Package ‘Crossover’

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Type Package
Title 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
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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 <rohmeyer@small-projects.de>

References


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**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 <rohmeyer@small-projects.de>

References

See the documentation for the data files.

Examples

buildSummaryTable()

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 <rohmeyer@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)

---

Crossover designs

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, federerAtkinson5tb, 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, lewisFletcherMatthews21, lewisFletcherMatthews22, lewisFletcherMatthews23, lewisFletcherMatthews24, lewisFletcherMatthews25, lewisFletcherMatthews26, lewisFletcherMatthews27, lewisFletcherMatthews28, lewisFletcherMatthews29, lewisFletcherMatthews30, lewisFletcherMatthews31, lewisFletcherMatthews32, lewisFletcherMatthews33, lewisFletcherMatthews34, lewisFletcherMatthews35, lewisFletcherMatthews36, lewisFletcherMatthews37, lewisFletcherMatthews38, lewisFletcherMatthews39, lewisFletcherMatthews40, lewisFletcherMatthews41, lewisFletcherMatthews42, lewisFletcherMatthews5, lewisFletcherMatthews6, lewisFletcherMatthews7, lewisFletcherMatthews8, lewisFletcherMatthews9, orthogonalLatinSquare3t, orthogonalLatinSquare4t,

Source


Examples

getDesign("williams4t")

data(fletcher)
ls(pattern="fletcher")
fletcherT10

CrossoverGUI

Graphical User Interface for Crossover Designs

Description

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

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 <rohmeyer@small-projects.de>

Examples

```r
## 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 <rohmeyer@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.efficiency

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.efficiency(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 <rohmeyer@small-projects.de>
References

Examples

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

designNefficiencyHgetdesignHBfletcher1BII
designNefficiencyHgetdesignHBswitchbackTtBIL model=7I

Description
Calculate variances of paramater 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 <rohmeyer@small-projects.de>
getDesign

Extract Design from a CrossoverSearchResult

Description

Extract Design from a CrossoverSearchResult

Usage

```r
## 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 <rohmeyer@small-projects.de>

Examples

```r
# 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 <rohmeyer@small-projects.de>

Examples
```r
## 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=FALSE)
```

rcd

Create a row column design

Description
Create a row column design

Usage
```r
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).
rcdMatrix

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

<table>
<thead>
<tr>
<th></th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>X</td>
<td>row-column design</td>
</tr>
<tr>
<td>v</td>
<td>number of treatments</td>
</tr>
</tbody>
</table>
| 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**

```r
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 = PI)
```

**Arguments**

- `s` Number of sequences.
- `p` Number of periods.
- `v` Number of treatments.
- `model` 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.
- `eff.factor` Weights for different efficiency factors. (Not used in the moment.)
- `v.rep` Integer vector specifying how often each treatment should be assigned (sum must equal s*p).
- `balance.s` Boolean specifying whether to allocate the treatments as equally as possible to each sequence (can result in loss of efficiency).
- `balance.p` 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 placebos, 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 to 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 \( n \) 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 <rohmeyer@small-projects.de>

**References**


**Examples**

```r
## 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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