

Package ‘gmvalid’

November 3, 2009

Type Package

Title Validation of graphical models

Version 1.21

Date 2009-11-01

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Description Simulate data sets given a dependence model, validate graphical models using the bootstrap, find the best prediction model using cross validation.

License GPL (>= 2)

Depends R (>= 2.7.0), grid, epitools, CoCo, CoCoObjects, CoCoRaw, CoCoCore, gtools

Suggests mimR

Repository CRAN

Date/Publication 2009-11-03 11:42:50

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`gm.chi`*Conditional chi-squared test*

Description

Conducts a conditional chi-squared test for the null hypothesis X independent Y given Z.

Usage

```
gm.chi(data, X = 1, Y = 2, Z = 3)
```

Arguments

<code>data</code>	Data frame or a table (array). Variables should have names, <code>data</code> has to be discrete.
<code>X</code>	Number of column of the first variable in data.
<code>Y</code>	Number of column of the second variable in data.
<code>Z</code>	Number of column of the variable in condition in data.

Details

The conditional chi-squared test is conducted like a marginal chi-squared test where the expected cell counts are calculated as: $E(i,j,k) = E(i,+,k) * E(+,j,k) / E(+,+,k)$

Value

<code>chi.squared</code>	Value of the chi-squared statistic.
<code>DF</code>	Degrees of freedom.
<code>p.value</code>	P-value of the test.

Author(s)

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References

Agresti A (1990) *Categorical Data Analysis* Wiley, New York.

See Also

[gm.gamma](#), [chisq.test](#)

Examples

```

data(dp)
gm.chi(dp, 1, 2, 3)
gm.chi(dp, 2, 3, 1)
gm.chi(dp, 1, 3, 2)

```

gm.csi

*Conditional Synergy Index***Description**

Computes the conditional synergy index of two dichotomous variables in relation to a binary group variable.

Usage

```
gm.csi(X, Y, group, data=0, reference=c(1,1,2), pen = NULL, conf.level = 0.95)
```

Arguments

X	Index of the variable's position in <code>data</code> or a vector.
Y	Index of the variable's position in <code>data</code> or a vector.
group	Binary group or outcome variable addressed as variable index in <code>data</code> or a vector. By default, 2 is the reference category.
data	Data frame or table.
reference	Vector to define the reference categories of X, Y and group. By default, 2 is the reference category for group and 1 for X and Y.
pen	If FALSE the penetrance $P(\text{group} X, Y)$ is estimated from the data.
conf.level	Confidence level of the interval (default is 0.95).

Details

Foraita's conditional synergy index (CSI) is an interaction measure on the penetrance scale between two dichotomous variables on a binary outcome. The index equals 1 under additivity, $\text{CSI} > 1$ in the case of antagonism and $\text{CSI} < 1$ in the presence of synergy.

The confidence intervals are calculated using an asymptotic variance given in Foraita (2008).

Value

A list containing:

penetrance	A matrix containing the joint penetrance. If <code>pen = NULL</code> , the penetrance will be estimated from the data using relative frequencies.
measure	A matrix containing the estimate, variance, standard error, confidence interval and p-value. Figures in brackets show the reference category respectively the category under consideration.

Author(s)

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References

Foraita R (2008) *A conditional synergy index to assess biological interaction*. <http://nbn-resolving.de/urn:nbn:de:gbv:46-diss000111139>

See Also

[gm.si](#)

Examples

```
data(idd35)
gm.csi(1,2,3,data=idd35)

### >> constructing an additive and multiplicative penetrance
x <- c(0.1,0.4)
y <- c(0.05,0.5)
add.pen <- outer(x,y,FUN="+")
mult.pen <- outer(x,y)
het.pen <- outer(x,y,FUN="+") - outer(x,y)

### >> Function that samples data using the penetrance
make.data <- function(R,pen,category)
{
  s.vec <- sample(c(1,2,3,4),R,replace=TRUE,prob=as.vector(pen))
  fact.1 <- fact.2 <- vector()
  for( i in 1:R ) {
    ifelse( s.vec[i] == 1 || s.vec[i] == 3 , fact.1[i] <- 1, fact.1[i] <- 2 )
    ifelse( s.vec[i] == 1 || s.vec[i] == 2 , fact.2[i] <- 1, fact.2[i] <- 2 )
  }
  cbind(X=fact.1,Y=fact.2,group=rep(category,R))
}

### >>> Building datasets with affected and unaffected subjects
add.aff <- make.data(200,add.pen,2)
add.uaf <- make.data(200,1-add.pen,1)
add.df <- as.data.frame(rbind(add.uaf,add.aff))

mult.aff <- make.data(200,mult.pen,2)
mult.uaf <- make.data(200,1-mult.pen,1)
mult.df <- as.data.frame(rbind(mult.uaf,mult.aff))

het.aff <- make.data(200,het.pen,2)
het.uaf <- make.data(200,1-het.pen,1)
het.df <- as.data.frame(rbind(het.uaf,het.aff))

gm.csi(1,2,3,add.df,pen=add.pen) # Additivity
```

```
gm.csi(1,2,3,mult.df,pen=mult.pen) # Synergy
gm.csi(1,2,3,het.df,pen=het.pen)  # Antagonism
```

gm.gamma

Conditional Gamma coefficient estimation and confidence intervals

Description

Calculates conditional gamma coefficients of two binary or ordinal variables X and Y given a set of variables {A,B,...}.

Usage

```
gm.gamma(X = 0, Y = 0, data = 0, conditions = 0,
         type = c("conditional", "single", "marginal"), conf.level = 0.95)
```

Arguments

X	Index of the variable's position in data or a vector.
Y	Index of the variable's position in data or a vector.
data	Data frame or table
conditions	Variable indices in data or a data frame of the conditioning variables.
type	Character string specifying the method, must be one of "conditional" (default), "single" or "marginal". May be abbreviated.
conf.level	Confidence level of the interval (default is 0.95).

Details

The gamma coefficient is a correlation measure between two binary or ordinal variables. It ranges between -1 and 1, where -1 or respectively +1 stands for a purely negative or positive monotone relation. The relation has not to be of linear nature!

If `type = "conditional"`, the conditional gamma coefficients are calculated and if `type = "marginal"`, the marginal gamma coefficients are computed.

If X and Y are given, the "single" gamma coefficient between both variables are computed.

If X or Y are zero, the function computes all possible conditional gamma coefficients.

Confidence intervals are calculated using the asymptotic variance given in Olszak and Ritschard (1995).

Value

A matrix containing the gamma estimate(s), standard deviation(s), confidence interval(s) and p-value(s).

Author(s)

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References

Davis JA (1967) *A partial coefficient for Goodman and Kruskal's gamma*. Journal of the American Statistical Association, 62:189-193.

Olszak M, Ritschard G (1995) *The behaviour of nominal and ordinal partial association measures*. The Statistician, 44(2):195-212.

See Also

[gm.or](#), [gm.rr](#)

Examples

```
data(dp)

### Conditional Gamma by victime
gm.gamma(1,3,conditions=2,data=dp)
### the same
gm.gamma(dp$Defendants.Race,dp$Death.Penalty,data=dp,conditions=dp$Victims.Race)

### Stratified Gamma
dp.black <- data.frame(victime=dp$Victims.Race[dp$Victims.Race=="black"],
                      killer=dp$Defendants.Race[dp$Victims.Race=="black"],
                      death.penalty=dp$Death.Penalty[dp$Victims.Race=="black"])
dp.white <- data.frame(victime=dp$Victims.Race[dp$Victims.Race=="white"],
                      killer=dp$Defendants.Race[dp$Victims.Race=="white"],
                      death.penalty=dp$Death.Penalty[dp$Victims.Race=="white"])
table(dp.black[,c(2,3,1)])
table(dp.white[,c(2,3,1)])

gm.gamma(2,3,data=dp.black)
gm.gamma(2,3,data=dp.white)

### Marginal Gamma
gm.gamma(1,3,data=dp)

### Analyse complete data set
gm.gamma(data=dp,type="m")

### Plot model
gamma <- gm.gamma(data=dp)
#> all edges
mat <- matrix(NA,nrow=3,ncol=3)
mat[upper.tri(mat)] <- gamma[,1]
gm.plot(model="abc",data.analysis=mat)
#> only significant edges
```

```
mat <- matrix(NA,nrow=3,ncol=3)
tmp <- vector()
for( i in 1:dim(gamma)[1] ) ifelse(gamma[i,5]<0.05, tmp[i] <- gamma[i,1], tmp[i] <-NA)
mat[upper.tri(mat)] <- tmp
gm.plot(model="ab,bc",data.analysis=mat)
```

gm.generate

Random data frames of binary variables given fixed marginals

Description

Generates a random data frame of independent binary variables given fixed marginals.

Usage

```
gm.generate(N, p = c(0.5, 0.5, 0.5))
```

Arguments

N	Number of observations, sample size.
p	Probability vector. Each element assigns the probability to draw a "2". The user-defined number of elements determines the number of variables in the resulting data frame.

Value

A data frame with number of rows equal to N and number of columns equal to the length of p.

Author(s)

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See Also

[gm.modelsim](#), [gm.sim.ixj](#), [r2dtable](#)

Examples

```
gm.generate(10,c(.5,.2,.2))
gm.generate(15,c(.5,.5,.5,.5,.5,.5))
```

gm.modelsim	<i>Random data frames with given dependence model and fixed marginals</i>
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Description

Generates a random data frame of discrete variables given a dependence model and marginals.

Usage

```
gm.modelsim(N, model, categories = 0)
```

Arguments

N	Number of observations, sample size.
model	A character string assigning a dependence model expressed as clique structure. Each variable has to be expressed as a letter, e.g. "ABC,CDE".
categories	a list of weight vectors that assigns the weight of each category. Number of list elements must equal the number of variables in model. Default is "list(c(.5,.5),c(.5,.5),...)".

Value

A data frame with number of rows approximately equal to N and number of columns equal to the number of variables used in model.

Note

Observed marginal probabilities reflect the given marginal probabilities only approximately. Works best with large sample sizes, like e.g. N=10,000.

Author(s)

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See Also

[gm.generate](#), [gm.sim.ixj](#), [r2dtable](#)

Examples

```
gm.modelsim(100, "AB,AC")
table( gm.modelsim(100, "a,b,c" ) )

tmp.df <- gm.modelsim(10000, "abf,cd,cf,bdeg,bfg")

# with given number of categories
```

```

tmp.df <- gm.modelsim(1000, "AB,C", list(c(1,1,1), c(1,1), c(1,1,1)))

# with given number of categories and marginals
tmp.df <- gm.modelsim(1000, "ABC", list(c(0.3,0.3,0.4), c(0.6, .4), c(0.25,0.25,0.5)))
table(tmp.df)

## Not run:
tmp.df <- gm.modelsim(100, "ABC", list(3,2,3))# (number of categories will be 2 x 2 x 2 )
      gm.modelsim(100, "123")

## End(Not run)

```

gm.or, gm.rr

Stratified odds ratios and risk ratios

Description

Computes (stratified) odds ratios or risk ratios and their asymptotic confidence interval.

Usage

```

gm.or(X, Y, data = 0, conditions = 0,
      reference = c("last", "biggest", "first"), conf.level = 0.95)

gm.rr(X, Y, data = 0, conditions = 0,
      reference = c("last", "biggest", "first"), conf.level = 0.95)

```

Arguments

X	Index of the variable's position in data or a vector.
Y	Index of the variable's position in data or a vector.
data	Data frame or table
conditions	Variable indices in data or a data frame of the conditional variables.
reference	Character string specifying the reference category. Must be one of "last" (default), "biggest" (largest) or "first", may be abbreviated.
conf.level	Confidence level of the interval (default is 0.95).

Details

Calculates odds ratios by conditional maximum likelihood estimation (Fisher) for stratified odds ratios and odds ratios by unconditional maximum likelihood estimation (Wald) for marginal odds ratios. Confidence intervals are calculated using exact methods.

Calculates risk ratios by unconditional maximum likelihood estimation (Wald). Confidence intervals are calculated using normal approximation.

Is based on the functions `oddsratio.fisher`, `oddsratio.wald` and `riskratio.wald` (package: epitools).

Value

A matrix containing estimate(s), confidence interval(s) and p-value(s).

Author(s)

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References

<http://www.epitools.net>

Rothman KJ, Greenland S (1998) *Modern Epidemiology*. (2nd) Lippincott-Raven Publisher

See Also

[oddsratio](#), [riskratio](#)

Examples

```
group <- c("treatment", "placebo1", "placebo2")
target <- c("low", "medium", "high")
mat <- matrix(c(78, 35, 53, 77, 10, 89, 16, 119, 32), nrow=3, ncol=3, byrow=TRUE,
              dimnames=list("group"=group, "target"=target))
treat <- data.frame(expand.table(mat))
table(treat)

### Marginal OR
gm.or(1,2,treat,reference="f")
gm.or(treat$target,treat$group)

### Stratified OR
data <- gm.modelsim(1000,"ab,bcd",list(c(1,1),c(1,1),c(1,1),c(1,1)))
gm.or(1,2,conditions=c(3,4),data=data)

### Marginal RR
gm.rr(1,2,treat,reference="f")
gm.rr(treat$target,treat$group)

### Stratified RR
data <- gm.modelsim(1000,"ab,bcd",list(c(1,1),c(1,1),c(1,1),c(1,1)))
gm.rr(1,2,conditions=c(3,4),data=data)

### ALSO
gm.or(X=data$a,Y=data$b,conditions=data$d)
```

`gm.plot`*Plot graphical models*

Description

Plots given graphical models and writes provided measures next to the edges.

Usage

```
gm.plot(model, significant = TRUE, data.analysis = 0)
```

Arguments

<code>model</code>	String vector with model formulas. See gm.modelsim .
<code>significant</code>	If TRUE only significant edges in the selected models are plotted (in solid lines). If FALSE also not significant edges are plotted as dashed lines.
<code>data.analysis</code>	Upper-tri matrix of estimates for the edge between variables i and j ($i > j$) at matrix position $[i,j]$. If the length of the <code>model</code> is bigger than 1, <code>data.analysis</code> has to be a list of matrices.

Details

The line width of the edges will depend on the size of the numbers in `data.analysis`.

Value

TRUE

Note

Every use of the plot function opens a new window.

Author(s)

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See Also

[gm.analysis](#)

Examples

```
gm.plot("ABC,CDE")

gm.plot("VBA,EVC")

gm.plot(c("ABC,CDE","AB,BC,CD,DE","ABC,DEF,GHI"))

gm.plot("AB,AC",FALSE,matrix(0.5,nrow=3,ncol=3))
```

gm.screening

Model Screening

Description

Preliminary model search procedure for categorical data in three steps, using Goodman's and Kruskal's gamma and chi-squared tests.

Usage

```
gm.screening(data, conf.level = 0.95)
```

Arguments

`data` Data frame or array. Variables need to be discrete and should have names.
`conf.level` Confidence level (default is 0.95).

Details

The initial model screening divides into three parts: (1) An edge is added to the main effects model, if the marginal gamma coefficient or the chi-squared statistic is significant. (2) An edge is added between two vertices, if either the conditional gamma coefficient or the conditional chi-squared statistic is significant for the two variables given any possible variable in condition. (3) All triplets of variables whose vertices build a complete subgraph are tested for removal using the conditional gamma coefficient and conditional chi-squared statistic. An edge is removed if the corresponding p-value is larger than $1 - \text{conf.level}$.

Value

`mat` Adjacency matrix of the screened model.
`model` String of the graphical model.

Note

The model screening is not a model selection strategy! It 'just' searches for a good start model to initialize a model selection. Common usage is to select a model after screening based on a backwards and forwards selection as implemented in [gm.coco](#).

Author(s)

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References

- Kreiner S and Edwards D (1983) *The analysis of contingency tables by graphical models* Biometrika, 70(3):553-565
- Kreiner S (2008) *DIGRAM* <http://staff.pubhealth.ku.dk/~skm/skm/> last accessed 30.06.2008
- Siersma V (2007) *Studies in the interactions between disease development and interventions* PhD thesis, Faculty of Health Sciences, University of Copenhagen.

See Also

[backward](#), [gm.coco](#), [gm.chi](#), [gm.gamma](#)

Examples

```
data(wam)
model <- gm.screening(wam)
gm.coco(wam, recursive=TRUE, criterion="aic", model=model$model)
```

gm.si

Synergy Index

Description

Computes the synergy index of two discrete variables in relation to a binary group variable.

Usage

```
gm.si(X, Y, group, data=0, reference=c(1, 1, 2), conf.level = 0.95)
```

Arguments

X	Index of the variable's position in data or a vector.
Y	Index of the variable's position in data or a vector.
group	Binary group or outcome variable addressed as variable index in data or as vector.
data	Data frame or table.
reference	Vector to define the reference categories of X, Y and group. By default, 2 is the reference category for group.
conf.level	Confidence level of the interval (default is 0.95).

Details

Rothman's synergy index (S) is an interaction measure between two discrete variables on a dichotomous outcome. The index equals 1 under additivity, $S > 1$ in the case of synergy and $S < 1$ in the presence of antagonism.

The synergy index is originally constructed on (2×2) -tables, but $(i \times j)$ -tables can also be analyzed. Then $(i-1) \times (j-1)$ synergy indices are computed and combined to an overall synergy index.

The confidence intervals are calculated using the asymptotic variance given in Rothman (1974).

Value

A list containing:

OddsRatio	A odds ratio table.
covariance	Covariance matrix for category specific synergy indices. Not written if X or Y are binary.
measure	Matrix containing the estimate(s), standard deviation(s), confidence interval(s) and p-value(s). Figures in brackets show the reference category respectively the category under consideration. If both factors X and Y are binary, confidence intervals for case-control as well as cohort designs are computed. If at least one factor has more than 2 categories, the overall synergy index with its corresponding confidence interval is computed that follows a case-control design.

Note

It can occur that certain combinations of categories lead to a negative synergy indices. In that case confidence intervals cannot be computed. If so, use the `reference` option to re-order the categories of the variable(s) in question (see example below).

Author(s)

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(BIPS) <http://www.bips.uni-bremen.de>

References

- Rothman K (1974) *The estimation of synergy or antagonism*. American Journal of Epidemiology, 103(5):506-511
- Rothman K (1986) *Modern Epidemiology*. Little, Brown and Company, Boston/Toronto.

See Also

[gm.csi](#)

Examples

```

data(wynder)
gm.si(1,2,3,wynder)

# Smoking and alcohol in relation to oral cancer among male veterans under age 60.
# (from "Modern Epidemiology")
oral <- array(c(20,3,18,8,12,6,166,225),dim=c(2,2,2),
             dimnames=list(Group=c("control","cases"),
                             Smoker=c("no","yes"),Alcohol=c("no","yes")))
oral.df <- expand.table(oral)
# grouping variable is first in data frame
gm.si(2,3,1,oral.df)

# Effects must be ascending in respect to the reference category
show.effect <- array(c(1,7,2,7,7,12,106,48),dim=c(2,2,2),
                    dimnames=list(A=1:2,B=1:2,C=1:2))

# produces NaN
gm.si(1,2,3,expand.table(show.effect))
# > re-ordering variable B helps
gm.si(1,2,3,expand.table(show.effect),reference=c(1,2,2))

```

gm.sim.ixj

Random (i x j)-way dependency table with given marginals

Description

Generates random (i x j)-way dependency table with given marginals.

Usage

```
gm.sim.ixj(N, pa, pb)
```

Arguments

N	Number of observations; sample size.
pa	Weight vector of length i to assign the distribution of the row totals.
pb	Weight vector of length j to assign the distribution of the column totals.

Value

A (i x j)-matrix.

Note

Observed totals that were generated according to the shorter weight vector reflect the given weights only approximatively.

Author(s)

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See Also

[gm.generate](#), [gm.modelsim](#), [r2dtable](#)

Examples

```
gm.sim.ixj(1000,c(1,1,1),c(1,1,1,1,1))
gm.sim.ixj(1000,c(.2,.3,.4,.1),c(.5,.2,.3))

round(gm.sim.ixj(30,c(1,1),c(1,1)))

tab <- round(gm.sim.ixj(500,c(.5,.5),c(.5,.5)))
chisq.test(tab)
```

idd35

Type 1 Diabetes susceptibility loci Idd3 and Idd5

Description

Loci Idd3 and Idd5 are susceptible to be associated with type 1 diabetes. This data reflects an animal experiment from Hill et al. (2000).

Usage

```
data(idd35)
```

Format

A data frame with 313 observations on the following 3 variables.

idd3 a factor with levels NN and BB

idd5 a factor with levels NN and BB

group a factor with levels `controls` `cases`

Details

Data was used from Cordell et al. (2001) to model the joint effect of alleles at loci Idd3 and Idd5 on the outcome "type 1 diabetes". Only homozygous genotypes were available.

Source

Hill NJ, Lyons PA, Armitage N, Todd JA, Wicker LS and Peterson LB (2000) *NOD Idd5 locus controls insulinitis and diabetes and overlaps the orthologous CTLA4/IDDM12 and NRAMP1 loci in humans*. Diabetes, 49:1744-1747.

References

Cordell HJ, Todd JA, Hill NJ, Lord CJ, Lyons PA, Peterson LB, Wicker LS and Clayton DG (2001) *Statistical modeling of interlocus interactions in a complex disease: Rejection of the multiplicative model of epistasis in type 1 diabetes*. *Genetics*, 158:357-367.

Examples

```
data(idd35)
table(idd35)
```

wynder

Alcohol, Smoking and Oral Cancer

Description

Alcohol drinking and smoking among cases of oral cancer and controls.

Usage

```
data(wynder)
```

Format

A data frame with 443 observations on the following 3 variables.

Alc a numeric vector indicating the units of alcohol.

Smoking a numeric vector indicating the units of smoked cigarettes.

Group a numeric vector indicating whether the subject is "control" (1) or "case" (2).

Details

One unit of alcohol equals 1 oz (30 cc) of whiskey or 8 oz (237 cc) of beer.

Source

Wynder EE, Bross IJ, Feldman R (1957) *A study of etiological factors in cancer of the mouth*. *Cancer*, 10:1300-1323.

References

Rothman K (1974) *The estimation of synergy or antagonism*. *American Journal of Epidemiology*, 103(5):506-511

Examples

```
data(wynder)
tab <- table(wynder)
dimnames(tab) <- list(c("<1", "1-6", ">6"), c("<15", "16-34", ">34"), c("controls", "cases"))
names(dimnames(tab)) <- c("Alcohol (unit/day)", "Smoking (cigarettes/day)", "Group")
tab
```

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