

Package ‘dae’

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Title Functions Useful in the Design and ANOVA of Experiments

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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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R topics documented:

dae-package	4
ABC.Interact.dat	8
as.data.frame.pstructure	9

as.numfac	10
BIBDWheat.dat	11
blockboundaryPlot	11
Casuarina.dat	13
correct.degfree	14
dae-deprecated	15
daeTips	15
decomp.relate	16
degfree	17
designAmeasures	18
designAnatomy	20
designLatinSqrSys	24
designPlot	24
designPlotlabels	27
designRandomize	29
designTwophaseAnatomies	31
detect.diff	34
efficiencies	35
efficiency.criteria	37
elements	38
Exp249.mplot.des	39
extab	40
fac.ar1mat	41
fac.combine	42
fac.divide	43
fac.gen	44
fac.layout	46
fac.match	48
fac.meanop	49
fac.nested	50
fac.recode	51
fac.sumop	52
fac.vcmat	53
Fac4Proc.dat	54
fitted.aovlist	54
fitted.errors	56
get.daeTolerance	57
harmonic.mean	58
interaction.ABC.plot	58
is.allzero	60
is.projector	61
LatticeSquare_t49.des	62
marginality	62
mat.ar1	64
mat.ar2	64
mat.ar3	65
mat.arma	67
mat.banded	68

mat.dirprod	69
mat.dirsum	70
mat.exp	71
mat.gau	71
mat.I	72
mat.J	73
mat.ma1	74
mat.ma2	74
mat.ncssvar	75
mat.sar	76
mat.sar2	77
mat.Vpred	78
mat.Vpredicts	80
McIntyreTMV.dat	83
meanop	83
mpone	84
no.reps	85
Oats.dat	86
p2canon.object	87
pcanon.object	88
power.exp	89
print.aliasing	90
print.projector	91
print.pstructure	92
print.summary.p2canon	93
print.summary.pcanon	94
proj2.combine	95
proj2.efficiency	96
proj2.eigen	98
projector	99
projector-class	100
projs.2canon	102
projs.combine.p2canon	103
pstructure.formula	104
pstructure.object	108
qqyeffects	109
resid.errors	110
residuals.aovlist	111
rmvnorm	112
Sensory3Phase.dat	113
set.daeTolerance	114
show-methods	115
SPLGrass.dat	116
strength	116
summary.p2canon	118
summary.pcanon	119
tukey.1df	121
yates.effects	122

Zncsspline 123

Index **125**

dae-package

Functions Useful in the Design and ANOVA of Experiments

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/>.

Version: 3.0-32

Date: 2019-05-15

Index

(i) Data

ABC.Interact.dat	Randomly generated set of values indexed by three factors
BIBDWheat.dat	Data for a balanced incomplete block experiment
Casuarina.dat	Data for an experiment with rows and columns from Williams (2002)
Exp249.mplot.des	Systematic, main-plot design for an experiment to be run in a greenhouse
Fac4Proc.dat	Data for a 2 ⁴ factorial experiment
LatticeSquare_t49.des	A Lattice square design for 49 treatments
McIntyreTMV.dat	The design and data from McIntyre (1955) two-phase experiment
Oats.dat	Data for an experiment to investigate nitrogen response of 3 oats varieties
Sensory3Phase.dat	Data for the three-phase sensory evaluation experiment in Brien, C.J. and Payne, R.W. (1999)
Sensory3PhaseShort.dat	Data for the three-phase sensory evaluation experiment in Brien, C.J. and Payne, R.W. (1999), but with short factor names
SPLGrass.dat	Data for an experiment to investigate the effects of grazing patterns on pasture composition

(ii) Factor manipulation functions

as.numfac	Convert a factor to a numeric vector
---------------------------	--------------------------------------

<code>fac.combine</code>	Combines several factors into one
<code>fac.divide</code>	Divides a factor into several individual factors
<code>fac.gen</code>	Generate all combinations of several factors and, optionally, replicate them
<code>fac.match</code>	Match, for each combination of a set of columns in 'x', the row that has the same combination in 'table'
<code>fac.nested</code>	Creates a factor whose values are generated within those of the factor nesting.fac
<code>fac.recode</code>	Recodes factor 'levels' using possibly nonunique values in a vector.
<code>mpone</code>	Converts the first two levels of a factor into the numeric values -1 and +1
 (iii) Design functions	
<code>blockboundaryPlot</code>	This function plots a block boundary on a plot produced by 'designPlot'. It supersedes <code>blockboundary.plot</code> .
<code>designAmeasures</code>	Calculates the A-optimality measures from the variance matrix for predictions that can be obtained using <code>mat.Vpredicts</code>
<code>designAnatomy</code>	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.
<code>designLatinSqrSys</code>	Generate a systematic plan for a Latin Square design.
<code>designPlot</code>	A graphical representation of an experimental design using labels stored in a matrix. It superseded <code>design.plot</code> .
<code>designPlotlabels</code>	Plots labels on a two-way grid using <code>ggplot2</code> .
<code>designRandomize</code>	Randomize allocated to recipient factors to produce a layout for an experiment. It supersedes <code>fac.layout</code> .
<code>designTwophaseAnatomies</code>	Given the layout for a design and three structure formulae, obtain the anatomies for the two-phase, first-phase, cross-phase and second-phase designs.
<code>marginality.pstructure</code>	Extracts the marginality matrix from a <code>pstructure.object</code>
<code>marginality.pstructure</code>	Extracts a list containing the marginality matrices from a <code>pcanon.object</code>
<code>print.aliasing</code>	Prints an aliasing data.frame
<code>no.reps</code>	Computes the number of replicates for an experiment
<code>detect.diff</code>	Computes the detectable difference for an experiment
<code>power.exp</code>	Computes the power for an experiment
<code>summary.pcanon</code>	Summarizes the anatomy of a design, being the decomposition of the sample space based on its canonical analysis

(iv) ANOVA functions

<code>fitted.aovlist</code>	Extract the fitted values for a fitted model from an aovlist object
<code>fitted.errors</code>	Extract the fitted values for a fitted model
<code>interaction.ABC.plot</code>	Plots an interaction plot for three factors
<code>qqyeffects</code>	Half or full normal plot of Yates effects
<code>resid.errors</code>	Extract the residuals for a fitted model
<code>residuals.aovlist</code>	Extract the residuals from an aovlist object
<code>strength</code>	Generate paper strength values
<code>tukey.1df</code>	Performs Tukey's one-degree-of-freedom-test-for-nonadditivity
<code>yates.effects</code>	Extract Yates effects
 (v) Matrix functions	
<code>elements</code>	Extract the elements of an array specified by the subscripts
<code>fac.ar1mat</code>	Forms the ar1 correlation matrix for a (generalized) factor
<code>fac.sumop</code>	Computes the summation matrix that produces sums corresponding to a (generalized) factor
<code>fac.vcmat</code>	Forms the variance matrix for the variance component of a (generalized) factor
<code>mat.I</code>	Forms a unit matrix
<code>mat.J</code>	Forms a square matrix of ones
<code>mat.ar1</code>	Forms an ar1 correlation matrix
<code>mat.ar2</code>	Forms an ar2 correlation matrix
<code>mat.ar3</code>	Forms an ar3 correlation matrix
<code>mat.arma</code>	Forms an arma correlation matrix
<code>mat.banded</code>	Forms a banded matrix
<code>mat.exp</code>	Forms an exponential correlation matrix
<code>mat.gau</code>	Forms a gaussian correlation matrix
<code>mat.ma1</code>	Forms an ma1 correlation matrix
<code>mat.ma2</code>	Forms an ma2 correlation matrix
<code>mat.ncssvar</code>	Forms a variance matrix for random cubic smoothing spline effects
<code>mat.sar</code>	Forms an sar correlation matrix
<code>mat.sar2</code>	Forms an sar2 correlation matrix
<code>mat.dirprod</code>	Forms the direct product of two matrices
<code>mat.dirsum</code>	Forms the direct sum of a list of matrices
<code>mat.Vpred</code>	Forms the variance matrix of predictions
<code>mat.Vpredicts</code>	Forms the variance matrix of predictions, based on supplied matrices or formulae.
<code>Zncsspline</code>	Forms the design matrix for fitting the random effects for a natural cubic smoothing spline.

(vi) Projector and canonical efficiency functions

Projector class:

`projector`
`projector-class`
`is.projector`

`print.projector`
`correct.degfree`

`degfree`

Create projectors
 Class projector
 Tests whether an object is a valid object of class projector
 Print projectors
 Check the degrees of freedom in an object of class projector
 Degrees of freedom extraction and replacement

Accepts two or more formulae:

`designAnatomy`

`summary.pcanon`

`print.summary.pcanon`
`efficiencies.pcanon`

An anatomy of a design, obtained from a canonical analysis of the relationships between sets of projectors.
 Summarizes the anatomy of a design, being the decomposition of the sample space based on its canonical analysis
 Prints the values in an 'summary.pcanon' object
 Extracts the canonical efficiency factors from a list of class 'pcanon'

Accepts exactly two formulae:

`projs.2canon`

`projs.combine.p2canon`
`summary.p2canon`

`print.summary.p2canon`

`efficiencies.p2canon`

A canonical analysis of the relationships between two sets of projectors
 Extract, from a p2canon object, the projectors
 A summary of the results of an analysis of the relationships between two sets of projectors
 Prints the values in an 'summary.p2canon' object that give the combined decomposition
 Extracts the canonical efficiency factors from a list of class 'p2canon'

Accepts a single formula:

`as.data.frame.pstructure`
`print.pstructure`
`pstructure.formula`

Coerces a pstructure.object to a data.frame
 Prints a pstructure.object
 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

<code>efficiency.criteria</code>	Computes efficiency criteria from a set of efficiency factors
<code>fac.meanop</code>	Computes the projection matrix that produces means
<code>proj2.eigen</code>	Canonical efficiency factors and eigenvectors in joint decomposition of two projectors
<code>proj2.efficiency</code>	Computes the canonical efficiency factors for the joint decomposition of two projectors
<code>proj2.combine</code>	Compute the projection and Residual operators for two, possibly nonorthogonal, projectors
<code>show-methods</code>	Methods for Function 'show' in Package dae
(vii) Miscellaneous functions	
<code>extab</code>	Expands the values in table to a vector
<code>get.daeTolerance</code>	Gets the value of daeTolerance for the package dae
<code>harmonic.mean</code>	Calculates the harmonic mean.
<code>is.allzero</code>	Tests whether all elements are approximately zero
<code>rmvnorm</code>	Generates a vector of random values from a multivariate normal distribution
<code>set.daeTolerance</code>	Sets the value of daeTolerance for the package dae

Author(s)

NA

Maintainer: NA

ABC.Interact.dat

*Randomly generated set of values indexed by three factors***Description**

This data set has randomly generated values of the response variable MOE (Measure Of Effectiveness) which is indexed by the two-level factors A, B and C.

Usage

```
data(ABC.Interact.dat)
```

Format

A data.frame containing 8 observations of 4 variables.

Source

Generated by Chris Brien

`as.data.frame.pstructure`*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

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

Arguments

<code>x</code>	The pstructure.object , which is of class <code>pstructure</code> and is to be coerced.
<code>row.names</code>	NULL or a character vector giving the row names for the data frame. Missing values are not allowed.
<code>optional</code>	A logical passed to <code>as.data.frame</code> . If TRUE, setting row names and converting column names (to syntactic names: see <code>make.names</code>) is optional. Note that all of R's base package <code>as.data.frame()</code> methods use <code>optional</code> only for column names treatment, basically with the meaning of <code>data.frame(*, check.names = !optional)</code> .
<code>...</code>	Further arguments passed to or from other methods.
<code>omit.marginality</code>	A logical , which, if TRUE, results in the marginality matrix being omitted from the <code>data.frame</code> .

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	<i>Convert a factor to a numeric vector</i>
-----------	---

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.recode](#) 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.recode](#) 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 *daeDesignNotes.pdf*.

Usage

```
data(BIBDWheat.dat)
```

Format

A data.frame containing 30 observations of 4 variables.

Source

Joshi, D. D. (1987) *Linear Estimation and Design of Experiments*. Wiley Eastern, New Delhi.

`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

```
## 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,
                  blocklinewidth = 3,blockcolour = "blue")
blockboundaryPlot(blockdefinition = cbind(10,16), blocklinewidth=3, blockcolour="blue",
                  nrows=10, ncolumns=16)
#Plot border and internal block boundaries only
blockboundaryPlot(blockdefinition = cbind(8,14), cstart = 1, rstart= 1,
                  nrows = 9, ncolumns = 15,
                  blocklinewidth = 3, blockcolour = "blue")
blockboundaryPlot(blockdefinition = cbind(10,16),
                  blocklinewidth = 3, blockcolour = "blue",
                  nrows = 10, ncolumns = 16)

## End(Not run)

```

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 *daeDesignNotes.pdf*.

Usage

```
data(Casuarina.dat)
```

Format

A data.frame containing 240 observations of 7 variables.

Source

Williams, E. R., Matheson, A. C. and Harwood, C. E. (2002) *Experimental design and analysis for tree improvement*. 2nd edition. CSIRO, Melbourne, Australia.

correct.degfree	<i>Check the degrees of freedom in an object of class projector</i>
-----------------	---

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)
```

dae-deprecated

Deprecated 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.canon(...)  
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>.

Author(s)

Chris Brien

decomp.relate	<i>Examines the relationship between the eigenvectors for two decompositions</i>
---------------	--

Description

Two decompositions produced by [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 [proj2.eigen](#) have the same Q1.

Usage

```
decomp.relate(decomp1, decomp2)
```

Arguments

decomp1	A list containing components efficiencies and eigenvectors such as is produced by proj2.eigen .
decomp2	Another list containing components efficiencies and eigenvectors such as is produced by 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 `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 [matrix](#) that is $r1 \times r2$ where `r1` and `r2` are the numbers of efficiencies of `decomp1` and `decomp2`, respectively. The rownames and columnnames of the [matrix](#) are the values of the efficiency factors from `decomp1` and `decomp2`, respectively.

Author(s)

Chris Brien

See Also

[proj2.eigen](#), [proj2.combine](#) in package `dae`, [eigen](#).

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"]])

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

```
degfree(object)
```

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

Arguments

object	An object of class <code>"projector"</code> 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 <code>"projector"</code> or <code>"matrix"</code> 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

```
## 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	<i>Calculates the average variance of pairwise differences from the variance matrix for predictions that can be obtained using mat.Vpredicts</i>
-----------------	--

Description

Calculates the average variance of pairwise differences between (of elementary contrasts of) predictions, possibly for different subgroups of the predictions, from the variance matrix for 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

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

Arguments

Vpred	The variance matrix of the predictions.
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 specifies a 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.

Value

A [matrix](#) containing the within and between group A-optimality measures.

Author(s)

Chris Brien

References

Smith, A. B., D. G. Butler, C. R. Cavanagh and B. R. Cullis (2015). Multi-phase variety trials using both composite and individual replicate samples: a model-based design approach. *Journal of Agricultural Science*, **153**, 1017-1029.

See Also

[mat.Vpred](#), [designAnatomy](#).

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 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 varaince 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)))
grpsizes <- c(4,2)
names(grpsizes) <- c("fldUndup", "fldDup")
designAmeasures(Vp, groupsizes = grpsizes)
designAmeasures(Vp, groupsizes = c(4))
designAmeasures(Vp, groups=list(c(1,4),c(5,6)))

## Calculate the variance matrix of the predicted fixed Variety effects, elminating 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 its use also see the vignette *daeDesignNotes.pdf*.

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 <code>list</code> whose components are of class <code>formula</code> . 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 <code>summary.pcanon</code> object. They will also be used to name the terms, sources and marginality lists in the <code>pcanon.object</code> .
data	A <code>data.frame</code> contains the values of the factors and variables that occur in formulae.
keep.order	A <code>logical</code> 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 <code>logical</code> indicating whether the projector for the grand mean is to be included for each structure.
orthogonalize	A <code>character</code> vector indicating the method for orthogonalizing a projector to those for terms that occurred previously in a single formula. Three options are available: <code>hybrid</code> ; <code>differencing</code> ; <code>eigenmethods</code> . The <code>hybrid</code> option 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 <code>eigenmethods</code> . The <code>differencing</code> option subtracts, from the current projector, those previously orthogonalized projectors for terms whose factors are a subset of the current projector's factors. The <code>eigenmethods</code> 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 formulae.
labels	A <code>character</code> 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 <code>terms</code> and <code>sources</code> . <code>Terms</code> have all factors/variables in it separated by colons (<code>:</code>). <code>Sources</code> have factors/variables in them that represent interactions separated by hashes (<code>#</code>); if some factors are nested within others, the nesting factors are surrounded by square brackets (<code>[</code> and <code>]</code>) and separated by colons (<code>:</code>). If some generalized, or combined, factors have no marginal terms, the constituent factors are separated by colons (<code>:</code>) and if they interact with other factors in the source they will be parenthesized.
marginality	A <code>list</code> 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 <code>list</code> is the same length as the formulae <code>list</code> , they will be associated in parallel with the components of formulae, irrespective of the naming of the two <code>lists</code> . If the number of components in <code>marginality</code> is less than the number of components in formulae then both <code>lists</code> must be named so that those in the marginality <code>list</code> can be matched with those in the formulae <code>list</code> . Each component of the marginality <code>list</code> must be either <code>NULL</code> or a square <code>matrix</code> 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.

`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 `pcanon.object`.

Author(s)

Chris Brien

References

Brien, C. J. (2017) Multiphase experiments in practice: A look back. *Australian & New Zealand Journal of Statistics*, **59**, 327-352.

Brien, C. J. (2019) Multiphase experiments with at least one later laboratory phase . II. Northogonal designs. *Australian & New Zealand Journal of Statistics*, accepted for publication.

Brien, C. J. and R. A. Bailey (2009). Decomposition tables for multitiered experiments. I. A chain of randomizations. *The Annals of Statistics*, **36**, 4184 - 4213.

James, A. T. and Wilkinson, G. N. (1971) Factorization of the residual operator and canonical decomposition of nonorthogonal factors in the analysis of variance. *Biometrika*, **58**, 279-294.

Payne, R. W. and R. D. Tobias (1992). General balance, combination of information and the analysis of covariance. *Scandinavian Journal of Statistics*, **19**, 3-23.

See Also

[designRandomize](#), [designLatinSqrSys](#), [designPlot](#), [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

```
## 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)
```

designLatinSqrSys	<i>Generate a systematic plan for a Latin Square design</i>
-------------------	---

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	<i>A graphical representation of an experimental design using labels stored in a matrix.</i>
------------	--

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.
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 <code>labels</code> is <code>NULL</code> , 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 <code>labels</code> is <code>NULL</code> then the number of colours must at least equal the number of unique labels in <code>designMatrix</code> . The default, <code>NA</code> , is to leave the cells unfilled. See also <code>Colour</code> specification under the <code>par</code> 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: <ul style="list-style-type: none"> • 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. <p>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.</p>
blocklinecolour	A character string specifying the colour of the block boundary. See also <code>Colour</code> specification under the <code>par</code> function.
blocklinewidth	A numeric giving the width of the block boundary to be plotted.
rotate	A logical which, if <code>TRUE</code> , 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 <code>polygon</code> in plotting the cell.

Value

no values are returned, but a plot is produced.

Author(s)

Chris Brien

References

Coombes, N. E. (2009). *DiGGer design search tool in R*. <http://nswdpibiom.org/austatgen/software/>

See Also

[blockboundaryPlot](#), [designPlotlabels](#), [designLatinSqrSys](#), [designRandomize](#), [designAnatomy](#) in package **dae**.

Also, [par](#), [polygon](#), [DiGGer](#)

Examples

```
## Not run:
designPlot(des.mat, labels=1:4, cellfillcolour="lightblue", new=TRUE,
          plotcellboundary = TRUE, chardivisor=3,
          rtitle="Lanes", ctitle="Positions",
          rcellpropn = 1, ccellpropn=1)
designPlot(des.mat, labels=5:87, plotlabels=TRUE, cellfillcolour="grey", new=FALSE,
          plotcellboundary = TRUE, chardivisor=3)
designPlot(des.mat, labels=88:434, plotlabels=TRUE, cellfillcolour="lightgreen",
          new=FALSE, plotcellboundary = TRUE, chardivisor=3,
          blocksequence=TRUE, blockdefinition=cbind(4,10,12),
          blocklinewidth=3, blockcolour="blue")
## End(Not run)
```

designPlotlabels	<i>Plots labels on a two-way grid using ggplot2</i>
------------------	---

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

<code>data</code>	A data.frame containing labels, <code>grid.x</code> , <code>grid.y</code> and, if specified, <code>colour.column</code> .
<code>labels</code>	A character giving the name of the column in <code>data</code> containing the labels to be plotted on the grid.
<code>grid.x</code>	A character giving the name of the column in <code>data</code> that specifies the x-coordinates of the plot grid.
<code>grid.y</code>	A character giving the name of the column in <code>data</code> that specifies the y-coordinates of the plot grid.
<code>reverse.x</code>	A logical which, if true, causes the order of values on the x-axis to be reversed.
<code>reverse.y</code>	A logical which, if true, causes the order of values on the y-axis to be reversed.
<code>colour.column</code>	A character giving the name of the column in <code>data</code> that is to be used to colour the values plotted on the grid.
<code>colour.values</code>	A character giving the name of the column in <code>data</code> that is to be used to colour the values plotted on the grid.
<code>xlab</code>	Label for the x-axis. By default it is the name of the <code>grid.x</code> .
<code>ylab</code>	Label for the y-axis. By default it is the name of the <code>grid.y</code> .
<code>title</code>	Title for plot window. By default it is "Plot of labels".
<code>printPlot</code>	A logical indicating whether to print the plot.
<code>ggplotFuncs</code>	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.
<code>...</code>	Other arguments that are passed down to geom_text .

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	<i>Randomize allocated to recipient factors to produce a layout for an experiment</i>
-----------------	---

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 *daeDesignNotes.pdf*.

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. It is emphasized that the nesting is a property of the design that is being employed (it is only partly based on the intrinsic nesting).

except	A <code>character</code> vector containing the names recipient <code>factors</code> that are to be excepted from the permutation; any allocated <code>factors</code> whose values differ between the levels of the <code>factors</code> in this vector will not have those values randomized.
seed	A single <code>numeric</code> value, interpreted as an integer, that specifies the starting value of the random number generator.
unit.permutation	A logical indicating whether to include the <code>.Unit</code> and <code>.Permutation</code> columns in the <code>data.frame</code> .
...	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. This permutation 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 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

Bailey, R.A. (1981) A unified approach to design of experiments. *Journal of the Royal Statistical Society, Series A*, **144**, 214–223.

See Also

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

designTwophaseAnatomies

Given the layout for a design and three structure formulae, obtain the anatomies for the two-phase, first-phase, cross-phase and second-phase designs.

Description

Uses [designAnatomy](#) to obtain the four species of designs associated with a two-phase design that are described by Brien (2019): the anatomies for the two-phase, first-phase, cross-phase and second-phase designs.

Usage

```
designTwophaseAnatomies(formulae, data,
                        which.designs = "all", printAnatomies = TRUE,
                        orthogonalize = "hybrid",
                        marginality = NULL,
                        which.criteria = c("aefficiency", "eefficiency",
                                          "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 second-phase; all, the default, results in all four being obtained. |
| printAnatomies | A logical indicating whether or not the anatomies are to be printed. |
| 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 subtract 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 formulae. |

- 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 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 *i*th row and *j*th column will be one if the *i*th term is marginal to the *j*th term i.e. the column space of the *i*th term is a subspace of that for the *j*th term and so the source for the *j*th term is to be made orthogonal to that for the *i*th 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 formulae supplied in formulae, the first-phase anatomy uses the second and third formulae, the cross-phase anatomy derives from the first and third formulae and the second-phase anatomy is obtained with the first and second formulae.

Value

A **list** containing the components twophase, first, cross and second. 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.

Author(s)

Chris Brien

References

- Brien, C. J. (2017) Multiphase experiments in practice: A look back. *Australian & New Zealand Journal of Statistics*, **59**, 327-352.
- Brien, C. J. (2019) Multiphase experiments with at least one later laboratory phase . II. Northogonal designs. *Australian & New Zealand Journal of Statistics*, accepted for publication.

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

```
##### 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)

## 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

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

Value

A single numeric value containing the computed detectable difference.

Author(s)

Chris Brien

See Also

[power.exp](#), [no.reps](#) in package **dae**.

Examples

```
## 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](#).


```
##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 `a`efficiency criterion is the harmonic mean of the nonzero efficiency factors. The `m`efficiency criterion is the mean of the nonzero efficiency factors. The `e`efficiency criterion is the minimum of the nonzero efficiency factors. The `s`efficiency criterion is the variance of the nonzero efficiency factors. The `x`efficiency is the maximum of the efficiency factors. The `o`order is the order of balance and is the number of unique nonzero efficiency factors. The `d`forthog is the number of efficiency factors that are equal to one.

Value

A list whose components are `a`efficiency, `m`efficiency, `s`efficiency, `e`efficiency, `x`efficiency, `o`order and `d`forthog.

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 `subscripts` are extracted. The number of columns of `subscripts` corresponds to the number of dimensions of `x`. The effect of supplying less columns in `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.
`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 `subscripts` object.

Author(s)

Chris Brien

See Also

Extract

Examples

```
## 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")])
```

Exp249.mplot.des

Systematic, main-plot design for an experiment to be run in a greenhouse

Description

In this main-plot design, there are 24 lanes by 11 Positions, the lanes being blocked into 6 Zones of 4 lanes. The design for the main plots is for assigning 75 wheat lines, of which 73 are Nested Association Mapping (NAM) wheat lines and the other two are two check lines, Scout and Gladius. A row and column design was generated with DiGger (Coombes, 2009). For more details see the vignette *daeDesignNotes.pdf*.

Usage

```
data(Exp249.mplot.des)
```

Format

A data.frame containing 264 observations of 3 variables.

Source

Coombes, N. E. (2009) codeDigger: *design search tool in R*. URL: <http://nswdpiom.org/austatgen/software/>, (accessed June 3, 2015).

extab	<i>Expands the values in table to a vector</i>
-------	--

Description

Expands the values in table to a vector according to the `index.factors` that are considered to index the table, either in standard or Yates order. The order of the values in the vector is determined by the order of the values of the `index.factors`.

Usage

```
extab(table, index.factors, order="standard")
```

Arguments

<code>table</code>	A numeric vector containing the values to be expanded. Its length must equal the product of the number of used levels for the <code>factors</code> in <code>index.factors</code> and the values in it correspond to all levels combinations of these <code>factors</code> . That is, the values of the <code>index.factors</code> are irrelevant to <code>table</code> .
<code>index.factors</code>	A list of <code>factors</code> that index the table. All the <code>factors</code> must be the same length.
<code>order</code>	The order in which the levels combinations of the <code>index.factors</code> are to be considered as numbered in indexing <code>table</code> ; <code>standard</code> numbers them as if they are arranged in standard order, that is with the first factor moving slowest and the last factor moving fastest; <code>yates</code> 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

```
## 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

```
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

```
## 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

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

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 from the observed combinations of the levels of the individual [factors](#).

Author(s)

Chris Brien

See Also

[fac.divide](#) in package **dae**.

Examples

```
## 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))
```

fac.divide	<i>Divides a factor into several individual factors</i>
------------	---

Description

Takes a [factor](#) and divides it into several individual [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 individual [factors](#) when these are arranged in standard or Yates order.

Usage

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

Arguments

combined.factor	A factor that is to be divided into the individual factors listed in <code>factor.names</code> .
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 <code>standard</code> or <code>yates</code> . The order in which the levels combinations of the factors in <code>factor.names</code> are to be considered as numbered; <code>standard</code> numbers them as if they are arranged in standard order, that is with the first factor moving slowest and the last factor moving fastest; <code>yates</code> 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.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 factor A nd B
CRD.facs <- fac.divide(CRD.lay$treat, factor.names = list(A = 2, B = 2))
```

fac.gen	<i>Generate all combinations of several factors and, optionally, replicate them</i>
---------	---

Description

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

Usage

```
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 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 generated levels with columns corresponding to the codefactors in the generate list.

Warning

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

Author(s)

Chris Brien

See Also

[fac.combine](#) in package **dae**

Examples

```
## 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)
```

fac.layout	<i>Generate a randomized layout for an experiment</i>
------------	---

Description

Warning: `fac.layout` will be deprecated in future versions, its synonym `designRandomize` being preferred.

Given a systematic design, generate a layout for an experiment consisting of randomized `factors` that are randomized to the unrandomized `factors`, taking into account the nesting between the unrandomized factors for the design.

Usage

```
fac.layout(unrandomized, nested.factors=NULL, except=NULL,
          randomized, seed=NULL, unit.permutation=TRUE)
```

Arguments

- unrandomized A `data.frame` or a `list` of `factors`, along with their levels. If a `list`, the name of each component of the `list` is a `factor` name and the component is either a single numeric value that is the number of levels, a numeric vector that contains the levels of the `factor` or a character codevector that contains the labels of the levels of the `factor`.
- nested.factors A `list` of the unrandomized `factors` that are nested in other `factors` in unrandomized. 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. It is emphasized that the nesting is a property of the design that is being employed (it is only partly based on the intrinsic nesting).
- except A `character` vector containing the names unrandomized `factors` that are to be excepted from the randomization.
- randomized A `factor` or a `data.frame` containing the values of the `factor(s)` to be randomized.
- seed A single 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`.

Details

This function uses the method of randomization described by Bailey (1981). That is, a permutation of the units that respects the nesting for the design, but does not permute any of the factors in the `except` vector, is obtained. This permutation is applied to the unrandomized `factors` and then a `data.frame` containing both the permuted unrandomized and unpermuted randomized `factors` is formed. To produce the randomized layout, the rows of the joint `data.frame` are reordered so

that its unrandomized `factors` are in either standard order or, if a `data.frame` was supplied to unrandomized, data frame order.

The `.Units` and `.Permutation` vectors enable one to swap between this 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` consisting of the values for `.Units` and `.Permutation` vectors, provided `unit.permutation` is `TRUE`, along with the values for the unrandomized and randomized `factors` that specify the randomized layout for the experiment.

Author(s)

Chris Brien

References

Bailey, R.A. (1981) A unified approach to design of experiments. *Journal of the Royal Statistical Society, Series A*, **144**, 214–223.

See Also

`fac.gen` in package `dae`.

Examples

```
## generate a randomized layout for a 4 x 4 Latin square
## (the nested.factors argument is not needed here as none of the
## factors are nested)
LS.unit <- data.frame(row = ordered(rep(c("I","II","III","IV"), times=4)),
                     col = factor(rep(c(0,2,4,6), each=4)))
LS.ran <- data.frame(treat = factor(c(1:4, 2,3,4,1, 3,4,1,2, 4,1,2,3)))
data.frame(LS.unit, LS.ran)
LS.lay <- fac.layout(unrandomized=LS.unit, randomized=LS.ran, seed=7197132)
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
RCBD.unit <- list(rep = 2, plot=1:3, block = c("I","II"))
## specify that plot is nested in block and rep and that block is nested
## in rep
RCBD.nest <- list(plot = c("block","rep"), block="rep")
## generate treatment factor in systematic order so that they correspond
## to plot
tr <- factor(rep(1:3, each=2, times=2))
## obtain randomized layout
RCBD.lay <- fac.layout(unrandomized=RCBD.unit,
                     nested.factors=RCBD.nest,
                     randomized=tr, seed=9719532)
```

```
#sort into the original standard order
RCBD.perm <- RCBD.lay[RCBD.lay$.Permutation,]
#resort into randomized order
RCBD.lay <- RCBD.perm[order(RCBD.perm$.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.
SPL.lay <- fac.layout(unrandomized=list(block = 2, main.unit = 4, split.unit = 3),
  nested.factors=list(main.unit = "block",
    split.unit = c("block", "main.unit")),
  randomized=fac.gen(list(A = 4, B = 3), times = 2),
  seed=155251978, unit.permutation=FALSE)
```

fac.match	<i>Match, for each combination of a set of columns in x, the row that has the same combination in table</i>
-----------	---

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

```
fac.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 <code>match</code> 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

See Also[match](#)**Examples**

```
## Not run:
#A single unmatched combination
kdata <- data.frame(Expt="D197-5",
                  Row=8,
                  Column=20, stringsAsFactors=FALSE)
index <- fac.match(kdata, D197.dat, c("Expt", "Row", "Column"))

# A matched and an unmatched combination
kdata <- data.frame(Expt=c("D197-5", "D197-4"),
                  Row=c(8, 10),
                  Column=c(20, 8), stringsAsFactors=FALSE)
index <- fac.match(kdata, D197.dat, c("Expt", "Row", "Column"))

## End(Not run)
```

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 $X \%*\% (1/\text{diag}(r) \%*\% \text{t}(X))$, 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

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.nested	<i>creates a factor whose values are generated within those of the factor nesting.fac</i>
------------	---

Description

Creates a [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, levels=NA, labels=NA, ...)
```

Arguments

<code>nesting.fac</code>	The factor within each of whose levels the created factor is to be generated.
<code>levels</code>	Optional vector of levels for the factor . Any data value that does not match a value in <code>levels</code> will be NA in the factor . The default value of <code>levels</code> is the the list of numbers from 1 to the maximum replication of the levels of <code>nesting.fac</code> , represented as characters.
<code>labels</code>	Optional vector of values to use as labels for the levels of the factor . The default is <code>as.character(levels)</code> .
<code>...</code>	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.

Note

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

Author(s)

Chris Brien

See Also

[fac.gen](#) in package **dae**, [factor](#).

Examples

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

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

fac.recode	<i>Recodes factor levels using values in a vector. The values in the vector do not have to be unique.</i>
------------	---

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](#).

Usage

```
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[as.numfac](#) and [mpone](#) in package [dae](#), [factor](#), [relevel](#).**Examples**

```
## set up a factor with labels
a <- 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(a, c(1,2,2,1), labels = c("a","b"))
```

fac.sumop	<i>computes the summation matrix that produces sums corresponding to a (generalized) factor</i>
-----------	---

Description

Computes the matrix that produces the sums corresponding to a (generalized) [factor](#).

Usage

```
fac.sumop(factor)
```

Arguments

factor The (generalized) [factor](#) whose sums the summation 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 summation matrix is formed as $X \%*\% t(X)$.

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 symmetric matrix.

Author(s)

Chris Brien

See Also

[fac.combine](#), [fac.meanop](#) in package **dae**.

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
S.AB <- fac.sumop(AB)
```

fac.vcmat	<i>forms the variance matrix for the variance component of a (generalized) factor</i>
-----------	---

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

```
## 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 2⁴ factorial experiment

Description

The data set come from an unreplicated 2⁴ 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 aranged 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

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

Arguments

object	An aovlist object created from a call to <code>aov</code> .
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 occur twice.

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,
                       85,87,92,89,84,79,81,80,88)

## 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 fitted values
fit <- fitted.aovlist(RCBDPen.aov)
fit <- fitted(RCBDPen.aov, error.term = "Blend:Flask")
```

fitted.errors	<i>Extract the fitted values for a fitted model</i>
---------------	---

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

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

Arguments

<code>object</code>	An <code>aovlist</code> object created from a call to <code>aov</code> .
<code>error.term</code>	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 <code>error.term</code> is NULL effects are extracted from all Error terms.
<code>...</code>	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

```
## 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)

## 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")
```

get.daeTolerance *Gets the value of daeTolerance for the package dae*

Description

A function that gets the vector of values such that, in **dae** functions, values less than it are considered to be zero.

Usage

```
get.daeTolerance()
```

Value

The vector of two values for daeTolerance, one named `element.tol` that is used for elements of matrices and a second named `element.eigen` that is used for eigenvalues and quantities based on them, such as efficiency factors.

Author(s)

Chris Brien

See Also

[set.daeTolerance](#).

Examples

```
## get daeTolerance.
get.daeTolerance()
```

harmonic.mean	<i>Calculates the harmonic mean.</i>
---------------	--------------------------------------

Description

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

Usage

```
harmonic.mean(x)
```

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	<i>Plots an interaction plot for three factors</i>
----------------------	--

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".
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.
...	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

```
## 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 combination 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	<i>Tests whether an object is a valid object of class projector</i>
--------------	---

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 *daeDesignNotes.pdf*.

Usage

```
data(LatticeSquare_t49.des)
```

Format

A data.frame containing 196 observations of 4 variables.

Source

Cochran and Cox (1957) *Experimental Designs*. 2nd edn Wiley, New York.

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 ternon-aliased term. Its elements are zeroes and ones, the entry in the *i*th row and *j*th column indicates whether or not the *i*th term is marginal to the *j*th term i.e. the column space of the *i*th term is a subspace of that for the *j*th term and so the source for the *j*th term will be orthogonal to that for the *i*th 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.combine](#), [proj2.eigen](#),
[pstructure](#) 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 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 i th row and j th column equal to ρ^k where $k = |i - j|$.

Usage

```
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

```
corr <- mat.ar1(rho=0.4, order=4)
```

mat.ar2 *Forms an ar2 correlation matrix*

Description

Form the correlation [matrix](#) of order `order` whose correlations follow the ar2 pattern. The resulting [matrix](#) is banded.

Usage

```
mat.ar2(ARparameters, order)
```


Arguments

- ARparameters A **numeric** containing the two autoregressive parameter values of the process, being the weights given to the lag 1 and lag 2 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 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 ar2 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](#), [mat.arma](#)

Examples

```
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`.

Let $\omega = 1 - \text{ARparameters}[2] - \text{ARparameters}[3] * (\text{ARparameters}[1] + \text{ARparameters}[3])$.
Then the values in

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

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

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

mat.arma	<i>Forms an arma correlation matrix</i>
----------	---

Description

Form the correlation [matrix](#) of order `order` whose correlations follow the arma pattern. The resulting [matrix](#) is banded.

Usage

```
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 $\text{ARparameters}[1]/(1-\text{ARparameters}[2])$;
- in subsequent diagonal bands, ($k = 3:\text{order}$), of `corr` are $\text{ARparameters}[1]*\text{corr}[k-1] + \text{ARparameters}[2]*\text{corr}[k-2]$.

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

```
corr <- mat.arma(ARparameter = 0.4, MAparameter = -0.2, order = 4)
```

`mat.banded`*Form a banded matrix from a vector of values*

Description

Takes the first value in `x` and places it down the diagonal of the `matrix`. Takes the second value in `x` and places it down the first subdiagonal, both below and above the diagonal of the `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 `matrix` will be zero.

Usage

```
mat.banded(x, nrow, ncol)
```

Arguments

<code>x</code>	A <code>numeric</code> containing the values for each band from 1 to the length of <code>x</code> .
<code>nrow</code>	The number of rows in the banded <code>matrix</code> being formed.
<code>ncol</code>	The number of columns in the banded <code>matrix</code> being formed.

Value

An $nrow \times ncol$ `matrix`.

Author(s)

Chris Brien

See Also

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

Examples

```
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)
```

`mat.dirprod`*Forms the direct product of two matrices*

Description

Form the direct product of the $m \times n$ **matrix** **A** and the $p \times q$ **matrix** **B**. It is also called the Kroneker 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	<i>Forms the direct sum of a list of matrices</i>
------------	---

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

```
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

```
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	<i>Forms an exponential correlation matrix</i>
---------	--

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 ρ^k where $k = |\text{coordinate}[i] - \text{coordinate}[j]|$.

Usage

```
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)
```

mat.gau	<i>Forms an exponential correlation matrix</i>
---------	--

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 ρ^k where $k = (\text{coordinate}[i] - \text{coordinate}[j])^2$.

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	<i>Forms a square matrix of ones</i>
-------	--------------------------------------

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)
```

mat.ma1 *Forms an ma1 correlation matrix*

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)
```

mat.ma2 *Forms an ma2 correlation matrix*

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

- MParameters A **numeric** containing the two moving average parameter values of the process, being the weights given to the lag 1 and lag 2 random perturbations.
- 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, `MParameters`. The values in

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

where $div = 1 + MMParameters[1]*MParameter[1] + MParameters[2]*MParameters[2]$.

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(MParameters = c(0.4, -0.2), order = 4)
```

<code>mat.ncssvar</code>	<i>Calculates the variance matrix of the random effects for a natural cubic smoothing spline</i>
--------------------------	--

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 orderd 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

Verbyla, A. P., Cullis, B. R., Kenward, M. G., and Welham, S. J. (1999). The analysis of designed experiments and longitudinal data by using smoothing splines (with discussion). *Journal of the Royal Statistical Society, Series C (Applied Statistics)*, **48**, 269-311.

See Also

[Zncsspline](#).

Examples

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

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 $\text{gamma}/(1 + (\text{gamma} * \text{gamma} / 4))$;
- the subsequent subdiagonal bands, ($k = 3:\text{order}$), of `corr` are equal to $\text{gamma} * \text{corr}[k-1] - (\text{gamma} * \text{gamma}/4) * \text{corr}[k-2]$.

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

<code>gamma</code>	A <code>numeric</code> containing the two values of <code>gamma</code> , being parameters linked with spatial dependence and competition.
<code>order</code>	The order of the <code>matrix</code> to be formed.
<code>print</code>	A <code>character</code> giving the object to be printed. Currently, only the calculated values of the <code>ar3</code> parameters can be printed. If <code>NULL</code> , nothing is printed.

Details

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

```
phi[1] = gamma[1] + 2 * gamma[2]; phi[2] = -gamma[2] * (2*gamma[2] + gamma[1]);
phi[3] = gamma[1] * gamma[2] * gamma[2].
```

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

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

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

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

mat.Vpred

Calculates the variances of a set of predicted effects from a mixed model

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 [mat.Vpredicts](#), which allows the use of both matrices and [formulae](#).

Usage

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

Arguments

W	The $n \times w$ incidence matrix for the w effects to be predicted.
Gg	The $w \times w$ variance matrix of the w effects to be predicted. If the effects to be predicted are fixed, set to 0.
X	The $n \times f$ incidence matrix for the f nuisance fixed factors and covariates. The default is a column vector of ones.
Vu	The $n \times r$ variance matrix of the r nuisance random effects. If there are none, set to zero.
R	The residual variance matrix .
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.

Details

Firstly the information matrix is calculated as

$A \leftarrow t(W) \%*\% \text{Vinv} \%*\% W + \text{ginv}(Gg) - A \%*\% \text{ginv}(t(X) \%*\% \text{Vinv} \%*\% X) \%*\% t(A)$, where $\text{Vinv} \leftarrow \text{ginv}(Vu + R)$, $A = t(W) \%*\% \text{Vinv} \%*\% X$ and $\text{ginv}(B)$ 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 $A \leftarrow (I - \text{eliminate}) \text{Vinv} (I - \text{eliminate})$.

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

Value

A $w \times w$ [matrix](#) containing the variances and covariances of the predicted effects.

Author(s)

Chris Brien

References

Smith, A. B., D. G. Butler, C. R. Cavanagh and B. R. Cullis (2015). Multi-phase variety trials using both composite and individual replicate samples: a model-based design approach. *Journal of Agricultural Science*, **153**, 1017-1029.

See Also

[designAmeasures](#), [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 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)
designAmeasures(Vp)

## 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))
designAmeasures(Vp.reduc)
```

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

```
mat.Vpredicts(target, Gt = 0, fixed = ~ 1, random, G, R, design,
              eliminate, keep.order = TRUE)
```


Arguments

target	The $n \times w$ incidence matrix for the w effects targetted for prediction, or a formula from which the matrix can be generated.
Gt	The value of the variance component for the targetted effects or the $w \times w$ variance matrix of the w targetted effects. If the targetted 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	The $n \times r$ incidence matrix for the r nuisance random effects, or a formula from which the matrix can be generated. The default is 0, which implies that there are no random effects.
G	The $r \times r$ variance matrix of the r nuisance random effects. 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.

Details

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

As described in Hooks et al. (2009, Equation 19), the information matrix is calculated as $\mathbf{A} \leftarrow \mathbf{t}(\mathbf{W}) \%*\% \mathbf{V}_{\text{inv}} \%*\% \mathbf{W} + \text{ginv}(\mathbf{G}_g) - \mathbf{A} \%*\% \text{ginv}(\mathbf{t}(\mathbf{X}) \%*\% \mathbf{V}_{\text{inv}} \%*\% \mathbf{X}) \%*\% \mathbf{t}(\mathbf{A})$, where $\mathbf{V}_{\text{inv}} \leftarrow \text{ginv}(\mathbf{V}\mathbf{u} + \mathbf{R})$, $\mathbf{A} = \mathbf{t}(\mathbf{W}) \%*\% \mathbf{V}_{\text{inv}} \%*\% \mathbf{X}$ and $\text{ginv}(\mathbf{B})$ is the unique Moore-Penrose inverse of \mathbf{B} formed using the eigendecomposition of \mathbf{B} .

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

Finally, the variance of the predicted effects is calculated: `Vpred <- ginv(A)`.

Value

A $w \times w$ `matrix` containing the variances and covariances of the predicted effects.

Author(s)

Chris Brien

References

Hooks, T., Marx, D., Kachman, S., and Pedersen, J. (2009). Optimality criteria for models with random effects. *Revista Colombiana de Estadística*, **32**, 17-31.

Smith, A. B., D. G. Butler, C. R. Cavanagh and B. R. Cullis (2015). Multi-phase variety trials using both composite and individual replicate samples: a model-based design approach. *Journal of Agricultural Science*, **153**, 1017-1029.

See Also

[designAmeasures](#), [mat.Vpred](#).

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
terms <- c("Variety", "Frep", "Frep:Fplot", "Mrep", "Mrep:Mday", "Mrep:Mday:Mord")
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)
```

```

## 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[c(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
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 *daeDesignNotes.pdf*.

Usage

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

Format

A data.frame containing 196 observations of 4 variables.

Source

McIntyre, G. A. (1955) Design and Analysis of Two Phase Experiments. *Biometrics*, **11**, 324–334.

meanop

computes the projection matrix that produces means

Description

Replaced by [fac.meanop](#).

mpone	<i>Converts the first two levels of a factor into the numeric values -1 and +1</i>
-------	--

Description

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 levles of A and B
Frf3.trt$C <- factor(mpone(Frf3.trt$A)*mpone(Frf3.trt$B), labels = mp)
```

no.reps	<i>Computes the number of replicates for an experiment</i>
---------	--

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

```
## 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)
```

Oats.dat	<i>Data for an experiment to investigate nitrogen response of 3 oats varieties</i>
----------	--

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

Yates, F. (1937). The Design and Analysis of Factorial Experiments. *Imperial Bureau of Soil Science, Technical Communication*, **35**, 1-95.

p2canon.object	<i>Description of a p2canon object</i>
----------------	--

Description

An object of class p2canon that contains information derived from two formulae using [projs.2canon](#).

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

The terms, sources, marginalty 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	<i>Computes the power for an experiment</i>
-----------	---

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)
```

print.aliasing *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

```
## 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
```

print.projector	<i>Print projectors</i>
-----------------	-------------------------

Description

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

Usage

```
## 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

```
## 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.criteria = c("aefficiency", "efficiency", "order"), ...)
```

Arguments

`x` The `pstructure.object`, which is of class `pstructure` 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 or from other methods.

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

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

Arguments

<code>x</code>	A <code>summary.p2canon</code> object.
<code>...</code>	further arguments passed to <code>print</code> .

Value

No value is returned.

Author(s)

Chris Brien

See Also

[summary.p2canon](#)

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 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

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

Arguments

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

Value

No value is returned.

Author(s)

Chris Brien

See Also

[summary.pcanon](#)

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 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	<i>Compute the projection and Residual operators for two, possibly nonorthogonal, projectors</i>
---------------	--

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 $Q1 \% \% Q2 \% \% Q1$ (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 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, $Qres = Q1 - Q1 \% \% ginv(Q2 \% \% Q1 \% \% Q2) \% \% Q1$. `Qconf` is obtained by subtracting `Qres` from `Q1`.

Value

A list with the following components:

1. **efficiencies:** a vector containing the nonzero canonical efficiency factors;
2. **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. **Qconf:** a projector onto the part of the range of Q1 with which Q2 is confounded;
4. **Qres:** a projector onto the part of the range of Q1 that is orthogonal to the range of Q2.

Author(s)

Chris Brien

References

James, A. T. and Wilkinson, G. N. (1971) Factorization of the residual operator and canonical decomposition of nonorthogonal factors in the analysis of variance. *Biometrika*, **58**, 279–294.

Payne, R. W. and R. D. Tobias (1992). General balance, combination of information and the analysis of covariance. *Scandinavian Journal of Statistics*, **19**, 3–23.

See Also

[proj2.eigen](#), [proj2.efficiency](#), [decomp.relate](#) in package **dae**.
[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 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".

Details

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`.

Value

A vector containing the nonzero canonical efficiency factors.

Author(s)

Chris Brien

References

James, A. T. and Wilkinson, G. N. (1971) Factorization of the residual operator and canonical decomposition of nonorthogonal factors in the analysis of variance. *Biometrika*, **58**, 279-294.

See Also

[efficiency.criteria](#), [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.intra <- proj2.efficiency(unit.struct$Q[["Block"]], trt.struct$Q[["trt"]])
```

proj2.eigen	<i>Canonical efficiency factors and eigenvectors in joint decomposition of two projectors</i>
-------------	---

Description

Computes the canonical efficiency factors for the joint decomposition of two projectors and the eigenvectors corresponding to the first projector (James and Wilkinson, 1971).

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 $n \times r$ [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. 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

James, A. T. and Wilkinson, G. N. (1971) Factorization of the residual operator and canonical decomposition of nonorthogonal factors in the analysis of variance. *Biometrika*, **58**, 279-294.

See Also

[proj2.estimate](#), [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
```

projector

Create projectors

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

```
## 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

Class "[matrix](#)", from data part. Class "[array](#)", by class "matrix", distance 2. Class "[structure](#)", by class "matrix", distance 3. Class "[vector](#)", by class "matrix", distance 4, with explicit coerce.

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

```
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	<i>A canonical analysis of the relationships between two sets of projectors</i>
--------------	---

Description

Computes the canonical efficiency factors for the joint decomposition of two structures or sets of mutually orthogonal 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 orthogonality 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`.

Value

A `p2canon.object`.

Author(s)

Chris Brien

References

Brien, C. J. and R. A. Bailey (2009). Decomposition tables for multitiered experiments. I. A chain of randomizations. *The Annals of Statistics*, **36**, 4184 - 4213.

James, A. T. and Wilkinson, G. N. (1971) Factorization of the residual operator and canonical decomposition of nonorthogonal factors in the analysis of variance. *Biometrika*, **58**, 279-294.

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

Brien, C. J. and R. A. Bailey (2009). Decomposition tables for multitiered experiments. I. A chain of randomizations. *The Annals of Statistics*, **36**, 4184 - 4213.

See Also

[projs.2canon](#), [proj2.eigen](#), [proj2.combine](#) in package **dae**.

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

pstructure.formula	<i>Takes a formula and constructs a pstructure.object that includes the orthogonalized projectors for the terms in a formula</i>
--------------------	--

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", "efficiency", "order"),
           aliasing.print = TRUE, data = NULL, ...)
```

Arguments

formula	An object of class <code>formula</code> from which the terms will be obtained.
keep.order	A <code>logical</code> 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 <code>logical</code> indicating whether the projector for the grand mean is to be included in the set produced.
orthogonalize	A <code>character</code> vector indicating the method for orthogonalizing a projector to those for terms that occurred previously in the formula. Three options are available: <code>hybrid</code> ; <code>differencing</code> ; <code>eigenmethods</code> . The <code>hybrid</code> option is the most general and uses the relationships between the projection operators for the terms in the formula to decide which <code>projectors</code> to subtract and which to orthogonalize using <code>eigenmethods</code> . The <code>differencing</code> option subtracts, from the current <code>projector</code> , those previously orthogonalized <code>projectors</code> for terms whose factors are a subset of the current <code>projector</code> 's factors. The <code>eigenmethods</code> option recursively orthogonalizes the <code>projectors</code> using an eigenanalysis of each <code>projector</code> with previously orthogonalized <code>projectors</code> .
labels	A <code>character</code> 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 <code>terms</code> and <code>sources</code> . <code>Terms</code> have all factors/variables in it separated by colons (<code>:</code>). <code>Sources</code> have factors/variables in them that represent interactions separated by hashes (<code>#</code>); if some factors are nested within others, the nesting factors are surrounded by square brackets (<code>[</code> and <code>]</code>) and separated by colons (<code>:</code>). If some generalized, or combined, factors have no marginal terms, the constituent factors are separated by colons (<code>:</code>) and if they interact with other factors in the source they will be parenthesized.
marginality	A square <code>matrix</code> that can be used to supply the marginality <code>matrix</code> when it is desired to overwrite the calculated marginality <code>matrix</code> or when it is not being calculated. It should consist 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 <i>i</i> th row and <i>j</i> th column will be one if the <i>i</i> th term is marginal to the <i>j</i> th term i.e. the column space of the <i>i</i> th term is a subspace of that for the <i>j</i> th term and so the source for the <i>j</i> th term is to be made orthogonal to that for the <i>i</i> th term. Otherwise, the entries are zero. A row and column should not be included for the grand mean even if <code>grandMean</code> is <code>TRUE</code> .

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 , efficiency , 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 $\mathbf{X}(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'$, where \mathbf{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.

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 \mathbf{Q}_i and \mathbf{Q}_j are two projectors for two different terms, with $i < j$, then

1. if $\mathbf{Q}_j\mathbf{Q}_i \neq \mathbf{0}$ then have to orthogonalize \mathbf{Q}_j to \mathbf{Q}_i .
2. if $\mathbf{Q}_j\mathbf{Q}_i = \mathbf{Q}_j$ then, if $\mathbf{Q}_i = \mathbf{Q}_j$, they are equal and \mathbf{Q}_j will be removed from the list of terms; otherwise they are marginal and \mathbf{Q}_i is subtracted from \mathbf{Q}_j .

3. if have to orthogonalize and $\mathbf{Q}_j\mathbf{Q}_i = \mathbf{Q}_i$ then \mathbf{Q}_j is aliased with previous terms and will be removed from the list of terms; otherwise \mathbf{Q}_i is partially aliased with \mathbf{Q}_j and \mathbf{Q}_j is orthogonalized to \mathbf{Q}_i using eigenmethods.

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

Value

A `pstructure.object`.

Author(s)

Chris Brien

References

James, A. T. and Wilkinson, G. N. (1971) Factorization of the residual operator and canonical decomposition of nonorthogonal factors in the analysis of variance. *Biometrika*, **58**, 279-294.

See Also

[proj2.efficiency](#), [proj2.combine](#), [proj2.eigen](#), [projs.2canon](#) 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)

## 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)

##obtain projectors using pstructure.formula
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, which = c("aeff","eeff","order"))
```

pstructure.object *Description of a pstructure object*

Description

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 projector 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 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**

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

Arguments

aov.obj	An aov object or aovlistobject 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 <code>help(points)</code> for details).
full	whether a full or half normal plot is to be produced. The default is for a half-normal plot; <code>full=TRUE</code> produces a full normal plot.
...	Further graphical parameters may be specified (use <code>help(par)</code> 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

```
## analysis of 2^4 factorial experiment from Table 10.6 of Box, Hunter and
## Hunter (1978) Statistics for Experimenters. New York, Wiley.
## use ?Fac4Proc.dat for data set details
data(Fac4Proc.dat)
Fac4Proc.aov <- aov(Conv ~ Catal * Temp * Press * Conc + Error(Runs),
                   Fac4Proc.dat)
qqeffects(Fac4Proc.aov, error.term="Runs", data=Fac4Proc.dat)
```

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

```
resid.errors(...)
```

Arguments

... 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

```
## 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

<code>object</code>	An <code>aovlist</code> object created from a call to aov .
<code>error.term</code>	The term from the <code>Error</code> function for which the residuals are to be extracted. If <code>error.term</code> is <code>NULL</code> the residuals are extracted from the last <code>Error</code> term.
<code>...</code>	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(89,88,97,94,84,84,77,92,79,81,87,87,
                      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")
```

rmvnorm	<i>generates a vector of random values from a multivariate normal distribution</i>
---------	--

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 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

Ripley, B. D. (1987) *Stochastic simulation*. Wiley, New York.

See Also

[fac.ar1mat](#), [fac.vcmat](#), in package [dae](#), [rnorm](#), and [chol](#).

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))

## 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)
```

Sensory3Phase.dat

Data for the three-phase sensory evaluation experiment in Brien, C.J. and Payne, R.W. (1999)

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 halplots 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 halplots 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 judges 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 give: Occasion, Judges, Interval, Sitings, 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, Sitings and Position are in standard order; the remaining factors are in randomized order.

See also the vignette *daeDesignNotes.pdf*.

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

Brien, C.J. and Payne, R.W. (1999) Tiers, structure formulae and the analysis of complicated experiments. *The Statistician*, **48**, 41-52.

<code>set.daeTolerance</code>	<i>Sets the values of daeTolerance for the package dae</i>
-------------------------------	--

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

```
## set daeTolerance.  
set.daeTolerance(1E-04, 1E-08)
```

show-methods

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	<i>Data for an experiment to investigate the effects of grazing patterns on pasture composition</i>
--------------	---

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

Example 14.1 from Mead, R. (1990). *The Design of Experiments: Statistical Principles for Practical Application*. Cambridge, Cambridge University Press.

strength	<i>Generate paper strength values</i>
----------	---------------------------------------

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

```
## 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	<i>Summarize a canonical analysis of the relationships between two sets of projectors</i>
-----------------	---

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

```
## S3 method for class 'p2canon'
summary(object, which.criteria = c("aefficiency", "efficiency", "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

Brien, C. J. and R. A. Bailey (2009). Decomposition tables for multitiered experiments. I. A chain of randomizations. *The Annals of Statistics*, **36**, 4184 - 4213.

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

```
## 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)
```

summary.pcanon	<i>Summarizes the anatomy of a design, being the decomposition of the sample space based on its canonical analysis, as produced by designAnatomy</i>
----------------	--

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

```
## S3 method for class 'pcanon'
summary(object, labels.swap = FALSE,
        which.criteria = c("aefficiency", "eefficiency", "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 dforthog – 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

Brien, C. J. and R. A. Bailey (2009). Decomposition tables for multitiered experiments. I. A chain of randomizations. *The Annals of Statistics*, **36**, 4184 - 4213.

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

```
## 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	<i>Performs Tukey's one-degree-of-freedom-test-for-nonadditivity</i>
-----------	--

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**

```
## 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)

## 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

```
## analysis of 2^4 factorial experiment from Table 10.6 of Box, Hunter and
## Hunter (1978) Statistics for Experimenters. New York, Wiley.
## 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 σ_s^2 .

Usage

```
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 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 Δ and G_s matrices.

Value

A [matrix](#) containing the design matrix.

Author(s)

Chris Brien

References

Verbyla, A. P., Cullis, B. R., Kenward, M. G., and Welham, S. J. (1999). The analysis of designed experiments and longitudinal data by using smoothing splines (with discussion). *Journal of the Royal Statistical Society, Series C (Applied Statistics)*, **48**, 269-311.

See Also

[mat.ncssvar](#).

Examples

```
Z <- Zncsspline(knot.points = 1:10, Gpower = 0.5)
```

Index

*Topic **aplot**

- designPlotlabels, 27
- interaction.ABC.plot, 58

*Topic **array**

- as.data.frame.pstructure, 9
- correct.degfree, 14
- decomp.relate, 16
- degfree, 17
- designAnatomy, 20
- designLatinSqrSys, 24
- designTwophaseAnatomies, 32
- efficiencies, 35
- efficiency.criteria, 37
- elements, 38
- fac.ar1mat, 41
- fac.meanop, 49
- fac.sumop, 52
- fac.vcmat, 53
- is.projector, 61
- marginality, 62
- mat.ar1, 64
- mat.ar2, 64
- mat.ar3, 65
- mat.arma, 67
- mat.banded, 68
- mat.dirprod, 69
- mat.dirsum, 70
- mat.exp, 71
- mat.gau, 71
- mat.I, 72
- mat.J, 73
- mat.ma1, 74
- mat.ma2, 74
- mat.ncssvar, 75
- mat.sar, 76
- mat.sar2, 77
- mat.Vpred, 78
- mat.Vpredicts, 80
- p2canon.object, 87

- p2canon.object, 88
- print.aliasing, 90
- print.projector, 91
- print.pstructure, 92
- proj2.combine, 95
- proj2.efficiency, 96
- proj2.eigen, 98
- projector, 99
- projector-class, 100
- projs.2canon, 102
- projs.combine.p2canon, 103
- pstructure.formula, 104
- pstructure.object, 108
- show-methods, 115
- summary.p2canon, 118
- summary.pcanon, 119
- Zncsspline, 123

*Topic **asreml**

- daeTips, 15

*Topic **classes**

- projector-class, 100

*Topic **datagen**

- designRandomize, 29
- fac.gen, 44
- fac.layout, 46
- rmvnorm, 112
- strength, 116

*Topic **datasets**

- ABC.Interact.dat, 8
- BIBDWheat.dat, 11
- Casuarina.dat, 13
- Exp249.mplot.des, 39
- Fac4Proc.dat, 54
- LatticeSquare_t49.des, 62
- McIntyreTMV.dat, 83
- Oats.dat, 86
- Sensory3Phase.dat, 113
- SPLGrass.dat, 116

*Topic **design**

- blockboundaryPlot, 11
- decomp.relate, 16
- designAmeasures, 18
- designAnatomy, 20
- designLatinSqrSys, 24
- designPlot, 24
- designPlotlabels, 27
- designRandomize, 29
- designTwophaseAnatomies, 32
- detect.diff, 34
- efficiencies, 35
- efficiency.criteria, 37
- fac.gen, 44
- fac.layout, 46
- fac.match, 48
- interaction.ABC.plot, 58
- marginality, 62
- mat.ncssvar, 75
- mat.Vpred, 78
- mat.Vpredicts, 80
- no.reps, 85
- p2canon.object, 87
- pcanon.object, 88
- power.exp, 89
- print.summary.p2canon, 93
- print.summary.pcanon, 94
- proj2.combine, 95
- proj2.efficiency, 96
- proj2.eigen, 98
- projs.2canon, 102
- projs.combine.p2canon, 103
- pstructure.formula, 104
- pstructure.object, 108
- qqyeffects, 109
- strength, 116
- summary.p2canon, 118
- summary.pcanon, 119
- yates.effects, 122
- Zncsspline, 123
- *Topic **factor**
 - as.numfac, 10
 - designRandomize, 29
 - fac.combine, 42
 - fac.divide, 43
 - fac.gen, 44
 - fac.layout, 46
 - fac.match, 48
 - fac.nested, 50
 - fac.recode, 51
 - mpone, 84
- *Topic **hplot**
 - designPlotlabels, 27
 - interaction.ABC.plot, 58
 - qqyeffects, 109
- *Topic **htest**
 - fitted.aovlist, 54
 - fitted.errors, 56
 - qqyeffects, 109
 - resid.errors, 110
 - residuals.aovlist, 111
 - tukey.1df, 121
 - yates.effects, 122
- *Topic **iplot**
 - qqyeffects, 109
- *Topic **manip**
 - as.numfac, 10
 - elements, 38
 - extab, 40
 - fac.combine, 42
 - fac.divide, 43
 - fac.nested, 50
 - fac.recode, 51
 - get.daeTolerance, 57
 - harmonic.mean, 58
 - is.allzero, 60
 - mpone, 84
 - set.daeTolerance, 114
- *Topic **methods**
 - fitted.aovlist, 54
 - residuals.aovlist, 111
 - show-methods, 115
- *Topic **models**
 - fitted.aovlist, 54
 - fitted.errors, 56
 - resid.errors, 110
 - residuals.aovlist, 111
 - tukey.1df, 121
- *Topic **package**
 - dae-package, 4
- *Topic **plot**
 - blockboundaryPlot, 11
 - designPlot, 24
- *Topic **projector**
 - as.data.frame.pstructure, 9
 - correct.degfree, 14
 - decomp.relate, 16

- degfree, 17
 - designAnatomy, 20
 - designTwophaseAnatomies, 32
 - efficiencies, 35
 - efficiency.criteria, 37
 - fac.meanop, 49
 - fac.sumop, 52
 - get.daeTolerance, 57
 - is.projector, 61
 - marginality, 62
 - p2canon.object, 87
 - pcanon.object, 88
 - print.aliasing, 90
 - print.projector, 91
 - print.pstructure, 92
 - print.summary.p2canon, 93
 - print.summary.pcanon, 94
 - proj2.combine, 95
 - proj2.efficiency, 96
 - proj2.eigen, 98
 - projector, 99
 - projector-class, 100
 - projs.2canon, 102
 - projs.combine.p2canon, 103
 - pstructure.formula, 104
 - pstructure.object, 108
 - set.daeTolerance, 114
 - show-methods, 115
 - summary.p2canon, 118
 - summary.pcanon, 119
- ABC.Interact.dat, 4, 8
- Ameasures (dae-deprecated), 15
- aov, 55, 56, 109–111, 121–123
- array, 101
- as.data.frame, 9
- as.data.frame.pstructure, 7, 9
- as.numeric, 10
- as.numfac, 4, 10, 52
- BIBDWheat.dat, 4, 11
- blockboundary.plot (dae-deprecated), 15
- blockboundaryPlot, 5, 11, 27
- Casuarina.dat, 4, 13
- character, 9, 12, 21, 22, 25, 26, 29, 30, 32, 33, 46, 77, 88, 105, 108, 120
- chol, 113
- coerce,projector,matrix-method
(projector-class), 100
- coerce<-,projector,matrix-method
(projector-class), 100
- correct.degfree, 7, 14, 17, 18, 50, 61, 100, 101
- dae (dae-package), 4
- dae-deprecated, 15
- dae-package, 4
- daeTips, 15
- data.frame, 9, 21, 28–30, 32, 43–47, 59, 81, 88, 90, 108
- decomp.relate, 7, 16, 96
- degfree, 7, 14, 17, 50, 100, 101
- degfree<- (degfree), 17
- design.plot (dae-deprecated), 15
- designAmeasures, 5, 18, 79, 82
- designAnatomy, 5, 7, 19, 20, 24, 27, 30, 32–36, 62, 63, 87, 88, 119, 120
- designLatinSqrSys, 5, 23, 24, 27, 30
- designPlot, 5, 11, 12, 23, 24, 24, 28, 30
- designPlotlabels, 5, 27, 27
- designRandomize, 5, 23, 24, 27, 29, 46
- designTwophaseAnatomies, 5, 31
- detect.diff, 5, 34, 86, 89
- efficiencies, 35
- efficiencies.p2canon, 7, 103
- efficiencies.pcanon, 7, 23, 34
- efficiency.criteria, 8, 22, 23, 33, 34, 37, 87, 90, 92, 97, 103, 106, 108, 118, 120
- eigen, 16, 23, 34, 36, 37, 63, 97, 98, 103, 107, 118, 120
- elements, 6, 38
- Exp249.mplot.des, 4, 39
- extab, 8, 40
- fac.ar1mat, 6, 41, 54, 113
- fac.combine, 5, 28, 42, 44, 45, 49, 50, 52, 53, 58, 59
- fac.divide, 5, 43, 43
- fac.gen, 5, 29, 30, 44, 47, 51
- fac.layout, 46
- fac.match, 5, 48
- fac.meanop, 8, 41, 49, 53, 54, 83
- fac.nested, 5, 50
- fac.recode, 5, 10, 51

- fac.sumop, [6](#), [41](#), [50](#), [52](#), [54](#)
- fac.vcmat, [6](#), [41](#), [53](#), [113](#)
- Fac4Proc.dat, [4](#), [54](#)
- factor, [10](#), [29](#), [30](#), [40–47](#), [49–53](#), [58](#), [59](#), [84](#), [117](#)
- fitted, [54](#), [56](#)
- fitted(fitted.aovlist), [54](#)
- fitted.aovlist, [6](#), [54](#), [56](#)
- fitted.errors, [6](#), [55](#), [56](#), [110](#), [111](#), [122](#)
- formula, [21](#), [32](#), [78](#), [80](#), [81](#), [88](#), [105](#), [108](#)
- geom_text, [28](#)
- get.daeTolerance, [8](#), [57](#), [115](#)
- ggplot, [28](#), [59](#)
- harmonic.mean, [8](#), [58](#)
- integer, [25](#)
- interaction.ABC.plot, [6](#), [58](#)
- interaction.plot, [59](#)
- is.allzero, [8](#), [60](#)
- is.projector, [7](#), [61](#), [100](#)
- LatticeSquare_t49.des, [4](#), [62](#)
- list, [16](#), [19](#), [21](#), [28–30](#), [32](#), [33](#), [42–44](#), [46](#), [59](#), [81](#), [88](#), [120](#)
- logical, [9](#), [12](#), [21](#), [22](#), [25](#), [26](#), [28](#), [32](#), [76](#), [81](#), [94](#), [105](#), [106](#), [120](#), [124](#)
- marginality, [62](#)
- marginality.pstructure, [5](#)
- mat.ar1, [6](#), [64](#), [65–68](#), [71–73](#), [75](#), [77](#), [78](#)
- mat.ar2, [6](#), [64](#), [64](#), [66](#), [68](#), [71](#), [72](#), [74](#), [77](#), [78](#)
- mat.ar3, [6](#), [64](#), [65](#), [65](#), [67](#), [68](#), [71](#), [72](#), [74](#), [75](#), [77](#), [78](#)
- mat.arma, [6](#), [64–66](#), [67](#), [68](#), [71](#), [72](#), [74](#), [75](#), [77](#), [78](#)
- mat.banded, [6](#), [64–67](#), [68](#), [71](#), [72](#), [74](#), [75](#), [77](#), [78](#)
- mat.dirprod, [6](#), [69](#), [69](#), [70](#)
- mat.dirsum, [6](#), [70](#)
- mat.exp, [6](#), [64–68](#), [71](#), [72](#), [74](#), [75](#), [77](#), [78](#)
- mat.gau, [6](#), [64–68](#), [71](#), [71](#), [74](#), [75](#), [77](#), [78](#)
- mat.I, [6](#), [64–68](#), [71](#), [72](#), [72](#), [73–75](#), [77](#), [78](#)
- mat.J, [6](#), [64–68](#), [71–73](#), [73](#), [74](#), [75](#), [77](#), [78](#)
- mat.ma1, [6](#), [64–68](#), [71](#), [72](#), [74](#), [75](#), [77](#), [78](#)
- mat.ma2, [6](#), [64–68](#), [71](#), [72](#), [74](#), [74](#), [77](#), [78](#)
- mat.ncssvar, [6](#), [75](#), [124](#)
- mat.sar, [6](#), [76](#), [78](#)
- mat.sar2, [6](#), [64–68](#), [71](#), [72](#), [74](#), [75](#), [77](#), [77](#)
- mat.Vpred, [6](#), [19](#), [78](#), [80](#), [82](#)
- mat.Vpredicts, [6](#), [78](#), [79](#), [80](#)
- match, [48](#), [49](#)
- matrices, [80](#)
- matrix, [11](#), [16](#), [19](#), [21](#), [25](#), [26](#), [33](#), [41](#), [53](#), [61](#), [62](#), [64–82](#), [88](#), [95](#), [98–101](#), [105](#), [108](#), [115](#), [124](#)
- McIntyreTMV.dat, [4](#), [83](#)
- meanop, [83](#)
- mpone, [5](#), [52](#), [84](#), [84](#)
- no.reps, [5](#), [35](#), [85](#), [89](#)
- numeric, [12](#), [19](#), [24–26](#), [30](#), [65–68](#), [75–77](#), [124](#)
- Oats.dat, [4](#), [86](#)
- p2canon.object, [23](#), [34](#), [35](#), [87](#), [88](#), [102](#)
- par, [12](#), [25–27](#)
- pcanon.object, [5](#), [21–23](#), [32–36](#), [62](#), [63](#), [87](#), [88](#), [119](#), [120](#)
- polygon, [26](#), [27](#)
- power.exp, [5](#), [35](#), [86](#), [89](#)
- print, [90–92](#)
- print,projector-method
(print.projector), [91](#)
- print.aliasing, [5](#), [90](#)
- print.default, [90–92](#)
- print.projector, [7](#), [91](#)
- print.pstructure, [7](#), [92](#)
- print.summary.p2canon, [7](#), [93](#), [118](#)
- print.summary.pcanon, [7](#), [94](#), [120](#)
- proj2.combine, [8](#), [16](#), [23](#), [34](#), [36](#), [37](#), [63](#), [95](#), [97](#), [98](#), [102–104](#), [107](#), [118](#), [120](#)
- proj2.decomp (dae-deprecated), [15](#)
- proj2.entropy, [8](#), [23](#), [34](#), [36](#), [37](#), [63](#), [96](#), [96](#), [98](#), [103](#), [107](#), [118](#), [120](#)
- proj2.eigen, [8](#), [16](#), [23](#), [34](#), [36](#), [37](#), [63](#), [87](#), [96](#), [97](#), [98](#), [103](#), [104](#), [107](#), [118](#), [120](#)
- proj2.ops (dae-deprecated), [15](#)
- projector, [7](#), [14](#), [17](#), [18](#), [23](#), [34](#), [36](#), [37](#), [50](#), [61](#), [63](#), [79](#), [81](#), [91](#), [96–99](#), [99](#), [100–107](#), [109](#), [115](#), [118](#), [120](#)
- projector-class, [7](#), [100](#)
- projs.2canon, [7](#), [22](#), [23](#), [34–36](#), [87](#), [88](#), [102](#), [103](#), [104](#), [107](#), [118](#)
- projs.canon, [120](#)
- projs.canon (dae-deprecated), [15](#)
- projs.combine.p2canon, [7](#), [103](#), [103](#)

- projs.structure (dae-deprecated), 15
- pstructure, 22, 23, 34, 36, 63, 103, 118, 120
- pstructure (pstructure.formula), 104
- pstructure.formula, 7, 22, 62, 63, 88, 104, 106, 108, 109
- pstructure.object, 5, 9, 62, 63, 88, 92, 104, 107, 108

- qqnorm, 110
- qqeffects, 6, 109, 123

- relevel, 52, 84
- resid.errors, 6, 55, 56, 110, 111, 122
- residuals, 110, 111
- residuals (residuals.aovlist), 111
- residuals.aovlist, 6, 110, 111
- rmvnorm, 8, 112
- rnorm, 113

- Sensory3Phase.dat, 4, 113
- Sensory3PhaseShort.dat, 4
- Sensory3PhaseShort.dat (Sensory3Phase.dat), 113
- set.daeTolerance, 8, 14, 16, 17, 57, 58, 60, 61, 95, 97–99, 102, 114
- show, 90–92
- show, ANY-method (show-methods), 115
- show, classRepresentation-method (show-methods), 115
- show, genericFunction-method (show-methods), 115
- show, MethodDefinition-method (show-methods), 115
- show, MethodSelectionReport-method (show-methods), 115
- show, MethodWithNext-method (show-methods), 115
- show, ObjectsWithPackage-method (show-methods), 115
- show, oldClass-method (show-methods), 115
- show, projector-method (show-methods), 115
- show, signature-method (show-methods), 115
- show, traceable-method (show-methods), 115
- show-methods, 8, 115
- SPLGrass.dat, 4, 116
- strength, 6, 116

- structure, 101
- summary, p2canon-method (summary.p2canon), 118
- summary, pcanon-method (summary.pcanon), 119
- summary.p2canon, 7, 93, 103, 118
- summary.pcanon, 5, 7, 21, 23, 32, 34, 36, 63, 94, 119

- text, 25
- tukey.1df, 6, 55, 56, 110, 111, 121

- vector, 48, 101, 113

- yates.effects, 6, 110, 122

- Zncsspline, 6, 76, 123