Package ‘algstat’

February 19, 2015

Type Package
Title Algebraic statistics in R
Version 0.0.2
Date 2014-12-04
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Description algstat provides functionality for algebraic statistics in R.
   Current applications include exact inference in log-linear models for
   contingency table data, analysis of ranked and partially ranked data, and
   general purpose tools for multivariate polynomials, building on the mpoly
   package. To aid in the process, algstat has ports to Macaulay2, Bertini,
   LattE-integrale and 4ti2.
Depends mpoly
LinkingTo Rcpp
Imports stringr, reshape2, Rcpp
License GPL-2
SystemRequirements Optionally Latte-integrale, Bertini, and Macaulay2.
   Cygwin is required for each of the above for Windows users. See
   INSTALL file for details.
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NeedsCompilation yes
Repository CRAN
Date/Publication 2014-12-06 02:23:38

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abortion

Description

A multi-way contingency table with the results of a survey concerning attitudes concerning abortion.

Usage

data(abortion)

Format

A 3x3x3 (contingency) table

Author(s)

1972 National Opinion Research Center

References


algstat

alcstat : Algebraic statistics in R

Description

algstat is a package for algebraic statistics in R. Current applications include exact inference in log-linear models for contingency table data, analysis of ranked and partially ranked data, and general purpose tools for multivariate polynomials, building on the mpoly package. To aid in the process, algstat has ports to Macaulay2, Bertini, Latte-Integrale and 4ti2.
**Amaker**

*Distance transitive matrix*

**Description**

Compute the distance transitive matrix for a survey in which k objects are selected from a group of m objects.

**Usage**

Amaker(m, k)

**Arguments**

- **m**: the number of objects
- **k**: the number of objects selected

**Value**

...

**See Also**

Tmaker, Emaker, Mmaker, Pmaker, Smaker

**Examples**

Amaker(4, 2)

---

**bertini**

*Evaluate Bertini Code*

**Description**

Write a Bertini file, evaluate it through a back-end connection to Bertini, and bring the output back into R.

**Usage**

bertini(code, dir = tempdir(), opts = "", quiet = TRUE)

**Arguments**

- **code**: Bertini code as either a character string or function; see examples
- **dir**: directory to place the files in, without an ending /
- **opts**: options for bertini
- **quiet**: show bertini output
**Value**

an object of class bertini

**Examples**

```r
## Not run:

# where does the circle intersect the line y = x?
code <- "
INPUT

variable_group x, y;
function f, g;

f = x^2 + y^2 - 1;
g = y - x;

END;
"
bertini(code)

c(sqrt(2)/2, sqrt(2)/2)

# where do the surfaces intersect?
# x^2 - y^2 - z^2 - 1/2
# x^2 + y^2 + z^2 - 9
# x^2/4 + y^2/4 - z^2
# intersect?
#
# code <- "
INPUT

variable_group x, y, z;
function f, g, h;

f = x^2 - y^2 - z^2 - 1/2;
g = x^2 + y^2 + z^2 - 9;
h = x^2/4 + y^2/4 - z^2;

END;
"
bertini(code)

# algebraic solution :
c(sqrt(19)/2, 7/(2*sqrt(5)), 3/sqrt(5)) # +/- each ordinate
```
# example from bertini manual

code <- "
INPUT

variable_group x, y;
function f, g;

f = x^2 - 1;
g = x + y - 1;

END;
"

out <- bertini(code)
summary(out)

# non zero-dimensional example

code <- "
CONFIG
    TRACKTYPE: 1;
END;

INPUT
    variable_group x, y, z;
    function f1, f2;
    f1 = x^2 - y;
    f2 = x^3 - z;
END;
"

out <- bertini(code)
# bertini(code, quiet = FALSE) # print broken here

### End(Not run)
Description

Convert dimensions of approval data, see details for more.

Usage

\texttt{bump(x, n, k, vin, vout, method = c("popular", "even"))}

Arguments

- **x**: the summary given
- **n**: the number of objects in the running
- **k**: the number of objects approved
- **vin**: the level of summary given
- **vout**: the level of summary/expectation desired
- **method**: "popular" (default) or "even", see details

Details

In a survey in which \( k \) objects are approved from a list of \( n \) objects by \( N \) voters, the survey responses can be summarized with \( \text{choose}(n, k) \) frequencies. \texttt{bump} can summarize these frequencies by computing the number of votes for any lower order grouping primarily using the \texttt{Tmaker} function. We refer to this as "bumping down". Given an \( i \)th summary (the number of votes for each \( i \)-grouping), we can compute the expected \((i+1)\)-group votes by evenly distributing each \( i \)-groups votes to the \((i+1)\)-groups containing the \( i \)-groups and summing over each \( i \)-group’s contribution. This is "bumping up".

See examples for the cookie example.

As a simple example of bumping up, suppose we have a survey in which 100 individuals select their favorite 3 items out of 6 items. The total number of votes cast is therefore 100*3 = 300.

If that is all that is known, then the (one) bumped up expected dataset would simply expect each of the 6 items to be listed equally frequently: a vector of length 6 with each element equal to 300/6 = 50. We would expect each of the 15 pairings to have 300/\text{choose}(6, 2) = 300 / 15 = 20 votes, and each of the 20 triples to have 300/\text{choose}(6, 3) = 5 votes.

Now suppose we learn that the six objects were voted for 30, 40, 50, 50, 60, and 70 times, respectively, but nothing more. Obviously, we could then compute 300 votes had been cast (\( V_0 = 100 \) voters), but "looking up" we could also guess that the pairing [12] was voted for 30/\text{choose}(5, 1) + 40/\text{choose}(5, 1) = 14 times. The reasoning is that if object 1 were observed 30 times and 2 40 times, if each were paired evenly with each of the others 1 would contribute 30/\text{choose}(5, 1) votes to the pairing and 2 40/\text{choose}(5, 1). The \text{choose}(5, 1) corresponds to the number of pairings that 1 (or 2) is present in: [12], [13], [14], [15], [16]. The same idea can be used to estimate the number of votes for each of the \text{choose}(6, 2) = 15 pairs. (See examples.) This is bumping up; for any level of summary, we can bump it up as far as we like (all the way up to the set itself).
Bumping down is easier. The only thing needed to know is that it follows the order of the subsets function. For example, in the above voting example, the 15 pairs votes are assumed to be in the order subsets(6, 2), and the result is given in the order of subsets(6, 1).

If method = "even", exactly the above is done. If method = "popular", then when bumping up the number of votes for [12] isn’t determined by each of 1 and 2 donating their samples evenly to each of their upstream pairs; but rather 1 and 2 donating to each other (as contributors of the pair [12]) according to how popular it is amongst the alternatives. In other words, 1 is thought to have (in this case) 30 votes to "give" to either 2, 3, 4, 5, or 6. If method = "even", it donates 30/5 to each. If method = "popular", it donates 40/(40+50+50+60+70) of the 30 votes to 2 (as a contributor of [12]), 50/(40+50+50+60+70) of the 30 votes to 3, and so on. The expected frequency of [12] is therefore made up as the sum of such contributions from each of the places the contribution might come. Here, the contributors of [12] are [1] and [2], with contributions 30*40/(40+50+50+60+70) and 40*30/(30+50+50+60+70), for a total of 9.06 expected [12] votes. The same is done for higher order votes; e.g. [123] takes even or popular contributions from [12], [13], and [14].

## Value

...  

## Examples

```r
## Not run:

V0 <- 100 # V0 = number of voters (not votes)
bump(V0, 6, 3, 0, 0) # no bump
bump(V0, 6, 3, 0, 1) # 1-up
bump(V0, 6, 3, 0, 2) # 2-up
bump(V0, 6, 3, 0, 3) # 3-up

V1 <- c(30, 40, 50, 50, 60, 70)
bump(V1, 6, 3, 1, 0) # bump down
bump(V1, 6, 3, 1, 1) # no bump
bump(V1, 6, 3, 1, 2) # 1-up
bump(V1, 6, 3, 1, 3) # 2-up

cbind(  
bump(V1, 6, 3, 1, 2, "popular"),  
bump(V1, 6, 3, 1, 2, "even")  
)

data(cookie)
(out <- spectral(cookie$freq, 6, 3, cookie$cookies))

(V0 <- out$obs$V0)
bump(V0, 6, 3, 0, 0)
bump(V0, 6, 3, 0, 1)
bump(V0, 6, 3, 0, 2)
```
bump(V0, 6, 3, 0, 3)
out$fullExp$V0
out$decompose(out$effects[,1])

(V1 <- out$obs$V1)
bump(V1, 6, 3, 1, 0) # cbind(bump(V1, 6, 3, 1, 0), out$fullExp$V1[[1]])
bump(V1, 6, 3, 1, 1) # cbind(bump(V1, 6, 3, 1, 1), out$fullExp$V1[[2]])
bump(V1, 6, 3, 1, 2) # cbind(bump(V1, 6, 3, 1, 2), out$fullExp$V1[[3]])
bump(V1, 6, 3, 1, 3) # cbind(bump(V1, 6, 3, 1, 3), out$fullExp$V1[[4]])
out$fullExp$V1 # the sampler doesn't distribute its samples up evenly

(V2 <- out$obs$V2)
bump(V2, 6, 3, 2, 0) # cbind(bump(V2, 6, 3, 2, 0), out$fullExp$V2[[1]])
bump(V2, 6, 3, 2, 1) # cbind(bump(V2, 6, 3, 2, 1), out$fullExp$V2[[2]])
bump(V2, 6, 3, 2, 2) # cbind(bump(V2, 6, 3, 2, 2), out$fullExp$V2[[3]])
bump(V2, 6, 3, 2, 3) # cbind(bump(V2, 6, 3, 2, 3), out$fullExp$V2[[4]])

(V3 <- out$obs$V3)
bump(V3, 6, 3, 3, 0)
bump(V3, 6, 3, 3, 1)
bump(V3, 6, 3, 3, 2)
bump(V3, 6, 3, 3, 3)

## End(Not run)

city

| Living Location Preference Dataset |

Description

1439 people were asked to rank three areas in which to live, the city (1), suburbs (2), and the country (3). 637 of these individuals themselves lived in a city, 500 in the suburbs, and 302 in the country.

Usage

data(city)

Format

A 6x3 matrix

Author(s)

1972 National Opinion Research Center Amalgam Survey

References

condorcet

Find a Condorcet Choice.

Description
Try to compute find a Condorcet choice given a full ranking of m objects.

Usage
condorcet(data, names)

Arguments
data the data, a vector of counts of each permutation of the m objects (m is the length of data)
names character vector of the names of the m objects

Details
In a ranking of m objects, the Condorcet choice is the choice that wins over every other choice in pairwise comparisons. See Marden (1995), p.20 for details.

Value
...

References

See Also
Pmaker

Examples
data(city)

condorcet(city[,"city"], colnames(city)) # among city-dwellers
condorcet(city[,"suburb"], colnames(city)) # among suburb-dwellers
condorcet(city[,"country"], colnames(city)) # among country-dwellers
condorcet(rowSums(city), colnames(city)) # overall winner
**Girl Scout Cookie Preferences**

**Description**
A small approval dataset on Girl Scout cookies.

**Usage**
```r
data(cookie)
```

**Format**
A list with elements "freq", "raw", "sorted", and "cookies"

**Author(s)**
Ann Johnston and Michael Orrison

**References**

---

**Count Integer Points in a Polytope**

**Description**
count uses LattE’s count function to count the (integer) lattice points in a polytope and compute Ehrhart polynomials.

**Usage**
```r
count(spec, dir = tempdir(), opts = "", quiet = TRUE, mpoly = TRUE)
```

**Arguments**
- `spec`: specification, see details and examples
- `dir`: directory to place the files in, without an ending /
- `opts`: options for count; "" for a hyperplane representation, "-vrep" for a vertex representation; see the LattE manual at [http://www.math.ucdavis.edu/~latte](http://www.math.ucdavis.edu/~latte) for more details.
- `quiet`: show latte output
- `mpoly`: when opts = "-ehrhart-polynomial", return the mpoly version of it
Details

The specification should be one of the following: (1) a character string or strings containing an inequality in the mpoly expression format (see examples), (2) a list of vertices, or (3) raw code for LattE's count program. If a character vector is supplied, (1) and (3) are distinguished by the number of strings.

Behind the scenes, count works by writing a latte file and running count on it. If a specification other than a length one character is given to it (which is considered to be the code), count attempts to convert it into LattE code and then run count on it.

Value

the count. if the count is a number has less than 10 digits, an integer is returned. if the number has 10 or more digits, an integer in a character string is returned. you may want to use the gmp package's as.bigz to parse it.

Examples

## Not run:

```r
spec <- c("x + y <= 10", "x >= 1", "y >= 1")
count(spec)
count(spec, opts = "--dilation=10")
count(spec, opts = "--homog")

# by default, the output from LattE is in
list.files(tempdir())
list.files(tempdir(), recursive = TRUE)

# ehrhart polynomials
count(spec, opts = "--ehrhart-polynomial")
count(spec, opts = "--ehrhart-polynomial", mpoly = FALSE)

# ehrhart series (raw since mpoly can't handle rational functions)
count(spec, opts = "--ehrhart-series")

# simplified ehrhart series - not yet implemented
# count(spec, opts = "--simplified-ehrhart-polynomial")

# first 3 terms of the ehrhart series
count(spec, opts = "--ehrhart-taylor=3")

# multivariate generating function
count(spec, opts = "--multivariate-generating-function")

# the number of tables with the same marginals
data(politics)
```
countTables

Count Similarly Margined Contingency Tables

Description

Count the number of contingency tables with the same marginals as a given table.

Usage

countTables(table, margins = as.list(1:length(dim(table))), dir = tempdir(),
opts = "", quiet = TRUE)

Arguments

table  the table of interest
margins the margins to be fixed
dir    directory to place the files in, without an ending /
opts   options for count
quiet  show latte output
Details

`countTables` uses LattE’s count function (via algstat’s `count` function) to count the tables. In many cases, the number of such tables is enormous. In these cases, instead of giving back an integer `countTables` provides a character string with the integer in it; see examples.

Value

an integer

See Also

count

Examples

```r
## Not run:

data(politics)
countTables(politics)

data(handy)
countTables(handy)

data(HairEyeColor)
eyeHairColor <- margin.table(HairEyeColor, 2:1)
countTables(eyeHairColor)

library(gmp)
as.bigz(countTables(eyeHairColor))

# notice that even tables with small cells can have
# huge fibers
data(drugs)
countTables(drugs)

countTables(eyeHairColor, quiet = FALSE)
```

## End(Not run)

---

drugs Use of Alcohol, Cigarettes, and Marijuana by High School Students

Description

A multi-way contingency table of alcohol, cigarettes, and marijuana use by high school students.
Emaker

Usage

data(drugs)

Format

A 2x2x2 (contingency) table

Author(s)

Wright State University School of Medicine and the United Health Services in Dayton, Ohio

References


| Emaker          | Create the expected higher-order statistics calculating matrix for approval data |

Description

Create the expected higher-order statistics calculating matrix for approval data

Usage

Emaker(m, vin, vout)

Arguments

- m the number of objects
- vin the (lower order) grouping level of the data
- vout the desired higher order grouping level

Value

...

See Also

Tmaker, Amaker, Mmaker, Pmaker, Smaker
Examples

Emaker(6, 0, 1)
Emaker(6, 0, 2)
Emaker(6, 0, 3)
Emaker(6, 0, 4)

Emaker(6, 1, 1)
Emaker(6, 1, 2)
Emaker(6, 1, 3)
Emaker(6, 1, 4)
Emaker(6, 1, 5)
Emaker(6, 1, 6)

# compare to Tmaker
Emaker(6, 1, 3) # contributors when bumping up from 1-groups to 3-groups
Tmaker(6, 3, 1)

---

data(haberman)

Description

Haberman’s example of a log-linear model (the no-three way interaction model) that lacks an MLE even though it has positive margins.

Usage

data(haberman)

Format

A 2x2x2 (contingency) table

Author(s)

unknown

References

**Handy**

*Handedness Data*

**Description**

A small fictional dataset on handedness.

**Usage**

```r
data(handy)
```

**Format**

A 2x2 (contingency) table

**Author(s)**

David Kahle

---

**Hierarchical**

*Fitting Hierarchical Log-linear Models with Algebraic Methods*

**Description**

Run the Metropolis-Hastings algorithm using a Markov basis computed with 4ti2 to sample from the conditional distribution of the data given the sufficient statistics of a hierarchical model.

**Usage**

```r
hierarchical(formula, data, iter = 10000, burn = 1000, thin = 10,
             engine = c("Cpp", "R"), method = c("ipf", "mcmc"), moves)
```

**Arguments**

- `formula`: formula for the hierarchical log-linear model
- `data`: data, typically as a table but can be in different formats. see `teshape`
- `iter`: number of chain iterations
- `burn`: burn-in
- `thin`: thinning
- `engine`: C++ or R? (C++ yields roughly a 20-25x speedup)
- `method`: should the expected value (exp) be fit using iterative proportional fitting (via `loglin`) or the MCMC as the average of the steps?
- `moves`: the markov moves for the mcmc
Details

Hierarchical fits and tests a hierarchical log-linear model on a contingency table. In many ways, hierarchical is like stats::loglin or MASS::loglm; however, there are a few key differences in the functionality of hierarchical.

The first difference is methodological. The tests conducted with hierarchical are exact tests based on the conditional distribution of the data given the sufficient statistics for the model. In other words, they are Fisher’s exact test analogues for log-linear models. These tests are made possible by advances in algebraic statistics; see the first and second references below. In particular, hierarchical leverages Markov bases through the software 4ti2 to construct a Metropolis-Hastings algorithm to sample from the conditional distribution of the table given the sufficient statistics.

A second way that hierarchical differs from stats::loglin or MASS::loglm is in generalizing the kinds of tests performed. While those allow for the asymptotic unconditional testing using Pearson’s X^2 test and the likelihood ratio test (MASS::loglm is simply a wrapper for stats::loglin), hierarchical gives several test statistics: Pearson’s X^2, the likelihood ratio G^2, Freeman-Tukey, Cressie-Read (lambda = 2/3), and Neyman’s modified X^2., see the last reference. In other words, to compute the exact p-value, iter = 1e4 samples are sampled from the conditional distribution of the table given the sufficient statistics, and then the proportion of tables that have X^2, G^2, etc. values greater than or equal to that of the observed table is the p value for the (conditional) exact test. A similar, but perhaps preferable approach, simply adds up the probabilities of the tables that have probabilities less than or equal to that of the observed table; this is the first line output in hierarchical and does not use a test statistic.

Some authors (see the third reference) suggest that for discrete problems, a "mid p value" is preferable to the traditional p value, and when presented should be interpreted in the same way. If the p value is defined to be, say, P(samps >= obs), the mid p value is defined to be P(samps > obs) + P(samps == obs)/2. The mid p value is computed for each test.

Since the tests make use of Monte Carlo sampling, standard errors (SE) are reported for each statistic. For the test statistics, this is just the standard deviation of the samples divided by the square root of the sample size, iter; they are computed and returned by the print method. The standard errors of the p values use the CLT asymptotic approximation and, therefore, warrant greater consideration when the p value is close to 0 or 1.

Value

a list containing named elements

- steps: an integer matrix whose columns represent individual samples from the mcmc.
- moves: the moves used for the proposal distribution in the mcmc, computed with 4ti2 (note that only the positive moves are given).
- acceptProb: the average acceptance probability of the moves, including the thinned moves.
- param: the fitted parameters of the log linear model.
- df: parameters per term in the model
- quality: model selection statistics AIC, AICc, and BIC.
- residuals: the (unstandardized) pearson residuals (O - E) / sqrt(E)
- call: the call.
- obs: the contingency table given.
hierarchical

- `exp`: the fit contingency table as an integer array.
- `A`: the sufficient statistics computing matrix (from Tmaker).
- `p.value`: the exact p-values of individual tests, accurate to Monte-Carlo error. These are computed as the proportion of samples with statistics equal to or larger than the observed statistic.
- `mid_p.value`: the mid p-values, see Agresti pp.20–21.
- `statistic`: the pearson’s chi-squared (X2), likelihood ratio (G2), Freeman-Tukey (FT), Cressie-Read (CR), and Neyman modified chi-squared (NM) statistics computed for the table given.
- `sampsStats`: the statistics computed for each mcmc sample.
- `cells`: the number of cells in the table.
- `method`: the method used to estimate the table.

Author(s)

David Kahle

References


See Also

`loglin`, `loglm`, `metropolis`

Examples

```r
## Not run:
```
```r
data(handy)
(out <- hierarchical(~ Gender + Handedness, data = handy))
```
```r
# hierarchical performs the same tasks as loglin and loglm,
# but hierarchical gives the exact test p values and more statistics
statsFit <- stats::loglin(handy, list(c(1),c(2)), fit = TRUE, param = TRUE)
```
massFit <- MASS::loglm(~ Gender + Handedness, data = handy)
# loglm is just a wrapper of loglin

# comparisons between hierarchical and loglin

# the expected table given the sufficient statistics can be computed
# via two methods, iterative proportional fitting, and the mcmc itself:
# #ipf
hierarchical(~ Gender + Handedness, data = handy, method = "mcmc")$exp
statsFit$fit # the equivalent in loglin; this is used by default in hierarchical

# the parameter values of the loglinear model can be accessed
out$param
statsFit$param

# the p-value for the overall model is available as well
# hierarchical gives the exact conditional p-value
# (conditional on the sufficient statistics)
# the five numbers correspond the probability of tables that are
# "more weird" than the observed table, where "more weird" is determined
# by having a larger X2 value (or G2, FT, CR, or NM)
out$p.value
fisher.test(handy)$p.value # out$p.value["X2"] is accurate to monte carlo error

# loglin gives the p-values using the unconditional asymptotic distributions
# (X2 = pchisq(statsFit$pearson, df = statsFit$df, lower.tail = FALSE),
# G2 = pchisq(statsFit$lrt, df = statsFit$df, lower.tail = FALSE))
out$mid.p.value # the mid (exact conditional) p-value is also available
# the test statistics based on the observed table and the expected
table under the model are available
out$statistic
c(statsFit$pearson, statsFit$lrt) # loglin only gives X2 and G2

# the markov basis used for the proposal distribution of the metropolis-hastings
# algorithm are returned. the proposal distribution is uniform on +/-
# the moves added to the current table
out$moves
# they are easier understood as tables
vec2tab(out$moves, dim(handy))
# notice that the marginals stay fixed:
handy + vec2tab(out$moves, dim(handy))

# these were computed as the markov basis of the integer matrix
out$A
markov(out$A)
out$moves

# the moves are also sometimes written in tableau form (LAS p.13)
tableau(out$moves, dim(handy))
# that's +1 the the table in elements [1,1] and [2,2]
# and -1 in the table in elements [1,2] and [2,1]

# the acceptance probability of the MCMC is retained
out$acceptProb

# various model assessment measures are also available
out$quality

# the number of independent parameters per term are in df
out$df

# as an added help, you may find the visuals in vcd useful:
# library(vcd)
# mosaic(~ Gender + Handedness, data = handy, shade = TRUE, legend = TRUE)

## politics example - with computing the exact p value by hand

```r
data(politics)

(out <- hierarchical(~ Personality + Party, data = politics))
statsFit <- stats::loglin(politics, as.list(1:2), fit = TRUE, param = TRUE)

out$p.value
# exact without monte-carlo error
sum(dhyper(c(0:3,6:9), 10, 10, 9))
fisher.test(politics)$p.value
round(dhyper(0:9, 10, 10, 9), 4)

# comparisons :
out$exp
statsFit$fit

out$param
statsFit$param

out$p.value # exact
c("X2" = pchisq(statsFit$pearson, df = statsFit$df, lower.tail = FALSE),
```
```r
"G^2" = pchiq(statsFit$lrt, df = statsFit$df, lower.tail = FALSE)
) # asymptotic approximation
fisher.test(politics)$p.value # accurate to monte carlo error

out$statistic # accurate to monte carlo error
c(statsFit$pearson, statsFit$lrt)

# mosaic(~ Personality + Party, data = politics, shade = TRUE, legend = TRUE)

## eyeHairColor from the Diaconis and Sturmfels reference
#########################################################################
data(HairEyeColor)
eyeHairColor <- margin.table(HairEyeColor, 2:1)

outC <- hierarchical(~ Eye + Hair, data = eyeHairColor)
outR <- hierarchical(~ Eye + Hair, data = eyeHairColor, engine = "R")

# doesn't work even with workspace = 2E9 (with over 4.5Gb in memory)
# fisher.test(eyeHairColor, hybrid = TRUE, workspace = 2E9)
tableau(outC$moves, dim(eyeHairColor))

# library(microbenchmark)
# microbenchmark(
#   hierarchical(~ Eye + Hair, data = eyeHairColor),
#   hierarchical(~ Eye + Hair, data = eyeHairColor, engine = "R")
# )
# 5-10 times faster; much faster with increased iter

# mosaic(~ Eye + Hair, data = HairEyeColor, shade = TRUE, legend = TRUE)

## abortion preference example from the
## Diaconis and Sturmfels reference pp. 379--381
## a no 3-way interaction model
#########################################################################```
data(abortion)

out <- hierarchical(
  ~ Education*Abortion + Abortion*Denomination + Education*Denomination,
  data = abortion,
  iter = 10000, burn = 50000, thin = 50
)
out$p.value

vec2tab(rowMeans(out$steps), dim(abortion)) # cf. p. 380
loglin(abortion, subsets(1:3, 2), fit = TRUE)$fit

out$param
loglin(abortion, subsets(1:3, 2), param = TRUE)$param

qqplot(rchisq(1055, df = 8), out$sampsStats$Xs2s)
curve(1*x, from = 0, to = 30, add = TRUE, col = "red")

(nMoves <- 2*ncol(out$move)) # DS uses 110
# the markov basis is larger than it needs to be

# loglin no three-way interaction model example
#---------------------------------------------------------------------------------
# the help for fits the no three-way interaction model on HairEyeColor,
# finds a .66196 p-value using the asymptotic distribution, and concludes
# a good fit:
data(HairEyeColor)

fit <- loglin(HairEyeColor, subsets(1:3, 2), fit = TRUE, param = TRUE)
mod <- hierarchical(~ Eye*Hair + Hair*Sex + Eye*Sex, data = HairEyeColor)

# p values
pchisq(fit$lrt, fit$df, lower.tail = FALSE) # see ?loglin
mod$p.value
# test statistics
c(fit$pearson, fit$lr)
mod$statistic

# fits (estimated tables)
fit$fit
mod$exp
mod$obs

# checking the autocorrelation
acf(mod$sampsStats$PRs)
mod <- hierarchical(~ Eye*Hair + Hair*Sex + Eye*Sex, data = HairEyeColor, thin = 100)
acf(mod$sampsStats$PRs) # got it!

# the slight differences in fit$fit and mod$exp (both done with ipf from loglin)
# are due to differences in variable order:
loglin(HairEyeColor, subsets(1:3, 2), fit = TRUE)$fit
loglin(HairEyeColor, subsets(1:3, 2)[c(1,3,2)], fit = TRUE)$fit

# a few model moves
vec2tab(mod$move[,1], dim(HairEyeColor))
vec2tab(mod$move[,50], dim(HairEyeColor))
~vec2tab(mod$move[,50], dim(HairEyeColor))

# they contribute 0 to the marginals of the table
vec2tab(mod$move[,50], dim(HairEyeColor))
mod$A %*% mod$move[,50]
vec2tab(mod$A %*% mod$move[,50], dim(HairEyeColor))

HairEyeColor
HairEyeColor + vec2tab(mod$move[,50], dim(HairEyeColor))

## a table with positive marginals but no MLE for
## the no-three way interaction model

### data(haberman)

mod <- hierarchical(~ X1*X2 + X2*X3 + X1*X3, data = haberman)

statsFit <- loglin(haberman, subsets(1:3, 2), param = TRUE, fit = TRUE)
statsFit$fit
statsFit$param
c(statsFit$pearson, statsFit$lrt)

algstatFit <- hierarchical(~ X1*X2 + X2*X3 + X1*X3, data = haberman, method = "mcmc")
algstatFit$exp
algstatFit$param
algstatFit$statistic

### an example from agresti, p.322

```r
# an example from agresti, p.322

data(drugs)
ftable(aperm(drugs, c(3, 1, 2))) # = table 8.3

out <- hierarchical(~Alcohol + Cigarette + Marijuana, data = drugs)
matrix(round(aperm(out$exp, c(2,1,3)), 1), byrow = FALSE)

loglin(drugs, as.list(1:3), fit = TRUE)$fit
loglin(drugs, as.list(1:3), param = TRUE)$param

# # the saturated model issues a warning from markov, but works :
# out <- hierarchical(~Alcohol * Cigarette * Marijuana, data = drugs)
# matrix(round(aperm(out$exp, c(2,1,3)), 1), byrow = FALSE)

ftable(aperm(out$exp, c(3,1,2)))

stats <- loglin(drugs, as.list(1:3), fit = TRUE, param = TRUE)

# considered via glm

df <- as.data.frame(drugs)
mod <- glm(Freq ~ Alcohol + Cigarette + Marijuana, data = df, family = poisson)
summary(mod)
mod$fitted.values

# the same can be done with glm :

mod <- glm(
  Freq ~ Alcohol + Cigarette + Marijuana,
Construct a Hierarchical Model Matrix

Description

Determine the A matrix associated with a hierarchical model on a contingency table. In algebraic
statistics, the A matrix of a log-linear model is the transpose of the design matrix of the (cell-means
parameterized) ANOVA corresponding to the model.

Usage

hmat(varlvls, facets)
is.bertini

Arguments

varlvls  a vector containing the number of levels of each variable
facets   the facets generating the hierarchical model, a list of vectors of variable indices

Value

a named matrix

References


Examples

```r
# LAS example 1.2.11, p.16
varlvls <- c(2,2,2,2)
facets <- list(c(1,2), c(1,4), c(2,3))
( A <- hmat(varlvls, facets) )

# 2x2 independence example
# following convention, the first index indicates rows
varlvls <- c(2,2)
facets <- list(1,2)
( A <- hmat(varlvls, facets) )

printForMarkov <- function(A){
  cat(paste(nrow(A), ncol(A)))
  cat("\n")
  cat(apply(unname(A), 1, paste, collapse = " ", sep = "\n"), collapse = "\n")
}
printForMarkov(A)
```

is.bertini  *Bertini Object Check*

Description

Test whether an object is an bertini object.

Usage

```r
is.bertini(x)
```

Arguments

x  object to be tested
**is.linear**

**Value**

Vector of logicals.

**Examples**

# see ?bertini

---

**is.linear**  
*Test whether an mpoly object is linear.*

**Description**

Test whether an mpoly object is linear.

**Usage**

```r
is.linear(x)
```

**Arguments**

- `x` an mpoly or mpolyList object

**Value**

a logical vector

**Examples**

```r
## Not run:

is.linear(mp("\theta"))
is.linear(mp("x + 1"))
is.linear(mp("x + y"))
is.linear(mp(c("\theta", "x + y")))

is.linear(mp("x + x y"))
is.linear(mp(c("x + x y", "x")))

## End(Not run)
```
is.m2  

Macaulay2 Object Check

Description
Test whether an object is an m2 object.

Usage
is.m2(x)

Arguments
x  object to be tested

Value
Vector of logicals.

Examples
## Not run:

is.m2(m2("13^1000"))

## End(Not run)

kprod  

Iterated Kronecker product

Description
Compute the Kronecker product of several matrices.

Usage
kprod(...)

Arguments
...  a listing of matrices

Details
If kronecker is the function that computes A x B, kprod computes A x B x C and so on; it’s a wrapper of Reduce and kronecker.
latteMax

Value

... a matrix that is the kronecker product of those matrices (from left to right)

Examples

```r
kprod(diag(2), t(ones(2)))
kprod(t(ones(2)), diag(2))

kprod(diag(2), t(ones(2)), t(ones(2)))
kprod(t(ones(2)), diag(2), t(ones(2)))
kprod(t(ones(2)), t(ones(2)), diag(2))
```

```r
rbind(
  kprod(diag(2), t(ones(2))),
  kprod(t(ones(2)), diag(2))
)
```

Description

latteMax uses LattE’s maximize function to find the maximum of a linear objective function over the integers satisfying linearity constraints. This makes use of the digging algorithm; see the LattE manual at http://www.math.ucdavis.edu/~latte for details.

Usage

```r
latteMax(objective, constraints, method = c("lp", "cones"), dir = tempfile(),
  opts = "", quiet = TRUE)
```

Arguments

- **objective**: a linear polynomial to pass to mp, see examples
- **constraints**: a collection of linear polynomial (in)equalities that define the feasibility region, the integers in the polytope
- **method**: method LP or cones
- **dir**: directory to place the files in, without an ending /
- **opts**: options; see the LattE manual at http://www.math.ucdavis.edu/~latte
- **quiet**: show latte output

Value

the count. if the count is a number has less than 10 digits, an integer is returned. if the number has 10 or more digits, an integer in a character string is returned. you may want to use the gmp package’s as.bigz to parse it.
Examples

```r
## Not run:

latteMax("-2 x + 3 y", c("x + y <= 10", "x >= 0", "y >= 0"))

df <- expand.grid(x = 0:10, y = 0:10)
df <- subset(df, x + y <= 10)
df$val <- apply(df, 1, function(v) -2*v[1] + 3*v[2])
df[which.max(df$val),]

library(ggplot2)
qplot(x, y, data = df, size = val)

## End(Not run)
```

`latteMin`  
_Solve a Linear Program (Minimization)_

Description

`latteMin` uses LattE’s minimize function to find the minimum of a linear objective function over the integers satisfying linearity constraints. This makes use of the digging algorithm; see the LattE manual at [http://www.math.ucdavis.edu/~latte](http://www.math.ucdavis.edu/~latte) for details.

Usage

```r
latteMin(objective, constraints, method = c("lp", "cones"), dir = tempdir(),
         opts = "", quiet = TRUE)
```

Arguments

- **objective**: a linear polynomial to pass to mp, see examples
- **constraints**: a collection of linear polynomial (in)equalities that define the feasibility region, the integers in the polytope
- **method**: method LP or cones
- **dir**: directory to place the files in, without an ending /
- **opts**: options; see the LattE manual at [http://www.math.ucdavis.edu/~latte](http://www.math.ucdavis.edu/~latte)
- **quiet**: show latte output

Value

the count. if the count is a number has less than 10 digits, an integer is returned. if the number has 10 or more digits, an integer in a character string is returned. you may want to use the gmp package’s as.bigz to parse it.
Examples

## Not run:

```r
latteMin("-2 x + 3 y", c("x + y <= 10", "x >= 0", "y >= 0"))
latteMin("-2 x + 3 y", c("x + y <= 10", "x >= 0", "y >= 0"),
  method = "cones") # ??

df <- expand.grid(x = 0:10, y = 0:10)
df <- subset(df, x + y <= 10)
df$val <- apply(df, 1, function(v) -2*v[1] + 3*v[2])
df[which.min(df$val),]

library(ggplot2)
qplot(x, y, data = df, size = val)
```

```r
latteMin("-2 x - 3 y - 4 z", c(
  "3 x + 2 y + z <= 10",
  "2 x + 5 y + 3 z <= 15",
  "x >= 0", "y >= 0", "z >= 0"
), "cones", quiet = FALSE)

df <- expand.grid(x = 0:10, y = 0:10, z = 0:10)
df <- subset(df,
  (3*x + 2*y + 1*z <= 10) &
  (2*x + 5*y + 3*z <= 15)
)

df$val <- apply(df, 1, function(v) -2*v[1] + -3*v[2] + -4*v[3])
df[which.min(df$val),]
```

## End(Not run)

---

**lower**

*Create a lower triangular matrix*

**Description**

Create a lower triangular matrix.
Usage

lower(x)

Arguments

x a vector

Value

...

See Also

upper

Examples

upper(1:3)
lower(1:3)

upper(1:6)
lower(1:6)

upper(rnorm(6))

---

\textbf{lpnorm} \hspace{2cm} \textit{Lp Norm}

\textbf{Description}

Compute the Lp norm of a vector.

Usage

lpnorm(x, p = 2)

Arguments

x x

p p

Value

...
Evaluate Macaulay2 Code

Description
Write a Macaulay2 file, evaluate it through a back-end connection to Macaulay2, and bring the output back into R.

Usage
m2(code, dir = tempdir(), opts = "--script")

Arguments
code Macaulay2 code as either a character string or function; see examples
dir directory to place the files in
opts options for m2

Value
an object of class m2

Examples
## Not run:

options(digits = 20)
13^20
m2("13^20") # correct answer
m2("toRR(20,(190049637748808000571392-13^20)/13^20))") # relative error
options(digits = 7)

Examples

lpnorm(1:10)
lpnorm(matrix(1:25, 5, 5))
lpnorm(split(1:25, rep(1:5, each = 5)))

lpnorm(1:10, 1)
lpnorm(matrix(1:25, 5, 5), 1)
lpnorm(split(1:25, rep(1:5, each = 5)), 1)

lpnorm(rnorm(10), 0)
lpnorm(matrix(rnorm(25), 5, 5), 0)
lpnorm(split(rnorm(25), rep(1:5, each = 5)), 0)

lpnorm(-5:5, Inf)
lpnorm(matrix(-25:-1, 5, 5), Inf)
lpnorm(split(-25:-1, rep(1:5, each = 5)), Inf)
Compute a Markov Basis with 4ti2

Description

A Markov basis of a matrix A is computed with the markov function of 4ti2, obtained with the LattE-integrale bundle.

Usage

```r
markov(mat, format = c("mat", "vec", "tab"), dim = NULL, all = FALSE, dir = tempdir(), opts = "-parb", quiet = TRUE, dbName)
```

Arguments

- `mat`: a matrix; for example the output of hmat
- `format`: how the moves should be returned (if "mat", moves are columns)
- `dim`: the dimension to be used in vec2tab if format = "tab" is used, oftentimes a vector of the number of levels of each variable in order
- `all`: if TRUE, all moves (+ and -) are given. if FALSE, only the + moves are given.
markov

dir directory to place the files in, without an ending /
opts options for markov
quiet show 4ti2 output
dbName the name of the model in the markov bases database, http://markov-bases.de, see examples

Value

a matrix containing the Markov basis as its columns (for easy addition to tables)

References


Examples

## Not run:

```r

# 2x2 independence example
# following convention, the first index indicates rows
varlvs <- c(2,2)
facets <- list(1,2)
( A <- hmat(varlvs, facets) )
markov(A)
markov(A, "vec")
markov(A, "tab", varlvs)
markov(A, "tab", varlvs, TRUE)

# 3x3 independence example
# following convention, the first index indicates rows
varlvs <- c(3,3)
facets <- list(1,2)
( A <- hmat(varlvs, facets) )
markov(A)
markov(A, "vec")
markov(A, "tab", varlvs)
markov(A, "tab", varlvs, TRUE)

# LAS example 1.2.1, p. 12 (2x3 independence)
varlvs <- c(2,3)
facets <- list(1, 2)
```
```
(A <- hmat(varlvs, facets))
markov(A, "tab", varlvs)
# Prop 1.2.2 says that there should be
2*choose(2, 2)*choose(3, 2) # = 6
# moves.
markov(A, "tab", varlvs, TRUE)

# LAS example 1.2.12, p.17 (no 3-way interaction)
varlvs <- c(2,2,2)
facets <- list(c(1,2), c(1,3), c(2,3))
(A <- hmat(varlvs, facets))
markov(A)

# LAS example 1.2.12, p.16 (no 3-way interaction)
varlvs <- c(2,2,2,2)
facets <- list(c(1,2), c(1,4), c(2,3))
(A <- hmat(varlvs, facets))
markov(A)
markov(A, "tab", varlvs) # hard to understand
tableau(markov(A), varlvs)

# using the markov bases database, must be connected to internet
# A <- markov(dbName = "ind3-3")
B <- markov(hmat(c(3,3), list(1,2)))
# all(A == B)
```
mchoose

```
markov(diag(1, 10))

## End(Not run)
```

mchoose | Multinomial Coefficient

**Description**

Compute the multinomial coefficient.

**Usage**

```
mchoose(n, x)
```

**Arguments**

- `n`: an integer
- `x`: a vector of integers

**Details**

This function computes the multinomial coefficient by computing the factorial of each number on a log scale, differencing \( \log(n!) - \text{sum}(\log(x!)) \), and then exponentiating. It then checks to see if this is an integer; if it’s not, it issues a warning.

**Value**

... 

**Examples**

```
mchoose(6, c(2, 2, 1, 1))
```
Description

Given a starting table (as a vector) and a loglinear model matrix A, compute the Markov basis of A with 4ti2 and then run the Metropolis-Hastings algorithm starting with the starting table.

Usage

`metropolis(init, moves, iter = 1000, burn = 1000, thin = 10, engine = c("Cpp", "R"))`

Arguments

- `init`: the initial step
- `moves`: the markov basis (the negatives will be added). see ?markov
- `iter`: number of chain iterations
- `burn`: burn-in
- `thin`: thinning
- `engine`: C++ or R? (C++ yields roughly a 20-25x speedup)

Details

See Algorithm 1.1.13 in LAS, the reference below.

Value

a list

Author(s)

David Kahle

References

Examples

## Not run:

data(handy)

```
exp <- loglin(handy, as.list(1:2), fit = TRUE)$fit
e <- unname(tab2vec(exp))
h <- t(t(unname(tab2vec(handy))))
chisq <- algstat:::computeChisqsCpp(h, e)
```

```
out <- hierarchical(~ Gender + Handedness, data = handy)
chisqs <- algstat:::computeChisqsCpp(out$steps, e)
```

```
mean(chisqs >= chisq)
fisher.test(handy)$p.value
```

```
A <- hmat(c(2,2), as.list(1:2))
moves <- markov(A)
outC <- metropolis(tab2vec(handy), moves, 1e4, engine = "Cpp")
str(outC)
outR <- metropolis(tab2vec(handy), moves, 1e4, engine = "R", thin = 20)
str(outR)
```

```
# showSteps(out$steps)
```

```
library(microbenchmark)
microbenchmark(
  metropolis(tab2vec(handy), moves, engine = "Cpp"),
  metropolis(tab2vec(handy), moves, engine = "R"))
```

```
# cpp ~ 20-25x faster
```
showSteps <- function(steps){
  apply(steps, 2, function(x){
    x <- format(x)
    tab <- vec2tab(x, dim(handy))
    message(
      paste(
        apply(tab, 1, paste, collapse = " "),
        collapse = " 
      )
    )
    message(" ", appendLF = F)
  })
  invisible()
}
# showSteps(out$steps)

## End(Not run)

### Mmaker

<table>
<thead>
<tr>
<th>Mmaker</th>
<th>Marginals matrix</th>
</tr>
</thead>
</table>

**Description**

Compute the marginals matrix for a full ranking of m objects

**Usage**

Mmaker(m)

**Arguments**

- **m** the number of objects

**Details**

This is the transpose of the marginals matrix presented in Marden (1995).

**Value**

...
ones

References


See Also

`Tmaker, Amaker, Emaker, Pmaker, Smaker`

Examples

data(city)

Mmaker(3)
Mmaker(3) %% city

---

<table>
<thead>
<tr>
<th>ones</th>
<th>Ones Vector</th>
</tr>
</thead>
</table>

Description

Make a column vector of ones.

Usage

ones(n)

Arguments

n how many ones

Value

a column vector of ones as an integer matrix

Examples

ones(5)
str(ones(5))
Pmaker

Pairs matrix

Description

Compute the pairs matrix for a full ranking of m objects

Usage

Pmaker(m)

Arguments

m
the number of objects

Details

This is the transpose of the pairs matrix presented in Marden (1995).

Value

...

References


See Also

Tmaker, Amaker, Emaker, Mmaker, Smaker

Examples

data(city)

Pmaker(3)
Pmaker(3) %>% city
# 1 = city, 2 = suburb, 3 = country

# looking just among city folk, generate the pairs matrix
city[,"city",drop=FALSE] # the data
m <- sum(city[,"city"])
k <- (Pmaker(3) %>% city)[,1]
Khat <- upper(k) + lower(m-k)
colnames(Khat) <- row.names(Khat) <- colnames(city)
Khat
round(Khat / m, 2) # % times row is rated over column

# worked out: city is voted over suburb in 123, 132, and 231, equaling
210 + 23 + 8 = khat[1,2]  
# whereas suburb is rated over city in 213, 312, 321, equaling 
111 + 204 + 81 = khat[2,1]  

# is there a condorcet choice?  

p <- ncol(khat)  
Khat[which(diag(p) == 1)] <- NA  
K2 <- t(apply(Khat, 1, function(v) v[is.na(v)]))  
# remove diag elts  
boole <- apply(K2/m, 1, function(x) all(x > .5))  
if(any(boole)) names(boole)[which(boole)]  
# suburb is a condorcet choice  

<table>
<thead>
<tr>
<th>politicalGoals</th>
<th>Relative Rankings of Importance of Four Political Goals</th>
</tr>
</thead>
<tbody>
<tr>
<td>politicalGoals</td>
<td>Relative Rankings of Importance of Four Political Goals</td>
</tr>
</tbody>
</table>

**Description**  
2262 Germans were asked to rank the following in order of importance: (1) maintain order in the nation, "order"; (2) give people more say in decisions in the government, "say"; (3) fight rising prices, "prices"; and (4) protect freedom of speech, "freedom".

**Usage**  
data(politicalGoals)

**Format**  
An atomic named vector of length 4! = 24

**Author(s)**  
The first reference

**References**  

politics  Politics by Personality

Description
A 2-by-2 contingency table comparing political identification and personality.

Usage
data(politics)

Format
A 2x2 (contingency) table

Author(s)
David Kahle, simplifying the dataset found on p.622 of Sheskin (see References)

References

polyOptim  Polynomial Optimization

Description
Find the collection of critical points of a multivariate polynomial unconstrained or constrained to an affine variety (algebraic set; solution set of multivariate polynomials).

Usage
polyOptim(objective, constraints, varOrder, ...)

Arguments
objective the objective polynomial (as a character or mpoly)
constraints (as a character or mpoly/mpolyList)
varOrder variable order (see examples)
... stuff to pass to bertini

Value
an object of class bertini
Examples

## Not run:

# unconstrained optimization of polynomial functions is available
polyOptim("x^2")
polyOptim("-x^2")
polyOptim("-(x - 2)^2")
polyOptim("-(x^2 + y^2)")
polyOptim("-(x^2 + (y - 2)^2")

polyOptim("(x - 1) (x - 2) (x - 3)") # fix global labeling

# constrained optimization over the affine varieties is also available
# (affine variety = solution set of polynomial equations)

# find the critical points of the plane f(x,y) = x + y
# over the unit circle x^2 + y^2 = 1
polyOptim("x + y", "x^2 + y^2 = 1")

# you can specify them as a combo of mpoly, mpolyList, and characters
o <- mp("x + y")
c <- "x^2 + y^2 = 1"
polyOptim(o, c)

out <- polyOptim("x + y", c)
str(out)

# another example, note the solutions are computed over the complex numbers
polyOptim("x^2 y", "x^2 + y^2 = 3")
# solutions: (+-sqrt(2), +-1) and (0, +-sqrt(3))

## End(Not run)

---

polySolve  Solve a System of Polynomial Equations

Description

polySolve solves a system of polynomial equations, specifiable in any of several ways.

Usage

polySolve(lhs, rhs, varOrder, ...)
polySolve

Arguments

  lhs   a mpolyList or character vector of left hand sides
  rhs   a mpolyList or character vector of right hand sides
  varOrder variable order (see examples)
  ...   stuff to pass to bertini

Value

  an object of class bertini

See Also

  variety, bertini

Examples

## Not run:

# it can solve linear systems
# (here where the line y = x intersects y = 2 - x)
polySolve(c("y", "y"), c("x", "2 - x"), c("x", "y"))

# or nonlinear systems
polySolve(c("y", "y"), c("x^2", "2 - x^2"), c("x", "y"))

# perhaps an easier specification is equations themselves
# with either the " = " or " == " specifications
# varOrder is used to order the solutions returned
polySolve(c("y = x^2", "y = 2 - x^2"), varOrder = c("x", "y"))
polySolve(c("y == x^2", "y == 2 - x^2"), varOrder = c("x", "y"))

# mpoly objects can be given instead of character strings
lhs <- mp(c("y - (2 - x)", "x y"))
rhs <- mp(c("0", "0"))
polySolve(lhs, rhs, varOrder = c("x", "y"))

# if no default right hand side is given, and no "=" or "==" is found,
# rhs is taken to be 0's.
# below is where the lines y = x and y = -x intersect the unit circle
polySolve(c("y - x") (y + x), "x^2 + y^2 - 1")

# the output object is a bertini object
out <- polySolve(c("(y - x) (y + x)", "x^2 + y^2 - 1")
str(out,1)

# here is the code that was run :
cat(out$bertiniCode)

# the finite and real solutions:
out$finite_solutions
print.bertini

Pretty Printing of Bertini Output

Description

Pretty printing of Bertini output.

Usage

```r
## S3 method for class 'bertini'
print(x, digits = 3, ...)
```

Arguments

- `x`: an object of class `bertini`
- `digits`: digits to round to
- `...`: additional parameters

Value

Invisible string of the printed object.

Examples

```r
## Not run:

# see ?bertini

variety("x^2 + 1")
variety(c("x^2 + 1 + y","y"))
```

## End(Not run)
print.hierarchical  Pretty Printing of Hierarchical’s Output

Description
Pretty printing of hierarchical’s output.

Usage
## S3 method for class 'hierarchical'
print(x, digits = 4, ...)

Arguments
x  an object of class hierarchical
digits  digits to round to
...  additional parameters

Value
Invisible string of the printed object.

Examples
# see ?hierarchical

print.m2  Pretty printing of Macaulay2 output.

Description
Pretty printing of Macaulay2 output.

Usage
## S3 method for class 'm2'
print(x, ...)

Arguments
x  an object of class m2
...  additional parameters

Value
Invisible string of the printed object.
print.polyOptim

Examples

## Not run:

m2("13^1000")

## End(Not run)

---

print.polyOptim  Pretty printing of polyOptim (Bertini) output.

Description

Pretty printing of polyOptim (Bertini) output.

Usage

## S3 method for class 'polyOptim'

print(x, lagrange = FALSE, digits = 3, ...)

Arguments

- `x`: an object of class polyOptim, bertini
- `lagrange`: show values of lagrange multipliers?
- `digits`: digits to round to
- `...`: additional parameters

Value

Invisible string of the printed object.

Examples

# see ?polyOptim
print.spectral  Pretty Printing of Spectral's Output

Description
Pretty printing of spectral's output.

Usage
## S3 method for class 'spectral'
print(x, digits = 3, ...)

Arguments
x  an object of class spectral
digits  digits to round to
...  additional parameters

Value
Invisible string of the printed object.

Examples
# see ?spectral

print.tableau  Pretty printing of tableau output.

Description
Pretty printing of tableau output.

Usage
## S3 method for class 'tableau'
print(x, ...)

Arguments
x  an object of class tableau
...  ...

Value
Invisible string of the printed object.
**projectOnto**

**Examples**

```r
# see ?tableau
```

---

**projectOnto**  \hspace{1cm} \textit{Vector Projection onto col(A)}

---

**Description**

Project a vector onto the column space of a matrix.

**Usage**

```r
projectOnto(A, x)
```

**Arguments**

- \texttt{A} \hspace{1cm} a matrix
- \texttt{x} \hspace{1cm} a vector

**Value**

...  

**See Also**

`qr.fitted`

**Examples**

```r
A <- diag(5)[,1:2]
x <- 1:5
projectOnto(A, x)
```

---

**projectOntoPerp**  \hspace{1cm} \textit{Vector Projection onto the orthogonal complement of col(A)}

---

**Description**

Project a vector onto the orthogonal complement of the column space of a matrix; the null space of \( A \) transpose

**Usage**

```r
projectOntoPerp(A, x)
```
Arguments

\[ A \]
\[ x \]

a matrix

a vector

Value

...

Examples

\[ A \leftarrow \text{diag}(5)[1:2] \]
\[ x \leftarrow 1:5 \]
\[ \text{projectOnto}(A, x) \]

---

**rvotes**

*Random Spectral Data*

---

Description

Generate spectral data for testing purposes.

Usage

\[ \text{rvotes}(\text{nVoters, nObjects, kSelected}) \]

Arguments

\[ \text{nVoters} \]
\[ \text{nObjects} \]
\[ \text{kSelected} \]

number of voters voting

number of objects up for selection

number of objects selected by each voter

Value

...

Examples

\[ \text{rvotes}(100, 10, 3) \]
**setBertiniPath**  

*Set Bertini Path*

**Description**

This function sets the Bertini path either by (1) passing it a character string or (2) using file.choose.

**Usage**

```r
setBertiniPath(path)
```

**Arguments**

- `path`: a character string, the path to Bertini

**Value**

```
invisible bertiniPath
```

**Examples**

```r
## Not run:
setBertiniPath()

## End(Not run)
```

---

**setLattePath**  

*Set LattE Path*

**Description**

This function sets the LattE path either by (1) passing it a character string or (2) using file.choose.

**Usage**

```r
setLattePath(path)
```

**Arguments**

- `path`: a character string, the path to LattE (the function count, for example)

**Value**

```
invisible lattePath
```
**Examples**

```r
## Not run:
setLattePath()

## End(Not run)
```

---

**setM2Path**  
*Set Macaulay2 Path*

**Description**

This function sets the Macaulay2 path either by (1) passing it a character string or (2) using `file.choose`.

**Usage**

```r
setM2Path(path)
```

**Arguments**

- `path`: a character string, the path to m2

**Value**

invisible `m2Path`

**Examples**

```r
## Not run:
setM2Path()

## End(Not run)
```
setMarkovPath

Description
This function sets the 4ti2 path either by (1) passing it a character string or (2) using file.choose.

Usage
setMarkovPath(path)

Arguments
path a character string, the path to 4ti2 (the function markov, for example)

Value
invisible markovPath

Examples
## Not run:
setMarkovPath()

## End(Not run)

smaker

Means matrix (rank data)

Description
Compute the means matrix for a full ranking of m objects

Usage
smaker(m)

Arguments
m the number of objects

Details
This is the transpose of the means matrix presented in Marden (1995); it projects onto the means subspace of a collection of ranked data. See the examples for how to compute the average rank.
**Value**

...

**References**


**See Also**

Tmaker, Amaker, Emaker, Mmaker, Pmaker

**Examples**

data(city)

X <- permutations(3)

# the average rank can be computed without this function
normalize <- function(x) x / sum(x)
factorial(3) * apply(t(X) %%*% city, 2, normalize)
# the dataset city is really like three datasets; they can be pooled back
# into one via:
rowSums(city)
factorial(3) * apply(t(X) %%*% rowSums(city), 2, normalize)

# the means matrix is used to summarize the data to the means subspace
# which is the subspace of m! spanned by the columns of permutations(m)
# note that when we project onto that subspace, the projection has the
# same average rank vector :
Smaker(3) %%*% city # the projections, table 2.8
factorial(3) * apply(t(X) %%*% Smaker(3) %%*% city, 2, normalize)

# the residuals can be computed by projecting onto the orthogonal complement
(diag(6) - Smaker(3)) %%*% city # residuals

apply(t(X) %%*% city, 2, function(x) x / sum(x) * factorial(3)) # average ranks by group

apply(t(X) %%*% rowSums(city), 2, function(x) x / sum(x) * factorial(3)) # average ranks pooled

---

**spectral**

**Analyze a Rank Dataset**

**Description**

spectral analyzes a rank dataset for order interactions; see examples for details.
spectral

Usage

spectral(data, n, k, levels, iter = 10000, burn = 1000, thin = 10)

Arguments

data: a vector in the frequency format (see examples)
n: the number of objects to select from
k: the number of objects selected
levels: the names of the outcomes, in the proper order
iter: iterations in metropolis
burn: burn in
thin: thinning

Value

a list containing named elements

• effects: the pure ith order effects as a data frame computed by projecting the data onto the isotypic subspaces. the length of each is the same as the data, choose(n, k).
• effectsNorms: the l2 norms of each effect.
• statsMatrices: the lower order statistics calculating matrices, made with Tmaker.
• moves: the markov moves for moving around each V, computed with markov on the statsMatrices. only the positive moves are given.
• samps: the samples from each space conditioned on each level of statistics. this is the output of metropolis.
• obs: a list of the observed data and its lower level summaries.
• exp: a list of the expected number of samples at each level given the summary statistics at the previous (lower) level. these are computed from the samples from metropolis by (1) summarizing them with Tmaker and then (2) averaging the samples. the expected V2 samples (for example), are determined by taking the samples with the same V1 statistics (in V3, say), summarizing them to V2 with Tmaker, and then averaging every cell across the samples.
• fullExp: this is the result of taking each of the samples with the same lower-order statistics and averaging them. see exp, which is a reduction of fullExp.
• residuals: obs - exp
• isotypicBases: a list of the basis vectors of each isotypic subspace; computed as the eigenvalues of the result of Amaker, and grouped by eigenvalue.
• sampsEffects: the effects determined by each of the samples, projected onto the isotypic subspaces.
• sampsEffectsNorms: the norms of the effects of the samples.
• sampsEffectsNormSummary: a summary of the norms of the effects of the samples.
• showStages: a function that prints out the observed, expected, and residuals of sequentially conditioning on the sample size, first order statistics, second order statistics, and so on.
• showFit: a function that prints out a summary of the fit of the model.
• decompose: a function that takes a vector of the same length of the table given and summarizes it to its lower level statistics.
• sampsDecomposed: every sample decomposed.
• statistic: the pearson’s chi-squared (X2), likelihood ratio (G2), Freeman-Tukey (FT), Cressie-Read (CR), and Neyman modified chi-squared (NM) statistics computed using the observed data (obs) and expected data (exp) at each level.
• sampsStats: the statistics computed on each of the samples.
• p.value: the exact p-values of individual tests, accurate to Monte-Carlo error. these are computed as the proportion of samples with statistics equal to or larger than the observed statistic.
• p.value.se: the standard errors of the p-values computed using the standard asymptotic formula of sqrt(p(1-p)/n), a measure of the Monte-Carlo error.

Examples

```r
## Not run:

## voting statistics at different levels
# load the cookies dataset:
data(cookie)
cookie$freq
cookie$cookies

# performing the spectral analysis
(out <- spectral(cookie$freq, 6, 3, cookie$cookies))

out$obs # the original observations, and the summary statistics

out$exp # each level is conditional on the previous level’s statistics
  # (e.g. what you would expect for 1st order effects given sample size)
  # these are generated using 10k markov bases based mcmc samples

out$p.value # these are approximate exact test p-values using various
  # popular test statistics. the approximations are good to
  # monte carlo error

out$p.value.se # these are the standard errors using the sqrt(p*(1-p)/n)
  # asymptotic formula, known to have poor performance
  # for small/large p; see package binom for better

out$statistic # the individual statistics are also available
  # the values are not comparable across Vi levels (the rows)
  # as they have asymptotic chi-squared distributions with
  # different degrees of freedom
```
out$fullExp # you can also get the expected number of samples at each scale
    # for tables with the same ith order statistics, i = 0, ..., k-1

# these can be seen to (re)construct an expected picture of the
# complete data given each successive collection of statistics
cbind(
    obs = cookie$freq,
    as.data.frame(lapply(out$fullExp, function(x) round(x[[4]],1)))[c(2:4,1)]
) # notice that the reconstruction given only the first order statistics
 # (the number of individual cookies selected) is quite good

# instead of using the reconstructions from the exp coming from
# the samples, you could reconstruct the summaries of the observed
# data using bump; it's not quite as good :
V0 <- bump(cookie$freq, 6, 3, 3, 0)
V1 <- bump(cookie$freq, 6, 3, 3, 1)
V2 <- bump(cookie$freq, 6, 3, 3, 2)
cbind(
    obs = cookie$freq,
    round(data.frame(
        V0 = bump(V0, 6, 3, 0, 3),
        V1 = bump(V1, 6, 3, 1, 3),
        V2 = bump(V2, 6, 3, 2, 3)
    ), 2)
)[c(2:4,1)]

# you can see the model step-by-step with showStages() :
out$showStages()
# notice (1) the significant reduction in the residuals after conditioning
# on the first order statistics and also (2) the powdery noise after
# conditioning on the second order statistics.
# the p-values reflect the same:
# * the residuals from conditioning on the sample size show the first
# order effects are strongly significant (in out$p.value V1 = 0)
# * the residuals from conditioning on the first order effects suggest
# the second order effects might be significant (V2 = .04-.13ish)
# * the residuals from conditioning on the second order effects indicate
# the third order effects are entirely insignificant (V3 > .2)

# the isotypic subspaces can be used to determine the pure order effects :
out$isotypicBases # bases of the isotypic subspaces (here 4)
out$effects # pure ith order effects; cookie$freq projected onto the bases
    # these are their effects at the data level, so they all have
    # the same length as the original dataset: choose(n, k)
    zapsmall(rowSums(out$effects)) # the effects sum to the data

    # if the Vk effects are 0, then the conclusion is that Vk is perfectly
    # predicted with the (k-1)st level statistics. this may lead to the
    # conclusion that the l2 norms (say) of the effects might be used to
    # gauge the relative strength of effects :
    out/effectsNorms # = apply(out/effects, 2, lpnorm)

    # the natural (not full-dimensional) residuals can be seen with the summary
    out
    # or with
    out$residuals
    # these are the residuals (obs ith level stats) - (exp ith level stats)
    # given the (i-1)st statistics

    # bump is a useful function :
    out$obs
    bump(cookie$freq, 6, 3, 3, 0) # the 0 level is the number of voters, not votes
    bump(cookie$freq, 6, 3, 3, 1)
    bump(cookie$freq, 6, 3, 3, 2)
    bump(cookie$freq, 6, 3, 3, 3)

    V1 <- out$obs$V1 # = bump(cookie$freq, 6, 3, 3, 1)
    bump(V1, 6, 3, 1, 0)
    bump(V1, 6, 3, 1, 1)
    bump(V1, 6, 3, 1, 2) # cbind(bump(V1, 6, 3, 1, 2), out$exp$V2)
    bump(V1, 6, 3, 1, 3) # cbind(bump(V1, 6, 3, 1, 3), out$fullExp$V1[[4]])
    # the differences here are between an observation and an expectation
out$obs$V1 - out$exp$V1
out$residuals$V1
out$decompose(out$effects$V1)$V1

out$obs$V2 - out$exp$V2
out$residuals$V2

out$decompose(out$effects$V0)$V2 +
out$decompose(out$effects$V1)$V2 +
out$decompose(out$effects$V2)$V2 -
out$exp$V2

# this is how to reconstruct the observation given the effects
# the cols of out$effects are the V_k order effects reconstructed
# from the lower level effects
out$obs$V0
zapsmall(
  out$decompose(out$effects$V0)$V0
)

out$obs$V1
zapsmall(
  out$decompose(out$effects$V0)$V1 +
  out$decompose(out$effects$V1)$V1
)

out$obs$V2
zapsmall(
  out$decompose(out$effects$V0)$V2 +
  out$decompose(out$effects$V1)$V2 +
  out$decompose(out$effects$V2)$V2
)

out$obs$V3
zapsmall(
  out$decompose(out$effects$V0)$V3 +
  out$decompose(out$effects$V1)$V3 +
  out$decompose(out$effects$V2)$V3 +
  out$decompose(out$effects$V3)$V3
)
zapsmall(rowSums(out$effects))

all(cookie$freq == zapsmall(rowSums(out$effects)))

out$effects$V0
out$effects$V0 + out$effects$V1
out$effects$V0 + out$effects$V2
out$effects$V0 + out$effects$V3

str(out$sampsDecomposed)
as.data.frame(lapply(out$sampsDecomposed, function(l) rowMeans(l$V3)))

eff0 <- rowMeans(out$sampsDecomposed$V0$V3)
cbind(eff0, out$effects$V0)

eff1 <- rowMeans(out$sampsDecomposed$V1$V3 - eff0)
cbind(eff1, out$effects$V1)

eff2 <- rowMeans(out$sampsDecomposed$V2$V3 - eff0 - eff1)
cbind(eff2, out$effects$V2)

sum(eff0)
sum(eff1)
sum(eff2)

str(out$sampsEffectsNORMS)
data <- out$sampsEffectsNORMS$V0$V3
plot(density(data))
curve(dnorm(x, mean(data), sd(data)), col = “red”, add = TRUE)

data <- out$sampsEffectsNORMS$V0$V2
plot(density(data))
curve(dnorm(x, mean(data), sd(data)), col = “red”, add = TRUE)

data <- out$sampsEffectsNORMS$V0$V1
plot(density(data))
curve(dnorm(x, mean(data), sd(data)), col = “red”, add = TRUE)

data <- out$sampsEffectsNORMS$V1$V3
plot(density(data))
curve(dnorm(x, mean(data), sd(data)), col = “red”, add = TRUE)

data <- out$sampsEffectsNORMS$V1$V2
plot(density(data))
curve(dnorm(x, mean(data), sd(data)), col = “red”, add = TRUE)

data <- out$sampsEffectsNORMS$V2$V3
plot(density(data))
curve(dnorm(x, mean(data), sd(data)), col = "red", add = TRUE)

## how to convert data into the right format
# this essentially just uses some clever indexing tricks
# to reorder the data in the way you want

data <- cookie$raw  # an example raw, unordered dataset
levels <- cookie$cookies # the order of the objects you want
levsNndcs <- 1:length(levels)
names(levsNndcs) <- levels

# arrange selections within rows (order of selection doesn't matter)
data <- t(apply(data, 1, function(x) x[order(levsNndcs[x]) ] ))

# arrange rows (order of selectors doesn't matter)
for(k in ncol(data):1) data <- data[order(levsNndcs[data[,k]]),]

# check that you've done the right thing
all( data == cookie$sorted )

# the data frequency order should match that of subsets:
subsets(levels, 1)
subsets(levels, 2)
sapply(subsets(levels, 2), paste, collapse = ", ")
subsets(levels, 3)
sapply(subsets(levels, 3), paste, collapse = ", ")

names(cookie$freq)
names(cookie$freq) == sapply(subsets(levels, 3), paste, collapse = ", ")
## Other examples

```r
# rvotes provides uniform samples

n <- 4
k <- 2

raw <- rvotes(250, n, k)
rawTogether <- apply(raw, 1, paste, collapse = " ")
levels <- sapply(subsets(n, k), paste, collapse = " ")
freq <- table(factor(rawTogether, levels = levels))
(out <- spectral(freq, n, k))

out$p.value
out$showStages()
out$obs
out$exp

n <- 6
k <- 3
raw <- rvotes(250, n, k)
rawTogether <- apply(raw, 1, paste, collapse = " ")
levels <- sapply(subsets(n, k), paste, collapse = " ")
freq <- table(factor(rawTogether, levels = levels))
(out <- spectral(freq, n, k))

n <- 7
k <- 3
raw <- rvotes(250, n, k)
rawTogether <- apply(raw, 1, paste, collapse = " ")
levels <- sapply(subsets(n, k), paste, collapse = " ")
freq <- table(factor(rawTogether, levels = levels))
(out <- spectral(freq, n, k))

n <- 8
k <- 3
raw <- rvotes(250, n, k)
rawTogether <- apply(raw, 1, paste, collapse = " ")
levels <- sapply(subsets(n, k), paste, collapse = " ")
freq <- table(factor(rawTogether, levels = levels))
# out <- spectral(freq, n, k) # breaks
```
subsets

Compute Subsets

Description

Compute the subsets of a given set.

Usage

subsets(set, sizes = 1:length(set), include_null = FALSE)

Arguments

- set: the original set
- sizes: desired size(s) of subsets
- include_null: should the empty vector be included?

Details

Note that this algorithm is run in R: it is therefore not intended to be the most efficient algorithm for computing subsets.

Value

a list of subsets as vectors

See Also

combn

Examples

subsets(1:3)
subsets(1:3, size = 2)
subsets(1:3, include_null = TRUE)

subsets(c('a','b','c','d'))
subsets(c('a','b','c','d'), include_null = TRUE)
summary.bertini  

**Summarize Bertini Output**

**Description**
This function summarizes the output from Bertini.

**Usage**
```r
## S3 method for class 'bertini'
summary(object, ...)
```

**Arguments**
- `object`: an object of class bertini
- `...`: additional parameters

**Value**
Invisible string of the printed object.

**Examples**
```
# see ?bertini
```

---

tab2vec  

**Array to Vector conversion**

**Description**
Convert an array into a vector.

**Usage**
```r
tab2vec(tab)
```

**Arguments**
- `tab`: an array of counts

**Details**
This function converts an array (or a multi-way contingency table) into a vector, using a consistent ordering of the cells. The ordering of the cells is lexicographical and cannot be specified by the user.
tableau

Value

a named integer vector. the names correspond to the cell indices in the table.

See Also

vec2tab

Examples

a <- array(1:24, c(2,3,4))
tab2vec(a)

data(Titanic)
tab2vec(Titanic)
Titanic[1,1,1,1]
Titanic[1,1,1,2]

---

tableau Tableau Notation for Markov

Description

Print the tableau notation for a Markov move. See the reference provided, p. 13.

Usage

tableau(move, dim)

Arguments

move a markov move matrix, where the columns are moves in vector form (e.g. the output of markov)
dim the dimensions of the table form of the move, oftentimes a vector of the number of levels of each variable in order

Value

an object of class tableau

References

### Examples

```r
## Not run:

# 2x2 independence example
# following convention, the first index indicates rows
varlvs <- c(2,2)
facets <- list(1,2)
(A <- hmat(varlvs, facets))
markov(A)
markov(A, "vec")
markov(A, "tab", varlvs)
markov(A, "tab", varlvs, TRUE)
tableau(markov(A), varlvs)

# LA5 example 1.2.12, p.17 (no 3-way interaction)
varlvs <- c(2,2,2)
facets <- list(c(1,2), c(1,3), c(2,3))
(A <- hmat(varlvs, facets))
markov(A)

## End(Not run)
```

---

**teshape**  
*Interconvert data structures*

### Description

Interconvert an array, a raw data frame, and frequency distribution data.frame.

### Usage

```r
treshape(data, out = c("freq", "tab", "raw"))
```

### Arguments

- **data**: a data frame or array
- **out**: the output format, see examples
Details
Multivariate categorical data can be represented in several ways. Three common ways are: a contingency table, a data frame of raw observations (1 row = 1 subject), and a long data frame with a variable containing the counts in the contingency table.

Value
a matrix containing the Markov basis as its columns (for easy addition to tables)

Examples
```r
data(Titanic)

# array to others
teshape(Titanic, "freq")
teshape(Titanic, "tab") # what it was
teshape(Titanic, "raw")

# freq to others
TitanicFreq <- teshape(Titanic, "freq")
teshape(TitanicFreq, "freq") # what it was
teshape(TitanicFreq, "tab") # == Titanic
teshape(TitanicFreq, "raw")

# raw to others
TitanicRaw <- teshape(Titanic, "raw")
teshape(TitanicRaw, "freq")
teshape(TitanicRaw, "tab")
teshape(TitanicRaw, "raw")
```

Description
Create the sufficient statistics calculating matrix for approval data

Usage
```r
tmaker(m, k, d)
```

Arguments
- `m`: the number of objects
- `k`: the number of objects selected
- `d`: the order-effect for the desired matrix (0 to k)
Value

...

See Also

Emaker, Amaker, Mmaker, Pmaker, Smaker

Examples

Tmaker(4, 2, 0) # m
Tmaker(4, 2, 1) # generates how many of each
Tmaker(4, 2, 2) # gives data (order = subsets(1:4, 2))

Tmaker(5, 2, 0)
Tmaker(5, 2, 1)
Tmaker(5, 2, 2)

Tmaker(4, 3, 0) #
Tmaker(4, 3, 1) # subsets(1:4, 3), 1 is in 1, 2, and 3
Tmaker(4, 3, 2) # subsets(1:4, 2)
Tmaker(4, 3, 3)

data(cookie)

## voting statistics at different levels

# projection onto V0: the number of people in survey
effectsOnV0 <- Tmaker(6, 3, 0) %% cookie$freq
colnames(effectsOnV0) <- "Total Votes"
effectsOnV0 # = sum(cookie$freq)

effectsOnV1 <- Tmaker(6, 3, 1) %% cookie$freq
row.names(effectsOnV1) <- cookie$cookies
colnames(effectsOnV1) <- "Total Votes"
effectsOnV1
# projection onto V2: the number of people voting for each cookie-pair
effectsOnV2 <- Tmaker(6, 3, 2) %*% cookie$freq
row.names(effectsOnV2) <- sapply(subsets(cookie$cookies, 2), paste, collapse = "", ")
colnames(effectsOnV2) <- "Total Votes"
effectsOnV2

# projection onto V3: the number of people voting for each cookie-triple
effectsOnV3 <- Tmaker(6, 3, 3) %*% cookie$freq
row.names(effectsOnV3) <- sapply(subsets(cookie$cookies, 3), paste, collapse = "", ")
colnames(effectsOnV3) <- "Total Votes"
effectsOnV3 # = t(t(cookie$freq)) = the (freq) data

---

**Umaker**

*U matrix (rank data)*

**Description**

Compute the generalized marginals matrix for a full ranking of m objects. Umaker generalized Mmaker.

**Usage**

`Umaker(m)`

**Arguments**

- `m` the number of objects

**Details**

This is the transpose of the generalized marginals matrix presented in Marden (1995).

**Value**

...

**References**


**See Also**

*Mmaker, Pmaker, Smaker*

**Examples**

data(politicalGoals)

lambdas <- apply(partitions(4), 1, function(v) v[!v == 0])
**upper**

Create an upper triangular matrix

**Description**

Create an upper triangular matrix.

**Usage**

upper(x)

**Arguments**

x  a vector

**Value**

...

**See Also**

lower

**Examples**

upper(1:3)
lower(1:3)

upper(1:6)
lower(1:6)

upper(rnorm(6))

**variety**

Compute a Variety

**Description**

The variety of a collection of multivariate polynomials is the collection of points at which those polynomials are (simultaneously) equal to 0. variety uses Bertini to find this set.

**Usage**

variety(mpolyList, varOrder, ...)
Arguments

mpolyList Bertini code as either a character string or function; see examples
varOrder variable order (see examples)
... stuff to pass to bertini

Value

an object of class bertini

Examples

```r
## Not run:

polys <- mp(c(
  "x^2 - y^2 - z^2 - .5",
  "x^2 + y^2 + z^2 - 9",
  ".25 x^2 + .25 y^2 - z^2"
))
variety(polys)

# algebraic solution :
c(sqrt(19)/2, 7/(2*sqrt(5)), 3/sqrt(5)) # +/- each ordinate

# character vectors can be taken in; they're passed to mp
variety(c("y - x^2", "y - x - 2"))

# an example of how varieties are invariant to the
# the generators of the ideal
variety(c("2 x^2 + 3 y^2 - 11", "x^2 - y^2 - 3"))

# the following takes a few seconds to initialize, feel free to them
# gb <- grobner(mp(c("2 x^2 + 3 y^2 - 11", "x^2 - y^2 - 3")))
# variety(gb)

m2("R = QQ[x,y]
gens gb ideal(2*x^2 + 3*y^2 - 11, x^2 - y^2 - 3)
")
variety(c("y^2 - 1", "x^2 - 4"))
variety(c("x^2 - 4", "y^2 - 1"))

# variable order is by default equal to vars(mpolyList)
# (this finds the zeros of y = x^2 - 1)
variety(c("y", "y - x^2 + 1")) # y, x
```
vec2tab

Vector to Array conversion

Description

Convert a vector into an array given a set of dimensions; it therefore simply wraps `aperm` and `array`.

Usage

`vec2tab(vec, dim)`

Arguments

Parameter | Description
---|---
`vec` | a vector
`dim` | the desired array dimensions, oftentimes a vector of the number of levels of each variable in order

Details

This function converts an array (or a multi-way contingency table) into a vector, using a consistent ordering of the cells. The ordering of the cells is lexicographical and cannot be specified by the user.
vec2tab

Value
an array

See Also
\texttt{tab2vec}, \texttt{aperm}, \texttt{array}

Examples
\begin{verbatim}
data(Titanic) Titanic tab2vec(Titanic) vec2tab(tab2vec(Titanic), dim(Titanic)) vec2tab(tab2vec(Titanic), dim(Titanic)) == Titanic all(vec2tab(tab2vec(Titanic), dim(Titanic)) == Titanic)
\end{verbatim}
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