

# Package ‘Crossover’

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**Type** Package

**Title** Analysis and Search of Crossover Designs

**Version** 0.1-21

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**Description** Generate and analyse crossover designs from combinatorial or search algorithms as well as from literature and a GUI to access them.

**Depends** R (>= 3.0.2), ggplot2

**Imports** MASS, crossdes (>= 1.1-1), xtable, methods, Matrix, rJava (>= 0.8-3), CommonJavaJars (>= 1.0.5), Rcpp (>= 0.10.3), RcppArmadillo (>= 0.2.0), JavaGD, multcomp, stats4, digest

**Suggests** knitr, testthat, nlme

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

**SystemRequirements** Java (>= 5.0)

**License** GPL-2

**VignetteBuilder** knitr

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

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

**RoxygenNote** 7.2.3

**NeedsCompilation** yes

**Repository** CRAN

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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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Lucas, H.L. (1956) Switch-back trials for more than two treatments. *Journal of Dairy Science*, 39, 146–154.

Williams, E.J. (1949) Experimental designs balanced for the estimation of residual effects of treatments. *Australian Journal of Science Res(A)*, 2, 14900168.

## 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.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 <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 <rohrmeyer@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	Eiher "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**

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 $s \cdot p$ ).
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 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)**

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**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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