

# Package ‘dae’

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**Title** Functions Useful in the Design and ANOVA of Experiments

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**Suggests** testthat, vdiffR, R.rsp

**VignetteBuilder** R.rsp

**Description** The content falls into the following groupings: (i) Data, (ii) Factor manipulation functions, (iii) Design functions, (iv) ANOVA functions, (v) Matrix functions, (vi) Projector and canonical efficiency functions, and (vii) Miscellaneous functions. There is a vignette describing how to use the design functions for randomizing and assessing designs available as a vignette called 'DesignNotes'. The ANOVA functions facilitate the extraction of information when the 'Error' function has been used in the call to 'aov'. The package 'dae' can also be installed from <http://chris.brien.name/rpackages/>.

**License** GPL (>=2)

**URL** <http://chris.brien.name>

**BugReports** <https://github.com/briencj/dae/issues>

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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/>.

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## Index

### (i) Data

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

### (ii) Factor manipulation functions

Forms a new or revised factor:

<a href="#">fac.combine</a>	Combines several factors into one
<a href="#">fac.multinested</a>	Creates several factors, one for each level of a nesting.fac

	and each of whose values are either generated within those of the level of nesting.fac or using the values of a nested.fac
<code>fac.nested</code>	Creates a factor, the nested factor, whose values are generated within those of a nesting factor
<code>fac.recast</code>	Recasts a factor by modifying the values in the factor vector and/or the levels attribute, possibly combining some levels into a single level.
<code>fac.recode</code>	Recodes factor 'levels' using possibly nonunique values in a vector. (May be deprecated in future.)
<code>fac.uselogical</code>	Forms a two-level factor from a logical object
<code>mpone</code>	Converts the first two levels of a factor into the numeric values -1 and +1
Forms multiple new factors:	
<code>fac.divide</code>	Divides a factor into several separate factors
<code>fac.gen</code>	Generate all combinations of several factors and, optionally, replicate them
<code>fac.genfactors</code>	Generate all combinations of the levels of the supplied factors, without replication
<code>fac.split</code>	Splits a factor whose levels consist of several delimited strings into several factors.
<code>fac.uncombine</code>	Cleaves a single factor, each of whose levels has delimited strings, into several factors using the separated strings.
Operates on factors:	
<code>as.numfac</code>	Convert a factor to a numeric vector
<code>fac.match</code>	Match, for each combination of a set of columns in 'x', the row that has the same combination in 'table'
(iii) Design functions	
Designing experiments:	
<code>designLatinSqrSys</code>	Generate a systematic plan for a Latin Square design.
<code>designRandomize</code>	Randomize allocated to recipient factors to produce a layout for an experiment. It supersedes <code>fac.layout</code> .
<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
Plotting designs:	
<code>blockboundaryPlot</code>	This function plots a block boundary on a plot produced by 'designPlot'. It supersedes <code>blockboundary.plot</code> .
<code>designBlocksGGPlot</code>	Adds block boundaries to a plot produced by <code>designGGPlot</code> .
<code>designGGPlot</code>	Plots labels on a two-way grid of coloured cells using <code>ggplot2</code> to represent an experimental 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> .
Assessing designs:	
<code>designAmeasures</code>	Calculates the A-optimality measures from the variance matrix for predictions.
<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>designTwophaseAnatomies</code>	Given the layout for a design and three structure formulae, obtain the anatomies for the (i) two-phase, (ii) first-phase, (iii) cross-phase, treatments, and (iv) combined-units designs.
<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 <code>data.frame</code>
<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 <code>aovlist</code> 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>qqeffects</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 <code>aovlist</code> 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	
Operates on matrices:	
<code>elements</code>	Extract the elements of an array specified by the subscripts
<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.ginv</code>	Computes the generalized inverse of a matrix
<code>Zncsspline</code>	Forms the design matrix for fitting the random effects for a natural cubic smoothing spline.

Compute variance matrices for  
supplied variance component values:

`mat.random`

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

`mat.Vpred`

Forms the variance matrix of predictions  
based on supplied matrices

`mat.Vpredicts`

Forms the variance matrix of predictions,  
based on supplied matrices or formulae.

Forms matrices using factors  
stored in a `data.frame`:

`fac.ar1mat`

Forms the ar1 correlation matrix for a  
(generalized) factor

`fac.sumop`

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

`fac.vcmat`

Forms the variance matrix for the variance  
component of a (generalized) factor

Forms patterned matrices:

`mat.I`

Forms a unit matrix

`mat.J`

Forms a square matrix of ones

`mat.ncssvar`

Forms a variance matrix for random cubic  
smoothing spline effects

Forms correlation matrices:

`mat.cor`

Forms a correlation matrix in which all  
correlations have the same value

`mat.corg`

Forms a general correlation matrix in which  
all correlations have different values

`mat.ar1`

Forms an ar1 correlation matrix

`mat.ar2`

Forms an ar2 correlation matrix

`mat.ar3`

Forms an ar3 correlation matrix

`mat.arma`

Forms an arma correlation matrix

`mat.banded`

Forms a banded matrix

`mat.exp`

Forms an exponential correlation matrix

`mat.gau`

Forms a gaussian correlation matrix

`mat.ma1`

Forms an ma1 correlation matrix

`mat.ma2`

Forms an ma2 correlation matrix

`mat.sar`

Forms an sar correlation matrix

`mat.sar2`

Forms an sar2 correlation matrix

(vi) Projector and canonical efficiency functions

Projector class:

`projector`

Create projectors

<code>projector-class</code>	Class projector
<code>is.projector</code>	Tests whether an object is a valid object of class projector
<code>print.projector</code>	Print projectors
<code>correct.degfree</code>	Check the degrees of freedom in an object of class projector
<code>degfree</code>	Degrees of freedom extraction and replacement
Accepts two or more formulae:	
<code>designAnatomy</code>	An anatomy of a design, obtained from a canonical analysis of the relationships between sets of projectors.
<code>summary.pcanon</code>	Summarizes the anatomy of a design, being the decomposition of the sample space based on its canonical analysis
<code>print.summary.pcanon</code>	Prints the values in an 'summary.pcanon' object
<code>efficiencies.pcanon</code>	Extracts the canonical efficiency factors from a list of class 'pcanon'
Accepts exactly two formulae:	
<code>projs.2canon</code>	A canonical analysis of the relationships between two sets of projectors
<code>projs.combine.p2canon</code>	Extract, from a p2canon object, the projectors
<code>summary.p2canon</code>	A summary of the results of an analysis of the relationships between two sets of projectors
<code>print.summary.p2canon</code>	Prints the values in an 'summary.p2canon' object that give the combined decomposition
<code>efficiencies.p2canon</code>	Extracts the canonical efficiency factors from a list of class 'p2canon'
Accepts a single formula:	
<code>as.data.frame.pstructure</code>	Coerces a pstructure.object to a data.frame
<code>print.pstructure</code>	Prints a pstructure.object
<code>pstructure.formula</code>	Takes a formula and constructs a pstructure.object that includes the orthogonalized projectors for the terms in a formula
<code>porthogonalize.list</code>	Takes a list of <code>projector</code> s and constructs a <code>pstructure.object</code> that includes projectors, each of which has been orthogonalized to all projectors preceding it in the list.
Others:	
<code>decomp.relate</code>	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>rep. data. frame</code>	Replicate the rows of a data.frame by repeating each row consecutively and/or repeating all rows as a group.
<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

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Maintainer: Chris Brien <[chris.brien@adelaide.edu.au](mailto:chris.brien@adelaide.edu.au)>

---

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 <a href="#">pstructure.object</a> , which is of class <code>pstructure</code> and is to be coerced.
<code>row.names</code>	NULL or a <a href="#">character</a> vector giving the row names for the data frame. Missing values are not allowed.
<code>optional</code>	A <a href="#">logical</a> 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 <a href="#">logical</a> , 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

*Convert a factor to a numeric vector*

---

## Description

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

## Usage

```
as.numfac(factor)
```

## Arguments

factor            The [factor](#) to be converted.

## Value

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

## Author(s)

Chris Brien

## See Also

[as.numeric](#), [fac.recast](#) in package [dae](#), [factor](#).

## Examples

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

---

BIBDWheat.dat	<i>Data for a balanced incomplete block experiment</i>
---------------	--

---

### Description

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

### Usage

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

### Format

A data.frame containing 30 observations of 4 variables.

### Source

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

---

blockboundaryPlot	<i>This function plots a block boundary on a plot produced by <a href="#">designPlot</a>.</i>
-------------------	---

---

### 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 <a href="#">logical</a> that determines whether block numbers are repetitions or sequences of block numbers.
rstart	A <a href="#">numeric</a> speccifying the row after which the plotting of block boundaries is to start.
cstart	A <a href="#">numeric</a> speccifying the column after which the plotting of block boundaries is to start.
nrows	A <a href="#">numeric</a> the number of rows (nrows), from the starting unit, that the blocks to be plotted are to cover.
ncolumns	A <a href="#">numeric</a> the number of columns (ncolumns), from the starting unit, that the blocks to be plotted are to cover.
blocklinecolour	A <a href="#">character</a> string specifying the colour of the block boundary. See Colour specification under the <a href="#">par</a> function.
blocklinewidth	A <a href="#">numeric</a> 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)

```

---

Cabinet1.des	<i>A design for one of the growth cabinets in an experiment with 50 lines and 4 harvests</i>
--------------	--

---

### Description

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

### Usage

```
data(Cabinet1.des)
```

### Format

A data.frame containing 160 observations of 15 variables.

---

Casuarina.dat	<i>Data for an experiment with rows and columns from Williams (2002)</i>
---------------	--

---

### Description

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

### Usage

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

### Format

A data.frame containing 240 observations of 7 variables.

## 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





```
##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 " <a href="#">projector</a> " 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 " <a href="#">projector</a> " or "matrix" from which the degrees of freedom are to be calculated.

**Details**

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

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

**Value**

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

**Author(s)**

Chris Brien

**See Also**

[correct.degfree](#), [projector](#) in package **dae**.  
[projector](#) for further information about this class.

**Examples**

```
## 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</i>
-----------------	---

---

**Description**

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

**Usage**

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

**Arguments**

Vpred	The variance <b>matrix</b> of the predictions. It can be obtained using <code>mat.Vpredicts</code> .
replications	A <b>numeric</b> vector whose length is equal to the number of rows (columns) in Vpred and whose elements are to be used to calculate weights for each pair of differences.
groupsizes	A <b>numeric</b> 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 <b>list</b> , each element of which is a <b>numeric</b> , vector with integers that specify the subgroup of the predictions over whose pairwise differences the variances are to be averaged. If there is more than one group, the variances of all between and within group pairwise differences are averaged. If the elements of groups are named, the names are used to label the groups. If groups is NULL, either groupsizes is used or the average for all pairwise differences is obtained.

## Details

The variance matrix of pairwise differences is calculated as  $v_{ii} + v_{jj} - 2v_{ij}$ , where  $v_{ij}$  is the element from the  $i$ th row and  $j$ th column of  $V_{pred}$ . If replication is not NULL then weights are computed as  $r_i * r_j / \text{mean}(\mathbf{r})$ , where  $\mathbf{r}$  is the replication vector and  $r_i$  and  $r_j$  are elements of  $\mathbf{r}$ . The  $(i, j)$  element of the variance matrix of pairwise differences is multiplied by the  $(i, j)$ th weight. Then the mean of the variances of the pairwise differences is computed for the nominated groups.

## Value

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

## Author(s)

Chris Brien

## References

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.

Williams, E. R., and Piepho, H.-P. (2015). Optimality and contrasts in block designs with unequal treatment replication. *Australian & New Zealand Journal of Statistics*, **57**, 203-209.

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

## Calculate A-optimality measure
designAmeasures(Vp)
designAmeasures(Vp, groups=list(fldUndup = c(1:4), fldDup = c(5,6)))
```

```

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

```

---

designAnatomy	<i>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.</i>
---------------	--

---

## Description

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

## Usage

```

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

```

## Arguments

formulae	An object of class <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 <a href="#">logical</a> indicating whether the projector for the grand mean is to be included for each structure.
orthogonalize	A <a href="#">character</a> 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.
labels	A <a href="#">character</a> nominating the type of labels to be used in labelling the projectors, and which will be used also in the output tables, such the tables of the aliasing in the structure. The two alternatives are terms and sources. Terms have all factors/variables in it separated by colons (:). Sources have factors/variables in them that represent interactions separated by hashes (#); if some factors are nested within others, the nesting factors are surrounded by square brackets ([ and ]) and separated by colons (:). If some generalized, or combined, factors have no marginal terms, the constituent factors are separated by colons (: ) and if they interact with other factors in the source they will be parenthesized.
marginality	<p>A <a href="#">list</a> 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 <a href="#">list</a> is the same length as the formulae <a href="#">list</a>, they will be associated in parallel with the components of formulae, irrespective of the naming of the two <a href="#">lists</a>. If the number of components in marginality is less than the number of components in formulae then both <a href="#">lists</a> must be named so that those in the marginality <a href="#">list</a> can be matched with those in the formulae <a href="#">list</a>.</p> <p>Each component of the marginality <a href="#">list</a> must be either NULL or a square <a href="#">matrix</a> 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.</p>
check.marginality	A <a href="#">logical</a> indicating whether the marginality matrix, when it is supplied, is to be checked against that computed by <a href="#">pstructure.formula</a> . It is ignored when orthogonalize is set to eigenmethods.
which.criteria	A <a href="#">character</a> 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 <a href="#">efficiency.criteria</a> . If none, no summary is printed.
aliasing.print	A <a href="#">logical</a> indicating whether the aliasing between sources is to be printed.
omit.projectors	A <a href="#">character</a> 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 products 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.

The hybrid method is recommended for general use. However, of the three methods, `eigenmethods` is least likely to fail, but it does not establish the marginality between the terms. It is often needed when there is nonorthogonality between terms, such as when there are several linear covariates. It can also be more efficient in these circumstances.

The process can be computationally expensive, particularly for a large data set (500 or more observations) and/or when many terms are to be orthogonalized.

If the error Matrix is not idempotent should occur then, especially if there are many terms, one might try using `set.daeTolerance` to reduce the tolerance used in determining if values are either the same or are zero; it may be necessary to lower the tolerance to as low as 0.001. Also, setting `orthogonalize` to `eigenmethods` is worth a try.

## 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*, **61**, 234-268.
- 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.
- Brien, C. J., Sermarini, R. A., & Demetrio, C. G. B. (2023). Exposing the confounding in experimental designs to understand and evaluate them, and formulating linear mixed models for analyzing the data from a designed experiment. *Biometrical Journal*, accepted for publication.
- 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](#), [proj2.2canon](#), [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)
```

---

designBlocksGGPlot      Adds block boundaries to a plot produced by [designGGPlot](#).

---

### Description

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



**Usage**

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

**Arguments**

- `ggplot.obj` An object produced by `ggplot`.
- `blockdefinition` A [matrix](#) of block sizes:
- if there is only one row, then the first element is interpreted as the no. rows in each block and blocks with this number of rows are to be repeated across the rows of the design.
  - if there is more than one row, then each row of the matrix specifies a block, with the sequence of rows in the matrix specifying a corresponding sequence of blocks down the rows of the design.
- Similarly, a single value for a column specifies a repetition of blocks of that size across the columns of the design, while several column values specifies a sequence of blocks across the columns of the size specified.
- `blocksequence` A [logical](#) that determines whether block numbers are repetitions or sequences of block numbers.
- `originrow` A [numeric](#) speccifying the row after which the plotting of block boundaries is to start.
- `origincolumn` A [numeric](#) speccifying the column after which the plotting of block boundaries is to start.
- `nrows` A [numeric](#) the number of rows (`nrows`), from the starting unit, that the blocks to be plotted are to cover.
- `ncolumns` A [numeric](#) the number of columns (`ncolumns`), from the starting unit, that the blocks to be plotted are to cover.
- `blocklinecolour` A [character](#) string specifying the colour of the block boundary. See Colour specification under the [par](#) function.
- `blocklinesize` A [numeric](#) giving the width of the block boundary to be plotted.
- `facetstrips.placement` A character nominating where the strip is to be placed with respect to axes text and titles, either "inside" both text and titles, "outside.text" or "outside.title". This argument is important only when axes and strips are on the same side of the plot. When this occurs, the default is to place them inside the axis text. **Note:** This argument must be specified only once in the constructor of the plot and after every other aspect of the plot has been finalized. In particular, if `designBlocksGGPlot` is to be called after `designGGPlot` to add block boundaries, then `facetstrips.placement` should be specified in the last call to `designBlocksGGPlot`, not in the call to `designGGPlot`.
- `printPlot` A [logical](#) indicating whether to print the plot after adding the block boundaries.

**Value**

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

**Author(s)**

Chris Brien

**Source**

Brien, C.J., Harch, B.D., Correll, R.L., and Bailey, R.A. (2011) Multiphase experiments with at least one later laboratory phase. I. Orthogonal designs. *Journal of Agricultural, Biological, and Environmental Statistics*, 16:422-450.

**See Also**

[designGGPlot](#), [par](#), [DiGger](#)

**Examples**

```
## Construct a randomized layout for the split-unit design described by
## Brien et al. (2011, Section 5)
split.sys <- cbind(fac.gen(list(Months = 4, Athletes = 3, Tests = 3)),
                  fac.gen(list(Intensities = LETTERS[1:3], Surfaces = 3),
                           times = 4))
split.lay <- designRandomize(allocated = split.sys[c("Intensities", "Surfaces")],
                            recipient = split.sys[c("Months", "Athletes", "Tests")],
                            nested.recipients = list(Athletes = "Months",
                                                      Tests = c("Months", "Athletes")),
                            seed = 2598)

## Plot the design
cell.colours <- c("lightblue", "lightcoral", "lightgoldenrod", "lightgreen", "lightgrey",
                 "lightpink", "lightsalmon", "lightcyan", "lightyellow", "lightseagreen")

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

#Add Month boundaries
designBlocksGGPlot(plt, nrows = 3, ncolumns = 3, blockdefinition = rbind(c(3,3)))

#### A layout for a growth cabinet experiment that allows for edge effects
data(Cabinet1.des)
plt <- designGGPlot(Cabinet1.des, labels = "Combinations", cellalpha = 0.75,
                   title = "Lines and Harvests allocation for Cabinet 1",
                   printPlot = FALSE)

## Plot Mainplot boundaries
plt <- designBlocksGGPlot(plt, blockdefinition = cbind(4,16), originrow = 1 ,
                        blocklinecolour = "green", nrows = 9, ncolumns = 16,
```

```

                                printPlot = FALSE)
plt <- designBlocksGGPlot(plt, blockdefinition = cbind(1,4),
                          blocklinecolour = "green", nrows = 1, ncolumns = 16,
                          printPlot = FALSE)
plt <- designBlocksGGPlot(plt, blockdefinition = cbind(1,4), originrow= 9,
                          blocklinecolour = "green", nrows = 10, ncolumns = 16,
                          printPlot = FALSE)
## Plot all 4 block boundaries
plt <- designBlocksGGPlot(plt, blockdefinition = cbind(8,5,5,4), blocksequence = TRUE,
                          origincolumn = 1, originrow= 1,
                          blocklinecolour = "blue", nrows = 9, ncolumns = 15,
                          printPlot = FALSE)
plt <- designBlocksGGPlot(plt, blockdefinition = cbind(10,16),
                          blocklinecolour = "blue", nrows = 10, ncolumns = 16,
                          printPlot = FALSE)
## Plot border and internal block boundaries only
plt <- designBlocksGGPlot(plt, blockdefinition = cbind(8,14), origincolumn = 1, originrow= 1,
                          blocklinecolour = "blue", nrows = 9, ncolumns = 15,
                          printPlot = FALSE)
plt <- designBlocksGGPlot(plt, blockdefinition = cbind(10,16),
                          blocklinecolour = "blue", nrows = 10, ncolumns = 16)

```

---

designGGPlot

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


---

## Description

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

## Usage

```

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

```

## Arguments

`design` A [data.frame](#) containing labels, `column.factors`, `row.factors` and, if specified, `colour.column`.

labels	A character giving the name of the column in data containing the labels to be plotted on the grid. If labels is NULL, no labels are added.
label.size	A numeric giving the size of the labels.
row.factors	A character giving the names of the <code>factors</code> (or <code>numerics</code> ) in data that index the rows of the plot grid used to represent the design. If there is more than one name, then <code>facet_grid</code> is used to facet the plot in the y direction, based on all but the last name. The <code>factor</code> corresponding to the last name will index the rows in each facet.
column.factors	A character giving the names of the <code>factors</code> (or <code>numerics</code> ) in data that index the columns of the plot grid used to represent the design. If there is more than one name, then <code>facet_grid</code> is used to facet the plot in the x direction, based on all but the last name. The <code>factor</code> corresponding to the last name will index the columns in each facet.
scales.free	When plots are faceted, a character specifying whether scales are shared across all facets ( <code>fixed</code> ), or vary across rows ( <code>free_x</code> ), columns ( <code>free_y</code> ), or both rows and columns (the default, <code>free</code> ). The <code>free_x</code> , <code>free_y</code> and <code>free</code> options may not work when the plot grid is indexed using <code>numerics</code> .
facetstrips.switch	When plots are faceted, the strip text are displayed on the top and right of the plot by default. If <code>facetstrips.switch</code> is "x", the top strip text will be switched to the bottom. If "y", the right-hand side labels will be switched to the left. The argument can also be set to "both". The argument <code>facetstrips.placement</code> can be used to change the relationship between the strip text and the <code>axis.text</code> and the <code>axis.title</code> .
facetstrips.placement	A character nominating where the strip is to be placed with respect to axes text and titles, either "inside" both text and titles, "outside.text" or "outside.title". This argument is important only when axes and strips are on the same side of the plot. When this occurs, the default is to place them inside the axis text. <b>Note:</b> This argument must be specified only once in the construction of the plot and after every other aspect of the plot has been finalized. In particular, if <code>designBlocksGGPlot</code> is to be called after <code>designGGPlot</code> to add block boundaries, then <code>facetstrips.placement</code> should be specified in the call to <code>designBlocksGGPlot</code> , not in the call to <code>designGGPlot</code> .
reverse.x	A logical which, if true, causes the order of values on the x-axis to be reversed, the natural order being to increase from left to right.
reverse.y	A logical which, if true, causes the order of values on the y-axis to be reversed, the natural order being to increase from bottom to top.
x.axis.position	A character giving the position of the x-axis; can be top or bottom.
cellfillcolour.column	A character giving the name of the column in data that is to be used to vary the colour the used to fill a cell.
colour.values	A character giving the name or names of the colours to be used in filling the cell. If <code>cellfillcolour.column</code> is not NULL then the number of colours specified needs to match the number of unique values in the <code>cellfillcolour.column</code> .
cellalpha	A numeric specifying the degree of transparency to be used in cell fill. It is a ratio in which the denominator specifies the number of points (or lines) that must be overplotted to give a solid cover.

celllinetype	A numeric or character giving the type of line for the cell border. An integer or name: 0 = blank, 1 = solid, 2 = dashed, 3 = dotted, 4 = dotdash, 5 = longdash, 6 = twodash. For more information see <code>vignette("ggplot2-specs")</code> .
celllinesize	A numeric specifying the size of the line in mm.
celllinecolour	A character giving the name of the colour to use for the cell outline.
cellheight	A numeric specifying the height of a cell.
cellwidth	A numeric specifying the width of of a cell.
xlab	Label for the x-axis. By default it is the last name in the <code>column.factors</code> .
ylab	Label for the y-axis. By default it is the last name in the <code>row.factors</code> .
title	Title for plot window. By default it is "Plot of labels".
labeller	A function for specifying the formatting of the strip labels of the facet grids used when there is more than one <code>row.factors</code> or <code>column.factors</code> . (See <a href="#">labellers</a> for <code>ggplot2</code> .)
title.size	A numeric giving the size for all titles: <code>xlab</code> , <code>ylab</code> and <code>title</code> .
axis.text.size	A numeric giving the size for tick labels.
blocksequence	A <a href="#">logical</a> that determines whether block numbers are repetitions or sequences of block numbers.
blockdefinition	A <a href="#">matrix</a> of block sizes: <ul style="list-style-type: none"> <li>• 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.</li> <li>• 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.</li> </ul> <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 <a href="#">character</a> string specifying the colour of the block boundary. See also the <code>scale_colour_*</code> functions or Colour specification under the <a href="#">par</a> function.
blocklinesize	A <a href="#">numeric</a> giving the width of the block boundary to be plotted.
printPlot	A <a href="#">logical</a> indicating whether to print the plot produced.
ggplotFuncs	A <a href="#">list</a> , each element of which contains the results of evaluating a <code>ggplot</code> function. It is created by calling the <code>list</code> function with a <code>ggplot</code> function call for each element. These functions are applied in creating the <code>ggplot</code> object.
...	Other arguments that are passed down to the <code>geom_text</code> call that plots the labels.

**Value**

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

**Author(s)**

Chris Brien

**See Also**

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

**Examples**

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

## Plot without labels
designGGPlot(RCBD.lay, cellfillcolour.column = "Treatments",
            row.factors = "Blocks", column.factors = "Units",
            colour.values = c("lightblue", "lightcoral", "lightgoldenrod",
                              "lightgreen", "lightgrey", "lightpink"),
            blockdefinition = cbind(1,6))

#### Plot a lattice square design
data(LatticeSquare_t49.des)
designGGPlot(LatticeSquare_t49.des, labels = "Lines", label.size = 5,
            row.factors = c("Intervals", "Runs"), column.factors = "Times",
            blockdefinition = cbind(7,7))
```

---

designLatinSqrSys

*Generate a systematic plan for a Latin Square design*

---

**Description**

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

**Usage**

```
designLatinSqrSys(order, start = NULL)
```

**Arguments**

order	The number of treatments.
start	A <a href="#">numeric</a> 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 <b>matrix</b> containing a set of numerics or characters being the labels as they have been assigned to the cells of the grid represented by the <b>matrix</b> .
labels	A <b>numeric</b> or <b>character</b> 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 <a href="#">text</a> for more information on specifying the labels.
altlabels	Either a <b>character</b> vector containing an alternative set of labels for the labels currently being plotted or a single <b>integer</b> 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.

<code>plotlabels</code>	A <a href="#">logical</a> to indicate whether labels are to be plotted in the cells. If TRUE, print all labels or the specific labels listed in <code>labels</code> . If FALSE, no labels are printed in the cells.
<code>rtitle</code>	A <a href="#">character</a> string to use as a title for rows of the plot. If <code>rtitle</code> is NULL then no title is plotted.
<code>ctitle</code>	A <a href="#">character</a> string to use as a title for columns of the plot. If <code>ctitle</code> is NULL then no title is plotted.
<code>rlabelsreverse</code>	A <a href="#">logical</a> indicating whether to reverse the row labels.
<code>clabelsreverse</code>	A <a href="#">logical</a> indicating whether to reverse the column labels.
<code>font</code>	An <a href="#">integer</a> specifying the font to be used for row and column labelling. See <a href="#">par</a> for further details.
<code>chardivisor</code>	A <a href="#">numeric</a> that changes the size of text and symbols in the cells by dividing the default size by it.
<code>rchardivisor</code>	A <a href="#">numeric</a> that changes the size of the labels of the rows of the design by dividing the default size by it.
<code>cchardivisor</code>	A <a href="#">numeric</a> that changes the size of the labels of the columns of the design by dividing the default size by it.
<code>cellfillcolour</code>	A <a href="#">character</a> 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 NULL, the number of colours must at least equal the number of labels and then the fill colours will be matched, one for one from the first colour, with the labels. If <code>labels</code> is NULL then the number of colours must at least equal the number of unique labels in <code>designMatrix</code> . The default, NA, is to leave their cells unfilled. See also <a href="#">Colour specification</a> under the <a href="#">par</a> function.
<code>plotcellboundary</code>	A <a href="#">logical</a> indicting whether a boundary is to plotted around a cell.
<code>rcellpropn</code>	a value between 0 and 1 giving the proportion of the standard row size of a cell size to be plotted as a cell.
<code>ccellpropn</code>	a value between 0 and 1 giving the proportion of the standard column size of a cell size to be plotted as a cell.
<code>blocksequence</code>	A <a href="#">logical</a> that determines whether block numbers are repetitions or sequences of block numbers.
<code>blockdefinition</code>	A <a href="#">matrix</a> of block sizes: <ul style="list-style-type: none"> <li>• 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.</li> <li>• 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.</li> </ul> <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 <a href="#">character</a> string specifying the colour of the block boundary. See also Colour specification under the <a href="#">par</a> function.
blocklinewidth	A <a href="#">numeric</a> giving the width of the block boundary to be plotted.
rotate	A <a href="#">logical</a> which, if TRUE, results in the matrix being rotated 90 degrees for plotting.
new	A <a href="#">logical</a> indicating if a new plot is to be produced or the current plot is added to.
...	further arguments passed to <a href="#">polygon</a> 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      *Plots labels on a two-way grid using ggplot2*

---

### Description

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

### Usage

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

### Arguments

<code>data</code>	A <a href="#">data.frame</a> 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 <a href="#">logical</a> indicating whether to print the plot.
<code>ggplotFuncs</code>	A <a href="#">list</a> , each element of which contains the results of evaluating a <a href="#">ggplot</a> function. It is created by calling the <a href="#">list</a> function with a <a href="#">ggplot</a> function call for each element. These functions are applied in creating the <a href="#">ggplot</a> object.
<code>...</code>	Other arguments that are passed down to the <a href="#">geom_text</a> call that plots the labels.

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

**Usage**

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

**Arguments**

allocated	A <b>factor</b> or a <b>data.frame</b> containing the systematically allocated values of the <b>factor</b> (s). If NULL, a random permutation of the recipient <b>factors</b> is produced that is consistent with their nesting as specified by nested.recipients.
recipient	A <b>data.frame</b> or a <b>list</b> of <b>factors</b> , along with their levels that specify the set of recipient <b>factors</b> that are allocated levels of the allocated <b>factors</b> . If a <b>list</b> , the name of each component of the <b>list</b> is a <b>factor</b> 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 <b>factor</b> , (iii) or a <b>character</b>

vector that contains the labels of the levels of the `factor`. The values of `factor`s will be generated in standard order using `fac.gen` and so the values in allocated must match this.

<code>nested.recipients</code>	A <code>list</code> of the recipient <code>factor</code> s that are nested in other <code>factor</code> s in recipient. The name of each component is the name of a <code>factor</code> that is nested and the component is a character vector containing the <code>factor</code> s within which it is nested. The randomization is controlled by <code>nested.recipients</code> : nested recipient factors are permuted within those factors that nest them. Only the nesting is specified: it is assumed that if two factors are not nested then they must be crossed. It is emphasized that the nesting is a property of the design that is being employed (it is only partly based on the intrinsic or physical crossing and nesting).
<code>except</code>	A <code>character</code> vector containing the names of recipient <code>factor</code> s that are to be excepted from the permutation; any allocated <code>factor</code> s whose values differ between the levels of the <code>factor</code> s in this vector will not have those values randomized.
<code>seed</code>	A single <code>numeric</code> value, interpreted as an integer, that specifies the starting value of the random number generator.
<code>unit.permutation</code>	A logical indicating whether to include the <code>.Unit</code> and <code>.Permutation</code> columns in the <code>data.frame</code> .
<code>...</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 `factor`s. If recipient is a `list` then `fac.gen` is used to generate a `data.frame` with the combinations of the levels of the recipient `factor`s 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 `factor`s with the values of recipient `factor`s in the recipient `data.frame`.

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

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

## Value

A `data.frame` with the values for the recipient and allocated `factor`s 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**.

**Examples**

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

## Generate a randomized layout for a replicated randomized complete
## block design, with the block factors arranged in standard order for
## rep then plot and then block
## Firstly, generate a systematic order such that levels of the
## treatment factor coincide with plot
RCBD.sys <- cbind(fac.gen(list(rep = 2, plot=1:3, block = c("I", "II"))),
                tr = factor(rep(1:3, each=2, times=2)))
## obtain randomized layout
RCBD.lay <- designRandomize(allocated = RCBD.sys["tr"],
                          recipient = RCBD.sys[c("rep", "block", "plot")],
                          nested.recipients = list(plot = c("block", "rep"),
                                                    block="rep"),
                          seed = 9719532,
                          unit.permutation = TRUE)
#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.
## Firstly, generate a systematic layout
SPL.sys <- cbind(fac.gen(list(block = 2, main.unit = 4, split.unit = 3)),
                fac.gen(list(A = 4, B = 3), times = 2))
## obtain randomized layout
SPL.lay <- designRandomize(allocated = SPL.sys[c("A", "B")],
                        recipient = SPL.sys[c("block", "main.unit", "split.unit")],
```

```

nested.recipients = list(main.unit = "block",
                          split.unit = c("block", "main.unit")),
seed=155251978)

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

```

---

designTwophaseAnatomies

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

---

## Description

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

## Usage

```

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

```

## Arguments

formulae	An object of class <a href="#">list</a> with three components of class <a href="#">formula</a> . 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 <a href="#">summary.pcanon</a> object. They will also be used to name the terms, sources and marginality lists in the <a href="#">pcanon.object</a> .
data	A <a href="#">data.frame</a> contains the values of the factors and variables that occur in formulae.

- which.designs A **character** vector indicating the species of designs that are to be obtained. It should include one or more of two-phase, first-phase, cross-phase and combined-units; all, the default, results in all four being obtained.
- printAnatomies titles A **logical** indicating whether or not the anatomies are to be printed.
- A **character** vector of length four providing titles for the printed anatomies. It should have the titles, in the following order, for the anatomies based on : (i) all three formulae, (ii) the second and third formulae, (iii) the first and third formulae, and (iv) the first and second formulae. If any element of titles is NA then that element is replaced with the corresponding default element of titles, these being, in order: Anatomy for the full two-phase design; Anatomy for the first-phase design; Anatomy for the cross-phase, treatments design; and Anatomy for the combined-units design. The titles generated will be saved as an attribute of the returned list.
- 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, treatments anatomy derives from the first and third formulae and the combined-units anatomy is obtained with the first and second formulae.

### Value

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

### Author(s)

Chris Brien

### References

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* **61**, 234-268.

### 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

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.
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 detectable difference.
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 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	<i>Extracts the canonical efficiency factors from a <a href="#">pcanon.object</a> or a <a href="#">p2canon.object</a>.</i>
--------------	--

---

### Description

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

### Usage

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

### Arguments

object	A <a href="#">pcanon.object</a> or an object of class <code>p2canon</code> produced by <a href="#">projs.2canon</a> .
which	A character string, either <code>adjusted</code> or <code>pairwise</code> . For <code>adjusted</code> , the canonical efficiency factor are adjusted for other projectors from from the same set. For <code>pairwise</code> , they are the unadjusted canonical efficiency factors between pairs of projectors consisting of one projector from each of two sets.
...	Further arguments passed to or from other methods. Unused at present.

### Value

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

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

### Author(s)

Chris Brien

### References

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

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

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

---

efficiency.criteria     *Computes efficiency criteria from a set of efficiency factors*

---

**Description**

Computes efficiency criteria from a set of efficiency factors.

**Usage**

```
efficiency.criteria(efficiencies)
```

**Arguments**

efficiencies     A numeric containing a set of efficiency factors.

**Details**

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

**Value**

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

**Author(s)**

Chris Brien

**See Also**

[proj2.efficiency](#), [proj2.eigen](#), [proj2.combine](#) in package **dae**, **eigen**.  
[projector](#) for further information about this class.

**Examples**

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

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

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

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

---

elements

---

*Extract the elements of an array specified by the subscripts*


---

**Description**

Elements of the array  $x$  corresponding to the rows of the two dimensional object 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.munit.des	<i>Systematic, main-unit design for an experiment to be run in a greenhouse</i>
------------------	---

---

**Description**

In this main-unit design, there are 24 lanes by 11 Positions, the lanes being blocked into 6 Zones of 4 lanes. The design for the main units 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 accessed via `vignette("DesignNotes", package="dae")`.

**Usage**

```
data(Exp249.munit.des)
```

**Format**

A data.frame containing 264 observations of 3 variables.

**Source**

Coombes, N. E. (2009) Digger: *design search tool in R*. URL: <http://nswdpiibiom.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**

table	A numeric vector containing the values to be expanded. Its length must equal the product of the number of used levels for the <code>index.factors</code> and the values in it correspond to all levels combinations of these <code>index.factors</code> . That is, the values of the <code>index.factors</code> are irrelevant to <code>table</code> .
index.factors	A list of <code>factor</code> s that index the table. All the <code>factor</code> s must be the same length.
order	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 `factor`s 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) <a href="#">factor</a> 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 <a href="#">list</a> of <a href="#">factors</a> all of the same length.
order	Either standard or yates. The order in which the levels combinations of the <a href="#">factors</a> are to be considered as numbered when forming the levels of the combined <a href="#">factor</a> ; 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 <a href="#">factor</a> are to be combined from those of the <a href="#">factors</a> 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 <a href="#">factors</a> , numbering the levels according to order.
sep	A character string to separate the levels when combine.levels = TRUE.
...	Further arguments passed to the <a href="#">factor</a> call creating the new <a href="#">factor</a> .

**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.uncombine](#), [fac.split](#), [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

*Divides a factor into several separate factors*

---

**Description**

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

**Usage**

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



## Arguments

combined.factor	A <a href="#">factor</a> that is to be divided into the individual <a href="#">factors</a> listed in factor.names.
factor.names	A <a href="#">list</a> of <a href="#">factors</a> to be formed. The names in the <a href="#">list</a> are the names of the <a href="#">factors</a> 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 <a href="#">factor</a> , or c) a character vector that contains the labels of the levels of the <a href="#">factor</a> .
order	Either standard or yates. The order in which the levels combinations of the <a href="#">factors</a> in factor.names are to be considered as numbered; standard numbers them as if they are arranged in standard order, that is with the first factor moving slowest and the last factor moving fastest; yates numbers them as if they are arranged in Yates order, that is with the first factor moving fastest and last factor moving slowest.

## Value

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

## Note

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

## Author(s)

Chris Brien

## See Also

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

## Examples

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

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

---

fac.gen	<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 <b>list</b> of named objects and numbers that specify the <b>factor</b> s whose levels are to be generated and the pattern in these levels. If a component of the <b>list</b> 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 <b>factor</b> , or c) a character vector that contains the labels of the levels of the <b>factor</b> .
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 <b>factor</b> s are to be considered as numbered; standard cycles through the levels of the first factor slowest and the last factor moving fastest; yates cycles through the levels of the first factor fastest and last factor moving slowest.

### Details

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

### Value

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

### Warning

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

### Author(s)

Chris Brien

**See Also**

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

**Examples**

```
## 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.genfactors	<i>Generate all combinations of the levels of the supplied factors, without replication</i>
----------------	---

---

**Description**

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

**Usage**

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

**Arguments**

factors	A <a href="#">list</a> of <a href="#">factors</a> , or an object of <a href="#">factor</a> s that is coercible to a <a href="#">list</a> .
...	Further arguments passed to the <a href="#">fac.gen</a> in creating the <a href="#">data.frame</a> of new <a href="#">factors</a> .

**Details**

The levels of each [factor](#) are generated in standard order, unless order is supplied to [fac.gen](#) via the '...' argument. The levels of the new [factor](#)s will be in the same order as in the supplied factors.

**Value**

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

**Author(s)**

Chris Brien

**See Also**[fac.gen](#) in package **dae****Examples**

```
## generate a treatments key for the Variety and Nitrogen treatments factors in Oats.dat
data(Oats.dat)
trts.key <- fac.genfactors(factors = Oats.dat[c("Variety", "Nitrogen")])
trts.key$Treatment <- factor(1:nrow(trts.key))
```

---

 fac.match

---

*Match, for each combination of a set of columns in x, the row that has the same combination in table*


---

**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 <code>multiples.allow</code> is FALSE, an error is generated. If <code>multiples.allow</code> is TRUE, the first occurrence in table is matched. This function can be viewed as a generalization to multiple vectors of the <a href="#">match</a> 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  $X \%*\% (1/\text{diag}(r)) \%*\% t(X)$ , 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.multinested	<i>Creates several factors, one for each level of nesting.fac and each of whose values are either generated within those of a level of nesting.fac or using the values of nested.fac within a levels of nesting.fac.</i>
-----------------	--

---

**Description**

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

**Usage**

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

**Arguments**

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

nested.levs	Optional vector of levels for the nested <b>factors</b> . Any data value that does not match a value in nested.levs will be NA in the nested <b>factor</b> being generated. The default value of nested.levs is the list of numbers from 1 to the replication of the levels of nesting.fac, represented as characters. When nested.fac is not NULL, nested.levs is not used.
nested.labs	Optional vector of values to use as labels for the levels of the new nested <b>factors</b> ; they are combined with outlabel. The default is as.character(levels).
outlevel	The level to use in the new <b>factor</b> for all values of old <b>factor</b> that do not correspond to the level of the nesting.fac to which the new <b>factor</b> corresponds.
outlabel	The label to use the outlevel level.
...	Further arguments passed to the <b>factor</b> call creating a new <b>factor</b> .

**Value**

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

**Note**

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

**Author(s)**

Chris Brien

**See Also**

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

**Examples**

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

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

#Add factors for B within each level of A, but with levels and outlabel given
lay2 <- cbind(lay, fac.multinested(lay$A, nested.levs = seq(10,60,10), outlabel = "other"))

canon2 <- designAnatomy(list(~A/(a+b+c)), data = lay2)
summary(canon2)

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

#Add factors for B within each level of A
lay4 <- cbind(lay3, fac.multinested(nesting.fac = lay$A, nested.fac = lay$B))

canon4 <- designAnatomy(list(~A/(a+b+c))/sample), data = lay4)
summary(canon4)
```

```
#Add factors for sample within each combination of A and B
lay5 <- with(lay4, cbind(lay4,
                        fac.multinested(nesting.fac = a, fac.prefix = "a"),
                        fac.multinested(nesting.fac = b, fac.prefix = "b"),
                        fac.multinested(nesting.fac = c, fac.prefix = "c")))

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

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

---

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

---

## Description

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

## Usage

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

## Arguments

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

## Value

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

## Note

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



**Author(s)**

Chris Brien

**See Also**[fac.gen](#), [fac.multinested](#) 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.recast`*Recasts a factor by modifying the values in the factor vector and/or the levels attribute, possibly combining some levels into a single level.*

---

**Description**

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

**Usage**

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

**Arguments**

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

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

... Further arguments passed to the [factor](#) call creating the new [factor](#).

**Value**

A [factor](#).

**Author(s)**

Chris Brien

**See Also**

[fac.uselogical](#), [as.numfac](#) and [mpone](#) in package [dae](#), [factor](#), [relevel](#).

**Examples**

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

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

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

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

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

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

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

---

fac.recode

*Recodes factor levels using values in a vector. The values in the vector do not have to be unique.*

---

**Description**

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

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

**Usage**

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

**Arguments**

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

**Value**

A `factor`.

**Author(s)**

Chris Brien

**See Also**

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

**Examples**

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

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

---

`fac.split`

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

---

**Description**

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

**Usage**

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

**Arguments**

combined.factor	A <a href="#">factor</a> to be split into several <a href="#">factors</a> .
factor.names	A <a href="#">list</a> of names for factors and associated levels, if required. The names of the components of the <a href="#">list</a> are used for the names of the new factors. Each component of the <a href="#">list</a> should either be NULL or a vector of levels for the new <a href="#">factor</a> . If a component is NULL then the unique values for the supplied factor are used as the levels, which are sorted into alphabetical order. If a either a <a href="#">numeric</a> or a <a href="#">character</a> vector is supplied for a component, then these are supplied as the levels of the new factor.
sep	A character string that separates the levels in the combined.factor.
...	Further arguments passed to the <a href="#">factor</a> call creating the new <a href="#">factor</a> .

**Value**

A [data.frame](#) containing the new [factors](#).

**Author(s)**

Chris Brien

**See Also**

[fac.divide](#), [fac.uncombine](#), [fac.combine](#) in package **dae** and [strsplit](#).

**Examples**

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

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

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

---

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)
```

---

<code>fac.uncombine</code>	<i>Cleaves a single factor, each of whose levels has delimited strings, into several factors using the separated strings.</i>
----------------------------	---

---

**Description**

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

**Usage**

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

**Arguments**

factor	A <a href="#">factor</a> or <a href="#">character</a> that has values that are strings delimited by the delimiter specified by sep.
new.factors	A <a href="#">list</a> , whose component names are the names of the new <a href="#">factors</a> to be formed. If a component is not NULL, then they are used as the levels of the corresponding factor.
sep	A character string that separates the levels of the new.factors in the levels factor.
...	Further arguments passed to the <a href="#">factor</a> call creating the new <a href="#">factor</a> .

**Value**

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

**Author(s)**

Chris Brien

**See Also**

[fac.split](#), [fac.combine](#), [fac.divide](#) in package **dae** and [strsplit](#).

**Examples**

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

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

---

fac.uselogical

*Forms a two-level [factor](#) from a [logical](#) object.*

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

A [factor](#).

**Author(s)**

Chris Brien

**See Also**

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

**Examples**

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

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

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

---

fac.vcmat

*forms the variance matrix for the variance component of a (generalized) factor*

---

**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) <a href="#">factor</a> 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  $\sigma^2$ .

**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 2<sup>4</sup> factorial experiment*

---

**Description**

The data set come from an unreplicated  $2^4$  factorial experiment to investigate a chemical process. The response variable is the Conversion percentage (Conv) and this is indexed by the 4 two-level factors Catal, Temp, Press and Conc, with levels “-” and “+”. The data is 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	<i>Extract the fitted values for a fitted model from an aovlist object</i>
----------------	--

---

### 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

<code>object</code>	An aovlist 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.

### 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	<i>Gets the value of daeTolerance for the package dae</i>
------------------	---

---

### 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`    *Plots an interaction plot for three factors*

---

**Description**

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

**Usage**

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

**Arguments**

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

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

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

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

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

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

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



---

is.allzero	<i>Tests whether all elements are approximately zero</i>
------------	--

---

**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 accessed via `vignette("DesignNotes", package="dae")`.

## 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	<i>Extracts the marginality matrix (matrices) from a <a href="#">pstructure.object</a> or a <a href="#">pcanon.object</a>.</i>
-------------	--

---

**Description**

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

A marginality matrix for a set of terms is a square [matrix](#) with a row and a column for each term-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 <a href="#">pstructure.object</a> produced by <a href="#">pstructure.formula</a> or <a href="#">pcanon.object</a> produced by <a href="#">designAnatomy</a> .
...	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  $\rho^k$  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.cor](#), [mat.corg](#), [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.cor](#), [mat.corg](#), [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.cor](#), [mat.corg](#), [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

*Forms an arma correlation matrix*


---

### 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 <a href="#">numeric</a> value for the autoregressive parameter of the process, being the weight given to the lag 1 response values.
MAparameter	A <a href="#">numeric</a> value for the moving average parameter of the process, being the weight given to the lag 1 random variable.
order	The order of the <a href="#">matrix</a> 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.cor](#), [mat.corg](#), [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	<i>Form a banded matrix from a vector of values</i>
------------	---

---

### 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

[mat.cor](#), [mat.corg](#), [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.cor	<i>Forms a correlation matrix in which all correlations have the same value.</i>
---------	--

---

**Description**

Form the correlation [matrix](#) of order `order` in which all correlations have the same value.

**Usage**

```
mat.cor(rho, order)
```

**Arguments**

rho	A <a href="#">numeric</a> containing the single correlation value.
order	The order of the correlation <a href="#">matrix</a> to be formed.

**Value**

A correlation [matrix](#).

**Author(s)**

Chris Brien

**See Also**

[mat.I](#), [mat.J](#), [mat.corg](#), [mat.banded](#), [mat.exp](#), [mat.gau](#), [mat.ar1](#), [mat.ar2](#), [mat.sar2](#), [mat.ma1](#), [mat.ma2](#), [mat.arma](#)

**Examples**

```
corr <- mat.cor(rho = 0.4, order = 3)
```

---

mat.corg	<i>Forms a general correlation matrix</i>
----------	---

---

**Description**

Form the correlation [matrix](#) of order `order` for which all correlations potentially differ.

**Usage**

```
mat.corg(rhos, order, byrow = FALSE)
```

**Arguments**

rhos	A <a href="#">numeric</a> containing the $p(p-1)/2$ correlation values ordered either by columns (if <code>byrow</code> is <code>FALSE</code> ) or by rows (if <code>byrow</code> is <code>TRUE</code> ).
order	The order of the correlation <a href="#">matrix</a> to be formed.
byrow	A <a href="#">logical</a> . If <code>FALSE</code> the lower-triangle of the matrix is filled by columns, otherwise the the ower triangle is filled by rows.

**Value**

A correlation [matrix](#).

**Author(s)**

Chris Brien

**See Also**

[mat.I](#), [mat.J](#), [mat.cor](#), [mat.banded](#), [mat.exp](#), [mat.gau](#), [mat.ar1](#), [mat.ar2](#), [mat.sar2](#), [mat.ma1](#), [mat.ma2](#), [mat.arma](#)

**Examples**

```
corr <- mat.corg(rhos = c(0.4, 0.2, 0.1), order = 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

*Forms the direct sum of a list of matrices*

---

## Description

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

## Usage

```
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

*Forms an exponential correlation matrix*


---

**Description**

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

**Usage**

```
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.cor](#), [mat.corg](#), [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

*Forms an exponential correlation matrix*


---

**Description**

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

**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.cor](#), [mat.corg](#), [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.ginv

*Computes the generalized inverse of a matrix*

---

**Description**

Computes the Moore-Penrose generalized inverse of a matrix.

**Usage**

```
mat.ginv(x, tol = .Machine$double.eps ^ 0.5)
```

**Arguments**

x                    A [matrix](#) whose generalized inverted is to be computed.  
tol                   A [numeric](#) specifying the relative tolerance to determine whether an eigenvalue of x is nonzero.

**Value**

A [matrix](#). An NA is returned if [svd](#) fails during the computation of the generalized inverse.

**Author(s)**

Chris Brien

**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)
## Compute the projector for a linear trend across Blocks
PBIBD2.lay <- within(PBIBD2.lay,
                    {
                      cBlock <- as.numfac(Block)
                      cBlock <- cBlock - mean(unique(cBlock))
                    })
X <- model.matrix(~ cBlock, data = PBIBD2.lay)
Q.cB <- projector((X %>% mat.ginv(t(X) %>% X) %>% t(X)))

```

---

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	<i>Forms an ma1 correlation matrix</i>
---------	--

---

**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 perturbation.

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.cor](#), [mat.corg](#), [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**

MAparameters    A [numeric](#) containing the two moving average parameter values of the process, being the weights given to the lag 1 and lag 2 random 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, MAparameters. The values in

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

where  $div = 1 + MMAparameters[1]*MAparameter[1] + MAparameters[2]*MAparameters[2]$ .

**Value**

A banded correlation [matrix](#) whose elements follow an ma2 pattern.

**Author(s)**

Chris Brien

**See Also**

[mat.I](#), [mat.J](#), [mat.cor](#), [mat.corg](#), [mat.exp](#), [mat.gau](#), [mat.banded](#), [mat.ar1](#), [mat.ar3](#), [mat.sar2](#), [mat.ma1](#), [mat.arma](#)

**Examples**

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

---

 mat.ncssvar

*Calculates the variance matrix of the random effects for a natural cubic smoothing spline*

---

**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 <a href="#">numeric</a> 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 <a href="#">numeric</a> giving the values of the knots point used in fitting the spline. These must be orderd in increasing order.
print	A <a href="#">logical</a> 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.random	<i>Calculates the variance matrix for the random effects from a mixed model, based on a supplied formula or a matrix.</i>
------------	---

---

**Description**

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

**Usage**

```
mat.random(random, G, design, keep.order = TRUE)
```

**Arguments**

random	A <code>formula</code> or a <code>matrix</code> . If a <code>formula</code> , it specifies the random effects from which the <code>matrix</code> for the contribution of the random effects to the variance matrix can be generated. If it is a <code>matrix</code> , it must be an $n \times n$ <code>matrix</code> and will be passed through as the required variance matrix for the random effects. The default is 0, which implies that there are no random effects.
G	This term only needs to be set if random is a <code>formula</code> . Then it is set to a <code>list</code> , in which each component is either a single value or a <code>matrix</code> ; there needs to be a component for each term in the expanded <code>formula</code> , 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.
design	A <code>data.frame</code> containing the design to be used in an experiment and for which the variance matrix is required. It is not required when the only <code>formula</code> specified is an intercept-only <code>formula</code> .
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.

**Details**

If  $\mathbf{Z}_i$  is the incidence matrix for the random nuisance effects in  $\mathbf{u}_i$  for a term in random and  $\mathbf{u}_i$  has variance matrix  $\mathbf{G}_i$  so that the contribution of the random effects to the variance matrix for  $\mathbf{Y}$  is  $\mathbf{V}_u = \Sigma(\mathbf{Z}_i \mathbf{G}_i (\mathbf{Z}_i)^T)$ .

**Value**

A  $n \times n$  `matrix` containing the variance matrix for the random effects.

**Author(s)**

Chris Brien

**See Also**[mat.Vpredicts](#).**Examples**

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

## Set gammas
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
Vu <- with(start.design, fac.vcmat(Mrep, gammas["Mrep"]) +
           fac.vcmat(fac.combine(list(Mrep,Mday)), gammas["Mrep:Mday"]) +
           fac.vcmat(Frep, gammas["Frep"]) +
           fac.vcmat(fac.combine(list(Frep,Fplot)), gammas["Frep:Fplot"]))

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

mat.sar

*Forms an sar correlation matrix***Description**

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

**Usage**

```
mat.sar(SARparameter, order)
```

**Arguments**

SARparameter	A <a href="#">numeric</a> containing the single value of the parameter from which the correlations are calculated.
order	The order of the <a href="#">matrix</a> 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.cor](#), [mat.corg](#), [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 ar3parameters 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.cor](#), [mat.corg](#), [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 <a href="#">matrix</a> for the $w$ effects to be predicted.
Gg	The $w \times w$ variance <a href="#">matrix</a> of the $w$ effects to be predicted. If the effects to be predicted are fixed, set to 0.
X	The $n \times f$ incidence <a href="#">matrix</a> for the $f$ nuisance fixed factors and covariates. The default is a column vector of ones.
Vu	The $n \times r$ variance <a href="#">matrix</a> of the $r$ nuisance random effects. If there are none, set to zero.
R	The residual variance <a href="#">matrix</a> .
eliminate	The $n \times n$ <a href="#">projector</a> onto the subspace corresponding to the effects to be eliminated from the information matrix prior to inverting it to form the variance <a href="#">matrix</a> 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

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

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

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

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

---

## 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, result = "variance.matrix")
```

## Arguments

target	The $n \times w$ incidence <a href="#">matrix</a> for the $w$ effects targetted for prediction, or a <a href="#">formula</a> from which the <a href="#">matrix</a> can be generated.
Gt	The value of the variance component for the targetted effects or the $w \times w$ variance <a href="#">matrix</a> of the $w$ targetted effects. If the targetted effects are fixed, set Gt to 0.
fixed	The $n \times f$ incidence <a href="#">matrix</a> for the $f$ nuisance fixed effects and covariates, or a <a href="#">formula</a> from which the <a href="#">matrix</a> can be generated. The default is a <a href="#">formula</a> for an intercept-only model.

random	A <a href="#">formula</a> or a <a href="#">matrix</a> . If a <a href="#">formula</a> , it specifies the random effects from which the <a href="#">matrix</a> for the contribution of the random effects to the variance matrix can be generated. If it is a matrix, it must be an $n \times n$ <a href="#">matrix</a> and will be passed on to form the variance matrix of the observations. The default is 0, which implies that there are no random effects.
G	This term only needs to be set if random is a <a href="#">formula</a> . Then it is set to a <a href="#">list</a> , in which each component is either a single value or a <a href="#">matrix</a> ; there needs to be a component for each term in the expanded <a href="#">formula</a> , 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 <a href="#">matrix</a> . If R is not set in the call, then it is set to the identity <a href="#">matrix</a> .
design	A <a href="#">data.frame</a> containing the design to be used in an experiment from which predictions are to be obtained. It is not required when the only <a href="#">formula</a> specified is an intercept-only <a href="#">formula</a> .
eliminate	The $n \times n$ <a href="#">projector</a> onto the subspace corresponding to the effects to be eliminated from the information matrix prior to inverting it to form the variance <a href="#">matrix</a> of the predicted effects. It is only appropriate to use this option when the effects to be predicted are fixed.
keep.order	A <a href="#">logical</a> indicating whether the terms should keep their position in the expanded formula projector, or reordered so that main effects precede two-factor interactions, which precede three-factor interactions and so on.
result	A <a href="#">character</a> indicating which matrix is to be returned: <code>variance.matrix</code> or <code>information.matrix</code> .

## Details

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

As described in Hooks et al. (2009, Equation 19), the information matrix is calculated as  $A \leftarrow t(W) \%*\% Vinv \%*\% W + ginv(Gg) - A \%*\% ginv(t(X) \%*\% Vinv \%*\% X) \%*\% t(A)$ , where  $Vinv \leftarrow ginv(Vu + R)$ ,  $A = t(W) \%*\% Vinv \%*\% X$  and  $ginv(B)$  is the unique Moore-Penrose inverse of  $B$  formed using the eigendecomposition of  $B$ .

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

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

**Value**

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

**Author(s)**

Chris Brien

**References**

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.random](#), [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, design = start.design)

## Calculate the variance matrix of the predicted random Variety effects using formulae
Vp <- mat.Vpredicts(target = ~ -1 + Variety, Gt = 1,
                   fixed = ~ 1,
                   random = ~ -1 + Mrep/Mday + Frep/Fplot,
                   G = as.list(gammas[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 accessed via `vignette("DesignNotes", package="dae")`.

### 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](#), [p`canon`.object](#).

---

p`canon`.object

*Description of a p`canon` 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`.

- 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`.

---

<code>porthogonalize.list</code>	<i>Takes a list of <code>projectors</code> and constructs a <code>pstructure.object</code> that includes projectors, each of which has been orthogonalized to all projectors preceding it in the list.</i>
----------------------------------	--

---

### Description

Constructs a `pstructure.object` that includes a set of mutually orthogonal projectors, one for each of the `projectors` in the `list`. These specify a structure, or an orthogonal decomposition of the data space. This function externalizes the process previously performed within `pstructure.formula` to orthogonalize `projectors`. There are three methods available for carrying out orthogonalization: `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 'list'
porthogonalize(projectors, formula = NULL, keep.order = TRUE,
               grandMean = FALSE, orthogonalize = "hybrid", labels = "sources",
               marginality = NULL, check.marginality = TRUE,
               omit.projectors = FALSE,
               which.criteria = c("aefficiency", "eefficiency", "order"),
               aliasing.print = TRUE, ...)
```

**Arguments**

projectors	A <b>list</b> each of whose components is a <b>projector</b> .
formula	An object of class <b>formula</b> from which the <b>projectors</b> have been obtained. If NULL, then the differencing option of orthogonalize is not available.
keep.order	A <b>logical</b> 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 <b>logical</b> indicating whether the projector for the grand mean is to be included in the set produced.
orthogonalize	A <b>character</b> vector indicating the method for orthogonalizing a projector to those for terms that occurred previously in the formula. Three options are available: hybrid; differencing; eigenmethods, unless formula is NULL in which case differencing is not available. The hybrid option is the most general and uses the relationships between the projection operators for the terms in the formula to decide which <b>projectors</b> to subtract and which to orthogonalize using eigenmethods. The differencing option subtracts, from the current <b>projector</b> , those previously orthogonalized <b>projectors</b> for terms whose factors are a subset of the current <b>projector</b> 's factors. The eigenmethods option recursively orthogonalizes the <b>projectors</b> using an eigenanalysis of each <b>projector</b> with previously orthogonalized <b>projectors</b> .
labels	A <b>character</b> nominating the type of labels to be used in labelling the projectors, and which will be used also in the output tables, such the tables of the aliasing in the structure. The two alternatives are terms and sources. Terms have all factors/variables in it separated by colons (:). Sources have factors/variables in them that represent interactions separated by hashes (#); if some factors are nested within others, the nesting factors are surrounded by square brackets ([ and ]) and separated by colons (:). If some generalized, or combined, factors have no marginal terms, the constituent factors are separated by colons (:) and if they interact with other factors in the source they will be parenthesized.
marginality	A square <b>matrix</b> that can be used to supply the marginality <b>matrix</b> when it is desired to overwrite the calculated marginality <b>matrix</b> 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 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 <b>logical</b> indicating whether the marginality matrix, when it is supplied, is to be checked against that computed by <b>porthogonalize.list</b> . It is ignored when orthogonalize is set to eigenmethods.
omit.projectors	A <b>logical</b> , which, if TRUE, results in the <b>projectors</b> 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 <b>projectors</b> are not required for further analysis.
which.criteria	A character vector nominating the efficiency criteria to be included in the summary of aliasing between terms. It can be none, all or some combination

of aefficiency, mefficiency, sefficiency, eefficiency, xefficiency, order and dforthog – for details see [efficiency.criteria](#). If none, no summary is printed.

aliasing.print A [logical](#) indicating whether the aliasing between sources within the structure is to be printed.

... further arguments passed to terms.

## Details

It is envisaged that the [projectors](#) in the [list](#) supplied to the `projectors` argument correspond to the terms in a linear model. One way to generate them is to obtain the design matrix  $\mathbf{X}$  for a term and then calculate its projector as  $\mathbf{X}(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'$ . There are three methods available for orthogonalizing the supplied projectors: differencing, eigenmethods or the default hybrid method.

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

Eigenmethods forces each projector to be orthogonal to all terms previous to it in the expanded formula. It uses equation 4.10 of James and Wilkinson (1971), which involves calculating the canonical efficiency factors for pairs of primary projectors. It produces a table of efficiency criteria for partially aliased terms. Again, the order of terms is crucial. This method has the disadvantage that the marginality of terms is not determined and so sources names are set to be the same as the term names, unless a marginality matrix is supplied.

The hybrid method is the most general and uses the relationships between the projection operators for the terms in the formula to decide which projectors to subtract and which to orthogonalize using eigenmethods. If  $\mathbf{Q}_i$  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.

The order of projections matrices in the [list](#) is crucial in this process.

Of the three methods, eigenmethods is least likely to fail, but it does not establish the marginality between the terms. It is often needed when there is nonorthogonality between terms, such as when there are several linear covariates. It can also be more efficient in these circumstances.

The process can be computationally expensive, particularly for a large data set (500 or more observations) and/or when many terms are to be orthogonalized.

If the error Matrix is not idempotent should occur then, especially if there are many terms, one might try using [set.daeTolerance](#) to reduce the tolerance used in determining if values are either the same or are zero; it may be necessary to lower the tolerance to as low as 0.001. Also, setting `orthogonalize` to `eigenmethods` is worth a try.

**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**

`pstructure.formula`, `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.BU <- projector(diag(1, nrow=24))

## manually obtain projector for trt
Q.T <- projector(fac.meanop(PBIBD2.lay$trt) - Q.G)

##Orthogonalize the projectors using porthogonalize.list
Qs <- list(Mean = Q.G, Block = Q.B, "Block:Unit" = Q.BU)
struct <- porthogonalize(Qs, grandMean = TRUE)
Qs <- struct$Q
(lapply(Qs, degfree))

#Add a linear covariate
PBIBD2.lay <- within(PBIBD2.lay,
                    {
                      cBlock <- as.numfac(Block)
                      cBlock <- cBlock - mean(unique(cBlock))
                    })
X <- model.matrix(~ cBlock, data = PBIBD2.lay)
Q.cB <- projector(X %*% mat.ginv(t(X) %*% X) %*% t(X))
Qs <- list(cBlock = Q.cB, Block = Q.B, "Block:Unit" = Q.BU)
struct <- porthogonalize(Qs, grandMean = FALSE)
Qs <- struct$Q
(lapply(Qs, degfree))
```

---

`power.exp`*Computes the power for an experiment*

---

**Description**

Computes the power for an experiment.

**Usage**

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

**Arguments**

<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>delta</code>	The true difference between a pair of means.
<code>sigma</code>	The population standard deviation.
<code>alpha</code>	The significance level to be used.
<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 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	<i>Print an aliasing data.frame</i>
----------------	-------------------------------------

---

### Description

Prints an aliasing [data.frame](#).

### Usage

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

### Arguments

x	The <a href="#">data.frame</a> that is also of class <code>aliasing</code> 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 <code>aefficiency</code> , <code>mefficiency</code> , <code>sefficiency</code> , <code>eefficiency</code> , <code>xefficiency</code> , <code>order</code> and <code>dforthog</code> – for details see <a href="#">efficiency.criteria</a> . If none, no criteria are printed.
...	Further arguments passed to the <code>print</code> method for <code>data.frame</code> .

### 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      Print projectors
```

---

**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 = "all", ...)
```

**Arguments**

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

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

`...` Further arguments passed to `print.aliasing`.

**Author(s)**

Chris Brien

**See Also**

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

**Examples**

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

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

## print the object either using the Method function, the generic function or show
print.pstructure(ABCD.struct)
print(ABCD.struct)
ABCD.struct
```

---

`print.summary.p2canon` *Prints the values in an `summary.p2canon` object*

---

**Description**

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

**Usage**

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

**Arguments**

`x` A `summary.p2canon` object.

`...` further arguments passed to `print`.

**Value**

No value is returned.

**Author(s)**

Chris Brien

**See Also**

[summary.p2canon](#)

**Examples**

```
## 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 <a href="#">logical</a> 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

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

---

**Description**

The canonical relationship between a pair of projectors is established by decomposing the range of  $Q_1$  into a part that pertains to  $Q_2$  and a part that is orthogonal to  $Q_2$ . It also produces the nonzero canonical efficiency factors for the joint decomposition of  $Q_1$  and  $Q$  and the corresponding eigenvectors of  $Q_1$  (James and Wilkinson, 1971).  $Q_1$  and  $Q_2$  may be nonorthogonal.

**Usage**

```
proj2.combine(Q1, Q2)
```

**Arguments**

$Q_1$             A symmetric projector whose range is to be decomposed.  
 $Q_2$             A symmetric projector whose range in  $Q_1$  is required.

**Details**

The nonzero canonical efficiency factors are the nonzero eigenvalues of  $Q_1 \%*\% Q_2 \%*\% Q_1$  (James and Wilkinson, 1971). An eigenvalue is regarded as zero if it is less than `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  $Q_1$  corresponding to the nonzero canonical efficiency factors. The eigenvectors for  $Q_2$  can be obtained by premultiplying those for  $Q_1$  by  $Q_2$ .

$Q_{res}$  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  $Q_{res}$ . In this latter case,  $Q_{res} = Q_1 - Q_1 \%*\% g_{inv}(Q_2 \%*\% Q_1 \%*\% Q_2) \%*\% Q_1$ .  $Q_{conf}$  is obtained by subtracting  $Q_{res}$  from  $Q_1$ .

**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  $Q_1$  corresponding to the nonzero canonical efficiency factors.
3. **Qconf**: a projector onto the part of the range of  $Q_1$  with which  $Q_2$  is confounded;
4. **Qres**: a projector onto the part of the range of  $Q_1$  that is orthogonal to the range of  $Q_2$ .

**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	<i>Computes the canonical efficiency factors for the joint decomposition of two projectors</i>
------------------	--

---

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

[projector](#) for further information about this class.

**Examples**

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

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

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

#extract intrablock efficiencies
decomp.intra$efficiencies
```

---

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, summetric, 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	<i>Class projector</i>
-----------------	------------------------

---

**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

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

---

**Description**

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

**Usage**

```
projs.2canon(Q1, Q2)
```



```
##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      *Takes a formula and constructs a [pstructure.object](#) that includes the orthogonalized projectors for the terms in a formula*

---

### Description

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

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

### Usage

```

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

```

### Arguments

formula	An object of class <a href="#">formula</a> from which the terms will be obtained.
keep.order	A <a href="#">logical</a> 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 <a href="#">logical</a> indicating whether the projector for the grand mean is to be included in the set produced.
orthogonalize	A <a href="#">character</a> vector indicating the method for orthogonalizing a projector to those for terms that occurred previously in the formula. Three options are available: hybrid; differencing; eigenmethods. The hybrid option is the most general and uses the relationships between the projection operators for the terms in the formula to decide which <a href="#">projectors</a> to subtract and which to orthogonalize using eigenmethods. The differencing option subtracts, from the current <a href="#">projector</a> , those previously orthogonalized <a href="#">projectors</a> for terms whose factors are a subset of the current <a href="#">projector</a> 's factors. The eigenmethods option recursively orthogonalizes the <a href="#">projectors</a> using an eigenanalysis of each <a href="#">projector</a> with previously orthogonalized <a href="#">projectors</a> .

labels	A <a href="#">character</a> nominating the type of labels to be used in labelling the projectors, and which will be used also in the output tables, such the tables of the aliasing in the structure. The two alternatives are terms and sources. Terms have all factors/variables in it separated by colons (:). Sources have factors/variables in them that represent interactions separated by hashes (#); if some factors are nested within others, the nesting factors are surrounded by square brackets ([ and ]) and separated by colons (:). If some generalized, or combined, factors have no marginal terms, the constituent factors are separated by colons (: ) and if they interact with other factors in the source they will be parenthesized.
marginality	A square <a href="#">matrix</a> that can be used to supply the marginality <a href="#">matrix</a> when it is desired to overwrite the calculated marginality <a href="#">matrix</a> 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 grandMean is TRUE.
check.marginality	A <a href="#">logical</a> indicating whether the marginality matrix, when it is supplied, is to be checked against that computed by <a href="#">pstructure.formula</a> . It is ignored when orthogonalize is set to eigenmethods.
omit.projectors	A <a href="#">logical</a> , which, if TRUE, results in the <a href="#">projectors</a> in the Q of the <a href="#">pstructure.object</a> 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 <a href="#">projectors</a> are not required for further analysis.
which.criteria	A character vector nominating the efficiency criteria to be included in the summary of aliasing between terms. It can be none, all or some combination of aefficiency, mefficiency, sefficiency, eefficiency, xefficiency, order and dforthog – for details see <a href="#">efficiency.criteria</a> . If none, no summary is printed.
aliasing.print	A <a href="#">logical</a> 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 using [porthogonalize.list](#), either by differencing, eigenmethods or the default hybrid method.

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

may happen that differencing does not produce a projector, in which case eigenmethods must be used.

Eigenmethods forces each projector to be orthogonal to all terms previous to it in the expanded formula. It uses equation 4.10 of James and Wilkinson (1971), which involves calculating the canonical efficiency factors for pairs of primary projectors. It produces a table of efficiency criteria for partially aliased terms. Again, the order of terms is crucial. This method has the disadvantage that the marginality of terms is not determined and so sources names are set to be the same as the term names, unless a marginality matrix is supplied.

The hybrid method is the most general and uses the relationships between the projection operators for the terms in the formula to decide which projectors to subtract and which to orthogonalize using eigenmethods. If  $\mathbf{Q}_i$  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.

The order of terms is crucial in this process.

Of the three methods, eigenmethods is least likely to fail, but it does not establish the marginality between the terms. It is often needed when there is nonorthogonality between terms, such as when there are several linear covariates. It can also be more efficient in these circumstances.

The process can be computationally expensive, particularly for a large data set (500 or more observations) and/or when many terms are to be orthogonalized.

If the error Matrix is not idempotent should occur then, especially if there are many terms, one might try using `set.daeTolerance` to reduce the tolerance used in determining if values are either the same or are zero; it may be necessary to lower the tolerance to as low as 0.001. Also, setting orthogonalize to eigenmethods is worth a try.

## 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

`orthogonalize.list`, `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	<i>Description of a pstructure object</i>
-------------------	---

---

**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 projectors for each non-aliased term/source in the formula; if grandMean is TRUE in the call to [pstructure.formula](#) then it also includes the projector for it;
2. terms: a [character](#) vector with the non-aliased term names; if grandMean is TRUE in the call to [pstructure.formula](#) then the first term will be "Mean";
3. sources: a [character](#) vector with the non-aliased source names;
4. marginality: a [matrix](#) of zeroes and ones with the same number of rows and columns as number of non-aliased terms, excluding the term for the grand mean even when grandMean is TRUE; the row names and column names are the elements terms, excluding "Mean";

the entry in the  $i$ 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 will have been made orthogonal to that for the  $i$ th term; otherwise, the entries are zero.

5. aliasing: a `data.frame` containing the information about the (partial) aliasing between the sources in the formula. The columns are:
  - Source: the source names, or associated term name, for those that are (partially) aliased with previous sources;
  - df: the remaining degrees of freedom for the source;
  - Alias: the source with which the current entry is (partially) aliased;
  - efficiency criteria: a set of columns for the complete set of criteria calculated by `efficiency.criteria`; the criteria reflect the amount of information that is aliased with previous sources and a line is included in the component that reports the information remaining after adjustment for previous sources.

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

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

### Author(s)

Chris Brien

### See Also

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

---

qqyeffects

*Half or full normal plot of Yates effects*

---

### Description

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

### Usage

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

### Arguments

<code>aov.obj</code>	An aov object or aovlistobject created from a call to <code>aov</code> .
<code>error.term</code>	The term from the Error function from which the Yates effects are estimated. Only required when Error used in call to <code>aov</code> .

data	A data.frame in which the variables specified in the aov.obj will be found. If missing, the variables are searched for in the standard way.
pch	The number of a plotting symbol to be drawn when plotting points (use help(points) for details).
full	whether a full or half normal plot is to be produced. The default is for a half-normal plot; full=TRUE produces a full normal plot.
...	Further graphical parameters may be specified (use help(par) for possibilities).

### Details

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

### Value

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

### Author(s)

Chris Brien

### See Also

[yates.effects](#) in package **dae**, [qqnorm](#).

### Examples

```
## 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)
qqyeffects(Fac4Proc.aov, error.term="Runs", data=Fac4Proc.dat)
```

---

rep.data.frame	<i>Replicate the rows of a data.frame by repeating each row consecutively and/or repeating all rows as a group</i>
----------------	--

---

### Description

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

### Usage

```
## S3 method for class 'data.frame'
rep(x, times=1, each=1, ...)
```

**Arguments**

x	A <code>data.frame</code> whose rows are to be repeated.
times	The number of times to repeat the whole set of rows, after the rows have been replicated consecutively each times.
each	The number of times to replicate consecutively each row in the <code>data.frame</code> .
...	Further arguments passed to or from other methods. Unused at present.

**Value**

A `data.frame` with replicated rows.

**Author(s)**

Chris Brien

**See Also**

`fac.gen` in package **dae** and `rep`

**Examples**

```
rep(fac.gen(list(a = 2, b = 2)), times=2, each=2)
```

---

resid.errors

*Extract the residuals for a fitted model*

---

**Description**

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

**Usage**

```
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(89,88,97,94,84,84,77,92,79,81,87,87,
                      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 <a href="#">aov</a> .
<code>error.term</code>	The term from the Error function for which the residuals are to be extracted. If <code>error.term</code> is NULL the residuals are extracted from the last Error 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(89,88,97,94,84,77,92,79,81,87,87,
                      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 accessed via `vignette("DesignNotes", package="dae")`.

### Usage

```
data(Sensory3Phase.dat)
data(Sensory3PhaseShort.dat)
```

### Format

A data.frame containing 576 observations of 12 variables. There are two versions, one with shorter factor names than the other.

### References

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

---

set.daeTolerance	<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

<code>element.tol</code>	The value to to which the first element of the <code>daeTolerance</code> vector is to be set. If more than one value is supplied, only the first value is used.
<code>eigen.tol</code>	The value to to which the second element of the <code>daeTolerance</code> 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

---

*Data for an experiment to investigate the effects of grazing patterns on pasture composition*


---

**Description**

The response variable is the percentage area covered by the principal grass (Main.Grass). The design for the experiment is a split-unit design. The main units are arranged in 3 Rows x 3 Columns. Each main unit is split into 2 SubRows x 2 SubColumns.

The factor Period, with levels 3, 9 and 18 days, is assigned to the main units using a 3 x 3 Latin square. The two-level factors Spring and Summer are assigned to split-units using a criss-cross design within each main unit. The levels of each of Spring and Summer are two different grazing patterns in its season.

**Usage**

data(SPLGrass.dat)

**Format**

A data.frame containing 36 observations of 8 variables.

**Source**

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 <a href="#">factor</a> 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", "eefficiency", "order"), ...)
```

### Arguments

object	A list of class p2canon produced by <a href="#">projs.2canon</a> .
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 <a href="#">efficiency.criteria</a> .
...	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 <a href="#">pcanon.object</a> .
labels.swap	A <a href="#">logical</a> indicating whether to swap between "sources" and 'terms' in the output. The default is established by the labels argument of <a href="#">designAnatomy</a> and <a href="#">projs.canon</a> .

`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`, `efficiency`, `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

*Performs Tukey's one-degree-of-freedom-test-for-nonadditivity*


---

### Description

Performs Tukey's one-degree-of-freedom-test-for-nonadditivity on a set of residuals from an analysis of variance.

### Usage

```
tukey.1df(aov.obj, data, error.term="Within")
```

### Arguments

aov.obj	An aov object or aovlist object created from a call to <a href="#">aov</a> .
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 <a href="#">aov</a> .

### Value

A list containing Tukey.SS, Tukey.F, Tukey.p, Devn.SS<sub>q</sub> being the SS<sub>q</sub> 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(89,88,97,94,84,84,77,92,79,81,87,87,
```

```

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	<i>Extract Yates effects</i>
---------------	------------------------------

---

## 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 <a href="#">aov</a> .
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	<i>Calculates the design matrix for fitting the random component of a natural cubic smoothing spline</i>
------------	--

---

**Description**

Calculates the design matrix,  $\mathbf{Z}$ , of the random effects for a natural cubic smoothing spline as described by Verbyla et al., (1999). An initial design matrix,  $\mathbf{\Delta}\mathbf{\Delta}^{-1}\mathbf{\Delta}$ , based on the knot points is computed. It can then be post multiplied by the power of the tri-diagonal matrix  $\mathbf{G}_s$  that is proportional to the variance matrix of the random spline effects. If the power is set to 0.5 then the random spline effects based on the resulting  $\mathbf{Z}$  matrix will be independent with variance  $\sigma_s^2$ .

**Usage**

```
Zncsspline(knot.points, Gpower = 0, print = FALSE)
```

**Arguments**

knot.points	A <b>numeric</b> giving the values of the knot points to be used in fitting the spline. These must be orderd in increasing order.
Gpower	A <b>numeric</b> giving the power of the tri-diagonal matrix $\mathbf{G}_s$ from which the variance matrix of the random spline effects is caluclated. 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 <b>logical</b> indicating whether to print the $\mathbf{\Delta}$ and $\mathbf{G}_s$ 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)
```

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