption("digit")),
          robust = FALSE, df = TRUE, ...)

## S3 method for class 'lme2'
summary2(object, digit = max(3,getOption("digit")),
          robust = FALSE, df = TRUE, ...)

## S3 method for class 'lvmfit2'
summary2(object, cluster = NULL, robust = FALSE,
          df = TRUE, ...)

### Arguments

- **object**
  - a gls, lme or lvm object.
- ... arguments passed to the summary method of the object.
- **df**
  - [logical] should the degree of freedoms of the Wald statistic be computed using the Satterthwaite correction? Otherwise the degree of freedoms are set to Inf, i.e. a normal distribution is used instead of a Student's t distribution when computing the p-values.
- **bias.correct**
  - [logical] should the standard errors of the coefficients be corrected for small sample bias? See `sCorrect` for more details.
- **cluster**
  - [integer vector] the grouping variable relative to which the observations are iid.
- **digit**
  - [integer > 0] the number of decimal places to use when displaying the summary.
- **robust**
  - [logical] should the robust standard errors be used instead of the model based standard errors?

### Details

`summary2` is the same as `summary` except that it first computes the small sample correction (but does not store it). So if `summary2` is to be called several times, it is more efficient to pre-compute the quantities for the small sample correction using `sCorrect` and then call `summary2`.

### See Also

- `sCorrect` for more detail about the small sample correction.

### Examples

```r
m <- lvm(Y~X1+X2)
set.seed(10)
```
d <- lava::sim(m, 2e1)

## Gold standard
summary(lm(Y~X1+X2, d))$coef

## gls models
library(nlme)
e.gls <- gls(Y~X1+X2, data = d, method = "ML")
summary(e.gls)$tTable
sCorrect(e.gls, cluster = 1:NROW(d)) <- FALSE ## no small sample correction
summary2(e.gls)$tTable
sCorrect(e.gls, cluster = 1:NROW(d)) <- TRUE ## small sample correction
summary2(e.gls)$tTable

## lvm models
e.lvm <- estimate(m, data = d)
summary(e.lvm)$coef
sCorrect(e.lvm) <- FALSE ## no small sample correction
summary2(e.lvm)$coef
sCorrect(e.lvm) <- TRUE ## small sample correction
summary2(e.lvm)$coef

---

tryWithWarnings Run an Expression and Catch Warnings and Errors

Description

Similar to `try` but also returns warnings.

Usage

`tryWithWarnings(expr)`

Arguments

`expr` the line of code to be evaluated

Details

Value
A list containing:

- value the result of the evaluation of the expression
- warnings warning(s) generated during the evaluation of the expression
- error error generated during the evaluation of the expression

Examples

FctTest <- function(x){
  return(log(x))
}
tryWithWarnings(FctTest(-1))
tryWithWarnings(FctTest(1))
tryWithWarnings(FctTest(xxxx))

vcov2

Extract the Variance Covariance Matrix of the Model Parameters

Description
Extract the variance covariance matrix of the model parameters from a Gaussian linear model.

Usage

vcov2(object, ...)

## S3 method for class 'lm'
vcov2(object, param = NULL, data = NULL,
       bias.correct = TRUE, ...)

## S3 method for class 'gls'
vcov2(object, param = NULL, data = NULL,
       bias.correct = TRUE, ...)

## S3 method for class 'lme'
vcov2(object, param = NULL, data = NULL,
       bias.correct = TRUE, ...)

## S3 method for class 'lvmfit'
vcov2(object, param = NULL, data = NULL,
       bias.correct = TRUE, ...)

## S3 method for class 'lm2'
vcov2(object, param = NULL, data = NULL, ...)

## S3 method for class 'gls2'
vcov2(object, param = NULL, data = NULL, ...)

## S3 method for class 'lme2'
vcov2(object, param = NULL, data = NULL, ...)

## S3 method for class 'lvmfit2'
vcov2(object, param = NULL, data = NULL, ...)

### Arguments

- **object**: a linear model or a latent variable model
- **...**: arguments to be passed to sCorrect.
- **param**: [optional] the fitted parameters.
- **data**: [optional] the data set.
- **bias.correct**: [logical] should the standard errors of the coefficients be corrected for small sample bias? Only relevant if the sCorrect function has not yet be applied to the object.

### Details

If argument `p` or `data` is not null, then the small sample size correction is recomputed to correct the influence function.

### Value

A matrix.

### See Also

- `sCorrect` to obtain `lm2`, `gls2`, `lme2`, or `lvmfit2` objects.

### Examples

```r
n <- 5e1
p <- 3
X.name <- paste0("X",1:p)
link.lvm <- paste0("Y","",X.name)
formula.lvm <- as.formula(paste0("Y","",paste0(X.name,collapse="+")))

m <- lvm(formula.lvm)
distribution(m,~1d) <- Sequence.lvm(0)
set.seed(10)
d <- lava::sim(m,n)

## linear model
e.lm <- lm(formula.lvm, data=d)
v cov2.temp <- vcov2(e.lm, bias.correct = TRUE)
v cov2.temp[rownames(v cov2(e.lm)), colnames(v cov2(e.lm))]/vcov(e.lm)
```
## latent variable model

e.lvm <- estimate(lvm(formula.lvm), data=d)
vcov.tempo <- vcov2(e.lvm, bias.correct = FALSE)
vcov.tempo/vcov(e.lvm)
Index

.compare2(compare2), 22
.addLink, 3
.autoplot.calibrateType1
    (autoplot_calibrateType1), 5
.autoplot.intDensTri, 4
.autoplot.modelsearch2
    (autplot-modelsearch2), 6
.autoplot_calibrateType1, 5
.autoplot-modelsearch2, 6
.calcDistMax, 7
.calcDistMaxBootstrap (calcDistMax), 7
.calcDistMaxIntegral (calcDistMax), 7
.calcType1postSelection, 9
.calibrateType1, 5, 11, 50
.checkData, 14
.clean, 15
.coefByType, 16
.coefCov (coefByType), 16
.coefExtra (coefByType), 16
.coefIndexModel (coefByType), 16
.coefIntercept (coefByType), 16
.coefRef (coefByType), 16
.coefReg (coefByType), 16
.coefType, 19
.coefVar (coefByType), 16
.combineFormula, 21
.compare2, 22, 50
.convFormulaCharacter, 25
.createContrast, 24, 25, 39, 40, 50
.dSigma, 28
.dSigmaRobust, 28
.effects2, 29
.estfun, 30
.extractData, 31
.findNewLink, 33

.formula2character
    (convFormulaCharacter), 25

.getNewLink, 34
.getNewModel, 35
.getStep, 36
.getVarCov2, 37, 50
.glht2, 39, 50

.iid2, 41
.iidJack, 43, 50
.information2, 45
.initVarLink, 47
.initVarLinks (initVarLink), 47
.intDensTri, 4, 10, 48

.lavaSearch2, 50
.lavaSearch2, (lavaSearch2), 50
.lavaSearch2-package (lavaSearch2), 50
.leverage2, 51

.matrixPower, 53
.modelsearch2, 50, 54

.nStep, 57

.residuals2, 58

.score2, 59
.sCorrect, 24, 40, 42, 46, 52, 59, 60, 61, 67, 70
.sCorrect<-(sCorrect), 61
.setLink, 64
.summary.calibrateType1, 65
.summary.modelsearch2, 66
.summary2, 50, 66

.tryWithWarnings, 68

.vcov2, 69