

Package ‘gRbase’

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Version 1.1.2

Title A package for graphical modelling in R

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Description The gRbase package provides certain general constructs which are used by other graphical modelling packages. This includes 1) the concept of gmData (graphical meta data), 2) several graph algorithms 3) facilities for table operations, 4) functions for testing for conditional independence. gRbase also illustrates how hierarchical log-linear models (hllm) may be implemented.

License GPL (>= 2)

URL <http://genetics.agrsci.dk/~sorenh/public/R/gRbaseweb/>

Depends R (>= 2.7.0),MASS,graph,RBGL

Suggests Rgraphviz

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breastcancer	<i>Gene expression signatures for p53 mutation status in 250 breast cancer samples</i>
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Description

Perturbations of the p53 pathway are associated with more aggressive and therapeutically refractory tumours. We preprocessed the data using Robust Multichip Analysis (RMA). Dataset has been truncated to the 1000 most informative genes (as selected by Wilcoxon test statistics) to simplify computation. The genes have been standardised to have zero mean and unit variance (i.e. z-scored).

Usage

```
data(breastcancer)
```

Format

A data frame with 250 observations on the following 1001 variables.

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A.218877_s_at a numeric vector
A.218883_s_at a numeric vector
A.218894_s_at a numeric vector
A.218936_s_at a numeric vector
A.218966_at a numeric vector
A.218976_at a numeric vector
A.218982_s_at a numeric vector
A.218987_at a numeric vector
A.219000_s_at a numeric vector
A.219004_s_at a numeric vector
A.219010_at a numeric vector
A.219031_s_at a numeric vector
A.219061_s_at a numeric vector
A.219065_s_at a numeric vector
A.219091_s_at a numeric vector
A.219105_x_at a numeric vector
A.219132_at a numeric vector
A.219148_at a numeric vector
A.219197_s_at a numeric vector
A.219252_s_at a numeric vector
A.219286_s_at a numeric vector
A.219304_s_at a numeric vector
A.219306_at a numeric vector
A.219396_s_at a numeric vector
A.219413_at a numeric vector
A.219417_s_at a numeric vector
A.219436_s_at a numeric vector
A.219440_at a numeric vector

- A.219455_at** a numeric vector
- A.219463_at** a numeric vector
- A.219469_at** a numeric vector
- A.219490_s_at** a numeric vector
- A.219493_at** a numeric vector
- A.219494_at** a numeric vector
- A.219510_at** a numeric vector
- A.219555_s_at** a numeric vector
- A.219588_s_at** a numeric vector
- A.219646_at** a numeric vector
- A.219650_at** a numeric vector
- A.219686_at** a numeric vector
- A.219687_at** a numeric vector
- A.219689_at** a numeric vector
- A.219713_at** a numeric vector
- A.219787_s_at** a numeric vector
- A.219833_s_at** a numeric vector
- A.219918_s_at** a numeric vector
- A.219922_s_at** a numeric vector
- A.219978_s_at** a numeric vector
- A.219990_at** a numeric vector
- A.220011_at** a numeric vector
- A.220060_s_at** a numeric vector
- A.220094_s_at** a numeric vector
- A.220173_at** a numeric vector
- A.220239_at** a numeric vector
- A.220276_at** a numeric vector
- A.220324_at** a numeric vector
- A.220540_at** a numeric vector
- A.220651_s_at** a numeric vector
- A.220789_s_at** a numeric vector
- A.220865_s_at** a numeric vector
- A.220917_s_at** a numeric vector
- A.221203_s_at** a numeric vector
- A.221207_s_at** a numeric vector
- A.221221_s_at** a numeric vector
- A.221258_s_at** a numeric vector

A.221272_s_at a numeric vector
A.221275_s_at a numeric vector
A.221276_s_at a numeric vector
A.221436_s_at a numeric vector
A.221505_at a numeric vector
A.221520_s_at a numeric vector
A.221521_s_at a numeric vector
A.221562_s_at a numeric vector
A.221588_x_at a numeric vector
A.221590_s_at a numeric vector
A.221676_s_at a numeric vector
A.221677_s_at a numeric vector
A.221685_s_at a numeric vector
A.221740_x_at a numeric vector
A.221856_s_at a numeric vector
A.221913_at a numeric vector
A.221922_at a numeric vector
A.221951_at a numeric vector
A.222010_at a numeric vector
A.222011_s_at a numeric vector
A.222039_at a numeric vector
A.222043_at a numeric vector
A.222077_s_at a numeric vector
A.222118_at a numeric vector
A.222195_s_at a numeric vector
A.36129_at a numeric vector
A.37152_at a numeric vector
A.38158_at a numeric vector
A.39854_r_at a numeric vector
A.40016_g_at a numeric vector
A.40093_at a numeric vector
A.45297_at a numeric vector
A.45633_at a numeric vector
A.57703_at a numeric vector
A.AFFX.HUMGAPDH.M33197_3_at a numeric vector
A.AFFX.HUMGAPDH.M33197_M_at a numeric vector
B.200039_s_at a numeric vector

B.200076_s_at a numeric vector
B.200079_s_at a numeric vector
B.200086_s_at a numeric vector
B.222396_at a numeric vector
B.222423_at a numeric vector
B.222453_at a numeric vector
B.222602_at a numeric vector
B.222606_at a numeric vector
B.222608_s_at a numeric vector
B.222640_at a numeric vector
B.222680_s_at a numeric vector
B.222740_at a numeric vector
B.222752_s_at a numeric vector
B.222767_s_at a numeric vector
B.222820_at a numeric vector
B.222835_at a numeric vector
B.222843_at a numeric vector
B.222848_at a numeric vector
B.222889_at a numeric vector
B.222958_s_at a numeric vector
B.222962_s_at a numeric vector
B.223054_at a numeric vector
B.223056_s_at a numeric vector
B.223062_s_at a numeric vector
B.223068_at a numeric vector
B.223096_at a numeric vector
B.223100_s_at a numeric vector
B.223119_s_at a numeric vector
B.223126_s_at a numeric vector
B.223186_at a numeric vector
B.223204_at a numeric vector
B.223225_s_at a numeric vector
B.223229_at a numeric vector
B.223234_at a numeric vector
B.223274_at a numeric vector
B.223307_at a numeric vector
B.223315_at a numeric vector

B.223348_x_at a numeric vector
B.223361_at a numeric vector
B.223381_at a numeric vector
B.223387_at a numeric vector
B.223452_s_at a numeric vector
B.223480_s_at a numeric vector
B.223491_at a numeric vector
B.223515_s_at a numeric vector
B.223556_at a numeric vector
B.223570_at a numeric vector
B.223666_at a numeric vector
B.223700_at a numeric vector
B.223864_at a numeric vector
B.224217_s_at a numeric vector
B.224320_s_at a numeric vector
B.224333_s_at a numeric vector
B.224428_s_at a numeric vector
B.224468_s_at a numeric vector
B.224471_s_at a numeric vector
B.224521_s_at a numeric vector
B.224523_s_at a numeric vector
B.224566_at a numeric vector
B.224578_at a numeric vector
B.224610_at a numeric vector
B.224674_at a numeric vector
B.224686_x_at a numeric vector
B.224699_s_at a numeric vector
B.224752_at a numeric vector
B.224753_at a numeric vector
B.224903_at a numeric vector
B.224944_at a numeric vector
B.225004_at a numeric vector
B.225064_at a numeric vector
B.225071_at a numeric vector
B.225083_at a numeric vector
B.225092_at a numeric vector
B.225099_at a numeric vector

B.225100_at a numeric vector
B.225142_at a numeric vector
B.225162_at a numeric vector
B.225191_at a numeric vector
B.225268_at a numeric vector
B.225291_at a numeric vector
B.225300_at a numeric vector
B.225309_at a numeric vector
B.225327_at a numeric vector
B.225365_at a numeric vector
B.225379_at a numeric vector
B.225402_at a numeric vector
B.225454_at a numeric vector
B.225468_at a numeric vector
B.225501_at a numeric vector
B.225592_at a numeric vector
B.225611_at a numeric vector
B.225613_at a numeric vector
B.225629_s_at a numeric vector
B.225655_at a numeric vector
B.225656_at a numeric vector
B.225676_s_at a numeric vector
B.225686_at a numeric vector
B.225687_at a numeric vector
B.225723_at a numeric vector
B.225748_at a numeric vector
B.225777_at a numeric vector
B.225804_at a numeric vector
B.225834_at a numeric vector
B.225841_at a numeric vector
B.225866_at a numeric vector
B.226030_at a numeric vector
B.226108_at a numeric vector
B.226118_at a numeric vector
B.226198_at a numeric vector
B.226274_at a numeric vector
B.226298_at a numeric vector

B.226303_at a numeric vector
B.226308_at a numeric vector
B.226344_at a numeric vector
B.226346_at a numeric vector
B.226349_at a numeric vector
B.226358_at a numeric vector
B.226410_at a numeric vector
B.226437_at a numeric vector
B.226439_s_at a numeric vector
B.226456_at a numeric vector
B.226466_s_at a numeric vector
B.226473_at a numeric vector
B.226506_at a numeric vector
B.226519_s_at a numeric vector
B.226522_at a numeric vector
B.226582_at a numeric vector
B.226661_at a numeric vector
B.226831_at a numeric vector
B.226833_at a numeric vector
B.226846_at a numeric vector
B.226914_at a numeric vector
B.226915_s_at a numeric vector
B.226936_at a numeric vector
B.226974_at a numeric vector
B.226977_at a numeric vector
B.226980_at a numeric vector
B.226992_at a numeric vector
B.227021_at a numeric vector
B.227047_x_at a numeric vector
B.227068_at a numeric vector
B.227081_at a numeric vector
B.227103_s_at a numeric vector
B.227165_at a numeric vector
B.227182_at a numeric vector
B.227198_at a numeric vector
B.227211_at a numeric vector
B.227212_s_at a numeric vector

- B.227227_at a numeric vector
- B.227232_at a numeric vector
- B.227279_at a numeric vector
- B.227350_at a numeric vector
- B.227363_s_at a numeric vector
- B.227419_x_at a numeric vector
- B.227423_at a numeric vector
- B.227436_at a numeric vector
- B.227478_at a numeric vector
- B.227512_at a numeric vector
- B.227533_at a numeric vector
- B.227651_at a numeric vector
- B.227700_x_at a numeric vector
- B.227703_s_at a numeric vector
- B.227718_at a numeric vector
- B.227762_at a numeric vector
- B.227809_at a numeric vector
- B.227811_at a numeric vector
- B.227873_at a numeric vector
- B.227874_at a numeric vector
- B.227920_at a numeric vector
- B.227928_at a numeric vector
- B.227982_at a numeric vector
- B.228044_at a numeric vector
- B.228069_at a numeric vector
- B.228081_at a numeric vector
- B.228252_at a numeric vector
- B.228273_at a numeric vector
- B.228281_at a numeric vector
- B.228318_s_at a numeric vector
- B.228323_at a numeric vector
- B.228327_x_at a numeric vector
- B.228361_at a numeric vector
- B.228468_at a numeric vector
- B.228469_at a numeric vector
- B.228476_at a numeric vector
- B.228504_at a numeric vector

B.228505_s_at a numeric vector
B.228528_at a numeric vector
B.228550_at a numeric vector
B.228554_at a numeric vector
B.228559_at a numeric vector
B.228560_at a numeric vector
B.228597_at a numeric vector
B.228692_at a numeric vector
B.228718_at a numeric vector
B.228729_at a numeric vector
B.228730_s_at a numeric vector
B.228750_at a numeric vector
B.228799_at a numeric vector
B.228811_at a numeric vector
B.228854_at a numeric vector
B.228868_x_at a numeric vector
B.228915_at a numeric vector
B.228931_at a numeric vector
B.228955_at a numeric vector
B.229030_at a numeric vector
B.229062_at a numeric vector
B.229097_at a numeric vector
B.229127_at a numeric vector
B.229150_at a numeric vector
B.229169_at a numeric vector
B.229170_s_at a numeric vector
B.229181_s_at a numeric vector
B.229342_at a numeric vector
B.229381_at a numeric vector
B.229437_at a numeric vector
B.229466_at a numeric vector
B.229490_s_at a numeric vector
B.229538_s_at a numeric vector
B.229551_x_at a numeric vector
B.229610_at a numeric vector
B.229764_at a numeric vector
B.229886_at a numeric vector

B.230021_at a numeric vector
B.230123_at a numeric vector
B.230142_s_at a numeric vector
B.230165_at a numeric vector
B.230250_at a numeric vector
B.230451_at a numeric vector
B.230469_at a numeric vector
B.230863_at a numeric vector
B.230966_at a numeric vector
B.231002_s_at a numeric vector
B.231034_s_at a numeric vector
B.231472_at a numeric vector
B.231577_s_at a numeric vector
B.232065_x_at a numeric vector
B.232210_at a numeric vector
B.232238_at a numeric vector
B.232278_s_at a numeric vector
B.232286_at a numeric vector
B.232307_at a numeric vector
B.232398_at a numeric vector
B.232459_at a numeric vector
B.232596_at a numeric vector
B.232855_at a numeric vector
B.232944_at a numeric vector
B.232968_at a numeric vector
B.233110_s_at a numeric vector
B.233388_at a numeric vector
B.233413_at a numeric vector
B.233520_s_at a numeric vector
B.234222_at a numeric vector
B.234294_x_at a numeric vector
B.234749_s_at a numeric vector
B.234863_x_at a numeric vector
B.234944_s_at a numeric vector
B.234954_at a numeric vector
B.234992_x_at a numeric vector
B.235040_at a numeric vector

B.235046_at a numeric vector
B.235117_at a numeric vector
B.235124_at a numeric vector
B.235181_at a numeric vector
B.235193_at a numeric vector
B.235363_at a numeric vector
B.235369_at a numeric vector
B.235425_at a numeric vector
B.235542_at a numeric vector
B.235545_at a numeric vector
B.235547_at a numeric vector
B.235570_at a numeric vector
B.235572_at a numeric vector
B.235609_at a numeric vector
B.235662_at a numeric vector
B.235709_at a numeric vector
B.235771_at a numeric vector
B.235786_at a numeric vector
B.235789_at a numeric vector
B.235800_at a numeric vector
B.236050_at a numeric vector
B.236064_at a numeric vector
B.236312_at a numeric vector
B.236641_at a numeric vector
B.236787_at a numeric vector
B.236953_s_at a numeric vector
B.237086_at a numeric vector
B.237168_at a numeric vector
B.237301_at a numeric vector
B.237339_at a numeric vector
B.238001_at a numeric vector
B.238045_at a numeric vector
B.238075_at a numeric vector
B.238077_at a numeric vector
B.238116_at a numeric vector
B.238425_at a numeric vector
B.238447_at a numeric vector

B.238656_at a numeric vector
B.238756_at a numeric vector
B.238781_at a numeric vector
B.238898_at a numeric vector
B.239002_at a numeric vector
B.239349_at a numeric vector
B.239432_at a numeric vector
B.239758_at a numeric vector
B.239890_s_at a numeric vector
B.240099_at a numeric vector
B.240422_at a numeric vector
B.241310_at a numeric vector
B.241408_at a numeric vector
B.241577_at a numeric vector
B.241789_at a numeric vector
B.241937_s_at a numeric vector
B.242218_at a numeric vector
B.242255_at a numeric vector
B.242323_at a numeric vector
B.242560_at a numeric vector
B.242657_at a numeric vector
B.242890_at a numeric vector
B.243754_at a numeric vector
B.243806_at a numeric vector
B.244116_at a numeric vector
B.244375_at a numeric vector
B.244571_s_at a numeric vector
B.244677_at a numeric vector
B.244696_at a numeric vector
B.AFFX.HUMGAPDH.M33197_3_at a numeric vector
B.AFFX.HUMGAPDH.M33197_M_at a numeric vector
code a factor with levels `case control`

Details

The factor `code` defines whether there was a mutation in the p53 sequence (`code=case`) or not (`code=control`).

Source

Dr. Chris Holmes, c.holmes at stats dot. ox . ac .uk

References

Miller et al (2005, PubMed ID:16141321)

Examples

```
data(breastcancer)
## maybe str(breastcancer) ; plot(breastcancer) ...
```

cad

Coronary artery disease data

Description

A cross classified table with observational data from a Danish heart clinic. The response variable is CAD.

Usage

```
data(cad1)
```

Format

A data frame with 236 observations on the following 14 variables.

Sex a factor with levels Female Male

AngPec a factor with levels Atypical None Typical

AMI a factor with levels Definite NotCertain

QWave a factor with levels No Yes

QWavecode a factor with levels Nonusable Usable

STcode a factor with levels Nonusable Usable

STchange a factor with levels No Yes

SuffHeartF a factor with levels No Yes

Hypertrophi a factor with levels No Yes

Hyperchol a factor with levels No Yes

Smoker a factor with levels No Yes

Inherit a factor with levels No Yes

Heartfail a factor with levels No Yes

CAD a factor with levels No Yes

Details

cad1: Complete dataset, 236 cases. cad2: Incomplete dataset, 67 cases. Information on (some of) the variables Hyperchol, Smoker, Inherit is missing.

References

Højsgaard, Søren and Thiesson, Bo (1995). BIFROST - Block recursive models Induced From Relevant knowledge, Observations and Statistical Techniques. Computational Statistics and Data Analysis, vol. 19, p. 155-175

Hansen, J. F. (1980). The clinical diagnosis of ichaeme heart disease du to coronary artery disease. Danish Medical Bulletin

Examples

```
data(cad1)
## maybe str(cad1) ; plot(cad1) ...
```

carcass	<i>lean meat contents of pig carcasses</i>
---------	--

Description

Measurement of lean meat percentage of 344 pig carcasses together with auxillary information collected at three Danish slaughter houses

Usage

```
data(carcass)
data(carcassall)
```

Format

carcassall: A data frame with 344 observations on the following 17 variables.

weight Weight of carcass

lengthc Length of carcass from back toe to head (when the carcass hangs in the back legs)

lengthf Length of carcass from back toe to front leg (that is, to the shoulder)

lengthp Length of carcass from back toe to the pelvic bone

F02, F03, F11, F12, F13, F14, F16 Thickness of fat layer at different locations on the back of the carcass (FXX refers to thickness at (or rather next to) rib no. XX. Notice that 02 is closest to the head

M11, M12, M13 Thickness of meat layer at different locations on the back of the carcass, see description above

LMP Lean meat percentage determined by dissection

slhouse Slaughter house; a factor with levels a b c

sex Sex of the pig; a factor with a b c. Notice that it is no an error to have three levels; the third level refers to castrates

carcass: Contains only the variables F11, F12, F13, M11, M12, M13, LMP

Source

Busk, H., Olsen, E. V., Brøndum, J. (1999) Determination of lean meat in pig carcasses with the Autofom classification system, Meat Science, 52, 307-314

chestSim

Simulated data from the Chest Clinic example

Description

Simulated data from the Chest Clinic example (also known as the Asia example) from Lauritzen and Spiegelhalter, 1988.

Usage

```
data(chestSim500)
```

Format

A data frame with 500 observations on the following 8 variables.

asia a factor with levels yes no

tub a factor with levels yes no

smoke a factor with levels yes no

lung a factor with levels yes no

bronc a factor with levels yes no

either a factor with levels yes no

xray a factor with levels yes no

dysp a factor with levels yes no

References

Lauritzen and Spiegelhalter (1988) Local Computations with Probabilities on Graphical Structures and their Application to Expert Systems (with Discussion). J. Roy. Stat. Soc. 50, p. 157-224.

Examples

```
data(chestSim500)
## maybe str(chestSim500) ; plot(chestSim500) ...
```

`cov2pcor`*Partial correlation (matrix)*

Description

`cov2pcor` calculates the partial correlation matrix from an (empirical) covariance matrix

Usage

```
cov2pcor(V)
```

Arguments

`V` Covariance matrix

Value

A matrix with the same dimension as `V`.

Author(s)

Søren Højsgaard, sorenh@agrsci.dk

Examples

```
data(math)
S <- cov.wt(math)$cov
cov2pcor(S)
```

`dietox`*Growth curves of pigs in a 3x3 factorial experiment*

Description

The `dietox` data frame has 861 rows and 7 columns.

Usage

```
data(dietox)
```

Format

This data frame contains the following columns: Weight, Feed, Time, Pig, Evit, Cu, Litter.

Source

Lauridsen, C., Højsgaard, S., Sørensen, M.T. C. (1999) Influence of Dietary Rapeseed Oil, Vitamin E, and Copper on Performance and Antioxidant and Oxidative Status of Pigs. *J. Anim. Sci.* 77:906-916

Examples

```
data(dietox)
```

gmData

Class "gmData" graphical meta data

Description

A common class for representing data. No matter the actual representation of data, the important characteristics are contained in a graphical metadata object.

Usage

```
newgmData (varNames,
           varTypes=rep (validVarTypes () [1], length (varNames)),
           nLevels=NULL,
           latent=NULL,
           valueLabels=NULL,
           observations=NULL,
           description=NULL,
           shortNames=NULL
          )
```

Arguments

varNames	a vector of strings with names of variables.
varTypes	a vector of strings with values from validVarTypes giving the types of the variables; typical types are "Discrete", "Ordinal", "Continuous", but others can be defined. The types can be abbreviated.
nLevels	a numeric vector with integer values for discrete or ordinal variables giving the number of levels.
latent	a vector of strings with names of the latent variables.
valueLabels	a list of vectors of strings with names of the levels for each discrete or ordinal variable.
observations	an object containing the observations, eg. a dataframe or a table.
description	a string describing the origin of the data.
shortNames	a vector of strings giving a short name of each variable.

Details

If neither `nLevels` nor `valueLabels` are given, then all categorical variables are assumed to be binary. If `valueLabels` are given then `nLevels` are inferred from these. `valueLabels / nLevels` are recycled if necessary.

Value

An object of class `gmData` holds information about the data and can be retrieved and changed by accessor functions.

Objects from the Class

Objects can be created by calls of the form `newgmData(varNames, varTypes, nLevels, latent, valueLabels, observations, description)`.

More often, `gmData` objects will be created from a `data.frame` or `table`.

A `gmData` object contains the abstraction of data into a meta data object including variable names and types etc. However, the actual data might not be present or may be represented by a reference to data, such as a database file. Also, it may be possible to work without data, which may be valuable if the point of interest is in the model alone. Separating the specification of the variables from data has the benefit, that some properties of a model can be investigated without any reference to data, for example decomposability and collapsibility.

Author(s)

Søren Højsgaard, (sorenh@agrsci.dk),
Claus Dethlefsen, (dethlef@math.aau.dk)

See Also

`demo(gmData)`

Examples

```
vn <- c("a", "b", "c", "d")
z<-newgmData(vn, varTypes=c("dis", "dis", "con", "con"))
summary(z)
z<-newgmData(vn, varTypes=c("dis", "dis", "con", "con"), nLevels=c(4, 3, NA, NA))
summary(z)
z<-newgmData(vn, varTypes=c("dis", "dis", "con", "con"), nLevels=c(4, NA, NA, NA))
summary(z)
z<-newgmData(vn, varTypes=c("dis", "dis", "ord", "con"), valueLabels=list("a"=1:2, "b"=1:4))
summary(z)

ccnames <- c("asia", "smoke", "tub", "lung", "bronc", "either", "xray", "dysp")
gmd <- newgmData(ccnames, valueLabels=c("yes", "no"), description="Chest clinic")
summary(gmd)

data(mathmark)
as.gmData(mathmark)
```

```
data(HairEyeColor)
as.gmData(HairEyeColor)
```

gModel

Class "gModel" - graphical models

Description

The general class `gModel` contains a formula object and a `gmData` object. Implementations of different specific graphical model classes can inherit from this class and provide methods for parsing the formula. This is illustrated in the implementation of a class for hierarchical log-linear models, [hllm](#).

Usage

```
gModel(formula, gmData)
```

Arguments

`formula` an object of class [formula](#).
`gmData` an object of class [gmData](#).

Value

`gModel` creates an object of class `gModel` with the two components `formula` and `gmData`. These components can be retrieved or replaced using the accessor functions of the same names. Also, a `gModel` object may be manipulated using the `dynamicGraph` interface.

Author(s)

Søren Højsgaard, sorenh@agrsci.dk,
 Claus Dethlefsen, cld@rn.dk

See Also

[gmData](#), [gRfit](#), [hllm](#).

Examples

```
data(rats)
rats <- as.gmData(rats)

m1 <- gModel(~.^., rats)
m1.form <- formula(m1)
m1.data <- gmData(m1)
observations(gmData(m1)) <- observations(rats)[1:10,]
```

graph-operations1 *Simple operations on undirected and directed acyclic graphs.*

Description

Make operations on undirected and directed acyclic graphs.

Usage

```
as.adjMAT(object)
ancestors(set, object)
ancestralGraph(set, object)
ancestralSet(set, object)
children(set, object)
closure(set, object)
edgeList(object, matrix=FALSE)
nonEdgeList(object, matrix=FALSE)
vpar(object)
is.complete(object, set)
is.decomposition(set, set2, set3, object)
is.simplicial(set, object)
parents(set, object)
simplicialNodes(object)
```

Arguments

set, set2, set3	Vectors of sets
object	A graph nel object
matrix	If TRUE the result is returned as a p x 2 matrix; otherwise as a matrix list.

Details

Notice that `as.adjMAT(g)` does the same as `as(g, "matrix")` but `as.adjMAT()` is considerably faster.

Author(s)

Søren Højsgaard, sorenh@agrsci.dk

See Also

[mcs](#) [rip](#) [moralize](#) [jTree](#)

Examples

```
ugr <- ug(~me:ve, ~me:al, ~ve:al, ~al:an, ~al:st, ~an:st)
closure("me", ugr)
```

graph-operations2 *More advanced operations on undirected and directed acyclic graphs.*

Description

Make operations on undirected and directed acyclic graphs.

Usage

```
mcs(object, root=NULL, index=FALSE)
mcsMAT(amat, vn = colnames(amat), root = NULL, index = FALSE)
rip(object, root=NULL, nLevels=NULL)
ripMAT(amat, root = NULL, nLevels = NULL)
moralize(object)
moralizeMAT(amat)
maxCliqueMAT(amat)
jTree(object, method="mcwh", nLevels=rep(2, length(nodes(object))), control=list())
```

Arguments

<code>object</code>	An undirected graph (of class "graphNEL")
<code>root</code>	Variables to be considered first when doing the orderings
<code>index</code>	If TRUE, then a permutation is returned
<code>nLevels</code>	Number of levels of the nodes in the graph
<code>amat</code>	Adjacency matrix
<code>vn</code>	Nodes in the graph given by adjacency matrix
<code>method</code>	The triangulation method, "mcwh" is a C implementation of a minimum clique weight heuristic, "R" is a corresponding R implementation (experimental)
<code>control</code>	Currently not used

Details

The `RIP` and `RIPMAT` functions return a RIP ordering of the cliques. This is obtained by first ordering the variables linearly with maximum cardinality search (by MCS). The `root` argument is transferred to MCS as a way of controlling which clique will be the first in the RIP ordering.

The `jTree` (for "junction tree") is just a wrapper for a call of `triangulate` followed by a call of `RIP`.

Value

`moralize` and `triangulate` returns objects of class "graphsh".

`MCS` and `MCSMAT` return a vector with a linear ordering (obtained by maximum cardinality search) of the variables or `character(0)` if such an ordering can not be created.

`RIP` and `RIPMAT` returns a list with cliques, separators etc. if a RIP ordering can be made and an empty list if not.

Author(s)

Søren Højsgaard, sorenh@agrsci.dk

See Also

[ug](#), [dag](#)

Examples

```
## Undirected graphs
##
ugr <- ug(~me+ve,~me+al,~ve+al,~al+an,~al+st,~an+st)
ugm <- as.adjMAT(ugr)
edges(ugr)
nodes(ugr)
mcs(ugr)
mcsMAT(ugm)
rip(ugr)
ripMAT(ugm)

maxClique(ugr)
maxCliqueMAT(ugm)

## Directed graphs
##
dagr <- dag(~me+ve,~me+al,~ve+al,~al+an,~al+st,~an+st)
edges(dagr)
nodes(dagr)
moralize(dagr)
```

gRbase

The package 'gRbase': summary information

Description

This package provides a basis for graphical modelling in R

Details

- gRbase provides the general framework for setting up data and model structures and provide examples for fitting hierarchical log linear models for contingency tables and graphical Gaussian models for the multivariate normal distribution.
- Other graphical model software on CRAN includes: [mimR](#), [deal](#), [CoCo](#), [ggm](#) and [SIN](#).

The package is intended as a contribution to the gR-project described by Lauritzen (2002).

Authors

Søren Højsgaard, Aarhus University, DK-8830 Tjele, Denmark

Claus Dethlefsen, Center for Cardiovascular Research, Aalborg Hospital, Århus University Hospital, DK-9000 Aalborg, Denmark

Acknowledgements

Thanks to the other members of the gR initiative, in particular to David Edwards for providing functions for formula-manipulation.

References

Lauritzen, S. L. (2002). gRaphical Models in R. *R News*, 3(2)39.

gRbase-utilities *Utility functions for gRbase*

Description

Utility functions for gRbase package. Includes 'faster versions' of certain standard R functions.

Usage

```
uniquePrim(x)
setdiffPrim(x, y)
intersectPrim(x, y)
unlistPrim(l, recursive = TRUE, use.names = TRUE)
```

Arguments

<code>x, y</code>	Vectors
<code>l</code>	A list (of vectors)
<code>recursive</code>	logical. Should unlisting be applied to list components of x?
<code>use.names</code>	logical. Should names be preserved?

Value

A vector or a logical.

Note

Use the xxxxPrim functions with caution!

Author(s)

Søren Højsgaard, sorenh@agrsci.dk

See Also

[unique](#), [setdiff](#), [unlist](#)

Examples

```
uniquePrim(c(1,2,3,2,1,2))
setdiffPrim(c(1,3,2), c(2,3,4,5))
unlistPrim(list(c(1,2), c(2,3)))
```

gRfit

Class "gRfit" - fitted graphical models

Description

Objects of class `gRfit` are created when the function `fit` is applied to a `gModel` object. When adding new types of `gModel` objects, one must also supply the appropriate `fit` function. The `gRfit` object contains the output of the fit which can be accessed by `getFit`. Separate `print` and `summary` methods exist for `gRfit` objects.

Usage

```
fit(m, ...)
getFit(x)
```

Arguments

<code>m</code>	An object for which a fit method has been defined
<code>x</code>	an object of class <code>gRfit</code> as created from <code>fit</code> applied to a <code>gModel</code> object.
<code>...</code>	Additional arguments

Value

`fit` creates an object of class `gRfit`. `getFit` returns the fit information created by the fitting algorithm.

Author(s)

Søren Højsgaard, sorenh@agrsci.dk,
Claus Dethlefsen, cld@rn.dk

See Also

[gModel](#).

Examples

```

data(reinis)
reinis <- as.gmData(reinis)

m1 <- hllm(~.^., reinis)
m1 <- fit(m1, engine="loglm")

```

hllm

*Hierarchical log-linear models***Description**

An implementation of hierarchical log-linear models using the framework of [gRbase](#). A model object is defined using `hllm`, fitted using `fit` (which calls `loglm`) and a model search performed using `stepwise`. The models may be displayed and manipulated using the [gRbase](#).

Usage

```

hllm(formula = ~.^1, gmData, marginal)
## S3 method for class 'hllm':
fit(m, engine="loglm", ...)

```

Arguments

<code>formula</code>	an object of class formula . The right hand side of the formula is a list of the generators separated by <code>+</code> . A generator is specified by variable names with separated by <code>*</code> . Commonly used models have short hand notations: saturated model (<code>~.^.</code>), main effects (<code>~.^1</code>), all k 'th order interactions (<code>~.^k</code>).
<code>gmData</code>	an object of class gmData .
<code>marginal</code>	an optional argument specifying a subset of the variables from the <code>gmData</code> object.
<code>m</code>	A <code>hllm</code> object
<code>engine</code>	Defining the fitting engine. For <code>hllm</code> objects only "loglm" is implemented.
<code>...</code>	Additional arguments

Value

`hllm` returns an object of class `hllm`, inheriting from the superclass `gModel`.

Author(s)

Søren Højsgaard, (sorenh@agrsci.dk),
 Claus Dethlefsen, (cld@rn.dk)

See Also

[gmData](#), [gRfit](#), [ggm](#)

Examples

```
data(reinis)
reinis <- as.gmData(reinis)
m2 <-
hllm(~smoke*phys*protein+mental*phys+mental*family+smoke*systol*protein,
reinis)
m2 <- fit(m2,engine="loglm")
## plot(m2)
```

lizard

Lizard behaviour

Description

In a study of lizard behaviour, characteristics of 409 lizards were recorded, namely species (S), perch diameter (D) and perch height (H). The focus of interest is in how the propensities of the lizards to choose perch height and diameter are related, and whether and how these depend on species.

Usage

```
data(lizard)
```

Format

A 3-dimensional array with factors diam: "<=4" ">4" height: ">4.75" "<=4.75" species: "anoli" "dist"

References

Schoener TW (1968) The anolis lizards of bimini: Resource partitioning in a complex fauna. Ecology 49:704-726

Examples

```
data(lizard)
## maybe str(lizard) ; plot(lizard) ...
```

 mathmark

Mathematics marks for students

Description

The `mathmark` data frame has 88 rows and 5 columns.

Usage

```
data(mathmark)
```

Format

This data frame contains the following columns: mechanics, vectors, algebra, analysis, statistics.

Author(s)

Søren Højsgaard, sorenh@agrsci.dk

References

David Edwards, *An Introduction to Graphical Modelling*, Second Edition, Springer Verlag, 2000

Examples

```
data(mathmark)
```

mildew

Mildew fungus

Description

The data stem from a cross between two isolates of the barley powdery mildew fungus. For each offspring 6 binary characteristics, each corresponding to a single locus, were recorded. The object of the analysis is to determine the order of the loci along the chromosome.

Usage

```
data(mildew)
```

Format

The format is: table [1:2, 1:2, 1:2, 1:2, 1:2, 1:2] 0 0 0 0 3 0 1 0 0 1 ... - attr(*, "dimnames")=List of 6 ..*la10* : *chr*[1 : 2]"1""2".. *locc*: *chr* [1:2] "1" "2" ..*mp58* : *chr*[1 : 2]"1""2".. *c365*: *chr* [1:2] "1" "2" ..*p53a* : *chr*[1 : 2]"1""2".. *a367*: *chr* [1:2] "1" "2"

References

Christiansen, S.K., Giese, H (1991) Genetic analysis of obligate barley powdery mildew fungus based on RFLP and virulence loci. *Theor. Appl. Genet.* 79:705-712

Examples

```
data(mildew)
## maybe str(mildew) ; plot(mildew) ...
```

ptable *Representation of and operations on multidimensional tables*

Description

General representation of multidimensional tables (by `ptable` objects).

Usage

```
ptable(varNames, levels, values = 1, normalize = c("none", "first", "all"), smooth
as.ptable <- function(values, normalize=c("none","first","all"), smooth=0)
tableMarginPrim(t1, margin, normalize=FALSE)

## S3 method for class 'ptable':
varNames(x)
## S3 method for class 'ptable':
nLevels(x)
## S3 method for class 'ptable':
valueLabels(x)
```

Arguments

<code>varNames</code>	Names of variables defining table
<code>levels</code>	Either vector with number of levels of the factors in <code>varNames</code> or list with specification of the levels of the factors in <code>varNames</code> . See 'examples' below.
<code>values</code>	Table values
<code>x</code>	Objects of class "ptable"
<code>t1</code>	Objects of class "ptable"
<code>margin</code>	Set of nodes to marginalize onto
<code>normalize</code>	Should result be normalized, see 'Details' below.
<code>smooth</code>	Should values be smoothed, see 'Details' below.

Details

A ptable object represents a table defined by a set of variables and their levels, together with the values of the table. E.g. $f(a,b,c)$ can be a table with a,b,c representing levels of binary variable

If `normalize="first"` then for each configuration of the parents, "pa", the probabilities are normalized to sum to one. Thus $f(a,b,c)$ becomes a conditional probability table of the form $p(alb,c)$.

If `normalize="all"` then the sum over all entries of $f(a,b,c)$ is one.

If `smooth` is positive then `smooth` is added to `values` before normalization takes place.

as `.ptable` can be used for coercing an array to a ptable object.

Value

An object of class `ptable`.

Author(s)

Søren Højsgaard, sorenh@agrsci.dk

Examples

```
t1 <- ptable(c("gender", "answer"), list(c('male', 'female'), c('yes', 'no')), values=1:4)
t1 <- ptable(~gender+answer, list(c('male', 'female'), c('yes', 'no')), values=1:4)
t1 <- ptable(~gender+answer, c(2,2), values=1:4)
```

```
t2 <- ptable(c("answer", "category"), list(c('yes', 'no'), c(1,2)), values=1:4+10)
t3 <- ptable(c("category", "foo"), c(2,2), values=1:4+100)
```

```
varNames(t1)
nLevels(t1)
valueLabels(t1)
```

querygraph

Query a graph

Description

`queryg` is a general function for querying a graph object, specifically graphs as created with `newug` and `newdag`.

Usage

```
querygraph(object, type, set = NULL, set2 = NULL, set3 = NULL)
```

Arguments

object	A graph object; i.e. either an undirected graph (ugsh) or a directed acyclic graph (dagsh)
type	Query type, see 'details' below.
set, set2, set3	Possible arguments to a graph query of type type

Details

The type can be:

- adj: Nodes adjacent to set
- an: Ancestors of set
- ancestralGraph: Ancestral graph induced by set
- ancestralSet: Ancestral set of set
- cl: Closure of set
- ch: Children of set
- maxClique: The cliques
- connectedComp The connected components
- edges: Edges of graph
- ne: Neighbours of set
- nodes: Nodes of graph
- is.complete:
- edgeList
- vpar
- is.simplicial:
- is.triangulated:
- pa: Parents of set
- separates: Is set and set2 separated by set3
- simplicialNodes: The simplicial nodes of graph
- subgraph: Subgraph induced by set

Value

Depending on the type, the output will be either a new graph or a vector or a list.

Author(s)

Søren Højsgaard, sorenh@agrsci.dk

See Also

[ug](#), [dag](#)

Examples

```
ug0 <- ug(~a:b, ~b:c:d, ~e)

querygraph(ug0, "nodes")
querygraph(ug0, "edges")

querygraph(ug0, "subgraph", c("b", "c", "d", "e"))

querygraph(ug0, "adj", "c")
querygraph(ug0, "closure", "c")
querygraph(ug0, "is.simplicial", "b")
querygraph(ug0, "simplicialNodes")

querygraph(ug0, "is.complete")
querygraph(ug0, "is.complete", c("b", "c", "d"))
querygraph(ug0, "maxClique")

querygraph(ug0, "is.triangulated")
querygraph(ug0, "is.decomposition", "a", "d", c("b", "c"))
```

rats

Weightloss of rats

Description

An artificial dataset. 24 rats (12 female, 12 male) have been randomized to use one of three drugs (products for losing weight). The weightloss for each rat is noted after one and two weeks.

Usage

```
data(rats)
```

Format

A dataframe with 4 variables. Sex: "M" (male), "F" (female). Drug: "D1", "D2", "D3" (three types). W1 weightloss, week one. W2 weightloss, week 2.

References

Morrison, D.F. (1976). *Multivariate Statistical Methods*. McGraw-Hill, USA.

Edwards, D. (1995). *Introduction to Graphical Modelling*, Springer-Verlag. New York.

reinis	<i>Risk factors for coronary heart disease.</i>
--------	---

Description

Data collected at the beginning of a 15 year follow-up study of probable risk factors for coronary thrombosis. Data are from all men employed in a car factory.

Usage

```
data(reinis)
```

Format

A table with 6 discrete variables. A: smoking, B: strenuous mental work, D: strenuous physical work, E: systolic blood pressure, F: ratio of lipoproteins, G: Family anamnesis of coronary heart disease.

References

Edwards and Havranek (1985): A fast procedure for model search in multidimensional contingency tables. *Biometrika*, 72: 339-351.

Reinis et al (1981): Prognostic significance of the risk profile in the prevention of coronary heart disease. *Bratis. lek. Listy*. 76: 137-150.

Setoperations	<i>Set operations</i>
---------------	-----------------------

Description

Miscellaneous set operations.

Usage

```
is.subsetof(x, set)
is.insetlist(x, setlist, index=FALSE)
removeRedundant(setlist, maximal = TRUE, index = FALSE)
```

Arguments

<code>x, set</code>	Vectors representing sets
<code>setlist</code>	List of vectors (representing a set of subsets)
<code>maximal</code>	Logical; see section 'Details' for a description.
<code>index</code>	Logical; should indices (in setlist) be returned or a set of subsets.

Details

'setlist' is a list of vectors representing a set of subsets; i.e. V_1, \dots, V_Q where V_k is a subset of some base set V .

`is.insetlist`: Checks if the set x is in one of the V_k 's.

`removeRedundant`: Returns those V_k which are not contained in other subsets; i.e. gives the maximal sets. If `maximal` is `FALSE` then returns the minimal sets; i.e. V_k is returned if V_k is contained in one of the other sets V_l and there are no set V_n contained in V_k .

Notice that the comparisons are made by turning the elements into characters and then comparing these. Hence 1 is identical to "1".

Author(s)

Søren Højsgaard, sorenh@agrsci.dk

Examples

```
is.subsetof(c(1,2), c(1,2,3))
is.subsetof(c(1,2,3), c(1,2))

l <- list(c(1,2), c(1,2,3), c(2,4), c(5,6), 5)

#subsetofList(c(1,2), l)
#subsetofList(c(1,2,3,4), l)

removeRedundant(l)
removeRedundant(l, maximal=FALSE)

is.insetlist(c(2,4), l)
is.insetlist(c(2,8), l)
```

table-operations *Compute table margin or table slice*

Description

For a contingency table in array form, compute the sum of table entries for a given index (i.e. a marginal table) or find the slice of the table defined by specific margins being at a specific level.

Usage

```
tableOp(t1, t2, op = "*")
tableMargin(x, margin, keep.class=FALSE)
tableSlice(x, margin, level, impose)
tablePerm(a, perm, resize = TRUE, keep.class=FALSE)
```

Arguments

<code>x, t1, t2, a</code>	An array
<code>margin</code>	An index, either numerical or character
<code>keep.class</code>	If TRUE the result will be forced to have the same class as the input; otherwise the result will be an array.
<code>level</code>	A value, either numerical or character
<code>impose</code>	Possible value used to fill up a slice to give it full dimension
<code>op</code>	Either "*" or "/"
<code>perm</code>	The subscript permutation vector, which must be a permutation of the integers 1:n, where n is the number of dimensions of a OR a permutation of the dimension names of a. The default is to reverse the order of the dimensions. A permutation of the dimensions of a.
<code>resize</code>	A flag indicating whether the vector should be resized as well as having its elements reordered.

Details

`tableMargin`: `tableMargin` is analogous to `margin.table` except that `margin` can be given both as array indices or as variable names

`tableSlice`: If the table `x` has dimensions Z,U,V where V has levels 1 and 2 then `tableSlice` can extract the slice of `x` (in this case a 2-way table) defined by e.g. `U=2`. Setting `impose=1000` implies that a 3-way table is returned with the `U=2` slice in the right place and the `U=1`-slice consisting of 1000 in each cell.

`tableOp`: If `t1` has dimnames A and B and `t2` has dimnames B and C then `tableOp(t1,t2)` will return a table (an array) with dimnames A, B and C containing the product.

`tablePerm`: A wrapper for `aperm`, but `tablePerm` accepts dimnames in addition to indices.

See examples below.

Value

An array.

Author(s)

Søren Højsgaard

See Also

[margin.table](#)

Examples

```

data(HairEyeColor)

tableMargin(HairEyeColor, "Hair")
tableMargin(HairEyeColor, 1)
tableMargin(HairEyeColor, c("Hair", "Eye"))
tableMargin(HairEyeColor, c(1,2))

tableSlice(HairEyeColor, "Sex", "Male")
tableSlice(HairEyeColor, 3,1)
tableSlice(HairEyeColor, "Sex", "Male", impose=1000)
tableSlice(HairEyeColor, 3,1, impose=1000)

t1 <- array(1:4, dim=c(2,2), dimnames=list(gender=c('male','female'), answer=c('yes','no')))
t2 <- array(1:4+10, dim=c(2,2), dimnames=list(answer=c('yes','no'), category=c(1,2)))

tableOp(t1,t2, "*")
tableOp(t1,t2, "/")

data(reinis)

t1 <- tableMargin(reinis, c(6,5,2,1))
t2 <- tableMargin(reinis, c(6,5,3,4))

tt1 <- tableOp(t1,t2)

t1 <- tableMargin(reinis, c(6,5,2,4,1))
t2 <- tableMargin(reinis, c(6,5,4))

tt1 <- tableOp2(t1,t2)

```

triangulate

Triangulation of an undirected graph

Description

This function will triangulate an undirected graph by adding fillins.

Usage

```

triangulate(object, method="mcwh", nLevels = rep(2,length(nodes(object))), matrix=
triangulateMAT(amat, method="mcwh", nLevels=rep(2,ncol(amat)))

```

Arguments

object	An undirected graph (of class 'graphNEL')
amat	An adjacency matrix (symmetrical)

<code>method</code>	Triangulation method. Either "mcwh" (minimum clique weight heuristic) which is implemented in C or "r" (an experimental R version)
<code>nLevels</code>	Typically, the number of levels of the variables (nodes) when these are discrete. Used in determining the triangulation using a "minimum clique weight heuristic". See section 'details'.
<code>matrix</code>	If TRUE the adjacency matrix is returned; if FALSE a graphNEL object is returned

Details

The triangulation is made so as the total state space is kept low.

Value

A triangulated graph (an object of class 'graphNEL') or an adjacency matrix.

Author(s)

Søren Højsgaard, sorenh@agrsci.dk

See Also

[mcs rip](#)

Examples

```
ugr <- ug(~a:b+b:c+c:d+d:e+e:f+f:a)
triangulate(ugr)
```

ug

Create undirected and directed graphs

Description

These functions are wrappers for creation of graphs as implemented by graphNEL objects in the graph package.

Usage

```
ug(...)
dag(...)
ugList(x)
dagList(x)
```

Arguments

`...` A generating class for a graph, see examples below
`x` A list containing a generating class for a graph, see examples below

Value

Functions `ug()`, `dag()`, `ugList()` and `dagList()` return a 'graphNEL' object.

Functions `ugMAT()` and `ugListMAT()` return an adjacency matrix.

Author(s)

Søren Højsgaard, `sorenh at agrsci.dk`

Examples

```

ugr <- ug(~me:ve,~me:al,~ve:al,~al:an,~al:st,~an:st)

ugr <- ug(~me:ve:al,~al:an:st)

ugr <- ug(c("me","ve"),c("me","al"),c("ve","al"),c("al","an"),c("al","st"),c("an","st"))

ugr <- ug(~me:ve:al, c("me","ve"),c("me","al"),c("ve","al"),c("al","an"),c("al","st"),c("an","st"))

dagr <- dag(c("me","ve"),c("me","al"),c("ve","al"),c("al","an"),c("al","st"),c("an","st"))

dagr <- dag(~me:ve,~me:al,~ve:al,~al:an,~al:st,~an:st)

dagr <- dag(~me:ve:al,~ve:al:an)

edges(ugr)
nodes(ugr)

edges(dagr)
nodes(dagr)

ugList(list(~me:ve:al,~al:an:st))
dagList(list(~me:ve:al,~ve:al:an))

```

`validVarTypes`

Admissible variable types in gmData objects

Description

The variable types in a `gmData` object must be from a vector predefined types which may be inspected by the command `validVarTypes()`. The available types may be extended by the package developers as demonstrated in the example.

Usage

```
validVarTypes()
```

Value

A character vector with the names of the admissible variable types.

Author(s)

Søren Højsgaard, (sorenh@agrsci.dk),
Claus Dethlefsen, (cld@m.dk)

See Also

[gmData](#)

Examples

```
oldtypes <- validVarTypes()
validVartypes <- function() c(oldtypes, "MyVarType")
validVartypes()
```

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