

Package ‘Crossover’

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Type Package

Title Analysis and Search of Crossover Designs

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Description Package Crossover provides different crossover designs from combinatorial or search algorithms as well as from literature and a GUI to access them.

Depends R (>= 3.0.2), rJava (>= 0.8-3), CommonJavaJars (>= 1.0.5), JavaGD, ggplot2

Imports MASS, crossdes (>= 1.1-1), xtable, methods, Matrix, multcomp, stats4, digest

Suggests knitr, testthat, nlme

SystemRequirements Java (>= 5.0)

LinkingTo Rcpp (>= 0.10.3), RcppArmadillo (>= 0.2.0)

License GPL-2

VignetteBuilder knitr

URL <https://github.com/kornl/Crossover/wiki>

BugReports <https://github.com/kornl/Crossover/issues>

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Crossover-package	<i>This package provides more than two hundred cross-over design from literature, a search algorithm to find efficient cross-over designs for various models and a graphical user interface to find/generate appropriate designs.</i>
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Description

This package provides more than two hundred cross-over design from literature, a search algorithm to find efficient cross-over designs for various models and a graphical user interface to find/generate appropriate designs.

Author(s)

Maintainer: Kornelius Rohmeyer <rohmeier@small-projects.de>

References

Jones, B., & Kenward, M. G. (2003). Design and analysis of cross-over trials (Vol. 98). Chapman & Hall.

John, J. A., Russell, K. G., & Whitaker, D. (2004). CrossOver: an algorithm for the construction of efficient cross-over designs. *Statistics in medicine*, 23(17), 2645-2658.

buildSummaryTable *Build Summary Table For All Examples From Literature*

Description

Build Summary Table For All Examples From Literature

Usage

```
buildSummaryTable(extended = FALSE)
```

Arguments

extended If TRUE the summary table will have further columns with extended information as how balanced the design is and whether all treatment effect differences are estimable under all models.

Details

See also the documentation for the data files.

Value

TODO

Author(s)

Kornelius Rohmeyer <rohrmeyer@small-projects.de>

References

See the documentation for the data files.

Examples

```
buildSummaryTable()
```

canonicalOrder	<i>Sorts sequences of a design into a canonical order</i>
----------------	---

Description

Sorts sequences of a design into a canonical order.

Usage

```
canonicalOrder(design)
```

Arguments

design Cross-over design.

Details

When comparing bigger designs this ordering easily allows to check whether two designs are equal.

Author(s)

Kornelius Rohmeyer <rohrmeyer@small-projects.de>

Examples

```
getDesign("switchback5t")
canonicalOrder(getDesign("switchback5t"))
```

contrMat2	<i>Create the design matrix, variance-covariance matrix, the variance of each pairwise comparison and the efficiency of each pairwise comparison for a cross-over design</i>
-----------	--

Description

Function to read in a cross-over design and create the design matrix X, the variance of each pairwise comparison and the efficiency of each pairwise comparison.

Usage

```
contrMat2(type, v, model, eff.factor = rep(1,
length(parameterCount(model, v))))
```

Arguments

type	Type of contrast. A character vector containing the following: "Dunnett", "Tukey", "none". If the length is 1, this contrast is only applied for the treatment effects and for carry-over effects a "Tukey" contrast is used. Otherwise the specified contrasts are used, see also the examples.
v	Number of treatments
model	Model - one of the following: 1) "Standard additive model", 2) "Second-order carry-over effects", 3) "Full set of interactions", 4) "Self-adjacency model", 5) "Placebo model", 6) "No carry-over into self model", 7) "Treatment decay model", 8) "Proportionality model", 9) "No carry-over effects". Can be specified as number or as character string.
eff.factor	Weight applied to the different sub contrast matrices. A warning is given if it does not sum up to one. See examples.

Details

See the vignette of this package for further details.

Value

A contrast matrix

Author(s)

Kornelius Rohmeyer <rohrmeyer@small-projects.de>

Examples

```
contrMat2("Tukey", v=3, model=1)
contrMat2("Dunnett", v=3, model=1)
contrMat2(c("Dunnett", "Dunnett"), v=3, model=1)
contrMat2(c("Dunnett", "none"), v=3, model=1)
contrMat2(c("Dunnett", "none", "none"), v=3, model=8)
contrMat2("Dunnett", v=3, model=1, eff.factor=c(0.9, 0.1))
contrMat2("Dunnett", v=3, model=8, eff.factor=c(0.5, 0.3, 0.2))
```

CrossoverDesign-class *Class CrossoverDesign*

Description

A S4 class for Crossover designs: CrossoverDesign

Slots

list("design") Matrix specifying the design. Rows represent periods and columns the subjects.

list("s") Number of sequences.

list("p") Number of periods.

list("v") Number of treatments.

list("model") A numeric specifying the model the design was searched for or -1 if unknown.

list("description") Optional description of design or reference.

list("attr") List with attributes.

list("misc") List with miscellaneous stuff - not used yet.

Author(s)

Kornelius Rohmeyer <rohmeier@small-projects.de>

Examples

```
design <- t(rbind(c(1,1,2,2),
                c(2,2,1,1),
                c(1,1,2,2),
                c(2,2,1,1),
                c(1,2,2,1),
                c(2,1,1,2)))
new("CrossoverDesign", design)
```

Crossoverdesigns

Selected Cross-Over designs from literature

Description

Selected Cross-Over designs from literature.

You can access all designs via the function `getDesign` as in the example `getDesign("williams4t")`.

Format

A integer matrix specifying the design. Rows represent periods and columns the subjects.

Details

These data sets are stored combined by prefix, so alternatively to using the recommended function `getDesign` you could access for example design `fletcher10` by using the command `data(fletcher10)` and afterwards all 31 design from `fletcher1` up to `fletcher31` are loaded.

The available data sets are:

`federerAtkinson3ta`, `federerAtkinson3tb`, `federerAtkinson4ta`, `federerAtkinson4tb`, `federerAtkinson5ta`, `fletcher1`, `fletcher10`, `fletcher11`, `fletcher12`, `fletcher13`, `fletcher14`, `fletcher15`, `fletcher16`, `fletcher17`, `fletcher18`, `fletcher19`, `fletcher2`, `fletcher20`, `fletcher21`, `fletcher22`, `fletcher23`, `fletcher24`, `fletcher25`, `fletcher26`, `fletcher27`, `fletcher28`, `fletcher29`, `fletcher3`, `fletcher30`, `fletcher31`, `fletcher4`, `fletcher5`, `fletcher6`, `fletcher7`, `fletcher8`, `fletcher9`, `iqbalJones1`, `iqbalJones10`, `iqbalJones11`, `iqbalJones12`, `iqbalJones13`, `iqbalJones14`, `iqbalJones15`, `iqbalJones16`, `iqbalJones17`, `iqbalJones18`, `iqbalJones19`, `iqbalJones2`, `iqbalJones20`, `iqbalJones21`, `iqbalJones22`, `iqbalJones23`, `iqbalJones24`, `iqbalJones25`, `iqbalJones26`, `iqbalJones27`, `iqbalJones28`, `iqbalJones29`, `iqbalJones3`, `iqbalJones30`, `iqbalJones31`, `iqbalJones32`, `iqbalJones33`, `iqbalJones34`, `iqbalJones35`, `iqbalJones36`, `iqbalJones37`, `iqbalJones38`, `iqbalJones39`, `iqbalJones4`, `iqbalJones40`, `iqbalJones41`, `iqbalJones42`, `iqbalJones5`, `iqbalJones6`, `iqbalJones7`, `iqbalJones8`, `iqbalJones9`, `lewisFletcherMatthews1`, `lewisFletcherMatthews10`, `lewisFletcherMatthews11`, `lewisFletcherMatthews12`, `lewisFletcherMatthews13`, `lewisFletcherMatthews14`, `lewisFletcherMatthews15`, `lewisFletcherMatthews16`, `lewisFletcherMatthews17`, `lewisFletcherMatthews18`, `lewisFletcherMatthews19`, `lewisFletcherMatthews2`, `lewisFletcherMatthews20`, `lewisFletcherMatthews3`, `lewisFletcherMatthews4`, `lewisFletcherMatthews5`, `lewisFletcherMatthews6`, `lewisFletcherMatthews7`, `lewisFletcherMatthews8`, `lewisFletcherMatthews9`, `orthogonalLatinSquare3t`, `orthogonalLatinSquare4t`, `orthogonalLatinSquare5t`, `orthogonalLatinSquare7t`, `pattersonLucasExtraPeriod30`, `pattersonLucasExtraPeriod31`, `pattersonLucasExtraPeriod32`, `pattersonLucasExtraPeriod33`, `pattersonLucasExtraPeriod34`, `pattersonLucasExtraPeriod35`, `pattersonLucasExtraPeriod36`, `pattersonLucasExtraPeriod37`, `pattersonLucasExtraPeriod38`, `pattersonLucasExtraPeriod39`, `pattersonLucasExtraPeriod40`, `pattersonLucasExtraPeriod41`, `pattersonLucasExtraPeriod42`, `pattersonLucasExtraPeriod43`, `pattersonLucasExtraPeriod44`, `pattersonLucasExtraPeriod45`, `pattersonLucasExtraPeriod46`, `pattersonLucasExtraPeriod47`, `pattersonLucasExtraPeriod48`, `pattersonLucasExtraPeriod49`, `pattersonLucasExtraPeriod86`, `pattersonLucasPBIBD100`, `pattersonLucasPBIBD101`, `pattersonLucasPBIBD102`, `pattersonLucasPBIBD103`, `pattersonLucasPBIBD104`, `pattersonLucasPBIBD105`, `pattersonLucasPBIBD106`, `pattersonLucasPBIBD107`, `pattersonLucasPBIBD125`, `pattersonLucasPBIBD126`, `pattersonLucasPBIBD127`, `pattersonLucasPBIBD128`, `pattersonLucasPBIBD131`, `pattersonLucasPBIBD132`, `pattersonLucasPBIBD133`, `pattersonLucasPBIBD134`, `pattersonLucasPBIBD135`, `pattersonLucasPBIBD136`, `pattersonLucasPBIBD137`, `pattersonLucasPBIBD138`, `pattersonLucasPBIBD139`, `pattersonLucasPBIBD140`, `pattersonLucasPBIBD141`, `pattersonLucasPBIBD153`, `pattersonLucasPBIBD154`, `pattersonLucasPBIBD155`, `pattersonLucasPBIBD156`, `pattersonLucasPBIBD99`, `pattersonLucasPltT1`, `pattersonLucasPltT10`, `pattersonLucasPltT12`, `pattersonLucasPltT13`, `pattersonLucasPltT15`, `pattersonLucasPltT16`, `pattersonLucasPltT17`, `pattersonLucasPltT18`, `pattersonLucasPltT19`, `pattersonLucasPltT20`, `pattersonLucasPltT21`, `pattersonLucasPltT22`, `pattersonLucasPltT23`, `pattersonLucasPltT3`, `pattersonLucasPltT4`, `pattersonLucasPltT5`, `pattersonLucasPltT7`, `pattersonLucasPltT8`, `pattersonLucasPltT9`, `pidgeon1`, `pidgeon10`, `pidgeon11`, `pidgeon12`, `pidgeon13`, `pidgeon14`, `pidgeon15`, `pidgeon16`, `pidgeon17`, `pidgeon18`, `pidgeon19`, `pidgeon2`, `pidgeon20`, `pidgeon3`, `pidgeon4`, `pidgeon5`, `pidgeon6`, `pidgeon7`, `pidgeon8`, `pidgeon9`, `prescott1`, `prescott2`, `quenouille3t1`, `quenouille3t2`, `quenouille4t1`, `quenouille4t2`, `quenouille4t3`, `russel4t`, `russel7t`, `switchback3t`, `switchback4t`, `switchback5t`, `switchback6t`, `switchback7t`, `williams3t`, `williams4t`, `williams5t`, `williams6t`, `williams7t`, `williams8t`, `williams9t`, `pb2.64`.

Source

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Examples

```
getDesign("williams4t")

data(fletcher)
ls(pattern="fletcher*")
fletcher10
```

CrossoverGUI

Graphical User Interface for Crossover Designs

Description

Starts a graphical user interface for accessing and creating crossover designs.

Usage

```
CrossoverGUI()
```

Details

See the vignette of this package for further details, since describing a GUI interface is better done with some nice pictures.

Value

The function itself returns nothing of interest. But from the GUI designs and objects can be created or edited that will be available in R under the specified variable name after saving.

Author(s)

Kornelius Rohmeyer <rohmeier@small-projects.de>

Examples

```
## Not run:
CrossoverGUI()

## End(Not run)
```

CrossoverSearchResult-class

Class CrossoverSearchResult

Description

A S4 class for the search result for Crossover designs: CrossoverSearchResult

Slots

list("design") An object of class CrossoverDesign describing the best design that was found.

list("startDesigns") A list of start designs to search from.

list("model") A numeric specifying the model the design was searched for or -1 if unknown.

list("eff") List, Progress of the algorithm. TODO: Explain further.

list("search") List, TODO

list("time") Named numeric with the time in seconds the algorithm was searching.

list("misc") List - in the moment not used.

Author(s)

Kornelius Rohmeyer <rohmeier@small-projects.de>

Examples

```
# n=c(100,10) is very small, but it's just an example and should not take much time
x <- searchCrossOverDesign(s=9, p=5, v=4, model=4, n=c(100,10))
print(x)
```

design.ency

Create the design matrix, variance-covariance matrix, the variance of each pairwise comparison and the efficiency of each pairwise comparison for a cross-over design

Description

Function to read in a cross-over design and create the design matrix X, the variance of each pairwise comparison and the efficiency of each pairwise comparison.

Usage

```
design.ency(design, model = 1, model.param = list(),
  v = length(levels(as.factor(design))))
```

Arguments

design	Cross-over design.
model	Model - one of the following: 1) "Standard additive model", 2) "Second-order carry-over effects", 3) "Full set of interactions", 4) "Self-adjacency model", 5) "Placebo model", 6) "No carry-over into self model", 7) "Treatment decay model", 8) "Proportionality model", 9) "No carry-over effects".
model.param	List of additional model specific parameters. In the moment these are ppp, the proportionality parameter for the proportionality model, and placebos, the number of placebo treatments in the placebo model.
v	Number of treatments

Details

See the vignette of this package for further details.

Value

A list with the following elements:

- xmat Design matrix for the given model (including subject and period effects)
- var.trt.pair.adj Matrix of treatment difference variances
- eff.trt.pair.adj Matrix of treatment difference efficiencies

Author(s)

Kornelius Rohmeyer <rohrmeyer@small-projects.de>

References

Jones, B., & Kenward, M. G. (2003). Design and analysis of cross-over trials (Vol. 98). Chapman & Hall.

Examples

```
design.efficiency(getDesign("fletcher1"))
design.efficiency(getDesign("fletcher1"), model=7)
design.efficiency(getDesign("switchback4t"), model=7)
```

exampleSearchResults2t

Example search results for two treatments

Description

A list of 16 integer matrices specifying the design. Rows represent periods and columns the subjects.

Format

A list of 16 integer matrices specifying the design. Rows represent periods and columns the subjects.

Details

See vignette.

Source

Found by method searchCrossOverDesign.

general.carryover

Calculate variances of parameter contrasts

Description

Calculate variances of parameter contrasts

Usage

```
general.carryover(design, v = length(table(design)), model, ppp = 0.5,
  placebos = 1, contrasts)
```

Arguments

design	Cross-over design.
v	Number of treatments
model	Model - one of the following numbers or Strings: 1 = "Standard additive model", 2 = "Self-adjacency model", 3 = "Proportionality model", 4 = "Placebo model", 5 = "No carry-over into self model", 6 = "Treatment decay model", 7 = "Full set of interactions", 8 = "Second-order carry-over effects"
ppp	The proportionality parameter for the proportionality model.
placebos	The number of placebo treatments in the placebo model.
contrasts	Optionally a contrast matrix or a list of contrast matrix. If missing pairwise differences for treatment and carry-over parameters are calculated.

Details

See the vignette of this package for further details.

Value

A list with the variances of the pairwise differences or specified contrasts. If contrasts are not estimable, NA is returned for variances.

Author(s)

Kornelius Rohmeyer <rohmeier@small-projects.de>

References

Jones, B., & Kenward, M. G. (2003). Design and analysis of cross-over trials (Vol. 98). Chapman & Hall.

Examples

```
general.carryover(getDesign("fletcher1"), model=1)
general.carryover(getDesign("fletcher1"), model=2)
general.carryover(getDesign("fletcher1"), model=3)
general.carryover(getDesign("switchback4t"), model=7)
```

getDesign

Extract Design from a CrossoverSearchResult

Description

Extract Design from a CrossoverSearchResult

Usage

```
## S4 method for signature 'CrossoverSearchResult'
getDesign(object, ...)
```

Arguments

object A searchCrossOverDesign object from which the design should be extracted.
... Possible parameters for subclasses (not yet used).

Value

Returns a numeric matrix representing the crossover design. Rows represent periods, columns represent sequences.

Author(s)

Kornelius Rohmeyer <rohmeier@small-projects.de>

Examples

```
# n=c(100,10) is very small, but it's just an example and should not take much time
x <- searchCrossOverDesign(s=9, p=5, v=4, model=4, n=c(100,10))
getDesign(x)

getDesign("williams4t")
```

getModelNr

Get the number or character string specifying the model

Description

Get the number or character string specifying the model

Usage

```
getModelNr(model, type = "numeric")
```

Arguments

model	Number or character string specifying the model
type	Either "numeric" or "character". If numeric the number of the model will be returned. Otherwise the character string description of the model.

Value

Either number or character string specifying the model.

Examples

```
Crossover:::getModelNr("Self-adjacency model")==Crossover:::getModelNr(2)
"Self-adjacency model"==Crossover:::getModelNr(2, type="character")
Crossover:::getModelNr("Self-adjacency model")==2
```

plot *Plots information about the search algorithm and its process.*

Description

Plots information about the search algorithm and its process.

Usage

```
## S4 method for signature 'CrossoverSearchResult,missing'  
plot(x, y, type = 1,  
      show.jumps = FALSE)
```

Arguments

x	Result from searchCrossOverDesign.
y	Missing.
type	Type of plot. Number 1 is more colorful, but number 2 perhaps a bit easier to understand.
show.jumps	If TRUE vertical lines will show where the specified jumps occurred.

Details

The x-axis corresponds to the consecutive simulation runs and the y-axis to the design criterion E that depending on the model is either a weighted average of efficiency factors or standardized pairwise variances and described in detail in the vignette of this package. Also see the vignette for a few examples and a discussion what can be derived from this plots.

Value

Returns a ggplot object of the plot.

Author(s)

Kornelius Rohmeyer <rohmeier@small-projects.de>

Examples

```
## Not run:  
x <- searchCrossOverDesign(s=9, p=5, v=4, model=4)  
plot(x)  
  
## End(Not run)  
  
x <- searchCrossOverDesign(s=9, p=5, v=4, model=4, n=c(50,10), jumps=c(10, 10))  
plot(x, show.jumps=TRUE)  
plot(x, type=2)
```

rcd *Create a row column design*

Description

Create a row column design

Usage

```
rcd(X, v, model)
```

Arguments

X cross-over design
v number of treatments
model String or number describing the model. See [getModelNr](#).

Value

A row-column design (as matrix - but not the design matrix).

See Also

[rcdMatrix](#) gives the row-column design matrix.

Examples

```
# TODO
```

rcdMatrix *Create the design matrix for a given row column design*

Description

Create the design matrix for a given row column design

Usage

```
rcdMatrix(X, v, model)
```

Arguments

X row-column design
v number of treatments
model String or number describing the model. See [getModelNr](#).

Value

The design matrix for a row-column design.

See Also

`rcd` gives the row-column design to a given crossover design.

Examples

```
# TODO
```

searchCrossOverDesign *Search for a Cross-Over Design*

Description

Search for a Cross-Over Design

Usage

```
searchCrossOverDesign(s, p, v, model = "Standard additive model",
  eff.factor = 1, v.rep, balance.s = FALSE, balance.p = FALSE,
  verbose = 0, model.param = list(), n = c(5000, 20), jumps = c(5,
  50), start.designs, random.subject = FALSE, contrast,
  correlation = NULL, rho = 0)
```

Arguments

<code>s</code>	Number of sequences.
<code>p</code>	Number of periods.
<code>v</code>	Number of treatments.
<code>model</code>	Model - one of the following: "Standard additive model" (2), "Second-order carry-over effects" (3), "Full set of interactions" (3), "Self-adjacency model" (3), "Placebo model" (2), "No carry-over into self model" (2), "Treatment decay model" (2), "Proportionality model" (1), "No carry-over effects" (0). The number in parentheses is the number of different efficiency factors that can be specified.
<code>eff.factor</code>	Weights for different efficiency factors. (Not used in the moment.)
<code>v.rep</code>	Integer vector specifying how often each treatment should be assigned (sum must equal $s \cdot p$).
<code>balance.s</code>	Boolean specifying whether to allocate the treatments as equally as possible to each sequence (can result in loss of efficiency).
<code>balance.p</code>	Boolean specifying whether to allocate the treatments as equally as possible to each period (can result in loss of efficiency).

verbose	Level of verbosity, a number between 0 and 10. The default verbose=0 does not print any output, while verbose=10 prints any available notes.
model.param	List of additional model specific parameters. In the moment these are ppp, the proportionality parameter for the proportionality model, and placebo, the number of placebo treatments in the placebo model.
n	$n=c(n1, n2)$ with $n1$ the number of hill climbing steps per trial and $n2$ the number of searches from random start matrices.
jumps	To reduce the possibility of the hill-climbing algorithm to get stuck in local extrema long jumps of distance d can be performed all k steps. This can be specified as $long.jumps=c(d, k)$. If $long.jumps$ has only length 1 the default for k is 50. If after $k/2$ hill-climbing steps the old design criterion is not enhanced (or at least reached), the algorithm returns to the design from before the jump.
start.designs	A single design or a list of start designs. If missing or too few start designs are specified (with regard to parameter n which specifies a number of 20 start designs as default) the start designs are generated randomly with the sample function. Alternatively $start.designs="catalog"$ can be used to take start designs from the catalog to which random designs are added till $n2$ start designs are at hand.
random.subject	Should the subject effects be random ($random.subject=TRUE$) or fixed effects ($random.subject=FALSE$).
contrast	Contrast matrix to be optimised. TODO: Example and better explanation for contrast.
correlation	Either a correlation matrix for the random subject effects or one of the following character strings: "equicorrelated", "autoregressive"
rho	Parameter for the correlation if parameter correlation is a character string.

Details

See the vignette of this package for further details.

Value

Returns the design as an integer matrix.

Author(s)

Kornelius Rohmeyer <rohrmeyer@small-projects.de>

References

John, J. A., Russell, K. G., & Whitaker, D. (2004). CrossOver: an algorithm for the construction of efficient cross-over designs. *Statistics in medicine*, 23(17), 2645-2658.

Examples

```
## Not run:  
x <- searchCrossOverDesign(s=9, p=5, v=4, model=4)  
  
jumps <- c(10000, 200) # Do a long jump (10000 changes) every 200 steps  
n <- c(1000, 5) # Do 5 trials with 1000 steps in each trial  
result <- searchCrossOverDesign(s=9, p=5, v=4, model=4, jumps=jumps, n=n)  
plot(result)  
  
## End(Not run)
```

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