

Package ‘lava’

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Type Package

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BugReports <https://github.com/kkholst/lava/issues>

License GPL-3

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lava-package	<i>Estimation and simulation of latent variable models</i>
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Description

Framework for estimating parameters and simulate data from Latent Variable Models.

Author(s)

Klaus K. Holst Maintainer: <k.k.holst@biostat.ku.dk>

Examples

lava()

addvar	<i>Add variable to (model) object</i>
--------	---------------------------------------

Description

Generic method for adding variables to model object

Usage

addvar(x, ...)

Arguments

- x Model object
- ... Additional arguments

Author(s)

Klaus K. Holst

backdoor	<i>Backdoor criterion</i>
----------	---------------------------

Description

Check backdoor criterion of a lvm object

Usage

```
backdoor(object, f, cond, ..., return.graph = FALSE)
```

Arguments

object	lvm object
f	formula. Conditioning, z, set can be given as $y \sim x z$
cond	Vector of variables to conditon on
...	Additional arguments to lower level functions
return.graph	Return moral ancestral graph with z and effects from x removed

Examples

```
m <- lvm(y~c2,c2~c1,x~c1,m1~x,y~m1, v1~c3, x~c3,v1~y,
        x~z1, z2~z1, z2~z3, y~z3+z2+g1+g2+g3)
ll <- backdoor(m, y~x)
backdoor(m, y~x|c1+z1+g1)
```

baptize	<i>Label elements of object</i>
---------	---------------------------------

Description

Generic method for labeling elements of an object

Usage

```
baptize(x, ...)
```

Arguments

x	Object
...	Additional arguments

Author(s)

Klaus K. Holst

blockdiag	<i>Combine matrices to block diagonal structure</i>
-----------	---

Description

Combine matrices to block diagonal structure

Usage

```
blockdiag(x, ..., pad = 0)
```

Arguments

x	Matrix
...	Additional matrices
pad	Value outside block-diagonal

Author(s)

Klaus K. Holst

Examples

```
A <- diag(3)+1
blockdiag(A,A,A,pad=NA)
```

bmd	<i>Longitudinal Bone Mineral Density Data (Wide format)</i>
-----	---

Description

Bone Mineral Density Data consisting of 112 girls randomized to receive calcium or placebo. Longitudinal measurements of bone mineral density (g/cm^2) measured approximately every 6th month in 3 years.

Format

data.frame

Source

Vonesh & Chinchilli (1997), Table 5.4.1 on page 228.

See Also

calcium

bmidata	<i>Data</i>
---------	-------------

Description

Description

Format

data.frame

bootstrap	<i>Generic bootstrap method</i>
-----------	---------------------------------

Description

Generic method for calculating bootstrap statistics

Usage

bootstrap(x, ...)

Arguments

x	Model object
...	Additional arguments

Author(s)

Klaus K. Holst

See Also

bootstrap.lvm bootstrap.lvmfit

bootstrap.lvm	<i>Calculate bootstrap estimates of a lvm object</i>
---------------	--

Description

Draws non-parametric bootstrap samples

Usage

```
## S3 method for class 'lvm'
bootstrap(x,R=100,data,fun=NULL,control=list(),
          p, parametric=FALSE, bollenstine=FALSE,
          constraints=TRUE,sd=FALSE,silent=FALSE,
          parallel=lava.options()$parallel,
          mc.cores=NULL,
          ...)

## S3 method for class 'lvmfit'
bootstrap(x,R=100,data=model.frame(x),
          control=list(start=coef(x)),
          p=coef(x), parametric=FALSE, bollenstine=FALSE,
          estimator=x$estimator,weights=Weights(x),...)
```

Arguments

x	lvm-object.
R	Number of bootstrap samples
data	The data to resample from
fun	Optional function of the (bootstrapped) model-fit defining the statistic of interest
control	Options to the optimization routine
p	Parameter vector of the null model for the parametric bootstrap
parametric	If TRUE a parametric bootstrap is calculated. If FALSE a non-parametric (row-sampling) bootstrap is computed.
bollenstine	Bollen-Stine transformation (non-parametric bootstrap) for bootstrap hypothesis testing.
constraints	Logical indicating whether non-linear parameter constraints should be included in the bootstrap procedure
sd	Logical indicating whether standard error estimates should be included in the bootstrap procedure
silent	Suppress messages
parallel	If TRUE parallel backend will be used
mc.cores	Number of threads (if NULL foreach::foreach will be used, otherwise parallel::mclapply)

- ... Additional arguments, e.g. choice of estimator.
- estimator String definining estimator, e.g. 'gaussian' (see estimator)
- weights Optional weights matrix used by estimator

Value

A bootstrap.lvm object.

Author(s)

Klaus K. Holst

See Also

[confint.lvmfit](#)

Examples

```
m <- lvm(y~x)
d <- sim(m,100)
e <- estimate(y~x, d)
## Reduce Ex.Timings
B <- bootstrap(e,R=50,parallel=FALSE)
B
```

brisa	<i>Simulated data</i>
-------	-----------------------

Description

Simulated data

Format

data.frame

Source

Simulated

By	<i>Apply a Function to a Data Frame Split by Factors</i>
----	--

Description

Apply a Function to a Data Frame Split by Factors

Usage

By(x, INDICES, FUN, COLUMNS, array = FALSE, ...)

Arguments

x	Data frame
INDICES	Indices (vector or list of indices, vector of column names, or formula of column names)
FUN	A function to be applied to data frame subsets of 'data'.
COLUMNS	(Optional) subset of columns of x to work on
array	if TRUE an array/matrix is always returned
...	Additional arguments to lower-level functions

Details

Simple wrapper of the 'by' function

Author(s)

Klaus K. Holst

Examples

By(datasets::C02,~Treatment+Type,colMeans,~conc)
By(datasets::C02,~Treatment+Type,colMeans,~conc+uptake)

calcium	<i>Longitudinal Bone Mineral Density Data</i>
---------	---

Description

Bone Mineral Density Data consisting of 112 girls randomized to receive calcium og placebo. Longitudinal measurements of bone mineral density (g/cm^2) measured approximately every 6th month in 3 years.

Format

A data.frame containing 560 (incomplete) observations. The 'person' column defines the individual girls of the study with measurements at visiting times 'visit', and age in years 'age' at the time of visit. The bone mineral density variable is 'bmd' (g/cm²).

Source

Vonesh & Chinchilli (1997), Table 5.4.1 on page 228.

cancel	<i>Generic cancel method</i>
--------	------------------------------

Description

Generic cancel method

Usage

```
cancel(x, ...)
```

Arguments

x	Object
...	Additional arguments

Author(s)

Klaus K. Holst

children	<i>Extract children or parent elements of object</i>
----------	--

Description

Generic method for memberships from object (e.g. a graph)

Usage

```
children(object, ...)
```

Arguments

object	Object
...	Additional arguments

Author(s)

Klaus K. Holst

click	<i>Identify points on plot</i>
-------	--------------------------------

Description

Extension of the identify function

Usage

```
## Default S3 method:  
click(x, y=NULL, label=TRUE, n=length(x), pch=19, col="orange", cex=3, ...)  
idplot(x,y,...,id=list())
```

Arguments

x	X coordinates
...	Additional arguments parsed to plot function
y	Y coordinates
label	Should labels be added?
n	Max number of inputs to expect
pch	Symbol
col	Colour
cex	Size
id	List of arguments parsed to click function

Details

For the usual 'X11' device the identification process is terminated by pressing any mouse button other than the first. For the 'quartz' device the process is terminated by pressing either the pop-up menu equivalent (usually second mouse button or 'Ctrl'-click) or the 'ESC' key.

Author(s)

Klaus K. Holst

See Also

[idplot](#), [identify](#)

Examples

```

if (interactive()) {
  n <- 10; x <- seq(n); y <- runif(n)
  plot(y ~ x); click(x,y)

  data(iris)
  l <- lm(Sepal.Length ~ Sepal.Width*Species,iris)
  res <- plotConf(l,var2="Species")## ylim=c(6,8), xlim=c(2.5,3.3))
  with(res, click(x,y))

  with(iris, idplot(Sepal.Length,Petal.Length))
}

```

closed.testing	<i>Closed testing procedure</i>
----------------	---------------------------------

Description

Closed testing procedure

Usage

```

closed.testing(object, idx = seq_along(coef(object)), null = rep(0,
  length(idx)), ...)

```

Arguments

object	estimate object
idx	Index of parameters to adjust for multiple testing
null	Null hypothesis value
...	Additional arguments

Examples

```

m <- lvm()
regression(m, c(y1,y2,y3,y4,y5,y6,y7)~x) <- c(0,0.25,0,0.25,0.25,0,0)
regression(m, to=endogenous(m), from="u") <- 1
variance(m,endogenous(m)) <- 1
set.seed(2)
d <- sim(m,200)
l1 <- lm(y1~x,d)
l2 <- lm(y2~x,d)
l3 <- lm(y3~x,d)
l4 <- lm(y4~x,d)
l5 <- lm(y5~x,d)
l6 <- lm(y6~x,d)
l7 <- lm(y7~x,d)

```

```
(a <- merge(l1,l2,l3,l4,l5,l6,l7,subset=2))
if (requireNamespace("mets",quietly=TRUE)) {
  p.correct(a)
}
as.vector(closed.testing(a))
```

Col

Generate a transparent RGB color

Description

This function transforms a standard color (e.g. "red") into an transparent RGB-color (i.e. α -blend<1).

Usage

```
Col(col, alpha = 0.2, locate = 0)
```

Arguments

col	Color (numeric or character)
alpha	Degree of transparency (0,1)
locate	Choose colour (with mouse)

Details

This only works for certain graphics devices (Cairo-X11 (x11 as of R>=2.7), quartz, pdf, ...).

Value

A character vector with elements of 7 or 9 characters, '"\#"' followed by the red, blue, green and optionally alpha values in hexadecimal (after rescaling to '0 ... 255').

Author(s)

Klaus K. Holst

Examples

```
plot(runif(1000),cex=runif(1000,0,4),col=Col(c("darkblue","orange"),0.5),pch=16)
```

colorbar	<i>Add color-bar to plot</i>
----------	------------------------------

Description

Add color-bar to plot

Usage

```
colorbar(clut = Col(rev(rainbow(11, start = 0, end = 0.69))), alpha,
  x.range = c(-0.5, 0.5), y.range = c(-0.1, 0.1), values = seq(clut),
  digits = 2, label.offset, srt = 45, cex = 0.5, border = NA,
  alpha = 0.5, position = 1, direction = c("horizontal", "vertical"), ...)
```

Arguments

clut	Color look-up table
x.range	x range
y.range	y range
values	label values
digits	number of digits
label.offset	label offset
srt	rotation of labels
cex	text size
border	border of color bar rectangles
alpha	Alpha (transparency) level 0-1
position	Label position left/bottom (1) or top/right (2) or no text (0)
direction	horizontal or vertical color bars
...	additional low level arguments (i.e. parsed to text)

Examples

```
## Not run:
plotNeuro(x,roi=R,mm=-18,range=5)
colorbar(clut=Col(rev(rainbow(11,start=0,end=0.69))),0.5),
  x=c(-40,40),y.range=c(84,90),values=c(-5:5))

colorbar(clut=Col(rev(rainbow(11,start=0,end=0.69))),0.5),
  x=c(-10,10),y.range=c(-100,50),values=c(-5:5),
  direction="vertical",border=1)

## End(Not run)
```

Combine

*Report estimates across different models***Description**

Report estimates across different models

Usage

Combine(x, ...)

Arguments

x list of model objects

... additional arguments to lower level functions

Author(s)

Klaus K. Holst

Examples

```
data(serotonin)
m1 <- lm(cau ~ age*gene1 + age*gene2,data=serotonin)
m2 <- lm(cau ~ age + gene1,data=serotonin)
m3 <- lm(cau ~ age*gene2,data=serotonin)

Combine(list(A=m1,B=m2,C=m3),fun=function(x)
  c("-----"=="",R2=" " %+ %format(summary(x)$r.squared,digits=2)))
```

commutation

*Finds the unique commutation matrix***Description**Finds the unique commutation matrix K : $K \text{vec}(A) = \text{vec}(A^t)$ **Usage**

commutation(m, n = m)

Arguments

m rows

n columns

Author(s)

Klaus K. Holst

compare

*Statistical tests***Description**

Performs Likelihood-ratio, Wald and score tests

Usage

compare(object, ...)

Arguments

object	lvmfit-object
...	Additional arguments to low-level functions

Value

Matrix of test-statistics and p-values

Author(s)

Klaus K. Holst

See Also[modelsearch](#), [equivalence](#)**Examples**

```

m <- lvm();
regression(m) <- c(y1,y2,y3) ~ eta; latent(m) <- ~eta
regression(m) <- eta ~ x
m2 <- regression(m, c(y3,eta) ~ x)
set.seed(1)
d <- sim(m,1000)
e <- estimate(m,d)
e2 <- estimate(m2,d)

compare(e)

compare(e,e2) ## LRT, H0: y3<-x=0
compare(e,scoretest=y3~x) ## Score-test, H0: y3~x=0
compare(e2,par=c("y3~x")) ## Wald-test, H0: y3~x=0

B <- diag(2); colnames(B) <- c("y2~eta","y3~eta")

```

```
compare(e2,contrast=B,null=c(1,1))

B <- rep(0,length(coef(e2))); B[1:3] <- 1
compare(e2,contrast=B)

compare(e,scoretest=list(y3~x,y2~x))
```

complik

Composite Likelihood for probit latent variable models

Description

Estimate parameters in a probit latent variable model via a composite likelihood decomposition.

Usage

```
complik(x, data, k = 2, type = c("nearest", "all"), pairlist,
  silent = TRUE, estimator = "normal", ...)
```

Arguments

x	lvm-object
data	data.frame
k	Size of composite groups
type	Determines number of groups. With type="nearest" (default) only neighboring items will be grouped, e.g. for k=2 (y1,y2),(y2,y3),... With type="all" all combinations of size k are included
pairlist	A list of indices specifying the composite groups. Optional argument which overrides k and type but gives complete flexibility in the specification of the composite likelihood
silent	Turn output messages on/off
estimator	Model (pseudo-likelihood) to use for the pairs/groups
...	Additional arguments parsed on to lower-level functions

Value

An object of class clprobit inheriting methods from lvm

Author(s)

Klaus K. Holst

See Also

estimate

confband	<i>Add Confidence limits bar to plot</i>
----------	--

Description

Add Confidence limits bar to plot

Usage

```
confband(x, lower, upper, center = NULL, line = TRUE, delta = 0.07,  
         centermark = 0.03, pch, blank = TRUE, vert = TRUE, polygon = FALSE,  
         step = FALSE, ...)
```

Arguments

x	Position (x-coordinate if vert=TRUE, y-coordinate otherwise)
lower	Lower limit (if NULL no limits is added, and only the center is drawn (if not NULL))
upper	Upper limit
center	Center point
line	If FALSE do not add line between upper and lower bound
delta	Length of limit bars
centermark	Length of center bar
pch	Center symbol (if missing a line is drawn)
blank	If TRUE a white ball is plotted before the center is added to the plot
vert	If TRUE a vertical bar is plotted. Otherwise a horizontal bar is used
polygon	If TRUE polygons are added between 'lower' and 'upper'.
step	Type of polygon (step-function or piecewise linear)
...	Additional low level arguments (e.g. col, lwd, lty,...)

Author(s)

Klaus K. Holst

See Also

confband

Examples

```

plot(0,0,type="n",xlab="",ylab="")
confband(0.5,-0.5,0.5,0,col="darkblue")
confband(0.8,-0.5,0.5,0,col="darkred",vert=FALSE,pch=1,cex=1.5)

set.seed(1)
K <- 20
est <- rnorm(K)
se <- runif(K,0.2,0.4)
x <- cbind(est,est-2*se,est+2*se,runif(K,0.5,2))
x[c(3:4,10:12),] <- NA
rownames(x) <- unlist(lapply(letters[seq(K)],function(x) paste(rep(x,4),collapse="")))
rownames(x)[which(is.na(est))] <- ""
signif <- sign(x[,2])==sign(x[,3])
forestplot(x,text.right=FALSE)
forestplot(x[, -4],sep=c(2,15),col=signif+1,box1=TRUE,delta=0.2,pch=16,cex=1.5)
forestplot(x,vert=TRUE,text=FALSE)
forestplot(x,vert=TRUE,text=FALSE,pch=NA)
##forestplot(x,vert=TRUE,text.vert=FALSE)
##forestplot(val,vert=TRUE,add=TRUE)

z <- seq(10)
zu <- c(z[-1],10)
plot(z,type="n")
confband(z,zu,rep(0,length(z)),col=Col("darkblue"),polygon=TRUE,step=TRUE)
confband(z,zu,zu-2,col=Col("darkred"),polygon=TRUE,step=TRUE)

z <- seq(0,1,length.out=100)
plot(z,z,type="n")
confband(z,z,z^2,polygon="TRUE",col=Col("darkblue"))

set.seed(1)
k <- 10
x <- seq(k)
est <- rnorm(k)
sd <- runif(k)
val <- cbind(x,est,est-sd,est+sd)
par(mfrow=c(1,2))
plot(0,type="n",xlim=c(0,k+1),ylim=range(val[, -1]),axes=FALSE,xlab="",ylab="")
axis(2)
confband(val[,1],val[,3],val[,4],val[,2],pch=16,cex=2)
plot(0,type="n",ylim=c(0,k+1),xlim=range(val[, -1]),axes=FALSE,xlab="",ylab="")
axis(1)
confband(val[,1],val[,3],val[,4],val[,2],pch=16,cex=2,vert=FALSE)

```

confint.lvmfit

Calculate confidence limits for parameters

Description

Calculate Wald og Likelihood based (profile likelihood) confidence intervals

Usage

```
## S3 method for class 'lvmfit'
confint(object, parm = seq_len(length(coef(object))),
  level = 0.95, profile = FALSE, curve = FALSE, n = 20,
  interval = NULL, lower = TRUE, upper = TRUE, ...)
```

Arguments

object	lvm-object.
parm	Index of which parameters to calculate confidence limits for.
level	Confidence level
profile	Logical expression defining whether to calculate confidence limits via the profile log likelihood
curve	if FALSE and profile is TRUE, confidence limits are returned. Otherwise, the profile curve is returned.
n	Number of points to evaluate profile log-likelihood in over the interval defined by interval
interval	Interval over which the profiling is done
lower	If FALSE the lower limit will not be estimated (profile intervals only)
upper	If FALSE the upper limit will not be estimated (profile intervals only)
...	Additional arguments to be passed to the low level functions

Details

Calculates either Wald confidence limits:

$$\hat{\theta} \pm z_{\alpha/2} * \hat{\sigma}_{\hat{\theta}}$$

or profile likelihood confidence limits, defined as the set of value τ :

$$\log Lik(\hat{\theta}_{\tau}, \tau) - \log Lik(\hat{\theta}) < q_{\alpha}/2$$

where q_{α} is the α fractile of the χ^2_1 distribution, and $\hat{\theta}_{\tau}$ are obtained by maximizing the log-likelihood with tau being fixed.

Value

A 2xp matrix with columns of lower and upper confidence limits

Author(s)

Klaus K. Holst

See Also

[bootstrap{lvm}](#)

Examples

```
m <- lvm(y~x)
d <- sim(m,100)
e <- estimate(y~x, d)
confint(e,3,profile=TRUE)
confint(e,3)
## Reduce Ex.timings
B <- bootstrap(e,R=50)
B
```

constrain<-	<i>Add non-linear constraints to latent variable model</i>
-------------	--

Description

Add non-linear constraints to latent variable model

Usage

```
## Default S3 replacement method:
constrain(x,par,args,...) <- value

## S3 replacement method for class 'multigroup'
constrain(x,par,k=1,...) <- value

constraints(object,data=model.frame(object),vcov=object$vcov,level=0.95,
            p=pars.default(object),k,idx,...)
```

Arguments

x	lvm-object
...	Additional arguments to be passed to the low level functions
value	Real function taking args as a vector argument
par	Name of new parameter. Alternatively a formula with lhs specifying the new parameter and the rhs defining the names of the parameters or variable names defining the new parameter (overruling the args argument).
args	Vector of variables names or parameter names that are used in defining par
k	For multigroup models this argument specifies which group to add/extract the constraint
object	lvm-object
data	Data-row from which possible non-linear constraints should be calculated
vcov	Variance matrix of parameter estimates
level	Level of confidence limits
p	Parameter vector
idx	Index indicating which constraints to extract

Details

Add non-linear parameter constraints as well as non-linear associations between covariates and latent or observed variables in the model (non-linear regression).

As an example we will specify the follow multiple regression model:

$$E(Y|X_1, X_2) = \alpha + \beta_1 X_1 + \beta_2 X_2$$

$$V(Y|X_1, X_2) = v$$

which is defined (with the appropriate parameter labels) as

```
m <- lvm(y ~ f(x,beta1) + f(x,beta2))
```

```
intercept(m) <- y ~ f(alpha)
```

```
covariance(m) <- y ~ f(v)
```

The somewhat strained parameter constraint

$$v = \frac{(\beta_1 - \beta_2)^2}{\alpha}$$

can then specified as

```
constrain(m,v ~ beta1 + beta2 + alpha) <- function(x) (x[1]-x[2])^2/x[3]
```

A subset of the arguments args can be covariates in the model, allowing the specification of non-linear regression models. As an example the non-linear regression model

$$E(Y | X) = \nu + \Phi(\alpha + \beta X)$$

where Φ denotes the standard normal cumulative distribution function, can be defined as

```
m <- lvm(y ~ f(x,0)) # No linear effect of x
```

Next we add three new parameters using the parameter assigment function:

```
parameter(m) <- ~nu+alpha+beta
```

The intercept of Y is defined as mu

```
intercept(m) <- y ~ f(mu)
```

And finally the newly added intercept parameter mu is defined as the appropriate non-linear function of α , ν and β :

```
constrain(m, mu ~ x + alpha + nu) <- function(x) pnorm(x[1]*x[2])+x[3]
```

The constraints function can be used to show the estimated non-linear parameter constraints of an estimated model object (lvmfit or multigroupfit). Calling constrain with no additional arguments beyond x will return a list of the functions and parameter names defining the non-linear restrictions.

The gradient function can optionally be added as an attribute grad to the return value of the function defined by value. In this case the analytical derivatives will be calculated via the chain rule when evaluating the corresponding score function of the log-likelihood. If the gradient attribute is omitted the chain rule will be applied on a numeric approximation of the gradient.

Value

A lvm object.

Author(s)

Klaus K. Holst

See Also

[regression](#), [intercept](#), [covariance](#)

Examples

```
#####
### Non-linear parameter constraints 1
#####
m <- lvm(y ~ f(x1,gamma)+f(x2,beta))
covariance(m) <- y ~ f(v)
d <- sim(m,100)
m1 <- m; constrain(m1,beta ~ v) <- function(x) x^2
## Define slope of x2 to be the square of the residual variance of y
## Estimate both restricted and unrestricted model
e <- estimate(m,d,control=list(method="NR"))
e1 <- estimate(m1,d)
p1 <- coef(e1)
p1 <- c(p1[1:2],p1[3]^2,p1[3])
## Likelihood of unrestricted model evaluated in MLE of restricted model
logLik(e,p1)
## Likelihood of restricted model (MLE)
logLik(e1)

#####
### Non-linear regression
#####

## Simulate data
m <- lvm(c(y1,y2)~f(x,0)+f(eta,1))
latent(m) <- ~eta
covariance(m,~y1+y2) <- "v"
intercept(m,~y1+y2) <- "mu"
covariance(m,~eta) <- "zeta"
intercept(m,~eta) <- 0
set.seed(1)
d <- sim(m,100,p=c(v=0.01,zeta=0.01))[,manifest(m)]
d <- transform(d,
               y1=y1+2*pnorm(2*x),
               y2=y2+2*pnorm(2*x))

## Specify model and estimate parameters
constrain(m, mu ~ x + alpha + nu + gamma) <- function(x) x[4]*pnorm(x[3]+x[1]*x[2])
## Reduce Ex.Timings
e <- estimate(m,d,control=list(trace=1,constrain=TRUE))
```



```

constraints(e,data=d)
## Plot model-fit
plot(y1~x,d,pch=16); points(y2~x,d,pch=16,col="gray")
x0 <- seq(-4,4,length.out=100)
lines(x0,coef(e)["nu"] + coef(e)["gamma"]*pnorm(coef(e)["alpha"]*x0))

#####
### Multigroup model
#####
### Define two models
m1 <- lvm(y ~ f(x,beta)+f(z,beta2))
m2 <- lvm(y ~ f(x,psi) + z)
### And simulate data from them
d1 <- sim(m1,500)
d2 <- sim(m2,500)
### Add 'non'-linear parameter constraint
constrain(m2,psi ~ beta2) <- function(x) x
## Add parameter beta2 to model 2, now beta2 exists in both models
parameter(m2) <- ~ beta2
ee <- estimate(list(m1,m2),list(d1,d2),control=list(method="NR"))
summary(ee)

m3 <- lvm(y ~ f(x,beta)+f(z,beta2))
m4 <- lvm(y ~ f(x,beta2) + z)
e2 <- estimate(list(m3,m4),list(d1,d2),control=list(method="NR"))
e2

```

contr

Create contrast matrix

Description

Create contrast matrix typically for use with 'estimate' (Wald tests).

Usage

```
contr(p, n, diff = TRUE, ...)
```

Arguments

p	index of non-zero entries (see example)
n	Total number of parameters (if omitted the max number in p will be used)
diff	If FALSE all non-zero entries are +1, otherwise the second non-zero element in each row will be -1.
...	Additional arguments to lower level functions

Examples

```

contr(2,n=5)
contr(as.list(2:4),n=5)
contr(list(1,2,4),n=5)
contr(c(2,3,4),n=5)
contr(list(c(1,3),c(2,4)),n=5)
contr(list(c(1,3),c(2,4),5))

parsesdesign(c("aa","b","c"),"?","?",diff=c(FALSE,TRUE))

```

correlation	<i>Generic method for extracting correlation coefficients of model object</i>
-------------	---

Description

Generic correlation method

Usage

```
correlation(x, ...)
```

Arguments

x	Object
...	Additional arguments

Author(s)

Klaus K. Holst

covariance	<i>Add covariance structure to Latent Variable Model</i>
------------	--

Description

Define covariances between residual terms in a lvm-object.

Usage

```

## S3 replacement method for class 'lvm'
covariance(object, var1=NULL, var2=NULL, constrain=FALSE, pairwise=FALSE,...) <- value

```

Arguments

object	lvm-object
...	Additional arguments to be passed to the low level functions
var1	Vector of variables names (or formula)
var2	Vector of variables names (or formula) defining pairwise covariance between var1 and var2)
constrain	Define non-linear parameter constraints to ensure positive definite structure
pairwise	If TRUE and var2 is omitted then pairwise correlation is added between all variables in var1
value	List of parameter values or (if var1 is unspecified)

Details

The covariance function is used to specify correlation structure between residual terms of a latent variable model, using a formula syntax.

For instance, a multivariate model with three response variables,

$$Y_1 = \mu_1 + \epsilon_1$$

$$Y_2 = \mu_2 + \epsilon_2$$

$$Y_3 = \mu_3 + \epsilon_3$$

can be specified as

```
m <- lvm(~y1+y2+y3)
```

Pr. default the two variables are assumed to be independent. To add a covariance parameter $r = cov(\epsilon_1, \epsilon_2)$, we execute the following code

```
covariance(m) <- y1 ~ f(y2,r)
```

The special function f and its second argument could be omitted thus assigning an unique parameter the covariance between y_1 and y_2 .

Similarly the marginal variance of the two response variables can be fixed to be identical ($var(Y_i) = v$) via

```
covariance(m) <- c(y1,y2,y3) ~ f(v)
```

To specify a completely unstructured covariance structure, we can call

```
covariance(m) <- ~y1+y2+y3
```

All the parameter values of the linear constraints can be given as the right handside expression of the assignment function `covariance<-` if the first (and possibly second) argument is defined as well.

E.g:

```
covariance(m,y1~y1+y2) <- list("a1","b1")
```

```
covariance(m,~y2+y3) <- list("a2",2)
```

Defines

$$\text{var}(\epsilon_1) = a1$$

$$\text{var}(\epsilon_2) = a2$$

$$\text{var}(\epsilon_3) = 2$$

$$\text{cov}(\epsilon_1, \epsilon_2) = b1$$

Parameter constraints can be cleared by fixing the relevant parameters to NA (see also the regression method).

The function `covariance` (called without additional arguments) can be used to inspect the covariance constraints of a `lvm`-object.

Value

A `lvm`-object

Author(s)

Klaus K. Holst

See Also

`regression<-`, `intercept<-`, `constrain<-` `parameter<-`, `latent<-`, `cancel<-`, `kill<-`

Examples

```
m <- lvm()
### Define covariance between residuals terms of y1 and y2
covariance(m) <- y1~y2
covariance(m) <- c(y1,y2)~f(v) ## Same marginal variance
covariance(m) ## Examine covariance structure
```

density.sim	<i>Plot sim object</i>
-------------	------------------------

Description

Plot sim object

Usage

```
## S3 method for class 'sim'
density(x, ..., plot.type = "single")
```

Arguments

x	sim object
...	Graphical arguments to plot.sim
plot.type	Single or multiple plots

Examples

```
n <- 1000
val <- cbind(est1=rnorm(n,sd=1),est2=rnorm(n,sd=0.2),est3=rnorm(n,1,sd=0.5),
             sd1=runif(n,0.8,1.2),sd2=runif(n,0.1,0.3),sd3=runif(n,0.25,0.75))

plot.sim(val,estimate=c(1,2),true=c(0,0),se=c(4,5),equal=TRUE)
plot.sim(val,estimate=c(1,3),true=c(0,1),se=c(4,6),density.xlim=c(-3,3),ylim=c(-3,3))
plot.sim(val,estimate=c(1,2),true=c(0,0),se=c(4,5),equal=TRUE,plot.type="single")
plot.sim(val,estimate=c(1),se=c(4,5,6),plot.type="single")
plot.sim(val,estimate=c(1,2,3),equal=TRUE)
plot.sim(val,estimate=c(1,2,3),equal=TRUE,byrow=TRUE)
plot.sim(val,estimate=c(1,2,3),plot.type="single")
plot.sim(val,estimate=1,se=c(3,4,5),plot.type="single")

density.sim(val,estimate=c(1,2,3),polygon.density=c(0,10,10),polygon.angle=c(0,45,-45))
```

devcoords	<i>Returns device-coordinates and plot-region</i>
-----------	---

Description

Returns device-coordinates and plot-region

Usage

```
devcoords()
```

Value

A list with elements

dev.x1	Device: Left x-coordinate
dev.x2	Device: Right x-coordinate
dev.y1	Device Bottom y-coordinate
dev.y2	Device Top y-coordinate
fig.x1	Plot: Left x-coordinate
fig.x2	Plot: Right x-coordinate
fig.y1	Plot: Bottom y-coordinate
fig.y2	Plot: Top y-coordinate

Author(s)

Klaus K. Holst

diagtest

Calculate diagnostic tests for 2x2 table

Description

Calculate prevalence, sensitivity, specificity, and positive and negative predictive values

Usage

```
diagtest(table, positive = 2, exact = FALSE, p0 = NA,
  confint = c("logit", "arcsin", "pseudoscore", "exact"), ...)
```

Arguments

table	Table or (matrix/data.frame with two columns)
positive	Switch reference
exact	If TRUE exact binomial proportions CI/test will be used
p0	Optional null hypothesis (test prevalenc, sensitivity, ...)
confint	Type of confidence limits
...	Additional arguments to lower level functions

Details

Table should be in the format with outcome in columns and test in rows. Data.frame should be with test in the first column and outcome in the second column.

Author(s)

Klaus Holst

Examples

```
M <- as.table(matrix(c(42,12,
                      35,28),ncol=2,byrow=TRUE,
                      dimnames=list(rater=c("no","yes"),gold=c("no","yes"))))
diagtest(M,exact=TRUE)
```

dsep.lvm	<i>Check d-separation criterion</i>
----------	-------------------------------------

Description

Check for conditional independence (d-separation)

Usage

```
## S3 method for class 'lvm'
dsep(object, x, cond = NULL, return.graph = FALSE, ...)
```

Arguments

object	lvm object
x	Variables for which to check for conditional independence
cond	Conditioning set
return.graph	If TRUE the moralized ancestral graph with the conditioning set removed is returned
...	Additional arguments to lower level functions

Details

The argument 'x' can be given as a formula, e.g. $x \sim y | z + v$ or $\sim x + y | z + v$. With everything on the rhs of the bar defining the variables on which to condition on.

Examples

```
m <- lvm(x5 ~ x4+x3, x4~x3+x1, x3~x2, x2~x1)
if (interactive()) {
  plot(m,layoutType='neato')
}
dsep(m,x5~x1|x2+x4)
dsep(m,x5~x1|x3+x4)
dsep(m,~x1+x2+x3|x4)
```

equivalence	<i>Identify candidates of equivalent models</i>
-------------	---

Description

Identifies candidates of equivalent models

Usage

```
equivalence(x, rel, tol = 0.001, k = 1, omitrel = TRUE, ...)
```

Arguments

x	lvmfit-object
rel	Formula or character-vector specifying two variables to omit from the model and subsequently search for possible equivalent models
tol	Define two models as empirical equivalent if the absolute difference in score test is less than tol
k	Number of parameters to test simultaneously. For equivalence the number of additional associations to be added instead of rel.
omitrel	if k greater than 1, this boolean defines whether to omit candidates containing rel from the output
...	Additional arguments to be passed to the low level functions

Author(s)

Klaus K. Holst

See Also

[compare](#), [modelsearch](#)

estimate.default	<i>Estimation of functional of parameters</i>
------------------	---

Description

Estimation of functional of parameters. Wald tests, robust standard errors, cluster robust standard errors, LRT (when f is not a function)...

Usage

```
## Default S3 method:
estimate(x = NULL, f = NULL, ..., data, id, iddata,
  stack = TRUE, average = FALSE, subset, score.deriv, level = 0.95,
  iid = TRUE, type = c("robust", "df", "mbn"), keep, use, contrast, null,
  vcov, coef, robust = TRUE, df = NULL, print = NULL, labels, label.width,
  only.coef = FALSE, back.transform = NULL, folds = 0, cluster, R = 0,
  null.sim)
```

Arguments

<code>x</code>	model object (glm, lvmfit, ...)
<code>f</code>	transformation of model parameters and (optionally) data, or contrast matrix (or vector)
<code>...</code>	additional arguments to lower level functions
<code>data</code>	data.frame
<code>id</code>	(optional) id-variable corresponding to iid decomposition of model parameters.
<code>iddata</code>	(optional) id-variable for 'data'
<code>stack</code>	if TRUE (default) the i.i.d. decomposition is automatically stacked according to 'id'
<code>average</code>	if TRUE averages are calculated
<code>subset</code>	(optional) subset of data.frame on which to condition (logical expression or variable name)
<code>score.deriv</code>	(optional) derivative of mean score function
<code>level</code>	level of confidence limits
<code>iid</code>	if TRUE (default) the iid decompositions are also returned (extract with iid method)
<code>type</code>	type of small-sample correction
<code>keep</code>	(optional) index of parameters to keep from final result
<code>use</code>	(optional) index of parameters to use in calculations
<code>contrast</code>	(optional) Contrast matrix for final Wald test
<code>null</code>	(optional) null hypothesis to test
<code>vcov</code>	(optional) covariance matrix of parameter estimates (e.g. Wald-test)
<code>coef</code>	(optional) parameter coefficient
<code>robust</code>	if TRUE robust standard errors are calculated. If FALSE p-values for linear models are calculated from t-distribution
<code>df</code>	degrees of freedom (default obtained from 'df.residual')
<code>print</code>	(optional) print function
<code>labels</code>	(optional) names of coefficients
<code>label.width</code>	(optional) max width of labels
<code>only.coef</code>	if TRUE only the coefficient matrix is return

back.transform (optional) transform of parameters and confidence intervals
 folds (optional) aggregate influence functions (divide and conquer)
 cluster (obsolete) alias for 'id'.
 R Number of simulations (simulated p-values)
 null.sim Mean under the null for simulations

Details

iid decomposition

$$\sqrt{n}(\hat{\theta} - \theta) = \sum_{i=1}^n \epsilon_i + o_p(1)$$

can be extracted with the iid method.

Examples

```
## Simulation from logistic regression model
m <- lvm(y~x+z);
distribution(m,y~x) <- binomial.lvm("logit")
d <- sim(m,1000)
g <- glm(y~z+x,data=d,family=binomial())
g0 <- glm(y~1,data=d,family=binomial())

## LRT
estimate(g,g0)

## Plain estimates (robust standard errors)
estimate(g)

## Testing contrasts
estimate(g,null=0)
estimate(g,rbind(c(1,1,0),c(1,0,2)))
estimate(g,rbind(c(1,1,0),c(1,0,2)),null=c(1,2))
estimate(g,2:3) ## same as cbind(0,1,-1)
estimate(g,as.list(2:3)) ## same as rbind(c(0,1,0),c(0,0,1))
## Alternative syntax
estimate(g,"z","z"-x,2*z-3*x)
estimate(g,z,z-x,2*z-3*x)
estimate(g,"?") ## Wilcards
estimate(g,"*Int*","z")
estimate(g,"1","2"-3,null=c(0,1))
estimate(g,2,3)

## Usual (non-robust) confidence intervals
estimate(g,robust=FALSE)

## Transformations
estimate(g,function(p) p[1]+p[2])

## Multiple parameters
```

```

e <- estimate(g,function(p) c(p[1]+p[2],p[1]*p[2]))
e
vcov(e)

## Label new parameters
estimate(g,function(p) list("a1"=p[1]+p[2],"b1"=p[1]*p[2]))
##'
## Multiple group
m <- lvm(y~x)
m <- baptize(m)
d2 <- d1 <- sim(m,50)
e <- estimate(list(m,m),list(d1,d2))
estimate(e) ## Wrong
estimate(e,id=rep(seq(nrow(d1)),2))
estimate(lm(y~x,d1))

## Marginalize
f <- function(p,data)
  list(p0=lava::expit(p["(Intercept)"] + p["z"]*data[, "z"]),
        p1=lava::expit(p["(Intercept)"] + p["x"] + p["z"]*data[, "z"]))
e <- estimate(g, f, average=TRUE)
e
estimate(e,diff)
estimate(e,cbind(1,1))

## Clusters and subset (conditional marginal effects)
d$id <- rep(seq(nrow(d)/4),each=4)
estimate(g,function(p,data)
  list(p0=lava::expit(p[1] + p["z"]*data[, "z"]),
        subset=d$id>0, id=d$id, average=TRUE))

## More examples with clusters:
m <- lvm(c(y1,y2,y3)~u+x)
d <- sim(m,10)
l1 <- glm(y1~x,data=d)
l2 <- glm(y2~x,data=d)
l3 <- glm(y3~x,data=d)

## Some random id-numbers
id1 <- c(1,1,4,1,3,1,2,3,4,5)
id2 <- c(1,2,3,4,5,6,7,8,1,1)
id3 <- seq(10)

## Un-stacked and stacked i.i.d. decomposition
iid(estimate(l1,id=id1,stack=FALSE))
iid(estimate(l1,id=id1))

## Combined i.i.d. decomposition
e1 <- estimate(l1,id=id1)
e2 <- estimate(l2,id=id2)
e3 <- estimate(l3,id=id3)
(a2 <- merge(e1,e2,e3))

```

```
## If all models were estimated on the same data we could use the
## syntax:
## Reduce(merge,estimate(list(l1,l2,l3)))

## Same:
iid(a1 <- merge(l1,l2,l3,id=list(id1,id2,id3)))

iid(merge(l1,l2,l3,id=TRUE)) # one-to-one (same clusters)
iid(merge(l1,l2,l3,id=FALSE)) # independence

## Monte Carlo approach, simple trend test example

m <- categorical(lvm(),~x,K=5)
regression(m,additive=TRUE) <- y~x
d <- simulate(m,100,seed=1,'y~x'=0.1)
l <- lm(y~1+factor(x),data=d)

f <- function(x) coef(lm(x~seq_along(x)))[2]
null <- rep(mean(coef(l)),length(coef(l))) ## just need to make sure we simulate under H0: slope=0
estimate(l,f,R=1e2,null.sim=null)

estimate(l,f)
```

estimate.lvm

Estimation of parameters in a Latent Variable Model (lvm)

Description

Estimate parameters. MLE, IV or user-defined estimator.

Usage

```
## S3 method for class 'lvm'
estimate(x, data = parent.frame(), estimator = NULL,
  control = list(), missing = FALSE, weights, weightsname, data2, id, fix,
  index = !quick, graph = FALSE, silent = lava.options()$silent,
  quick = FALSE, method, param, cluster, p, ...)
```

Arguments

x	lvm-object
data	data.frame
estimator	String defining the estimator (see details below)
control	control/optimization parameters (see details below)
missing	Logical variable indicating how to treat missing data. Setting to FALSE leads to complete case analysis. In the other case likelihood based inference is obtained by integrating out the missing data under assumption the assumption that data is missing at random (MAR).

<code>weights</code>	Optional weights to used by the chosen estimator.
<code>weightsname</code>	Weights names (variable names of the model) in case <code>weights</code> was given as a vector of column names of data
<code>data2</code>	Optional additional dataset used by the chosen estimator.
<code>id</code>	Vector (or name of column in data) that identifies correlated groups of observations in the data leading to variance estimates based on a sandwich estimator
<code>fix</code>	Logical variable indicating whether parameter restriction automatically should be imposed (e.g. intercepts of latent variables set to 0 and at least one regression parameter of each measurement model fixed to ensure identifiability.)
<code>index</code>	For internal use only
<code>graph</code>	For internal use only
<code>silent</code>	Logical argument indicating whether information should be printed during estimation
<code>quick</code>	If TRUE the parameter estimates are calculated but all additional information such as standard errors are skipped
<code>method</code>	Optimization method
<code>param</code>	set parametrization (see <code>help(lava.options)</code>)
<code>cluster</code>	Obsolete. Alias for 'id'.
<code>p</code>	Evaluate model in parameter 'p' (no optimization)
<code>...</code>	Additional arguments to be passed to the low level functions

Details

A list of parameters controlling the estimation and optimization procedures is parsed via the `control` argument. By default Maximum Likelihood is used assuming multivariate normal distributed measurement errors. A list with one or more of the following elements is expected:

start: Starting value. The order of the parameters can be shown by calling `coef` (with `mean=TRUE`) on the `lvm`-object or with `plot(..., labels=TRUE)`. Note that this requires a check that it is actual the model being estimated, as `estimate` might add additional restriction to the model, e.g. through the `fix` and `exo.fix` arguments. The `lvm`-object of a fitted model can be extracted with the `Model`-function.

starterfun: Starter-function with syntax `function(lvm, S, mu)`. Three builtin functions are available: `startvalues`, `startvalues0`, `startvalues1`, ...

estimator: String defining which estimator to use (Defaults to "gaussian")

meanstructure Logical variable indicating whether to fit model with meanstructure.

method: String pointing to alternative optimizer (e.g. `optim` to use simulated annealing).

control: Parameters passed to the optimizer (default `stats::nlminb`).

tol: Tolerance of optimization constraints on lower limit of variance parameters.

Value

A `lvmfit`-object.

Author(s)

Klaus K. Holst

See Also

estimate.default score, information

Examples

```

dd <- read.table(header=TRUE,
text="x1 x2 x3
0.0 -0.5 -2.5
-0.5 -2.0 0.0
1.0 1.5 1.0
0.0 0.5 0.0
-2.5 -1.5 -1.0")
e <- estimate(lvm(c(x1,x2,x3)~u),dd)

## Simulation example
m <- lvm(list(y~v1+v2+v3+v4,c(v1,v2,v3,v4)~x))
covariance(m) <- v1~v2+v3+v4
dd <- sim(m,10000) ## Simulate 10000 observations from model
e <- estimate(m, dd) ## Estimate parameters
e

## Using just sufficient statistics
n <- nrow(dd)
e0 <- estimate(m,data=list(S=cov(dd)*(n-1)/n,mu=colMeans(dd),n=n))
rm(dd)

## Multiple group analysis
m <- lvm()
regression(m) <- c(y1,y2,y3)~u
regression(m) <- u~x
d1 <- sim(m,100,p=c("u,u"=1,"u~x"=1))
d2 <- sim(m,100,p=c("u,u"=2,"u~x"=-1))

mm <- baptize(m)
regression(mm,u~x) <- NA
covariance(mm,~u) <- NA
intercept(mm,~u) <- NA
ee <- estimate(list(mm,mm),list(d1,d2))

## Missing data
d0 <- makemissing(d1,cols=1:2)
e0 <- estimate(m,d0,missing=TRUE)
e0

```

eventTime	<i>Add an observed event time outcome to a latent variable model.</i>
-----------	---

Description

For example, if the model 'm' includes latent event time variables are called 'T1' and 'T2' and 'C' is the end of follow-up (right censored), then one can specify

Usage

```
eventTime(object, formula, eventName = "status", ...)
```

Arguments

object	Model object
formula	Formula (see details)
eventName	Event names
...	Additional arguments to lower levels functions

Details

```
eventTime(object=m, formula=ObsTime~min(T1=a, T2=b, C=0, "ObsEvent"))
```

when data are simulated from the model one gets 2 new columns:

- "ObsTime": the smallest of T1, T2 and C - "ObsEvent": 'a' if T1 is smallest, 'b' if T2 is smallest and '0' if C is smallest

Note that "ObsEvent" and "ObsTime" are names specified by the user.

Author(s)

Thomas A. Gerds, Klaus K. Holst

Examples

```
# Right censored survival data without covariates
m0 <- lvm()
distribution(m0, "eventtime") <- coxWeibull.lvm(scale=1/100, shape=2)
distribution(m0, "censtime") <- coxExponential.lvm(rate=10)
m0 <- eventTime(m0, time~min(eventtime=1, censtime=0), "status")
sim(m0, 10)

# Alternative specification of the right censored survival outcome
## eventTime(m, "Status") <- ~min(eventtime=1, censtime=0)

# Cox regression:
# lava implements two different parametrizations of the same
# Weibull regression model. The first specifies
```

```

# the effects of covariates as proportional hazard ratios
# and works as follows:
m <- lvm()
distribution(m,"eventtime") <- coxWeibull.lvm(scale=1/100,shape=2)
distribution(m,"censtime") <- coxWeibull.lvm(scale=1/100,shape=2)
m <- eventTime(m,time~min(eventtime=1,censtime=0),"status")
distribution(m,"sex") <- binomial.lvm(p=0.4)
distribution(m,"sbp") <- normal.lvm(mean=120,sd=20)
regression(m,from="sex",to="eventtime") <- 0.4
regression(m,from="sbp",to="eventtime") <- -0.01
sim(m,6)
# The parameters can be recovered using a Cox regression
# routine or a Weibull regression model. E.g.,
## Not run:
  set.seed(18)
  d <- sim(m,1000)
  library(survival)
  coxph(Surv(time,status)~sex+sbp,data=d)

  sr <- survreg(Surv(time,status)~sex+sbp,data=d)
  library(SurvRegCensCov)
  ConvertWeibull(sr)

## End(Not run)

# The second parametrization is an accelerated failure time
# regression model and uses the function weibull.lvm instead
# of coxWeibull.lvm to specify the event time distributions.
# Here is an example:

ma <- lvm()
distribution(ma,"eventtime") <- weibull.lvm(scale=3,shape=0.7)
distribution(ma,"censtime") <- weibull.lvm(scale=2,shape=0.7)
ma <- eventTime(ma,time~min(eventtime=1,censtime=0),"status")
distribution(ma,"sex") <- binomial.lvm(p=0.4)
distribution(ma,"sbp") <- normal.lvm(mean=120,sd=20)
regression(ma,from="sex",to="eventtime") <- 0.7
regression(ma,from="sbp",to="eventtime") <- -0.008
set.seed(17)
sim(ma,6)
# The regression coefficients of the AFT model
# can be transformed into log(hazard ratios):
# coef.coxWeibull = - coef.weibull / shape.weibull
## Not run:
  set.seed(17)
  da <- sim(ma,1000)
  library(survival)
  fa <- coxph(Surv(time,status)~sex+sbp,data=da)
  coef(fa)
  c(0.7,-0.008)/0.7

## End(Not run)

```



```

# The Weibull parameters are related as follows:
# shape.coxWeibull = 1/shape.weibull
# scale.coxWeibull = exp(-scale.weibull/shape.weibull)
# scale.AFT = log(scale.coxWeibull) / shape.coxWeibull
# Thus, the following are equivalent parametrizations
# which produce exactly the same random numbers:

model.aft <- lvm()
distribution(model.aft,"eventtime") <- weibull.lvm(scale=-log(1/100)/2,shape=0.5)
distribution(model.aft,"censtime") <- weibull.lvm(scale=-log(1/100)/2,shape=0.5)
set.seed(17)
sim(model.aft,6)

model.cox <- lvm()
distribution(model.cox,"eventtime") <- coxWeibull.lvm(scale=1/100,shape=2)
distribution(model.cox,"censtime") <- coxWeibull.lvm(scale=1/100,shape=2)
set.seed(17)
sim(model.cox,6)

# The minimum of multiple latent times one of them still
# being a censoring time, yield
# right censored competing risks data

mc <- lvm()
distribution(mc,~X2) <- binomial.lvm()
regression(mc) <- T1~f(X1,-.5)+f(X2,0.3)
regression(mc) <- T2~f(X2,0.6)
distribution(mc,~T1) <- coxWeibull.lvm(scale=1/100)
distribution(mc,~T2) <- coxWeibull.lvm(scale=1/100)
distribution(mc,~C) <- coxWeibull.lvm(scale=1/100)
mc <- eventTime(mc,time~min(T1=1,T2=2,C=0),"event")
sim(mc,6)

```

Expand

Create a Data Frame from All Combinations of Factors

Description

Create a Data Frame from All Combinations of Factors

Usage

```
Expand(`_data`, ...)
```

Arguments

<code>_data</code>	Data.frame
<code>...</code>	vectors, factors or a list containing these

Details

Simple wrapper of the 'expand.grid' function. If x is a table then a data frame is returned with one row pr individual observation.

Author(s)

Klaus K. Holst

Examples

```
dd <- Expand(iris, Sepal.Length=2:8, Species=c("virginica","setosa"))
summary(dd)

T <- with(warpbreaks, table(wool, tension))
Expand(T)
```

fplot

fplot

Description

Faster plot via RGL

Usage

```
fplot(x, y, z = NULL, xlab, ylab, ..., z.col = topo.colors(64),
      data = parent.frame(), add = FALSE)
```

Arguments

<code>x</code>	X variable
<code>y</code>	Y variable
<code>z</code>	Z variable (optional)
<code>xlab</code>	x-axis label
<code>ylab</code>	y-axis label
<code>...</code>	additional argument to lower level plot functions
<code>z.col</code>	Color
<code>data</code>	data.frame
<code>add</code>	If TRUE use current active device

Examples

```
if (interactive()) {  
  data(iris)  
  fplot(Sepal.Length ~ Petal.Length+Species, data=iris, size=2, type="s")  
}
```

`getMplus`*Read Mplus output*

Description

Read Mplus output files

Usage

```
getMplus(infile = "template.out", coef = TRUE, ...)
```

Arguments

<code>infile</code>	Mplus output file
<code>coef</code>	Coefficients only
<code>...</code>	additional arguments to lower level functions

Author(s)

Klaus K. Holst

See Also

`getSAS`

`getSAS`*Read SAS output*

Description

Run SAS code like in the following:

Usage

```
getSAS(infile, entry = "Parameter Estimates", ...)
```

Arguments

infile	file (csv file generated by ODS)
entry	Name of entry to capture
...	additional arguments to lower level functions

Details

ODS CSVALL BODY="myest.csv"; proc nlmixed data=aj qpoints=2 dampstep=0.5; ... run; ODS CSVALL Close;

and read results into R with:

```
getsas("myest.csv", "Parameter Estimates")
```

Author(s)

Klaus K. Holst

See Also

getMplus

gof

Extract model summaries and GOF statistics for model object

Description

Calculates various GOF statistics for model object including global chi-squared test statistic and AIC. Extract model-specific mean and variance structure, residuals and various predictions.

Usage

```
gof(object, ...)
```

```
## S3 method for class 'lvmfit'
```

```
gof(object, chisq=FALSE, level=0.90, rmsea.threshold=0.05, all=FALSE, ...)
```

```
moments(x, ...)
```

```
## S3 method for class 'lvm'
```

```
moments(x, p, debug=FALSE, conditional=FALSE, data=NULL, latent=FALSE, ...)
```

```
## S3 method for class 'lvmfit'
```

```
logLik(object, p=coef(object),
        data=model.frame(object),
        model=object$estimator,
        weights=Weights(object),
        data2=object$data$data2,
```

```

... )

## S3 method for class 'lvmfit'
score(x, data=model.frame(x), p=pars(x), model=x$estimator,
      weights=Weights(x), data2=x$data$data2, ...)

## S3 method for class 'lvmfit'
information(x,p=pars(x),n=x$data$n,data=model.frame(x),
           model=x$estimator,weights=Weights(x), data2=x$data$data2, ...)

```

Arguments

<code>object</code>	Model object
<code>...</code>	Additional arguments to be passed to the low level functions
<code>x</code>	Model object
<code>p</code>	Parameter vector used to calculate statistics
<code>data</code>	Data.frame to use
<code>latent</code>	If TRUE predictions of latent variables are included in output
<code>data2</code>	Optional second data.frame (only for censored observations)
<code>weights</code>	Optional weight matrix
<code>n</code>	Number of observations
<code>conditional</code>	If TRUE the conditional moments given the covariates are calculated. Otherwise the joint moments are calculated
<code>model</code>	String defining estimator, e.g. "gaussian" (see <code>estimate</code>)
<code>debug</code>	Debugging only
<code>chisq</code>	Boolean indicating whether to calculate chi-squared goodness-of-fit (always TRUE for estimator='gaussian')
<code>level</code>	Level of confidence limits for RMSEA
<code>rmsea.threshold</code>	Which probability to calculate, $\Pr(\text{RMSEA} < \text{rmsea.threshold})$
<code>all</code>	Calculate all (ad hoc) FIT indices: TLI, CFI, NFI, SRMR, ...

Value

A `htest`-object.

Author(s)

Klaus K. Holst

Examples

```
m <- lvm(list(y~v1+v2+v3+v4,c(v1,v2,v3,v4)~x))
set.seed(1)
dd <- sim(m,1000)
e <- estimate(m, dd)
gof(e,all=TRUE,rmsea.threshold=0.05,level=0.9)

set.seed(1)
m <- lvm(list(c(y1,y2,y3)~u,y1~x)); latent(m) <- ~u
regression(m,c(y2,y3)~u) <- "b"
d <- sim(m,1000)
e <- estimate(m,d)
rsq(e)
##'
rr <- rsq(e,TRUE)
rr
estimate(rr,contrast=rbind(c(1,-1,0),c(1,0,-1),c(0,1,-1)))
```

Graph	<i>Extract graph</i>
-------	----------------------

Description

Extract or replace graph object

Usage

```
Graph(x, ...)
```

```
Graph(x, ...) <- value
```

Arguments

- | | |
|-------|--|
| x | Model object |
| ... | Additional arguments to be passed to the low level functions |
| value | New graphNEL object |

Author(s)

Klaus K. Holst

See Also

[Model](#)

Examples

```
m <- lvm(y~x)
Graph(m)
```

hubble	<i>Hubble data</i>
--------	--------------------

Description

Velocity (v) and distance (D) measures of 36 Type Ia super-novae from the Hubble Space Telescope

Format

data.frame

Source

Freedman, W. L., et al. 2001, AstroPhysicalJournal, 553, 47.

hubble2	<i>Hubble data</i>
---------	--------------------

Description

Hubble data

Format

data.frame

See Also

hubble

iid	<i>Extract i.i.d. decomposition (influence function) from model object</i>
-----	--

Description

Extract i.i.d. decomposition (influence function) from model object

Usage

```
iid(x,...)

## Default S3 method:
iid(x,bread,id=NULL,folds=0,maxsize=(folds>0)*1e6,...)
```

Arguments

x	model object
...	additional arguments
id	(optional) id/cluster variable
bread	(optional) Inverse of derivative of mean score function
folds	(optional) Calculate aggregated iid decomposition (0:=disabled)
maxsize	(optional) Data is split in groups of size up to 'maxsize' (0:=disabled)

Examples

```
m <- lvm(y~x+z)
distribution(m, ~y+z) <- binomial.lvm("logit")
d <- sim(m,1e3)
g <- glm(y~x+z,data=d,family=binomial)
crossprod(iid(g))
```

images	<i>Organize several image calls (for visualizing categorical data)</i>
--------	--

Description

Visualize categorical by group variable

Usage

```
images(x, group, ncol = 2, byrow = TRUE, colorbar = 1,
  colorbar.space = 0.1, label.offset = 0.02, order = TRUE,
  colorbar.border = 0, main, rowcol = FALSE, plotfun = NULL, axis1, axis2,
  mar, col = list(c("#EFF3FF", "#BDD7E7", "#6BAED6", "#2171B5"), c("#FEE5D9",
  "#FCAE91", "#FB6A4A", "#CB181D"), c("#EDF8E9", "#BAE4B3", "#74C476",
  "#238B45"), c("#FEEDDE", "#FDBE85", "#FD8D3C", "#D94701")), ...)
```


Arguments

<code>x</code>	data.frame or matrix
<code>group</code>	group variable
<code>ncol</code>	number of columns in layout
<code>byrow</code>	organize by row if TRUE
<code>colorbar</code>	Add color bar
<code>colorbar.space</code>	Space around color bar
<code>label.offset</code>	label offset
<code>order</code>	order
<code>colorbar.border</code>	Add border around color bar
<code>main</code>	Main title
<code>rowcol</code>	switch rows and columns
<code>plotfun</code>	Alternative plot function (instead of 'image')
<code>axis1</code>	Axis 1
<code>axis2</code>	Axis 2
<code>mar</code>	Margins
<code>col</code>	Colours
<code>...</code>	Additional arguments to lower level graphics functions

Author(s)

Klaus Holst

Examples

```
X <- matrix(rbinom(400,3,0.5),20)
group <- rep(1:4,each=5)
images(X,colorbar=0,zlim=c(0,3))
images(X,group=group,zlim=c(0,3))
## Not run:
images(X,group=group,col=list(RColorBrewer::brewer.pal(4,"Purples"),
                             RColorBrewer::brewer.pal(4,"Greys"),
                             RColorBrewer::brewer.pal(4,"YlGn"),
                             RColorBrewer::brewer.pal(4,"PuBuGn")),colorbar=2,zlim=c(0,3))

## End(Not run)
images(list(X,X,X,X),group=group,zlim=c(0,3))
images(list(X,X,X,X),ncol=1,group=group,zlim=c(0,3))
images(list(X,X),group,axis2=c(FALSE,FALSE),axis1=c(FALSE,FALSE),
       mar=list(c(0,0,0,0),c(0,0,0,0)),yaxs="i",xaxs="i",zlim=c(0,3))
```

indoorenv	<i>Data</i>
Description	
Description	
Format	
data.frame	
Source	
Simulated	
<hr/>	
intercept	<i>Fix mean parameters in 'lvm'-object</i>

Description

Define linear constraints on intercept parameters in a lvm-object.

Usage

```
## S3 replacement method for class 'lvm'  
intercept(object, vars, ...) <- value
```

Arguments

object	lvm-object
...	Additional arguments
vars	character vector of variable names
value	Vector (or list) of parameter values or labels (numeric or character) or a formula defining the linear constraints (see also the regression or covariance methods).

Details

The intercept function is used to specify linear constraints on the intercept parameters of a latent variable model. As an example we look at the multivariate regression model

$$E(Y_1|X) = \alpha_1 + \beta_1 X$$
$$E(Y_2|X) = \alpha_2 + \beta_2 X$$

defined by the call

```
m <- lvm(c(y1,y2) ~ x)
```

To fix $\alpha_1 = \alpha_2$ we call

```
intercept(m) <- c(y1,y2) ~ f(mu)
```

Fixed parameters can be reset by fixing them to NA. For instance to free the parameter restriction of Y_1 and at the same time fixing $\alpha_2 = 2$, we call

```
intercept(m, ~y1+y2) <- list(NA,2)
```

Calling `intercept` with no additional arguments will return the current intercept restrictions of the `lvm`-object.

Value

A `lvm`-object

Note

Variables will be added to the model if not already present.

Author(s)

Klaus K. Holst

See Also

[covariance<-](#), [regression<-](#), [constrain<-](#), [parameter<-](#), [latent<-](#), [cancel<-](#), [kill<-](#)

Examples

```
## A multivariate model
m <- lvm(c(y1,y2) ~ f(x1,beta)+x2)
regression(m) <- y3 ~ f(x1,beta)
intercept(m) <- y1 ~ f(mu)
intercept(m, ~y2+y3) <- list(2,"mu")
intercept(m) ## Examine intercepts of model (NA translates to free/unique parameter)
```

kill	<i>Remove variables from (model) object.</i>
------	--

Description

Generic method for removing elements of object

Usage

```
kill(x, ...) <- value
```

Arguments

x	Model object
...	additional arguments to lower level functions
value	Vector of variables or formula specifying which nodes to remove

Author(s)

Klaus K. Holst

See Also

cancel

Examples

```
m <- lvm()
addvar(m) <- ~y1+y2+x
covariance(m) <- y1~y2
regression(m) <- c(y1,y2) ~ x
### Cancel the covariance between the residuals of y1 and y2
cancel(m) <- y1~y2
### Remove y2 from the model
rmvar(m) <- ~y2
```

ksmooth2 *Plot/estimate surface*

Description

Plot/estimate surface

Usage

```
ksmooth2(x, data, h = NULL, xlab = NULL, ylab = NULL, zlab = "",
  gridsize = rep(51L, 2), ...)
```

Arguments

x	formula or data
data	data.frame
h	bandwidth
xlab	X label
ylab	Y label
zlab	Z label
gridsize	grid size of kernel smoother
...	Additional arguments to graphics routine (persp3d or persp)

Examples

```
ksmooth2(rmvn(1e4, sigma=diag(2)*.5+.5), c(-3.5, 3.5), h=1,
  rgl=FALSE, theta=30)

if (interactive()) {
  ksmooth2(rmvn(1e4, sigma=diag(2)*.5+.5), c(-3.5, 3.5), h=1)
  ksmooth2(function(x,y) x^2+y^2, c(-20, 20))
  ksmooth2(function(x,y) x^2+y^2, xlim=c(-5, 5), ylim=c(0, 10))

  f <- function(x,y) 1-sqrt(x^2+y^2)
  surface(f, xlim=c(-1, 1), alpha=0.9, aspect=c(1, 1, 0.75))
  surface(f, xlim=c(-1, 1), clut=heat.colors(128))
  ##play3d(spin3d(axis=c(0, 0, 1), rpm=8), duration=5)
}

if (interactive()) {
  surface(function(x) dmvn(x, sigma=diag(2)), c(-3, 3), lit=FALSE, smooth=FALSE, box=FALSE, alpha=0.8)
  surface(function(x) dmvn(x, sigma=diag(2)), c(-3, 3), box=FALSE, specular="black")##'
}

if (!inherits(try(find.package("fields"), silent=TRUE), "try-error")) {
  f <- function(x,y) 1-sqrt(x^2+y^2)
  ksmooth2(f, c(-1, 1), rgl=FALSE, image=fields::image.plot)
}
```

labels<-	<i>Define labels of graph</i>
----------	-------------------------------

Description

Alters labels of nodes and edges in the graph of a latent variable model

Usage

```
## Default S3 replacement method:
labels(object, ...) <- value
## S3 replacement method for class 'lvm'
edgelabels(object, to, ...) <- value
## Default S3 replacement method:
nodecolor(object, var=vars(object),
border, labcol, shape, lwd, ...) <- value
```

Arguments

object	lvm-object.
...	Additional arguments (lwd, cex, col, labcol), border.
value	node label/edge label/color
to	Formula specifying outcomes and predictors defining relevant edges.
var	Formula or character vector specifying the nodes/variables to alter.
border	Colors of borders
labcol	Text label colors
shape	Shape of node
lwd	Line width of border

Author(s)

Klaus K. Holst

Examples

```
m <- lvm(c(y,v)~x+z)
regression(m) <- c(v,x)~z
labels(m) <- c(y=expression(psi), z=expression(zeta))
nodecolor(m,~y+z+x,border=c("white","white","black"),
labcol="white", lwd=c(1,1,5),
lty=c(1,2)) <- c("orange","indianred","lightgreen")
edgelabels(m,y~z+x, cex=c(2,1.5), col=c("orange","black"),labcol="darkblue",
arrowhead=c("tee","dot"),
lwd=c(3,1)) <- expression(phi,rho)
edgelabels(m,c(v,x)~z, labcol="red", cex=0.8,arrowhead="none") <- 2
if (interactive()) {
```

```

    plot(m,addstyle=FALSE)
  }

  m <- lvm(y~x)
  labels(m) <- list(x="multiple\nlines")
  if (interactive()) {
    op <- par(mfrow=c(1,2))
    plot(m,plain=TRUE)
    plot(m)
    par(op)

    d <- sim(m,100)
    e <- estimate(m,d)
    plot(e,type="sd")
  }

```

lava.options	<i>Set global options for lava</i>
--------------	------------------------------------

Description

Extract and set global parameters of lava. In particular optimization parameters for the estimate function.

Usage

```
lava.options(...)
```

Arguments

... Arguments

Details

- param: 'relative' (factor loading and variance of one endogenous variables in each measurement model are fixed to one), 'absolute' (mean and variance of latent variables are set to 0 and 1, respectively), 'hybrid' (intercept of latent variables is fixed to 0, and factor loading of at least one endogenous variable in each measurement model is fixed to 1), 'none' (no constraints are added)
- layout: One of 'dot', 'fdp', 'circo', 'twopi', 'neato', 'osage'
- silent: Set to FALSE to disable various output messages
- ...

see control parameter of the estimate function.

Value

list of parameters

Author(s)

Klaus K. Holst

Examples

```
## Not run:
lava.options(iter.max=100,silent=TRUE)

## End(Not run)
```

lvm

Initialize new latent variable model

Description

Function that constructs a new latent variable model object

Usage

```
lvm(x = NULL, ..., latent = NULL, silent = lava.options()$silent)
```

Arguments

x	Vector of variable names. Optional but gives control of the sequence of appearance of the variables. The argument can be given as a character vector or formula, e.g. <code>~y1+y2</code> is equivalent to <code>c("y1", "y2")</code> . Alternatively the argument can be a formula specifying a linear model.
...	Additional arguments to be passed to the low level functions
latent	(optional) Latent variables
silent	Logical variable which indicates whether messages are turned on/off.

Value

Returns an object of class `lvm`.

Author(s)

Klaus K. Holst

See Also

[regression](#), [covariance](#), [intercept](#), ...

Examples

```
m <- lvm() # Empty model
m1 <- lvm(y~x) # Simple linear regression
m2 <- lvm(~y1+y2) # Model with two independent variables (argument)
m3 <- lvm(list(c(y1,y2,y3)~u,u~x+z)) # SEM with three items
```

makemissing	<i>Create random missing data</i>
-------------	-----------------------------------

Description

Generates missing entries in data.frame/matrix

Usage

```
makemissing(data, p = 0.2, cols = seq_len(ncol(data)), rowwise = FALSE,
  nafun = function(x) x)
```

Arguments

data	data.frame
p	Fraction of missing data in each column
cols	Which columns (name or index) to alter
rowwise	Should missing occur row-wise (either none or all selected columns are missing)
nafun	(Optional) function to be applied on data.frame before return (e.g. na.omit to return complete-cases only)

Value

data.frame

Author(s)

Klaus K. Holst

measurement.error	<i>Two-stage (non-linear) measurement error</i>
-------------------	---

Description

Two-stage measurement error

Usage

```
measurement.error(model1, formula, data = parent.frame(),
  predictfun = function(mu, var, data, ...) mu[, 1]^2 + var[1], id1, id2, ...)
```

Arguments

model1	Stage 1 model
formula	Formula specifying observed covariates in stage 2 model
data	data.frame
predictfun	Predictions to be used in stage 2
id1	Optional id-vector of stage 1
id2	Optional id-vector of stage 2
...	Additional arguments to lower level functions

See Also

stack.estimate

Examples

```
m <- lvm(c(y1,y2,y3)~u,c(y3,y4,y5)~v,u~~v,c(u,v)~x)
transform(m,u2~u) <- function(x) x^2
transform(m,uv~u+v) <- prod
regression(m) <- z~u2+u+v+uv+x
set.seed(1)
d <- sim(m,1000,p=c("u,u"=1))

## Stage 1
m1 <- lvm(c(y1[0:s],y2[0:s],y3[0:s])~1*u,c(y3[0:s],y4[0:s],y5[0:s])~1*v,u~b*x,u~~v)
latent(m1) <- ~u+v
e1 <- estimate(m1,d)

pp <- function(mu,var,data,...) {
  cbind(u=mu[, "u"],u2=mu[, "u"]^2+var["u", "u"],v=mu[, "v"],uv=mu[, "u"]*mu[, "v"]+var["u", "v"])
}
(e <- measurement.error(e1, z~1+x, data=d, predictfun=pp))

## uu <- seq(-1,1,length.out=100)
## pp <- estimate(e,function(p,...) p["(Intercept)"]+p["u"]*uu+p["u2"]*uu^2)$coefmat
```

```

if (interactive()) {
  plot(e, intercept=TRUE, vline=0)

  f <- function(p) p[1]+p["u"]*u+p["u2"]*u^2
  u <- seq(-1,1,length.out=100)
  plot(e, f, data=data.frame(u), ylim=c(-.5,2.5))
}

```

Missing

*Missing value generator***Description**

Missing value generator

Usage

```
Missing(object, formula, Rformula, missing.name, suffix = "0", ...)
```

Arguments

object	lvm-object.
formula	The right hand side specifies the name of a latent variable which is not always observed. The left hand side specifies the name of a new variable which is equal to the latent variable but has missing values. If given as a string then this is used as the name of the latent (full-data) name, and the observed data name is 'missing.data'
Rformula	Missing data mechanism with left hand side specifying the name of the observed data indicator (may also just be given as a character instead of a formula)
missing.name	Name of observed data variable (only used if 'formula' was given as a character specifying the name of the full-data variable)
suffix	If missing.name is missing, then the name of the observed data variable will be the name of the full-data variable + the suffix
...	Passed to binomial.lvm.

Details

This function adds a binary variable to a given lvm model and also a variable which is equal to the original variable where the binary variable is equal to zero

Value

lvm object

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>

Examples

```

library(lava)
set.seed(17)
m <- lvm(y0~x01+x02+x03)
m <- Missing(m, formula=x1~x01, Rformula=R1~0.3*x02+-0.7*x01, p=0.4)
sim(m, 10)

m <- lvm(y~1)
m <- Missing(m, "y", "r")
## same as
## m <- Missing(m, y~1, r~1)
sim(m, 10)

## same as
m <- lvm(y~1)
Missing(m, "y") <- r~x
sim(m, 10)

m <- lvm(y~1)
m <- Missing(m, "y", "r", suffix=".")
## same as
## m <- Missing(m, "y", "r", missing.name="y.")
## same as
## m <- Missing(m, y.~y, "r")
sim(m, 10)

```

missingdata

*Missing data example***Description**

Simulated data generated from model

$$E(Y_i | X) = X, \quad cov(Y_1, Y_2 | X) = 0.5$$

Format

list of data.frames

Details

The list contains four data sets 1) Complete data 2) MCAR 3) MAR 4) MNAR (missing mechanism depends on variable V correlated with Y1, Y2)

Source

Simulated

Examples

```

data(missingdata)
e0 <- estimate(lvm(c(y1,y2)~b*x,y1~~y2),missingdata[[1]]) ## No missing
e1 <- estimate(lvm(c(y1,y2)~b*x,y1~~y2),missingdata[[2]]) ## CC (MCAR)
e2 <- estimate(lvm(c(y1,y2)~b*x,y1~~y2),missingdata[[2]],missing=TRUE) ## MCAR
e3 <- estimate(lvm(c(y1,y2)~b*x,y1~~y2),missingdata[[3]]) ## CC (MAR)
e4 <- estimate(lvm(c(y1,y2)~b*x,y1~~y2),missingdata[[3]],missing=TRUE) ## MAR

```

Model

Extract model

Description

Extract or replace model object

Usage

```

Model(x, ...)

Model(x, ...) <- value

```

Arguments

x	Fitted model
...	Additional arguments to be passed to the low level functions
value	New model object (e.g. lvm or multigroup)

Value

Returns a model object (e.g. lvm or multigroup)

Author(s)

Klaus K. Holst

See Also

[Graph](#)

Examples

```

m <- lvm(y~x)
e <- estimate(m, sim(m,100))
Model(e)

```

modelsearch

Model searching

Description

Performs Wald or score tests

Usage

```
modelsearch(x, k = 1, dir = "forward", type = "all", ...)
```

Arguments

x	lvmfit-object
k	Number of parameters to test simultaneously. For equivalence the number of additional associations to be added instead of rel.
dir	Direction to do model search. "forward" := add associations/arrows to model/graph (score tests), "backward" := remove associations/arrows from model/graph (wald test)
type	If equal to 'correlation' only consider score tests for covariance parameters. If equal to 'regression' go through direct effects only (default 'all' is to do both)
...	Additional arguments to be passed to the low level functions

Value

Matrix of test-statistics and p-values

Author(s)

Klaus K. Holst

See Also

[compare](#), [equivalence](#)

Examples

```
m <- lvm();
regression(m) <- c(y1,y2,y3) ~ eta; latent(m) <- ~eta
regression(m) <- eta ~ x
m0 <- m; regression(m0) <- y2 ~ x
dd <- sim(m0,100)[,manifest(m0)]
e <- estimate(m,dd);
modelsearch(e,silent=TRUE)
modelsearch(e,silent=TRUE,type="cor")
```

multinomial

Estimate probabilities in contingency table

Description

Estimate probabilities in contingency table

Usage

```
multinomial(x, marginal = FALSE, transform, ...)
```

Arguments

x	Matrix or data.frame with observations (1 or 2 columns)
marginal	If TRUE the marginals are estimated
transform	Optional transformation of parameters (e.g., logit)
...	Additional arguments to lower-level functions

Author(s)

Klaus K. Holst

Examples

```
set.seed(1)
breaks <- c(-Inf,-1,0,Inf)
m <- lvm(); covariance(m,pairwise=TRUE) <- ~y1+y2+y3+y4
d <- transform(sim(m,5e2),
               z1=cut(y1,breaks=breaks),
               z2=cut(y2,breaks=breaks),
               z3=cut(y3,breaks=breaks),
               z4=cut(y4,breaks=breaks))

multinomial(d[,5])
(a1 <- multinomial(d[,5:6]))
(K1 <- kappa(a1)) ## Cohen's kappa

K2 <- kappa(d[,7:8])
## Testing difference K1-K2:
estimate(merge(K1,K2,id=TRUE),diff)

estimate(merge(K1,K2,id=FALSE),diff) ## Wrong std.err ignoring dependence
sqrt(vcov(K1)+vcov(K2))

## Average of the two kappas:
estimate(merge(K1,K2,id=TRUE),function(x) mean(x))
estimate(merge(K1,K2,id=FALSE),function(x) mean(x)) ## Independence
##'
```

```
## Goodman-Kruskal's gamma
m2 <- lvm(); covariance(m2) <- y1~y2
breaks1 <- c(-Inf,-1,0,Inf)
breaks2 <- c(-Inf,0,Inf)
d2 <- transform(sim(m2,5e2),
                 z1=cut(y1,breaks=breaks1),
                 z2=cut(y2,breaks=breaks2))

(g1 <- gkgamma(d2[,3:4]))
## same as
## Not run:
gkgamma(table(d2[,3:4]))
gkgamma(multinomial(d2[,3:4]))

## End(Not run)

##partial gamma
d2$x <- rbinom(nrow(d2),2,0.5)
gkgamma(z1~z2|x,data=d2)
```

nldata	<i>Example data (nonlinear model)</i>
--------	---------------------------------------

Description

Example data (nonlinear model)

Format

data.frame

Source

Simulated

nsem	<i>Example SEM data (nonlinear)</i>
------	-------------------------------------

Description

Simulated data

Format

data.frame

Source

Simulated

ordreg	<i>Univariate cumulative link regression models</i>
--------	---

Description

Ordinal regression models

Usage

```
ordreg(formula, data = parent.frame(), offset,
       family = stats::binomial("probit"), start, fast = FALSE, ...)
```

Arguments

formula	formula
data	data.frame
offset	offset
family	family (default proportional odds)
start	optional starting values
fast	If TRUE standard errors etc. will not be calculated
...	Additional arguments to lower level functions

Author(s)

Klaus K. Holst

Examples

```
m <- lvm(y~x)
ordinal(m,K=3) <- ~y
d <- sim(m,100)
e <- ordreg(y~x,d)
```

org	<i>Convert object to ascii suitable for org-mode</i>
-----	--

Description

Convert object to ascii suitable for org-mode

Usage

```
org(x, ..., ncol, include.rownames = TRUE, include.colnames = TRUE,
    header = TRUE, frame = "topbot", rownames = NULL, colnames = NULL,
    type = "org", tab = FALSE, margins = TRUE, print = TRUE, html, latex,
    sep = " ")
```

Arguments

<code>x</code>	R object
<code>...</code>	additional arguments to lower level functions
<code>ncol</code>	If <code>x</code> is a vector and <code>ncol</code> is given as argument, the resulting output will be a matrix with <code>ncol</code> columns
<code>include.rownames</code>	If FALSE row names are removed
<code>include.colnames</code>	If FALSE column names are removed
<code>header</code>	If TRUE the header is included
<code>frame</code>	Frame argument (see <code>ascii</code>)
<code>rownames</code>	Optional vector of row names
<code>colnames</code>	Optional vector of column names
<code>type</code>	Type argument (see <code>ascii</code>)
<code>tab</code>	Tabulate?
<code>margins</code>	Add margins to table?
<code>print</code>	print or return result
<code>html</code>	HTML prefix (added to <code>ATTR_HTML</code>)
<code>latex</code>	LaTeX prefix (added to <code>ATTR_LaTeX</code>)
<code>sep</code>	separator with <code>type='ascii'</code>

Author(s)

Klaus K. Holst

 parpos

Generic method for finding indeces of model parameters

Description

Generic method for finding indeces of model parameters

Usage

parpos(x, ...)

Arguments

<code>x</code>	Model object
<code>...</code>	Additional arguments

Author(s)

Klaus K. Holst

partialcor	<i>Calculate partial correlations</i>
------------	---------------------------------------

Description

Calculate partial correlation coefficients and confidence limits via Fishers z-transform

Usage

```
partialcor(formula, data, level = 0.95, ...)
```

Arguments

formula	formula specifying the covariates and optionally the outcomes to calculate partial correlation for
data	data.frame
level	Level of confidence limits
...	Additional arguments to lower level functions

Value

A coefficient matrix

Author(s)

Klaus K. Holst

Examples

```
m <- lvm(c(y1,y2,y3)~x1+x2)
covariance(m) <- c(y1,y2,y3)~y1+y2+y3
d <- sim(m,500)
partialcor(~x1+x2,d)
```

path	<i>Extract pathways in model graph</i>
------	--

Description

Extract all possible paths from one variable to another connected component in a latent variable model. In an estimated model the effect size is decomposed into direct, indirect and total effects including approximate standard errors.

Usage

```
## S3 method for class 'lvm'
path(object, to = NULL, from, all=FALSE, ...)
## S3 method for class 'lvmfit'
effects(object, to, from, silent=FALSE, ...)
```

Arguments

object	Model object (lvm)
...	Additional arguments to be passed to the low level functions
to	Outcome variable (string). Alternatively a formula specifying response and predictor in which case the argument from is ignored.
from	Response variable (string), not necessarily directly affected by to.
all	If TRUE all simple paths (in undirected graph) is returned
silent	Logical variable which indicates whether messages are turned on/off.

Value

If object is of class `lvmfit` a list with the following elements is returned

idx	A list where each element defines a possible pathway via a integer vector indicating the index of the visited nodes.
V	A List of covariance matrices for each path.
coef	A list of parameters estimates for each path
path	A list where each element defines a possible pathway via a character vector naming the visited nodes in order.
edges	Description of 'comp2'

If object is of class `lvm` only the path element will be returned.

The effects method returns an object of class `effects`.

Note

For a `lvmfit`-object the parameters estimates and their corresponding covariance matrix are also returned. The `effects`-function additionally calculates the total and indirect effects with approximate standard errors

Author(s)

Klaus K. Holst

See Also

children, parents

Examples

```

m <- lvm(c(y1,y2,y3)~eta)
regression(m) <- y2~x1
latent(m) <- ~eta
regression(m) <- eta~x1+x2
d <- sim(m,500)
e <- estimate(m,d)

path(Model(e),y2~x1)
parents(Model(e), ~y2)
children(Model(e), ~x2)
children(Model(e), ~x2+eta)
effects(e,y2~x1)
## All simple paths (undirected)
path(m,y1~x1,all=TRUE)

```

pcor

Polychoric correlation

Description

Maximum likelihood estimates of polychoric correlations

Usage

```
pcor(x, y, X, start, ...)
```

Arguments

x	Variable 1
y	Variable 2
X	Optional covariates
start	Optional starting values
...	Additional arguments to lower level functions

PD	<i>Dose response calculation for binomial regression models</i>
----	---

Description

Dose response calculation for binomial regression models

Usage

```
PD(model, intercept = 1, slope = 2, prob = NULL, x, level = 0.5,
    ci.level = 0.95, vcov, family, EB = NULL)
```

Arguments

model	Model object or vector of parameter estimates
intercept	Index of intercept parameters
slope	Index of intercept parameters
prob	Index of mixture parameters (only relevant for zibreg models)
x	Optional weights $\text{length}(x) = \text{length}(\text{intercept}) + \text{length}(\text{slope}) + \text{length}(\text{prob})$
level	Probability at which level to calculate dose
ci.level	Level of confidence limits
vcov	Optional estimate of variance matrix of parameter estimates
family	Optional distributional family argument
EB	Optional ratio of treatment effect and adverse effects used to find optimal dose (regret-function argument)

Author(s)

Klaus K. Holst

pdfconvert	<i>Convert pdf to raster format</i>
------------	-------------------------------------

Description

Convert PDF file to print quality png (default 300 dpi)

Usage

```
pdfconvert(files, dpi = 300, resolution = 1024, gs, gsopt, resize,
    format = "png", ...)
```

Arguments

files	Vector of (pdf-)filenames to process
dpi	DPI
resolution	Resolution of raster image file
gs	Optional ghostscript command
gsopt	Optional ghostscript arguments
resize	Optional resize arguments (mogrify)
format	Raster format (e.g. png, jpg, tif, ...)
...	Additional arguments

Details

Access to ghostscript program 'gs' is needed

Author(s)

Klaus K. Holst

See Also

dev.copy2pdf, printdev

plot.lvm

Plot path diagram

Description

Plot the path diagram of a SEM

Usage

```
## S3 method for class 'lvm'
plot(x, diag = FALSE, cor = TRUE, labels = FALSE,
     intercept = FALSE, addcolor = TRUE, plain = FALSE, cex,
     fontsize1 = 10, noplot = FALSE, graph = list(rankdir = "BT"),
     attrs = list(graph = graph), unexpr = FALSE, addstyle = TRUE,
     plot.engine = lava.options()$plot.engine, init = TRUE,
     layout = lava.options()$layout, edgecolor = lava.options()$edgecolor,
     graph.proc = lava.options()$graph.proc, ...)
```

Arguments

<code>x</code>	Model object
<code>diag</code>	Logical argument indicating whether to visualize variance parameters (i.e. diagonal of variance matrix)
<code>cor</code>	Logical argument indicating whether to visualize correlation parameters
<code>labels</code>	Logical argument indicating whether to add labels to plot (Unnamed parameters will be labeled p1,p2,...)
<code>intercept</code>	Logical argument indicating whether to add intercept labels
<code>addcolor</code>	Logical argument indicating whether to add colors to plot (overrides <code>nodecolor</code> calls)
<code>plain</code>	if TRUE strip plot of colors and boxes
<code>cex</code>	Fontsize of node labels
<code>fontsize1</code>	Fontsize of edge labels
<code>noplot</code>	if TRUE then return <code>graphNEL</code> object only
<code>graph</code>	Graph attributes (<code>Rgraphviz</code>)
<code>attrs</code>	Attributes (<code>Rgraphviz</code>)
<code>unexpr</code>	if TRUE remove expressions from labels
<code>addstyle</code>	Logical argument indicating whether additional style should automatically be added to the plot (e.g. dashed lines to double-headed arrows)
<code>plot.engine</code>	default 'Rgraphviz' if available, otherwise <code>visNetwork</code> , <code>igraph</code>
<code>init</code>	Reinitialize graph (for internal use)
<code>layout</code>	Graph layout (see <code>Rgraphviz</code> or <code>igraph</code> manual)
<code>edgecolor</code>	if TRUE plot style with colored edges
<code>graph.proc</code>	Function that post-process the graph object (default: subscripts are automatically added to labels of the nodes)
<code>...</code>	Additional arguments to be passed to the low level functions

Author(s)

Klaus K. Holst

Examples

```

if (interactive()) {
  m <- lvm(c(y1,y2) ~ eta)
  regression(m) <- eta ~ z+x2
  regression(m) <- c(eta,z) ~ x1
  latent(m) <- ~eta
  labels(m) <- c(y1=expression(y[scriptscriptstyle(1)]),
    y2=expression(y[scriptscriptstyle(2)]),
    x1=expression(x[scriptscriptstyle(1)]),
    x2=expression(x[scriptscriptstyle(2)]),

```



```

eta=expression(eta))
edgelabels(m, eta ~ z+x1+x2, cex=2, lwd=3,
           col=c("orange","lightblue","lightblue")) <- expression(rho,phi,psi)
nodecolor(m, vars(m), border="white", labcol="darkblue") <- NA
nodecolor(m, ~y1+y2+z, labcol=c("white","white","black")) <- NA
plot(m,cex=1.5)

d <- sim(m,100)
e <- estimate(m,d)
plot(e)

m <- lvm(c(y1,y2) ~ eta)
regression(m) <- eta ~ z+x2
regression(m) <- c(eta,z) ~ x1
latent(m) <- ~eta
plot(lava::beautify(m,edgecol=FALSE))
}

```

plotConf

*Plot regression lines***Description**

Plot regression line (with interactions) and partial residuals.

Usage

```

plotConf(model, var1 = NULL, var2 = NULL, data = NULL, ci.lty = 0,
         ci = TRUE, level = 0.95, pch = 16, lty = 1, lwd = 2,
         npoints = 100, xlim, col = NULL, colpt, alpha = 0.5, cex = 1,
         delta = 0.07, centermark = 0.03, jitter = 0.2, cidiff = FALSE,
         mean = TRUE, legend = ifelse(is.null(var1), FALSE, "topright"),
         trans = function(x) { x }, partres = inherits(model, "lm"),
         partse = FALSE, labels, vcov, predictfun, plot = TRUE, new = TRUE, ...)

```

Arguments

model	Model object (e.g. lm)
var1	predictor (Continuous or factor)
var2	Factor that interacts with var1
data	data.frame to use for prediction (model.frame is used as default)
ci.lty	Line type for confidence limits
ci	Boolean indicating whether to draw pointwise 95% confidence limits
level	Level of confidence limits (default 95%)
pch	Point type for partial residuals
lty	Line type for estimated regression lines

lwd	Line width for regression lines
npoints	Number of points used to plot curves
xlim	Range of x axis
col	Color (for each level in var2)
colpt	Color of partial residual points
alpha	Alpha level
cex	Point size
delta	For categorical var1
centermark	For categorical var1
jitter	For categorical var1
cidiff	For categorical var1
mean	For categorical var1
legend	Boolean (add legend)
trans	Transform estimates (e.g. exponential)
partres	Boolean indicating whether to plot partial residuals
partse	.
labels	Optional labels of var2
vcov	Optional variance estimates
predictfun	Optional predict-function used to calculate confidence limits and predictions
plot	If FALSE return only predictions and confidence bands
new	If FALSE add to current plot
...	additional arguments to lower level functions

Value

list with following members:

x	Variable on the x-axis (var1)
y	Variable on the y-axis (partial residuals)
predict	Matrix with confidence limits and predicted values

Author(s)

Klaus K. Holst

See Also

termplot

Examples

```

n <- 100
x0 <- rnorm(n)
x1 <- seq(-3,3, length.out=n)
x2 <- factor(rep(c(1,2),each=n/2), labels=c("A","B"))
y <- 5 + 2*x0 + 0.5*x1 + -1*(x2=="B")*x1 + 0.5*(x2=="B") + rnorm(n, sd=0.25)
dd <- data.frame(y=y, x1=x1, x2=x2)
lm0 <- lm(y ~ x0 + x1*x2, dd)
plotConf(lm0, var1="x1", var2="x2")
abline(a=5,b=0.5,col="red")
abline(a=5.5,b=-0.5,col="red")
### points(5+0.5*x1 -1*(x2=="B")*x1 + 0.5*(x2=="B") ~ x1, cex=2)

data(iris)
l <- lm(Sepal.Length ~ Sepal.Width*Species,iris)
plotConf(l,var2="Species")
plotConf(l,var1="Sepal.Width",var2="Species")

```

predict.lvm

*Prediction in structural equation models***Description**

Prediction in structural equation models

Usage

```

## S3 method for class 'lvm'
predict(object, x = NULL, y = NULL, residual = FALSE, p,
        data, path = FALSE, quick = is.null(x) & !(residual | path), ...)

```

Arguments

object	Model object
x	optional list of (endogenous) variables to condition on
y	optional subset of variables to predict
residual	If true the residuals are predicted
p	Parameter vector
data	Data to use in prediction
path	Path prediction
quick	If TRUE the conditional mean and variance given covariates are returned (and all other calculations skipped)
...	Additional arguments to lower level function

See Also

predictlvm

Examples

```
m <- lvm(list(c(y1,y2,y3)~u,u~x)); latent(m) <- ~u
d <- sim(m,100)
e <- estimate(m,d)

## Conditional mean (and variance as attribute) given covariates
r <- predict(e)
## Best linear unbiased predictor (BLUP)
r <- predict(e,vars(e))
## Conditional mean of y3 giving covariates and y1,y2
r <- predict(e,y3~y1+y2)
## Conditional mean gives covariates and y1
r <- predict(e,~y1+y2)
## Predicted residuals (conditional on all observed variables)
r <- predict(e,vars(e),residual=TRUE)
```

predictlvm

Predict function for latent variable models

Description

Predictions of conditional mean and variance and calculation of jacobian with respect to parameter vector.

Usage

```
predictlvm(object, formula, p = coef(object), data = model.frame(object),
...)
```

Arguments

object	Model object
formula	Formula specifying which variables to predict and which to condition on
p	Parameter vector
data	Data.frame
...	Additional arguments to lower level functions

See Also

predict.lvm

Examples

```

m <- lvm(c(x1,x2,x3)~u1,u1~z,
         c(y1,y2,y3)~u2,u2~u1+z)
latent(m) <- ~u1+u2
d <- simulate(m,10,"u2,u2"=2,"u1,u1"=0.5,seed=123)
e <- estimate(m,d)

## Conditional mean given covariates
predictlvm(e,c(x1,x2)~1)$mean
## Conditional variance of u1,y1 given x1,x2
predictlvm(e,c(u1,y1)~x1+x2)$var

```

Range.lvm	<i>Define range constraints of parameters</i>
-----------	---

Description

Define range constraints of parameters

Usage

```
Range.lvm(a = 0, b = 1)
```

Arguments

a	Lower bound
b	Upper bound

Value

function

Author(s)

Klaus K. Holst

regression<-	<i>Add regression association to latent variable model</i>
--------------	--

Description

Define regression association between variables in a lvm-object and define linear constraints between model equations.

Usage

```
## S3 method for class 'lvm'
regression(object = lvm(), to, from, fn = NA,
  silent = lava.options()$silent, additive=TRUE, y, x, value, ...)
## S3 replacement method for class 'lvm'
regression(object, to=NULL, quick=FALSE, ...) <- value
```

Arguments

object	lvm-object.
...	Additional arguments to be passed to the low level functions
value	A formula specifying the linear constraints or if to=NULL a list of parameter values.
to	Character vector of outcome(s) or formula object.
from	Character vector of predictor(s).
fn	Real function defining the functional form of predictors (for simulation only).
silent	Logical variable which indicates whether messages are turned on/off.
additive	If FALSE and predictor is categorical a non-additive effect is assumed
y	Alias for 'to'
x	Alias for 'from'
quick	Faster implementation without parameter constraints

Details

The regression function is used to specify linear associations between variables of a latent variable model, and offers formula syntax resembling the model specification of e.g. lm.

For instance, to add the following linear regression model, to the lvm-object, m:

$$E(Y|X_1, X_2) = \beta_1 X_1 + \beta_2 X_2$$

We can write

```
regression(m) <- y ~ x1 + x2
```

Multivariate models can be specified by successive calls with regression, but multivariate formulas are also supported, e.g.

```
regression(m) <- c(y1,y2) ~ x1 + x2
```

defines

$$E(Y_i|X_1, X_2) = \beta_{1i}X_1 + \beta_{2i}X_2$$

The special function, `f`, can be used in the model specification to specify linear constraints. E.g. to fix $\beta_1 = \beta_2$, we could write

```
regression(m) <- y ~ f(x1,beta) + f(x2,beta)
```

The second argument of `f` can also be a number (e.g. defining an offset) or be set to `NA` in order to clear any previously defined linear constraints.

Alternatively, a more straight forward notation can be used:

```
regression(m) <- y ~ beta*x1 + beta*x2
```

All the parameter values of the linear constraints can be given as the right handside expression of the assignment function `regression<-` (or `regfix<-`) if the first (and possibly second) argument is defined as well. E.g:

```
regression(m,y1~x1+x2) <- list("a1","b1")
```

defines $E(Y_1|X_1, X_2) = a_1X_1 + b_1X_2$. The rhs argument can be a mixture of character and numeric values (and `NA`'s to remove constraints).

The function `regression` (called without additional arguments) can be used to inspect the linear constraints of a `lvm-object`.

For backward compatibility the "\$"-symbol can be used to fix parameters at a given value. E.g. to add a linear relationship between `y` and `x` with slope 2 to the model `m`, we can write `regression(m,"y") <- "x$2"`. Similarly we can use the "@"-symbol to name parameters. E.g. in a multiple regression we can force the parameters to be equal: `regression(m,"y") <- c("x1@b", "x2@b")`. Fixed parameters can be reset by fixing (with `\$`) them to `NA`.

Value

A `lvm-object`

Note

Variables will be added to the model if not already present.

Author(s)

Klaus K. Holst

See Also

[intercept<-](#), [covariance<-](#), [constrain<-](#), [parameter<-](#), [latent<-](#), [cancel<-](#), [kill<-](#)

Examples

```
m <- lvm() ## Initialize empty lvm-object
### E(y1|z,v) = beta1*z + beta2*v
regression(m) <- y1 ~ z + v
### E(y2|x,z,v) = beta*x + beta*z + 2*v + beta3*u
regression(m) <- y2 ~ f(x,beta) + f(z,beta) + f(v,2) + u
### Clear restriction on association between y and
### fix slope coefficient of u to beta
regression(m, y2 ~ v+u) <- list(NA,"beta")

regression(m) ## Examine current linear parameter constraints

## ## A multivariate model, E(yi|x1,x2) = beta[1i]*x1 + beta[2i]*x2:
m2 <- lvm(c(y1,y2) ~ x1+x2)
```

revdiag

Create/extract 'reverse'-diagonal matrix or off-diagonal elements

Description

Create/extract 'reverse'-diagonal matrix or off-diagonal elements

Usage

```
revdiag(x,...)
offdiag(x,type=0,...)

revdiag(x,...) <- value
offdiag(x,type=0,...) <- value
```

Arguments

x	vector
...	additional arguments to lower level functions
value	For the assignment function the values to put in the diagonal
type	0: upper and lower triangular, 1: upper triangular, 2: lower triangular, 3: upper triangular + diagonal, 4: lower triangular + diagonal

Author(s)

Klaus K. Holst

scheffe	<i>Calculate simultaneous confidence limits by Scheffe's method</i>
---------	---

Description

Function to compute the Scheffe corrected confidence interval for the regression line

Usage

```
scheffe(model, newdata = model.frame(model), conf.level = 0.95)
```

Arguments

model	Linear model
newdata	new data frame
conf.level	confidence level (0.95)

Examples

```
x <- rnorm(100)
d <- data.frame(y=rnorm(length(x),x),x=x)
l <- lm(y~x,d)
plot(y~x,d)
abline(l)
d0 <- data.frame(x=seq(-5,5,length.out=100))
d1 <- cbind(d0,predict(l,newdata=d0,interval="confidence"))
d2 <- cbind(d0,scheffe(l,d0))
lines(lwr~x,d1,lty=2,col="red")
lines(upr~x,d1,lty=2,col="red")
lines(lwr~x,d2,lty=2,col="blue")
lines(upr~x,d2,lty=2,col="blue")
```

semdata	<i>Example SEM data</i>
---------	-------------------------

Description

Simulated data

Format

data.frame

Source

Simulated

serotonin

*Serotonin data***Description**

This simulated data mimics a PET imaging study where the 5-HT2A receptor and serotonin transporter (SERT) binding potential has been quantified into 8 different regions. The 5-HT2A cortical regions are considered high-binding regions measurements. These measurements can be regarded as proxy measures of the extra-cellular levels of serotonin in the brain

day	numeric	Scan day of the year
age	numeric	Age at baseline scan
mem	numeric	Memory performance score
depr	numeric	Depression (mild) status 500 days after baseline
gene1	numeric	Gene marker 1 (HTR2A)
gene2	numeric	Gene marker 2 (HTTTLPR)
cau	numeric	SERT binding, Caudate Nucleus
th	numeric	SERT binding, Thalamus
put	numeric	SERT binding, Putamen
mid	numeric	SERT binding, Midbrain
aci	numeric	5-HT2A binding, Anterior cingulate gyrus
pci	numeric	5-HT2A binding, Posterior cingulate gyrus
sfc	numeric	5-HT2A binding, Superior frontal cortex
par	numeric	5-HT2A binding, Parietal cortex

Format

data.frame

Source

Simulated

serotonin2

*Data***Description**

Description

Format

data.frame

Source

Simulated

See Also

serotonin

sim	<i>Simulate model</i>
-----	-----------------------

Description

Simulate data from a general SEM model including non-linear effects and general link and distribution of variables.

Usage

```
## S3 method for class 'lvm'
sim(x, n = NULL, p = NULL, normal = FALSE, cond = FALSE,
    sigma = 1, rho = 0.5, X = NULL, unlink=FALSE, latent=TRUE,
    use.labels = TRUE, seed=NULL, ...)
```

Arguments

x	Model object
...	Additional arguments to be passed to the low level functions
n	Number of simulated values/individuals
p	Parameter value (optional)
normal	Logical indicating whether to simulate data from a multivariate normal distribution conditional on exogenous variables hence ignoring functional/distribution definition
cond	for internal use
sigma	Default residual variance (1)
rho	Default covariance parameter (0.5)
X	Optional matrix of covariates
unlink	Return Inverse link transformed data
latent	Include latent variables (default TRUE)
use.labels	convert categorical variables to factors before applying transformation
seed	Random seed

Author(s)

Klaus K. Holst

Examples

```
#####
## Logistic regression
#####
m <- lvm(y~x+z)
regression(m) <- x~z
distribution(m,~y+z) <- binomial.lvm("logit")
d <- sim(m,1e3)
head(d)
e <- estimate(m,d,estimator="glm")
e
## Simulate a few observation from estimated model
sim(e,n=5)
#####
## Poisson
#####
distribution(m,~y) <- poisson.lvm()
d <- sim(m,1e4,p=c(y=-1,"y~x"=2,z=1))
head(d)
estimate(m,d,estimator="glm")
mean(d$d); lava::expit(1)
summary(lm(y~x,sim(lvm(y[1:2]~4*x),1e3)))
#####
### Gamma distribution
#####
m <- lvm(y~x)
distribution(m,~y+x) <- list(Gamma.lvm(shape=2),binomial.lvm())
intercept(m,~y) <- 0.5
d <- sim(m,1e4)
summary(g <- glm(y~x,family=Gamma(),data=d))
## Not run: MASS::gamma.shape(g)
args(lava::Gamma.lvm)
distribution(m,~y) <- Gamma.lvm(shape=2,log=TRUE)
sim(m,10,p=c(y=0.5))[, "y"]
#####
### Beta
#####
m <- lvm()
distribution(m,~y) <- beta.lvm(alpha=2,beta=1)
var(sim(m,100,"y,y"=2))
distribution(m,~y) <- beta.lvm(alpha=2,beta=1,scale=FALSE)
var(sim(m,100))
#####
### Transform
#####
m <- lvm()
transform(m,xz~x+z) <- function(x) x[1]*(x[2]>0)
regression(m) <- y~x+z+xz
d <- sim(m,1e3)
summary(lm(y~x+z + x*I(z>0),d))
#####
### Non-random variables
```

```
#####
m <- lvm()
distribution(m,~x+z+v+w) <- list(sequence.lvm(0,5),## Seq. 0 to 5 by 1/n
                                ones.lvm(),      ## Vector of ones
                                ones.lvm(0.5),   ## 0.8n 0, 0.2n 1
                                ones.lvm(interval=list(c(0.3,0.5),c(0.8,1))))

sim(m,10)
#####
### Cox model
### piecewise constant hazard
#####
m <- lvm(t~x)
rates <- c(1,0.5); cuts <- c(0,5)
## Constant rate: 1 in [0,5), 0.5 in [5,Inf)
distribution(m,~t) <- coxExponential.lvm(rate=rates,timecut=cuts)
## Not run:
  d <- sim(m,2e4,p=c("t~x"=0.1)); d$status <- TRUE
  plot(timereg::aalen(survival::Surv(t,status)~x,data=d,
                        resample.iid=0,robust=0),spec=1)
  L <- approxfun(c(cuts,max(d$t)),f=1,
                 cumsum(c(0,rates*diff(c(cuts,max(d$t))))),
                 method="linear")
  curve(L,0,100,add=TRUE,col="blue")

## End(Not run)
#####
### Cox model
### piecewise constant hazard, gamma frailty
#####
m <- lvm(y~x+z)
rates <- c(0.3,0.5); cuts <- c(0,5)
distribution(m,~y+z) <- list(coxExponential.lvm(rate=rates,timecut=cuts),
                             loggamma.lvm(rate=1,shape=1))
## Not run:
  d <- sim(m,2e4,p=c("y~x"=0,"y~z"=0)); d$status <- TRUE
  plot(timereg::aalen(survival::Surv(y,status)~x,data=d,
                        resample.iid=0,robust=0),spec=1)
  L <- approxfun(c(cuts,max(d$y)),f=1,
                 cumsum(c(0,rates*diff(c(cuts,max(d$y))))),
                 method="linear")
  curve(L,0,100,add=TRUE,col="blue")

## End(Not run)
## Equivalent via transform (here with Aalens additive hazard model)
m <- lvm(y~x)
distribution(m,~y) <- aalenExponential.lvm(rate=rates,timecut=cuts)
distribution(m,~z) <- Gamma.lvm(rate=1,shape=1)
transform(m,t~y+z) <- prod
sim(m,10)
## Shared frailty
m <- lvm(c(t1,t2)~x+z)
rates <- c(1,0.5); cuts <- c(0,5)
distribution(m,~y) <- aalenExponential.lvm(rate=rates,timecut=cuts)
```

```

distribution(m,~z) <- loggamma.lvm(rate=1,shape=1)
## Not run:
mets::fast.reshape(sim(m,100),varying="t")

## End(Not run)
#####
### General multivariate distributions
#####
## Not run:
m <- lvm()
distribution(m,~y1+y2,oratio=4) <- VGAM::rbiplackcop
ksmooth2(sim(m,1e4),rgl=FALSE,theta=-20,phi=25)
m <- lvm()
distribution(m,~z1+z2,"or1") <- VGAM::rbiplackcop
distribution(m,~y1+y2,"or2") <- VGAM::rbiplackcop
sim(m,10,p=c(or1=0.1,or2=4))

## End(Not run)
m <- lvm()
distribution(m,~y1+y2+y3,TRUE) <- function(n,...) rmv(n,sigma=diag(3)+1)
var(sim(m,100))
## Syntax also useful for univariate generators, e.g.
m <- lvm(y~x+z)
distribution(m,~y,TRUE) <- function(n) rnorm(n,mean=1000)
sim(m,5)
distribution(m,~y,"m1",0) <- rnorm
sim(m,5)
sim(m,5,p=c(m1=100))
#####
### Regression design in other parameters
#####
## Variance heterogeneity
m <- lvm(y~x)
distribution(m,~y) <- function(n,mean,x) rnorm(n,mean,exp(x)^.5)
if (interactive()) plot(y~x,sim(m,1e3))
## Alternatively, calculate the standard error directly
addvar(m) <- ~sd ## If 'sd' should be part of the resulting data.frame
constrain(m,sd~x) <- function(x) exp(x)^.5
distribution(m,~y) <- function(n,mean,sd) rnorm(n,mean,sd)
if (interactive()) plot(y~x,sim(m,1e3))
## Regression on variance parameter
m <- lvm()
regression(m) <- y~x
regression(m) <- v~x
##distribution(m,~v) <- 0 # No stochastic term
## Alternative:
## regression(m) <- v[NA:0]~x
distribution(m,~y) <- function(n,mean,v) rnorm(n,mean,exp(v)^.5)
if (interactive()) plot(y~x,sim(m,1e3))
## Regression on shape parameter in Weibull model
m <- lvm()
regression(m) <- y ~ z+v
regression(m) <- s ~ exp(0.6*x-0.5*z)

```

```

distribution(m,~x+z) <- binomial.lvm()
distribution(m,~cens) <- coxWeibull.lvm(scale=1)
distribution(m,~y) <- coxWeibull.lvm(scale=0.1,shape=~s)
eventTime(m) <- time ~ min(y=1,cens=0)
if (interactive()) {
  d <- sim(m,1e3)
  require(survival)
  (cc <- coxph(Surv(time,status)~v+strata(x,z),data=d))
  plot(survfit(cc) ,col=1:4,mark.time=FALSE)
}
#####
### Categorical predictor
#####
m <- lvm()
## categorical(m,K=3) <- "v"
categorical(m,labels=c("A","B","C")) <- "v"
regression(m,additive=FALSE) <- y~v
## Not run:
plot(y~v,sim(m,1000,p=c("y~v:2"=3)))

## End(Not run)
m <- lvm()
categorical(m,labels=c("A","B","C"),p=c(0.5,0.3)) <- "v"
regression(m,additive=FALSE,beta=c(0,2,-1)) <- y~v
## equivalent to:
## regression(m,y~v,additive=FALSE) <- c(0,2,-1)
regression(m,additive=FALSE,beta=c(0,4,-1)) <- z~v
table(sim(m,1e4)$v)
glm(y~v, data=sim(m,1e4))
glm(y~v, data=sim(m,1e4,p=c("y~v:1"=3)))

transform(m,v2~v) <- function(x) x=="A"
sim(m,10)

#####
### Pre-calculate object
#####
m <- lvm(y~x)
m2 <- sim(m,'y~x'=2)
sim(m,10,'y~x'=2)
sim(m2,10) ## Faster

```

sim.default

Wrapper function for mclapply

Description

Wrapper function for mclapply

Usage

```
## Default S3 method:
sim(x = NULL, R = 100, f = NULL, colnames = NULL,
    messages = lava.options()$messages, mc.cores, blocksize = 2L * mc.cores,
    cl, type = 1L, seed = NULL, args = list(), iter = FALSE, ...)
```

Arguments

x	function or 'sim' object
R	Number of replications or data.frame with parameters
f	Optional function (i.e., if x is a matrix)
colnames	Optional column names
messages	Messages
mc.cores	Number of cores to use
blocksize	Split computations in blocks
cl	(optional) cluster to use for parallelization
type	type=0 is an alias for messages=1,mc.cores=1,blocksize=R
seed	(optional) Seed (needed with cl=TRUE)
args	(optional) list of named arguments passed to (mc)mapply
iter	If TRUE the iteration number is passed as first argument to (mc)mapply
...	Additional arguments to (mc)mapply

Examples

```
m <- lvm(y~x+e)
distribution(m,~y) <- 0
distribution(m,~x) <- uniform.lvm(a=-1.1,b=1.1)
transform(m,e~x) <- function(x) (1*x^4)*rnorm(length(x),sd=1)

onerun <- function(iter=NULL,...,n=2e3,b0=1,idx=2) {
  d <- sim(m,n,p=c("y~x"=b0))
  l <- lm(y~x,d)
  res <- c(coef(summary(l))[idx,1:2],
          confint(l)[idx,],
          estimate(l,only.coef=TRUE)[idx,2:4])
  names(res) <- c("Estimate","Model.se","Model.lo","Model.hi",
                "Sandwich.se","Sandwich.lo","Sandwich.hi")
  res
}

val <- sim(onerun,R=10,b0=1,messages=0,mc.cores=1)
val

val <- sim(val,R=40,b0=1,mc.cores=1) ## append results
summary(val,estimate=c(1,1),confint=c(3,4,6,7),true=c(1,1))

summary(val,estimate=c(1,1),se=c(2,5),names=c("Model","Sandwich"))
summary(val,estimate=c(1,1),se=c(2,5),true=c(1,1),names=c("Model","Sandwich"),confint=TRUE)
```



```

if (interactive()) {
  plot(val,estimate=1,c(2,5),true=1,names=c("Model","Sandwich"),polygon=FALSE)
  plot(val,estimate=c(1,1),se=c(2,5),main=NULL,
        true=c(1,1),names=c("Model","Sandwich"),
        line.lwd=1,density.col=c("gray20","gray60"),
        rug=FALSE)
  plot(val,estimate=c(1,1),se=c(2,5),true=c(1,1),
        names=c("Model","Sandwich"))
}

f <- function(a=1,b=1) {
  rep(a*b,5)
}
R <- Expand(a=1:3,b=1:3)
sim(f,R,type=0)
sim(function(a,b) f(a,b), 3, args=c(a=5,b=5),type=0)
sim(function(iter=1,a=5,b=5) iter*f(a,b), type=0, iter=TRUE, R=5)

```

spaghetti

*Spaghetti plot***Description**

Spaghetti plot for longitudinal data

Usage

```

spaghetti(formula, data, id = "id", group = NULL, type = "o", lty = 1,
  pch = NA, col = 1:10, alpha = 0.3, lwd = 1, level = 0.95,
  trend.formula = formula, tau = NULL, trend.lty = 1, trend.join = TRUE,
  trend.delta = 0.2, trend = !is.null(tau), trend.col = col,
  trend.alpha = 0.2, trend.lwd = 3, trend.jitter = 0, legend = NULL,
  by = NULL, xlab = "Time", ylab = "", add = FALSE, ...)

```

Arguments

formula	Formula (response ~ time)
data	data.frame
id	Id variable
group	group variable
type	Type (line 'l', stair 's', ...)
lty	Line type
pch	Colour
col	Colour
alpha	transparency (0-1)

lwd	Line width
level	Confidence level
trend.formula	Formula for trendline
tau	Quantile to estimate (trend)
trend.lty	Trend line type
trend.join	Trend polygon
trend.delta	Length of limit bars
trend	Add trend line
trend.col	Colour of trend line
trend.alpha	Transparency
trend.lwd	Trend line width
trend.jitter	Jitter amount
legend	Legend
by	make separate plot for each level in 'by' (formula, name of column, or vector)
xlab	Label of X-axis
ylab	Label of Y-axis
add	Add to existing device
...	Additional arguments to lower level arguments

Author(s)

Klaus K. Holst

Examples

```

if (interactive() & requireNamespace("mets")) {
  K <- 5
  y <- "y"%+%"seq(K)
  m <- lvm()
  regression(m,y=y,x=~u) <- 1
  regression(m,y=y,x=~s) <- seq(K)-1
  regression(m,y=y,x=~x) <- "b"
  N <- 50
  d <- sim(m,N); d$z <- rbinom(N,1,0.5)
  dd <- mets::fast.reshape(d); dd$num <- dd$num+3
  spaghetti(y~num,dd,id="id",lty=1,col=Col(1,.4),
            trend.formula=~factor(num),trend=TRUE,trend.col="darkblue")
  dd$num <- dd$num+rnorm(nrow(dd),sd=0.5) ## Unbalance
  spaghetti(y~num,dd,id="id",lty=1,col=Col(1,.4),
            trend=TRUE,trend.col="darkblue")
  spaghetti(y~num,dd,id="id",lty=1,col=Col(1,.4),
            trend.formula=~num+I(num^2),trend=TRUE,trend.col="darkblue")
}

```

stack.estimate	<i>Stack estimating equations</i>
----------------	-----------------------------------

Description

Stack estimating equations

Usage

```
## S3 method for class 'estimate'
stack(x, model2, D1u, inv.D2u, weights, dweights, U, k = 1,
      keep1 = FALSE, ...)
```

Arguments

x	Model 1
model2	Model 2
D1u	Derivative of score of model 2 w.r.t. parameter vector of model 1
inv.D2u	Inverse of deri
weights	weights (vector or function)
dweights	derivative of weight wrt parameters of model 1
U	Optional score function (model 2) as function of all parameters
k	Debug argument
keep1	If TRUE only parameters of model 2 i s returned
...	Additional arguments to lower level functions

startvalues	<i>For internal use</i>
-------------	-------------------------

Description

For internal use

Author(s)

Klaus K. Holst

subset.lvm	<i>Extract subset of latent variable model</i>
------------	--

Description

Extract measurement models or user-specified subset of model

Usage

```
## S3 method for class 'lvm'
subset(x, vars, ...)
```

Arguments

x	lvm-object.
vars	Character vector or formula specifying variables to include in subset.
...	Additional arguments to be passed to the low level functions

Value

A lvm-object.

Author(s)

Klaus K. Holst

Examples

```
m <- lvm(c(y1,y2)~x1+x2)
subset(m,~y1+x1)
```

timedep	<i>Time-dependent parameters</i>
---------	----------------------------------

Description

Add time-varying covariate effects to model

Usage

```
timedep(object, formula, rate, timecut, type = "coxExponential.lvm", ...)
```

Arguments

object	Model
formula	Formula with rhs specifying time-varying covariates
rate	Optional rate parameters. If given as a vector this parameter is interpreted as the raw (baseline-)rates within each time interval defined by timecut. If given as a matrix the parameters are interpreted as log-rates (and log-rate-ratios for the time-varying covariates defined in the formula).
timecut	Time intervals
type	Type of model (default piecewise constant intensity)
...	Additional arguments to lower level functions

Author(s)

Klaus K. Holst

Examples

```
## Piecewise constant hazard
m <- lvm(y~1)
m <- timedep(m,y~1,timecut=c(0,5),rate=c(0.5,0.3))

## Not run:
d <- sim(m,1e4); d$status <- TRUE
dd <- mets::lifetable(Surv(y,status)~1,data=d,breaks=c(0,5,10));
exp(coef(glm(events ~ offset(log(atrisk)) + -1 + interval, dd, family=poisson)))

## End(Not run)

## Piecewise constant hazard and time-varying effect of z1
m <- lvm(y~1)
distribution(m,~z1) <- ones.lvm(0.5)
R <- log(cbind(c(0.2,0.7,0.9),c(0.5,0.3,0.3)))
m <- timedep(m,y~z1,timecut=c(0,3,5),rate=R)

## Not run:
d <- sim(m,1e4); d$status <- TRUE
dd <- mets::lifetable(Surv(y,status)~z1,data=d,breaks=c(0,3,5,Inf));
exp(coef(glm(events ~ offset(log(atrisk)) + -1 + interval+z1:interval, dd, family=poisson)))

## End(Not run)

## Explicit simulation of time-varying effects
m <- lvm(y~1)
distribution(m,~z1) <- ones.lvm(0.5)
distribution(m,~z2) <- binomial.lvm(p=0.5)
#variance(m,~m1+m2) <- 0
```

```
#regression(m,m1[m1:0] ~ z1) <- log(0.5)
#regression(m,m2[m2:0] ~ z1) <- log(0.3)
regression(m,m1 ~ z1,variance=0) <- log(0.5)
regression(m,m2 ~ z1,variance=0) <- log(0.3)
intercept(m,~m1+m2) <- c(-0.5,0)
m <- timedep(m,y~m1+m2,timecut=c(0,5))

## Not run:
d <- sim(m,1e5); d$status <- TRUE
dd <- mets::lifetable(Surv(y,status)~z1,data=d,breaks=c(0,5,Inf))
exp(coef(glm(events ~ offset(log(atrisk)) + -1 + interval + interval:z1, dd, family=poisson)))

## End(Not run)
```

toformula

Converts strings to formula

Description

Converts a vector of predictors and a vector of responses (characters) into a formula expression.

Usage

```
toformula(y = ".", x = ".")
```

Arguments

y	vector of predictors
x	vector of responses

Value

An object of class formula

Author(s)

Klaus K. Holst

See Also

[as.formula](#),

Examples

```
toformula(c("age", "gender"), "weight")
```

tr	<i>Trace operator</i>
----	-----------------------

Description

Calculates the trace of a square matrix.

Usage

```
tr(x, ...)
```

Arguments

x	Square numeric matrix
...	Additional arguments to lower level functions

Value

numeric

Author(s)

Klaus K. Holst

See Also

[crossprod](#), [tcrossprod](#)

Examples

```
tr(diag(1:5))
```

trim	<i>Trim tring of (leading/trailing/all) white spaces</i>
------	--

Description

Trim tring of (leading/trailing/all) white spaces

Usage

```
trim(x, all = FALSE, ...)
```

Arguments

x	String
all	Trim all whitespaces?
...	additional arguments to lower level functions

Author(s)

Klaus K. Holst

twindata	<i>Twin menarche data</i>
----------	---------------------------

Description

Simulated data

id	numeric	Twin-pair id
zyg	character	Zygoty (MZ or DZ)
twinnum	numeric	Twin number (1 or 2)
agemena	numeric	Age at menarche (or censoring)
status	logical	Censoring status (observed:=T,censored:=F)
bw	numeric	Birth weight
msmoke	numeric	Did mother smoke? (yes:=1,no:=0)

Format

data.frame

Source

Simulated

twostage	<i>Two-stage estimator</i>
----------	----------------------------

Description

Generic function

Usage

twostage(object, ...)

Arguments

object	Model object
...	Additional arguments to lower level functions

See Also

twostage.lvm twostage.lvmfit twostage.lvm.mixture twostage.estimate

twostage.lvmfit	<i>Two-stage estimator (non-linear SEM)</i>
-----------------	---

Description

Two-stage estimator for non-linear structural equation models

Usage

```
## S3 method for class 'lvmfit'
twostage(object, model2, data = parent.frame(),
  predictfun = function(mu, var, data, ...) cbind(u1 = mu[, 1], u2 = mu[, 1]^2
    + var[1]), id1, id2, all = FALSE, ...)
```

Arguments

object	Stage 1 measurement model
model2	Stage 2 SEM
data	data.frame
predictfun	Prediction of latent variable
id1	Optional id-variable (stage 1 model)
id2	Optional id-variable (stage 2 model)
all	If TRUE return additional output (naive estimates)
...	Additional arguments to lower level functions

Examples

```
m <- lvm(c(x1,x2,x3)~f1,f1~z,
  c(y1,y2,y3)~f2,f2~f1+z)
latent(m) <- ~f1+f2
d <- simulate(m,100,p=c("f2,f2"=2,"f1,f1"=0.5),seed=1)

## Full MLE
ee <- estimate(m,d)

## Manual two-stage
## Not run:
```

```

m1 <- lvm(c(x1,x2,x3)~f1,f1~z); latent(m1) <- ~f1
e1 <- estimate(m1,d)
pp1 <- predict(e1,f1~x1+x2+x3)

d$u1 <- pp1[,]
d$u2 <- pp1[,]^2+attr(pp1,"cond.var")
m2 <- lvm(c(y1,y2,y3)~eta,c(y1,eta)~u1+u2+z); latent(m2) <- ~eta
e2 <- estimate(m2,d)

## End(Not run)

## Two-stage
m1 <- lvm(c(x1,x2,x3)~f1,f1~z); latent(m1) <- ~f1
m2 <- lvm(c(y1,y2,y3)~eta,c(y1,eta)~u1+u2+z); latent(m2) <- ~eta
pred <- function(mu,var,data,...)
  cbind("u1"=mu[,1],"u2"=mu[,1]^2+var[1])
(mm <- twostage(m1,model2=m2,data=d,predictfun=pred))

if (interactive()) {
  pf <- function(p) p["eta"]+p["eta~u1"]*u + p["eta~u2"]*u^2
  plot(mm,f=pf,data=data.frame(u=seq(-2,2,length.out=100)),lwd=2)
}

```

vars

*Extract variable names from latent variable model***Description**

Extract exogenous variables (predictors), endogenous variables (outcomes), latent variables (random effects), manifest (observed) variables from a lvm object.

Usage

```

vars(x,...)

endogenous(x,...)

exogenous(x,...)

manifest(x,...)

latent(x,...)

## S3 replacement method for class 'lvm'
exogenous(x,silent = FALSE, xfree = TRUE,...) <- value

## S3 method for class 'lvm'
exogenous(x,latent=FALSE,index=TRUE,...)

```

```
## S3 replacement method for class 'lvm'
latent(x,clear=FALSE,...) <- value
```

Arguments

x	lvm-object
...	Additional arguments to be passed to the low level functions
latent	Logical defining whether latent variables without parents should be included in the result
index	For internal use only
clear	Logical indicating whether to add or remove latent variable status
silent	Suppress messages
xfree	For internal use only
value	Formula or character vector of variable names.

Details

vars returns all variables of the lvm-object including manifest and latent variables. Similarly manifest and latent returns the observed resp. latent variables of the model. exogenous returns all manifest variables without parents, e.g. covariates in the model, however the argument latent=TRUE can be used to also include latent variables without parents in the result. Pr. default lava will not include the parameters of the exogenous variables in the optimisation routine during estimation (likelihood of the remaining observed variables conditional on the covariates), however this behaviour can be altered via the assignment function exogenous<- telling lava which subset of (valid) variables to condition on. Finally latent returns a vector with the names of the latent variables in x. The assignment function latent<- can be used to change the latent status of variables in the model.

Value

Vector of variable names.

Author(s)

Klaus K. Holst

See Also

[endogenous](#), [manifest](#), [latent](#), [exogenous](#), [vars](#)

Examples

```
g <- lvm(eta1 ~ x1+x2)
regression(g) <- c(y1,y2,y3) ~ eta1
latent(g) <- ~eta1
endogenous(g)
exogenous(g)
```

```
identical(latent(g), setdiff(vars(g),manifest(g)))
```

vec	<i>vec operator</i>
-----	---------------------

Description

vec operator

Usage

```
vec(x, matrix = FALSE, sep = ".", ...)
```

Arguments

x	Array
matrix	If TRUE a row vector (matrix) is returned
sep	Seperator
...	Additional arguments

Details

Convert array into vector

Author(s)

Klaus Holst

wrapvec	<i>Wrap vector</i>
---------	--------------------

Description

Wrap vector

Usage

```
wrapvec(x, delta = 0L, ...)
```

Arguments

x	Vector or integer
delta	Shift
...	Additional parameters

Examples

```
wrapvec(5,2)
```

zibreg

Regression model for binomial data with unkown group of immortals

Description

Regression model for binomial data with unkown group of immortals (zero-inflated binomial regression)

Usage

```
zibreg(formula, formula.p = ~1, data, family = stats::binomial(),
       offset = NULL, start, var = "hessian", ...)
```

Arguments

formula	Formula specifying
formula.p	Formula for model of disease prevalence
data	data frame
family	Distribution family (see the help page family)
offset	Optional offset
start	Optional starting values
var	Type of variance (robust, expected, hessian, outer)
...	Additional arguments to lower level functions

Author(s)

Klaus K. Holst

Examples

```
## Simulation
n <- 2e3
x <- runif(n,0,20)
age <- runif(n,10,30)
z0 <- rnorm(n,mean=-1+0.05*age)
z <- cut(z0,breaks=c(-Inf,-1,0,1,Inf))
p0 <- lava::expit(model.matrix(~z+age) %*% c(-.4, -.4, 0.2, 2, -0.05))
y <- (runif(n)<lava::tlogit(-1+0.25*x-0*age))*1
u <- runif(n)<p0
y[u==0] <- 0
d <- data.frame(y=y,x=x,u=u*1,z=z,age=age)
head(d)
```

```
## Estimation
e0 <- zibreg(y~x*z,~1+z+age,data=d)
e <- zibreg(y~x,~1+z+age,data=d)
compare(e,e0)
e
PD(e0,intercept=c(1,3),slope=c(2,6))

B <- rbind(c(1,0,0,0,20),
           c(1,1,0,0,20),
           c(1,0,1,0,20),
           c(1,0,0,1,20))
prev <- summary(e,pr.contrast=B)$prevalence

x <- seq(0,100,length.out=100)
newdata <- expand.grid(x=x,age=20,z=levels(d$z))
fit <- predict(e,newdata=newdata)
plot(0,0,type="n",xlim=c(0,101),ylim=c(0,1),xlab="x",ylab="Probability(Event)")
count <- 0
for (i in levels(newdata$z)) {
  count <- count+1
  lines(x,fit[which(newdata$z==i)],col="darkblue",lty=count)
}
abline(h=prev[3:4,1],lty=3:4,col="gray")
abline(h=prev[3:4,2],lty=3:4,col="lightgray")
abline(h=prev[3:4,3],lty=3:4,col="lightgray")
legend("topleft",levels(d$z),col="darkblue",lty=seq_len(length(levels(d$z))))
```

%++%	<i>Concatenation operator</i>
------	-------------------------------

Description

For matrices a block-diagonal matrix is created. For all other data types he operator is a wrapper of paste.

Usage

```
x %++% y
```

Arguments

- x First object
- y Second object of same class

Details

Concatenation operator

Author(s)

Klaus K. Holst

See Also

blockdiag, [paste](#), [cat](#),

Examples

```
matrix(rnorm(25),5)%++matrix(rnorm(25),5)
"Hello "%++%" World"
```

%ni%

Matching operator (x not in y) oposed to the %in%-operator (x in y)

Description

Matching operator

Usage

```
x %ni% y
```

Arguments

x	vector
y	vector of same type as x

Value

A logical vector.

Author(s)

Klaus K. Holst

See Also

[match](#)

Examples

```
1:10 %ni% c(1,5,10)
```

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