Package: gRbase (via r-universe)

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Title A Package for Graphical Modelling in R

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Description The 'gRbase' package provides graphical modelling features used by e.g. the packages 'gRain', 'gRim' and 'gRc'. 'gRbase' implements graph algorithms including (i) maximum cardinality search (for marked and unmarked graphs). (ii) moralization, (iii) triangulation, (iv) creation of 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. The facilities of the package are documented in the book by Højsgaard, Edwards and Lauritzen (2012, <doi:10.1007/978-1-4614-2299-0>) and in the paper by Dethlefsen and Højsgaard, (2005, <doi:10.18637/jss.v014.i17>). Please see 'citation(` `gRbase")' for citation details.

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`all_pairs` *Create all possible pairs*

Description

Create all possible pairs of two character vectors.

Usage

```
all_pairs(x, y = character(0), sort = FALSE, result = "matrix")

names2pairs(x, y = NULL, sort = TRUE, result = "list")
```

Arguments

`x, y`	Character vectors.
`sort`	Logical.
`result`	A list or a matrix.

Details

NOTICE: If y is not NULL then x and y must be disjoint (no checks are made); otherwise pairs of identical elements wil also be obtained.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

Examples

```
x <- letters[1:4]
y <- letters[5:7]

all_pairs(x)
all_pairs(x, result="matrix")

all_pairs(x, y)
all_pairs(x, y, result="matrix")
```

---

all_subsets *Create all subsets*

Description

Create all subsets of a vector

Usage

```
all_subsets(x)

all_subsets0(x)
```

Arguments

x	Vector

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

api-array-07 *Array operations (2007)*

Description

Array operations; created to facilitate the gRain package in 2007. Now largely replaceable by other (often 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)

tableOp0(tab1, tab2, op = `*`)

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

Details

tableOp0 is brute force implementation based on dataframes. It is very slow, but useful for error checking.

---

api-array-properties *Check if object is array*

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)

dimnames_match(a1, a2)
```

Arguments

obj	Some R object.
a1, a2	Arrays with named dimnames.

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))
```

```
ar1 = tabNew(c("a", "b"), levels=c(2, 3))
ar2 = tabNew(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 = tabNew(c("a", "b"), levels=c(2, 3))
ar2 = tabNew(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 = tabNew(c("c", "a"), levels=list(c=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)
```

---

api-cell *Table cell operations.*

Description

Low level table cell operations.

Usage

```
cell2entry(cell, dim)

entry2cell(entry, dim)

next_cell(cell, dim)

next_cell2(cell, dim)

next_cell_slice(cell, dim, slice_marg)

slice2entry(slice_cell, slice_marg, dim)

cell2entry_perm(cell, dim, perm)

perm_cell_entries(perm, dim)

fact_grid(dim, slice_cell = NULL, slice_marg = NULL)
```

Arguments

cell	Vector giving the cell, e.g. c(1, 1, 2) in 3-way table.
dim	Vector giving array dimension, eg c(2, 2, 2).
entry	An entry in an array (a number indexing a vector).
slice_marg	Vector giving the margin of a table, eg. c(2, 3)
slice_cell	Vector giving the corresponding cell of marginal table, e.g. c(1, 2)
perm	Vector giving permutaion of array, eg. c(1, 3, 2).

Examples

```
di <- c(2, 2, 3)

cell2entry(c(1, 1, 1), dim=di)
cell2entry(c(2, 2, 3), dim=di)

entry2cell(1, dim=di)
entry2cell(12, dim=di)

next_cell(c(1, 1, 1), dim=di)
next_cell(c(2, 1, 1), dim=di)

## The first two entries are kept fixed
next_cell_slice(c(2, 1, 1), dim=di, slice_marg=c(1, 2))
next_cell_slice(c(2, 1, 2), dim=di, slice_marg=c(1, 2))

## Cell (2, 2, 1) corresponds to entry 4
cell2entry(c(2, 2, 1), dim=di)
## Same as
cell2entry_perm(c(2, 2, 1), dim=di, perm=c(1, 2, 3))
## If the table dimensions are permuted as (3, 1, 2)
## the entry becomes
cell2entry_perm(c(2, 2, 1), dim=di, perm=c(3, 1, 2))
```

---

api-cell_ *Low level table cell operations implemented in c++*

Description

Corresponding R functions without the trailing underscore exist.

Usage

```
cell2entry_(cell, dim)

make_plevels_(dim)

entry2cell_(entry, dim)
```

```
next_cell_(cell, dim)

next_cell2_(cell, dim)

next_cell_slice_(cell, dim, slice_marg)

slice2entry_(slice_cell, slice_marg, dim)

cell2entry_perm_(cell, dim, perm)

perm_cell_entries_(perm, dim)
```

Arguments

cell	Vector giving the cell, e.g. c(1, 1, 2) in 3-way table.
dim	Vector giving array dimension, eg c(2, 2, 2).
entry	An entry in an array (a number indexing a vector).
slice_marg	Vector giving the margin of a table, eg. c(2, 3)
slice_cell	Vector giving the corresponding cell of marginal table, e.g. c(1, 2)
perm	Vector giving permutaion of array, eg. c(1, 3, 2).

---

api-parray *Representation of and operations on multidimensional arrays*

Description

General representation of multidimensional arrays (with named dimnames, also called named arrays.)

Usage

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

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

data2parray(data, varNames = NULL, normalize = "none", smooth = 0)

makeDimNames(varNames, levels, sep = "")
```

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 array
normalize	Either "none", "first" or "all". Should result be normalized, see 'Details' below.
smooth	Should values be smoothed, see 'Details' below.
data	Data to be coerced to a parray; can be data.frame, table, xtabs, matrix.
sep	Desired separator in dim names; defaults to "".

Details

A named array 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.

Value

A a named array.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

See Also

is.named.array

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")
```

---

api-pct-operations *Array algebra*

Description

Addition, subtraction etc. of arrays

Usage

```
a1 %a+% a2

a1 %a-% a2

a1 %a*% a2

a1 %a/% a2

a1 %a/0% a2

tab1 %a_% marg

tab1 %a==% tab2

tab1 %a^% extra

tab1 %aperm% perm

tab1 %aalign% tab2

tab1 %aslice% slice

tab1 %aslice*% slice

tab1 %amarg% marg
```

Arguments

tab1, tab2	Multidimensional arrays with named dimnames (we call them 'named arrays').
marg	A vector of indices or dimnames or a right hand sided formula giving the desired marginal.
extra	List defining the extra dimensions.
perm	A vector of indices or dimnames or a right hand sided formula giving the desired permutiation.
slice	A list of the form name=value.
a, a1, a2	Arrays (with named dimnames)

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

Examples

```
hec <- HairEyeColor
a1 <- tabMarg(hec, c("Hair", "Eye"))
a2 <- tabMarg(hec, c("Hair", "Sex"))
a3 <- tabMarg(hec, c("Eye", "Sex"))

## Binary operations
a1 %a+% a2
a1 %a-% a2
a1 %a*% a2
a1 %a/% a2
```

---

api-tabDist *Marginalize and condition in multidimensional array.*

Description

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

Usage

```
tabDist(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 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.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

Examples

```
hec <- HairEyeColor

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

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

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

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

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

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

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

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

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

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

`api-tabNew` *Create multidimensional arrays*

Description

Alternative ways of creating arrays

Usage

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

Arguments

`names`	Names of variables defining table; either 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 array.
`normalize`	Either "none", "first" or "all". Should result be normalized, see 'Details' below.
`smooth`	Should values be smoothed, see 'Details' below.

Details

1. 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).
2. If `normalize="all"` then the sum over all entries of f(a,b,c) is one.
3. 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>

Examples

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

---

api-tabX *Interface - operations on multidimensional arrays.*

Description

Interface functions and minor extensions to cpp functions.

Usage

```
tabAdd(tab1, tab2)

tabAlign(tab1, tab2)

tabDiv(tab1, tab2)

tabDiv0(tab1, tab2)

tabOp(tab1, tab2, op = "*")

tabEqual(tab1, tab2, eps = 1e-12)

tabExpand(tab, aux, type = 0L)

tabMult(tab1, tab2)

tabSubt(tab1, tab2)

tabListMult(lst)

tabListAdd(lst)

tabPerm(tab, perm)

tabMarg(tab, marg = NULL)

tabSum(tab, ...)
```

```
tabProd(tab, ...)

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

Arguments

op	The algebraic operation to be carried out.
eps	Criterion for checking equality of two arrays.
tab, tab1, tab2, ...	Arrays with named dimnames (we call them 'named arrays').
aux	Either a list with names and dimnames or a named array from which such a list can be extracted.
type	If 0 then entries are duplicated. If 3 then averages are computed. If 2 then 0 slices are inserted.
lst	List of arrays.
perm, marg	A vector of indices or dimnames or a right hand sided formula giving the desired permutation/margin.

---

api-tabX_ *Table operations implemented in c++*

Description

Table operations implemented in c++. Corresponding R functions without the trailing underscore exist.

Usage

```
tab_perm_(tab, perm)

tab_expand_(tab, aux, type = 0L)

tab_align_(tab1, tab2)

tab_marg_(tab, marg)

tab_op_(tab1, tab2, op = "*")

tab_add_(tab1, tab2)

tab_subt_(tab1, tab2)

tab_mult_(tab1, tab2)
```

```
tab_div_(tab1, tab2)

tab_div0_(tab1, tab2)

tab_equal_(tab1, tab2, eps = 1e-12)

tab_list_mult_(lst)

tab_list_add_(lst)
```

Arguments

tab, tab1, tab2	Tables (arrays)
perm, marg	A vector of indices or dimnames or a right hand sided formula giving the desired permutation/margin.
aux	Either a list with names and dimnames or a named array from which such a list can be extracted.
type	If 0 then entries are duplicated. If 3 then averages are computed. If 2 then 0 slices are inserted.
op	The operation to be carried out; "+", "-", "*", "/".
eps	Criterion for checking equality of two arrays.
lst	List of arrays.

---

api_tabSlice *Array slices*

Description

Functions for extracting slices of arrays

Usage

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

tabSlice2(tab, slice, margin.idx, drop = TRUE, as.array = FALSE)

tabSlicePrim(tab, slice, drop = TRUE)

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

tabSlice2Entries(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.
margin.idx	Indec of variables in slice.
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>

Examples

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

s1 = tabSlice(x, slice=s); s1

tabSlice2Entries(x, slice=s)
tabSlice2Entries(x, slice=s, complement=TRUE)

## tabSliceMult
s2 = tabSliceMult(x, slice=s); s2

sp = list(c(1,2), c(1,2), TRUE)
tabSlicePrim(x, slice=sp)
tabSlice(x, slice=s)
```

---

array-simulate *Simulate data from array.*

Description

Simulate data (slice of) an array: Simulate n observations from the array x conditional on the variables in margin (a vector of indices) takes values given by margin.value

Usage

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

## S3 method for class 'table'
simulate(object, nsim = 1, seed = NULL, margin, value.margin, ...)

## S3 method for class 'xtabs'
simulate(object, nsim = 1, seed = NULL, margin, value.margin, ...)

## S3 method for class 'array'
simulate(object, nsim = 1, seed = NULL, margin, value.margin, ...)
```

Arguments

x, object	An array.
nsim	Number of cases to simulate.
margin, value.margin	Specification of slice of array to simulate from.
seed	Seed to be used for random number generation.
...	Additional arguments, currently not used.

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)

x <- tabNew(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, 1000, margin=1, value.margin=2)
xtabs(~., as.data.frame(s))
```

```
## 2 x 2 x 2 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))
```

`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

`object`, `object2`	Model objects
`...`	Additional arguments

Value

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

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

`cov2pcor` *Partial correlation (matrix)*

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)
```

---

data-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

```
data(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)
head(ashtrees)
```

`data-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)

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 https://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)
```

---

data-breastcancer *Gene expression signatures for p53 mutation status in 250 breast cancer samples*

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 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) ...
```

`data-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

```
data(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

`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

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)
```

---

data-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 (see reference below).

Usage

```
data(chestSim500)
```

Format

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

`asia` Recent visit to Asia?; a factor with levels `yes no`

`tub` Has tuberculosis?; a factor with levels `yes no`

`smoke` Is a smoker?; a factor with levels `yes no`

`lung` Has lung cancer?; a factor with levels `yes no`

`bronc` Has bronchitis?; a factor with levels `yes no`

`either` Either lung cancer or tuberculosis?; a factor with levels `yes no`

`xray` Positive x-ray? a factor with levels `yes no`

`dysp` Dyspnoea (shortness of breath)?; a factor with levels `yes no`

Details

Notice that the chest clinic example is a contrieved example; it does not originate from an empirical study.

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) ...
```

---

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

Examples

```
data(dietox)
```

data-dumping *Gastric Dumping*

Description

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

Usage

```
data(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\ (removal of 50\ 75\

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)
```

data-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). Perch means preferred place to settle down (a branch on a tree). 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)

# 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)
```

---

data-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@math.aau.dk>

References

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

Examples

```
data(mathmark)
```

`data-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

A 6 dimensional array where each variable has levels "1" and "2". The variables are: `la10`, `locc`, `mp58`, `c365`, `p53a` and `a365`.

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) ...
```

data-milkcomp *Milk composition data*

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

```
data(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) ...
```

data-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

```
data(Nutrimouse)
```

Format

A data frame with 40 observations on 143 variables of which two are factors and 141 are numeric.

`genotype` a factor with levels `wt` `ppar`

`diet` a factor with levels `coc` `fish` `lin` `ref` `sun`

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, France.

References

Martin, P. G. P., Guillou, H., Lasserre, F., D'jean, S., Lan, A., Pascussi, J.-M., San Cristobal, M., Legrand, P., Besse, P. and Pineau, T. (2007). Novel aspects of PPARa-mediated regulation of lipid and xenobiotic metabolism revealed through a multrigenomic study. Hepatology 54, 767-777.

Examples

```
data(Nutrimouse)
```

`data-personality` *Personality traits*

Description

The `peronality` dataframe has 240 rows and 32 columns

Usage

```
data(personality)
```

Format

This dataframe has recordings on the following 32 variables: distant, talkatv, carelss, hardwrk, anxious, agreebl, tense, kind, opposng, relaxed, disorgn, outgoin, approvn, shy, discipl, harsh, persevr, friendl, worryin, respnsi, contrar, sociabl, lazy, coopera, quiet, organiz, criticl, lax, laidbck, withdrw, givinup, easygon

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

References

Origin unclear

Examples

```
data(personality)
str(personality)
```

data-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 loosing 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.

data-reinis *Risk factors for coronary heart disease.*

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: 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.

`data-wine` *Chemical composition of wine*

Description

Using chemical analysis determine the origin of wines

Usage

```
data(wine)
```

Format

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

`Cult` a factor with levels `v1` `v2` `v3`: 3 different graph 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 https://archive.ics.uci.edu/ml/. Irvine, CA: University of California, School of Information and Computer Science.

References

See references at https://archive.ics.uci.edu/ml/datasets/Wine/

Examples

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

`data_cad` *Coronary artery disease data*

Description

A cross classified table with observational data from a Danish heart clinic. The response variable is CAD (coronary artery disease, some times called heart attack).

Usage

```
data(cad1)
```

Format

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

`Sex` Sex; a factor with levels `Female` `Male`

`AngPec` Angina pectoris (chest pain attacks); a factor with levels `Atypical` `None` `Typical`

`AMI` Acute myocardic infarct; a factor with levels `Definite` `NotCertain`

`QWave` A reading from an electrocardiogram; a factor with levels `No` `Yes`; Yes means pathological and is a sign of previous myocardial infarction.

`QWavecode` a factor with levels `Nonusable` `Usable`. An assesment of whether QWave is reliable.

`STcode` a factor with levels `Nonusable` `Usable`. An assesment of whether STchange is reliable.

`STchange` A reading from an electrocardiogram; a factor with levels `No` `Yes`. An STchange indicates a blockage of the coronary artery.

`SuffHeartF` Sufficient heart frequency; a factor with levels `No`, `Yes`

`Hypertrophi` a factor with levels `No`, `Yes`. Hypertrophy refers to an increased size of the heart muscle due to exercise.

`Hyperchol` a factor with levels `No` `Yes`. Hypercholesterolemia, also called high cholesterol, is the presence of high levels of cholesterol in the blood.

`Smoker` Is the patient a smoker; a factor with levels `No`, `Yes`.

`Inherit` Hereditary predispositions for CAD; a factor with levels `No`, `Yes`.

`Heartfail` Previous heart failures; a factor with levels `No` `Yes`

`CAD` Coronary Artery Disease; a factor with levels `No` `Yes`. CAD refers to a reduction of blood flow to the heart muscle (commonly known as a heart attack). The diagnosis made from biopsies.

Details

Notice that data are collected at a heart clinic, so data do not represent the population, but are conditional on patients having ended up at the clinic.

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

References

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

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

Examples

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

---

data_handling *Utilities for data handling*

Description

Utilities for data handling

Usage

```
valueLabels(x)

## Default S3 method:
valueLabels(x)

varNames(x)

## Default S3 method:
varNames(x)

nLevels(x)

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

Arguments

x	Data, typically a dataframe.

`downstream-aliases` *Downstream aliases*

Description

Downstream aliases for other graphical modelling packages. Will be deprecated in due course.

`edge_matrix` *Coerce dag to edge matrix*

Description

A DAG can be represented as a triangular matrix of regression coefficients.

Usage

```
dag2edge_matrix(object, out = 1)

edge_matrix2dag(edge_matrix)
```

Arguments

object	A graph, either an igraph object or an adjacency matrix.
out	Format of the output, can be 1, 2, 3 or 4.
edge_matrix	Lower triangular matrix representing a dag

Examples

```
g <- dag(~x2|x1 + x3|x1:x2 + x4|x3)
dag2edge_matrix(g, out=1)
dag2edge_matrix(g, out=2)
dag2edge_matrix(g, out=3)
dag2edge_matrix(g, out=4)
d2 <- dag(~c|a:b+d:c)
dag2edge_matrix(d2)
```

`fastcombn` *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

```
fastcombn(x, m, FUN = NULL, simplify = TRUE, ...)

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

Arguments

`x`	vector source for combinations, or integer n for x <- seq(n).
`m`	number of elements to choose.
`FUN`	function to be applied to each combination; default 'NULL' means the identity, i.e., to return the combination (vector of length 'm').
`simplify`	logical indicating if the result should be simplified to a matrix; if FALSE, the function returns a list.
`...`	Further arguments passed on to `FUN`.

Details

- Factors `x` are accepted.
- `combn_prim` is a simplified (but faster) version of the `combn` function. Does nok take the `FUN` argument.
- `fastcombn` is intended to be a faster version of the `combn` function.

Value

A matrix or a list.

Author(s)

Søren Højsgaard

See Also

`combn`

Examples

```
x <- letters[1:5]; m <- 3

fastcombn(x, m)
combn(x, m)
combn_prim(x, m)

x <- letters[1:4]; m <- 3
fastcombn(x, m, simplify=FALSE)
combn(x, m, simplify=FALSE)
combn_prim(x, m, simplify=FALSE)

x <- 1:10; m <- 3
fastcombn(x, m, min)
combn(x, m, min)

x <- factor(letters[1:8]); m <- 5

if (require(microbenchmark)){
  microbenchmark(
    combn(x, m, simplify=FALSE),
    combn_prim(x, m, simplify=FALSE),
    fastcombn(x, m, simplify=FALSE),
    times=50
  )
}
```

---

gmwr_book *Functions from Graphical Modelling with R book*

Description

Functions that must be retained to make code from gmwr-book work

Usage

```
as.adjMAT(object)
```

Arguments

object	An object to be coerced.

graph-clique *Get cliques of an undirected graph*

Description

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

Usage

```
get_cliques(object)

max_cliqueMAT(amat)

getCliques(object)

maxCliqueMAT(amat)

maxClique(object)
```

Arguments

object	An undirected graph represented either as an igraph 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 triangualted graph is linear in the number of cliques.

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

Value

A list.

Synonymous functions

For backward compatibility with downstream packages we have the following synonymous functions:

- getCliques = get_cliques
- maxCliqueMAT = max_cliqueMAT

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

See Also

ug, dag, mcs, mcsMAT, rip, ripMAT, moralize, moralizeMAT

Examples

```
uG0 <- ug(~a:b + b:c + c:d + d:e + e:f + f:a)
get_cliques(uG0)

uG1 <- as(uG0, "igraph")
get_cliques(uG1)

uG2 <- as(uG0, "matrix")
get_cliques(uG2)

uG3 <- as(uG1, "dgCMatrix")
get_cliques(uG3)
```

---

graph-coerce *Graph coercion*

Description

Methods for changing graph representations

Usage

```
coerceGraph(object, class)

graph_as(object, outtype, intype = NULL)
```

Arguments

object	A graph object
class	The desired output class
outtype	The desired output outtype
intype	The desired output outtype (only relevant if object is a list)

Details

coerceGraph is used in the book "Graphical models with R". A more generic approach is as().

Examples

```
g1 <- ug(~a:b+b:c)
as(g1, "igraph")
as(g1, "matrix")
as(g1, "Matrix")
as(g1, "dgCMatrix")

## graph_as(g1, "ugList") ## Fails
## getCliques(g1)         ## Works

l1 <- list(c("a" ,"b"), c("b", "c"))
```

---

graph-coerce-api *API for coercing graph representations*

Description

API for coercing graph representations.

Usage

```
g_dm2sm_(object)

g_dm2ig_(object)

g_sm2dm_(object)

g_sm2ig_(object)

g_ig2dm_(object)

g_ig2sm_(object)

g_xm2ig_(object)

g_xm2dm_(object)

g_xm2sm_(object)

g_xm2xm_(object, result = "matrix")
```

Arguments

object	An object representing a graph
result	Either 'matrix' (dense) or 'dgCMatrix' (sparse, can be abbreviated to 'Matrix').

Details

No checking is made. In the function the following names are used:

- "ig": "igraph";
- "sm": "dgCMatrix" (sparse matrix);
- "dm": "matrix" (dense matrix)

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

See Also

ug, dag

---

graph-create *Create undirected and directed graphs*

Description

These functions are wrappers for creation of graphs as primarily igraph objects but also as adjacency matrices

Usage

```
ug(..., result = "igraph")

ugi(...)

ugList(x, result = "igraph")

dag(..., result = "igraph", forceCheck = FALSE)

dagi(..., forceCheck = FALSE)

dagList(x, result = "igraph", forceCheck = FALSE)
```

Arguments

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

Value

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

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"))

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

## 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
topo_sort( daG2 )
topo_sort( daG4 )

## Different representations
uG7 <- ug(~a:b:c + c:d, result="igraph")    # igraph
uG8 <- ug(~a:b:c + c:d, result="matrix")    # dense matrix
uG9 <- ug(~a:b:c + c:d, result="dgCMatrix") # sparse matrix
```

---

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 an igraph object or an adjacency matrix.

Usage

```
edgeList(object, matrix = FALSE)

edgeListMAT(adjmat, matrix = FALSE)

nonEdgeList(object, matrix = FALSE)

nonEdgeListMAT(adjmat, matrix = FALSE)
```

Arguments

object	An igraph object, a dense matrix or a sparse dgCMatrix (the two latter representing 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 <- as(g, "matrix")
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 <- as(g, "matrix")
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 dependence graph is in 1-1-correspondance with the genrators (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)

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

On the other hand, \code{g2 <- ~a:b:c + c:d} induces the same
graph in this case there is a 1-1-correspondance.

The graph induced by \code{g3 <- ~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-mcs *Maximum cardinality search on undirected graph.*

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)

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

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

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

Arguments

object	An undirected graph represented either as 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.
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
\code{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 \code{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, junction_tree, rip, ug, dag

Examples

```
uG <- ug(~ me:ve + me:al + ve:al + al:an + al:st + an:st)
mcs(uG)
mcsMAT(as(uG, "matrix"))
## 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:
mcs_marked(uG1, discrete=c("a","d"))
## Strongly decomposable:
mcs_marked(uG2, discrete=c("a","d"))
```

graph-min-triangulate *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

```
minimal_triang(
  object,
  tobject = triangulate(object),
  result = NULL,
  details = 0
)

minimal_triangMAT(amat, tamat = triangulateMAT(amat), details = 0)
```

Arguments

object	An undirected graph represented either as a igraph 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 "igraph", "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 superflous 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

`minimal_triang()` returns an igraph object while `minimal_triangMAT()` 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

```
## An igraph object
g1 <- ug(~a:b + b:c + c:d + d:e + e:f + a:f + b:e, result="igraph")
x <- minimal_triang(g1)

tt <- ug(~a:b:e:f + b:e:c:d, result="igraph")
x <- minimal_triang(g1, tobject=tt)

## g2 is a triangulation of g1 but it is not minimal
g2 <- ug(~a:b:e:f + b:c:d:e, result="igraph")
x <- minimal_triang(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 <- minimal_triangMAT(g1m)
```

---

graph-moralize *Moralize a directed acyclic graph*

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

Value

A moralized graph represented either as an igraph, 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, junction_tree, 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 = minimal_triang(object), details = 0)

## Default S3 method:
mpd(object, tobject = triangulate(object), details = 0)

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

Arguments

object	An undirected graph; an igraph or an adjacency matrix.
tobject	Any minimal triangulation of object; an igraph or an adjacency matrix.
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, minimal_triang, minimal_triangMAT, rip, ripMAT, triangulate, triangulateMAT

Examples

```
## Maximal prime subgraph decomposition
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")
x <- mpdMAT(g1m)
```

graph-randomdag *Random directed acyclic graph*

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

An igraph 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 *Create RIP ordering of the cliques of an undirected graph; create junction tree.*

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, ...)

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

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

junction_tree(object, ...)

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

junction_treeMAT(amat, nLevels = rep(2, ncol(amat)), ...)

jTree(object, ...)
```

Arguments

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

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 transfered to mcs as a way of controlling which clique will be the first in the RIP ordering. The junction_tree() (and junction_tree()) (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.)

Synonymous functions

For backward compatibility with downstream packages we have the following synonymous functions:

- jTree = junction_tree (Used in rags2ridges)
- junctionTree = junction_tree

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

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

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

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

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

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, ...)

triang_mcwh(object, ...)

triang_elo(object, ...)

triang(object, ...)

## Default S3 method:
triang(object, control = list(), ...)

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

## Default S3 method:
triang_elo(object, order = NULL, result = NULL, check = TRUE, ...)

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

triang_mcwhMAT_(amat, nLevels = rep(2, ncol(amat)), ...)

triang_eloMAT_(amat, order)

triang_eloMAT(amat, order = NULL)
```

Arguments

object	An undirected graph represented either as 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 "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 if FALSE
control	A list controlling the triangulation; see 'examples'.
order	Elimation order; a character vector or numeric vector.
amat	Adjacency matrix; a (dense) matrix, or a (sparse) dgCMatrix.

Details

There are two type of functions: triang and triangulate

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 (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

```
uG1 <- ug(~a:b + b:c + c:d + d:e + e:f + f:a)
uG2 <- ug(~a:b + b:c + c:d + d:e + e:f + f:a, result="matrix")
uG3 <- ug(~a:b + b:c + c:d + d:e + e:f + f:a, result="dgCMatrix")

## Default triangulation: minimum clique weight heuristic
# (default is that each node is given the same weight):
```

```
tuG1 <- triang(uG1)
## Same as
triang_mcwh(uG1)

## Alternative: Triangulation from a desired elimination order
# (default is that the order is order of the nodes in the graph):

triang(uG1, control=list(method="elo"))
## Same as:
triang_elo(uG1)

## More control: Define the number of levels for each node:
tuG1 <- triang(uG1, control=list(method="mcwh", nLevels=c(2, 3, 2, 6, 4, 9)))
tuG1 <- triang_mcwh(uG1, nLevels=c(2, 3, 2, 6, 4, 9))

tuG1 <- triang(uG1, control=list(method="elo", order=c("a", "e", "f")))
tuG1 <- triang_elo(uG1, order=c("a", "e", "f"))

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="dgCMatrix")
tuG2 <- triangulate(uG2)
```

`graph_coerce_list` *Coercion of graphs represented as lists*

Description

Coercion of graphs represented as lists to various graph formats.

Usage

```
g_ugl2ig_(zz, vn = NULL)

g_ugl2dm_(zz, vn = NULL)

g_ugl2sm_(zz, vn = NULL)

g_ugl2XX_(zz, outtype, vn = NULL)

g_dagl2ig_(zz, vn = NULL)
```

```
g_dagl2dm_(zz, vn = NULL)

g_dagl2sm_(zz, vn = NULL)

g_dagl2XX_(zz, outtype, vn = NULL)

g_adl2ig_(zz)

g_adl2dm_(zz)

g_adl2sm_(zz)

g_adl2XX_(zz, outtype)

g_M2adl_(amat)

g_M2ugl_(amat)

g_M2dagl_(amat)

g_ugl2M_(glist, vn = NULL, result = "matrix")

g_dagl2M_(glist, vn = NULL, result = "matrix")

g_adl2M_(alist, result = "matrix")
```

Arguments

zz	An object representing a graph.
vn	The names of the vertices in the graphs. These will be the row and column names of the matrix.
outtype	What should a list be coerced to.
amat	Adjacency matrix (dense or sparse dgCMatrix).
glist	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 (v1,...,vn) means that there will be arrows from v2,...,vn to v1.
result	A graph object.
alist	An adjacency list.

Examples

```
## 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")
g_M2adl_( g1 )

## Sparse and dense adjacency matrices converted to cliques
```

```
g_M2ugl_( g1 )

## Sparse and dense adjacency matrices converted to cliques
g_M2dagl_( g1 )

## g_M2adl_( g2 ) ## FIXME FAILS for sparse matrix
## g_M2ugl_( g2 ) ## FIXME Is there an issue here??
## g_M2dagList( g2 ) ## Fails for sparse matrix
```

---

graph_iplot *Function for plotting graphs using the 'igraph' package.*

Description

Generic function for plotting graphs using the 'igraph' package.

Usage

```
iplot(x, ...)

## S3 method for class 'igraph'
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).

Usage

```
is_dag(object)

is_dagMAT(object)

is_ug(object)

is_ugMAT(object)

is_tug(object)

is_tugMAT(object)

is_dg(object)

is_dgMAT(object)

is_adjMAT(object)

is.adjMAT(object)
```

Arguments

object	A graph represented as an igraph (igraph package), an adjacency matrix or 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.
- The function is_ug() checks if the adjacency matrix is symmetric.
- 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 seach.

- 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.

Synonymous functions

The functions

- `is.TUG`/`is.DAG`/`is.DG`/`is.UG`/`is.adjMAT`

are synonymous with

- `is_tug`/`is_dag`/`is_dg`/`is_ug`/`is_adjMAT`.

The `is.X` group of functions will be deprecated.

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

See Also

dag, ug

Examples

```
## DAGs
dag_  <- dag(~ a:b:c + c:d:e)

## Undirected graphs
ug_  <- ug(~a:b:c + c:d:e)

## Is graph a DAG?
is_dag(dag_)
is_dag(ug_)

## Is graph an undirected graph
is_ug(dag_)
is_ug(ug_)

## Is graph a triangulated (i.e. chordal) undirected graph
is_tug(dag_)
is_tug(ug_)

## Example where the graph is not triangulated
ug2_  <- ug(~ a:b + b:c + c:d + d:a)
```

```
is_tug(ug2_)
```

---

graph_query *Query a graph*

Description

Unified approach to query a graph about its properties (based partly on functionality from gRbase and functionality imported from RBGL).

Usage

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

qgraph(object, op, set = NULL, set2 = NULL, set3 = NULL)

ancestors(set, object)

subGraph(set, object)

is.triangulated(object)

connComp(object)

ancestralSet(set, object)

ancestralGraph(set, object)

parents(set, object)

children(set, object)

separates(set, set2, set3, object)

closure(set, object)

adj(object, set)

is.simplicial(set, object)

simplicialNodes(object)

is.complete(object, set = NULL)

is.decomposition(set, set2, set3, object)
```

```
nodes_(object)

nodes(object, ...)

## S4 method for signature 'igraph'
nodes(object, ...)

edges(object)

edges_(object)

addEdge(v1, v2, object)

removeEdge(v1, v2, object)
```

Arguments

object	A graph.
op	The operation or query.
set, set2, set3	Sets of nodes in graph.
...	additional arguments
v1, v2	Vertex names

Examples

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

separates("a", "d", c("b", "c"), ug0)
separates("a", "d", "c", ug0)
is.simplicial("b", ug0)
simplicialNodes(ug0)

simplicialNodes(ug0)
```

---

graph_topo_sort *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

```
topo_sort(object, index = FALSE)

topo_sortMAT(amat, index = FALSE)

topoSort(object, index = FALSE)

topoSortMAT(amat, index = FALSE)
```

Arguments

object	An graph represented either as 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.

Synonymous functions

The functions topo_sort / topoSort are synonymous with topo_sortMAT / topoSortMAT. One of the groups may be deprecated in the future.

Note

The workhorse is the topo_sortMAT 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")

topo_sort(dagMAT)
topo_sort(dagMATS)
```

graph_vpar *List of vertices and their parents for graph.*

Description

Get list of vertices and their parents for graph.

Usage

```
vchi(object, getv = TRUE, forceCheck = TRUE)

vchiMAT(object, getv = TRUE, forceCheck = TRUE)

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

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

Arguments

object	An object representing a graph. Valid objects are an adjacency matrix or an igraph.
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
dag_mat <- dag(~a:b:c + c:d:e, result="matrix")
dag_ig <- dag(~a:b:c + c:d:e)
vpar(dag_mat)
vpar(dag_ig)
vpar(dag_mat, getv=FALSE)
vpar(dag_ig, getv=FALSE)
## Undirected graphs
ug_mat <- ug(~a:b:c + c:d:e, result="matrix")
ug_ig <- ug(~a:b:c + c:d:e)
## Not run:
```

```
## This will fail because the adjacency matrix is symmetric and the
## graph has undirected edges
vpar(ug_mat)
vpar(ug_ig)

## End(Not run)
## When forceCheck is FALSE, it will not be detected that the
#g raphs are undirected.
vpar(ug_mat, forceCheck=FALSE)
vpar(ug_ig, forceCheck=FALSE)
```

---

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

Soren Hojsgaard, Department of Mathematical Sciences, Aalborg University, Denmark

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-utilities *gRbase utilities*

Description

Various utility functions for gRbase. Includes 'faster versions' of certain standard R functions.

Usage

```
rhsFormula2list(form)

rhsf2list(form)

rhsf2vec(form)

listify_dots(dots)

list2rhsFormula(form)

list2rhsf(form)

rowmat2list(X)

colmat2list(X)

matrix2list(X, byrow = TRUE)

which.arr.index(X)

which_matrix_index(X)

rowSumsPrim(X)

colSumsPrim(X)

colwiseProd(v, X)

lapplyV2I(setlist, item)

lapplyI2V(setlist, item)
```

Arguments

form	Formula specification (a right-hand sided formula, a numeric/character vector or a list of vectors).
dots	dot-arguments to be turned into a list

X	A matrix.
byrow	Should the split be by row or by column.
v	A vector.
setlist	A list of atomic vectors
item	An atomic vector

Details

which.arr.ind: Returns matrix n x 2 matrix with indices of non-zero entries in matrix X. Notice which_matrix_index__ is cpp implementation.

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

- lapplyV2I: same as but much faster than lapply(setlist, function(elt) match(elt, item))
- lapplyI2V: same as but faster than lapply(setlist, function(elt) item[elt])

Author(s)

Søren Højsgaard, <sorenh@math.aau.dk>

Examples

```
## colwiseProd
X <- matrix(1:16, nrow=4)
v <- 1:4
t(v * t(X))
colwiseProd(v, X)
## Not run:
system.time(for (ii in 1:100000)  t(v * t(X)))
system.time(for (ii in 1:100000)  colwiseProd(v, X))

## End(Not run)


setlist <- list(c(1,2,3), c(2,3,4), c(2,4,5))
item <- c(2,3)

lapplyV2I(setlist, item)
lapply(setlist, function(gg) match(gg, item))

lapplyI2V(setlist, item)
lapply(setlist, function(x) item[x])

if (require(microbenchmark)){
microbenchmark(
  lapplyV2I(setlist, item),
  lapply(setlist, function(elt) match(elt, item)))

microbenchmark::microbenchmark(
```

```
  lapplyI2V(setlist, item),
  lapply(setlist, function(elt) item[elt]))
}
```

---

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

---

internal *Internal functions for the gRbase package*

Description

These functions are not intended to be called directly.

prostate *Prostate Tumor Gene Expression Dataset*

Description

This is the Prostate Tumor Gene Expression dataset used in Chung and Keles (2010).

Usage

```
data(prostate)
```

Format

A list with two components:

x Gene expression data. A matrix with 102 rows and 6033 columns.

y Class index. A vector with 102 elements.

Details

The prostate dataset consists of 52 prostate tumor and 50 normal samples. Normal and tumor classes are coded in 0 and 1, respectively, in y vector. Matrix x is gene expression data and arrays were normalized, log transformed, and standardized to zero mean and unit variance across genes as described in Dettling (2004) and Dettling and Beuhlmann (2002). See Chung and Keles (2010) for more details.

Source

Singh D, Febbo P, Ross K, Jackson D, Manola J, Ladd C, Tamayo P, Renshaw A, DAmico A, Richie J, Lander E, Loda M, Kantoff P, Golub T, and Sellers W (2002), "Gene expression correlates of clinical prostate cancer behavior", *Cancer Cell*, Vol. 1, pp. 203–209.

References

Chung D and Keles S (2010), "Sparse partial least squares classification for high dimensional data", *Statistical Applications in Genetics and Molecular Biology*, Vol. 9, Article 17.

Dettling M (2004), "BagBoosting for tumor classification with gene expression data", *Bioinformatics*, Vol. 20, pp. 3583–3593.

Dettling M and Beuhlmann P (2002), "Supervised clustering of genes", *Genome Biology*, Vol. 3, pp. research0069.1–0069.15.

Examples

```
data(prostate)
prostate$x[1:5,1:5]
prostate$y
```

`set-operations` *Suite of set operations*

Description

Set operations for gRbase and related packages.

Usage

```
maximal_sets(setlist, index = FALSE)

minimal_sets(setlist, index = FALSE)

remove_redundant(setlist, maximal = TRUE, index = FALSE)

is_inset(x, setlist, index = FALSE)

filter_maximal_vectors(setlist, index = FALSE)

get_subset(x, setlist, all = FALSE)

get_superset(x, setlist, all = FALSE)

is_subsetof(set, set2)

is.subsetof(x, set)

subsetof(x, set)
```

Arguments

`setlist`	List of vectors (representing a set of subsets)
`index`	Logical; should indices (in setlist) be returned or a set of subsets.
`maximal`	Logical; see section 'Details' for a description.
`x`, `set`, `set2`	Vector representing a set.
`all`	Logical; see section 'Details' for a description.

Details

'setlist' is a list of vectors representing a set of subsets; i.e. V1,...VQ where Vk is a subset of some base set V.

'all' If true, `get_superset` will return index of all vectors containing the element; otherwise only the first index is returned.

`is_inset`: Checks if the set x is in one of the Vk's.

remove_redundant: Returns those Vk which are not contained in other subsets; i.e. gives the maximal sets. If maximal is FALSE then returns the minimal sets; i.e. Vk is returned if Vk is contained in one of the other sets Vl and there are no set Vn contained in Vk.

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

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

el1 <- c(2, 1)
el2 <- c(2, 3)
el3 <- c(4, 3)
el4 <- c(2, 1, 3)

maximal_sets(set)
minimal_sets(set)

remove_redundant(set)
remove_redundant(set, maximal=FALSE)

is_inset(el1, set)
is_inset(el2, set)
is_inset(el3, set)

get_subset(el1, set)
get_subset(el1, set)
get_subset(el2, set)
get_subset(el3, set)

get_superset(el1, set)
get_superset(el1, set, all=TRUE)
get_superset(el2, set)
get_superset(el3, set)

is_subsetof(el1, el1)
is_subsetof(el1, el2)
is_subsetof(el1, el4)
```

---

ug2dag *Coerce between undirected and directed graphs when possible*

Description

An undirected graph G can be converted to a dag if G is chordal.

Usage

```
ug2dag(object)
```

Arguments

object	An igraph object.

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