Package ‘dae’

August 8, 2023

Version 3.2.19
Date 2023-08-08
Title Functions Useful in the Design and ANOVA of Experiments
Depends R (>= 3.5.0), ggplot2
Imports ggpubr, graphics, methods, plyr, stats
Suggests testthat, vdiffr, R.rsp
VignetteBuilder R.rsp

Description The content falls into the following groupings: (i) Data, (ii) Factor manipulation functions, (iii) Design functions, (iv) ANOVA functions, (v) Matrix functions, (vi) Projector and canonical efficiency functions, and (vii) Miscellaneous functions. There is a vignette describing how to use the design functions for randomizing and assessing designs available as a vignette called ‘DesignNotes’. The ANOVA functions facilitate the extraction of information when the ‘Error’ function has been used in the call to ‘aov’.

The package ‘dae’ can also be installed from <http://chris.brien.name/rpackages/>.

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URL http://chris.brien.name
RoxygenNote 5.0.1
NeedsCompilation no
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Description

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<td>fac.gen</td>
<td>Generate all combinations of several factors and, optionally, replicate them</td>
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<tr>
<td>fac.gen</td>
<td>Generate all combinations of the levels of the supplied factors, without replication</td>
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**fac.match**  
Match, for each combination of a set of columns in 'x', the row that has the same combination in 'table'  

**fac.multinested**  
Creates several factors, one for each level of a nesting.fac and each of whose values are either generated within those of the level of nesting.fac or using the values of a nested.fac  

**fac.nested**  
Creates a factor, the nested factor, whose values are generated within those of a nesting factor  

**fac.recast**  
Recasts a factor by modifying the values in the factor vector and/or the levels attribute, possibly combining some levels into a single level.  

**fac.recode**  
Recodes factor 'levels' using possibly nonunique values in a vector. (May be deprecated in future.)  

**fac.split**  
Splits a factor whose levels consist of several delimited strings into several factors.  

**fac.uncombine**  
Cleaves a single factor, each of whose levels has delimited strings, into several factors using the separated strings.  

**fac.uselogical**  
Forms a two-level factor from a logical object  

**mpone**  
Converts the first two levels of a factor into the numeric values -1 and +1  

(iii) Design functions  

**blockboundaryPlot**  
This function plots a block boundary on a plot produced by 'designPlot'. It supersedes blockboundary.plot.  

**designAmeasures**  
Calculates the A-optimality measures from the variance matrix for predictions.  

**designAnatomy**  
Given the layout for a design, obtain its anatomy via the canonical analysis of its projectors to show the confounding and aliasing inherent in the design.  

**designBlocksGGPlot**  
Adds block boundaries to a plot produced by designGGPlot.  

**designGGPlot**  
Plots labels on a two-way grid of coloured cells using ggplot2 to represent an experimental design.  

**designLatinSqrSys**  
Generate a systematic plan for a Latin Square design.  

**designPlot**  
A graphical representation of an experimental design using labels stored in a matrix. It supersedes design.plot.  

**designPlotlabels**  
Plots labels on a two-way grid using ggplot2.  

**designRandomize**  
Randomize allocated to recipient factors to produce a layout for an experiment. It supersedes fac.layout.  

**designTwoPhaseAnatomies**  
Given the layout for a design and three structure formulae, obtain the anatomies for the (i) two-phase, (ii) first-phase, (iii) cross-phase, treatments, and (iv) combined-units designs.  

**marginality.pstructure**  
Extracts the marginality matrix from a pstructure.object  

**marginality.pstructure**  
Extracts a list containing the marginality matrices from a pcanoan.object  

**print.aliasing**  
Prints an aliasing data.frame  

**no.reps**  
Computes the number of replicates for an experiment
detect.diff  Computes the detectable difference for an experiment
power.exp  Computes the power for an experiment
summary.pcanon  Summarizes the anatomy of a design, being the
decomposition of the sample space based on its canonical analysis.

(iv) ANOVA functions

fitted.aovlist  Extract the fitted values for a fitted model
from an aovlist object
fitted.errors  Extract the fitted values for a fitted model
interaction.ABC.plot  Plots an interaction plot for three factors
qqyeffects  Half or full normal plot of Yates effects
resid.errors  Extract the residuals for a fitted model
residuals.aovlist  Extract the residuals from an aovlist object
strength  Generate paper strength values
tukey.1df  Performs Tukey’s
one-degree-of-freedom-test-for-nonadditivity
yates.effects  Extract Yates effects

(v) Matrix functions

elements  Extract the elements of an array specified by
the subscripts
fac.ar1mat  Forms the ar1 correlation matrix for a
(generalized) factor
fac.sumop  Computes the summation matrix that produces
sums corresponding to a (generalized) factor
fac.vcmat  Forms the variance matrix for the variance
component of a (generalized) factor
mat.I  Forms a unit matrix
mat.J  Forms a square matrix of ones
mat.ar1  Forms an ar1 correlation matrix
mat.ar2  Forms an ar2 correlation matrix
mat.ar3  Forms an ar3 correlation matrix
mat.arma  Forms an arma correlation matrix
mat.banded  Forms a banded matrix
mat.exp  Forms an exponential correlation matrix
mat.gau  Forms a gaussian correlation matrix
mat.ma1  Forms an ma1 correlation matrix
mat.ma2  Forms an ma2 correlation matrix
mat.ncssvar  Forms a variance matrix for random cubic
smoothing spline effects
mat.sar  Forms an sar correlation matrix
mat.sar2  Forms an sar2 correlation matrix
mat.dirprod  Forms the direct product of two matrices
mat.dirsum  Forms the direct sum of a list of matrices
mat.random  Calculates the variance matrix for the
random effects from a mixed model, based
on a formula or a supplied matrix
mat.Vpred  Forms the variance matrix of predictions
mat.Vpredicts  Forms the variance matrix of predictions,
Zncsspline

Forms the design matrix for fitting the random effects for a natural cubic smoothing spline.

(vi) Projector and canonical efficiency functions

Projector class:

\textbf{projector} \hspace{1cm} \text{Create projectors} \\
\textbf{projector-class} \hspace{1cm} \text{Class projector} \\
\textbf{is.projector} \hspace{1cm} \text{Tests whether an object is a valid object of class projector} \\
\textbf{print.projector} \hspace{1cm} \text{Print projectors} \\
\textbf{correct.degfree} \hspace{1cm} \text{Check the degrees of freedom in an object of class projector} \\
\textbf{degfree} \hspace{1cm} \text{Degrees of freedom extraction and replacement}

Accepts two or more formulae:

\textbf{designAnatomy} \hspace{1cm} \text{An anatomy of a design, obtained from a canonical analysis of the relationships between sets of projectors.} \\
\textbf{summary.pcanon} \hspace{1cm} \text{Summarizes the anatomy of a design, being the decomposition of the sample space based on its canonical analysis} \\
\textbf{print.summary.pcanon} \hspace{1cm} \text{Prints the values in an 'summary.pcanon' object} \\
\textbf{efficiencies.pcanon} \hspace{1cm} \text{Extracts the canonical efficiency factors from a list of class 'pcanon'}

Accepts exactly two formulae:

\textbf{projs.2canon} \hspace{1cm} \text{A canonical analysis of the relationships between two sets of projectors} \\
\textbf{projs.combine.p2canon} \hspace{1cm} \text{Extract, from a p2canon object, the projectors} \\
\textbf{summary.p2canon} \hspace{1cm} \text{A summary of the results of an analysis of the relationships between two sets of projectors} \\
\textbf{print.summary.p2canon} \hspace{1cm} \text{Prints the values in an 'summary.p2canon' object that give the combined decomposition} \\
\textbf{efficiencies.p2canon} \hspace{1cm} \text{Extracts the canonical efficiency factors from a list of class 'p2canon'}

Accepts a single formula:

\textbf{as.data.frame.pstructure} \hspace{1cm} \text{Coerces a pstructure.object to a data.frame} \\
\textbf{print.pstructure} \hspace{1cm} \text{Prints a pstructure.object} \\
\textbf{pstructure.formula} \hspace{1cm} \text{Takes a formula and constructs a pstructure.object that includes the orthogonalized projectors for the terms in a formula}

Others:
decomp.relate

Examines the relationship between the eigenvectors for two decompositions.

efficiency.criteria

Computes efficiency criteria from a set of efficiency factors.

fac.meanop

Computes the projection matrix that produces means.

proj2.eigen

Canonical efficiency factors and eigenvectors in joint decomposition of two projectors.

proj2.efficiency

Computes the canonical efficiency factors for the joint decomposition of two projectors.

proj2.combine

Compute the projection and Residual operators for two, possibly nonorthogonal, projectors.

show-methods

Methods for Function 'show' in Package dae

(vii) Miscellaneous functions

eextab

Expands the values in table to a vector.

get.daeTolerance

Gets the value of daeTolerance for the package dae.

harmonic.mean

Calculates the harmonic mean.

is.allzero

Tests whether all elements are approximately zero.

rep.data.frame

Replicate the rows of a data.frame by repeating each row consecutively and/or repeating all rows as a group.

rmvnorm

Generates a vector of random values from a multivariate normal distribution.

set.daeTolerance

Sets the value of daeTolerance for the package dae.

Author(s)

NA

Maintainer: NA
Coerces a `pstructure.object` to a `data.frame`.

Description

Coerces a `pstructure.object`, which is of class `pstructure`, to a `data.frame`. One can choose whether or not to include the marginality matrix in the `data.frame`. The aliasing component is excluded.

Usage

```r
## S3 method for class 'pstructure'
as.data.frame(x, row.names = NULL, optional = FALSE, ...,
               omit.marginality = FALSE)
```

Arguments

- `x`  
  The `pstructure.object`, which is of class `pstructure` and is to be coerced.

- `row.names`  
  NULL or a character vector giving the row names for the `data.frame`. Missing values are not allowed.

- `optional`  
  A logical passed to `as.data.frame`. If TRUE, setting row names and converting column names (to syntactic names: see `make.names`) is optional. Note that all of R’s base package `as.data.frame()` methods use `optional` only for column names treatment, basically with the meaning of `data.frame(*, check.names = !optional)`.

- `...`  
  Further arguments passed to or from other methods.

- `omit.marginality`  
  A logical, which, if TRUE, results in the marginality matrix being omitted from the `data.frame`.

Value

A `data.frame` with as many rows as there are non-aliased terms in the `pstructure.object`. The columns are `df`, `terms`, `sources` and, if `omit.marginality` is FALSE, the columns of the generated levels with columns of the marginality matrix that is stored in the marginality component of the object.

Author(s)

Chris Brien

See Also

`as.data.frame`. 
Examples

## Generate a data.frame with 4 factors, each with three levels, in standard order
ABCD.lay <- fac.gen(list(A = 3, B = 3, C = 3, D = 3))

## create a pstructure object based on the formula ((A*B)/C)*D
ABCD.struct <- pstructure.formula(~ ((A*B)/C)*D, data = ABCD.lay)

## print the object either using the Method function or the generic function
ABCS.dat <- as.data.frame.pstructure(ABCD.struct)
as.data.frame(ABCD.struct)

---

as.numfac

Convert a factor to a numeric vector

Description

Converts a factor to a numeric vector with approximately the numeric values of its levels. Hence, the levels of the factor must be numeric values, stored as characters. It uses the method described in factor. Use as.numeric to convert a factor to a numeric vector with integers 1, 2, ... corresponding to the positions in the list of levels. You can also use fac.recast to recode the levels to numeric values. If a numeric is supplied, it is left unchanged.

Usage

as.numfac(factor)

Arguments

factor

The factor to be converted.

Value

A numeric vector. An NA will be stored for any value of the factor whose level is not a number.

Author(s)

Chris Brien

See Also

as.numeric, fac.recast in package dae, factor.

Examples

## set up a factor and convert it to a numeric vector
a <- factor(rep(1:3, 4))
x <- as.numfac(a)
BIBDWheat.dat

Data for a balanced incomplete block experiment

Description

The data set comes from Joshi (1987) and is the data from an experiment to investigate six varieties of wheat that employs a balanced incomplete block design (BIBD) with ten blocks, each consisting of three plots. For more details see the vignette accessed via vignette("DesignNotes", package="dae").

Usage

data(BIBDWheat.dat)

Format

A data.frame containing 30 observations of 4 variables.

Source


blockboundaryPlot

This function plots a block boundary on a plot produced by designPlot.

Description

This function plots a block boundary on a plot produced by designPlot. It allows control of the starting unit, through rstart and cstart, and the number of rows (nrows) and columns (ncolumns) from the starting unit that the blocks to be plotted are to cover.

Usage

blockboundaryPlot(blockdefinition = NULL, blocksequence = FALSE, rstart= 0, cstart = 0, nrows, ncolumns, blocklinecolour = 1, blocklinewidth = 2)

Arguments

blockdefinition

A matrix of block sizes:

• if there is only one row, then the first element is interpreted as the no. rows in each block and blocks with this number of rows are to be repeated across the rows of the design.

• if there is more than one row, then each row of the matrix specifies a block, with the sequence of rows in the matrix specifying a corresponding sequence of blocks down the rows of the design.
Similarly, a single value for a column specifies a repetition of blocks of that size across the columns of the design, while several column values specifies a sequence of blocks across the columns of the size specified.

**blocksequence**  
A **logical** that determines whether block numbers are repetitions or sequences of block numbers.

**rstart**  
A **numeric** specifying the row after which the plotting of block boundaries is to start.

**cstart**  
A **numeric** specifying the column after which the plotting of block boundaries is to start.

**nrows**  
A **numeric** the number of rows (nrows), from the starting unit, that the blocks to be plotted are to cover.

**ncolumns**  
A **numeric** the number of columns (ncolumns), from the starting unit, that the blocks to be plotted are to cover.

**blocklinecolour**  
A **character** string specifying the colour of the block boundary.  
See Colour specification under the **par** function.

**blocklinewidth**  
A **numeric** giving the width of the block boundary to be plotted.

**Value**

No values are returned, but modifications are made to the currently active plot.

**Author(s)**

Chris Brien

**See Also**

designPlot, par, DiGGer

**Examples**

```r
## Not run:
SPL.Lines.mat <- matrix(as.numfac(Lines), ncol=16, byrow=T)
colnames(SPL.Lines.mat) <- 1:16
rownames(SPL.Lines.mat) <- 1:10
SPL.Lines.mat <- SPL.Lines.mat[10:1, 1:16]
designPlot(SPL.Lines.mat, labels=1:10, new=TRUE,
  rtitle="Rows", ctitle="Columns",
  chardivisor=3, rcellpropn = 1, ccellpropn=1, plotcellboundary = TRUE)
#Plot Mainplot boundaries
blockboundaryPlot(blockdefinition = cbind(4,16), rstart = 1,
  blocklinewidth = 3, blockcolour = "green",
  nrows = 9, ncolumns = 16)
blockboundaryPlot(blockdefinition = cbind(1,4),
  blocklinewidth = 3, blockcolour = "green",
  nrows = 1, ncolumns = 16)
blockboundaryPlot(blockdefinition = cbind(1,4), rstart= 9, nrows = 10, ncolumns = 16,
  blocklinewidth = 3, blockcolour = "green")
#Plot all 4 block boundaries
blockboundaryPlot(blockdefinition = cbind(8,5,5,4), blocksequence=T,
  cstart = 1, rstart= 1, nrows = 9, ncolumns = 15,
```

Cabinet1.des

A design for one of the growth cabinets in an experiment with 50 lines and 4 harvests

Description
The systematic design for a lattice square for 49 treatments consisting of four 7 x 7 squares. For more details see the vignette daeDesignNotes.pdf.

Usage
data(Cabinet1.des)

Format
A data.frame containing 160 observations of 15 variables.

Casuarina.dat

Data for an experiment with rows and columns from Williams (2002)

Description
Williams (2002, p.144) provides an example of a resolved, Latinized, row-column design with four rectangles (blocks) each of six rows by ten columns. The experiment investigated differences between 60 provenances of a species of Casuarina tree, these provenances coming from 18 countries; the trees were inoculated prior to planting at two different times, time of inoculation being assigned to the four replicates so that each occurred in two replicates. At 30 months, diameter at breast height (Dbh) was measured. For more details see the vignette accessed via vignette("DesignNotes", package="dae").

Usage
data(Casuarina.dat)

Format
A data.frame containing 240 observations of 7 variables.
correct.degfree

Check the degrees of freedom in an object of class projector

Description

Check the degrees of freedom in an object of class "projector".

Usage

correct.degfree(object)

Arguments

object An object of class "projector" whose degrees of freedom are to be checked.

Details

The degrees of freedom of the projector are obtained as its number of nonzero eigenvalues. An eigenvalue is regarded as zero if it is less than daeTolerance, which is initially set to Machine$double.eps^0.5 (about 1.5E-08). The function set.daeTolerance can be used to change daeTolerance.

Value

TRUE or FALSE depending on whether the correct degrees of freedom have been stored in the object of class "projector".

Author(s)

Chris Brien

See Also

degfree, projector in package dae.
projector for further information about this class.

Examples

## set up a 2 x 2 mean operator that takes the mean of a vector of 2 values
m <- matrix(rep(0.5,4), nrow=2)

## create a projector based on the matrix m
proj.m <- new("projector", data=m)

## add its degrees of freedom
degfree(proj.m) <- 1

## check degrees of freedom are correct
correct.degfree(proj.m)
**Deprecation Functions in Package dae**

**Description**

These functions have been renamed and deprecated in dae.

**Usage**

- `Ameasures(...)`
- `blockboundary.plot(...)`
- `design.plot(...)`
- `proj2.decomp(...)`
- `proj2.ops(...)`
- `projs.cannon(...)`
- `projs.structure(...)`

**Arguments**

... absorbs arguments passed from the old functions of the style foo.bar().

**Author(s)**

Chris Brien

---

**daeTips**

*The intermittent, randomly-presented, startup tips.*

**Description**

The intermittent, randomly-presented, startup tips.

**Startup tips**

Need help? Enter `help(package = 'dae')` and click on 'User guides, package vignettes and other docs'.

Need help? The manual is in the doc subdirectory of the package’s install directory.

Find out what has changed in dae: enter `news(package = 'dae')`.

Need help to produce randomized designs? Enter `vignette('DesignNotes', package = 'dae')`.

Need help to do the canonical analysis of a design? Enter `vignette('DesignNotes', package = 'dae')`.

Use `suppressPackageStartupMessages()` to eliminate all package startup messages.

To see all the intermittent, randomly-presented, startup tips enter `?daeTips`.

For versions between CRAN releases (and more) go to [http://chris.brien.name/rpackages](http://chris.brien.name/rpackages).

**Author(s)**

Chris Brien
decomp.relate  \hspace{1cm} Examines the relationship between the eigenvectors for two decompositions

Description

Two decompositions produced by \texttt{proj2.eigen} are compared by computing all pairs of crossproduct sums of eigenvectors from the two decompositions. It is most useful when the calls to \texttt{proj2.eigen} have the same \texttt{Q1}.

Usage

\begin{verbatim}
decomp.relate(decomp1, decomp2)
\end{verbatim}

Arguments

- \texttt{decomp1} A list containing components efficiencies and eigenvectors such as is produced by \texttt{proj2.eigen}.
- \texttt{decomp2} Another list containing components efficiencies and eigenvectors such as is produced by \texttt{proj2.eigen}.

Details

Each element of the \(r1 \times r2\) matrix is the sum of crossproducts of a pair of eigenvectors, one from each of the two decompositions. A sum is regarded as zero if it is less than \texttt{daeTolerance}, which is initially set to \(\text{.Machine}\$\text{double.eps}^{0.5}\) (about 1.5E-08). The function \texttt{set.daeTolerance} can be used to change \texttt{daeTolerance}.

Value

A matrix that is \(r1 \times r2\) where \(r1\) and \(r2\) are the numbers of efficiencies of \texttt{decomp1} and \texttt{decomp2}, respectively. The rownames and columnnames of the matrix are the values of the efficiency factors from \texttt{decomp1} and \texttt{decomp2}, respectively.

Author(s)

Chris Brien

See Also

\texttt{proj2.eigen}, \texttt{proj2.combine} in package \texttt{dae}, \texttt{eigen}.

Examples

\begin{verbatim}
## PBIBD(2) from p. 379 of Cochran and Cox (1957) Experimental Designs.  
## 2nd edn Wiley, New York
PBIBD2.unit <- list(Block = 6, Unit = 4)
PBIBD2.nest <- list(Unit = "Block")
trt <- factor(c(1,4,2,5, 2,5,3,6, 3,6,1,4, 4,1,5,2, 5,2,6,3, 6,3,4,1))
PBIBD2.lay <- designRandomize(allocated = trt, 
                         recipient = PBIBD2.unit,  
                         nested.recipients = PBIBD2.nest)
\end{verbatim}
## obtain sets of projectors
unit.struct <- pstructure(~ Block/Unit, data = PBIB2.lay)
trt.struct <- pstructure(~ trt, data = PBIB2.lay)

## obtain intra- and inter-block decompositions
decom.inter <- proj2.eigen(unit.struct$Q["Block"], trt.struct$Q["trt"])
decom.intra <- proj2.eigen(unit.struct$Q["Unit[Block]"], trt.struct$Q["trt"])

## check that intra- and inter-block decompositions are orthogonal
decomp.relate(decom.intra, decom.inter)

---

degfree

**Degrees of freedom extraction and replacement**

### Description

Extracts the degrees of freedom from or replaces them in an object of class "projector".

### Usage

```r
degfree(object)
degfree(object) <- value
```

### Arguments

- **object**
  - An object of class "projector" whose degrees of freedom are to be extracted or replaced.

- **value**
  - An integer to which the degrees of freedom are to be set or an object of class "projector" or "matrix" from which the degrees of freedom are to be calculated.

### Details

There is no checking of the correctness of the degrees of freedom, either already stored or as a supplied integer value. This can be done using `correct.degfree`.

When the degrees of freedom of the projector are to be calculated, they are obtained as the number of nonzero eigenvalues. An eigenvalue is regarded as zero if it is less than `daeTolerance`, which is initially set to `.Machine$double.eps ^ 0.5` (about 1.5E-08). The function `set.daeTolerance` can be used to change `daeTolerance`.

### Value

An object of class "projector" that consists of a square, symmetric, idempotent matrix and degrees of freedom (rank) of the matrix.

### Author(s)

Chris Brien

### See Also

- `correct.degfree`, `projector` in package `dae`.
- `projector` for further information about this class.
Examples

```r
## set up a 2 x 2 mean operator that takes the mean of a vector of 2 values
m <- matrix(rep(0.5,4), nrow=2)

## coerce to a projector
proj.m <- projector(m)

## extract its degrees of freedom
degfree(proj.m)

## create a projector based on the matrix m
proj.m <- new("projector", data=m)

## add its degrees of freedom and print the projector
degfree(proj.m) <- proj.m
print(proj.m)
```

designAmeasures

Calculates the average variance of pairwise differences from the variance matrix for predictions

**Description**

Calculates the average variance of pairwise differences between, or of elementary contrasts of, predictions using the variance matrix for the predictions. The weighted average variance of pairwise differences can be computed from a vector of replications, as described by Williams and Piepho (2015). It is possible to compute either A-optimality measure for different subgroups of the predictions. If groups are specified then the A-optimality measures are calculated for the differences between predictions within each group and for those between predictions from different groups. If groupsizes are specified, but groups are not, the predictions will be sequentially broken into groups of the size specified by the elements of groupsizes. The groups can be named.

**Usage**

```r
designAmeasures(Vpred, replications = NULL, groupsizes = NULL, groups = NULL)
```

**Arguments**

- **Vpred**: The variance matrix of the predictions. It can be obtained using `mat.Vpredicts`.
- **replications**: A numeric vector whose length is equal to the number of rows (columns) in `Vpred` and whose elements are to be used to calculate weights for each pair of differences.
- **groupsizes**: A numeric containing group sizes. The sum of the elements of groupsizes must be less than or equal to the order of `Vpred`. If groupsizes is a named vector, the names are used to label the groups. If `NULL`, either groups is used or the average for all pairwise differences is obtained.
- **groups**: A list, each element of which is a numeric, vector with integers that specify the subgroup of the predictions over whose pairwise differences the variances are to be averaged. If there is more than one group, the variances of all between and within group pairwise differences are averaged. If the elements of groups are named, the names are used to label the groups. If `groups` is `NULL`, either groupsizes is used or the average for all pairwise differences is obtained.
The variance matrix of pairwise differences is calculated as \( v_{ii} + v_{jj} - 2v_{ij} \), where \( v_{ij} \) is the element from the \( i \)th row and \( j \)th column of \( V_{\text{pred}} \). If replication is not NULL then weights are computed as \( r_i \times r_j / \text{mean}(r) \), where \( r \) is the replication vector and \( r_i \) and \( r_j \) are elements of \( r \). The \((i,j)\) element of the variance matrix of pairwise differences is multiplied by the \((i,j)\)th weight. Then the mean of the variances of the pairwise differences is computed for the nominated groups.

### Value

A matrix containing the within and between group A-optimality measures.

### Author(s)

Chris Brien

### References


### See Also

`mat.Vpred`, `designAnatomy`.

### Examples

```r
## Reduced example from Smith et al. (2015)
## Generate two-phase design
mill.fac <- fac.gen(list(Mrep = 2, Mday = 2, Mord = 3))
field.lay <- fac.gen(list(Frep = 2, Fplot = 4))
field.lay$Variety <- factor(c("D","E","Y","W","G","D","E","M"),
                            levels = c("Y","W","G","M","D","E"))
start.design <- cbind(mill.fac, field.lay[c(3,4,5,8,1,7,3,4,5,8,6,2),])
rownames(start.design) <- NULL

## Set up matrices
n <- nrow(start.design)
W <- model.matrix(~ -1+ Variety, start.design)
ng <- ncol(W)
Gg <- diag(1, ng)
Vu <- with(start.design, fac.vcmat(Mrep, 0.3) +
          fac.vcmat(fac.combine(list(Mrep, Mday)), 0.2) +
          fac.vcmat(Frep, 0.1) +
          fac.vcmat(fac.combine(list(Frep, Fplot)), 0.2))
R <- diag(1, n)

## Calculate the variance matrix of the predicted random Variety effects
Vp <- mat.Vpred(W = W, Gg = Gg, Vu = Vu, R = R)

## Calculate A-optimality measure
designAmeasures(Vp)
designAmeasures(Vp, groups=list(fldUndup = c(1:4), fldDup = c(5,6)))
```
designAnatomy<-c(4,2)
names(grpsizes)<-c("fldUndup","fldDup")
designAmeasures(Vp,grpsizes=grpsizes)
designAmeasures(Vp,grpsizes=c(4))
designAmeasures(Vp,groups=list(c(1,4),c(5,6)))

## Calculate the variance matrix of the predicted fixed Variety effects, eliminating the grand mean
Vp.reduc<-mat.Vpred(W=W,Gg=0,Vu=Vu,R=R,
eliminate=projector(matrix(1,nrow=n,ncol=n)/n))
## Calculate A-optimality measure
designAmeasures(Vp.reduc)

designAnatomy

Given the layout for a design, obtain its anatomy via the canonical analysis of its projectors to show the confounding and aliasing inherent in the design.

Description

Computes the canonical efficiency factors for the joint decomposition of two or more structures or sets of mutually orthogonally projectors (Brien and Bailey, 2009; Brien, 2017; Brien, 2019), orthogonalizing projectors in a set to those earlier in the set of projectors with which they are partially aliased. The results can be summarized in the form of a decomposition table that shows the confounding between sources from different sets. For examples of the function’s use also see the vignette accessed via vignette("DesignNotes",package="dae") and for a discussion of its use see Brien, Sermarini and Demetro (2023).

Usage

designAnatomy(formulae,data,keep.order=TRUE,grandMean=FALSE,
orthogonalize="hybrid",labels="sources",
marginality=NULL,check.marginality=TRUE,
which.criteria=c("aefficiency","eefficiency","order"),
aliasing.print=FALSE,
omit.projectors=c("pcanon","combined"),...)

Arguments

formulae An object of class list whose components are of class formula. Usually, the terms in a single formula have the same status in the allocation of factors in the design. For example, all involve only factors that were allocated, or all involve factors that were recipients of allocated factors. The names of the components are used to identify the sources in the summary.pcanon object. They will also be used to name the terms, sources and marginality lists in the pcanon.object.
data A data.frame contains the values of the factors and variables that occur in formulae.
keep.order A logical indicating whether the terms should keep their position in the expanded formula projector, or reordered so that main effects precede two-factor interactions, which precede three-factor interactions and so on.
**grandMean**  
A **logical** indicating whether the projector for the grand mean is to be included for each structure.

**orthogonalize**  
A **character** vector indicating the method for orthogonalizing a projector to those for terms that occurred previously in a single formula. Three options are available: hybrid; differencing; eigenmethods. The hybrid option is the most general and uses the relationships between the projection operators for the terms in the formula to decide which projectors to substract and which to orthogonalize using eigenmethods. The differencing option subtructs, from the current projector, those previously orthogonalized projectors for terms whose factors are a subset of the current projector’s factors. The eigenmethods option recursively orthogonalizes the projects using an eigenanalysis of each projector with previously orthogonlized projectors. If a single value is given, it is used for all formulae.

**labels**  
A **character** nominating the type of labels to be used in labelling the projectors, and which will be used also in the output tables, such the tables of the aliasing in the structure. The two alternatives are **terms** and **sources**. Terms have all factors/variables in it separated by colons (:). Sources have factors/variables in them that represent interactions separated by hashes (#); if some factors are nested within others, the nesting factors are surrounded by square brackets ([ and ]) and separated by colons (:). If some generalized, or combined, factors have no marginal terms, the constituent factors are separated by colons (:) and if they interact with other factors in the source they will be parenthesized.

**marginality**  
A **list** that can be used to supply some or all of the marginality matrices when it is desired to overwrite calculated marginality matrices or when they are not calculated. If the **list** is the same length as the formulae **list**, they will be associated in parallel with the components of formulae, irrespective of the naming of the two **lists**. If the number of components in marginality is less than the number of components in formulae then both lists must be named so that those in the marginality **list** can be matched with those in the formulae **list**.

Each component of the marginality **list** must be either **NULL** or a square **matrix** consisting of zeroes and ones that gives the marginalites of the terms in the formula. It must have the row and column names set to the terms from the expanded formula, including being in the same order as these terms. The entry in the ith row and jth column will be one if the ith term is marginal to the jth term i.e. the column space of the ith term is a subspace of that for the jth term and so the source for the jth term is to be made orthogonal to that for the ith term. Otherwise, the entries are zero. A row and column should not be included for the grand mean even if grandMean is TRUE.

**check.marginality**  
A **logical** indicating whether the marginality matrix, when it is supplied, is to be checked against that computed by **pstructure.formula**. It is ignored when orthogonalize is set to eigenmethods.

**which.criteria**  
A **character** vector nominating the efficiency criteria to be included in the summary of aliasing between terms within a structure. It can be none, all or some combination of aefficiency, mefficiency, sefficiency, eefficiency, xefficiency, order and dforthog – for details see **efficiency.criteria**. If none, no summary is printed.

**aliasing.print**  
A **logical** indicating whether the aliasing between sources is to be printed.

**omit.projectors**  
A **character** vector of the types of projectors to omit from the returned pcanon
object. If pcanon is included in the vector then the projectors in these objects will be replaced with a numeric containing their degrees of freedom. If combined is included in the vector then the projectors for the combined decomposition will be replaced with a numeric containing their degrees of freedom. If none is included in the vector then no projectors will be omitted.

... further arguments passed to terms.

Details

For each formula supplied in formulae, the set of projectors is obtained using pstructure; there is one projector for each term in a formula. Then projs.2canon is used to perform an analysis of the canonical relationships between two sets of projectors for the first two formulae. If there are further formulae, the relationships between its projectors and the already established decomposition is obtained using projs.2canon. The core of the analysis is the determination of eigenvalues of the product of pairs of projectors using the results of James and Wilkinson (1971). However, if the order of balance between two projection matrices is 10 or more or the James and Wilkinson (1971) methods fails to produce an idempotent matrix, equation 5.3 of Payne and Tobias (1992) is used to obtain the projection matrices for their joint decomposition.

Value

A pcano.object.

Author(s)

Chris Brien

References


See Also
designRandomize, designLatinSqrSys, designPlot, pcano.object, p2canon.object, summary.pcano, efficiencies.pcano, pstructure, projs.2canon, proj2.efficiency, proj2.combine, proj2.eigen, efficiency.criteria, in package dae,
eigen.

projector for further information about this class.
Examples

```r
## PBIBD(2) from p. 379 of Cochran and Cox (1957) Experimental Designs.
## 2nd edn Wiley, New York
PBIBD2.unit <- list(Block = 6, Unit = 4)
PBiBD2.nest <- list(Unit = "Block")
trt <- factor(c(1,4,2,5, 2,5,3,6, 3,6,1,4, 4,1,5,2, 5,2,6,3, 6,3,4,1))
PBiBD2.lay <- designRandomize(allocated = trt,
                          recipient = PBIBD2.unit,
                          nested.recipients = PBIBD2.nest)

##obtain combined decomposition and summarize
unit.trt.canon <- designAnatomy(formulae = list(unit=~ Block/Unit, trt=~ trt),
                                data = PBIBD2.lay)
summary(unit.trt.canon, which.criteria = c("aeff","eeff","order"))
summary(unit.trt.canon, which.criteria = c("aeff","eeff","order"), labels.swap = TRUE)

## Three-phase sensory example from Brien and Payne (1999)
## Not run:
data(Sensory3Phase.dat)
Eval.Field.Treat.canon <- designAnatomy(formulae = list(
    eval= ~ ((Occasions/Intervals/Sittings)*Judges)/Positions,
    field= ~ (Rows*(Squares/Columns))/Halfplots,
    treats= ~ Trellis*Method),
    data = Sensory3Phase.dat)
summary(Eval.Field.Treat.canon, which.criteria =c("aefficiency", "order"))

## End(Not run)
```

---

**designBlocksGGPlot**

* Adds block boundaries to a plot produced by *designGGPlot*.

---

**Description**

This function adds block boundaries to a plot produced by *designGGPlot*. It allows control of the starting unit, through `originrow` and `origincolumn`, and the number of rows (`nrows`) and columns (`ncolumns`) from the starting unit that the blocks to be plotted are to cover.

**Usage**

```r
designBlocksGGPlot(ggplot.obj, blockdefinition = NULL, blocksequence = FALSE, originrow= 0, origincolumn = 0, nrows, ncolumns, blocklinecolour = "blue", blocklinesize = 2, facetstrips.placement = "inside", printPlot = TRUE)
```

**Arguments**

- `ggplot.obj` An object produced by `ggplot`.
- `blockdefinition` A *matrix* of block sizes:
  - if there is only one row, then the first element is interpreted as the no. rows in each block and blocks with this number of rows are to be repeated across the rows of the design.
• if there is more than one row, then each row of the matrix specifies a block, with the sequence of rows in the matrix specifying a corresponding sequence of blocks down the rows of the design.

Similarly, a single value for a column specifies a repetition of blocks of that size across the columns of the design, while several column values specifies a sequence of blocks across the columns of the size specified.

blocksequence A logical that determines whether block numbers are repetitions or sequences of block numbers.

originrow A numeric specifying the row after which the plotting of block boundaries is to start.

origincolumn A numeric specifying the column after which the plotting of block boundaries is to start.

nrows A numeric the number of rows (nrows), from the starting unit, that the blocks to be plotted are to cover.

ncolumns A numeric the number of columns (ncolumns), from the starting unit, that the blocks to be plotted are to cover.

blocklinecolour A character string specifying the colour of the block boundary. See Colour specification under the par function.

blocklinesize A numeric giving the width of the block boundary to be plotted.

facetstrips.placement A character nominating where the strip is to be placed with respect to axes text and titles, either "inside" both text and titles, "outside.text" or "outside.title". This argument is important only when axes and strips are on the same side of the plot. When this occurs, the default is to place them inside the axis text. Note: This argument must be specified only once in the construction of the plot and after every other aspect of the plot has been finalized. In particular, if designBlocksGGPlot is to called after designGGPlot to add block boundaries, then facetstrips.placement should be specified in the last call to designBlocksGGPlot, not in the call to designGGPlot.

printPlot A logical indicating whether to print the plot after adding the block boundaries.

Value

An object of class 'ggplot', formed by adding to the input ggplot.obj and which can be plotted using print.

Author(s)

Chris Brien

Source


See Also

designGGPlot, par, DiGger
Examples

## Construct a randomized layout for the split-unit design described by
## Brien et al. (2011, Section 5)

```r
split.sys <- cbind(fac.gen(list(Months = 4, Athletes = 3, Tests = 3)),
                   fac.gen(list(Intensities = LETTERS[1:3], Surfaces = 3),
                           times = 4))

split.lay <- designRandomize(allocated = split.sys[c("Intensities", "Surfaces")],
                              recipient = split.sys[c("Months", "Athletes", "Tests")],
                              nested.recipients = list(Athletes = "Months",
                                          Tests = c("Months", "Athletes")),
                              seed = 2598)
```

## Plot the design

```r
cell.colours <- c("lightblue", "lightcoral", "lightgoldenrod", "lightgreen", "lightgrey",
                  "lightpink", "lightsalmon", "lightcyan", "lightyellow", "lightseagreen")

split.lay <- within(split.lay,
                    Treatments <- fac.combine(list(Intensities, Surfaces),
                                               combine.levels = TRUE))

plt <- designGGPlot(split.lay, labels = "Treatments",
                    row.factors = "Tests", column.factors = c("Months", "Athletes"),
                    colour.values = cell.colours[1:9], label.size = 6,
                    blockdefinition = rbind(c(3,1)), blocklinecolour = "darkgreen",
                    printPlot = FALSE)
```

## A layout for a growth cabinet experiment that allows for edge effects

```r
data(Cabinet1.des)

plt <- designGGPlot(Cabinet1.des, labels = "Combinations", cellalpha = 0.75,
                   title = "Lines and Harvests allocation for Cabinet 1",
                   printPlot = FALSE)
```

## Plot Mainplot boundaries

```r
plt <- designBlocksGGPlot(plt, ncolumns = 16, blockdefinition = cbind(4,16),
                                      originrow= 1, blocklinecolour = "green",
                                      nrows = 16, printPlot = FALSE)
plt <- designBlocksGGPlot(plt, ncolumns = 16, blockdefinition = cbind(1,4),
                                      blocklinecolour = "green", nrows = 16,
                                      printPlot = FALSE)
plt <- designBlocksGGPlot(plt, ncolumns = 16, blockdefinition = cbind(1,4),
                                      originrow= 1, blocklinecolour = "green",
                                      nrow = 16, printPlot = FALSE)
```

## Plot all 4 block boundaries

```r
plt <- designBlocksGGPlot(plt, blocksequence = TRUE, blockdefinition = cbind(8,5,5,4),
                                      blocklinecolour = "blue", nrows = 15, ncolumns = 15,
                                      printPlot = FALSE)
plt <- designBlocksGGPlot(plt, blockdefinition = cbind(10,16),
                                      blocklinecolour = "blue", nrows = 16, ncolumns = 16,
                                      printPlot = FALSE)
```

## Plot border and internal block boundaries only

```r
plt <- designBlocksGGPlot(plt, blockdefinition = cbind(8,14), originrow= 1,
                                      blocklinecolour = "blue", nrows = 9, ncolumns = 15,
                                      printPlot = FALSE)
```
designGGPlot

Plots labels on two-way grids of coloured cells using ggplot2 to represent an experimental design

Description

Plots the labels in a grid of cells specified by row.factors and column.factors. The cells can be coloured by the values of the column specified by column.name and can be divided into facets by specifying multiple row and or column factors.

Usage

```r
designGGPlot(design, labels = NULL, label.size = NULL, row.factors = "Rows", column.factors = "Columns", scales.free = "free", facetstrips.switch = NULL, facetstrips.placement = "inside", cellfillcolour.column = NULL, colour.values = NULL, cellalpha = 1, celllinetype = "solid", celllinesize = 0.5, celllinecolour = "black", cellheight = 1, cellwidth = 1, reverse.x = FALSE, reverse.y = TRUE, x.axis.position = "top", xlab, ylab, title, labeller = label_both, title.size = 15, axis.text.size = 15, blocksequence = FALSE, blockdefinition = NULL, blocklinecolour = "blue", blocklinesize = 2, printPlot = TRUE, ggplotFuncs = NULL, ...)
```

Arguments

- `design`: A `data.frame` containing labels, column.factors, row.factors and, if specified, colour.column.
- `labels`: A character giving the name of the column in data containing the labels to be plotted on the grid. If labels is `NULL`, no labels are added.
- `label.size`: A numeric giving the size of the labels.
- `row.factors`: A character giving the names of the factors (or numerics) in data that index the rows of the plot grid used to represent the design. If there is more than one name, then facet_grid is used to facet the plot in the y direction, based on all but the last name. The factor corresponding to the last name will index the rows in each facet.
- `column.factors`: A character giving the names of the factors (or numerics) in data that index the columns of the plot grid used to represent the design. If there is more than one name, then facet_grid is used to facet the plot in the x direction, based on all but the last name. The factor corresponding to the last name will index the columns in each facet.
- `scales.free`: When plots are faceted, a character specifying whether scales are shared across all facets (fixed), or vary across rows (free_x), columns (free_y), or both rows and columns (the default, free). The free_x, free_y and free options may not work when the plot grid is indexed using numerics.
When plots are facetted, the strip text are displayed on the top and right of the plot by default. If `facetstrips.switch` is "x", the top strip text will be switched to the bottom. If "y", the right-hand side labels will be switched to the left. The argument can also be set to "both". The argument `facetstrips.placement` can be used to change the relationship between the strip text and the axis.text and the axis.title.

**A character nominating where the strip is to be placed with respect to axes text and titles, either "inside" both text and titles, "outside.text" or "outside.title".**

This argument is important only when axes and strips are on the same side of the plot. When this occurs, the default is to place them inside the axis text. **Note:** This argument must be specified only once in the construction of the plot and after every other aspect of the plot has been finalized. In particular, if `designBlocksGGPlot` is to called after `designGGPlot` to add block boundaries, then `facetstrips.placement` should be specified in the call to `designBlocksGGPlot`, not in the call to `designGGPlot`.

A logical which, if true, causes the order of values on the x-axis to be reversed, the natural order being to increase from left to right.

A logical which, if true, causes the order of values on the y-axis to be reversed, the natural order being to increase from bottom to top.

A character giving the position of the x-axis; can be top or bottom.

A character giving the name of the column in data that is to be used to vary the colour the used to fill a cell.

A character giving the name or names of the colours to be used in filling the cell. If `cellfillcolour.column` is not NULL then the number of colours specified needs to match the number of unique values in the `cellfillcolour.column`.

A numeric specifying the degree of transparency to be used in cell fill. It is a ratio in which the denominator specifies the number of points (or lines) that must be overplotted to give a solid cover.

A numeric or character giving the type of line for the cell border. An integer or name: 0 = blank, 1 = solid, 2 = dashed, 3 = dotted, 4 = dotdash, 5 = longdash, 6 = twodash. For more information see vignette("ggplot2-specs").

A numeric specifying the size of the line in mm.

A character giving the name of the colour to use for the cell outline.

A numeric specifying the height of a cell.

A numeric specifying the width of of a cell.

Label for the x-axis. By default it is the last name in the `column.factors`.

Label for the y-axis. By default it is the last name in the `row.factors`.

Title for plot window. By default it is "Plot of labels".

A function for specifying the formatting of the strip labels of the facet grids used when there is more than one `row.factors` or `column.factors`. (See `labellers` for ggplot2.)

A numeric giving the size for all titles: `xlab`, `ylab` and `title`.

A numeric giving the size for tick labels.
blocksequence
A logical that determines whether block numbers are repetitions or sequences of block numbers.

blockdefinition
A matrix of block sizes:
- if there is only one row, then the first element is interpreted as the no. rows in each block and blocks with this number of rows are to be repeated across the rows of the design.
- if there is more than one row, then each row of the matrix specifies a block, with the sequence of rows in the matrix specifying a corresponding sequence of blocks down the rows of the design.

Similarly, a single value for a column specifies a repetition of blocks of that size across the columns of the design, while several column values specifies a sequence of blocks across the columns of the size specified.

blocklinecolour
A character string specifying the colour of the block boundary. See also the scale_colour_* functions or Colour specification under the par function.

blocklinesize
A numeric giving the width of the block boundary to be plotted.

printPlot
A logical indicating whether to print the plot produced.

ggplotFuncs
A list, each element of which contains the results of evaluating a ggplot function. It is created by calling the list function with a ggplot function call for each element. These functions are applied in creating the ggplot object.

... Other arguments that are passed down to the geom_text call that plots the labels.

Value
An object of class "ggplot", which can be plotted using print.

Author(s)
Chris Brien

See Also
designBlocksGGPlot, fac.combine in package dae, designPlot.

Examples

```r
#### Plot a randomized complete block design
Treatments <- factor(rep(1:6, times = 5))
RCBD.lay <- designRandomize(allocated = Treatments,
                           recipient = list(Blocks = 5, Units = 6),
                           nested.recipients = list(Units = "Blocks"),
                           seed = 74111)
designGGPlot(RCBD.lay, labels = "Treatments", label.size = 5,
             row.factors = "Blocks", column.factors = "Units",
             blockdefinition = cbind(1,5))

## Plot without labels
designGGPlot(RCBD.lay, cellfillcolour.column = "Treatments",
             row.factors = "Blocks", column.factors = "Units",
             ...)
designLatinSqrSys

Generate a systematic plan for a Latin Square design

Description

Generates a systematic plan for a Latin Square design using the method of cycling the integers 1 to the number of treatments. The start of the cycle for each row, or the first column, can be specified as a vector of integers.

Usage

designLatinSqrSys(order, start = NULL)

Arguments

order The number of treatments.

start A numeric containing order unique values between one and order. These are interpreted as the value for the first column for each row. If NULL, 1:order is used.

Value

A numeric containing order x order integers between 1 and order such that, when the numeric is considered as a square matrix of size order, each integer occurs once and only once in each row and column of the matrix.

See Also

designRandomize, designPlot, designAnatomy in package dae.

Examples

matrix(designLatinSqrSys(5, start = c(seq(1, 5, 2), seq(2, 5, 2))), nrow=5)
designLatinSqrSys(3)
designPlot

A graphical representation of an experimental design using labels stored in a matrix.

Description

This function uses labels, usually derived from treatment and blocking factors from an experimental design and stored in a matrix, to build a graphical representation of the matrix, highlighting the position of certain labels. It is a modified version of the function supplied with DiGGer. It includes more control over the labelling of the rows and columns of the design and allows for more flexible plotting of designs with unequal block size.

Usage

```
  designPlot(designMatrix, labels = NULL, altlabels = NULL, plotlabels = TRUE, 
             rtitle = NULL, ctitle = NULL, 
             rlabelsreverse = FALSE, clabelsreverse = FALSE, 
             font = 1, chardivisor = 2, rchardivisor = 1, 
             cchardivisor = 1, 
             cellfillcolour = NA, plotcellboundary = TRUE, 
             rcellpropn = 1, ccellpropn = 1, 
             blocksequence = FALSE, blockdefinition = NULL, 
             blocklinecolour = 1, blocklinewidth = 2, 
             rotate = FALSE, new = TRUE, ...)
```

Arguments

- `designMatrix` A matrix containing a set of numerics or characters being the labels as they have been assigned to the cells of the grid represented by the matrix.
- `labels` A numeric or character vector giving the cells in `designMatrix` that are to be plotted in this call to `designPlot`. If NULL then all the cells are plotted. What is actually plotted for a cell is controlled jointly by `labels`, `plotlabels`, `altlabels`, `plotcellboundary` and `cellfillcolour`. If `plotlabels` is TRUE and `altlabels` is NULL then labels are plotted in the cells, unless `labels` is NULL when the labels in `designMatrix` are plotted. Whatever is being plotted, `altlabels` and `cellfillcolour` must have an appropriate number of values. See text for more information on specifying the labels.
- `altlabels` Either a character vector containing an alternative set of labels for the labels currently being plotted or a single integer specifying an alternative symbol to be used in plotting cells when `plotlabels` is TRUE. The length of `altlabels` must be one or the same length as `labels`, unless `labels` is NULL in which case it must equal the number of unique labels in `designMatrix`. If `altlabels` is NULL, the labels specified in `labels` are plotted when `plotlabels` is TRUE. If `labels` is also NULL, the labels in `designMatrix` are plotted. See text for more information on specifying the labels.
- `plotlabels` A logical to indicate whether labels are to be plotted in the cells. If TRUE, print all labels or the specific labels listed in `labels`. If FALSE, no labels are printed in the cells.
- `rtitle` A character string to use as a title for rows of the plot. If `rtitle` is NULL then no title is plotted.
**designPlot**

A function to plot a design matrix as a table, with options for customizing the appearance of the plot.

- **ctitle**: A character string to use as a title for columns of the plot. If `ctitle` is `NULL` then no title is plotted.
- **rlabelsreverse**: A logical indicating whether to reverse the row labels.
- **clabelsreverse**: A logical indicating whether to reverse the column labels.
- **font**: An integer specifying the font to be used for row and column labelling. See `par` for further details.
- **chardivisor**: A numeric that changes the size of text and symbols in the cells by dividing the default size by it.
- **rchardivisor**: A numeric that changes the size of the labels of the rows of the design by dividing the default size by it.
- **cchardivisor**: A numeric that changes the size of the labels of the columns of the design by dividing the default size by it.
- **cellfillcolour**: A character string specifying the colour of the fill for the cells to be plotted in this call. If there is only one colour then all cells being plotted with that colour. If there is more than one colour then, unless `labels` is `NULL`, the number of colours must at least equal the number of labels and then the fill colours will be matched, one for one from the first colour, with the labels. If `labels` is `NULL` then the number of colours must at least equal the number of unique labels in `designMatrix`. The default, `NA`, is to leave their cells unfilled. See also Colour specification under the `par` function.
- **plotcellboundary**: A logical indicating whether a boundary is to be plotted around a cell.
- **rcellpropn**: A value between 0 and 1 giving the proportion of the standard row size of a cell size to be plotted as a cell.
- **ccellpropn**: A value between 0 and 1 giving the proportion of the standard column size of a cell size to be plotted as a cell.
- **blocksequence**: A logical that determines whether block numbers are repetitions or sequences of block numbers.
- **blockdefinition**: A matrix of block sizes:
  - if there is only one row, then the first element is interpreted as the no. rows in each block and blocks with this number of rows are to be repeated across the rows of the design.
  - if there is more than one row, then each row of the matrix specifies a block, with the sequence of rows in the matrix specifying a corresponding sequence of blocks down the rows of the design.

Similarly, a single value for a column specifies a repetition of blocks of that size across the columns of the design, while several column values specifies a sequence of blocks across the columns of the size specified.

- **blocklinecolour**: A character string specifying the colour of the block boundary. See also Colour specification under the `par` function.
- **blocklinewidth**: A numeric giving the width of the block boundary to be plotted.
- **rotate**: A logical which, if TRUE, results in the matrix being rotated 90 degrees for plotting.
- **new**: A logical indicating if a new plot is to be produced or the current plot is added to.
- **...**: further arguments passed to `polygon` in plotting the cell.
designPlotlabels

Plots labels on a two-way grid using ggplot2

Description

Plots the labels in a grid specified by grid.x and grid.y. The labels can be coloured by the values of the column specified by column.name.

Usage

designPlotlabels(data, labels, grid.x = "Columns", grid.y = "Rows",
                   colour.column=NULL, colour.values=NULL,
                   reverse.x = FALSE, reverse.y = TRUE,
                   xlab, ylab, title, printPlot = TRUE, ggplotFuncs = NULL, ...)
Arguments

data A data.frame containing labels, grid.x, grid.y and, if specified, colour.column.
labels A character giving the name of the column in data containing the labels to be plotted on the grid.
grid.x A character giving the name of the column in data that specifies the x-coordinates of the plot grid.
grid.y A character giving the name of the column in data that specifies the y-coordinates of the plot grid.
reverse.x A logical which, if true, causes the order of values on the x-axis to be reversed.
reverse.y A logical which, if true, causes the order of values on the y-axis to be reversed.
colour.column A character giving the name of the column in data that is to be used to colour the values plotted on the grid.
colour.values A character giving the name of the column in data that is to be used to colour the values plotted on the grid.
xlab Label for the x-axis. By default it is the name of the grid.x.
ylab Label for the y-axis. By default it is the name of the grid.y.
title Title for plot window. By default it is "Plot of labels".
printPlot A logical indicating whether to print the plot.
ggplotFuncs A list, each element of which contains the results of evaluating a ggplot function. It is created by calling the list function with a ggplot function call for each element. These functions are applied in creating the ggplot object.

Value

An object of class "ggplot", which can be plotted using print.

Author(s)

Chris Brien

See Also

fac.combine in package dae, designPlot.

Examples

Treatments <- factor(rep(1:6, times = 5))
RCBD.lay <- designRandomize(allocated = Treatments,
         recipient = list(Blocks = 5, Units = 6),
         nested.recipients = list(Units = "Blocks"),
         seed = 74111)
designPlotlabels(RCBD.lay, labels = "Treatments",
grid.x = "Units", grid.y = "Blocks",
colour.column = "Treatments", size = 5)
designRandomize

Randomize allocated to recipient factors to produce a layout for an experiment

Description

A systematic design is specified by a set of allocated factors that have been assigned to a set of recipient factors. In textbook designs the allocated factors are the treatment factors and the recipient factors are the factors indexing the units. To obtain a randomized layout for a systematic design it is necessary to provide (i) the systematic arrangement of the allocated factors, (ii) a list of the recipient factors or a data.frame with their values, and (iii) the nesting of the recipient factors for the design being randomized. Given this information, the allocated factors will be randomized to the recipient factors, taking into account the nesting between the recipient factors for the design. However, allocated factors that have different values associated with those recipient factors that are in the except vector will remain unchanged from the systematic design.

Also, if allocated is NULL then a random permutation of the recipient factors is produced that is consistent with their nesting as specified by nested.recipients.

For examples of its use also see the vignette accessed via vignette("DesignNotes", package="dae") and for a discussion of its use see Brien, Sermarini and Demetro (2023).

Usage

designRandomize(allocated = NULL, recipient, nested.recipients = NULL, except = NULL, seed = NULL, unit.permutation = FALSE, ...)

Arguments

allocated

A factor or a data.frame containing the systematically allocated values of the factor(s). If NULL, a random permutation of the recipient factors is produced that is consistent with their nesting as specified by nested.recipients.

recipient

A data.frame or a list of factors, along with their levels that specify the set of recipient factors that are allocated levels of the allocated factors. If a list, the name of each component of the list is a factor name and the component is either (i) a single numeric value that is the number of levels, (ii) a numeric vector that contains the levels of the factor, (iii) or a character vector that contains the labels of the levels of the factor. The values of factors will be generated in standard order using fac.gen and so the values in allocated must match this.

nested.recipients

A list of the recipient factors that are nested in other factors in recipient. The name of each component is the name of a factor that is nested and the component is a character vector containing the factors within which it is nested. The randomization is controlled by nested.recipients: nested recipient factors are permuted within those factors that nest them. Only the nesting is specified: it is assumed that if two factors are not nested then they must be crossed. It is emphasized that the nesting is a property of the design that is being employed (it is only partly based on the intrinsic or physical crossing and nesting).
except A character vector containing the names of recipient factors that are to be excepted from the permutation; any allocated factors whose values differ between the levels of the factors in this vector will not have those values randomized.

seed A single numeric value, interpreted as an integer, that specifies the starting value of the random number generator.

unit.permutation A logical indicating whether to include the .Unit and .Permutation columns in the data.frame.

... Further arguments passed to or from other methods. Unused at present.

Details

A systematic design is specified by the matching of the supplied allocated and recipient factors. If recipient is a list then fac.gen is used to generate a data.frame with the combinations of the levels of the recipient factors in standard order. Although, the data.frames are not combined at this stage, the systematic design is the combination, by columns, of the values of the allocated factors with the values of recipient factors in the recipient data.frame.

The method of randomization described by Bailey (1981) is used to randomize the allocated factors to the recipient factors. That is, a permutation of the recipient factors is obtained that respects the nesting for the design, but does not permute any of the factors in the except vector. A permutation is generated for all combinations of the recipient factors, except that a nested factor, specified using the nested.recipients argument, cannot occur in a combination without its nesting factor(s). These permutations are combined into a single, units permutation that is applied to the recipient factors. Then the data.frame containing the permuted recipient factors and that containing the unpermuted allocated factors are combined columnwise, as in cbind. To produce the randomized layout, the rows of the combined data.frame are reordered so that its recipient factors are in either standard order or, if a data.frame was supplied to recipient, the same order as for the supplied data.frame.

The .Units and .Permutation vectors enable one to swap between this combined, units permutation and the randomized layout. The $i$th value in .Permutation gives the unit to which unit $i$ was assigned in the randomization.

Value

A data.frame with the values for the recipient and allocated factors that specify the layout for the experiment and, if unit.permutation is TRUE, the values for .Units and .Permutation vectors.

Author(s)

Chris Brien

References


See Also

fac.gen, designLatinSqrSys, designPlot, designAnatomy in package dae.
Examples

```r
## Generate a randomized layout for a 4 x 4 Latin square
## (the nested.recipients argument is not needed here as none of the
## factors are nested)
## Firstly, generate a systematic layout
LS.sys <- cbind(fac.gen(list(row = c("I","II","III","IV"),
col = c(0,2,4,6))),
treat = factor(designLatinSqrSys(4), label = LETTERS[1:4]))
## obtain randomized layout
LS.lay <- designRandomize(allocated = LS.sys["treat"],
recipient = LS.sys[c("row","col")],
seed = 7197132, unit.permutation = TRUE)
LS.lay[LS.lay$.Permutation,]

## Generate a randomized layout for a replicated randomized complete
## block design, with the block factors arranged in standard order for
## rep then plot and then block
## Firstly, generate a systematic order such that levels of the
## treatment factor coincide with plot
RCBD.sys <- cbind(fac.gen(list(rep = 2, plot=1:3, block = c("I","II"))),
tr = factor(rep(1:3, each=2, times=2)))
## obtain randomized layout
RCBD.lay <- designRandomize(allocated = RCBD.sys["tr"],
recipient = RCBD.sys[c("rep", "block", "plot")],
nested.recipients = list(plot = c("block","rep"),
block="rep"),
seed = 9719532,
unit.permutation = TRUE)
RCBD.perm <- RCBD.lay[RCBD.lay$.Permutation,,]
RCBD.lay <- RCBD.perm[order(RCBD.perm$.Units),]

## Generate a layout for a split-unit experiment in which:
## - the main-unit factor is A with 4 levels arranged in
## a randomized complete block design with 2 blocks;
## - the split-unit factor is B with 3 levels.
## Firstly, generate a systematic layout
SPL.sys <- cbind(fac.gen(list(block = 2, main.unit = 4, split.unit = 3)),
fac.gen(list(A = 4, B = 3), times = 2))
## obtain randomized layout
SPL.lay <- designRandomize(allocated = SPL.sys["A","B"],
recipient = SPL.sys[c("block", "main.unit", "split.unit")],
nested.recipients = list(main.unit = "block",
split.unit = c("block", "main.unit")),
seed=155251978)

## Generate a permutation of Seedlings within Species
seed.permute <- designRandomize(recipient = list(Species = 3, Seedlings = 4),
nested.recipients = list(Seedlings = "Species"),
seed = 75724, except = "Species",
unit.permutation = TRUE)
```
designTwoPhaseAnatomies

Given the layout for a design and three structure formulae, obtain the anatomies for the (i) two-phase, (ii) first-phase, (iii) cross-phase, treatments, and (iv) combined-units designs.

Description

Uses designAnatomy to obtain the four species of designs, described by Brien (2019), that are associated with a standard two-phase design: the anatomies for the (i) two-phase, (ii) first-phase, (iii) cross-phase, treatments, and (iv) combined-units designs. (The names of the last two designs in Brien (2019) were cross-phase and second-phase designs.) For the standard two-phase design, the first-phase design is the design that allocates first-phase treatments to first-phase units. The cross-phase, treatments design allocates the first-phase treatments to the second-phase units and the combined-units design allocates the first-phase units to the second-phase units. The two-phase design combines the other three species of designs. However, it is not mandatory that the three formulae correspond to second-phase units, first-phase units and first-phase treatments, respectively, as is implied above; this is just the correspondence for a standard two-phase design. The essential requirement is that three structure formulae are supplied. For example, if there are both first- and second-phase treatments in a two-phase design, the third formula might involve the treatment factors from both phases. In this case, the default anatomy titles when printing occurs will not be correct, but can be modified using the titles argument.

Usage

designTwoPhaseAnatomies(formulae, data, which.designs = "all", printAnatomies = TRUE, titles, orthogonalize = "hybrid", marginality = NULL, which.criteria = c("aefficiency", "eeficiency", "order"), ...)

Arguments

formulae An object of class list with three components of class formula. Usually, the terms in a single formula have the same status in the allocation of factors in the design. For example, all involve only factors that were allocated, or all involve factors that were recipients of allocated factors. The names of the components are used to identify the sources in the summary.pcanon object. They will also be used to name the terms, sources and marginality lists in the pcanon.object.

data A data.frame contains the values of the factors and variables that occur in formulae.

which.designs A character vector indicating the species of designs that are to be obtained. It should include one or more of two-phase, first-phase, cross-phase and combined-units; all, the default, results in all four being obtained.

printAnatomies A logical indicating whether or not the anatomies are to be printed.

titles A character vector of length four providing titles for the printed anatomies. It should have the titles, in the following order, for the anatomies based on: (i) all three formulae, (ii) the second and third formulae, (iii) the first and third formulae, and (iv) the first and second formulae. If any element of titles is NA then that element is replaced with the corresponding default element of
orthogonalize A character vector indicating the method for orthogonalizing a projector to those for terms that occurred previously in a single formula. Three options are available: hybrid; differencing; eigenmethods. The hybrid option is the most general and uses the relationships between the projection operators for the terms in the formula to decide which projectors to substract and which to orthogonalize using eigenmethods. The differencing option subtracts, from the current projector, those previously orthogonalized projectors for terms whose factors are a subset of the current projector’s factors. The eigenmethods option recursively orthogonalizes the projects using an eigenanalysis of each projector with previously orthogonalized projectors. If a single value is given, it is used for all formulæ.

marginality A list that can be used to supply some or all of the marginality matrices when it is desired to overwrite calculated marginality matrices or when they are not calculated. If the list is the same length as the formulæ list, they will be associated in parallel with the components of formulæ, irrespective of the naming of the two lists. If the number of components in marginalita is less than the number of components in formulæ then both lists must be named so that those in the marginality list can be matched with those in the formulæ list.

Each component of the marginality list must be either NULL or a square matrix consisting of zeroes and ones that gives the marginalities of the terms in the formula. It must have the row and column names set to the terms from the expanded formula, including being in the same order as these terms. The entry in the ith row and jth column will be one if the ith term is marginal to the jth term i.e. the column space of the ith term is a subspace of that for the jth term and so the source for the jth term is to be made orthogonal to that for the ith term. Otherwise, the entries are zero. A row and column should not be included for the grand mean even if grandMean is TRUE.

which.criteria A character vector nominating the efficiency criteria to be included in the summary of aliasing between terms within a structure. It can be none, all or some combination of aefficiency, mefficiency, sefficiency, eefficiency, xefficiency, order and dforthog – for details see efficiency.criteria. If none, no summary is printed.

... further arguments passed to designAnatomy.

Details

To produce the anatomies, designAnatomy is called. The two-phase anatomy is based on the three formulæ supplied in formulæ, the first-phase anatomy uses the second and third formulæ, the cross-phase, treatments anatomy derives from the first and third formulæ and the combined-units anatomy is obtained with the first and second formulæ.

Value

A list containing the components twophase, first, cross and combined. Each contains the pcanon.object for one of the four designs produced by designTwophaseAnatomies, unless it is NULL because the design was omitted from the which.designs argument. The returned list
has an attribute `titles`, being a character vector of length four and containing the titles used in printing the anatomies.

Author(s)

Chris Brien

References


See Also

designAnatomy, pcanon.object, p2canon.object, summary.pcanon, efficiencies.pcanon, pstructure, projs.2canon, proj2.efficiency, proj2.combine, proj2.eigen, efficiency.criteria, in package `dae`, `eigen`.

`projector` for further information about this class.

Examples

```r
# Microarray example from Jarrett & Ruggiero (2008) - see Brien (2019)
jr.lay <- fac.gen(list(Set = 7, Dye = 2, Array = 3))
jr.lay <- within(jr.lay, {
  Block <- factor(rep(1:7, each=6))
  Plant <- factor(rep(c(1,2,3,2,3,1), times=7))
  Sample <- factor(c(rep(c(2,1,2,2,1,1, 1,2,1,1,2,2), times=3),
               2,1,2,2,1,1))
  Treat <- factor(c(1,2,4,2,4,1, 2,3,5,3,5,2, 3,4,6,4,6,3, 4,5,7,5,7,4, 5,6,1,6,1,5, 6,7,2,7,2,6, 7,1,3,1,3,7),
                  labels=c("A","B","C","D","E","F","G"))
})
jr.anat <- designTwophaseAnatomies(formulae = list(array = ~ (Set:Array)*Dye,
                    plot = ~ Block/Plant/Sample,
                    trt = ~ Treat),
               which.designs = c("first","cross"),
               data = jr.lay)

# Three-phase sensory example from Brien and Payne (1999)
# Not run:
data(Sensory3Phase.dat)
Sensory.canon <- designTwophaseAnatomies(formulae = list(
  eval = ~ ((Occasions/Intervals/Sittings)*Judges)/Positions,
  field = ~ (Rows*(Squares/Columns))/Halfplots,
  treats = ~ Trellis*Method),
  data = Sensory3Phase.dat)
```

```r
## End(Not run)
```
detect.diff

Computes the detectable difference for an experiment

Description

Computes the delta that is detectable for specified replication, power, alpha.

Usage

detect.diff(rm=5, df.num=1, df.denom=10, sigma=1, alpha=0.05, power=0.8, tol = 0.001, print=FALSE)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>rm</td>
<td>The number of observations used in computing a mean.</td>
</tr>
<tr>
<td>df.num</td>
<td>The degrees of freedom of the numerator of the F for testing the term involving the means.</td>
</tr>
<tr>
<td>df.denom</td>
<td>The degrees of freedom of the denominator of the F for testing the term involving the means.</td>
</tr>
<tr>
<td>sigma</td>
<td>The population standard deviation.</td>
</tr>
<tr>
<td>alpha</td>
<td>The significance level to be used.</td>
</tr>
<tr>
<td>power</td>
<td>The minimum power to be achieved.</td>
</tr>
<tr>
<td>tol</td>
<td>The maximum difference tolerated between the power required and the power computed in determining the detectable difference.</td>
</tr>
<tr>
<td>print</td>
<td>TRUE or FALSE to have or not have a table of power calculation details printed out.</td>
</tr>
</tbody>
</table>

Value

A single numeric value containing the computed detectable difference.

Author(s)

Chris Brien

See Also

power.exp, no.reps in package dae.

Examples

```r
## Compute the detectable difference for a randomized complete block design
## with four treatments given power is 0.8 and alpha is 0.05.
rm <- 5
detect.diff(rm = rm, df.num = 3, df.denom = 3 * (rm - 1), sigma = sqrt(20))
```
## Efficiencies

*Extracts the canonical efficiency factors from a `pcanon.object` or a `p2canon.object`.*

### Description

Produces a list containing the canonical efficiency factors for the joint decomposition of two or more sets of projectors (Brien and Bailey, 2009) obtained using `designAnatomy` or `projs.2canon`.

### Usage

```r
## S3 method for class 'pcanon'
efficiencies(object, which = "adjusted", ...)
## S3 method for class 'p2canon'
efficiencies(object, which = "adjusted", ...)
```

### Arguments

- **object**
  - A `pcanon.object` or an object of class `p2canon` produced by `projs.2canon`.

- **which**
  - A character string, either `adjusted` or `pairwise`. For `adjusted`, the canonical efficiency factor are adjusted for other projectors from from the same set. For `pairwise`, they are the unadjusted canonical efficiency factors between pairs of projectors consisting of one projector from each of two sets.

- **...**
  - Further arguments passed to or from other methods. Unused at present.

### Value

For a `pcanon.object`, a list with a component for each component of `object`, except for the last component – for more information about the components see `pcanon.object`.

For a `p2canon` object, a list with a component for each element of the `Q1` argument from `projs.2canon`. Each component is list, each its components corresponding to an element of the `Q2` argument from `projs.2canon`.

### Author(s)

Chris Brien

### References


### See Also

- `designAnatomy`, `summary.pcanon`, `proj2.efficiency`, `proj2.combine`, `proj2.eigen`, `pstructure` in package `dae`, `eigen`.
- `projector` for further information about this class.
Examples

```r
## PBIBD(2) from p. 379 of Cochran and Cox (1957) Experimental Designs.
## 2nd edn Wiley, New York
PBIBD2.unit <- list(Block = 6, Unit = 4)
PBIBD2.nest <- list(Unit = "Block")
trt <- factor(c(1,4,2,5, 2,5,3,6, 3,6,1,4, 4,1,5,2, 5,2,6,3, 6,3,4,1))
PBIBD2.lay <- designRandomize(allocated = trt,
                               recipient = PBIBD2.unit,
                               nested.recipients = PBIBD2.nest)

##obtain combined decomposition using designAnatomy and get the efficiencies
unit.trt.canon <- designAnatomy(list(unit=~ Block/Unit, trt=~ trt), data = PBIBD2.lay)
efficiencies.pcanon(unit.trt.canon)

##obtain the projectors for each formula using pstructure
unit.struct <- pstructure(~ Block/Unit, data = PBIBD2.lay)
trt.struct <- pstructure(~ trt, data = PBIBD2.lay)

##obtain combined decomposition projs.2canon and get the efficiencies
unit.trt.p2canon <- projs.2canon(unit.struct$Q, trt.struct$Q)
efficiencies.p2canon(unit.trt.p2canon)
```

efficiency.criteria

Computes efficiency criteria from a set of efficiency factors

Description

Computes efficiency criteria from a set of efficiency factors.

Usage

`efficiency.criteria(efficiencies)`

Arguments

`efficiencies` A numeric containing a set of efficiency factors.

Details

The `aefficiency` criterion is the harmonic mean of the nonzero efficiency factors. The `mefficiency` criterion is the mean of the nonzero efficiency factors. The `eefficiency` criterion is the minimum of the nonzero efficiency factors. The `sefficiency` criterion is the variance of the nonzero efficiency factors. The `xefficiency` is the maximum of the efficiency factors. The `order` is the order of balance and is the number of unique nonzero efficiency factors. The `dforthog` is the number of efficiency factors that are equal to one.

Value

A list whose components are `aefficiency`, `mefficiency`, `sefficiency`, `eefficiency`, `xefficiency`, `order` and `dforthog`.

Author(s)

Chris Brien
See Also

proj2.efficiency, proj2.eigen, proj2.combine in package dae.eigen.
projector for further information about this class.

Examples

## PBIBD(2) from p. 379 of Cochran and Cox (1957) Experimental Designs.
## 2nd edn Wiley, New York
PBIBD2.unit <- list(Block = 6, Unit = 4)
PBIBD2.nest <- list(Unit = "Block")
trt <- factor(c(1,4,2,5, 2,5,3,6, 3,6,1,4, 4,1,5,2, 5,2,6,3, 6,3,4,1))
PBIBD2.lay <- designRandomize(allocated = trt,
recipient = PBIBD2.unit,
nested.recipients = PBIBD2.nest)

## obtain sets of projectors
unit.struct <- pstructure(~ Block/Unit, data = PBIBD2.lay)
trt.struct <- pstructure(~ trt, data = PBIBD2.lay)

## save intrablock efficiencies
eff.inter <- proj2.efficiency(unit.struct$Q["Unit[Block]"], trt.struct$Q["trt"])

## calculate efficiency criteria
efficiency.criteria(eff.inter)

elements

Extract the elements of an array specified by the subscripts

Description

Elements of the array \( x \) corresponding to the rows of the two dimensional object \( \text{subscripts} \) are extracted. The number of columns of \( \text{subscripts} \) corresponds to the number of dimensions of \( x \). The effect of supplying less columns in \( \text{subscripts} \) than the number of dimensions in \( x \) is the same as for "[".

Usage

elements(x, subscripts)

Arguments

\( x \) An array with at least two dimensions whose elements are to be extracted.

\( \text{subscripts} \) A two dimensional object interpreted as elements by dimensions.

Value

A vector containing the extracted elements and whose length equals the number of rows in the \( \text{subscripts} \) object.

Author(s)

Chris Brien
See Also

Extract

Examples

```r
## Form a table of the means for all combinations of Row and Line.
## Then obtain the values corresponding to the combinations in the data frame x,
## excluding Row 3.
x <- fac.gen(list(Row = 2, Line = 4), each =2)
x$y <- rnorm(16)
RowLine.tab <- tapply(x$y, list(x$Row, x$Line), mean)
xs <- elements(RowLine.tab, subscripts=x[x$"Line" != 3, c("Row", "Line")])
```
Arguments

- **table**: A numeric vector containing the values to be expanded. Its length must equal the product of the number of used levels for the factors in `index.factors` and the values in it correspond to all levels combinations of these factors. That is, the values of the `index.factors` are irrelevant to `table`.

- **index.factors**: A list of factors that index the table. All the factors must be the same length.

- **order**: The order in which the levels combinations of the `index.factors` are to be considered as numbered in indexing `table`; standard numbers them as if they are arranged in standard order, that is with the first factor moving slowest and the last factor moving fastest; yates numbers them as if they are arranged in Yates order, that is with the first factor moving fastest and last factor moving slowest.

Value

A vector of length equal to the factors in `index.factor` whose values are taken from `table`.

Author(s)

Chris Brien

Examples

```r
## generate a small completely randomized design with the two-level
## factors A and B
n <- 12
CRD.unit <- list(Unit = n)
CRD.treat <- fac.gen(list(A = 2, B = 2), each = 3)
CRD.lay <- designRandomize(allocated = CRD.treat, recipient = CRD.unit, seed = 956)

## set up a 2 x 2 table of A x B effects
AB.tab <- c(12, -12, -12, 12)

## add a unit-length vector of expanded effects to CRD.lay
attach(CRD.lay)
CRD.lay$AB.effects <- extab(table=AB.tab, index.factors=list(A, B))
```

---

**fac.ar1mat**

forms the ar1 correlation matrix for a (generalized) factor

Description

Form the correlation matrix for a (generalized) factor where the correlation between the levels follows an autocorrelation of order 1 (ar1) pattern.

Usage

```r
fac.ar1mat(factor, rho)
```
Arguments

factor The (generalized) factor for which the correlation between its levels displays an ar1 pattern.
rho The correlation parameter for the ar1 process.

Details

The method is: a) form an \( n \times n \) matrix of all pairwise differences in the numeric values corresponding to the observed levels of the factor by taking the difference between the following two \( n \times n \) matrices are equal: 1) each row contains the numeric values corresponding to the observed levels of the factor, and 2) each column contains the numeric values corresponding to the observed levels of the factor, b) replace each element of the pairwise difference matrix with \( \rho \) raised to the absolute value of the difference.

Value

An \( n \times n \) matrix, where \( n \) is the length of the factor.

Author(s)

Chris Brien

See Also

fac.vcmat, fac.meanop, fac.sumop in package dae.

Examples

```r
## set up a two-level factor and a three-level factor, both of length 12
A <- factor(rep(1:2, each=6))
B <- factor(rep(1:3, each=2, times=2))

## create a 12 x 12 ar1 matrix corresponding to B
ar1.B <- fac.ar1mat(B, 0.6)
```

fac.combine Combines several factors into one

Description

Combines several factors into one whose levels are the combinations of the used levels of the individual factors.

Usage

```r
fac.combine(factors, order="standard", combine.levels=FALSE, sep="", ...)```
fac.divide

Description

Takes a factor and divides it into several separate factors as if the levels in the original combined.factor are numbered from one to its number of levels and correspond to the numbering of the levels combinations of the new factors when these are arranged in standard or Yates order.

Usage

fac.divide(combined.factor, factor.names, order="standard")

Arguments

- **factors**: A list of factors all of the same length.
- **order**: Either standard or yates. The order in which the levels combinations of the factors are to be considered as numbered when forming the levels of the combined factor; standard numbers them as if they are arranged in standard order, that is with the levels of the first factor moving slowest and those of the last factor moving fastest; yates numbers them as if they are arranged in Yates order, that is with the levels of the first factor moving fastest and those of the last factor moving slowest.
- **combine.levels**: A logical specifying whether the levels labels of the new factor are to be combined from those of the factors being combined. The default is to use the integers from 1 to the product of the numbers of combinations of used levels of the individual factors, numbering the levels according to order.
- **sep**: A character string to separate the levels when combine.levels = TRUE.
- **...**: Further arguments passed to the factor call creating the new factor.

Value

A factor whose levels are formed form the observed combinations of the levels of the individual factors.

Author(s)

Chris Brien

See Also

fac.uncombine, fac.split, fac.divide in package dae.

Examples

```r
## set up two factors
A <- factor(rep(1:2, each=6))
B <- factor(rep(1:3, each=2, times=2))

## obtain six-level factor corresponding to the combinations of A and B
AB <- fac.combine(list(A,B))
```

Divides a factor into several separate factors
Arguments

combined.factor

A factor that is to be divided into the individual factors listed in factor.names.

factor.names

A list of factors to be formed. The names in the list are the names of the factors and the component of a name is either a) a single numeric value that is the number of levels, b) a numeric vector that contains the levels of the factor, or c) a character vector that contains the labels of the levels of the factor.

order

Either standard or yates. The order in which the levels combinations of the factors in factor.names are to be considered as numbered; standard numbers them as if they are arranged in standard order, that is with the first factor moving slowest and the last factor moving fastest; yates numbers them as if they are arranged in Yates order, that is with the first factor moving fastest and last factor moving slowest.

Value

A data.frame whose columns consist of the factors listed in factor.names and whose values have been computed from the combined factor. All the factors will be of the same length.

Note

A single factor name may be supplied in the list in which case a data.frame is produced that contains the single factor computed from the numeric vector. This may be useful when calling this function from others.

Author(s)

Chris Brien

See Also

fac.split, fac.uncombine, fac.combine in package dae.

Examples

## generate a small completely randomized design for 6 treatments
n <- 12
CRD.unit <- list(Unit = n)
treat <- factor(rep(1:4, each = 3))
CRD.lay <- designRandomize(allocated = treat, recipient = CRD.unit, seed=956)

## divide the treatments into two two-level factors A and B
CRD.facs <- fac.divide(CRD.lay$treat, factor.names = list(A = 2, B = 2))
**fac.gen**

Generate all combinations of several factors and, optionally, replicate them.

### Usage

```r
fac.gen(generate, each=1, times=1, order="standard")
```

### Arguments

- **generate**: A list of named objects and numbers that specify the factors whose levels are to be generated and the pattern in these levels. If a component of the list is named, then the component should be either a) a single numeric value that is the number of levels, b) a numeric vector that contains the levels of the factor, or c) a character vector that contains the labels of the levels of the factor.
- **each**: The number of times to replicate consecutively the elements of the levels generated according to pattern specified by the `generate` argument.
- **times**: The number of times to repeat the whole generated pattern of levels generated according to pattern specified by the `generate` argument.
- **order**: Either `standard` or `yates`. The order in which the speed of cycling through the levels is to move; combinations of the factors are to be considered as numbered; standard cycles through the levels of the first factor slowest and the last factor moving fastest; yates cycles through the levels of the first factor fastest and last factor moving slowest.

### Details

The levels of each factor are generated in a hierarchical pattern, such as standard order, where the levels of one factor are held constant while those of the adjacent factor are cycled through the complete set once. If a number is supplied instead of a name, the pattern is generated as if a factor with that number of levels had been supplied in the same position as the number. However, no levels are stored for this unnamed factor.

### Value

A data.frame of factors whose generated levels are those supplied in the `generate` list. The number of rows in the data.frame will equal the product of the numbers of levels of the supplied factors and the values of the `each` and `times` arguments.

### Warning

Avoid using factor names F and T as these might be confused with FALSE and TRUE.

### Author(s)

Chris Brien
See Also

fac.genfactors, fac.combine in package dae

Examples

```r
## generate a 2^3 factorial experiment with levels - and +, and
## in Yates order
mp <- c("-", "+")
fnames <- list(Catal = mp, Temp = mp, Press = mp, Conc = mp)
Fac4Proc.Treats <- fac.gen(generate = fnames, order="yates")

## Generate the factors A, B and D. The basic pattern has 4 repetitions
## of the levels of D for each A and B combination and 3 repetitions of
## the pattern of the B and D combinations for each level of A. This basic
## pattern has each combination repeated twice, and the whole of this
## is repeated twice. It generates 864 A, B and D combinations.
gen <- list(A = 3, 3, B = c(0,100,200), 4, D = c("0","1"))
fac.gen(gen, times=2, each=2)
```

Description

Generate all combinations of the levels of the supplied factors, without replication. This function extracts the levels from the supplied factors and uses them to generate the new factors. On the other hand, the levels must supplied in the generate argument of the function fac.gen.

Usage

```r
fac.genfactors(factors, ...)
```

Arguments

- **factors**: A list of factors, or an object of factors that is coercible to a list.
- **...**: Further arguments passed to the fac.gen in creating the data.frame of new factors.

Details

The levels of each factor are generated in standard order, unless order is supplied to fac.gen via the `...` argument. The levels of the new factors will be in the same order as in the supplied factors.

Value

A data.frame whose columns correspond to factors in the factors list. The values in a column are the generated levels of the factor. The number of rows in the data.frame will equal the product of the numbers of levels of the supplied factors.
Description

Match, for each combination of a set of columns in x, the rows that has the same combination in table. The argument multiples.allow controls what happens when there are multiple matches in table of a combination in x.

Usage

defac.match(x, table, col.names, nomatch = NA_integer_, multiples.allow = FALSE)

Arguments

x
an R object, normally a data.frame, possibly a matrix.

Table
an R object, normally a data.frame, possibly a matrix.

col.names
A character vector giving the columns in x and table that are to be matched.

nomatch
The value to be returned in the case when no match is found. Note that it is coerced to integer.

multiples.allow
A logical indicating whether multiple matches of a combination in x to those in table is allowed. If multiples.allow is FALSE, an error is generated. If multiples.allow is TRUE, the first occurrence in table is matched. This function can be viewed as a generalization to multiple vectors of the match function that applies to single vectors.

Value

A vector of length equal to x that gives the rows in table that match the combinations of col.names in x. The order of the rows is the same as the order of the combinations in x. The value returned if a combination is unmatched is specified in the nomatch argument.

Author(s)

Chris Brien
fac.meanop

computes the projection matrix that produces means

Description

Computes the symmetric projection matrix that produces the means corresponding to a (generalized) factor.

Usage

fac.meanop(factor)

Arguments

factor

The (generalized) factor whose means the projection matrix computes from an observation-length vector.

Details

The design matrix $X$ for a (generalized) factor is formed with a column for each level of the (generalized) factor, this column being its indicator variable. The projection matrix is formed as $X \%\% (1/\text{diag}(r)) \%\% t(X)$, where $r$ is the vector of levels replications.

A generalized factor is a factor formed from the combinations of the levels of several original factors. Generalized factors can be formed using fac.combine.

Value

A projector containing the symmetric, projection matrix and its degrees of freedom.

Author(s)

Chris Brien
fac.multinested

See Also
fac.combine, projector, degfree, correct.degfree, fac.sumop in package dae.
projector for further information about this class.

Examples
## set up a two-level factor and a three-level factor, both of length 12
A <- factor(rep(1:2, each=6))
B <- factor(rep(1:3, each=2, times=2))

## create a generalized factor whose levels are the combinations of A and B
AB <- fac.combine(list(A,B))

## obtain the operator that computes the AB means from a vector of length 12
M.AB <- fac.meanop(AB)

fac.multinested

Creates several factors, one for each level of nesting.fac and each of whose values are either generated within those of a level of nesting.fac or using the values of nested.fac within a levels of nesting.fac.

Description

Creates several factors, one for each level of nesting.fac and each of whose values are either (i) generated within those of the level of nesting.fac or (ii) using the values of nested.fac within the levels of the nesting.fac. For (i), all elements having the same level of nesting.fac are numbered from 1 to the number of different elements having that level. For (ii), the values of nested.fac for a level of nesting.fac are copied. In both cases, for the values of nested.fac not equal to the level of the values of nested.fac for which a nested factor is being created, the levels are set to outlevel and labelled using outlabel. A factor is not created for a level of nesting.fac with label equal to outlabel. The names of the factors are equal to the levels of nesting.fac; optionally fac.prefix is added to the beginning of the names of the factors. The function is used to split up a nested term into separate terms for each level of nesting.fac.

Usage

fac.multinested(nesting.fac, nested.fac = NULL, fac.prefix = NULL,
nested.levs = NA, nested.labs = NA,
outlevel = 0, outlabel = "rest", ...)

Arguments

nesting.fac The factor for each of whose levels a nested facor is to be generated, except one is not generated for the outlabel level.
nested.fac The factor whose values for a level are to be used for the factor being created for that level. If nested.fac is NULL, then the values of the levels is the the list of numbers from 1 to the replication of the level of nesting.fac. represented as characters.
fac.prefix The prefix to be added to a level in naming a nested factor.
fac.multinested

nested.levs  Optional vector of levels for the nested factors. Any data value that does not match a value in nested.levs will be NA in the nested factor being generated. The default value of nested.levs is the list of numbers from 1 to the replication of the levels of nesting.fac, represented as characters. When nesting.fac is not NULL, nested.levs is not used.

nested.labs  Optional vector of values to use as labels for the levels of the new nested factors; they are combined with outlabel. The default is as.character(levels).

outlevel  The level to use in the new factor for all values of old factor that do not correspond to the level of the nesting.fac to which the new factor corresponds.

outlabel  The label to use the outlevel level.

...  Further arguments passed to the factor call creating a new factor.

Value

A data.frame containing a factor for each level of nesting.fac.

Note

The levels of nesting.fac do not have to be equally replicated.

Author(s)

Chris Brien

See Also

fac.gen, fac.nested in package dae, factor.

Examples

```r
lay <- data.frame(A = factor(rep(c(1:3), c(3,6,4)), labels = letters[1:3]))
lay$B <- fac.nested(lay$A)

#Add factors for B within each level of A
lay2 <- cbind(lay, fac.multinested(lay$A))
canon2 <- designAnatomy(list(~A/(a+b+c)), data = lay2)
summary(canon2)

#Add factors for B within each level of A, but with levels and outlabel given
lay2 <- cbind(lay, fac.multinested(lay$A, nested.levs = seq(10,60,10), outlabel = "other"))
canon2 <- designAnatomy(list(~A/(a+b+c)), data = lay2)
summary(canon2)

#Replicate the combinations of A and B three times and index them with the factor sample
lay3 <- rbind(lay,lay,lay)
lay3$sample <- with(lay3, fac.nested(fac.combine(list(A,B))))

#Add factors for B within each level of A
lay4 <- cbind(lay3, fac.multinested(nesting.fac = lay$A, nested.fac = lay$B))
canon4 <- designAnatomy(list(~(A/(a+b+c))/sample), data = lay4)
summary(canon4)
```
#Add factors for sample within each combination of A and B
lay5 <- with(lay4, cbind(lay4,
               fac.multinested(nesting.fac = a, fac.prefix = "a"),
               fac.multinested(nesting.fac = b, fac.prefix = "b"),
               fac.multinested(nesting.fac = c, fac.prefix = "c")))

canon5 <- designAnatomy(list(~A/(a/(a1+a2+a3)+b/(b1+b2+b3+b4+b5+b6)+c/(c1+c2+c3))), data = lay5)
summary(canon5)

#Add factors for sample within each level of A
lay6 <- cbind(lay4,
               fac.multinested(nesting.fac = lay4$A, nested.fac = lay$sample, fac.prefix = "samp"))
canon6 <- designAnatomy(list(~A/(a/sampa+b/sampb+c/sampc)), data = lay6)
summary(canon6)

fac.nested

creates a factor, the nested factor, whose values are generated within those of the factor nesting.fac

Description

Creates a nested factor whose levels are generated within those of the factor nesting.fac. All elements of nesting.fac having the same level are numbered from 1 to the number of different elements having that level.

Usage

fac.nested(nesting.fac, nested.levs=NA, nested.labs=NA, ...)

Arguments

- nesting.fac: The factor within each of whose levels the created factor is to be generated.
- nested.levs: Optional vector of levels for the factor. Any data value that does not match a value in levels will be NA in the factor. The default value of nested.levs is the list of numbers from 1 to the maximum replication of the levels of nesting.fac, represented as characters.
- nested.labs: Optional vector of values to use as labels for the levels of the factor. The default is as.character(nested.levs).
- ...: Further arguments passed to the factor call creating the new factor.

Value

A factor that is a character vector with class attribute "factor" and a levels attribute which determines what character strings may be included in the vector. It has a different level for each of the values of the nesting.fac with the same level.

Note

The levels of nesting.fac do not have to be equally replicated.
fac.recast

Author(s)

Chris Brien

See Also

fac.gen, fac.multinested in package dae, factor.

Examples

```r
## set up factor A
A <- factor(c(1, 1, 1, 2, 2))

## create nested factor
B <- fac.nested(A)
```

fac.recast

Recasts a factor by modifying the values in the factor vector and/or the levels attribute, possibly combining some levels into a single level.

Description

A factor is comprised of a vector of values and a levels attribute. This function can modify these separately or jointly. The newlevels argument recasts both the values of a factor vector and the levels attribute, using each value in the newlevels vector to replace the corresponding value in both factor vector and the levels attribute. The factor, possibly with the new levels, can have its levels attribute reordered and/or new labels associated with the levels using the levels.order and newlabels arguments.

Usage

`fac.recast(factor, newlevels = NULL, levels.order = NULL, newlabels = NULL, ...)`

Arguments

- `factor`: The factor to be recast.
- `newlevels`: A vector of length levels(factor) that changes both the values in the factor vector and its levels attribute. The values in the newlevels vector need not be unique, but there must be as many values as there are levels in the supplied factor. The levels in the vector of the supplied factor that have the same value in newlevels will be combined in the recast factor. The values in the new levels attribute can be re-ordered using levels.order.
- `levels.order`: A vector that specifies the order of the levels in the levels attribute of the recast factor. If newlevels is NULL, must be of length levels(factor) and contain the old levels in the new order for the recast factor. If newlevels is not NULL, the vector must be of length(unique(newlevels)) and contain the unique values in newlevels in the new order for the recast factor. The values in the factor vector whose levels are being re-ordered will be unchanged. If levels.order is NULL, then the current levels attribute of factor is used.
newlabels 

A vector of length levels(factor) if newlevels is NULL, and of length unique(newlevels) if it is not NULL. It should contain the values to be used as labels in the recast factor. Effectively, this changes the values in the factor vector to those given in newlabels and the levels attribute to newlabels.

Further arguments passed to the factor call creating the new factor.

Value

A factor.

Author(s)

Chris Brien

See Also

fac.use.logical, as.numfac and mpone in package dae, factor, relevel.

Examples

```r
## set up a factor with labels
Treats <- factor(rep(1:4, 4), labels=letters[1:4])

## recast to reduce the levels: "a" and "d" to 1 and "b" and "c" to 2, i.e. from 4 to 2 levels
A <- fac.recast(Treats, newlevels = c(1,2,2,1), labels = letters[1:2])
A <- fac.recast(Treats, newlevels = letters[c(1,2,2,1)])

# reduce the levels from 4 to 2, with re-ordering the levels vector without changing the values # of the new recast factor vector
A <- fac.recast(Treats, newlevels = letters[c(1,2,2,1)], levels.order = letters[2:1])

# reassign the values in the factor vector without re-ordering the levels attribute
A <- fac.recast(Treats, newlevels = letters[4:1])

# reassign the values in the factor vector, with re-ordering the levels attribute
A <- fac.recast(Treats, newlabels = letters[4:1])

# reorder the levels attribute with changing the values in the factor vector
A <- fac.recast(Treats, levels.order = letters[4:1])

# reorder the values in the factor vector without changing the levels attribute
A <- fac.recast(Treats, newlevels = 4:1, newlabels = levels(Treats))
```
**Description**

Recodes the levels and values of a factor using each value in the newlevels vector to replace the corresponding value in the vector of levels of the `factor`.

This function has been superseded by `fac.recast`, which has extended functionality. Calls to `fac.recast` that use only the `factor` and `newlevels` argument will produce the same results as a call to `fa.recode`. `fac.recode` may be deprecated in future versions of `dae` and is being retained for now to maintain backwards compatibility.

**Usage**

```r
fac.recode(factor, newlevels, ...)
```

**Arguments**

- `factor` - The `factor` to be recoded.
- `newlevels` - A vector of length `levels(factor)` containing values to use in the recoding.
- `...` - Further arguments passed to the `factor` call creating the new `factor`.

**Value**

A `factor`.

**Author(s)**

Chris Brien

**See Also**

`fac.recast, fac.uselogical, as.numfac` and `mpone` in package `dae, factor, relevel`.

**Examples**

```r
## set up a factor with labels
Treats <- factor(rep(1:4, 4), labels=c("A","B","C","D"))

## recode "A" and "D" to 1 and "B" and "C" to 2
B <- fac.recode(Treats, c(1,2,2,1), labels = c("a","b"))
```

---

**fac.split**

*Splits a factor whose levels consist of several delimited strings into several factors*

**Description**

Splits a `factor`, whose levels consist of strings delimited by a separator character, into several `factors`. It uses the function `strsplit`, with `fixed = TRUE` to split the levels.

**Usage**

```r
fac.split(combined.factor, factor.names, sep="", ...)
```
**Arguments**

combined.factor  
A **factor** to be split into several **factors**.

factor.names  
A **list** of names for factors and associated levels, if required. The names of the components of the **list** are used for the names of the new factors. Each component of the **list** should either be **NULL** or a vector of levels for the new **factor**. If a component is **NULL** then the unique values for the supplied factor are used as the levels, which are sorted into alphabetical order. If a either a **numeric** or a **character** vector is supplied for a component, then these are supplied as the levels of the new factor.

sep  
A **character** string that separates the levels in the **combined.factor**.

...  
Further arguments passed to the **factor** call creating the new **factor**.

**Value**

A **data.frame** containing the new **factors**.

**Author(s)**

Chris Brien

**See Also**

fac.divide, fac.uncombine, fac.combine in package **dae** and strsplit.

**Examples**

```r
## Form a combined factor to split
data(Oats.dat)
tmp <- within(Oats.dat, Trts <- fac.combine(list(Variety, Nitrogen), combine.levels = TRUE))

## Variety levels sorted into alphabetical order
trts.dat <- fac.split(combined.factor = tmp$Trts,
                      factor.names = list(Variety = NULL, Nitrogen = NULL))

## Variety levels order from Oats.dat retained
trts.dat <- fac.split(combined.factor = tmp$Trts,
                      factor.names = list(Variety = levels(tmp$Variety), Nitrogen = NULL))
```

---

**Description**

Computes the summation matrix that produces sums corresponding to a (generalized) **factor**.

**Usage**

`fac.sumop(factor)`
fac.uncombine

Cleaves a single factor, each of whose levels has delimited strings, into several factors using the separated strings.

Description

Cleaves a single factor into several factors whose levels, the levels of the original factor consisting of several delimited strings that can be separated to form the levels of the new factors. That is, it reverses the process of combining factors that fac.combine performs.

Usage

fac.uncombine(factor, new.factors, sep="",",...")
Arguments

factor A factor or character that has values that are strings delimited by the delimiter specified by sep.

new.factors A list, the names of whose components are the names of the new factors to be performed. If the contents of a component is not NULL, then they are used as the levels of the corresponding factor.

sep A character string that separates the levels of the new.factors in the levels factor.

Further arguments passed to the factor call creating the new factor.

Value

A data.frame whose columns consist of the factors listed in new.factors and whose values have been computed from the values of the combined factor.

Author(s)

Chris Brien

See Also

fac.split, fac.combine, fac.divide in package dae and strsplit.

Examples

## set up two factors and combine them
facs <- fac.gen(list(A = letters[1:3], B = 1:2), each = 4)
facs$AB <- with(facs, fac.combine(list(A, B), combine.levels = TRUE))

## now reverse the process and uncombine the two factors
new.facs <- fac.uncombine(factor = facs$AB,
new.factors = list(A = letters[1:3], B = NULL),
sep = "",
new.facs <- fac.uncombine(factor = facs$AB,
new.factors = list(A = NULL, B = NULL),
sep = ",")

fac.uselogical

Forms a two-level factor from a logical object.

Description

Forms a two-level factor from a logical object. It can be used to recode a factor when the resulting factor is to have only two levels.

Usage

fac.uselogical(x, levels = c(TRUE, FALSE), labels = c("yes", "no"), ...)
Arguments

- **x**: A logical vector with values TRUE or FALSE. If the vector is not a logical, as.logical will be used in an attempt to coerce it to logical.
- **levels**: A vector of length two with values TRUE or T and FALSE or F, in either order depending on which of TRUE or FALSE is to be the first level.
- **labels**: A vector of length two with values to be used as labels for the first and second levels, respectively.
- **...**: Further arguments passed to the factor call creating the new factor.

Value

A factor.

Author(s)

Chris Brien

See Also

fac.recast, as.numfac and mpone in package dae, factor, relevel.

Examples

```r
## set up a factor with labels
Treats <- factor(rep(1:4, 4), labels=c("A","B","C","D"))

## recode "A" and "D" to "a" and "B" and "C" to "b"
B <- fac.uselogical(Treats %in% c("A", "D"), labels = c("a","b"))
B <- fac.uselogical(Treats %in% c("A", "D"), labels = c(-1,1))

## suppose level A in factor a is a control treatment
## set up a factor Control to discriminate between control and treated
Control <- fac.uselogical(Treats == "A")
```

Description

Form the variance matrix for a (generalized) factor whose effects for its different levels are independently and identically distributed, with their variance given by the variance component; elements of the matrix will equal either zero or sigma2 and displays compound symmetry.

Usage

fac.vcmat(factor, sigma2)

Arguments

- **factor**: The (generalized) factor for which the variance matrix is required.
- **sigma2**: The variance component, being the of the random effects for the factor.
Details

The method is: a) form the $n \times n$ summation or relationship matrix whose elements are equal to zero except for those elements whose corresponding elements in the following two $n \times n$ matrices are equal: 1) each row contains the numeric values corresponding to the observed levels of the factor, and 2) each column contains the numeric values corresponding to the observed levels of the factor, b) multiply the summation matrix by sigma2.

Value

An $n \times n$ matrix, where $n$ is the length of the factor.

Author(s)

Chris Brien

See Also

fac.ar1mat, fac.meanop, fac.sumop in package dae.

Examples

```r
## set up a two-level factor and a three-level factor, both of length 12
A <- factor(rep(1:2, each=6))
B <- factor(rep(1:3, each=2, times=2))

## create a 12 x 12 ar1 matrix corresponding to B
vc.B <- fac.vcmat(B, 2)
```

Fac4Proc.dat

Data for a $2^4$ factorial experiment

Description

The data set come from an unreplicated $2^4$ factorial experiment to investigate a chemical process. The response variable is the Conversion percentage (Conv) and this is indexed by the 4 two-level factors Catal, Temp, Press and Conc, with levels “-” and “+”. The data is arranged in Yates order. Also included is the 16-level factor Runs which gives the order in which the combinations of the two-level factors were run.

Usage

data(Fac4Proc.dat)

Format

A data.frame containing 16 observations of 6 variables.

Source

Table 10.6 of Box, Hunter and Hunter (1978) Statistics for Experimenters. New York, Wiley.
fitted.aovlist

Extract the fitted values for a fitted model from an aovlist object

Description

Extracts the fitted values as the sum of the effects for all the fitted terms in the model, stopping at error.term if this is specified. It is a method for the generic function fitted.

Usage

```r
## S3 method for class 'aovlist'
fitted(object, error.term=NULL, ...)
```

Arguments

- `object`: An aovlist object created from a call to aov.
- `error.term`: The term from the Error function down to which effects are extracted for adding to the fitted values. The order of terms is as given in the ANOVA table. If error.term is NULL effects are extracted from all Error terms.
- `...`: Further arguments passed to or from other methods.

Value

A numeric vector of fitted values.

Note

Fitted values will be the sum of effects for terms from the model, but only for terms external to any Error function. If you want effects for terms in the Error function to be included, put them both inside and outside the Error function so they are occur twice.

Author(s)

Chris Brien

See Also

fitted.errors, resid.errors, tukey.1df in package dae.

Examples

```r
## set up data frame for randomized complete block design in Table 4.4 from
## Box, Hunter and Hunter (2005) Statistics for Experimenters. 2nd edn
## New York, Wiley.
RCBDPen.dat <- fac.gen(list(Blend=5, Flask=4))
RCBDPen.dat$Treat <- factor(rep(c("A","B","C","D"), times=5))
RCBDPen.dat$Yield <- c(89,88,97,94,77,92,79,81,87,87,
                      85,87,92,89,84,79,81,88,88)

## perform the analysis of variance
RCBDPen.aov <- aov(Yield ~ Blend + Treat + Error(Blend/Flask), RCBDPen.dat)
summary(RCBDPen.aov)
```
## two equivalent ways of extracting the fitted values
fit <- fitted.aovlist(RCBDPen.aov)
fit <- fitted(RCBDPen.aov, error.term = "Blend:Flask")

---

### Description

An alias for the generic function `fitted`. When it is available, the method `fitted.aovlist` extracts the fitted values, which is provided in the `dae` package to cover `aovlist` objects.

### Usage

```r
## S3 method for class 'errors'
fitted(object, error.term=NULL, ...)
```

### Arguments

- **object**: An `aovlist` object created from a call to `aov`.
- **error.term**: The term from the `Error` function down to which effects are extracted for adding to the fitted values. The order of terms is as given in the ANOVA table. If `error.term` is `NULL` effects are extracted from all `Error` terms.
- **...**: Further arguments passed to or from other methods.

### Value

A numeric vector of fitted values.

### Warning

See `fitted.aovlist` for specific information about fitted values when an `Error` function is used in the call to the `aov` function.

### Author(s)

Chris Brien

### See Also

- `fitted.aovlist`, `resid.errors`, `Tukey.1df` in package `dae`.

### Examples

```r
## set up data frame for randomized complete block design in Table 4.4 from
## Box, Hunter and Hunter (2005) Statistics for Experimenters. 2nd edn
## New York, Wiley.
RCBDPen.dat <- fac.gen(list(Blend=5, Flask=4))
RCBDPen.dat$Treat <- factor(rep(c("A","B","C","D"), times=5))
RCBDPen.dat$Yield <- c(89,88,97,94,84,77,92,79,81,87,87,
                       85,87,92,89,84,79,81,88,88)
```
## perform the analysis of variance
RCBDPen.aov <- aov(Yield ~ Blend + Treat + Error(Blend/Flask), RCBDPen.dat)
summary(RCBDPen.aov)

## three equivalent ways of extracting the fitted values
fit <- fitted.aovlist(RCBDPen.aov)
fit <- fitted(RCBDPen.aov, error.term = "Blend:Flask")
fit <- fitted.errors(RCBDPen.aov, error.term = "Blend:Flask")

### harmonic.mean

Calculates the harmonic mean.

#### Description
A function to calculate the harmonic mean of a set of nonzero numbers.

#### Usage

harmonic.mean(x)
interaction.ABC.plot

Arguments

x
An object from whose elements the harmonic mean is to be computed.

Details

All the elements of x are tested as being less than daeTolerance, which is initially set to .Machine$double.eps^0.5 (about 1.5E-08). The function set.daeTolerance can be used to change daeTolerance.

Value

A numeric. Returns Inf if x contains a value close to zero

Examples

y <- c(seq(0.1,1,0.2))
harmonic.mean(y)

interaction.ABC.plot
Plots an interaction plot for three factors

Description

Plots a function (the mean by default) of the response for the combinations of the three factors specified as the x.factor (plotted on the x-axis of each plot), the groups.factor (plotted as separate lines in each plot) and the trace.factor (its levels are plotted in different plots). Interaction plots for more than three factors can be produced by using fac.combine to combine all but two of them into a single factor that is specified as the trace.factor.

Usage

interaction.ABC.plot(response, x.factor, groups.factor, trace.factor, data, fun="mean", title="A:B:C Interaction Plot", xlab, ylab, key.title, lwd=4, columns=2, ggplotFuncs = NULL, ...)

Arguments

response
A numeric vector containing the response variable from which a function (the mean by default) is computed for plotting on the y-axis.

x.factor
The factor to be plotted on the x-axis of each plot. If the levels are numeric values stored as characters, they will be converted to numeric values for plotting. If they are actually numeric codes for nonnumeric categories and you want them plotted on a discrete scale then you should employ nonnumeric codings, such as '-' and '+' or 'N' and 'Y' or something similar.

groups.factor
The factor plotted as separate lines in each plot.

trace.factor
The factor for whose levels there are separate plots.

data
A data.frame containing the three factors and the response.

fun
The function to be computed from the response for each combination of the three factors x.factor, groups.factor and trace.factor. By default, the mean is computed for each combination.

title
Title for plot window. By default it is "A:B:C Interaction Plot".
interaction.ABC.plot

- **xlab**: Label for the x-axis. By default it is the name of the x.factor.
- **ylab**: Label for the y-axis. By default it is the name of the response.
- **key.title**: Label for the key (legend) to the lines in each plot. By default it is the name of the groups.factor.
- **lwd**: The width of the lines. By default it is 4.
- **columns**: The number of columns for arranging the several plots for the levels of the groups.factor. By default it is 2.
- **ggplotFuncs**: A list, each element of which contains the results of evaluating a `ggplot` function. It is created by calling the `list` function with a `ggplot` function call for each element. These functions are applied in creating the ggplot object.
  - **...**: Other arguments that are passed down to `ggplot` methods.

**Value**

An object of class "ggplot", which can be plotted using `print`.

**Author(s)**

Chris Brien

**See Also**

- `fac.combine` in package `dae`, `interaction.plot`.

**Examples**

```r
## Not run:
## plot for Example 14.1 from Mead, R. (1990). The Design of Experiments:
## Statistical Principles for Practical Application. Cambridge,
## Cambridge University Press.
## use ?SPLGrass.dat for details
data(SPLGrass.dat)
interaction.ABC.plot(Main.Grass, x.factor=Period,
                     groups.factor=Spring, trace.factor=Summer,
                     data=SPLGrass.dat,
                     title="Effect of Period, Spring and Summer on Main Grass")

## plot for generated data
## use ?ABC.Interact.dat for data set details
data(ABC.Interact.dat)
## Add standard errors for plotting
## - here data contains a single value for each combintion of A, B and C
## - need to supply name for data twice
ABC.Interact.dat$se <- rep(c(0.5,1), each=4)
interaction.ABC.plot(MOE, A, B, C, data=ABC.Interact.dat,
                     ggplotFunc=list(geom_errorbar(data=ABC.Interact.dat,
                                                aes(ymax=MOE+se, ymin=MOE-se),
                                                width=0.2)))

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

Tests whether all elements are approximately zero

Description

A single-line function that tests whether all elements are zero (approximately).

Usage

is.allzero(x)

Arguments

x

An object whose elements are to be tested.

Details

The mean of the absolute values of the elements of x is tested to determine if it is less than daeTolerance, which is initially set to .Machine$double.eps ^ 0.5 (about 1.5E-08). The function set.daeTolerance can be used to change daeTolerance.

Value

A logical.

Author(s)

Chris Brien

Examples

## create a vector of 9 zeroes and a one
y <- c(rep(0,9), 1)

## check that vector is only zeroes is FALSE
is.allzero(y)

is.projector

Tests whether an object is a valid object of class projector

Description

Tests whether an object is a valid object of class "projector".

Usage

is.projector(object)

Arguments

object

The matrix to be made into a projector.
Details

The function is.projector tests whether the object consists of a matrix that is square, symmetric and idempotent. In checking symmetry and idempotency, the equality of the matrix with either its transpose or square is tested. In this, a difference in elements is considered to be zero if it is less than daeTolerance, which is initially set to .Machine$double.eps ^ 0.5 (about 1.5E-08). The function set.daeTolerance can be used to change daeTolerance.

Value

TRUE or FALSE depending on whether the object is a valid object of class "projector".

Warning

The degrees of freedom are not checked. correct.degfree can be used to check them.

Author(s)

Chris Brien

See Also

projector, correct.degfree in package dae.
projector for further information about this class.

Examples

## set up a 2 x 2 mean operator that takes the mean of a vector of 2 values
m <- matrix(rep(0.5,4), nrow=2)

## create an object of class projector
proj.m <- projector(m)

## check that it is a valid projector
is.projector(proj.m)

LatticeSquare_t49.des  A Lattice square design for 49 treatments

Description

The systematic design for a lattice square for 49 treatments consisting of four 7 x 7 squares. For more details see the vignette accessed via vignette("DesignNotes", package="dae").

Usage

data(LatticeSquare_t49.des)

Format

A data.frame containing 196 observations of 4 variables.
marginality

Source


marginality

Extracts the marginality matrix (matrices) from a pstructure.object or a pcanon.object.

Description

Produces (i) a marginality matrix for the formula in a call to pstructure.formula or (ii) a list containing the marginality matrices, one for each formula in the formulae argument of a call to designAnatomy.

A marginality matrix for a set of terms is a square matrix with a row and a column for each term not aliased term. Its elements are zeroes and ones, the entry in the ith row and jth column indicates whether or not the ith term is marginal to the jth term i.e. the column space of the ith term is a subspace of that for the jth term and so the source for the jth term will be orthogonal to that for the ith term.

Usage

## S3 method for class 'pstructure'
marginality(object, ...)
## S3 method for class 'pcanon'
marginality(object, ...)

Arguments

object A pstructure.object produced by pstructure.formula or pcanon.object produced by designAnatomy.

... Further arguments passed to or from other methods. Unused at present.

Value

If object is a pstructure.object then a matrix containing the marginality matrix for the terms obtained from the formula in the call to pstructure.formula.

If object is a pcanon.object then a list with a component for each formula, each component having a marginality matrix that corresponds to one of the formulae in the call to designAnatomy. The components of the list will have the same names as the components of the formulae list and so will be unnamed if the components of the latter list are unnamed.

Author(s)

Chris Brien

See Also

pstructure.formula, designAnatomy, summary.pcanon, proj2.efficiency, proj2.combined, proj2.eigen, pstructure in package dae, eigen, projector for further information about this class.
Examples

```r
## PBIBD(2) from p. 379 of Cochran and Cox (1957) Experimental Designs.
## 2nd edn Wiley, New York
PBIBD2.unit <- list(Block = 6, Unit = 4)
PBIBD2.nest <- list(Unit = "Block")
trt <- factor(c(1,4,2,5, 2,5,3,6, 3,6,1,4, 4,1,5,2, 5,2,6,3, 6,3,4,1))
PBIBD2.lay <- designRandomize(allocated = trt,
                            recipient = PBIBD2.unit,
                            nested.recipients = PBIBD2.nest)

##obtain pstructure.object and extract marginality matrix
unit.struct <- pstructure(~ Block/Unit, data = PBIBD2.lay)
unit.marg <- marginality(unit.struct)

##obtain combined decomposition and extract marginality matrices
unit.trt.canon <- designAnatomy(list(unit=~ Block/Unit, trt=~ trt), data = PBIBD2.lay)
marg <- marginality(unit.trt.canon)
```

---

mat.ar1

Forms an ar1 correlation matrix

Description

Form the correlation matrix of order order whose correlations follow the ar1 pattern. The matrix is banded and has diagonal elements equal to one and the off-diagonal element in the ith row and jth column equal to $\rho^{|i-j|}$.

Usage

```r
mat.ar1(rho, order)
```

Arguments

- **rho**  
The correlation on the first off-diagonal.
- **order**  
The order of the matrix to be formed.

Value

A banded correlation matrix whose elements follow an ar1 pattern.

Author(s)

Chris Brien

See Also

- `mat.I`, `mat.J`, `mat.exp`, `mat.gau`, `mat.banded`, `mat.ar2`, `mat.ar3`, `mat.sar2`, `mat.ma1`, `mat.ma2`, `mat.arma`

Examples

```r
corr <- mat.ar1(rho=0.4, order=4)
```
Form the correlation matrix of order order whose correlations follow the ar2 pattern. The resulting matrix is banded.

mat.ar2(ARparameters, order)

A numeric containing the two autoregressive parameter values of the process, being the weights given to the lag 1 and lag 2 response values.

The order of the matrix to be formed.

The correlations in the correlation matrix, corr say, are calculated from the autoregressive parameters, ARparameters. The values in

- the diagonal (k = 1) of corr are one;
- the first subdiagonal band (k = 2) of corr are equal to ARparameters[1]/(1-ARparameters[2]);
- in subsequent diagonal bands, (k = 3:order), of corr are ARparameters[1]*corr[k-1] + ARparameters[2]*corr[k-2].

A banded correlation matrix whose elements follow an ar2 pattern.

Chris Brien

mat.I, mat.J, mat.exp, mat.gau, mat.banded, mat.ar1, mat.ar3, mat.sar2, mat.ma1, mat.ma2, mat.arma

corr <- mat.ar2(ARparameters = c(0.4, 0.2), order = 4)
**mat.ar3**

*Forms an ar3 correlation matrix*

**Description**

Form the correlation matrix of order order whose correlations follow the ar3 pattern. The resulting matrix is banded.

**Usage**

`mat.ar3(ARparameters, order)`

**Arguments**

- `ARparameters` A numeric containing the three autoregressive parameter values of the process, being the weights given to the lag 1, lag 2 and lag 3 response values.
- `order` The order of the matrix to be formed.

**Details**

The correlations in the correlation matrix, `corr` say, are calculated from the autoregressive parameters, `ARparameters`.


- the diagonal of `corr` (k = 1) are one;
- the first subdiagonal band (k = 2) of `corr` are equal to `(ARparameters[1] + ARparameters[2]*ARparameters[3]) / omega`;

**Value**

A banded correlation matrix whose elements follow an ar3 pattern.

**Author(s)**

Chris Brien

**See Also**

`mat.I, mat.J, mat.banded, mat.exp, mat.gau, mat.ar1, mat.ar2, mat.sar2, mat.ma1, mat.ma2, mat.arma`

**Examples**

```r
corr <- mat.ar3(ARparameters = c(0.4, 0.2, 0.1), order = 4)
```
**Description**

Form the correlation matrix of order order whose correlations follow the arma pattern. The resulting matrix is banded.

**Usage**

```r
mat.arma(ARparameter, MAparameter, order)
```

**Arguments**

- **ARparameter** A numeric value for the autoregressive parameter of the process, being the weight given to the lag 1 response values.
- **MAparameter** A numeric value for the moving average parameter of the process, being the weight given to the lag 1 random variable.
- **order** The order of the matrix to be formed.

**Details**

The correlations in the correlation matrix, corr say, are calculated from the correlation parameters, ARparameters. The values in

- the diagonal (k = 1) of corr are one;
- the first subdiagonal band (k = 2) of corr are equal to ARparameters[1]/(1-ARparameters[2]);
- in subsequent diagonal bands, (k = 3:order), of corr are ARparameters[1]*corr[k-1] + ARparameters[2]*corr[k-2].

**Value**

A banded correlation matrix whose elements follow an arma pattern.

**Author(s)**

Chris Brien

**See Also**

- `mat.I`, `mat.J`, `mat.exp`, `mat.gau`, `mat.banded`, `mat.ar1`, `mat.ar3`, `mat.sar2`, `mat.ma1`, `mat.ma2`

**Examples**

```r
corr <- mat.arma(ARparameter = 0.4, MAparameter = -0.2, order = 4)
```
Form a banded matrix from a vector of values

Description

Takes the first value in \( x \) and places it down the diagonal of the \texttt{matrix}. Takes the second value in \( x \) and places it down the first subdiagonal, both below and above the diagonal of the \texttt{matrix}. The third value is placed in the second subdiagonal and so on, until the bands for which there are elements in \( x \) have been filled. All other elements in the \texttt{matrix} will be zero.

Usage

\texttt{mat.banded}(x, nrow, ncol)

Arguments

\begin{itemize}
  \item \texttt{x} \hspace{1cm} A \texttt{numeric} containing the values for each band from 1 to the length of \( x \).
  \item \texttt{nrow} \hspace{1cm} The number of rows in the banded \texttt{matrix} being formed.
  \item \texttt{ncol} \hspace{1cm} The number of columns in the banded \texttt{matrix} being formed.
\end{itemize}

Value

An \( \texttt{nrow} \times \texttt{ncol} \) \texttt{matrix}.

Author(s)

Chris Brien

See Also

\texttt{matmult, mat.ar1, mat.ar2, mat.ar3, mat.sar2, mat.exp, mat.gau, mat.ma1, mat.ma2, mat.arma, mat.I, mat.J}

Examples

\begin{verbatim}
m <- mat.banded(c(1,0.6,0.5), 5,5) m <- mat.banded(c(1,0.6,0.5), 3,4) m <- mat.banded(c(1,0.6,0.5), 4,3)
\end{verbatim}
**Description**

Form the direct product of the $m \times n$ matrix $A$ and the $p \times q$ matrix $B$. It is also called the Kronecker product and the right direct product. It is defined to be the result of replacing each element of $A$, $a_{ij}$, with $a_{ij}B$. The result matrix is $mp \times nq$.

The method employed uses the `rep` function to form two $mp \times nq$ matrices: (i) the direct product of $A$ and $J$, and (ii) the direct product of $J$ and $B$, where each $J$ is a matrix of ones whose dimensions are those required to produce an $mp \times nq$ matrix. Then the elementwise product of these two matrices is taken to yield the result.

**Usage**

```
mat.dirprod(A, B)
```

**Arguments**

- **A** The left-hand matrix in the product.
- **B** The right-hand matrix in the product.

**Value**

An $mp \times nq$ matrix.

**Author(s)**

Chris Brien

**See Also**

`matmult`, `mat.dirprod`

**Examples**

```
col.I <- mat.I(order=4)
row.I <- mat.I(order=28)
V <- mat.dirprod(col.I, row.I)
```
**mat.dirsum**

*Forms the direct sum of a list of matrices*

**Description**

The direct sum is the partitioned matrices whose diagonal submatrices are the matrices from which the direct sum is to be formed and whose off-diagonal submatrices are conformable matrices of zeroes. The resulting matrix is $m \times n$, where $m$ is the sum of the numbers of rows of the contributing matrices and $n$ is the sum of their numbers of columns.

**Usage**

```r
mat.dirsum(matrices)
```

**Arguments**

- `matrices` A list, each of whose component is a `matrix`.

**Value**

An $m \times n$ matrix.

**Author(s)**

Chris Brien

**See Also**

`mat.dirprod`, `matmult`

**Examples**

```r
m1 <- matrix(1:4, nrow=2)
m2 <- matrix(11:16, nrow=3)
m3 <- diag(1, nrow=2, ncol=2)
dsum <- mat.dirsum(list(m1, m2, m3))
```

---

**mat.exp**

*Forms an exponential correlation matrix*

**Description**

Form the correlation matrix of order equal to the length of coordinates. The matrix has diagonal elements equal to one and the off-diagonal element in the $i$th row and $j$th column equal to $\rho^k$ where $k = |\text{coordinate}[i] - \text{coordinate}[j]|$.

**Usage**

```r
mat.exp(rho, coordinates)
```
Arguments

    rho       The correlation for points a distance of one apart.
    coordinates The coordinates of points whose correlation matrix is to be formed.

Value

A correlation matrix whose elements depend on the power of the absolute distance apart.

Author(s)

Chris Brien

See Also

mat.I, mat.J, mat.banded, mat.ar1, mat.ar2, mat.ar3, mat.sar2, mat.ma1, mat.ma2, mat.arma, mat.gau

Examples

corr <- mat.exp(coordinates=c(3:6, 9:12, 15:18), rho=0.1)

Form an exponential correlation matrix

Description

Form the correlation matrix of order equal to the length of coordinates. The matrix has diagonal elements equal to one and the off-diagonal element in the ith row and jth column equal to $\rho^k$ where $k = (coordinate[i] - coordinate[j])^2$.

Usage

mat.gau(rho, coordinates)

Arguments

    rho       The correlation for points a distance of one apart.
    coordinates The coordinates of points whose correlation matrix is to be formed.

Value

A correlation matrix whose elements depend on the power of the absolute distance apart.

Author(s)

Chris Brien

See Also

mat.I, mat.J, mat.banded, mat.ar1, mat.ar2, mat.ar3, mat.sar2, mat.ma1, mat.ma2, mat.arma, mat.exp
Examples

corr <- mat.gau(coordinates=c(3:6, 9:12, 15:18), rho=0.1)

---

**mat.I**

*Forms a unit matrix*

**Description**

Form the unit or identity matrix of order order.

**Usage**

mat.I(order)

**Arguments**

order

The order of the matrix to be formed.

**Value**

A square matrix whose diagonal elements are one and its off-diagonal are zero.

**Author(s)**

Chris Brien

**See Also**

mat.J, mat.ar1

**Examples**

col.I <- mat.I(order=4)

---

**mat.J**

*Forms a square matrix of ones*

**Description**

Form the square matrix of ones of order order.

**Usage**

mat.J(order)

**Arguments**

order

The order of the matrix to be formed.
Value
A square matrix all of whose elements are one.

Author(s)
Chris Brien

See Also
mat.I, mat.ar1

Examples
    col.J <- mat.J(order=4)

Description
Form the correlation matrix of order order whose correlations follow the ma1 pattern. The matrix is banded and has diagonal elements equal to one and subdiagonal element equal to -MAparameter / (1 + MAparameter*MAparameter).

Usage
mat.ma1(MAparameter, order)

Arguments
    MAparameter The moving average parameter, being the weight applied to the lag 1 random pertubation.
    order The order of the matrix to be formed.

Value
A banded correlation matrix whose elements follow an ma1 pattern.

Author(s)
Chris Brien

See Also
mat.I, mat.J, mat.exp, mat.gau, mat.banded, mat.ar2, mat.ar3, mat.sar2, mat.ma2, mat.arma

Examples
    corr <- mat.ma1(MAparameter=0.4, order=4)
Description

Form the correlation matrix of order order whose correlations follow the ma2 pattern. The resulting matrix is banded.

Usage

mat.ma2(MAparameters, order)

Arguments

MAparameters A numeric containing the two moving average parameter values of the process, being the weights given to the lag 1 and lag 2 random pertubations.

order The order of the matrix to be formed.

Details

The correlations in the correlation matrix, corr say, are calculated from the moving average parameters, MAparameters. The values in

- the diagonal (k = 1) of corr are one;
- the first subdiagonal band (k = 2) of corr are equal to -MAparameters[1]*(1 - MAparameters[2]) / div;
- the second subdiagonal band (k = 3) of corr are equal to -MAparameters[2] / div;
- in subsequent diagonal bands, (k = 4:order), of corr are zero,


Value

A banded correlation matrix whose elements follow an ma2 pattern.

Author(s)

Chris Brien

See Also

mat.I, mat.J, mat.exp, mat.gau, mat.banded, mat.ar1, mat.ar3, mat.sar2, mat.ma1, mat.arma

Examples

corr <- mat.ma2(MAparameters = c(0.4, -0.2), order = 4)
Description

Calculates the variance matrix of the random effects for a natural cubic smoothing spline. It is the tri-diagonal matrix $G_s$ given by Verbyla et al., (1999) multiplied by the variance component for the random spline effects.

Usage

mat.ncssvar(sigma2s = 1, knot.points, print = FALSE)

Arguments

sigma2s   A numeric giving the value of the variance component for the random spline effects. The smoothing parameter is then the inverse of the ratio of this component to the residual variance.

knot.points   A numeric giving the values of the knots point used in fitting the spline. These must be ordered in increasing order.

print   A logical indicating whether to print the matrix.

Value

A matrix containing the variances and covariances of the random spline effects.

Author(s)

Chris Brien

References


See Also

Zncsspline.

Examples

Gs <- mat.ncssvar(knot.points = 1:10)
mat.random

Calculates the variance matrix for the random effects from a mixed
model, based on a supplied formula or a matrix.

Description

For \( n \) observations, compute the variance matrix of the random effects. The \texttt{mat.random} can be specified using a \texttt{formula} for the random effects and a \texttt{list} of values of the variance components for the terms specified in the random \texttt{formula}. If a \texttt{matrix} specifying the variances of the nuisance random effects is supplied then it is returned as the value from the function.

Usage

\texttt{mat.random(random, G, design, keep.order = TRUE)}

Arguments

\begin{itemize}
  \item \texttt{random} A \texttt{formula} or a \texttt{matrix}. If a \texttt{formula}, it specifies the random effects from which the \texttt{matrix} for the contribution of the random effects to the variance matrix can be generated. If it is a \texttt{matrix}, it must be an \( n \times n \) \texttt{matrix} and will be passed through as the required variance matrix for the random effects. The default is 0, which implies that there are no random effects.
  \item \texttt{G} This term only needs to be set if \texttt{random} is a \texttt{formula}. Then it is set to a \texttt{list}, in which each component is either a single value or a \texttt{matrix}; there needs to be a component for each term in the expanded \texttt{formula}, with the order of the terms and components matching. If it is a single value, a diagonal matrix of dimension equal to the product of the numbers of levels of the factors in its term. If it is a \texttt{matrix}, its dimension must be equal to the product of the numbers of levels of the factors in its term.
  \item \texttt{design} A \texttt{data.frame} containing the design to be used in an experiment and for which the variance matrix is required. It is not required when the only \texttt{formula} specified is an intercept-only \texttt{formula}.
  \item \texttt{keep.order} A \texttt{logical} indicating whether the terms should keep their position in the expanded \texttt{formula} projector, or reordered so that main effects precede two-factor interactions, which precede three-factor interactions and so on.
\end{itemize}

Details

If \( Z_i \) is the is incidence matrix for the random nuisance effects in \( u_i \) for a term in \texttt{random} and \( u_i \) has variance matrix \( G_i \) so that the contribution of the random effectst to the variance matrix for \( Y \) is \( V_a = \Sigma(Z_i G_i(Z_i)^T) \).

Value

A \( n \times n \) \texttt{matrix} containing the variance matrix for the random effects.

Author(s)

Chris Brien
See Also

mat.Vpredicts.

Examples

## Reduced example from Smith et al. (2015)
## Generate two-phase design
mill.fac <- fac.gen(list(Mrep = 2, Mday = 2, Mord = 3))
field.lay <- fac.gen(list(Frep = 2, Fplot = 4))
field.lay$Variety <- factor(c("D","E","Y","W","G","D","E","M"),
                          levels = c("Y","W","G","M","D","E"))
start.design <- cbind(mill.fac, field.lay[c(3,4,5,8,1,7,3,4,5,8,6,2),])
rownames(start.design) <- NULL

## Set gammas
gammas <- c(1, 0.1, 0.2, 0.3, 0.2, 1)
names(gammas) <- terms

## Specify matrices to calculate the variance matrix of the predicted fixed Variety effects
Vu <- with(start.design, fac.vcmat(Mrep, gammas["Mrep"])
     + fac.vcmat(fac.combine(list(Mrep,Mday)), gammas["Mrep:Mday"])
     + fac.vcmat(Frep, gammas["Frep"])
     + fac.vcmat(fac.combine(list(Frep,Fplot)), gammas["Frep:Fplot"]))

## Calculate the variance matrix of the predicted random Variety effects using formulae
Vu <- mat.random(random = ~ -1 + Mrep/Mday + Frep/Fplot,
                 G = as.list(gammas[c(4,5,2,3)]),
                 design = start.design)

---

**mat.sar** Forms an sar correlation matrix

**Description**

Form the correlation matrix of order order whose correlations follow the sar pattern. The resulting matrix is banded.

**Usage**

mat.sar(SARparameter, order)

**Arguments**

SARparameter A numeric containing the single value of the parameter from which the correlations are calculated.

order The order of the matrix to be formed.
Details

The values of the correlations in the correlation matrix, \( corr \) say, are calculated from the SARparameter, \( gamma \) as follows. The values in

- the diagonal of \( corr (k = 1) \) are one;
- the first subdiagonal band \((k = 2)\) of \( corr \) are equal to \( gamma/(1 + (gamma * gamma / 4)) \);
- the subsequent subdiagonal bands, \((k = 3:order)\), of \( corr \) are equal to \( gamma * corr[k-1] - (gamma * gamma/4) * corr[k-2] \).

Value

A banded correlation matrix whose elements follow an sar pattern.

Author(s)

Chris Brien

See Also

mat.I, mat.J, mat.banded, mat.exp, mat.gau, mat.ar1, mat.ar2, mat.ar3, mat.sar2, mat.ma1, mat.ma2, mat.arma

Examples

\[
corr <- mat.sar(SARparameter = -0.4, order = 4)
\]

mat.sar2 Forms an sar2 correlation matrix

Description

Form the correlation matrix of order \( order \) whose correlations follow the sar2 pattern, a pattern used in crop competition models. The resulting matrix is banded and is a constrained AR3 matrix.

Usage

\[
mat.sar2(gamma, order, print = NULL)
\]

Arguments

- **gamma**: A numeric containing the two values of \( gamma \), being parameters linked with spatial dependence and competition.
- **order**: The order of the matrix to be formed.
- **print**: A character giving the object to be printed. Currently, only the calculated values of the ar3 parameters can be printed. If NULL, nothing is printed.
Details

The values of the AR3 parameters, \( \phi \), are calculated from the gammas as follows:

\[
\phi[1] = \gamma[1] + 2 \times \gamma[2]; \\
\phi[2] = -\gamma[2] \times (2 \times \gamma[2] + \gamma[1]); \\
\phi[3] = \gamma[1] \times \gamma[2] \times \gamma[2].
\]

Then the correlations in the correlation matrix, \( \text{corr} \) say, are calculated from the correlation parameters, \( \phi \). Let \( \omega = 1 - \phi[2] - \phi[3] \times (\phi[1] + \phi[3]) \). Then the values in

- the diagonal of \( \text{corr} \) (\( k = 1 \)) are one;
- the first subdiagonal band (\( k = 2 \)) of \( \text{corr} \) are equal to \( (\phi[1] + \phi[2] \times \phi[3]) / \omega \);
- the second subdiagonal band (\( k = 3 \)) of \( \text{corr} \) are equal to \( (\phi[1] \times (\phi[1] + \phi[3]) + \phi[2] \times (1 - \phi[2])) / \omega \);
- the subsequent subdiagonal bands, (\( k = 4: \text{order} \)), of \( \text{corr} \) are equal to \( \phi[1] \times \text{corr}[k-1] + \phi[2] \times \text{corr}[k-2] + \phi[3] \times \text{corr}[k-3] \).

Value

A banded correlation matrix whose elements follow an sar2 pattern.

Author(s)

Chris Brien

See Also

mat.I, mat.J, mat.banded, mat.exp, mat.gau, mat.ar1, mat.ar2, mat.ar3, mat.sar, mat.ma1, mat.ma2, mat.arma

Examples

```r
corr <- mat.sar2(gamma = c(-0.4, 0.2), order = 4)
corr <- mat.sar2(gamma = c(-0.4, 0.2), order = 4, print = "ar3")
```

Usage

```r
mat.Vpred(W, Gg = 0, X = matrix(1, nrow = nrow(W), ncol = 1), Vu = 0, R, eliminate)
```

Description

For \( n \) observations, \( w \) effects to be predicted, \( f \) nuisance fixed effects and \( r \) nuisance random effects, the variances of a set of predicted effects is calculated using the incidence matrix for the effects to be predicted and, optionally, a variance matrix of the effects, an incidence matrix for the nuisance fixed factors and covariates, the variance matrix of the nuisance random effects in the mixed model and the residual variance matrix.

This function has been superseded by \text{mat.Vpredicts}, which allows the use of both matrices and formulae.
Arguments

*W*  The n x w incidence matrix for the w effects to be predicted.

*G*  The w x w variance matrix of the w effects to be predicted. If the effects to be predicted are fixed, set to 0.

*X*  The n x f incidence matrix for the f nuisance fixed factors and covariates. The default is a column vector of ones.

*V*  The n x r variance matrix of the r nuisance random effects. If there are none, set to zero.

*R*  The residual variance matrix.

*eliminate*  The n x n projector onto the subspace corresponding to the effects to be eliminated from the information matrix prior to inverting it to form the variance matrix of the predicted effects. It is only appropriate to use this option when the effects to be predicted are fixed.

Details

Firstly the information matrix is calculated as

\[
A <- t(W) \times Vinv \times W + ginv(Gg) - A \times ginv(t(X) \times Vinv \times X) \times t(A),
\]

where \( Vinv \leftarrow ginv(Vu + R) \), \( A = t(W) \times Vinv \times X \) and \( ginv(B) \) is the unique Moore-Penrose inverse of \( B \) formed using the eigendecomposition of \( B \).

If *eliminate* is set and the effects to be predicted are fixed then the reduced information matrix is calculated as \( A \leftarrow (I - \text{eliminate}) Vinv (I - \text{eliminate}) \).

Finally, the variance of the predicted effects is calculated: \( Vpred \leftarrow ginv(A) \).

Value

A w x w matrix containing the variances and covariances of the predicted effects.

Author(s)

Chris Brien

References


See Also

designAmeasures, mat.Vpredicts.

Examples

```r
## Reduced example from Smith et al. (2015)
## Generate two-phase design
mill.fac <- fac.gen(list(Mrep = 2, Mday = 2, Mord = 3))
field.lay <- fac.gen(list(Frep = 2, Fplot = 4))
field.lay$Variety <- factor(c("D","E","Y","W","G","D","E","M"),
levels = c("Y","W","G","M","D","E"))
start.design <- cbind(mill.fac, field.lay[c(3,4,5,8,1,7,3,4,5,8,6,2),])
rownames(start.design) <- NULL
```
## Set up matrices

\[
\begin{align*}
  n &\leftarrow \text{nrow}(\text{start.design}) \\
  W &\leftarrow \text{model.matrix}(\sim \cdot-1+\text{Variety}, \text{start.design}) \\
  \text{ng} &\leftarrow \text{ncol}(W) \\
  \text{Gg} &\leftarrow \text{diag}(1, \text{ng}) \\
  \text{Vu} &\leftarrow \text{with}(\text{start.design}, \text{fac.vcmat}(\text{Mrep}, 0.3) + \text{fac.vcmat}(\text{fac.combine}(\text{list(Mrep, Mday)}), 0.2) + \text{fac.vcmat}(\text{Frep}, 0.1) + \text{fac.vcmat}(\text{fac.combine}(\text{list(Frep, Fplot)}), 0.2)) \\
  R &\leftarrow \text{diag}(1, n)
\end{align*}
\]

## Calculate the variance matrix of the predicted random Variety effects

\[
\begin{align*}
  \text{Vp} &\leftarrow \text{mat.Vpred}(W = W, \text{Gg} = \text{Gg}, \text{Vu} = \text{Vu}, R = R) \\
  \text{designAmeasures}(\text{Vp})
\end{align*}
\]

## Calculate the variance matrix of the predicted fixed Variety effects, eliminating the grand mean

\[
\begin{align*}
  \text{Vp.reduc} &\leftarrow \text{mat.Vpred}(W = W, \text{Gg} = 0, \text{Vu} = \text{Vu}, R = R, \text{eliminate} = \text{projector}(\text{matrix}(1, \text{nrow} = n, \text{ncol} = n)/n)) \\
  \text{designAmeasures}(\text{Vp.reduc})
\end{align*}
\]

---

**mat.Vpredicts**

**Calculates the variances of a set of predicted effects from a mixed model, based on supplied matrices or formulae.**

### Description

For \( n \) observations, \( w \) effects to be predicted, \( f \) nuisance fixed effects, \( r \) nuisance random effects and \( n \) residuals, the variances of a set of predicted effects is calculated using the incidence matrix for the effects to be predicted and, optionally, a variance matrix of these effects, an incidence matrix for the nuisance fixed factors and covariates, the variance matrix of the nuisance random effects and the residual variance matrix. The matrices can be supplied directly or using formulae and a matrix specifying the variances of the nuisance random effects. The difference between mat.Vpredicts and mat.Vpred is that the former has different names for equivalent arguments and the latter does not allow for the use of formulae.

### Usage

```r
mat.Vpredicts(target, Gt = 0, fixed = ~ -1, random, G, R, design, 
eliminate, keep.order = TRUE, result = "variance.matrix")
```

### Arguments

- **target**: The \( n \times w \) incidence matrix for the \( w \) effects targeted for prediction, or a formula from which the matrix can be generated.
- **Gt**: The value of the variance component for the targeted effects or the \( w \times w \) variance matrix of the \( w \) targeted effects. If the targeted effects are fixed, set \( Gt \) to 0.
- **fixed**: The \( n \times f \) incidence matrix for the \( f \) nuisance fixed effects and covariates, or a formula from which the matrix can be generated. The default is a formula for an intercept-only model.
random  A formula or a matrix. If a formula, it specifies the random effects from which the matrix for the contribution of the random effects to the variance matrix can be generated. If it is a matrix, it must be an $n \times n$ matrix and will be passed on to form the variance matrix of the observations. The default is 0, which implies that there are no random effects.

$G$  This term only needs to be set if random is a formula. Then it is set to a list, in which each component is either a single value or a matrix; there needs to be a component for each term in the expanded formula, with the order of the terms and components matching. If it is a single value, a diagonal matrix of dimension equal to the product of the numbers of levels of the factors in its term. If it is a matrix, its dimension must be equal to the product of the numbers of levels of the factors in its term.

$R$  The $n \times n$ residual variance matrix. If $R$ is not set in the call, then it is set to the identity matrix.

design  A data.frame containing the design to be used in an experiment from which predictions are to be obtained. It is not required when the only formula specified is an intercept-only formula.

eliminate  The $n \times n$ projector onto the subspace corresponding to the effects to be eliminated from the information matrix prior to inverting it to form the variance matrix of the predicted effects. It is only appropriate to use this option when the effects to be predicted are fixed.

keep.order  A logical indicating whether the terms should keep their position in the expanded formula projector, or reordered so that main effects precede two-factor interactions, which precede three-factor interactions and so on.

result  A character indicating which matrix is to be returned: variance.matrix or information.matrix.

Details

The mixed model for which the predictions are to be obtained is of the form $Y = X\beta + Ww + Zu + e$, where $W$ is the incidence matrix for the target predicted effects $w$, $X$ is the incidence matrix for the fixed nuisance effects $\beta$, $Z$ is the incidence matrix for the random nuisance effects $u$, $e$ are the residuals; the $u$ are assumed to have variance matrix $G$ so that their contribution to the variance matrix for $Y$ is $Vu = ZGZ^T$ and $e$ is assumed to have variance matrix $R$. If the target effects are random then the variance matrix for $w$ is $G_t$ so that their contribution to the variance matrix for $Y$ is $WG_tW^T$.

As described in Hooks et al. (2009, Equation 19), the information matrix is calculated as

\[
A \leftarrow t(W) \%\% Vinv \%\% W + ginv(Gg) - A \%\% ginv(t(X) \%\% Vinv \%\% X) \%\% t(A),
\]

where $Vinv \leftarrow ginv(Vu + R)$, $A = t(W) \%\% Vinv \%\% X$ and $ginv(B)$ is the unique Moore-Penrose inverse of $B$ formed using the eigendecomposition of $B$.

Then, if eliminate is set and the effects to be predicted are fixed then the reduced information matrix is calculated as $A \leftarrow (I - eliminate) \%\% Vinv (I - eliminate)$.

Finally, if result is set to variance.matrix, the variance of the predicted effects is calculated: $Vpred \leftarrow ginv(A)$ and returned; otherwise the information matrix $A$ is returned. The rank of the matrix to be returned is obtained via a singular value decomposition of the information matrix, it being the number of nonzero eigenvalues. An eigenvalue is regarded as zero if it is less than daeTolerance, which is initially set to $\text{Machine}$\$\text{double.eps ^ 0.5}$ (about 1.5E-08). The function set.daeTolerance can be used to change daeTolerance.
**Value**

A \( w \times w \) matrix containing the variances and covariances of the predicted effects or the information matrix for the effects, depending on the setting of `result`. The matrix has its rank as an attribute.

**Author(s)**

Chris Brien

**References**


**See Also**

`designAmeasures`, `mat.random`, `mat.Vpred`.

**Examples**

```r
## Reduced example from Smith et al. (2015)
## Generate two-phase design
mill.fac <- fac.gen(list(Mrep = 2, Mday = 2, Mord = 3))
field.lay <- fac.gen(list(Frep = 2, Fplot = 4))
field.lay$Variety <- factor(c("D","E","Y","W","G","D","E","M"),
levels = c("Y","W","G","M","D","E"))
start.design <- cbind(mill.fac, field.lay[3,4,5,8,1,7,3,4,5,8,6,2],)
rownames(start.design) <- NULL

## Set gammas
gammas <- c(1, 0.1, 0.2, 0.3, 0.2, 1)
names(gammas) <- terms

## Specify matrices to calculate the variance matrix of the predicted fixed Variety effects
W <- model.matrix(~ -1 + Variety, start.design)
Vu <- with(start.design, fac.vcmat(Mrep, gammas["Mrep"])
     + fac.vcmat(fac.combine(list(Mrep,Mday)), gammas["Mrep:Mday"])
     + fac.vcmat(Frep, gammas["Frep"])
     + fac.vcmat(fac.combine(list(Frep,Fplot)), gammas["Frep:Fplot"])
R <- diag(1, nrow(start.design))

## Calculate variance matrix
Vp <- mat.Vpredicts(target = W, random=Vu, R=R, design = start.design)

## Calculate the variance matrix of the predicted random Variety effects using formulae
Vp <- mat.Vpredicts(target = ~ -1 + Variety, Gt = 1,
fixed = ~ -1, random = ~ -1 + Mrep/Mday + Frep/Fplot,
G = as.list(gammas[4,5,2,3]),
R = R, design = start.design)
designAmeasures(Vp)
```
Calculate the variance matrix of the predicted fixed Variety effects, eliminating the grand mean

```r
n <- nrow(start.design)
Vp.reduc <- mat.Vpredicts(target = ~ -1 + Variety,
                        random = ~ -1 + Mrep/Mday + Frep/Fplot,
                        G = as.list(gammas[c(4,5,2,3)]),
                        eliminate = projector(matrix(1, nrow = n, ncol = n)/n),
                        design = start.design)
designAmeasures(Vp.reduc)
```

---

**McIntyreTMV.dat**  
*The design and data from McIntyre's (1955) two-phase experiment*

**Description**

McIntyre (1955) reports an investigation of the effect of four light intensities on the synthesis of tobacco mosaic virus in leaves of tobacco *Nicotiana tabacum* var. Hickory Pryor. It is a two-phase experiment: the first phase is a treatment phase, in which the four light treatments are randomized to the tobacco leaves, and the second phase is an assay phase, in which the tobacco leaves are randomized to the half-leaves of assay plants. For more details see the vignette accessed via vignette("DesignNotes", package="dae").

**Usage**

```r
data(McIntyreTMV.dat)
```

**Format**

A data.frame containing 196 observations of 4 variables.

**Source**


---

**meanop**  
*computes the projection matrix that produces means*

**Description**

Replaced by `fac.meanop`. 
mpone

Converts the first two levels of a factor into the numeric values -1 and +1.

Usage

mpone(factor)

Arguments

factor The factor to be converted.

Value

A numeric vector.

Warning

If the factor has more than two levels they will be coerced to numeric values.

Author(s)

Chris Brien

See Also

mpone in package dae, factor, relevel.

Examples

## generate all combinations of two two-level factors
mp <- c("-", "+")
Frf3.trt <- fac.gen(list(A = mp, B = mp))

## add factor C, whose levels are the products of the levels of A and B
Frf3.trt$C <- factor(mpone(Frf3.trt$A)*mpone(Frf3.trt$B), labels = mp)
no.reps

Computes the number of replicates for an experiment

Description

Computes the number of pure replicates required in an experiment to achieve a specified power.

Usage

no.reps(multiple=1., df.num=1.,
       df.denom=expression((df.num + 1.) * (r - 1.)), delta=1.,
       sigma=1., alpha=0.05, power=0.8, tol=0.1, print=FALSE)

Arguments

multiple The multiplier, m, which when multiplied by the number of pure replicates of a treatment, r, gives the number of observations rm used in computing means for some, not necessarily proper, subset of the treatment factors; m is the replication arising from other treatment factors. However, for single treatment factor experiments the subset can only be the treatment factor and m = 1.
df.num The degrees of freedom of the numerator of the F for testing the term involving the treatment factor subset.
df.denom The degrees of freedom of the denominator of the F for testing the term involving the treatment factor subset.
delta The true difference between a pair of means for some, not necessarily proper, subset of the treatment factors.
sigma The population standard deviation.
alpha The significance level to be used.
power The minimum power to be achieved.
tol The maximum difference tolerated between the power required and the power computed in determining the number of replicates.
print TRUE or FALSE to have or not have a table of power calculation details printed out.

Value

A list containing nreps, a single numeric value containing the computed number of pure replicates, and power, a single numeric value containing the power for the computed number of pure replicates.

Author(s)

Chris Brien

See Also

power.exp, detect.diff in package dae.
Examples

```r
## Compute the number of replicates (blocks) required for a randomized
## complete block design with four treatments.
no.reps(multiple = 1, df.num = 3,
       df.denom = expression(df.num * (r - 1)), delta = 5,
       sigma = sqrt(20), print = TRUE)
```

Description

Yates (1937) describes a split-plot experiment that investigates the effects of three varieties of oats and four levels of Nitrogen fertilizer. The varieties are assigned to the main plots using a randomized complete block design with 6 blocks and the nitrogen levels are randomly assigned to the subplots in each main plot.

The columns in the data frame are: Blocks, Wplots, Subplots, Variety, Nitrogen, xNitrogen, Yield. The column xNitrogen is a numeric version of the factor Nitrogen. The response variable is Yield.

Usage

data(Oats.dat)

Format

A data.frame containing 72 observations of 7 variables.

Author(s)

Chris Brien

Source


Description

An object of class p2canon that contains information derived from two formulae using projs.2canon.
pcanon.object

Value

A list of class p2canon. It has two components: decomp and aliasing. The decomp component is composed as follows:

- It has a component for each component of Q1.
- Each of the components for Q1 is a list; each of these lists has one component for each of Q2 and a component Pres.
- Each of the Q2 components is a list of three components: pairwise, adjusted and Qproj. These components are based on an eigenanalysis of the relationship between the projectors for the parent Q1 and Q2 components.
  1. Each pairwise component is based on the nonzero canonical efficiency factors for the joint decomposition of the two parent projectors (see proj2.eigen).
  2. An adjusted component is based on the nonzero canonical efficiency factors for the joint decomposition of the Q1 component and the Q2 component, the latter adjusted for all Q2 projectors that have occurred previously in the list.
  3. The Qproj component is the adjusted projector for the parent Q2 component.

- The pairwise and adjusted components have the following components: efficiencies, aefficiency, mefficiency, ssefficiency, eefficiency, xefficiency, order and dforthog – for details see efficiency.criteria.

The aliasing component is a data.frame describing the aliasing between terms corresponding to two Q2 projectors when estimated in subspaces corresponding to a Q1 projector.

Author(s)

Chris Brien

See Also

projs.2canon, designAnatomy, pcanon.object.

pcanon.object  Description of a pcanon object

Description

An object of class pcanon that contains information derived from several formulae using designAnatomy.

Value

A list of class pcanon that has four components: (i) Q, (ii) terms, (iii) sources, (iv) marginality, and (v) aliasing. Each component is a list with as many components as there are formulae in the formulae list supplied to designAnatomy.

The Q list is made up of the following components:

1. The first component is the joint decomposition of two structures derived from the first two formulae, being the p2canon.object produced by projs.2canon.
2. Then there is a component for each further formulae; it contains the p2canon.object obtained by applying projs.2canon to the structure for a formula and the already established joint decomposition of the structures for the previous formulae in the formulae.
power.exp

3. The last component contains the list of the projectors that give the combined canonical decomposition derived from all of the formulae.

The terms, sources, marginality and aliasing lists have a component for each formula in the formulae argument to designAnatomy. Each component of the terms and sources lists has a character vector containing the terms or sources derived from its formula. For the marginality component, each component is the marginality matrix for the terms derived from its formula. For the aliasing component, each component is the aliasing data.frame for the source derived from its formula. The components of these four lists are produced by pstructure.formula and are copied from the pstructure.object for the formula. The names of the components of these four lists will be the names of the components in the formulae list.

The object has the attribute labels, which is set to "terms" or "sources" according to which of these were used to label the projectors when the object was created.

Author(s)

Chris Brien

See Also

designAnatomy, p2canon.object.

power.exp Computes the power for an experiment

Description

Computes the power for an experiment.

Usage

power.exp(rm=5., df.num=1., df.denom=10., delta=1., sigma=1., alpha=0.05, print=FALSE)

Arguments

rm The number of observations used in computing a mean.
df.num The degrees of freedom of the numerator of the F for testing the term involving the means.
df.denom The degrees of freedom of the denominator of the F for testing the term involving the means.
delta The true difference between a pair of means.
sigma The population standard deviation.
alpha The significance level to be used.
print TRUE or FALSE to have or not have a table of power calculation details printed out.

Value

A single numeric value containing the computed power.
Author(s)

Chris Brien

See Also

no.reps, detect.diff in package dae.

Examples

## Compute power for a randomized complete block design with four treatments
## and five blocks.
rm <- 5
power.exp(rm = rm, df.num = 3, df.denom = 3 * (rm - 1), delta = 5,
          sigma = sqrt(20), print = TRUE)


description

Print an aliasing data.frame

Description

Prints an aliasing data.frame.

Usage

## S3 method for class 'aliasing'
print(x, which.criteria = c("aefficiency","eefficiency","order"), ...)

Arguments

x

The data.frame that is also of class aliasing and is to be printed.

which.criteria

A character vector nominating the efficiency criteria to be included in the summary of aliasing between terms. It can be none, all or some combination of aefficiency, mefficiency, sefficiency, eefficiency, xefficiency, order and dforthog – for details see efficiency.criteria. If none, no criteria are printed.

...

Further arguments passed to the print method for data.frame.

Author(s)

Chris Brien

See Also

print, print.default, show.
Examples

```r
## Generate a data.frame with 3 factors length 12
pseudo.lay <- data.frame(pl = factor(1:12),
                          ab = factor(rep(1:4, times=3)),
                          a = factor(rep(1:2, times=6)))

## create a pstructure object
trt.struct <- pstructure(~ ab+a, data = pseudo.lay)

## print the object either using the Method function, the generic function or show
print.aliasing(trt.struct$aliasing)
print(trt.struct$aliasing, which.criteria = "none")
trt.struct$aliasing
```

Description

Print an object of class "projector", displaying the matrix and its degrees of freedom (rank).

Usage

```r
## S3 method for class 'projector'
print(x, ...)  
```

Arguments

- `x` The object of class "projector" to be printed.
- `...` Further arguments passed to or from other methods.

Author(s)

Chris Brien

See Also

`print`, `print.default`, `show`

`projector` for further information about this class.

Examples

```r
## set up a 2 x 2 mean operator that takes the mean of a vector of 2 values
m <- matrix(rep(0.5,4), nrow=2)

## create an object of class projector
proj.m <- projector(m)

## print the object either using the Method function, the generic function or show
print.projector(proj.m)
print(proj.m)
proj.m
```
print.pstructure  

Prints a pstructure.object

Description

Prints a pstructure.object, which is of class pstructure. The df, terms and sources are coerced into a data.frame and printed; the marginality matrix is printed separately.

Usage

## S3 method for class 'pstructure'
print(x, which = "all", ...)  

Arguments

x  
The pstructure.object, which is of class pstructure and is to be printed.

which  
A character vector nominating the components of the pstructure.object to print. Must be all or some combination of projectors, marginality, and aliasing.

...  
Further arguments passed to print.aliasing.

Author(s)

Chris Brien

See Also

print, print.default, show.

Examples

## Generate a data.frame with 4 factors, each with three levels, in standard order
ABCD.lay <- fac.gen(list(A = 3, B = 3, C = 3, D = 3))

## create a pstructure object based on the formula ((A*B)/C)*D
ABCD.struct <- pstructure.formula(~ ((A*B)/C)*D, data =ABCD.lay)

## print the object either using the Method function, the generic function or show
print.pstructure(ABCD.struct)
print(ABCD.struct)
ABCD.struct
**print.summary.p2canon**  
*Prints the values in an summary.p2canon object*

**Description**
Prints a summary.p2canon object, which is also a data.frame, in a pretty format.

**Usage**
```r
## S3 method for class 'summary.p2canon'
print(x, ...)
```

**Arguments**
- `x` A summary.p2canon object.
- `...` Further arguments passed to print.

**Value**
No value is returned.

**Author(s)**
Chris Brien

**See Also**
- `summary.p2canon`

**Examples**
```r
## PBIBD(2) from p. 379 of Cochran and Cox (1957) Experimental Designs.  
## 2nd edn Wiley, New York
PBIBD2.unit <- list(Block = 6, Unit = 4)
PBIBD2.nest <- list(Unit = "Block")
trt <- factor(c(1,4,2,5, 2,5,3,6, 3,6,1,4, 4,1,5,2, 5,2,6,3, 6,3,4,1))
PBIBD2.lay <- designRandomize(allocated = trt,  
    recipient = PBIBD2.unit,  
    nested.recipients = PBIBD2.nest)

##obtain projectors using pstructure
unit.struct <- pstructure(~ Block/Unit, data = PBIBD2.lay)
trt.struct <- pstructure(~ trt, data = PBIBD2.lay)

##obtain combined decomposition and print summary
unit.trt.p2canon <- projs.2canon(unit.struct$Q, trt.struct$Q)
summ <- summary(unit.trt.p2canon)
print(summ)
```
print.summary.pcanon  

Prints the values in an `summary.pcanon` object

Description

Prints a `summary.pcanon` object, which is also a `data.frame`, in a pretty format.

Usage

```r
## S3 method for class 'summary.pcanon'
print(x, aliasing.print = TRUE, ...)  
```

Arguments

- `x`: A `summary.pcanon` object.
- `aliasing.print`: A logical indicating whether the aliasing between sources is to be printed. Ignored for legacy `summary.pcanon` objects resulting from versions prior to 3.0-0 and so using `projs.canon`
- `...`: further arguments passed to `print`

Value

No value is returned.

Author(s)

Chris Brien

See Also

`summary.pcanon`

Examples

```r
## PBIBD(2) from p. 379 of Cochran and Cox (1957) Experimental Designs.
## 2nd edn Wiley, New York
PBIBD2.unit <- list(Block = 6, Unit = 4)
PBIBD2.nest <- list(Unit = "Block")
trt <- factor(c(1,4,2,5, 2,5,3,6, 3,6,1,4, 4,1,5,2, 5,2,6,3, 6,3,4,1))
PBIBD2.lay <- designRandomize(allocated = trt,
                           recipient = PBIBD2.unit,
                           nested.recipients = PBIBD2.nest)

##obtain combined decomposition and summarize
unit.trt.canon <- designAnatomy(list(unit=~ Block/Unit, trt=~ trt),
                               data = PBIBD2.lay)
summ <- summary(unit.trt.canon, which = c("aeff","eeff","order"))
print(summ)
```
proj2.combine

Compute the projection and Residual operators for two, possibly nonorthogonal, projectors

Description

The canonical relationship between a pair of projectors is established by decomposing the range of Q1 into a part that pertains to Q2 and a part that is orthogonal to Q2. It also produces the nonzero canonical efficiency factors for the joint decomposition of Q1 and Q and the corresponding eigenvectors of Q1 (James and Wilkinson, 1971). Q1 and Q2 may be nonorthogonal.

Usage

proj2.combine(Q1, Q2)

Arguments

Q1 A symmetric projector whose range is to be decomposed.
Q2 A symmetric projector whose range in Q1 is required.

Details

The nonzero canonical efficiency factors are the nonzero eigenvalues of \( Q1 \times Q2 \times Q1 \) (James and Wilkinson, 1971). An eigenvalue is regarded as zero if it is less than \( \text{daeTolerance} \), which is initially set to \( \text{Machine$double.eps}^0.5 \) (about 1.5E-08). The function \text{set.daeTolerance} can be used to change \( \text{daeTolerance} \).

The eigenvectors are the eigenvectors of Q1 corresponding to the nonzero canonical efficiency factors. The eigenvectors for Q2 can be obtained by premultiplying those for Q1 by Q2.

Qres is computed using equation 4.10 from James and Wilkinson (1971), if the number of distinct canonical efficiency factors is less than 10. If this fails to produce a projector or the number of distinct canonical efficiency factors is 10 or more, equation 5.3 of Payne and Tobias (1992) is used to obtain Qres. In this latter case, \( Qres = Q1 - Q1 \times \text{ginv}(Q2 \times Q1 \times Q2) \times Q1 \). Qconf is obtained by subtracting Qres from Q1.

Value

A list with the following components:

1. \textbf{efficiencies}: a vector containing the nonzero canonical efficiency factors;
2. \textbf{eigenvectors}: an \( n \times r \) matrix, where \( n \) is the order of the projectors and \( r \) is the number of nonzero canonical efficiency factors; it contains the eigenvectors of Q1 corresponding to the nonzero canonical efficiency factors.
3. \textbf{Qconf}: a projector onto the part of the range of Q1 with which Q2 is confounded;
4. \textbf{Qres}: a projector onto the part of the range of Q1 that is orthogonal to the range of Q2.

Author(s)

Chris Brien
References


See Also

`proj2.eigen`, `proj2.efficiency`, `decomp.relate` in package `dae`.

`projector` for further information about this class.

Examples

```r
## PBIBD(2) from p. 379 of Cochran and Cox (1957) Experimental Designs.
## 2nd edn Wiley, New York
PBIBD2.unit <- list(Block = 6, Unit = 4)
PBIBD2.nest <- list(Unit = "Block")
trt <- factor(c(1, 4, 2, 5, 2, 5, 3, 6, 3, 6, 1, 4, 4, 1, 5, 2, 5, 2, 6, 3, 6, 3, 4, 1))
PBIBD2.lay <- designRandomize(allocated = trt,
                             recipient = PBIBD2.unit,
                             nested.recipients = PBIBD2.nest)

## obtain sets of projectors
unit.struct <- pstructure(~ Block/Unit, data = PBIBD2.lay)
trt.struct <- pstructure(~ trt, data = PBIBD2.lay)

## obtain the projection operators for the interblock analysis
PBIBD2.Bops <- proj2.combine(unit.struct$Q["Unit[Block]"], trt.struct$Q["trt"])
Q.B.T <- PBIBD2.Bops$Qconf
Q.B.res <- PBIBD2.Bops$Qres

## demonstrate their orthogonality
is.allzero(Q.B.T %*% Q.B.res)
```

---

**proj2.efficiency**

*Computes the canonical efficiency factors for the joint decomposition of two projectors*

Description

Computes the canonical efficiency factors for the joint decomposition of two projectors (James and Wilkinson, 1971).

Usage

`proj2.efficiency(Q1, Q2)`

Arguments

- **Q1**: An object of class "projector".
- **Q2**: An object of class "projector".
The nonzero canonical efficiency factors are the nonzero eigenvalues of \( Q_1 \%*\% Q_2 \%*\% Q_1 \) (James and Wilkinson, 1971). An eigenvalue is regarded as zero if it is less than \( \text{daeTolerance} \), which is initially set to \( \text{Machine}$\_\text{double.\_eps}^{0.5} \) (about 1.5E-08). The function \( \text{set.daeTolerance} \) can be used to change \( \text{daeTolerance} \).

A vector containing the nonzero canonical efficiency factors.

Chris Brien


See Also

\( \text{efficiency.criteria, proj2.eigen, proj2.combine} \) in package \( \text{dae, eigen}. \)
\( \text{projector} \) for further information about this class.

## Examples

```
## PBIBD(2) from p. 379 of Cochran and Cox (1957) Experimental Designs.
## 2nd edn Wiley, New York
PBIBD2.unit <- list(Block = 6, Unit = 4)
PBIBD2.nest <- list(Unit = "Block")
trt <- factor(c(1,4,2,5, 2,5,3,6, 3,6,1,4, 4,1,5,2, 5,2,6,3, 6,3,4,1))
PBIBD2.lay <- designRandomize(allocated = trt,
                              recipient = PBIBD2.unit,
                              nested.recipients = PBIBD2.nest)

## obtain sets of projectors
unit.struct <- pstructure(~ Block/Unit, data = PBIBD2.lay)
trt.struct <- pstructure(~ trt, data = PBIBD2.lay)

## save intrablock efficiencies
eff.intra <- proj2.efficiency(unit.struct$Q["Block"], trt.struct$Q["trt"])
```
Usage
proj2.eigen(Q1, Q2)

Arguments
Q1 An object of class "projector".
Q2 An object of class "projector".

Details
The component efficiencies is a vector containing the nonzero canonical efficiency factors for the joint decomposition of the two projectors. The nonzero canonical efficiency factors are the nonzero eigenvalues of Q1 %*% Q2 %*% Q1 (James and Wilkinson, 1971). An eigenvalue is regarded as zero if it is less than daeTolerance, which is initially set to .Machine$double.eps ^ 0.5 (about 1.5E-08). The function set.daeTolerance can be used to change daeTolerance.

The component eigenvectors is an n x r matrix, where n is the order of the projectors and r is the number of nonzero canonical efficiency factors; it contains the eigenvectors of Q1 corresponding to the nonzero canonical efficiency factors. The eigenvectors for Q2 can be obtained by premultiplying those for Q1 by Q2.

Value
A list with components efficiencies and eigenvectors.

Author(s)
Chris Brien

References

See Also
proj2.efficiency, proj2.combine in package dae, eigen. projector for further information about this class.

Examples
## PBIBD(2) from p. 379 of Cochran and Cox (1957) Experimental Designs.
## 2nd edn Wiley, New York
PBIBD2.unit <- list(Block = 6, Unit = 4)
PBIBD2.nest <- list(Unit = "Block")
trt <- factor(c(1,4,2,5, 2,5,3,6, 3,6,1,4, 4,1,5,2, 5,2,6,3, 6,3,4,1))
PBIBD2.lay <- designRandomize(allocated = trt,
                                  recipient = PBIBD2.unit,
                                  nested.recipients = PBIBD2.nest)

## obtain sets of projectors
unit.struct <- pstructure(~ Block/Unit, data = PBIBD2.lay)
trt.struct <- pstructure(~ trt, data = PBIBD2.lay)

## obtain intra- and inter-block decompositions
decomp.inter <- proj2.eigen(unit.struct$Q[["Block"]], trt.struct$Q[["trt"]])
decomp.intra <- proj2.eigen(unit.struct$Q[["Unit[Block]"]], trt.struct$Q[["trt"]])

#extract intrablock efficiencies
decomp.intra$efficiencies

---

**Description**

The class "projector" is the subclass of the class "matrix" in which matrices are square, symmetric and idempotent.

The function projector tests whether a matrix satisfies these criteria and if it does creates a "projector" object, computing the projector’s degrees of freedom and adding them to the object.

**Usage**

projector(Q)

**Arguments**

Q The matrix to be made into a projector.

**Details**

In checking that the matrix is square, symmetric and idempotent, the equality of the matrix with either its transpose or square is tested. In this, a difference in elements is considered to be zero if it is less than daeTolerance, which is initially set to .Machine$double$eps ^ 0.5 (about 1.5E-08). The function set.daeTolerance can be used to change daeTolerance.

**Value**

An object of Class "projector" that consists of a square, symmetric, idempotent matrix and degrees of freedom (rank) of the matrix.

**Author(s)**

Chris Brien

**See Also**

degfree, correct.degfree in package dae.

projector for further information about this class.
Examples

```r
## set up a 2 x 2 mean operator that takes the mean of a vector of 2 values
m <- matrix(rep(0.5,4), nrow=2)

## create an object of class projector
proj.m <- projector(m)

## check that it is a valid projector
is.projector(proj.m)
```

---

**projector-class**

*Class projector*

**Description**

The class "projector" is the subclass of matrices that are square, symmetric and idempotent. 

*is.projector* is the membership function for this class.

*degfree* is the extractor function for the degrees of freedom and *degfree<-* is the replacement function.

*correct.degfree* checks whether the stored degrees of freedom are correct.

**Objects from the Class**

An object of class "projector" consists of a square, symmetric, idempotent matrix along with its degrees of freedom (rank).

Objects can be created by calls of the form *new("projector", data, nrow, ncol, byrow, dimnames, ...)*. However, this does not add the degrees of freedom to the object. These can be added using the replacement function *degfree<-*. Alternatively, the function *projector* creates the new object from a *matrix*, adding its degrees of freedom at the same time.

**Slots**

.Data: Object of class "matrix"

.degfree: Object of class "integer"

**Extends**


**Methods**

*coerce* signature(from = "projector", to = "matrix")

*print* signature(x = "projector")

*show* signature(object = "projector")

**Author(s)**

Chris Brien
See Also

`projector`, `degfree`, `correct.degfree` in package `dae`.

Examples

```r
showClass("projector")

## set up a 2 x 2 mean operator that takes the mean of a vector of 2 values
m <- matrix(rep(0.5,4), nrow=2)

## create an object of class projector
proj.m <- projector(m)

## check that it is a valid projector
is.projector(proj.m)

## create a projector based on the matrix m
proj.m <- new("projector", data=m)

## add its degrees of freedom and print the projector
degfree(proj.m) <- proj.m
```

---

projs.2canon

*A canonical analysis of the relationships between two sets of projectors*

Description

Computes the canonical efficiency factors for the joint decomposition of two structures or sets of mutually orthogonally projectors (Brien and Bailey, 2009), orthogonalizing projectors in the Q2 list to those earlier in the list of projectors with which they are partially aliased. The results can be summarized in the form of a skeleton ANOVA table.

Usage

`projs.2canon(Q1, Q2)`

Arguments

Q1  
A list whose components are objects of class "projector".

Q2  
A list whose components are objects of class "projector".

Details

Two loops, one nested within the other, are performed. The first cycles over the components of Q1 and the nested loop cycles over the components of Q2. The joint decomposition of the two projectors in each cycle, one from Q1 (say Q1[i]) and the other from Q2 (say Q2[j]) is obtained using `proj2.combine`. In particular, the nonzero canonical efficiency factors for the joint decomposition of the two projectors is obtained. The nonzero canonical efficiency factors are the nonzero eigenvalues of `Q1[i] %*% Q2[j] %*% Q1[i]` (James and Wilkinson, 1971). An eigenvalue is regarded as zero if it is less than `daeTolerance`, which is initially set to `.Machine$double.eps ^ 0.5` (about 1.5E-08). The function `set.daeTolerance` can be used to change `daeTolerance`. 
However, a warning occurs if any pair of Q2 projectors (say Q2[[j]] and Q2[[k]]) do not have adjusted orthgonality with respect to any Q1 projector (say Q1[[i]]), because they are partially aliased. That is, if Q2[[j]] %*% Q1[[i]] %*% Q2[[k]] is nonzero for any pair of different Q2 projectors and any Q1 projector. When it is nonzero, the projector for the later term in the list of projectors is orthogonalized to the projector that is earlier in the list. A list of such projectors is returned in the aliasing component of the p2canon.object. The entries in the aliasing component gives the amount of information that is aliased with previous terms.

Value

A p2canon.object.

Author(s)

Chris Brien

References


See Also

summary.p2canon, efficiencies.p2canon, projs.combine.p2canon, pstructure, proj2.efficiency, proj2.combine, proj2.eigen, efficiency.criteria in package dae, eigen. projector for further information about this class.

Examples

## PBIBD(2) from p. 379 of Cochran and Cox (1957) Experimental Designs.
## 2nd edn Wiley, New York
PBIBD2.unit <- list(Block = 6, Unit = 4)
PBIBD2.nest <- list(Unit = "Block")
trt <- factor(c(1,4,2,5, 2,5,3,6, 3,6,1,4, 4,1,5,2, 5,2,6,3, 6,3,4,1))
PBIBD2.lay <- designRandomize(allocated = trt,
recipient = PBIBD2.unit,
nested.recipients = PBIBD2.nest)

##obtain projectors using pstructure
unit.struct <- pstructure(~ Block/Unit, data = PBIBD2.lay)
trt.struct <- pstructure(~ trt, data = PBIBD2.lay)

##obtain combined decomposition and summarize
unit.trt.p2canon <- projs.2canon(unit.struct$Q, trt.struct$Q)
summary(unit.trt.p2canon)
projs.combine.p2canon

Extract, from a p2canon object, the projectors that give the combined canonical decomposition

Description

Extracts, from a p2canon object obtained using projs.2canon, the projectors that give the combined canonical decomposition of two sets of projectors (Brien and Bailey, 2009).

Usage

projs.combine.p2canon(object)

Arguments

object A list of class p2canon produced by projs.2canon.

Value

A list, each of whose components is a projector in the decomposition.

Author(s)

Chris Brien

References


See Also

projs.2canon, proj2.eigen, proj2.combine in package dae.

projector for further information about this class.

Examples

```r
## PBIBD(2) from p. 379 of Cochran and Cox (1957) Experimental Designs.
## 2nd edn Wiley, New York
PBIBD2.unit <- list(Block = 6, Unit = 4)
PBIBD2.nest <- list(Unit = "Block")
trt <- factor(c(1,4,2,5, 2,5,3,6, 3,6,1,4, 4,1,5,2, 5,2,6,3, 6,3,4,1))
PBIBD2.lay <- designRandomize(allocated = trt,
                            recipient = PBIBD2.unit,
                            nested.recipients = PBIBD2.nest)

## obtain sets of projectors
unit.struct <- pstructure(~ Block/Unit, data = PBIBD2.lay)
trt.struct <- pstructure(~ trt, data = PBIBD2.lay)

## obtain combined decomposition
unit.trt.p2canon <- projs.2canon(unit.struct$Q, trt.struct$Q)
UcombineT <- projs.combine.p2canon(unit.trt.p2canon)
```
pstructure.formula

Takes a formula and constructs a pstructure.object that includes the orthogonalized projectors for the terms in a formula

Description

Constructs a pstructure.object that includes a set of mutually orthogonal projectors, one for each term in the formula. These are used to specify a structure, or an orthogonal decomposition of the data space. There are three methods available for orthogonalizing the projectors corresponding to the terms in the formula: differencing, eigenmethods or the default hybrid method.

It is possible to use this function to find out what sources are associated with the terms in a model and to determine the marginality between terms in the model. The marginality matrix can be saved.

Usage

## S3 method for class 'formula'
pstructure(formula, keep.order = TRUE, grandMean = FALSE, orthogonalize = "hybrid", labels = "sources", marginality = NULL, check.marginality = TRUE, omit.projectors = FALSE, which.criteria = c("aefficiency","eEfficiency","order"), aliasing.print = TRUE, data = NULL, ...)

Arguments

formula An object of class formula from which the terms will be obtained.
keep.order A logical indicating whether the terms should keep their position in the expanded formula projector, or reordered so that main effects precede two-factor interactions, which precede three-factor interactions and so on.
grandMean A logical indicating whether the projector for the grand mean is to be included in the set produced.
orthogonalize A character vector indicating the method for orthogonalizing a projector to those for terms that occurred previously in the formula. Three options are available: hybrid; differencing; eigenmethods. The hybrid option is the most general and uses the relationships between the projection operators for the terms in the formula to decide which projectors to substract and which to orthogonalize using eigenmethods. The differencing option subtracts, from the current projector, those previously orthogonalized projectors for terms whose factors are a subset of the current projector's factors. The eigenmethods option recursively orthogonalizes the projectors using an eigenanalysis of each projector with previously orthogonalized projectors.
labels A character nominating the type of labels to be used in labelling the projectors, and which will be used also in the output tables, such the tables of the aliasing in the structure. The two alternatives are terms and sources. Terms have all factors/variables in it separated by colons (:). Sources have factors/variables in them that represent interactions separated by hashes (#); if some factors are nested within others, the nesting factors are surrounded by square brackets ([ and ]) and separated by colons (:). If some generalized, or combined, factors have no marginal terms, the constituent factors are separated by colons (:) and if they interact with other factors in the source they will be parenthesized.
pstructure.formula

marginality

A square matrix that can be used to supply the marginality matrix when it is desired to overwrite the calculated marginality matrix or when it is not being calculated. It should consist of zeroes and ones that gives the marginalites of the terms in the formula. It must have the row and column names set to the terms from the expanded formula, including being in the same order as these terms. The entry in the ith row and jth column will be one if the ith term is marginal to the jth term i.e. the column space of the ith term is a subspace of that for the jth term and so the source for the jth term is to be made orthogonal to that for the ith term. Otherwise, the entries are zero. A row and column should not be included for the grand mean even if grandMean is TRUE.

check.marginality

A logical indicating whether the marginality matrix, when it is supplied, is to be checked against that computed by pstructure.formula. It is ignored when orthogonalize is set to eigenmethods.

omit.projectors

A logical, which, if TRUE, results in the projectors in the Q of the pstructure.object being replaced by their degrees of freedom. These will be the degrees of freedom of the sources. This option is included a device for saving storage when the projectors are not required for further analysis.

which.criteria

A character vector nominating the efficiency criteria to be included in the summary of aliasing between terms. It can be none, all or some combination of aefficiency, mefficiency, sefficiency, eefficiency, xefficiency, order and dforthog – for details see efficiency.criteria. If none, no summary is printed.

aliasing.print

A logical indicating whether the aliasing between sources within the structure is to be printed.

data

A data frame contains the values of the factors and variables that occur in formula.

... further arguments passed to terms.

Details

Firstly, the primary projector $X(X'X)^{-1}X'$, where $X$ is the design matrix for the term, is calculated for each term. Then each projector is made orthogonal to terms aliased with it, either by differencing, eigenmethods or the default hybrid method.

Differencing relies on comparing the factors involved in two terms, one previous to the other, to identify whether to subtract the orthogonalized projector for the previous term from the primary projector of the other. It does so if factors/variables for the previous term are a subset of the factors/variables for the other term. This relies on ensuring that all projectors whose factors/variables are a subset of the current projector occur before it in the expanded formula. It is checked that the set of matrices are mutually orthogonal. If they are not then a warning is given. It may happen that differencing does not produce a projector, in which case eigenmethods must be used.

Eigenmethods forces each projector to be orthogonal to all terms previous to it in the expanded formula. It uses equation 4.10 of James and Wilkinson (1971), which involves calculating the canonical efficiency factors for pairs of primary projectors. It produces a table of efficiency criteria for partially aliased terms. Again, the order of terms is crucial. This method has the disadvantage that the marginality of terms is not determined and so sources names are set to be the same as the term names, unless a marginality matrix is supplied.
The hybrid method is the most general and uses the relationships between the projection operators for the terms in the formula to decide which projectors to subtract and which to orthogonalize using eigenmethods. If $Q_i$ and $Q_j$ are two projectors for two different terms, with $i < j$, then

1. if $Q_j Q_i \neq 0$ then have to orthogonalize $Q_j$ to $Q_i$.
2. if $Q_j Q_i = Q_j$, then if $Q_i = Q_j$, they are equal and $Q_j$ will be removed from the list of terms; otherwise they are marginal and $Q_i$ is subtracted from $Q_j$.
3. if have to orthogonalize and $Q_j Q_i = Q_i$ then $Q_j$ is aliased with previous terms and will be removed from the list of terms; otherwise $Q_i$ is partially aliased with $Q_j$ and $Q_j$ is orthogonalized to $Q_i$ using eigenmethods.

Again, the order of terms is crucial in this process.

Value

A `pstructure.object`.

Author(s)

Chris Brien

References


See Also

`proj2.efficiency, proj2.combine, proj2.eigen, projs.2canon` in package `dae`.

`eigen`, `projector` for further information about this class.

Examples

```r
## PBIBD(2) from p. 379 of Cochran and Cox (1957) Experimental Designs.
## 2nd edn Wiley, New York
PBIBD2.unit <- list(Block = 6, Unit = 4)
PBIBD2.nest <- list(Unit = "Block")
trt <- factor(c(1,4,2,5, 2,5,3,6, 3,6,1,4, 4,1,5,2, 5,2,6,3, 6,3,4,1))
PBIBD2.lay <- designRandomize(allocated = trt,
                              recipient = PBIBD2.unit,
                              nested.recipients = PBIBD2.nest)
## manually obtain projectors for units
Q.G <- projector(matrix(1, nrow=24, ncol=24)/24)
Q.B <- projector(fac.meanop(PBIBD2.lay$Block) - Q.G)
Q.BP <- projector(diag(1, nrow=24) - Q.B - Q.G)
## manually obtain projector for trt
Q.T <- projector(fac.meanop(PBIBD2.lay$trt) - Q.G)
## compute intrablock efficiency criteria
effic <- proj2.efficiency(Q.BP, Q.T)
effic
efficiency.criteria(effic)
```
### pstructure.object

--

## obtain projectors using pstructure.formula

```r
unit.struct <- pstructure(~ Block/Unit, data = PBIBD2.lay)
trt.struct <- pstructure(~ trt, data = PBIBD2.lay)
```

## obtain combined decomposition and summarize

```r
unit.trt.p2canon <- projs.2canon(unit.struct$Q, trt.struct$Q)
summary(unit.trt.p2canon, which = c("aeff","eiff","order"))
```

---

### Description

Description of a pstructure object

An object of class `pstructure` that contains information derived from a `formula` using `pstructure.formula`. It also inherits from class `list`.

### Value

A list of class `pstructure` with the following components:

1. `Q`: a list with a component of class `projector`, being the orthogonalized projectors for each non-aliased term/source in the formula; if `grandMean` is `TRUE` in the call to `pstructure.formula` then it also includes the projector for it;
2. `terms`: a `character` vector with the non-aliased term names; if `grandMean` is `TRUE` in the call to `pstructure.formula` then the first term will be "Mean";
3. `sources`: a `character` vector with the non-aliased source names;
4. `marginality`: a `matrix` of zeroes and ones with the same number of rows and columns as number of non-aliased terms, excluding the term for the grand mean even when `grandMean` is `TRUE`; the row names and column names are the elements `terms`, excluding "Mean"; the entry in the ith row and jth column will be one if the ith term is marginal to the jth term i.e. the column space of the ith term is a subspace of that for the jth term and so the source for the jth term will have been made orthogonal to that for the ith term; otherwise, the entries are zero.
5. `aliasing`: a `data.frame` containing the information about the (partial) aliasing between the sources in the formula. The columns are:
   - `Source`: the source names, or associated term name, for those that are (partially) aliased with previous sources;
   - `df`: the remaining degrees of freedom for the source;
   - `Alias`: the source with which the current entry is (partially) aliased;
   - `efficiency criteria`: a set of columns for the complete set of criteria calculated by `efficiency.criteria`; the criteria reflect the amount of information that is aliased with previous sources and a line is included in the component that reports the information remaining after adjustment for previous sources.

The information provided depends on the setting of `orthogonalize`. All the information is provided for the "hybrid" option. For the option "differencing", no efficiency criteria are included and either the terms/sources of the `Alias` are set to "unknown" and the `df` are set to NA when these are unknown. For the option "eigenmethods", the previous terms/sources cannot be identified and so all values of `Alias` are set to NA. If there is no (partial) aliasing then the component is set to NULL.

The object has the attribute `labels`, which is set to "terms" or "sources" according to which of these label the projectors.
Author(s)

Chris Brien

See Also

`pstructure.formula` and, for further information about the projector class, `projector`.

**qqyeffects**

Half or full normal plot of Yates effects

Description

Produces a half or full normal plot of the Yates effects from a $2^k$ factorial experiment.

Usage

```r
qqyeffects(aov.obj, error.term="Within", data=NULL, pch=16, 
            full=FALSE, ...)
```

Arguments

- `aov.obj`: An `aov` object or `aovlist` object created from a call to `aov`.
- `error.term`: The term from the `Error` function from which the Yates effects are estimated. Only required when `Error` used in call to `aov`.
- `data`: A `data.frame` in which the variables specified in the `aov.obj` will be found. If missing, the variables are searched for in the standard way.
- `pch`: The number of a plotting symbol to be drawn when plotting points (use help(points) for details).
- `full`: Whether a full or half normal plot is to be produced. The default is for a half-normal plot; `full=TRUE` produces a full normal plot.
- `...`: Further graphical parameters may be specified (use help(par) for possibilities).

Details

A half or full normal plot of the Yates effects is produced. You will be able to interactively select effects to be labelled (click reasonably close to the point and on the side where you want the label placed). **Right click on the graph and select Stop when you have finished labelling effects.** A regression line fitted to the unselected effects and constrained to go through the origin is plotted. Also, a list of the labelled effects, if any, are printed to standard output.

Value

Returns, invisibly, a list with components `x` and `y`, giving coordinates of the plotted points.

Author(s)

Chris Brien

See Also

`yates.effects` in package `dae`, `qqnorm`. 
Examples

```r
## analysis of 2^4 factorial experiment from Table 10.6 of Box, Hunter and
## use ?Fac4Proc.dat for data set details
data(Fac4Proc.dat)
Fac4Proc.aov <- aov(Conv ~ Catal * Temp * Press * Conc + Error(Runs),
                     Fac4Proc.dat)
qqyeffects(Fac4Proc.aov, error.term="Runs", data=Fac4Proc.dat)
```

---

**rep.data.frame**

*Replicate the rows of a data.frame by repeating each row consecutively and/or repeating all rows as a group*

Description

Replicate the rows of a `data.frame` by repeating each row consecutively and/or repeating all rows as a group.

Usage

```r
## S3 method for class 'data.frame'
rep(x, times=1, each=1, ...)
```

Arguments

- `x`: A `data.frame` whose rows are to be repeated.
- `times`: The number of times to repeat the whole set of rows, after the rows have been replicated consecutively each times.
- `each`: The number of times to replicate consecutively each row in the `data.frame`.
- `...`: Further arguments passed to or from other methods. Unused at present.

Value

A `data.frame` with replicated rows.

Author(s)

Chris Brien

See Also

- `fac.gen` in package `dae` and `rep`

Examples

```r
rep(fac.gen(list(a = 2, b = 2)), times=2, each=2)
```
resid.errors  Extract the residuals for a fitted model

Description
An alias for the generic function `residuals`. When it is available, the method `residuals.aovlist` extracts residuals, which is provided in the package `dae` to cover `aovlist` objects.

Usage
```r
resid.errors(...)```

Arguments
```r
...
```
Arguments passed to `residuals.aovlist`.

Value
A numeric vector containing the residuals.

Note
See `residuals.aovlist` for specific information about the residuals when an `Error` function is used in the call to the `aov` function.

Author(s)
Chris Brien

See Also
`fitted.errors`, `residuals.aovlist`, `tukey.1df` in package `dae`.

Examples
```r
## set up data frame for randomized complete block design in Table 4.4 from ## Box, Hunter and Hunter (2005) Statistics for Experimenters. 2nd edn ## New York, Wiley.
RCBDPen.dat <- fac.gen(list(Blend=5, Flask=4))
RCBDPen.dat$Treat <- factor(rep(c("A","B","C","D"), times=5))
RCBDPen.dat$Yield <- c(89,88,97,94,84,77,92,79,81,87,87,85,87,92,89,84,79,81,80,88)

## perform the analysis of variance
RCBDPen.aov <- aov(Yield ~ Blend + Treat + Error(Blend/Flask), RCBDPen.dat)
summary(RCBDPen.aov)

## two equivalent ways of extracting the residuals
res <- residuals.aovlist(RCBDPen.aov)
res <- residuals(RCBDPen.aov, error.term = "Blend:Flask")
res <- resid.errors(RCBDPen.aov)
```
residuals.aovlist

Extract the residuals from an aovlist object

Description

Extracts the residuals from error.term or, if error.term is not specified, the last error.term in the analysis. It is a method for the generic function residuals.

Usage

## S3 method for class 'aovlist'
residuals(object, error.term=NULL, ...)

Arguments

object An aovlist object created from a call to aov.
error.term The term from the Error function for which the residuals are to be extracted. If error.term is NULL the residuals are extracted from the last Error term.
...
Further arguments passed to or from other methods.

Value

A numeric vector containing the residuals.

Author(s)

Chris Brien

See Also

fitted.errors, resid.errors, tukey.1df in package dae.

Examples

## set up data frame for randomized complete block design in Table 4.4 from
## Box, Hunter and Hunter (2005) Statistics for Experimenters. 2nd edn
## New York, Wiley.
RCBDPen.dat <- fac.gen(list(Blend=5, Flask=4))
RCBDPen.dat$Treat <- factor(rep(c("A","B","C","D"), times=5))
RCBDPen.dat$Yield <- c(89,88,97,94,84,77,92,79,81,87,87,
                       85,87,92,89,84,79,81,88,88)

## perform the analysis of variance
RCBDPen.aov <- aov(Yield ~ Blend + Treat + Error(Blend/Flask), RCBDPen.dat)
summary(RCBDPen.aov)

## two equivalent ways of extracting the residuals
res <- residuals.aovlist(RCBDPen.aov)
res <- residuals(RCBDPen.aov, error.term = "Blend:Flask")
rmvnorm generates a vector of random values from a multivariate normal distribution

Description

Generates a vector of random values from an n-dimensional multivariate normal distribution whose mean is given by the n-vector mean and variance by the n x n symmetric matrix V. It uses the method described by Ripley (1987, p.98)

Usage

rmvnorm(mean, V, method = 'eigenanalysis')

Arguments

- mean: The mean vector of the multivariate normal distribution from which the random values are to be generated.
- V: The variance matrix of the multivariate normal distribution from which the random values are to be generated.
- method: The method used to decompose the variance matrix in producing a matrix to transform the iid standard normal values. The two methods available are 'eigenanalysis' and 'choleski', where only the first letter of each option is obligatory. The default method is eigenanalysis, which is slower but is likely to be more stable than Choleski decomposition.

Details

The method is: a) uses either the eigenvalue or Choleski decomposition of the variance matrix, V, to form the matrix that transforms an iid vector of values to a vector with variance V; b) generate a vector of length equal to mean of standard normal values; c) premultiply the vector of standard normal values by the transpose of the upper triangular factor and, to the result, add mean.

Value

A vector of length n, equal to the length of mean.

Author(s)

Chris Brien

References


See Also

fac.ar1mat, fac.vcmat, in package dae, rnorm, and chol.
Examples

```r
## set up a two-level factor and a three-level factor, both of length 12
A <- factor(rep(1:2, each=6))
B <- factor(rep(1:3, each=2, times=2))

## generate random values from a multivariate normal for which
# the mean is 20 for all variables and
# the variance matrix has random effects for factor A, ar1 pattern for B and
# residual random variation
mean <- rep(20, 12)
V <- fac.vcmat(A, 5) + fac.ar1mat(B, 0.6) + 2*mat.I(12)
y <- rmvnorm(mean, V)
```

Description

The data is from an experiment involved two phases. In the field phase a viticultural experiment was conducted to investigate the differences between 4 types of trellising and 2 methods of pruning. The design was a split-plot design in which the trellis types were assigned to the main plots using two adjacent Youden squares of 3 rows and 4 columns. Each main plot was split into two subplots (or halfplots) and the methods of pruning assigned at random independently to the two halfplots in each main plot. The produce of each halfplot was made into a wine so that there were 24 wines altogether.

The second phase was an evaluation phase in which the produce from the halfplots was evaluated by 6 judges all of whom took part in 24 sittings. In the first 12 sittings the judges evaluated the wines made from the halfplots of one square; the final 12 sittings were to evaluate the wines from the other square. At each sitting, each judge assessed two glasses of wine from each of the halfplots of one of the main plots. The main plots allocated to the judges at each sitting were determined as follows. For the allocation of rows, each occasion was subdivided into 3 intervals of 4 consecutive sittings. During each interval, each judge examined plots from one particular row, these being determined using two 3x3 Latin squares for each occasion, one for judges 1-3 and the other for judges 4-6. At each sitting judges 1-3 examined wines from one particular column and judges 4-6 examined wines from another column. The columns were randomized to the 2 sets of 2 plots x 3 intervals x 4 sittings using duplicates of a balanced incomplete block design for v=4 and k=2 that were latinized. This balanced incomplete block design consists of three sets of 2 blocks, each set containing the 4 "treatments". For each interval, a different set of 2 blocks was taken and each block assigned to two sittings, but with the columns within the block placed in reverse order in one sitting compared to the other sitting. Thus, in each interval, a judge would evaluate a wine from each of the 4 columns.

The data frame contains the following factors, in the order given: Occasion, Judges, Interval, Sittings, Position, Squares, Rows, Columns, Halfplot, Trellis, Method. They are followed by the simulated response variable Score.

The scores are ordered so that the factors Occasion, Judges, Interval, Sittings and Position are in standard order; the remaining factors are in randomized order.

See also the vignette accessed via vignette("DesignNotes", package="dae").
Usage

data(Sensory3Phase.dat)
data(Sensory3PhaseShort.dat)

Format

A data.frame containing 576 observations of 12 variables. There are two versions, one with shorter factor names than the other.

References


---

set.daeTolerance

Sets the values of daeTolerance for the package dae

Description

A function that sets the values such that, in dae functions, values less than it are considered to be zero. The values are stored in a vector named daeTolerance in the daeEnv environment. The vector is of length two and, initially, both values are set to .Machine$double.eps ^ 0.5 (about 1.5E-08). One value is named element.tol and is used for elements of matrices; the second is named element.eigen and is used for eigenvalues and quantities based on them, such as efficiency factors.

Usage

set.daeTolerance(element.tol=NULL, eigen.tol=NULL)

Arguments

- **element.tol**: The value to to which the first element of the daeTolerance vector is to be set. If more than one value is supplied, only the first value is used.
- **eigen.tol**: The value to to which the second element of the daeTolerance vector is to be set. If more than one value is supplied, only the first value is used.

Value

The vector daeTolerance is returned invisibly.

Author(s)

Chris Brien

See Also

get.daeTolerance.

Examples

```r
## set daeTolerance.
set.daeTolerance(1E-04, 1E-08)
```
Methods for Function show in Package dae

Description

Methods for function show in Package dae

Methods

signature(object = "projector") Prints the matrix and its degrees of freedom.

See Also

projector for further information about this class.

SPLGrass.dat

Data for an experiment to investigate the effects of grazing patterns on pasture composition

Description

The response variable is the percentage area covered by the principal grass (Main.Grass). The design for the experiment is a split-unit design. The main units are arranged in 3 Rows x 3 Columns. Each main unit is split into 2 SubRows x 2 SubColumns.

The factor Period, with levels 3, 9 and 18 days, is assigned to the main units using a 3 x 3 Latin square. The two-level factors Spring and Summer are assigned to split-units using a criss-cross design within each main unit. The levels of each of Spring and Summer are two different grazing patterns in its season.

Usage

data(SPLGrass.dat)

Format

A data.frame containing 36 observations of 8 variables.

Source

**strength**

*Generate paper strength values*

**Description**

Generates paper strength values for an experiment with different temperatures.

**Usage**

strength(nodays, noruns, temperature, ident)

**Arguments**

- **nodays**: The number of days over which the experiment is to be run.
- **noruns**: The number of runs to be performed on each day of the experiment.
- **temperature**: A **factor** that encapsulates the layout by giving the temperature to be investigated for each run on each day. These must be ordered so that the temperatures for the first day are given in the order in which they are to be investigated on that day. These must be followed by the noruns temperatures for the second day and so on. Consequently, the factor temperature will have nodays*noruns values.
- **ident**: The digits of your student identity number. That is, leave out any letters.

**Value**

A **data.frame** object containing the factors day, run and temperature and a vector of the generated strengths.

**Author(s)**

Chris Brien

**Examples**

```r
## Here temperature is a factor with 4*3 = 12 values whose
## first 3 values specify the temperatures to be applied in
## the 3 runs on the first day, values 4 to 6 specify the
## temperatures for the 3 runs on day 2, and so on.
temperature <- factor(rep(c(80, 85, 90), 4))
exp.strength <- strength(nodays = 4, noruns = 3,
                          temperature = temperature, ident = 0123456)

## In this second example, a completely randomized design is generated
## for the same 3 temperatures replicated 4 times. The layout is stored
## in the data.frame called Design.
Design <- designRandomize(allocated = temperature,
                           recipient = list(runs = 12),
                           seed = 5847123)
## eradicate the unrandomized version of temperature
remove("temperature")

## The 12 temperatures in Design are to be regarded as being assigned to
## days and runs in the same manner as for the first example.
```
exp.strength <- strength(nodays = 4, noruns = 3, 
                         temperature = Design$temperature, ident = 0123456)

summary.p2canon

<table>
<thead>
<tr>
<th>Summary of a canonical analysis of the relationships between two sets of projectors</th>
</tr>
</thead>
</table>

**Description**

Produces a summary of the efficiency criteria computed from the canonical efficiency factors for the joint decomposition of two sets of projectors (Brien and Bailey, 2009) obtained using `projs.2canon`. It takes the form of a decomposition or skeleton ANOVA table.

**Usage**

```r
## S3 method for class 'p2canon'
summary(object, which.criteria = c("aefficiency", "eefficiency", "order"), ...) 
```

**Arguments**

- **object**: A list of class `p2canon` produced by `projs.2canon`.
- **which.criteria**: A character vector nominating the efficiency criteria to be included in the summary. It can be none, all or some combination of `aefficiency`, `mefficiency`, `sefficiency`, `eefficiency`, `xefficiency`, `order` and `dforthog` – for details see `efficiency.criteria`.
- **...**: further arguments affecting the summary produced.

**Value**

An object of classes `summary.p2canon` and `data.frame`, whose rows correspond to the pairs of projectors, one from the Q1 argument and the other from the Q2 argument from `projs.2canon`; only pairs with non-zero efficiency factors are included. In addition, a line is included for each nonzero Residual Q1 projector.

**Author(s)**

Chris Brien

**References**


**See Also**

`projs.2canon`, `proj2.efficiency`, `efficiency.criteria`, `proj2.combine`, `proj2.eigen`, `pstructure`, `print.summary.p2canon` in package `dae`, `eigen`.

`projector` for further information about this class.
Examples

```r
## PBIBD(2) from p. 379 of Cochran and Cox (1957) Experimental Designs.  
## 2nd edn Wiley, New York
PBIBD2.unit <- list(Block = 6, Unit = 4)
PBIBD2.nest <- list(Unit = "Block")
trt <- factor(c(1,4,2,5, 2,5,3,6, 3,6,1,4, 4,1,5,2, 5,2,6,3, 6,3,4,1))
PBIBD2.lay <- designRandomize(allocated = trt,  
  recipient = PBIBD2.unit,  
  nested.recipients = PBIBD2.nest)

##obtain projectors using pstructure
unit.struct <- pstructure(~ Block/Unit, data = PBIBD2.lay)
trt.struct <- pstructure(~ trt, data = PBIBD2.lay)

##obtain combined decomposition and summarize
unit.trt.p2canon <- projs.2canon(unit.struct$Q, trt.struct$Q)
summary(unit.trt.p2canon)
```

Description

Gives the anatomy of a design in a table; it summarizes the joint decomposition of two or more sets of projectors (Brien and Bailey, 2009) obtained using `designAnatomy`. It includes the efficiency criteria computed from the canonical efficiency factors for the joint decomposition. The labels in the table may be Terms or Sources. The terms are those that would be included in a mixed model for an experiment based on the design. The sources are the orthogonal subspaces, derived from the terms, that make up the decomposition and the degrees of freedom and efficiency factors relate to these subspaces. The table displays how the information for the different sources allowed for in the design are related. For more information about the notation used for sources see the `labels` argument of `designAnatomy`.

It is possible to supply an object that is a `pcanon.object` produced in versions prior to 3.0-0 using `projs.canon`.

Usage

```r
## S3 method for class 'pcanon'
summary(object, labels.swap = FALSE,  
  which.criteria = c("aeficiency", "eeficiency", "order"), ...)
```

Arguments

- `object` A `pcanon.object`.
- `labels.swap` A `logical` indicating whether to swap between "sources" and 'terms' in the output. The default is established by the `labels` argument of `designAnatomy` and `projs.canon`.
which.criteria  A character vector nominating the efficiency criteria to be included in the summary. It can be none, all or some combination of aefficiency, mefficiency, sefficiency, eefficiency, xefficiency, order and dorthog – for details see efficiency.criteria. If there is only one formula, this argument is ignored.

... further arguments affecting the summary produced.

Value

An object of class summary.pcanon that is a list with the two components decomp and aliasing.

The component decomp is a data.frame whose rows correspond to subspaces in the decomposition for a design. It has the following attributes: (i) title that is the title for printing with the decomposition table; (ii) ntiers that is equal to the number of tiers; (iii) orthogonal that is TRUE if the design is orthogonal; (iv) labels that is either "terms" or "sources" depending on the labels that have resulted from the setting of label.swap.

The component aliasing is a data.frame that is also of class aliasing. It contains information about the aliasing between terms that are derived from the same formula and has the attribute title that is the title to be printed with the aliasing table.

However, if the object supplied is a pcanon.object produced with versions prior to 3.0-0 using projs.canon, the value is a data.frame, instead of a list, that has the same attributes as the decomp component of the summary.pcanon object now produced, except that labels is always set to "terms".

Author(s)

Chris Brien

References


See Also
designAnatomy, designAnatomy, pstructure, efficiency.criteria, proj2.combine, proj2.efficiency, proj2.eigen, print.summary.pcanon in package dae, eigen, projector for further information about this class.

Examples

```r
## PBIBD(2) from p. 379 of Cochran and Cox (1957) Experimental Designs.
## 2nd edn Wiley, New York
PBIBD2.unit <- list(Block = 6, Unit = 4)
PBIBD2.nest <- list(Unit = "Block")
trt <- factor(c(1,4,2,5, 2,5,3,6, 3,6,1,4, 4,1,5,2, 5,2,6,3, 6,3,4,1))
PBIBD2.lay <- designRandomize(allocated = trt,
                               recipient = PBIBD2.unit,
                               nested.recipients = PBIBD2.nest)

##obtain combined decomposition and summarize
unit.trt.canon <- designAnatomy(list(unit=~ Block/Unit, trt=~ trt),
                                data = PBIBD2.lay)
summary(unit.trt.canon, which = c("aeff","eeff","order"))
summary(unit.trt.canon, which = c("aeff","eeff","order"), labels.swap = TRUE)
```
tukey.1df  

**Performs Tukey's one-degree-of-freedom-test-for-nonadditivity**

**Description**

Performs Tukey's one-degree-of-freedom-test-for-nonadditivity on a set of residuals from an analysis of variance.

**Usage**

tukey.1df(aov.obj, data, error.term="Within")

**Arguments**

- `aov.obj` An `aov` object or `aovlist` object created from a call to `aov`.
- `error.term` The term from the `Error` function whose residuals are to be tested for nonadditivity. Only required when the `Error` function used in call to `aov`, so that an `aovlist` object is created.
- `data` A `data.frame` containing the original response variable and factors used in the call to `aov`.

**Value**

A list containing Tukey.SS, Tukey.F, Tukey.p, Devn.SSq being the SSq for the 1df test, F value for test and the p-value for the test.

**Note**

In computing the test quantities fitted values must be obtained. If `error.term` is specified, fitted values will be the sum of effects extracted from terms from the `Error` function, but only down to that specified by `error.term`. The order of terms is as given in the ANOVA table. If `error.term` is unspecified, all effects for terms external to any `Error` terms are extracted and summed. Extracted effects will only be for terms external to any `Error` function. If you want effects for terms in the `Error` function to be included, put them both inside and outside the `Error` function so they are occur twice.

**Author(s)**

Chris Brien

**See Also**

`fitted.errors`, `resid.errors` in package `dae`.

**Examples**

```r
## set up data frame for randomized complete block design in Table 4.4 from
## Box, Hunter and Hunter (2005) Statistics for Experimenters. 2nd edn
## New York, Wiley.
RCBDPen.dat <- fac.gen(list(Blend=5, Flask=4))
RCBDPen.dat$Treat <- factor(rep(c("A","B","C","D"), times=5))
RCBDPen.dat$Yield <- c(89,88,97,94,84,77,92,79,81,87,93,
```
## perform the analysis of variance
RCBDPen.aov <- aov(Yield ~ Blend + Treat + Error(Blend/Flask), RCBDPen.dat)
summary(RCBDPen.aov)

## Obtain the quantities for Tukey's test
tukey.1df(RCBDPen.aov, RCBDPen.dat, error.term = "Blend:Flask")

---

### yates.effects

**Extract Yates effects**

**Description**

Extracts Yates effects from an aov object or aovlist object.

**Usage**

yates.effects(aov.obj, error.term="Within", data=NULL)

**Arguments**

- **aov.obj**: An aov object or aovlist object created from a call to `aov`.
- **error.term**: The term from the `Error` function from which the Yates effects are estimated. Only required when `Error` used in call to `aov`.
- **data**: A data.frame in which the variables specified in the `aov.obj` will be found. If missing, the variables are searched for in the standard way.

**Details**

Yates effects are specific to $2^k$ experiments, where Yates effects are conventionally defined as the difference between the upper and lower levels of a factor. We follow the convention used in Box, Hunter and Hunter (1978) for scaling of higher order interactions: all the Yates effects are on the same scale, and represent the average difference due to the interaction between two different levels. Effects are estimated only from the error term supplied to the `error.term` argument.

**Value**

A vector of the Yates effects.

**Author(s)**

Chris Brien

**See Also**

`qqyeffects` in package `dae, aov`
Examples

```r
## analysis of 2^4 factorial experiment from Table 10.6 of Box, Hunter and
## use ?Fac4Proc.dat for data set details
data(Fac4Proc.dat)
Fac4Proc.aov <- aov(Conv ~ Catal * Temp * Press * Conc + Error(Runs),
                   Fac4Proc.dat)
round(yates.effects(Fac4Proc.aov, error.term="Runs", data=Fac4Proc.dat), 2)
```

Zncsspline

Calculates the design matrix for fitting the random component of a
natural cubic smoothing spline

Description

Calculates the design matrix, $\mathbf{Z}$, of the random effects for a natural cubic smoothing spline as described by Verbyla et al., (1999). An initial design matrix, $\mathbf{\Delta} \mathbf{\Delta}^{-1} \mathbf{\Delta}$, based on the knot points is computed. It can then be post multiplied by the power of the tri-diagonal matrix $\mathbf{G}_s$ that is proportional to the variance matrix of the random spline effects. If the power is set to 0.5 then the random spline effects based on the resulting $\mathbf{Z}$ matrix will be independent with variance $\sigma^2_s$.

Usage

```r
Zncsspline(knot.points, Gpower = 0, print = FALSE)
```

Arguments

- **knot.points**
  
  A `numeric` giving the values of the knot points to be used in fitting the spline. These must be ordered in increasing order.

- **Gpower**
  
  A `numeric` giving the power of the tri-diagonal matrix $\mathbf{G}_s$ from which the variance matrix of the random spline effects is calculated. That the initial design matrix is to be the value of the variance component for the random spline effects. The smoothing parameter is then the inverse of the ratio of this component to the residual variance.

- **print**
  
  A `logical` indicating whether to print the $\mathbf{\Delta}$ and $\mathbf{G}_s$ matrices.

Value

A `matrix` containing the design matrix.

Author(s)

Chris Brien

References

Zncsspline

See Also

mat.ncssvar.

Examples

Z <- Zncsspline(knot.points = 1:10, Gpower = 0.5)
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