

Package ‘gRbase’

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Version 1.8-1

Title A Package for Graphical Modelling in R

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Description The 'gRbase' package provides general features which are used by other graphical modelling packages, in particular by the packages 'gRain', 'gRim' and 'gRc'. 'gRbase' contains several data sets relevant for use in connection with graphical models. Almost all data sets used in the book Graphical Models with R (2012) are contained in 'gRbase'. 'gRbase' implements several graph algorithms (based mainly on representing graphs as adjacency matrices - either in the form of a standard matrix or a sparse matrix). Some graph algorithms are:

- (i) maximum cardinality search (for marked and unmarked graphs).
- (ii) moralize.
- (iii) triangulate.
- (iv) junction tree.

'gRbase' facilitates array operations, 'gRbase' implements functions for testing for conditional independence. 'gRbase' illustrates how hierarchical log-linear models may be implemented and describes concept of graphical meta data. These features, however, are not maintained anymore and remains in 'gRbase' only because there exists a paper describing these facilities: A Common Platform for Graphical Models in R: The 'gRbase' Package, Journal of Statistical Software, Vol 14, No 17, 2005.

NOTICE Proper functionality of 'gRbase' requires that the packages graph, 'Rgraphviz' and 'RBGL' are installed from 'bioconductor'; for installation instructions please refer to the web page given below.

License GPL (>= 2)

URL <http://people.math.aau.dk/~sorenh/software/gR/>

ByteCompile Yes

Encoding UTF-8

Depends R (>= 3.0.2), methods

Imports graph, igraph, magrittr, Matrix, RBGL, Rcpp (>= 0.11.1)

Suggests Rgraphviz, microbenchmark

LinkingTo Rcpp (>= 0.11.1), RcppArmadillo, RcppEigen

RoxygenNote 5.0.1

NeedsCompilation yes

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R topics documented:

array-algebra	3
array-create	4
array-dimnames	6
array-distribution	7
array-normalize	8
array-operations	9
array-properties	11
array-slice	12
ashtrees	13
BodyFat	14
breastcancer	16
cad	17
carcass	18
chestSim	19
combnPrim	20
compareModels	21
cov2pcor	22
dietox	22
dumping	23
graph-cliques	24
graph-coerce	25
graph-create	26
graph-edgeList	27
graph-gcproperties	28
graph-iplot	30
graph-is	31
graph-mcs	33
graph-minimaltriang	35
graph-moralize	37
graph-mpd	38
graph-query	39
graph-randomdag	40
graph-rip	41
graph-toposort	43

graph-triangulate	44
graph-vpar	46
graph-xxx2yyy	47
gRbase	50
gRbase-generics	51
gRbase-utilities	52
lizard	52
mathmark	53
mildew	54
milkcomp	54
Nutrimouse	55
old-array-operations	60
old-parray	61
rats	63
reinis	64
Setoperations	64
simulateArray	65
wine	66

Index**68**

array-algebra

*Array algebra***Description**

Addition, subtraction etc. of arrays

Usage

a1 %a+% a2

a1 %a-% a2

a1 %a*% a2

a1 %a/% a2

aradd(a1, a2)

arsubt(a1, a2)

armult(a1, a2)

ardiv(a1, a2)

ardiv0(a1, a2)

```
arsum(...)  
arprod(...)
```

Arguments

a, a1, a2, ... Arrays (with named dimnames)

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

Examples

```
hec <- HairEyeColor  
a1 <- armarg(hec, c("Hair", "Eye"))  
a2 <- armarg(hec, c("Hair", "Sex"))  
a3 <- armarg(hec, c("Eye", "Sex"))  
  
## Binary operations  
a1 %a+% a2  
a1 %a-% a2  
a1 %a*% a2  
a1 %a/% a2  
  
arsum(a1, a2, a3)  
arprod(a1, a2, a3)
```

array-create

Create multidimensional arrays

Description

Alternative ways of creating arrays

Convert dataframe to contingency table

Usage

```
newar(names, levels, values, normalize = "none", smooth = 0)
```

```
df2xtabs(indata, names = NULL, normalize = "none", smooth = 0)
```

Arguments

names	Names of variables defining table; a character vector or a right hand sided formula.
levels	1) a list with specification of the levels of the factors in names or 2) a vector with number of levels of the factors in names. See 'examples' below.
values	values to go into the parray
normalize	Either "none", "first" or "all". Should result be normalized, see 'Details' below.
smooth	Should values be smoothed, see 'Details' below.
indata	A dataframe.

Details

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

Value

An array.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

See Also

[arperm](#), [aradd](#), [arprod](#) etc.

Examples

```
universe <- list(gender=c('male','female'),
                answer=c('yes','no'),
                rain=c('yes','no'))
t1 <- newar(c("gender","answer"), levels=universe, values=1:4)
t1
t2 <- newar(~gender:answer, levels=universe, values=1:4)
t2
t3 <- newar(~gender:answer, c(2,2), values=1:4)
t3

## Extract arrays from dataframe (much like xtabs()) but with more flexibility)
data(cad1)
df2xtabs(cad1, ~Sex:AngPec:AMI)
df2xtabs(cad1, c("Sex","AngPec","AMI"))
df2xtabs(cad1, c(1,2,3))

## Extract arrays from dataframe (much like xtabs()) but with more flexibility)
```

```
data(cad1)
df2xtabs(cad1, ~Sex:AngPec:AMI)
df2xtabs(cad1, c("Sex","AngPec","AMI"))
df2xtabs(cad1, c(1,2,3))
```

array-dimnames	<i>Check compatibility of dimnames</i>
----------------	--

Description

Check that the intersection of dimnames of two arrays are identical.

Usage

```
dimnames_match(a1, a2)

dimnames_match_(tab1, tab2, verbose = FALSE)
```

Arguments

a1, a2, tab1, tab2
 Arrays with named dimnames.

verbose
 Should errors be printed.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

See Also

[is.named.array](#)

Examples

```
ar1 = newar(c("a","b"), levels=c(2,3))
ar2 = newar(c("c","a"), levels=c(2,2))
ar1
ar2
## dimension a has levels a1,a2 in both ar1 and ar2.
# Hence we have a match.
dimnames_match(ar1, ar2)

ar1 = newar(c("a","b"), levels=c(2,3))
ar2 = newar(c("c","a"), levels=c(2,3))
ar1
ar2
## dimension a has levels a1,a2 in ar1 and levels a1,a2,a3 in ar2.
# Hence we do not have a match.
```

```
dimnames_match(ar1, ar2)

ar2 = newar(c("c","a"), levels=list(c="c1","c2"), a=c("a2","a1"))
ar2
## dimension a has levels a1,a2 in ar1 and levels a2,a1 in ar2.
# Hence we do not have a match.
dimnames_match(ar1, ar2)
```

array-distribution *Marginalize and condition in multidimensional array.*

Description

Marginalize and condition in a multidimensional array which is assumed to represent a discrete multivariate distribution.

Usage

```
ardist(tab, marg = NULL, cond = NULL, normalize = TRUE)
```

Arguments

tab	Multidimensional array with dimnames.
marg	A specification of the desired margin; a character vector, a numeric vector or a right hand sided formula.
cond	A specification of what is conditioned on. Can take two forms: Form one is a character vector, a numeric vector or a right hand sided formula. Form two is as a simple slice of the array, which is a list of the form var1=value1, var2=value2 etc.
normalize	Should the result be normalized to sum to 1.

Value

A multidimensional array.

Note

ardist is a recent addition and its functionality (and name) may change. ardist is based on calling arMarg and arSlice.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

See Also

[newar](#), [armarg](#), [arslice](#) etc.

Examples

```

hec <- HairEyeColor

is.named.array( hec )
## We need dimnames, and names on the dimnames

## Marginalize:
ardist(hec, marg= ~Hair + Eye)
ardist(hec, marg= ~Hair:Eye)
ardist(hec, marg= c("Hair", "Eye"))
ardist(hec, marg= 1:2)

ardist(hec, marg= ~Hair + Eye, normalize=FALSE)

## Condition
ardist(hec, cond= ~Sex + Hair)
ardist(hec, cond= ~Sex:Hair)
ardist(hec, cond= c("Sex", "Hair"))
ardist(hec, cond= c(3,1))

ardist(hec, cond= list(Hair="Black"))
ardist(hec, cond= list(Hair=1))

## Not run:
## This will fail
ardist(hec, cond= list(Hair=c("Black", "Brown")))
ardist(hec, cond= list(Hair=1:2))

## End(Not run)
## But this will do the trick
a <- arslice(hec, slice=list(Hair=c("Black", "Brown")))
ardist(a, cond=~Hair)

## Combined
ardist(hec, marg=~Hair+Eye, cond=~Sex)
ardist(hec, marg=~Hair+Eye, cond="Sex")

ardist(hec, marg=~Hair+Eye, cond=list(Sex="Male"))
ardist(hec, marg=~Hair+Eye, cond=list(Sex="Male"), normalize=FALSE)

ardist(hec, cond=list(Sex="Male"))
ardist(hec, cond=list(Sex="Male"), normalize=FALSE)

```

array-normalize

*Normalize an array***Description**

Normalize an array in various ways.

Usage

```
arnormalize(tab, type = "none")
```

Arguments

tab	A multidimensional array
type	Either "none", "first", or "all"

Value

An array

Examples

```
arnormalize( HairEyeColor, type="first")
arnormalize( HairEyeColor, type="all")
```

array-operations	<i>Operations on multidimensional arrays.</i>
------------------	---

Description

Operations like marginalize, permute, slicing etc on arrays A multidimensional table (an array) is here a vector with a dim and a dimnames attribute.

Usage

```
arperm(tab, perm)
armarg(tab, marg)
arequal(tab1, tab2, eps = 1e-12)
arexpand(tab1, tab2)
aralign(tab1, tab2)
```

Arguments

tab, tab1, tab2	Multidimensional arrays.
perm	A vector of indices or dimnames giving the desired permutation.
marg	Specification of marginal; either a character vector, a numeric vector or a right hand sided formula For arperm and ararg it can also be a right hand sided formula.
eps	Criterion for checking equality of two arrays.

Details

perm in arperm() can be a vector of indices (as in Rs own aperm()) but also a vector of dimnames. Currently there is no checking that the dimnames are actually in the array, so please take care.

Value

Most functions here return a multidimensional array.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

See Also

[aperm](#), [arslice](#), [arslice_entries](#)

Examples

```
ar1 <- array(1:8, dim=c(2,2,2), dimnames=list("a"=1:2,"b"=1:2,"c"=1:2))
ar2 <- array(1:8, dim=c(2,2,2), dimnames=list("b"=1:2,"c"=1:2,"d"=1:2))

## ## armarg ##
## Marginalize down to the bc-array
armarg(ar1, 2:3)
armarg(ar1, c("b","c"))
armarg(ar1, ~b + c)

## This gives an error
## armarg(ar1, c(2,5))
## armarg(ar1, c("b","w"))
## armarg(ar1, ~b + w)

## ## arperm ##
arperm(ar1, 1:3)      ## No change - an abc-table
arperm(ar1, c(2,3,1)) ## A bca-table
arperm(ar1, ~b + c + a)

## This gives error
## arperm(ar1, c(2,1))
## arperm(ar1, c(2,1,5))
## arperm(ar1, c(2,1,NA))

## ## armult etc ##
## Multiply two arrays
out <- armult(ar1, ar2)
out <- arperm(out, ~a+b+c+d) ## Just for comparison below
ftable(out)
## Alternative approach
df1 <- as.data.frame.table(ar1)
df2 <- as.data.frame.table(ar2)
df3 <- merge(df1, df2, by=c("b","c"))
```

```

df3 <- transform(df3, Freq=Freq.x*Freq.y)
ar3 <- xtabs(Freq ~ a + b + c + d, data=df3)
ftable(ar3)

## ## arexpend ##
ar1.e <- arexpend(ar1, ar2)
## ar1.e has dimnames b,c,d,a; values are simply replicated for each
## level of d.
dimnames(ar1.e)
ftable(ar1.e, row.vars="d")

## ## aralign ##
ar2.e <- arexpend(ar2, ar1)
names(dimnames(ar2.e))
names(dimnames(ar1.e))
out <- aralign(ar1.e, ar2.e)
names(dimnames(out)) ## Same as ar2.e

## arexpend:
ar1 <- array(1:8, dim=c(2,2,2), dimnames=list("a"=1:2,"b"=1:2,"c"=1:2))
ar2 <- array(1:8, dim=c(2,2,2), dimnames=list("b"=1:2,"c"=1:2,"d"=1:2))

arexpend(ar1, ar2) %>% ftable(row.vars=1) ## Same as
## arexpend(ar1, dimnames(ar2)) %>% ftable(row.vars=1)

```

array-properties	<i>Check if object is array</i>
------------------	---------------------------------

Description

Check if object is array (that it is a vector with a dim attribute) and that the object has dimnames and that dimnames are named.

Usage

```

is.named.array(obj)

is_named_array_(obj)

is_number_vector_(obj)

is_dimnames_(obj)

```

Arguments

obj Some R object.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

Examples

```

is.named.array( HairEyeColor )
is.named.array( matrix(1:4, nrow=2) )
is_named_array_( HairEyeColor )
is_named_array_( matrix(1:4, nrow=2) )
is_number_vector_(1:4)
is_number_vector_(list(1:4))

```

array-slice

Array slices

Description

Functions for extracting slices of arrays

Usage

```

arslice(tab, slice = NULL, margin = names(slice), drop = TRUE,
        as.array = FALSE)

```

```

arslice_prim(tab, slice, drop = TRUE)

```

```

arslice_mult(tab, slice, val = 1, comp = 0)

```

```

arslice_entries(tab, slice, complement = FALSE)

```

Arguments

tab	An array with named dimnames.
slice	A list defining the slice.
margin	Names of variables in slice.
drop	If TRUE then dimensions with only one level will be dropped from the output.
as.array	If the resulting array is one-dimensional the result will by default be a vector with no dim attribute unless as.array is TRUE.
val	The values that entries in the slice will be multiplied with.
comp	The values that entries NOT in the slice will be multiplied with.
complement	If TRUE the complement of the entries are returned.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

See Also

[arperm](#), [armarg](#), [armult](#), [ardiv](#), [aradd](#), [arsubt](#), [arsum](#), [arprod](#)

Examples

```
x = HairEyeColor
s = list(Hair=c("Black","Brown"), Eye=c("Brown", "Blue"))

## arslice
s1 = arslice(x, slice=s)
s1

## arslice_entries
arslice_entries(x, slice=s)
arslice_entries(x, slice=s, complement=TRUE)

## arslice_mult
s2 = arslice_mult(x, slice=s)
s2

## arslice_prim does the same as arslice - faster, but the function is less
# flexible
sp = list(c(1,2), c(1,2), TRUE)
arslice_prim(x, slice=sp)
arslice(x, slice=s)
if ( require(microbenchmark) ){
  microbenchmark(arslice_prim(x, slice=sp), arslice(x, slice=s))
}
```

ashtrees

Crown dieback in ash trees

Description

This dataset comes from a study of symptoms of crown dieback, cankers and symptoms caused by other pathogens and pests in ash trees (*Fraxinus excelsior*). In all 454 trees were observed in two plots. There are 8 categorical variables, 6 of which are binary and two are trichotomous with values representing increasing severity of symptoms, and one continuous variable, tree diameter at breast height (DBH).

Usage

```
ashtrees
```

Format

A data frame with 454 observations on the following 9 variables.

plot a factor with levels 2 6
 dieback a factor with levels 0 1 2
 dead50 a factor with levels 0 0.5 1
 bushy a factor with levels 0 1
 canker a factor with levels BRNCH MAIN NONE
 wilt a factor with levels 0 1
 roses a factor with levels 0 1
 discolour a factor with levels 0 1
 dbh a numeric vector

References

Skovgaard JP, Thomsen IM, Skovgaard IM and Martinussen T (2009). Associations among symptoms of dieback in even-aged stands of ash (*Fraxinus excelsior* L.). *Forest Pathology*.

Examples

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

BodyFat

Body Fat Data

Description

Estimates of the percentage of body fat determined by underwater weighing and various body circumference measurements for 252 men.

Usage

```
data(BodyFat)
```

Format

A data frame with 252 observations on the following 15 variables.

Density Density determined from underwater weighing, a numeric vector
 BodyFat Percent body fat from Siri's (1956) equation, a numeric vector
 Age in years, a numeric vector
 Weight in lbs, a numeric vector

Height in inches, a numeric vector
Neck circumference in cm, a numeric vector
Chest circumference in cm, a numeric vector
Abdomen circumference in cm, a numeric vector
Hip circumference in cm, a numeric vector
Thigh circumference in cm, a numeric vector
Knee circumference in cm, a numeric vector
Ankle circumference in cm, a numeric vector
Biceps circumference in cm, a numeric vector
Forearm circumference in cm, a numeric vector
Wrist circumference in cm, a numeric vector

Source

For more information see <http://lib.stat.cmu.edu/datasets/bodyfat>

References

- Bailey, Covert (1994). *Smart Exercise: Burning Fat, Getting Fit*, Houghton-Mifflin Co., Boston, pp. 179-186.
- Behnke, A.R. and Wilmore, J.H. (1974). *Evaluation and Regulation of Body Build and Composition*, Prentice-Hall, Englewood Cliffs, N.J.
- Siri, W.E. (1956), "Gross composition of the body", in *Advances in Biological and Medical Physics*, vol. IV, edited by J.H. Lawrence and C.A. Tobias, Academic Press, Inc., New York.
- Katch, Frank and McArdle, William (1977). *Nutrition, Weight Control, and Exercise*, Houghton Mifflin Co., Boston.
- Wilmore, Jack (1976). *Athletic Training and Physical Fitness: Physiological Principles of the Conditioning Process*, Allyn and Bacon, Inc., Boston.

Examples

```
data(BodyFat)
head(BodyFat)
```

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

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

```
breastcancer
```

Format

A data frame with 250 observations on 1001 variables. The first 1000 columns are numerical variables; the last column (named code) is a factor with levels case and 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	<i>Coronary artery disease data</i>
-----	-------------------------------------

Description

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

Usage

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.

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

Lean meat contents of 344 pig carcasses

Description

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

Usage

```
carcass
```

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

Fat02, Fat03, Fat11, Fat12, Fat13, Fat14, Fat16 Thickness of fat layer at different locations on the back of the carcass (FatXX refers to thickness at (or rather next to) rib no. XX. Notice that 02 is closest to the head

Meat11, Meat12, Meat13 Thickness of meat layer at different locations on the back of the carcass, see description above

LeanMeat Lean meat percentage determined by dissection

s1house 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

Note

carcass: Contains only the variables Fat11, Fat12, Fat13, Meat11, Meat12, Meat13, LeanMeat

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

Examples

```
data(carcass)
head(carcass)
```

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

```
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) ...
```

`combnPrim`*Generate All Combinations of n Elements Taken m at a Time*

Description

Generate all combinations of the elements of `x` taken `m` at a time. If `x` is a positive integer, returns all combinations of the elements of `seq(x)` taken `m` at a time.

Usage

```
combnPrim(x, m, simplify = TRUE)
```

Arguments

<code>x</code>	vector source for combinations, or integer <code>n</code> for <code>x <- seq(n)</code> .
<code>m</code>	number of elements to choose.
<code>simplify</code>	logical indicating if the result should be simplified to a matrix; if <code>FALSE</code> , the function returns a list.

Value

A matrix or a list.

Note

The `combnPrim` function is a simplified version of the `combn` function. However, `combnPrim` is implemented in C and is considerably faster than `combn`.

Author(s)

P. T. Wallace and Søren Højsgaard

See Also

[combn](#)

Examples

```
x <- letters[1:20]
m <- 3

combn(x, m)
combnPrim(x, m)

combn(m, m)
combnPrim(m, m)
```

```
combn(x,m, simplify=FALSE)
combnPrim(x,m, simplify=FALSE)

system.time({ for (i in 1:100) { combnPrim(x,m) }})
system.time({ for (i in 1:100) { combn(x,m) }})

system.time({ for (i in 1:100) { combnPrim(x,m, simplify=FALSE) }})
system.time({ for (i in 1:100) { combn(x,m, simplify=FALSE) }})
```

`compareModels`*Generic function for model comparison*

Description

`compareModels` is a generic functions which invoke particular methods which depend on the class of the first argument

Usage

```
compareModels(object, object2, ...)
```

Arguments

<code>object, object2</code>	Model objects
<code>...</code>	Additional arguments

Value

The value returned depends on the class of the first argument.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

cov2pcor	<i>Partial correlation (matrix)</i>
----------	-------------------------------------

Description

cov2pcor calculates the partial correlation matrix from an (empirical) covariance matrix while conc2pcor calculates the partial correlation matrix from a concentration matrix (inverse covariance matrix).

Usage

```
cov2pcor(V)
```

```
conc2pcor(K)
```

Arguments

V	Covariance matrix
K	Concentration matrix

Value

A matrix with the same dimension as V.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

Examples

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

dietox	<i>Growth curves of pigs in a 3x3 factorial experiment</i>
--------	--

Description

The dietox data frame has 861 rows and 7 columns.

Usage

```
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 Oli, Vitamin E, and Copper on Performance and Antioxidant and Oxidative Status of Pigs. *J. Anim. Sci.*77:906-916

Examples

```
data(dietox)
```

dumping

Gastric Dumping

Description

A contingency table relating surgical operation, centre and severity of gastric dumping, a syndrome associated with gastric surgery.

Usage

```
dumping
```

Format

A 3x4x4 table of counts cross-classified by Symptom (none/slight/moderate), Operation (Vd/Va/Vh/Gr) and Centre (1:4).

Details

Gastric dumping syndrome is a condition where ingested foods bypass the stomach too rapidly and enter the small intestine largely undigested. It is an undesirable side-effect of gastric surgery. The table summarizes the results of a study comparing four different surgical operations on patients with duodenal ulcer, carried out in four centres, as described in Grizzle et al (1969). The four operations were: vagotomy and drainage, vagotomy and antrectomy (removal of 25% of gastric tissue), vagotomy and hemigastrectomy (removal of 50% of gastric tissue), and gastric restriction (removal of 75% of gastric tissue).

Source

Grizzle JE, Starmer CF, Koch GG (1969) Analysis of categorical data by linear models. *Biometrics* 25(3):489-504.

Examples

```
data(dumping)
plot(dumping)
```

graph-cliques

Get cliques of an undirected graph

Description

Return a list of (maximal) cliques of an undirected graph.

Usage

```
getCliques(object)

## S3 method for class 'graphNEL'
getCliques(object)

## Default S3 method:
getCliques(object)

maxCliqueMAT(amat)
```

Arguments

object	An undirected graph represented either as a graphNEL object, a (dense) matrix, a (sparse) dgCMatrix
amat	An adjacency matrix.

Details

In graph theory, a clique is often a complete subset of a graph. A maximal clique is a clique which can not be enlarged. In statistics (and that is the convention we follow here) a clique is usually understood to be a maximal clique.

Finding the cliques of a general graph is an NP complete problem. Finding the cliques of triangulated graph is linear in the number of cliques.

The workhorse is the maxCliqueMAT function which calls the maxClique function in the RBGL package.

Value

A list.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

See Also

[ug](#), [dag](#), [mcs](#), [mcsMAT](#), [rip](#), [ripMAT](#), [moralize](#), [moralizeMAT](#)

Examples

```
## graphNEL
uG1 <- ug(~a:b+b:c+c:d+d:e+f+f:a)
getCliques(uG1)

## adjacency matrix
uG2 <- ug(~a:b+b:c+c:d+d:e+f+f:a, result="matrix")
getCliques(uG2)

## adjacency matrix (sparse)
uG3 <- ug(~a:b+b:c+c:d+d:e+f+f:a, result="Matrix")
getCliques(uG3)
```

graph-coerce

Graph coercion

Description

Methods for changing graph representations

Usage

```
coerceGraph(object, result)

## S3 method for class 'graphNEL'
coerceGraph(object, result)

## S3 method for class 'matrix'
coerceGraph(object, result)

## S3 method for class 'dgCMatrix'
coerceGraph(object, result)

## S3 method for class 'igraph'
coerceGraph(object, result)
```

Arguments

object	A graph object
result	The desired output type

graph-create	<i>Create undirected and directed graphs</i>
--------------	--

Description

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

Usage

```
ug(..., result = "graphNEL")
dag(..., result = "graphNEL", forceCheck = FALSE)
```

Arguments

result	The format of the graph. The possible choices are "graphNEL" (for a graphNEL object), "matrix" (for an adjacency matrix), "dgCMatrix" (for a sparse matrix), "igraph" (for an igraph object).
forceCheck	Logical determining if it should be checked if the graph is acyclical. Yes, one can specify graphs with cycles using the dag() function.
...	A generating class for a graph, see examples below

Value

Functions ug(), and dag() can return a graphNEL object, a sparse or dense adjacency matrix or an igraph object.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

Examples

```
## The following specifications of undirected graphs are equivalent:
uG1 <- ug(~ a:b:c + c:d)
uG2 <- ug(c("a","b","c"), c("c","d"))
uG3 <- ug(c("a","b"), c("a","c"), c("b","c"), c("c","d"))

graph::edges(uG1)
graph::nodes(uG1)
```

```

## The following specifications of directed acyclic graphs are equivalent:
daG1 <- dag(~ a:b:c + b:c + c:d)
daG2 <- dag(c("a","b","c"), c("b","c"), c("c","d"))

graph::edges(daG1)
graph::nodes(daG2)

## dag() allows to specify directed graphs with cycles:
daG4 <- dag(~ a:b + b:c + c:a) # A directed graph but with cycles
## A check for acyclicity can be done with
## daG5 <- dag(~ a:b + b:c + c:a, forceCheck=TRUE)

## A check for acyclicity is provided by topoSort
topoSort( daG2 )
topoSort( daG4 )

## Different representations
uG6 <- ug(~a:b:c + c:d, result="graphNEL") # default
uG6
uG7 <- ug(~a:b:c + c:d, result="NEL")      # same
uG7
uG8 <- ug(~a:b:c + c:d, result="matrix")   # dense matrix
uG8
uG9 <- ug(~a:b:c + c:d, result="dgMatrix") # sparse matrix
uG9

```

graph-edgeList *Find edges in a graph and edges not in a graph.*

Description

Returns the edges of a graph (or edges not in a graph) where the graph can be either a graphNEL object or an adjacency matrix.

Usage

```

edgeList(object, matrix = FALSE)

## Default S3 method:
edgeList(object, matrix = FALSE)

edgeListMAT(adjmat, matrix = FALSE)

nonEdgeList(object, matrix = FALSE)

## Default S3 method:
nonEdgeList(object, matrix = FALSE)

nonEdgeListMAT(adjmat, matrix = FALSE)

```

Arguments

object	A graphNEL object or an adjacency matrix.
matrix	If TRUE the result is a matrix; otherwise the result is a list.
adjmat	An adjacency matrix.

Examples

```
## A graph with edges
g <- ug(~a:b+b:c+c:d)
gm <- graphNEL2M(g)
edgeList(g)
edgeList(gm)
edgeListMAT(gm)
edgeList(g, matrix=TRUE)
edgeList(gm, matrix=TRUE)
edgeListMAT(gm, matrix=TRUE)
nonEdgeList(g)
nonEdgeList(gm)
nonEdgeListMAT(gm)
## A graph without edges
g <- ug(~a+b+c)
gm <- graphNEL2M(g)
edgeList(g)
edgeList(gm)
edgeListMAT(gm)
edgeList(g, matrix=TRUE)
edgeList(gm, matrix=TRUE)
edgeListMAT(gm, matrix=TRUE)
nonEdgeList(g)
nonEdgeList(gm)
nonEdgeListMAT(gm)
```

graph-gcproperties *Properties of a generating class (for defining a graph)*

Description

A set of generators define an undirected graph, here called a dependence graph. Given a set of generators it is checked 1) if the dependence graph is in 1-1-correspondance with the generators (such that the corresponding model is graphical) and 2) if the dependence graph is chordal (triangulated) (such that the corresponding model is decomposable).

Usage

```
isGraphical(x)

## Default S3 method:
isGraphical(x)

isDecomposable(x)

## Default S3 method:
isDecomposable(x)
```

Arguments

x A generating class given as right hand sided formula or a list; see 'examples' below

Details

A set of sets of variables, say A_1, A_2, \dots, A_K is called a generating class for a graph with vertices V and edges E . If two variables a, b are in the same generator, say A_j , then a and b are vertices in the graph and there is an undirected edge between a and b .

The graph induced by $g1 = \sim a:b + a:c + b:c + c:d$ has edges ab, ac, bc, cd . The cliques of this graph are abc, cd . Hence there is not a 1-1-correspondance between the graph and the generators.

On the other hand, $g2 \leftarrow \sim a:b:c + c:d$ induces the same graph in this case there is a 1-1-correspondance.

The graph induced by $g3 \leftarrow \sim a:b + b:c + c:d + d:a$ is in 1-1-correspondance with its dependence graph, but the graph is not chordal.

Value

TRUE or FALSE

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

See Also

[mcs](#), [rip](#)

Examples

```
g1 <- ~a:b+a:c+b:c+c:d
g2 <- ~a:b:c+c:d
g3 <- ~a:b + b:c + c:d + d:a

isGraphical( g1 ) # FALSE
isGraphical( g2 ) # TRUE
```

```
isGraphical( g3 ) # TRUE

isDecomposable( g1 ) # FALSE
isDecomposable( g2 ) # TRUE
isDecomposable( g3 ) # TRUE

## A generating class can be given as a list:
f <- list(c("a","b"), c("b","c"), c("a","c"))
isGraphical( f )
isDecomposable( f )
```

graph-iplot

Function for plotting graphs using the 'igraph' package.

Description

Generic function for plotting graphs using the 'igraph' package and a plot method for graphNEL objects.

Usage

```
iplot(x, ...)
```

S3 method for class 'graphNEL'

```
iplot(x, ...)
```

Arguments

x A graph object to be plotted.
... Additional arguments

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

Examples

```
UG <- ug(~a:b+b:c:d)
iplot(UG)
```

`graph-is`*Check properties of graphs.*

Description

Check if a graph is 1) a directed acyclic graph (DAG), 2) a directed graph (DG), 3) an undirected graph (UG), 4) a triangulated (chordal) undirected graph (TUG). This is done for graphs represented as 1) graphNEL (from the graph package), 2) an adjacency matrix, 3) a sparse adjacency matrix (a dgCMat from the Matrix package).

Usage

```
is.DAG(object)

## S3 method for class 'graphNEL'
is.DAG(object)

## Default S3 method:
is.DAG(object)

is.DAGMAT(object)

is.UG(object)

## S3 method for class 'graphNEL'
is.UG(object)

## Default S3 method:
is.UG(object)

is.UGMAT(object)

is.TUG(object)

## S3 method for class 'graphNEL'
is.TUG(object)

## Default S3 method:
is.TUG(object)

is.TUGMAT(object)

is.DG(object)

## S3 method for class 'graphNEL'
is.DG(object)
```

```
## Default S3 method:
is.DG(object)

is.DGMAT(object)
```

Arguments

object A graph represented as 1) graphNEL (from the graph package), 2) an adjacency matrix, 3) a sparse adjacency matrix (a dgCMatrix from the Matrix package).

Details

A non-zero value at entry (i,j) in an adjacency matrix A for a graph means that there is an edge from i to j. If also (j,i) is non-zero there is also an edge from j to i. In this case we may think of a bidirected edge between i and j or we may think of the edge as being undirected. We do not distinguish between undirected and bidirected edges in the gRbase package. On the other hand, graphNEL objects from the graph package makes such a distinction (the function `edgemode()` will tell if edges are "directed" or "undirected" in a graphNEL object).

The function `is.UG()` checks if the adjacency matrix is symmetric (If applied to a graphNEL, the adjacency matrix is created and checked for symmetry.)

The function `is.TUG()` checks if the graph is undirected and triangulated (also called chordal) by checking if the adjacency matrix is symmetric and the vertices can be given a perfect ordering using maximum cardinality search.

The function `is.DG()` checks if a graph is directed, i.e., that there are no undirected edges. This is done by computing the elementwise product of A and the transpose of A; if there are no non-zero entries in this product then the graph is directed.

The function `is.DAG()` will return TRUE if all edges are directed and if there are no cycles in the graph. (This is checked by checking if the vertices in the graph can be given a topological ordering which is based on identifying an undirected edge with a bidirected edge).

There is a special case, namely if the graph has no edges at all (such that the adjacency matrix consists only of zeros). Such a graph is both undirected, triangulated, directed and directed acyclic.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

See Also

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

Examples

```
## DAGs
dagNEL <- dag(~ a:b:c + c:d:e, result="NEL")
dagMAT <- dag(~ a:b:c + c:d:e, result="matrix")
dagMATS <- dag(~ a:b:c + c:d:e, result="Matrix")
```



```

## Undirected graphs
ugNEL <- ug(~a:b:c + c:d:e, result="NEL")
ugMAT <- ug(~a:b:c + c:d:e, result="matrix")
ugMATS <- ug(~a:b:c + c:d:e, result="Matrix")

## Is it a DAG?
is.DAG(dagNEL)
is.DAG(dagMAT)
is.DAG(dagMATS)

is.DAG(ugNEL)
is.DAG(ugMAT)
is.DAG(ugMATS)

## Is it an undirected graph
is.UG(dagNEL)
is.UG(dagMAT)
is.UG(dagMATS)

is.UG(ugNEL)
is.UG(ugMAT)
is.UG(ugMATS)

## Is it a triangulated (i.e. chordal) undirected graph
is.TUG(dagNEL)
is.TUG(dagMAT)
is.TUG(dagMATS)

is.TUG(ugNEL)
is.TUG(ugMAT)
is.TUG(ugMATS)

## Example where the graph is not triangulated
ug2NEL <- ug(~ a:b + b:c + c:d + d:a, result="NEL")
ug2MAT <- ug(~ a:b + b:c + c:d + d:a, result="matrix")
ug2MATS <- ug(~ a:b + b:c + c:d + d:a, result="Matrix")

is.TUG(ug2NEL)
is.TUG(ug2MAT)
is.TUG(ug2MATS)

## Bidirected graphs
graph::edgemode(ugNEL)
graph::edgemode(ugNEL) <- "directed"
graph::edgemode(ugNEL)
is.DAG(ugNEL)
is.UG(ugNEL)

```

Description

Returns (if it exists) a perfect ordering of the vertices in an undirected graph.

Usage

```
mcs(object, root = NULL, index = FALSE)

## Default S3 method:
mcs(object, root = NULL, index = FALSE)

mcsMAT(amat, vn = colnames(amat), root = NULL, index = FALSE)

mcsmarked(object, discrete = NULL, index = FALSE)

## Default S3 method:
mcsmarked(object, discrete = NULL, index = FALSE)

mcsmarkedMAT(amat, vn = colnames(amat), discrete = NULL, index = FALSE)
```

Arguments

object	An undirected graph represented either as a graphNEL object, an igraph, a (dense) matrix, a (sparse) dgCMatix.
root	A vector of variables. The first variable in the perfect ordering will be the first variable on 'root'. The ordering of the variables given in 'root' will be followed as far as possible.
index	If TRUE, then a permutation is returned
amat	Adjacency matrix
vn	Nodes in the graph given by adjacency matrix
discrete	A vector indicating which of the nodes are discrete. See 'details' for more information.

Details

An undirected graph is decomposable iff there exists a perfect ordering of the vertices. The maximum cardinality search algorithm returns a perfect ordering of the vertices if it exists and hence this algorithm provides a check for decomposability. The `mcs()` functions finds such an ordering if it exists.

The notion of strong decomposability is used in connection with e.g. mixed interaction models where some vertices represent discrete variables and some represent continuous variables. Such graphs are said to be marked. The `mcsmarked()` function will return a perfect ordering iff the graph is strongly decomposable. As graphs do not know about whether vertices represent discrete or continuous variables, this information is supplied in the `discrete` argument.

Value

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.

Note

The workhorse is the mcsMAT function.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

See Also

[moralize](#), [jTree](#), [rip](#), [ug](#), [dag](#)

Examples

```

uG <- ug(~ me:ve + me:al + ve:al + al:an + al:st + an:st)
mcs(uG)
mcsMAT( graphNEL2M(uG) )
## Same as
uG <- ug(~ me:ve + me:al + ve:al + al:an + al:st + an:st, result="matrix")
mcsMAT(uG)

## Marked graphs
uG1 <- ug(~ a:b + b:c + c:d)
uG2 <- ug(~ a:b + a:d + c:d)
## Not strongly decomposable:
mcsmarked(uG1, discrete=c("a","d"))
## Strongly decomposable:
mcsmarked(uG2, discrete=c("a","d"))

```

graph-minimaltriang *Minimal triangulation of an undirected graph*

Description

An undirected graph uG is triangulated (or chordal) if it has no cycles of length ≥ 4 without a chord which is equivalent to that the vertices can be given a perfect ordering. Any undirected graph can be triangulated by adding edges to the graph, so called fill-ins which gives the graph TuG . A triangulation TuG is minimal if no fill-ins can be removed without breaking the property that TuG is triangulated.

Usage

```

minimalTriang(object, tobject = triangulate(object), result = NULL,
  details = 0)

## Default S3 method:
minimalTriang(object, tobject = triangulate(object),

```

```

    result = NULL, details = 0)

minimalTriangMAT(amat, tamat = triangulateMAT(amat), details = 0)

```

Arguments

object	An undirected graph represented either as a graphNEL object, a (dense) matrix, a (sparse) dgCMatrix.
tobject	Any triangulation of object; must be of the same representation.
result	The type (representation) of the result. Possible values are "graphNEL", "matrix", "dgCMatrix". Default is the same as the type of object.
details	The amount of details to be printed.
amat	The undirected graph which is to be triangulated; a symmetric adjacency matrix.
tamat	Any triangulation of object; a symmetric adjacency matrix.

Details

For a given triangulation tobject it may be so that some of the fill-ins are superfluous in the sense that they can be removed from tobject without breaking the property that tobject is triangulated. The graph obtained by doing so is a minimal triangulation.

Notice: A related concept is the minimum triangulation, which is the the graph with the smallest number of fill-ins. The minimum triangulation is unique. Finding the minimum triangulation is NP-hard.

Value

minimalTriang() returns a graphNEL object while minimalTriangMAT() returns an adjacency matrix.

Author(s)

Clive Bowsher <C.Bowsher@statslab.cam.ac.uk> with modifications by Søren Højsgaard, <sorenh@math.aau.dk>

References

Kristian G. Olesen and Anders L. Madsen (2002): Maximal Prime Subgraph Decomposition of Bayesian Networks. IEEE TRANSACTIONS ON SYSTEMS, MAN AND CYBERNETICS, PART B: CYBERNETICS, VOL. 32, NO. 1, FEBRUARY 2002

See Also

[mpd](#), [rip](#), [triangulate](#)

Examples

```
## A graphNEL object
g1 <- ug(~a:b+b:c+c:d+d:e+e:f+a:f+b:e)
x <- minimalTriang(g1)

## g2 is a triangulation of g1 but it is not minimal
g2 <- ug(~a:b:e:f+b:c:d:e)
x<-minimalTriang(g1, tobject=g2)

## An adjacency matrix
g1m <- ug(~a:b+b:c+c:d+d:e+e:f+a:f+b:e, result="matrix")
x<-minimalTriangMAT(g1m)
```

graph-moralize	<i>Moralize a directed acyclic graph</i>
----------------	--

Description

Moralize a directed acyclic graph which means marrying parents and dropping directions.

Usage

```
moralize(object, ...)

## Default S3 method:
moralize(object, result = NULL, ...)
```

Arguments

object	A directed acyclic graph represented either as a graphNEL object, an igraph, a (dense) matrix, a (sparse) dgCMatrix.
result	The representation of the moralized graph. When NULL the representation will be the same as the input object.
...	Additional arguments, currently not used

Value

A moralized graph represented either as a graphNEL, a dense matrix or a sparse dgCMatrix.

Note

The workhorse is the moralizeMAT function.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

See Also

[mcs](#), [jTree](#), [rip](#), [ug](#), [dag](#)

Examples

```

daG <- dag(~me+ve,~me+al,~ve+al,~al+an,~al+st,~an+st)
moralize(daG)

daG <- dag(~me+ve,~me+al,~ve+al,~al+an,~al+st,~an+st, result="matrix")
moralizeMAT(daG)

if (require(igraph)){
M <- matrix(c(1,2,3,3), nrow=2)
G <- graph.edgelist(M)
G
V(G)$name
moralize(G)
}

```

graph-mpd

Maximal prime subgraph decomposition

Description

Finding a junction tree representation of the MPD (maximal prime subgraph decomposition) of an undirected graph. The maximal prime subgraph decomposition of a graph is the smallest subgraphs into which the graph can be decomposed.

Usage

```
mpd(object, tobject = minimalTriang(object), details = 0)
```

```
## Default S3 method:
```

```
mpd(object, tobject = triangulate(object), details = 0)
```

```
mpdMAT(amat, tamat = minimalTriangMAT(amat), details = 0)
```

Arguments

object	An undirected graph; a graphNEL object
tobject	Any minimal triangulation of object; a graphNEL object
details	The amount of details to be printed.
amat	An undirected graph; a symmetric adjacency matrix
tamat	Any minimal triangulation of object; a symmetric adjacency matrix

Value

A list with components "nodes", "cliques", "separators", "parents", "children", "nLevels". The component "cliques" defines the subgraphs.

Author(s)

Clive Bowsher <C.Bowsher@statslab.cam.ac.uk> with modifications by Søren Højsgaard, <sorenh@math.aau.dk>

References

Kristian G. Olesen and Anders L. Madsen (2002): Maximal Prime Subgraph Decomposition of Bayesian Networks. IEEE TRANSACTIONS ON SYSTEMS, MAN AND CYBERNETICS, PART B: CYBERNETICS, VOL. 32, NO. 1, FEBRUARY 2002

See Also

[mcs](#), [mcsMAT](#), [minimalTriang](#), [minimalTriangMAT](#), [rip](#), [ripMAT](#), [triangulate](#), [triangulateMAT](#)

Examples

```
## Maximal prime subgraph decomposition - a graphNEL object
g1 <- ug(~ a:b + b:c + c:d + d:e + e:f + a:f + b:e)
if (interactive()) plot(g1)
x <- mpd(g1)

## Maximal prime subgraph decomposition - an adjacency matrix
g1m <- ug(~ a:b + b:c + c:d + d:e + e:f + a:f + b:e, result="matrix")
if (interactive()) plot(as(g1m, "graphNEL"))
x <- mpdMAT(g1m)
```

graph-query

Query a graph

Description

Unified approach to query a graph about its properties

Usage

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

```
ancestors(set, object)
```

```
ancestralSet(set, object)
```

```
parents(set, object)
```

```

children(set, object)
closure(set, object)
simplicialNodes(object)
ancestralGraph(set, object)
is.complete(object, set = NULL)
is.decomposition(set, set2, set3, object)
is.simplicial(set, object)

```

Arguments

object	A graph
op	The operation or query
set, set2, set3	Sets of nodes in graph

graph-randomdag	<i>Random directed acyclic graph</i>
-----------------	--------------------------------------

Description

Generate a random directed acyclic graph (DAG)

Usage

```
random_dag(V, maxpar = 3, wgt = 0.1)
```

Arguments

V	The set of vertices.
maxpar	The maximum number of parents each node can have
wgt	A parameter controlling how likely it is for a node to have a certain number of parents; see 'Details'

Details

If the maximum number of parents for a node is, say 3 and wgt=0.1, then the probability of the node ending up with 0,1,2,3 parents is proportional to 0.1^0 , 0.1^1 , 0.1^2 , 0.1^3 .

Value

A graphNEL object.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

Examples

```
dg <- random_dag(1:1000, maxpar=5, wgt=.9)
table(sapply(vpar(dg),length))
```

```
dg <- random_dag(1:1000, maxpar=5, wgt=.5)
table(sapply(vpar(dg),length))
```

```
dg <- random_dag(1:1000, maxpar=5, wgt=.1)
table(sapply(vpar(dg),length))
```

graph-rip	<i>Create RIP ordering of the cliques of an undirected graph; create junction tree.</i>
-----------	---

Description

A RIP (running intersection property) ordering of the cliques is also called a perfect ordering. If the graph is not chordal, then no such ordering exists.

Usage

```
rip(object, root = NULL, nLevels = NULL)

## Default S3 method:
rip(object, root = NULL, nLevels = NULL)

ripMAT(amat, root = NULL, nLevels = rep(2, ncol(amat)))

jTree(object, ...)

## Default S3 method:
jTree(object, nLevels = NULL, ...)

jTreeMAT(amat, nLevels = rep(2, ncol(amat)), ...)
```

Arguments

object	An undirected graph represented either as a graphNEL object, an igraph, a (dense) matrix, a (sparse) dgCMatrix.
root	A vector of variables. The first variable in the perfect ordering will be the first variable on 'root'. The ordering of the variables given in 'root' will be followed as far as possible.
nLevels	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'.
amat	Adjacency matrix
...	Additional arguments; currently not used

Details

The RIP ordering of the cliques of a decomposable (i.e. chordal) graph 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() (and jTree()) (for "junction tree") is just a wrapper for a call of triangulate() followed by a call of rip().

Value

rip returns a list (an object of class ripOrder. A print method exists for such objects.)

Note

The workhorse is the ripMAT() function. The nLevels argument to the rip functions has no meaning.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

See Also

[mcs](#) [triangulate](#) [moralize](#) [ug](#), [dag](#)

Examples

```
## graphNEL
uG <- ug(~me:ve + me:al + ve:al + al:an + al:st + an:st)
mcs(uG)
rip(uG)
jTree(uG)

## Adjacency matrix
uG <- ug(~me:ve:al + al:an:st, result="matrix")
mcs(uG)
```

```

rip(uG)
jTree(uG)

## Sparse adjacency matrix
uG <- ug(c("me", "ve", "al"), c("al", "an", "st"), result="Matrix")
mcs(uG)
rip(uG)
jTree(uG)

## Non--decomposable graph
uG <- ug(~1:2+2:3+3:4+4:5+5:1)
mcs(uG)
rip(uG)
jTree(uG)

```

graph-toposort

Topological sort of vertices in directed acyclic graph

Description

A topological ordering of a directed graph is a linear ordering of its vertices such that, for every edge (u->v), u comes before v in the ordering. A topological ordering is possible if and only if the graph has no directed cycles, that is, if it is a directed acyclic graph (DAG). Any DAG has at least one topological ordering. Can hence be used for checking if a graph is a DAG.

Usage

```

topoSort(object, index = FALSE)

## Default S3 method:
topoSort(object, index = FALSE)

topoSortMAT(amat, index = FALSE)

```

Arguments

object	An graph represented either as a graphNEL object, an igraph, a (dense) matrix, a (sparse) dgCMatrix.
index	If FALSE, an ordering is returned if it exists and character(0) otherwise. If TRUE, the index of the variables in an adjacency matrix is returned and -1 otherwise.
amat	Adjacency matrix.

Value

If FALSE, an ordering is returned if it exists and character(0) otherwise. If TRUE, the index of the variables in an adjacency matrix is returned and -1 otherwise.

Note

The workhorse is the topoSortMAT function which takes an adjacency matrix as input

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

See Also

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

Examples

```
dagMAT <- dag(~a:b:c+c:d:e, result="matrix")
dagMATS <- as(dagMAT, "dgCMatrix")
dagNEL <- as(dagMAT, "graphNEL")

topoSort(dagMAT)
topoSort(dagMATS)
topoSort(dagNEL)
```

graph-triangulate

Triangulation of an undirected graph

Description

This function will triangulate an undirected graph by adding fill-ins.

Usage

```
triangulate(object, ...)

## Default S3 method:
triangulate(object, nLevels = NULL, result = NULL,
  check = TRUE, ...)

triangulateMAT(amat, nLevels = rep(2, ncol(amat)), ...)
```

Arguments

object	An undirected graph represented either as a graphNEL object, an igraph, a (dense) matrix, a (sparse) dgCMatrix.
...	Additional arguments, currently not used.
nLevels	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'.

result	The type (representation) of the result. Possible values are "graphNEL", "igraph", "matrix", "dgCMatrix". Default is the same as the type of object.
check	If TRUE (the default) it is checked whether the graph is triangulated before doing the triangulation; gives a speed up
amat	Adjacency matrix; a (dense) matrix, or a (sparse) dgCMatrix.

Details

The workhorse is the triangulateMAT function.

The triangulation is made so as the total state space is kept low by applying a minimum clique weight heuristic: When a fill-in is necessary, the algorithm will search for an edge to add such that the complete set to be formed will have as small a state-space as possible. It is in this connection that the nLevels values are used.

Default (when nLevels=NULL) is to take nLevels=2 for all nodes. If nLevels is the same for all nodes then the heuristic aims at keeping the clique sizes small.

Value

A triangulated graph represented either as a graphNEL, a (dense) matrix or a (sparse) dgCMatrix.

Note

Care should be taken when specifying nLevels for other representations than adjacency matrices: Since the triangulateMAT function is the workhorse, any other representation is transformed to an adjacency matrix and the order of values in nLevels most come in the order of the nodes in the adjacency matrix representation.

Currently there is no check for that the graph is undirected.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

See Also

[ug dag mcs](#), [mcsMAT rip](#), [ripMAT](#), [moralize](#), [moralizeMAT](#)

Examples

```
## graphNEL
uG1 <- ug(~a:b+b:c+c:d+d:e+e:f+f:a)
tuG1 <- triangulate(uG1)

## adjacency matrix
uG2 <- ug(~a:b+b:c+c:d+d:e+e:f+f:a, result="matrix")
tuG2 <- triangulate(uG2)

## adjacency matrix (sparse)
uG2 <- ug(~a:b+b:c+c:d+d:e+e:f+f:a, result="Matrix")
```

```
tuG2 <- triangulate(uG2)
```

graph-vpar

List of vertices and their parents for graph.

Description

Get list of vertices and their parents for graph.

Usage

```
vpar(object, getv = TRUE, forceCheck = TRUE)
vparMAT(object, getv = TRUE, forceCheck = TRUE)

## S3 method for class 'graphNEL'
vpar(object, getv = TRUE, forceCheck = TRUE)

## S3 method for class 'Matrix'
vpar(object, getv = TRUE, forceCheck = TRUE)

## S3 method for class 'matrix'
vpar(object, getv = TRUE, forceCheck = TRUE)
```

Arguments

object	An object representing a graph. Valid objects are an adjacency matrix or as a graphNEL.
getv	The result is by default a list of vectors of the form (v, pa1, pa2, ... paN) where pa1, pa2, ... paN are the parents of v. If getv is FALSE then the vectors will have the form (pa1, pa2, ... paN)
forceCheck	Logical indicating if it should be checked that the object is a DAG.

Value

A list of vectors where each vector will have the form (v, pa1, pa2, ... paN) where pa1, pa2, ... paN are the parents of v.

See Also

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

Examples

```

## DAGs
dagMAT <- dag(~a:b:c+c:d:e, result="matrix")
dagNEL <- dag(~a:b:c+c:d:e, result="NEL")
vpar(dagMAT)
vpar(dagNEL)
vpar(dagMAT, getv=FALSE)
vpar(dagNEL, getv=FALSE)
## Undirected graphs
ugMAT <- ug(~a:b:c+c:d:e, result="matrix")
ugNEL <- ug(~a:b:c+c:d:e, result="NEL")
## Not run:
## This will fail because the adjacency matrix is symmetric and the
## graphNEL has undirected edges
vpar(ugMAT)
vpar(ugNEL)

## End(Not run)
## When forceCheck is FALSE, it will not be detected that the graphs are undirected.
vpar(ugMAT, forceCheck=FALSE)
vpar(ugNEL, forceCheck=FALSE)
## Bidirected graphs
## This is, for graphNELs, the same as working with bidirected edges:
if (require(graph)){
  graph::edgemode(ugNEL)
  graph::edgemode(ugNEL) <- "directed"
  graph::edgemode(ugNEL)
  vpar(ugNEL, FALSE)
}

```

graph-xxx2yyy

Graph, matrix and generating class coercions

Description

Graph and matrix coercions where speed is an issue.

Usage

```

graphNEL2M(gn, result = "matrix")

graphNEL2MAT(gn, limit = 100)

graphNEL2ftM(gn)

graphNEL2tfM(gn)

graphNEL2igraph(gn)

```

```

M2igraph(amat)
M2graphNEL(amat)
M2adjList(amat)
M2ugList(amat)
M2dagList(amat)
ugList2graphNEL(glist, vn = NULL)
ugList2M(glist, vn = NULL, result = "matrix")
dagList2graphNEL(glist, vn = NULL)
dagList2M(glist, vn = NULL, result = "matrix")
adjList2M(alist, result = "matrix")
dagList2tfM(glist)
as.adjMAT(gn, result = "matrix")
ug2dag(gn)
MAT2matrix(mat)
MAT2dgCMatrix(mat)

```

Arguments

<code>gn</code>	A graphNEL object
<code>result</code>	Either "matrix" or "dgCMatrix" (for a sparse matrix representation)
<code>limit</code>	If number of nodes is larger than <code>limit</code> , the result will be a sparse dgCMatrix; otherwise a dense matrix.
<code>amat</code>	Adjacency matrix
<code>glist</code>	A list of generators where a generator is a character vector. If interpreted as generators of an undirected graph, a generator is a complete set of vertices in the graph. If interpreted as generators of a dag, a generator (v_1, \dots, v_n) means that there will be arrows from v_2, \dots, v_n to v_1 .
<code>vn</code>	The names of the vertices in the graphs. These will be the row and column names of the matrix
<code>alist</code>	An adjacency list.
<code>mat</code>	Either a dense matrix or a sparse dgCMatrix.

Value

An adjacency matrix (or NULL if glist has length 0)

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

See Also

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

Examples

```
glist <- list(1:3, 2:4, 4:5)
am1 <- ugList2M( glist )
am2 <- dagList2M( glist )
if (interactive()){
  plot(as(am1, "graphNEL"))
  plot(as(am2, "graphNEL"))
}

## Sparse and dense adjacency matrices converted to igraph
g1 <- ug(~a:b + b:c + c:d, result="matrix")
g2 <- ug(~a:b + b:c + c:d, result="dgCMatrix")
plot( M2igraph( g1 ) )
plot( M2igraph( g2 ) )

## Sparse and dense adjacency matrices converted to graphNEL
g1 <- ug(~a:b + b:c + c:d, result="matrix")
g2 <- ug(~a:b + b:c + c:d, result="dgCMatrix")
M2graphNEL( g1 )
M2graphNEL( g2 )

## Sparse and dense adjacency matrices converted to adjacency list
g1 <- ug(~a:b + b:c + c:d, result="matrix")
g2 <- ug(~a:b + b:c + c:d, result="dgCMatrix")
M2adjList( g1 )
## M2adjList( g2 ) FAILS for sparse matrix

## Sparse and dense adjacency matrices converted to cliques
g1 <- ug(~a:b + b:c + c:d, result="matrix")
g2 <- ug(~a:b + b:c + c:d, result="dgCMatrix")
M2ugList( g1 )
M2ugList( g2 )

## Sparse and dense adjacency matrices converted to cliques
g1 <- ug(~a:b + b:c + c:d, result="matrix")
g2 <- ug(~a:b + b:c + c:d, result="dgCMatrix")
M2dagList( g1 )
## M2dagList( g2 ) ## Fails for sparse matrix
```

```
g1 <- dag(~a:b + b:c + c:d, result="matrix")
g2 <- dag(~a:b + b:c + c:d, result="dgCMatrix")
M2dagList( g1 )
## M2dagList( g2 ) ## FIXME Fails for sparse matrix
```

gRbase

The package 'gRbase': summary information

Description

This package provides a basis for graphical modelling in R and in particular for other graphical modelling packages, most notably **gRim**, **gRain** and **gRc**.

Details

gRbase provides the following:

- Implementation of various graph algorithms, including maximum cardinality search, maximal prime subgraph decomposition, triangulation. See the vignette `graphs`.
- Implementation of various "high level" array operations, including multiplication/division, marginalization, slicing, permutation. See the vignette `ArrayOps`.
- Implementation of various "low level" array operations. See the vignette `ArrayOpsPrim`.
- A collection of datasets
- A 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. (Notice: This last part is not maintained / developed further.)

Authors

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Contributions from Claus Dethlefsen, Clive Bowsher, David Edwards.

Acknowledgements

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

References

Hojsgaard, S., Edwards, D., Lauritzen, S. (2012) Graphical models with R. Springer. ISBN: 978-1-4614-2298-3

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

gRbase-generics *Compile and propagate functions*

Description

compile and propagate are generic functions which invoke particular methods which depend on the class of the first argument

Usage

```
fit(object, ...)
```

```
compile(object, ...)
```

```
propagate(object, ...)
```

```
stepwise(object, ...)
```

Arguments

object An object

... Additional arguments which depends on the class of the object

Value

The value returned depends on the class of the first argument.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

References

Højsgaard, Søren; Edwards, David; Lauritzen, Steffen (2012): Graphical Models with R, Springer

See Also

[compile.grain](#), [propagate.grain](#)

gRbase-utilities *Utility functions for gRbase*

Description

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

Details

colwiseProd multiplies a vector and a matrix columnwise (as opposed to rowwise which is achieved by $v*M$). Hence colwiseProd does the same as $t(v*t(M))$ - but it does so faster for numeric values.

Value

A vector or a logical.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

Examples

```
## colwiseProd
M <- matrix(1:16, nrow=4)
v <- 1:4

t(v*t(M))
colwiseProd(v,M)

system.time(for (ii in 1:100000) t(v*t(M)))
system.time(for (ii in 1:100000) colwiseProd(v,M))
```

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

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)

# Datasets lizardRAW and lizardDF are generated with the following code
#lizardAGG <- as.data.frame(lizard)
#f <- lizardAGG$Freq
#idx <- unlist(mapply(function(i,n) rep(i,n),1:8,f))
#set.seed(0805)
#idx <- sample(idx)
#lizardRAW <- as.data.frame(lizardAGG[idx,1:3])
#rownames(lizardRAW) <- 1:NROW(lizardRAW)
```

mathmark

Mathematics marks for students

Description

The mathmark data frame has 88 rows and 5 columns.

Usage

```
mathmark
```

Format

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

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

References

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

Examples

```
data(mathmark)
```

mildew	<i>Mildew fungus</i>
--------	----------------------

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

```
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) ...
```

milkcomp	<i>Milk composition data</i>
----------	------------------------------

Description

Data from an experiment on composition of sow milk. Milk composition is measured on four occasions during lactation on a number of sows. The treatments are different types of fat added to the sows feed.

Usage

milkcomp

Format

A data frame with 214 observations on the following 7 variables.

sow a numeric vector

lactime a numeric vector

treat a factor with levels a b c d e f g

fat a numeric vector

protein a numeric vector

dm (dry matter) a numeric vector

lactose a numeric vector

Details

a is the control, i.e. no fat has been added.

fat + protein + lactose almost add up to dm (dry matter)

References

Charlotte Lauridsen and Viggo Danielsen (2004): Lactational dietary fat levels and sources influence milk composition and performance of sows and their progeny *Livestock Production Science* 91 (2004) 95-105

Examples

```
data(milkcomp)
## maybe str(milk) ; plot(milk) ...
```

Nutrimouse

The Nutrimouse Dataset

Description

The data come from a study of the effects of five dietary regimens with different fatty acid compositions on liver lipids and hepatic gene expression in 40 mice.

Usage

Nutrimouse

Format

A data frame with 40 observations on the following 143 variables.

genotype a factor with levels wt ppar

diet a factor with levels coc fish lin ref sun

X36b4 a numeric vector

ACAT1 a numeric vector

ACAT2 a numeric vector

ACBP a numeric vector

ACC1 a numeric vector

ACC2 a numeric vector

ACOTH a numeric vector

ADISP a numeric vector

ADSS1 a numeric vector

ALDH3 a numeric vector

AM2R a numeric vector

AOX a numeric vector

BACT a numeric vector

BIEN a numeric vector

BSEP a numeric vector

Bc1.3 a numeric vector

C16SR a numeric vector

CACP a numeric vector

CAR1 a numeric vector

CBS a numeric vector

CIDEA a numeric vector

COX1 a numeric vector

COX2 a numeric vector

CPT2 a numeric vector

CYP24 a numeric vector

CYP26 a numeric vector

CYP27a1 a numeric vector

CYP27b1 a numeric vector

CYP2b10 a numeric vector

CYP2b13 a numeric vector

CYP2c29 a numeric vector

CYP3A11 a numeric vector

CYP4A10 a numeric vector

CYP4A14 a numeric vector
CYP7a a numeric vector
CYP8b1 a numeric vector
FAS a numeric vector
FAT a numeric vector
FDFT a numeric vector
FXR a numeric vector
G6PDH a numeric vector
G6Pase a numeric vector
GK a numeric vector
GS a numeric vector
GSTa a numeric vector
GSTmu a numeric vector
GSTpi2 a numeric vector
HMGCoAred a numeric vector
HPNCL a numeric vector
IL.2 a numeric vector
L.FABP a numeric vector
LCE a numeric vector
LDLr a numeric vector
LPK a numeric vector
LPL a numeric vector
LXRa a numeric vector
LXRb a numeric vector
Lpin a numeric vector
Lpin1 a numeric vector
Lpin2 a numeric vector
Lpin3 a numeric vector
M.CPT1 a numeric vector
MCAD a numeric vector
MDR1 a numeric vector
MDR2 a numeric vector
MRP6 a numeric vector
MS a numeric vector
MTHFR a numeric vector
NGFiB a numeric vector
NURR1 a numeric vector

Ntcp a numeric vector
OCTN2 a numeric vector
PAL a numeric vector
PDK4 a numeric vector
PECI a numeric vector
PLTP a numeric vector
PMDCI a numeric vector
PON a numeric vector
PPARa a numeric vector
PPARd a numeric vector
PPARg a numeric vector
PXR a numeric vector
Pex11a a numeric vector
RARa a numeric vector
RARb2 a numeric vector
RXRa a numeric vector
RXRb2 a numeric vector
RXRg1 a numeric vector
S14 a numeric vector
SHP1 a numeric vector
SIAT4c a numeric vector
SPI1.1 a numeric vector
SR.BI a numeric vector
THB a numeric vector
THIOL a numeric vector
TRa a numeric vector
TRb a numeric vector
Tpalpha a numeric vector
Tpbeta a numeric vector
UCP2 a numeric vector
UCP3 a numeric vector
VDR a numeric vector
VLDLr a numeric vector
Waf1 a numeric vector
ap2 a numeric vector
apoA.I a numeric vector
apoB a numeric vector

apoC3 a numeric vector
apoE a numeric vector
c.fos a numeric vector
cHMGC0AS a numeric vector
cMOAT a numeric vector
eif2g a numeric vector
hABC1 a numeric vector
i.BABP a numeric vector
i.BAT a numeric vector
i.FABP a numeric vector
i.NOS a numeric vector
mABC1 a numeric vector
mHMGC0AS a numeric vector
C14.0 a numeric vector
C16.0 a numeric vector
C18.0 a numeric vector
C16.1n.9 a numeric vector
C16.1n.7 a numeric vector
C18.1n.9 a numeric vector
C18.1n.7 a numeric vector
C20.1n.9 a numeric vector
C20.3n.9 a numeric vector
C18.2n.6 a numeric vector
C18.3n.6 a numeric vector
C20.2n.6 a numeric vector
C20.3n.6 a numeric vector
C20.4n.6 a numeric vector
C22.4n.6 a numeric vector
C22.5n.6 a numeric vector
C18.3n.3 a numeric vector
C20.3n.3 a numeric vector
C20.5n.3 a numeric vector
C22.5n.3 a numeric vector
C22.6n.3 a numeric vector

Details

The data come from a study of the effects of five dietary regimens with different fatty acid compositions on liver lipids and hepatic gene expression in wild-type and PPAR-alpha-deficient mice (Martin et al., 2007).

There were 5 replicates per genotype and diet combination.

There are two design variables: (i) genotype, a factor with two levels: wild-type (wt) and PPAR-alpha-deficient (ppar), and (ii) diet, a factor with five levels. The oils used for experimental diet preparation were: corn and colza oils (50/50) for a reference diet (ref); hydrogenated coconut oil for a saturated fatty acid diet (coc); sunflower oil for an Omega6 fatty acid-rich diet (sun); linseed oil for an Omega3-rich diet (lin); and corn/colza/enriched (43/43/14) fish oils (fish).

There are 141 response variables: (i) the log-expression levels of 120 genes measured in liver cells, and (ii) the concentrations (in percentages) of 21 hepatic fatty acids measured by gas chromatography.

Source

The data were provided by Pascal Martin from the Toxicology and Pharmacology Laboratory, National Institute for Agronomic Research, French.

References

Martin, P. G. P., Guillou, H., Lasserre, F., Dejean, S., Lan, A., Pascussi, J.-M., San Cristobal, M., Legrand, P., Besse, P. and Pineau, T. (2007). Novel aspects of PPAR α -mediated regulation of lipid and xenobiotic metabolism revealed through a multigenomic study. *Hepatology* 54, 767-777.

Examples

```
data(Nutrimouse)
```

old-array-operations *Array operations (2007)*

Description

Array operations; created to facilitate the gRain package in 2007. Now largely replaceable by other faster functions implemented in Rcpp.

Usage

```
tablePerm(tab, perm, resize = TRUE, keep.class = FALSE)
```

```
tableMult(tab1, tab2)
```

```
tableDiv(tab1, tab2)
```

```

tableOp(tab1, tab2, op = "*")
tableOp2(tab1, tab2, op = `*\`, restore = FALSE)
tableSlice(tab, margin, level, impose)
tableSlicePrim(tab, mar.idx, lev.idx)
tableMargin(tab, margin, keep.class = FALSE)
tableGetSliceIndex(tab, margin, level, complement = FALSE)
tableSetSliceValue(tab, margin, level, complement = FALSE, value = 0)

```

Arguments

tab, tab1, tab2	Arrays with named dimnames.
perm	A permutation; either indices or names.
resize	A flag indicating whether the vector should be resized as well as having its elements reordered (default TRUE).
keep.class	Obsolete argument.
op	The operation; choices are "*", "/", "+", "-".
restore	Not so clear anymore.
margin	Index or name of margin.
level	Corresponding level of margin.
impose	Value to be imposed.
mar.idx	Index of margin
lev.idx	Index of level
complement	Should values be set for the complement?
value	Which value should be set

old-parray

Representation of and operations on multidimensional tables

Description

General representation of multidimensional tables (by parray objects).

Usage

```

parray(varNames, levels, values = 1, normalize = "none", smooth = 0)
as.parray(values, normalize = "none", smooth = 0)

```

Arguments

varNames	Names of variables defining table; can be a right hand sided formula.
levels	Either 1) a vector with number of levels of the factors in varNames or 2) a list with specification of the levels of the factors in varNames. See 'examples' below.
values	Values to go into the parray
normalize	Either "none", "first" or "all". Should result be normalized, see 'Details' below.
smooth	Should values be smoothed, see 'Details' below.

Details

A parray 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 all other variables than the first, the probabilities are normalized to sum to one. Thus $f(a,b,c)$ becomes a conditional probability table of the form $p(a|b,c)$. 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.parray` can be used for coercing an array or an `xtabs` to a parray object.

Value

An object of class `parray`.

Author(s)

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See Also

[tableOp](#), [tableMargin](#), [tableOp](#)

Examples

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

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

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

## Create 1-dimensional vector with dim and dimnames
x1 <- 1:5
```

```
as.parray(x1)
x2 <- parray("x", levels=length(x1), values=x1)
dim(x2)
dimnames(x2)

## Matrix
x1 <- matrix(1:6, nrow=2)
as.parray(x1)
parray(~a:b, levels=dim(x1), values=x1)

## Extract parrays from data
## 1) a dataframe
data(cad1)
data2parray(cad1, ~Sex:AngPec:AMI)
data2parray(cad1, c("Sex", "AngPec", "AMI"))
data2parray(cad1, c(1,2,3))
## 2) a table
data2parray(UCBAdmissions,c(1,2), normalize="first")
```

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

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

reinis

Format

A table with 6 discrete variables. A: smoking, B: strenous 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)
maximalSets(setlist, index = FALSE)
minimalSets(setlist, index = FALSE)
```

Arguments

x, set	Vectors representing sets
setlist	List of vectors (representing a set of subsets)
maximal	Logical; see section 'Details' for a description.
index	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@math.aau.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), 1)
#subsetofList(c(1,2,3,4), 1)

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

is.insetlist (c(2,4), 1)
is.insetlist (c(2,8), 1)
```

simulateArray

Simulate data from array.

Description

Simulate data (slice of) an array.

Usage

```
simulateArray(x, nsim = 1, margin, value.margin)
```

Arguments

`x` An array
`nsim` Number of cases to simulate
`margin, value.margin` Specification of slice of array to simulate from

Value

A matrix

Note

The current implementation is fragile in the sense that it is not checked that the input argument `x` is an array.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

Examples

```
## 2x2 array
x <- parray(c("a","b"), levels=c(2,2), values=1:4)

## Simulate from entire array
s <-simulateArray(x,1000)
xtabs(~., as.data.frame(s))

## Simulate from slice defined by that dimension 1 is fixed at level 2
s <-simulateArray(x,6000,1,2)
xtabs(~., as.data.frame(s))

## 2x2x2 array
x <- parray(c("a","b","c"), levels=c(2,2,2), values=1:8)

## Simulate from entire array
s <-simulateArray(x,36000)
xtabs(~., as.data.frame(s))

## Simulate from slice defined by that dimension 3 is fixed at level 1
s <-simulateArray(x,10000,3,1)
xtabs(~., as.data.frame(s))
```

wine

Chemical composition of wine

Description

Using chemical analysis determine the origin of wines

Usage

wine

Format

A data frame with 178 observations on the following 14 variables.

`Cult` a factor with levels `v1 v2 v3`: 3 different grape varieties

`Alch` Alcohol

`Mlca` Malic acid

`Ash` Ash

`Aloa` Alcalinity of ash

`Mgns` Magnesium

`Ttlp` Total phenols

`Flvn` Flavanoids

`Nnfp` Nonflavanoid phenols

`Prnt` Proanthocyanins

`Clri` Color intensity

`Hue` Hue

`Oodw` OD280/OD315 of diluted wines

`Prln` Proline

Details

Data comes from the UCI Machine Learning Repository. The grape variety `Cult` is the class identifier.

Source

Frank, A. & Asuncion, A. (2010). UCI Machine Learning Repository [<http://archive.ics.uci.edu/ml>]. Irvine, CA: University of California, School of Information and Computer Science.

References

See references at <http://archive.ics.uci.edu/ml/datasets/Wine>

Examples

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

Index

- *Topic **datasets**
 - ashtrees, [13](#)
 - BodyFat, [14](#)
 - breastcancer, [16](#)
 - cad, [17](#)
 - carcass, [18](#)
 - chestSim, [19](#)
 - dietox, [22](#)
 - dumping, [23](#)
 - lizard, [52](#)
 - mathmark, [53](#)
 - mildew, [54](#)
 - milkcomp, [54](#)
 - Nutrimouse, [55](#)
 - rats, [63](#)
 - reinis, [64](#)
 - wine, [66](#)
- *Topic **graphics**
 - graph-iplot, [30](#)
- *Topic **graphs**
 - gRbase, [50](#)
- *Topic **models**
 - graph-gcproperties, [28](#)
 - gRbase, [50](#)
- *Topic **multivariate**
 - gRbase, [50](#)
- *Topic **utilities**
 - array-create, [4](#)
 - array-distribution, [7](#)
 - array-operations, [9](#)
 - combnPrim, [20](#)
 - compareModels, [21](#)
 - cov2pcor, [22](#)
 - graph-cliques, [24](#)
 - graph-create, [26](#)
 - graph-gcproperties, [28](#)
 - graph-is, [31](#)
 - graph-mcs, [34](#)
 - graph-minimaltriang, [35](#)
 - graph-moralize, [37](#)
 - graph-mpd, [38](#)
 - graph-randomdag, [40](#)
 - graph-rip, [41](#)
 - graph-toposort, [43](#)
 - graph-triangulate, [44](#)
 - graph-xxx2yyy, [47](#)
 - gRbase-generics, [51](#)
 - gRbase-utilities, [52](#)
 - old-parray, [61](#)
 - Setoperations, [64](#)
 - simulateArray, [65](#)
 - %a*(array-algebra), [3](#)
 - %a+(array-algebra), [3](#)
 - %a-(array-algebra), [3](#)
 - %a/(array-algebra), [3](#)
 - adjList2adjMAT (graph-xxx2yyy), [47](#)
 - adjList2M (graph-xxx2yyy), [47](#)
 - ancestors (graph-query), [39](#)
 - ancestralGraph (graph-query), [39](#)
 - ancestralSet (graph-query), [39](#)
 - aperm, [10](#)
 - aperm__ (array-operations), [9](#)
 - aradd, [5](#), [13](#)
 - aradd (array-algebra), [3](#)
 - aralign (array-operations), [9](#)
 - ardist (array-distribution), [7](#)
 - ardiv, [13](#)
 - ardiv (array-algebra), [3](#)
 - ardiv0 (array-algebra), [3](#)
 - arEqual (array-operations), [9](#)
 - arequal (array-operations), [9](#)
 - arexpand (array-operations), [9](#)
 - arExt (array-operations), [9](#)
 - armarg, [7](#), [13](#)
 - armarg (array-operations), [9](#)
 - armult, [13](#)
 - armult (array-algebra), [3](#)
 - arnormalize (array-normalize), [8](#)

- arPerm (array-operations), 9
- arperm, 5, 13
- arperm (array-operations), 9
- arprod, 5, 13
- arprod (array-algebra), 3
- array-algebra, 3
- array-create, 4
- array-dimnames, 6
- array-distribution, 7
- array-normalize, 8
- array-operations, 9
- array-properties, 11
- array-slice, 12
- arSlice (array-operations), 9
- arslice, 7, 10
- arslice (array-slice), 12
- arslice_entries, 10
- arslice_entries (array-slice), 12
- arslice_mult (array-slice), 12
- arslice_prim (array-slice), 12
- arSliceMult (array-operations), 9
- arSlicePrim (array-operations), 9
- arsubt, 13
- arsubt (array-algebra), 3
- arsum, 13
- arsum (array-algebra), 3
- as.adjMAT (graph-xxx2yyy), 47
- as.parray (old-parray), 61
- ashtrees, 13

- BodyFat, 14
- breastcancer, 16

- cad, 17
- cad1 (cad), 17
- cad2 (cad), 17
- carcass, 18
- carcassall (carcass), 18
- chestSim, 19
- chestSim1000 (chestSim), 19
- chestSim10000 (chestSim), 19
- chestSim100000 (chestSim), 19
- chestSim500 (chestSim), 19
- chestSim50000 (chestSim), 19
- children (graph-query), 39
- closure (graph-query), 39
- coerceGraph (graph-coerce), 25
- colwiseProd (gRbase-utilities), 52
- combn, 20
- combnPrim, 20
- compareModels, 21
- compile (gRbase-generics), 51
- compile.grain, 51
- conc2pcor (cov2pcor), 22
- cov2pcor, 22

- dag, 25, 32, 35, 38, 42, 44–46, 49
- dag (graph-create), 26
- dagList (graph-create), 26
- dagList2dgCMatrix (graph-create), 26
- dagList2graphNEL (graph-xxx2yyy), 47
- dagList2M (graph-xxx2yyy), 47
- dagList2matrix (graph-create), 26
- dagList2tfM (graph-xxx2yyy), 47
- data2parray (old-parray), 61
- df2xtabs (array-create), 4
- dietox, 22
- dimnames_match (array-dimnames), 6
- dimnames_match_ (array-dimnames), 6
- dumping, 23

- edgeList (graph-edgeList), 27
- edgeListMAT (graph-edgeList), 27

- fit (gRbase-generics), 51

- get_subset_ (gRbase-utilities), 52
- get_superset_ (gRbase-utilities), 52
- getCliques (graph-cliques), 24
- glist2adjMAT (graph-xxx2yyy), 47
- graph-cliques, 24
- graph-coerce, 25
- graph-create, 26
- graph-edgeList, 27
- graph-gcproperties, 28
- graph-iplot, 30
- graph-is, 31
- graph-mcs, 33
- graph-minimaltriang, 35
- graph-moralize, 37
- graph-mpd, 38
- graph-query, 39
- graph-randomdag, 40
- graph-rip, 41
- graph-toposort, 43
- graph-triangulate, 44
- graph-vpar, 46
- graph-xxx2yyy, 47

- graphNEL2adjMAT (graph-xxx2yyy), 47
- graphNEL2dgCMatrix (graph-xxx2yyy), 47
- graphNEL2ftM (graph-xxx2yyy), 47
- graphNEL2igraph (graph-xxx2yyy), 47
- graphNEL2M (graph-xxx2yyy), 47
- graphNEL2MAT (graph-xxx2yyy), 47
- graphNEL2matrix (graph-xxx2yyy), 47
- graphNEL2tfM (graph-xxx2yyy), 47
- gRbase, 50
- gRbase-generics, 51
- gRbase-utilities, 52

- iplot (graph-ipplot), 30
- is.adjMAT (graph-is), 31
- is.complete (graph-query), 39
- is.DAG (graph-is), 31
- is.DAGMAT (graph-is), 31
- is.decomposition (graph-query), 39
- is.DG (graph-is), 31
- is.DGMAT (graph-is), 31
- is.insetlist (Setoperations), 64
- is.named.array, 6
- is.named.array (array-properties), 11
- is.simplicial (graph-query), 39
- is.subsetof (Setoperations), 64
- is.TUG (graph-is), 31
- is.TUGMAT (graph-is), 31
- is.UG (graph-is), 31
- is.UGMAT (graph-is), 31
- is_dimnames_ (array-properties), 11
- is_named_array_ (array-properties), 11
- is_number_vector_ (array-properties), 11
- is_subsetof_ (gRbase-utilities), 52
- isDecomposable (graph-gcproperties), 28
- isGraphical (graph-gcproperties), 28
- isin (Setoperations), 64

- jTree, 35, 38
- jTree (graph-rip), 41
- jTreeMAT (graph-rip), 41
- junctionTree (graph-rip), 41
- junctionTreeMAT (graph-rip), 41

- lizard, 52
- lizardAGG (lizard), 52
- lizardRAW (lizard), 52

- M2adjList (graph-xxx2yyy), 47
- M2dagList (graph-xxx2yyy), 47

- M2graphNEL (graph-xxx2yyy), 47
- M2igraph (graph-xxx2yyy), 47
- M2ugList (graph-xxx2yyy), 47
- MAT2dgCMatrix (graph-xxx2yyy), 47
- MAT2matrix (graph-xxx2yyy), 47
- math (mathmark), 53
- mathmark, 53
- maxCliqueMAT (graph-cliques), 24
- maximalSets (Setoperations), 64
- mcs, 25, 29, 38, 39, 42, 45
- mcs (graph-mcs), 34
- mcsmarked (graph-mcs), 34
- mcsmarkedMAT (graph-mcs), 34
- mcsMAT, 25, 39, 45
- mcsMAT (graph-mcs), 34
- mildew, 54
- milkcomp, 54
- milkcomp1 (milkcomp), 54
- minimalSets (Setoperations), 64
- minimalTriang, 39
- minimalTriang (graph-minimaltriang), 35
- minimalTriangMAT, 39
- minimalTriangMAT (graph-minimaltriang), 35
- moralize, 25, 35, 42, 45
- moralize (graph-moralize), 37
- moralizeMAT, 25, 45
- moralizeMAT (graph-moralize), 37
- mpd, 36
- mpd (graph-mpd), 38
- mpdMAT (graph-mpd), 38

- newar, 7
- newar (array-create), 4
- nonEdgeList (graph-edgeList), 27
- nonEdgeListMAT (graph-edgeList), 27
- Nutrimouse, 55

- old-array-operations, 60
- old-parray, 61

- parents (graph-query), 39
- parray (old-parray), 61
- propagate (gRbase-generics), 51
- propagate.grain, 51

- querygraph (graph-query), 39

- random_dag (graph-randomdag), 40

- rats, 63
- reinis, 64
- removeRedundant (Setoperations), 64
- rip, 25, 29, 35, 36, 38, 39, 45
- rip (graph-rip), 41
- ripMAT, 25, 39, 45
- ripMAT (graph-rip), 41

- Setoperations, 64
- simplicialNodes (graph-query), 39
- simulateArray, 65
- stepwise (gRbase-generics), 51
- subsetof (Setoperations), 64

- tab (array-create), 4
- tabAdd (array-algebra), 3
- tabAdd__ (array-operations), 9
- tabAlign (array-operations), 9
- tabAlign__ (array-operations), 9
- tabCondProb (array-operations), 9
- tabDist (array-distribution), 7
- tabDiv (array-algebra), 3
- tabDiv0 (array-algebra), 3
- tabDiv0__ (array-operations), 9
- tabDiv__ (array-operations), 9
- tabEqual (array-operations), 9
- tabEqual__ (array-operations), 9
- tabExpand (array-operations), 9
- tabExpand__ (array-operations), 9
- tabExt (array-operations), 9
- tableDiv (old-array-operations), 60
- tableGetSliceIndex
 (old-array-operations), 60
- tableMargin, 62
- tableMargin (old-array-operations), 60
- tableMult (old-array-operations), 60
- tableOp, 62
- tableOp (old-array-operations), 60
- tableOp2 (old-array-operations), 60
- tablePerm (old-array-operations), 60
- tableSetSliceValue
 (old-array-operations), 60
- tableSlice (old-array-operations), 60
- tableSlicePrim (old-array-operations),
 60
- tabListAdd (array-operations), 9
- tabListAdd__ (array-operations), 9
- tabListMult (array-operations), 9
- tabListMult__ (array-operations), 9

- tabMarg (array-operations), 9
- tabMarg__ (array-operations), 9
- tabMult (array-algebra), 3
- tabMult__ (array-operations), 9
- tabOp__ (array-operations), 9
- tabPerm (array-operations), 9
- tabPerm__ (array-operations), 9
- tabSlice (array-operations), 9
- tabSlice2 (array-operations), 9
- tabSlice2Entries (array-operations), 9
- tabSlice2Entries_ (array-operations), 9
- tabSliceMult (array-operations), 9
- tabSlicePrim (array-operations), 9
- tabSubt (array-algebra), 3
- tabSubt__ (array-operations), 9
- topoSort (graph-toposort), 43
- topoSort_vparList (graph-toposort), 43
- topoSortMAT (graph-toposort), 43
- triangulate, 36, 39, 42
- triangulate (graph-triangulate), 44
- triangulateMAT, 39
- triangulateMAT (graph-triangulate), 44

- ug, 25, 32, 35, 38, 42, 44–46, 49
- ug (graph-create), 26
- ug2dag (graph-xxx2yyy), 47
- ugList (graph-create), 26
- ugList2dgCMatrix (graph-create), 26
- ugList2graphNEL (graph-xxx2yyy), 47
- ugList2M (graph-xxx2yyy), 47
- ugList2matrix (graph-create), 26

- vpaL2tfM (graph-xxx2yyy), 47
- vpaList2adjMAT (graph-xxx2yyy), 47
- vpar (graph-vpar), 46
- vparMAT (graph-vpar), 46

- wine, 66