

Crossover - A search algorithm and GUI for cross-over designs

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1 Introduction

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 (GUI) to find/generate appropriate designs.

The computationally intensive parts of the package, i.e. the search algorithm, is written using the R packages Rcpp and RcppArmadillo (Eddelbuettel and François [2011] and Eddelbuettel and Sanderson [2013]). The GUI is written in Java and uses package rJava (Urbanek [2013]).

1.1 Installation

Once it is installed, whenever you start R you can load the Crossover package by entering `library(Crossover)` into the R Console. The graphical user interface as shown in figure 1 is started with the command `CrossoverGUI()`.

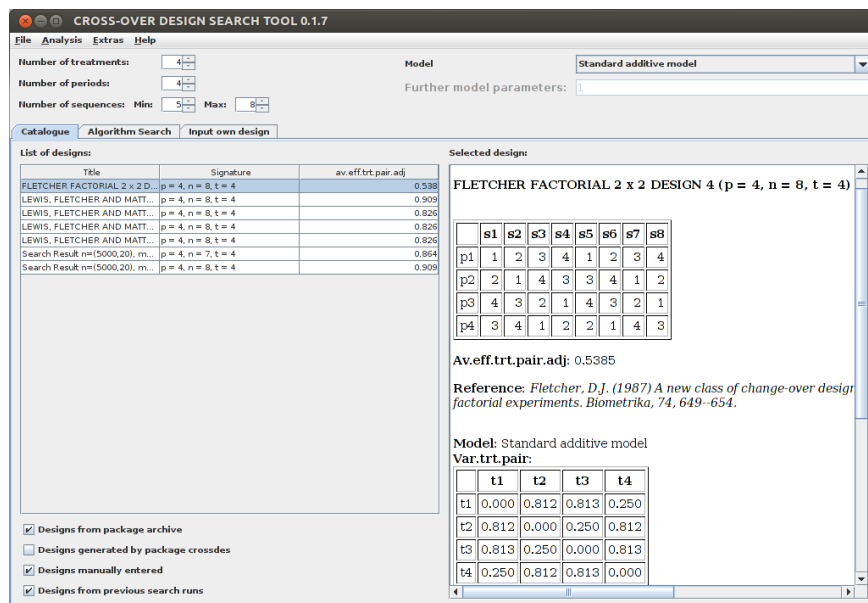


Figure 1: Cross-Over Design GUI.

1.2 GUI Overview

1.2.1 Catalogue

The catalogue, collected and compiled by Professor Byron Jones, contains 241 designs from the following literature: Anderson and Preece [2002], Archdeacon et al. [1980], Atkinson [1966], Balaam [1968], Berenblut [1964], Blaisdell Jr and Raghavarao [1980], Davis and Hall [1969], Federer and Atkinson [1964], Fletcher [1987], Iqbal and Jones [1994], Lewis et al. [1988], Cochran et al. [1941], Patterson and Lucas [1962], Pigeon [1985], Prescott [1999], Quenouille [1953], Russell [1991], Lucas [1956], Williams [1949], Prescott [1994], Bate and Jones [2002]

Depending on the numbers of treatments, periods and range of sequence you specify in the GUI appropriate designs from the catalogue will be shown.¹ Further functions from package `crossdes` (Sailer [2013]) are called to create designs for the specified values if possible.

¹You can get a table referencing all designs and the respective number of treatments, periods and sequences by calling `buildSummaryTable()`.

In figure 1 you can see the following four checkboxes, that allow you to see only specific subsets:

Designs from package archive The previously noted designs from literature are shown.

Designs generated by package crossdes Activating this option will result in short delays when displaying the catalogue, since the crossdes algorithms are called.

Designs manually entered All designs entered on tab "*Input own design*" are shown.

Designs from previous search runs All designs from previous search runs are shown.

1.2.2 Algorithm Search

In figure 2 the preliminary graphical interface for the search algorithm is shown with the following options:

- The drop-down menu for *model* let you specify which model you are interested. These models are described in detail in section 2.
- In case of the placebo or proportionality model you can specify *further model parameters* (namely the number of placebos and the proportionality parameter, respectively).
- Specify the exact *number of sequences*. (The number of treatments and periods is already specified in the top panel of the GUI.)
- Optionally specify the *exact number of treatment assignments*. The GUI default is to let the algorithm figure out good/optimal assignments. But depending on further information (information from theoretical results or treatments more important than the others², etc.) the number of treatment assignments can be specified.
- You can specify that the design should be constructed in a way that *in each sequence/period a treatment occur as evenly as possible*. This restriction will normally decrease the efficiency of the algorithm.
- The GUI default is an all-pair comparison of all treatments with equal weights. Change the *contrast weights* accordingly if you are interested in other contrasts or different weights.
User defined contrasts can be used and a R matrix of n contrasts (i.e. of dimension $n \times v$) will be used.
- Pressing the "*Compute Design*" button will start the search algorithm described in section 3. After a few seconds the result will be shown in the previous empty text area on the right.

1.2.3 Input own design

This tab provides you with the possibility to analyse your own designs easily or use them as starting points for the search algorithm.

2 Models

The package and GUI support the following eight models.

²Different weights of treatment importance should be specified as weighted contrasts. See item *contrasts*.

Figure 2: Panel for algorithmic search of cross-over designs.

2.1 Standard additive model

$$Y_{ijk} = \mu + \pi_j + \tau_{d[i,j]} + \lambda_{d[i,j-1]} + s_{ik} + e_{ijk}$$

with³

μ intercept,

π_j period effect for period j ,

$\tau_{d[i,j]}$ direct treatment effect for treatment $d[i,j]$ in period j of sequence i ,

$\lambda_{d[i,j-1]}$ first-order carry-over effect (0 for $j-1=0$),

s_{ik} k th subject effect on sequence i ,

e_{ijk} random error with zero mean and variance σ^2 .

which we can write as

$$E(Y) = \mu + X \begin{pmatrix} \tau \\ \lambda \end{pmatrix} + Z \begin{pmatrix} \pi \\ s \end{pmatrix}$$

with X and Z called the *treatment* and *block design matrices*, respectively.

We call H a *link matrix* if $X = X_r H$ were X_r is the design matrix for the row-column design. The rows of the link matrix specify all possible parameter combinations. Therefore H has as many columns as there are parameters and in the row-column-setting i parameter j is included h_{ij} times.

```
# Design:
design <- rbind(c(3,2,1),
              c(2,1,3),
              c(1,2,3),
              c(3,2,1))
design
```

³cf. Jones and Kenward [2003], page 8

```

##      [,1] [,2] [,3]
## [1,]   3   2   1
## [2,]   2   1   3
## [3,]   1   2   3
## [4,]   3   2   1

v <- 3 # number of treatments
# Link matrix:
H <- Crossover:::linkMatrix(model="Standard additive model", v)
H

##      [,1] [,2] [,3] [,4] [,5] [,6]
## [1,]   1   0   0   0   0   0
## [2,]   0   1   0   0   0   0
## [3,]   0   0   1   0   0   0
## [4,]   1   0   0   1   0   0
## [5,]   0   1   0   1   0   0
## [6,]   0   0   1   1   0   0
## [7,]   1   0   0   0   1   0
## [8,]   0   1   0   0   1   0
## [9,]   0   0   1   0   1   0
## [10,]  1   0   0   0   0   1
## [11,]  0   1   0   0   0   1
## [12,]  0   0   1   0   0   1

# Row-Column-Design: (cf. John et al. 2004, Table II and page 2649f.)
rcDesign <- Crossover:::rcd(design, v=v, model=1)
rcDesign

##      [,1] [,2] [,3]
## [1,]   3   2   1
## [2,]  11   7   6
## [3,]   7   5  12
## [4,]   6   8  10

# Design Matrix of Row-Column Design:
Xr <- Crossover:::rcdMatrix(rcDesign, v, model=1)
Xr

##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12]
## [1,]   0   0   1   0   0   0   0   0   0   0   0   0
## [2,]   0   1   0   0   0   0   0   0   0   0   0   0
## [3,]   1   0   0   0   0   0   0   0   0   0   0   0
## [4,]   0   0   0   0   0   0   0   0   0   0   1   0
## [5,]   0   0   0   0   0   0   1   0   0   0   0   0
## [6,]   0   0   0   0   0   1   0   0   0   0   0   0
## [7,]   0   0   0   0   0   0   1   0   0   0   0   0
## [8,]   0   0   0   0   1   0   0   0   0   0   0   0
## [9,]   0   0   0   0   0   0   0   0   0   0   0   1

```

```
## [10,] 0 0 0 0 0 1 0 0 0 0 0 0
## [11,] 0 0 0 0 0 0 0 1 0 0 0 0
## [12,] 0 0 0 0 0 0 0 0 0 1 0 0

# Design Matrix of Cross-Over Design:
X <- Xr %*% H
X

##      [,1] [,2] [,3] [,4] [,5] [,6]
## [1,] 0 0 1 0 0 0
## [2,] 0 1 0 0 0 0
## [3,] 1 0 0 0 0 0
## [4,] 0 1 0 0 0 1
## [5,] 1 0 0 0 1 0
## [6,] 0 0 1 1 0 0
## [7,] 1 0 0 0 1 0
## [8,] 0 1 0 1 0 0
## [9,] 0 0 1 0 0 1
## [10,] 0 0 1 1 0 0
## [11,] 0 1 0 0 1 0
## [12,] 1 0 0 0 0 1
```

2.2 Full set of interactions

This model has further interaction parameters γ_{ij} and a design matrix X with $2 * v + v^2$ columns:⁴

$$E(Y) = \mu + X \begin{pmatrix} \tau \\ \lambda \\ \gamma \end{pmatrix} + Z \begin{pmatrix} \pi \\ s \end{pmatrix}$$

```
H <- Crossover:::linkMatrix(model="Full set of interactions", v)
H

##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14] [,15]
## [1,] 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0
## [2,] 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0
## [3,] 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0
## [4,] 1 0 0 1 0 0 1 0 0 0 0 0 0 0 0
## [5,] 0 1 0 1 0 0 0 0 0 1 0 0 0 0 0
## [6,] 0 0 1 1 0 0 0 0 0 0 0 0 1 0 0
## [7,] 1 0 0 0 1 0 0 1 0 0 0 0 0 0 0
## [8,] 0 1 0 0 1 0 0 0 0 0 1 0 0 0 0
## [9,] 0 0 1 0 1 0 0 0 0 0 0 0 0 1 0
## [10,] 1 0 0 0 0 1 0 0 1 0 0 0 0 0 0
## [11,] 0 1 0 0 0 1 0 0 0 0 0 1 0 0 0
## [12,] 0 0 1 0 0 1 0 0 0 0 0 0 0 0 1
```

⁴Personally I think some of the overspecified parameters should be dropped, for example γ_{ii} - but I'll take a look at this later.

```

# Design Matrix of Cross-Over Design:
X <- Xr %*% H
X
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14] [,15]
## [1,]    0    0    1    0    0    0    0    0    0    0    0    0    0    0    0
## [2,]    0    1    0    0    0    0    0    0    0    0    0    0    0    0    0
## [3,]    1    0    0    0    0    0    0    0    0    0    0    0    0    0    0
## [4,]    0    1    0    0    0    1    0    0    0    0    0    1    0    0    0
## [5,]    1    0    0    0    1    0    0    1    0    0    0    0    0    0    0
## [6,]    0    0    1    1    0    0    0    0    0    0    0    0    1    0    0
## [7,]    1    0    0    0    1    0    0    1    0    0    0    0    0    0    0
## [8,]    0    1    0    1    0    0    0    0    0    1    0    0    0    0    0
## [9,]    0    0    1    0    0    1    0    0    0    0    0    0    0    0    1
## [10,]   0    0    1    1    0    0    0    0    0    0    0    0    1    0    0
## [11,]   0    1    0    0    1    0    0    0    0    0    1    0    0    0    0
## [12,]   1    0    0    0    0    1    0    0    1    0    0    0    0    0    0

```

2.3 Self-adjacency model

In the *self-adjacency model* λ_i is replaced by φ_i in case of carry-over into itself. The case $\varphi = 0$ represents the *no carry-over into self model*.

$$E(Y) = \mu + X \begin{pmatrix} \tau \\ \varphi \end{pmatrix} + Z \begin{pmatrix} \pi \\ s \end{pmatrix}$$

```

H <- Crossover:::linkMatrix(model="Self-adjacency model", v)
H
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9]
## [1,]    1    0    0    0    0    0    0    0    0
## [2,]    0    1    0    0    0    0    0    0    0
## [3,]    0    0    1    0    0    0    0    0    0
## [4,]    1    0    0    0    0    0    1    0    0
## [5,]    0    1    0    1    0    0    0    0    0
## [6,]    0    0    1    1    0    0    0    0    0
## [7,]    1    0    0    0    1    0    0    0    0
## [8,]    0    1    0    0    0    0    0    1    0
## [9,]    0    0    1    0    1    0    0    0    0
## [10,]   1    0    0    0    0    1    0    0    0
## [11,]   0    1    0    0    0    1    0    0    0
## [12,]   0    0    1    0    0    0    0    0    1

# Design Matrix of Cross-Over Design:
X <- Xr %*% H
X
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9]

```

```
## [1,] 0 0 1 0 0 0 0 0 0
## [2,] 0 1 0 0 0 0 0 0 0
## [3,] 1 0 0 0 0 0 0 0 0
## [4,] 0 1 0 0 0 1 0 0 0
## [5,] 1 0 0 0 1 0 0 0 0
## [6,] 0 0 1 1 0 0 0 0 0
## [7,] 1 0 0 0 1 0 0 0 0
## [8,] 0 1 0 1 0 0 0 0 0
## [9,] 0 0 1 0 0 0 0 0 1
## [10,] 0 0 1 1 0 0 0 0 0
## [11,] 0 1 0 0 0 0 0 1 0
## [12,] 1 0 0 0 0 1 0 0 0
```

2.4 Placebo model

In the placebo model there are no carry-over effects for the placebo treatment(s).

$$E(Y) = \mu + X\left(\begin{smallmatrix} \tau \\ \lambda \end{smallmatrix}\right) + Z\left(\begin{smallmatrix} \pi \\ s \end{smallmatrix}\right)$$

```
# Link matrix:
H <- Crossover:::linkMatrix(model="Placebo model", v, placebos=1)
H
##      [,1] [,2] [,3] [,4] [,5] [,6]
## [1,] 1 0 0 0 0 0
## [2,] 0 1 0 0 0 0
## [3,] 0 0 1 0 0 0
## [4,] 1 0 0 0 0 0
## [5,] 0 1 0 0 0 0
## [6,] 0 0 1 0 0 0
## [7,] 1 0 0 0 1 0
## [8,] 0 1 0 0 1 0
## [9,] 0 0 1 0 1 0
## [10,] 1 0 0 0 0 1
## [11,] 0 1 0 0 0 1
## [12,] 0 0 1 0 0 1

# Design Matrix of Cross-Over Design:
X <- Xr %*% H
X
##      [,1] [,2] [,3] [,4] [,5] [,6]
## [1,] 0 0 1 0 0 0
## [2,] 0 1 0 0 0 0
## [3,] 1 0 0 0 0 0
## [4,] 0 1 0 0 0 1
## [5,] 1 0 0 0 1 0
```



```
## [6,] 0 0 1 0 0 0
## [7,] 1 0 0 0 1 0
## [8,] 0 1 0 0 0 0
## [9,] 0 0 1 0 0 1
## [10,] 0 0 1 0 0 0
## [11,] 0 1 0 0 1 0
## [12,] 1 0 0 0 0 1
```

2.5 No carry-over into self model

This model differs from the standard additive model in the assumption that in the *no carry-over into self model* no carry-over effect occurs if current and previous treatment are the same.

$$E(Y) = \mu + X\left(\begin{smallmatrix} \tau \\ \lambda \end{smallmatrix}\right) + Z\left(\begin{smallmatrix} \pi \\ s \end{smallmatrix}\right)$$

```
H <- Crossover:::linkMatrix(model="No carry-over into self model", v)
H
##      [,1] [,2] [,3] [,4] [,5] [,6]
## [1,]  1  0  0  0  0  0
## [2,]  0  1  0  0  0  0
## [3,]  0  0  1  0  0  0
## [4,]  1  0  0  0  0  0
## [5,]  0  1  0  1  0  0
## [6,]  0  0  1  1  0  0
## [7,]  1  0  0  0  1  0
## [8,]  0  1  0  0  0  0
## [9,]  0  0  1  0  1  0
## [10,] 1  0  0  0  0  1
## [11,] 0  1  0  0  0  1
## [12,] 0  0  1  0  0  0

# Design Matrix of Cross-Over Design:
X <- Xr %*% H
X
##      [,1] [,2] [,3] [,4] [,5] [,6]
## [1,]  0  0  1  0  0  0
## [2,]  0  1  0  0  0  0
## [3,]  1  0  0  0  0  0
## [4,]  0  1  0  0  0  1
## [5,]  1  0  0  0  1  0
## [6,]  0  0  1  1  0  0
## [7,]  1  0  0  0  1  0
## [8,]  0  1  0  1  0  0
## [9,]  0  0  1  0  0  0
## [10,] 0  0  1  1  0  0
```

```
## [11,] 0 1 0 0 0 0
## [12,] 1 0 0 0 0 1
```

2.6 Treatment decay model

In contrast to the no carry-over into self model in the *treatment decay model* we assume there are only (negative) carry-over effects if the current and previous treatment are the same.

$$E(Y) = \mu + X\left(\begin{smallmatrix} \tau \\ \lambda \end{smallmatrix}\right) + Z\left(\begin{smallmatrix} \pi \\ s \end{smallmatrix}\right)$$

```
H <- Crossover:::linkMatrix(model="Treatment decay model", v)
```

```
H
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6]
## [1,]  1  0  0  0  0  0
## [2,]  0  1  0  0  0  0
## [3,]  0  0  1  0  0  0
## [4,]  1  0  0 -1  0  0
## [5,]  0  1  0  0  0  0
## [6,]  0  0  1  0  0  0
## [7,]  1  0  0  0  0  0
## [8,]  0  1  0  0 -1  0
## [9,]  0  0  1  0  0  0
## [10,] 1  0  0  0  0  0
## [11,] 0  1  0  0  0  0
## [12,] 0  0  1  0  0 -1
```

```
# Design Matrix of Cross-Over Design:
```

```
X <- Xr %*% H
```

```
X
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6]
## [1,]  0  0  1  0  0  0
## [2,]  0  1  0  0  0  0
## [3,]  1  0  0  0  0  0
## [4,]  0  1  0  0  0  0
## [5,]  1  0  0  0  0  0
## [6,]  0  0  1  0  0  0
## [7,]  1  0  0  0  0  0
## [8,]  0  1  0  0  0  0
## [9,]  0  0  1  0  0 -1
## [10,] 0  0  1  0  0  0
## [11,] 0  1  0  0 -1  0
## [12,] 1  0  0  0  0  0
```

2.7 Proportionality model

For the proportionality model we have no separate carry-over effects, but assume for period $i > 1$ an additive proportion p of the effect $\tau_{d(i-1,j)}$ from the previous treatment $d(i-1,j)$. This model is non-linear in p , therefore we assume p is known.

$$E(Y) = \mu + X_p\tau + Z\left(\frac{\pi}{s}\right)$$

```
H <- Crossover:::linkMatrix(model="Proportionality model", v)
H
##           [,1] [,2] [,3]
## [1,]  1.0  0.0  0.0
## [2,]  0.0  1.0  0.0
## [3,]  0.0  0.0  1.0
## [4,]  1.5  0.0  0.0
## [5,]  0.5  1.0  0.0
## [6,]  0.5  0.0  1.0
## [7,]  1.0  0.5  0.0
## [8,]  0.0  1.5  0.0
## [9,]  0.0  0.5  1.0
## [10,] 1.0  0.0  0.5
## [11,] 0.0  1.0  0.5
## [12,] 0.0  0.0  1.5

# Design Matrix of Cross-Over Design:
X <- Xr %*% H
X
##           [,1] [,2] [,3]
## [1,]  0.0  0.0  1.0
## [2,]  0.0  1.0  0.0
## [3,]  1.0  0.0  0.0
## [4,]  0.0  1.0  0.5
## [5,]  1.0  0.5  0.0
## [6,]  0.5  0.0  1.0
## [7,]  1.0  0.5  0.0
## [8,]  0.5  1.0  0.0
## [9,]  0.0  0.0  1.5
## [10,] 0.5  0.0  1.0
## [11,] 0.0  1.5  0.0
## [12,] 1.0  0.0  0.5
```

2.8 Second-order carry-over effects

In the model with second-order carry-over effects we do have another vector λ_2 of carry-over effects:

$$E(Y) = \mu + X \begin{pmatrix} \tau \\ \lambda_1 \\ \lambda_2 \end{pmatrix} + Z \begin{pmatrix} \pi \\ s \end{pmatrix}$$

Therefore the link matrix has $3 * v$ columns.

```
# Link matrix:
H <- Crossover:::linkMatrix(model="Second-order carry-over effects", v)
H
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9]
## [1,]  1  0  0  0  0  0  0  0  0
## [2,]  0  1  0  0  0  0  0  0  0
## [3,]  0  0  1  0  0  0  0  0  0
## [4,]  1  0  0  1  0  0  0  0  0
## [5,]  0  1  0  1  0  0  0  0  0
## [6,]  0  0  1  1  0  0  0  0  0
## [7,]  1  0  0  0  1  0  0  0  0
## [8,]  0  1  0  0  1  0  0  0  0
## [9,]  0  0  1  0  1  0  0  0  0
## [10,] 1  0  0  0  0  1  0  0  0
## [11,] 0  1  0  0  0  1  0  0  0
## [12,] 0  0  1  0  0  1  0  0  0
## [13,] 1  0  0  1  0  0  1  0  0
## [14,] 0  1  0  1  0  0  1  0  0
## [15,] 0  0  1  1  0  0  1  0  0
## [16,] 1  0  0  0  1  0  1  0  0
## [17,] 0  1  0  0  1  0  1  0  0
## [18,] 0  0  1  0  1  0  1  0  0
## [19,] 1  0  0  0  0  1  1  0  0
## [20,] 0  1  0  0  0  1  1  0  0
## [21,] 0  0  1  0  0  1  1  0  0
## [22,] 1  0  0  1  0  0  0  1  0
## [23,] 0  1  0  1  0  0  0  1  0
## [24,] 0  0  1  1  0  0  0  1  0
## [25,] 1  0  0  0  1  0  0  1  0
## [26,] 0  1  0  0  1  0  0  1  0
## [27,] 0  0  1  0  1  0  0  1  0
## [28,] 1  0  0  0  0  1  0  1  0
## [29,] 0  1  0  0  0  1  0  1  0
## [30,] 0  0  1  0  0  1  0  1  0
## [31,] 1  0  0  1  0  0  0  0  1
## [32,] 0  1  0  1  0  0  0  0  1
## [33,] 0  0  1  1  0  0  0  0  1
## [34,] 1  0  0  0  1  0  0  0  1
## [35,] 0  1  0  0  1  0  0  0  1
## [36,] 0  0  1  0  1  0  0  0  1
## [37,] 1  0  0  0  0  1  0  0  1
## [38,] 0  1  0  0  0  1  0  0  1
## [39,] 0  0  1  0  0  1  0  0  1
```

```
# Row-Column-Design: (cf. John et al. 2004, Table II and page 2649f.)
```

```
rcDesign <- Crossover:::rcd(design, v=v, model=8)
```

```
rcDesign
```

```
##      [,1] [,2] [,3]
```

```
## [1,]    3    2    1
```

```
## [2,]   11    7    6
```

```
## [3,]   34   23   21
```

```
## [4,]   24   17   37
```

```
# Design Matrix of Row-Column Design:
```

```
Xr <- Crossover:::rcdMatrix(rcDesign, v, model=8)
```

```
Xr
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14] [,15] [,16] [,17]
```

```
## [1,]    0    0    1    0    0    0    0    0    0    0    0    0    0    0    0    0    0
```

```
## [2,]    0    1    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
```

```
## [3,]    1    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
```

```
## [4,]    0    0    0    0    0    0    0    0    0    0    1    0    0    0    0    0    0
```

```
## [5,]    0    0    0    0    0    0    1    0    0    0    0    0    0    0    0    0    0
```

```
## [6,]    0    0    0    0    0    1    0    0    0    0    0    0    0    0    0    0    0
```

```
## [7,]    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
```

```
## [8,]    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
```

```
## [9,]    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
```

```
## [10,]   0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
```

```
## [11,]   0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    1
```

```
## [12,]   0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
```

```
##      [,22] [,23] [,24] [,25] [,26] [,27] [,28] [,29] [,30] [,31] [,32] [,33] [,34] [,35] [,36] [,37]
```

```
## [1,]    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
```

```
## [2,]    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
```

```
## [3,]    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
```

```
## [4,]    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
```

```
## [5,]    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
```

```
## [6,]    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
```

```
## [7,]    0    0    0    0    0    0    0    0    0    0    0    0    0    1    0    0
```

```
## [8,]    0    1    0    0    0    0    0    0    0    0    0    0    0    0    0    0
```

```
## [9,]    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
```

```
## [10,]   0    0    1    0    0    0    0    0    0    0    0    0    0    0    0    0
```

```
## [11,]   0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
```

```
## [12,]   0    0    0    0    0    0    0    0    0    0    0    0    0    0    0    0
```

```
# Design Matrix of Cross-Over Design:
```

```
X <- Xr %*% H
```

```
X
```

```
##      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9]
```

```
## [1,]    0    0    1    0    0    0    0    0    0
```

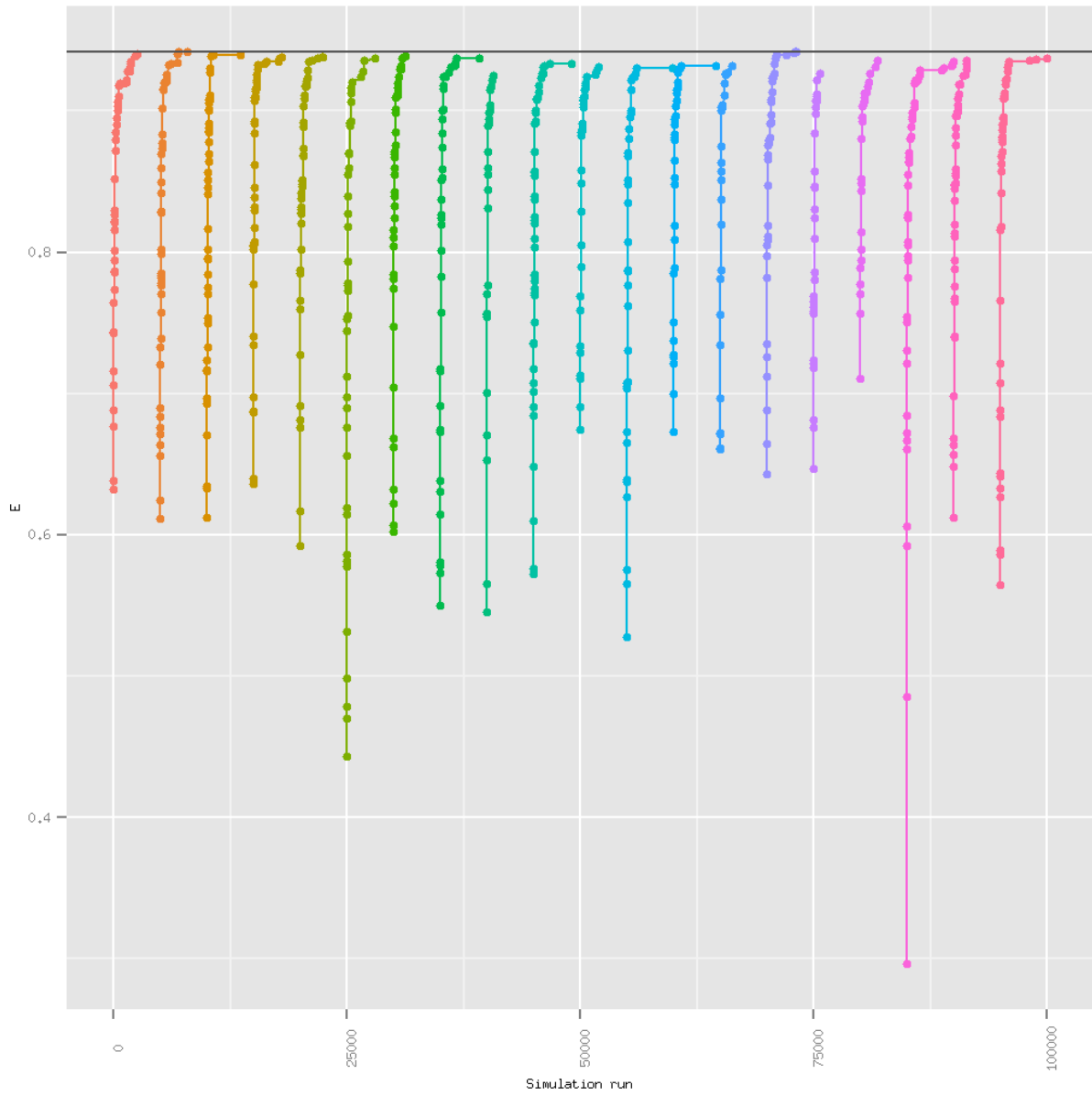
```
## [2,]    0    1    0    0    0    0    0    0    0
```

```
## [3,] 1 0 0 0 0 0 0 0 0 0
## [4,] 0 1 0 0 0 0 1 0 0 0
## [5,] 1 0 0 0 1 0 0 0 0 0
## [6,] 0 0 1 1 0 0 0 0 0 0
## [7,] 1 0 0 0 1 0 0 0 0 1
## [8,] 0 1 0 1 0 0 0 0 1 0
## [9,] 0 0 1 0 0 0 1 1 0 0
## [10,] 0 0 1 1 0 0 0 0 1 0
## [11,] 0 1 0 0 1 0 1 0 0 0
## [12,] 1 0 0 0 0 0 1 0 0 1
```

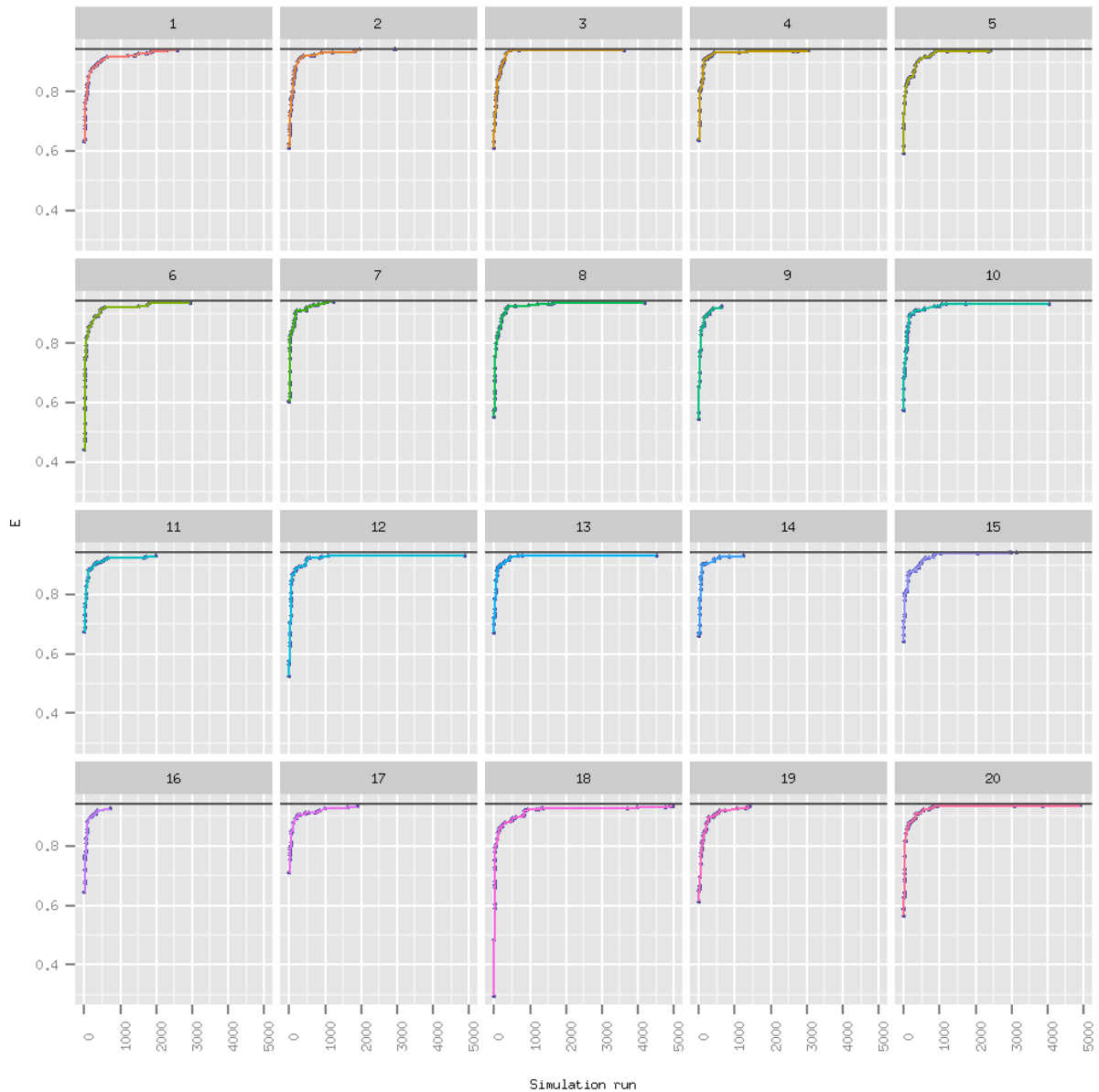
3 Search strategy

Monte-Carlo search for first candidates, followed by parallel hill climbing search, extended by long jumps. In the following graphic we see 100.000 design evaluations (that take less than 7 seconds on my computer), consisting out of 20 hill climbing search *runs* from 20 different designs as starting point which were selected by a Monte-Carlo search. We can see that 10 out of the 20 search runs were not able to achieve the efficiency the other 10 achieved. We can see, that there were most likely at least four local maxima the hill climbing search found and got stuck:

```
set.seed(42)
x <- searchCrossOverDesign(s=9, p=5, v=4, model=4)
plot(x)
```



```
plot(x, type=2)
```



There are different approaches to calculate the Information matrix A_r of the row-column design. In the following code fragment we compare the two different approaches:

$$A_r = r^\delta - \frac{1}{s}N_p N_p' - \frac{1}{p}N_s N_s' + \frac{1}{ps}rr'$$

and

$$A_r = X_r'(I - P_z)X_r.$$

For details (what are N_p , N_s , P_z , etc.) see John and Williams [1995] and John et al. [2004].

```
attach(loadNamespace("Crossover"), name="namespace:Crossover", pos=3, warn.conflicts=FALSE)

s <- 6
p <- 3
v <- 3
model <- 1
data(williams)
design <- williams3t
```



```

rcDesign <- rcd(design, v, model)
# JRW, p 2650, first equation on that page, without number
Ar <- infMatrix(rcDesign, v, model)
Xr <- rcdMatrix(rcDesign, v, model)
# JRW, p 2650, second equation on that page, number 11
Ar2 <- t(Xr) %*% (diag(s*p)-Crossover:::getPZ(s,p)) %*% Xr
max(abs(Ar-Ar2))

## [1] 6.661e-16

fXr <- cbind(Xr, getZ(s,p))
Ar3 <- t(fXr) %*% fXr
ginv(Ar3)[1:12,1:12]-ginv(Ar2)

##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]      [,7]      [,8]
## [1,]  8.781e-03  8.781e-03  8.781e-03  1.988e-16 -1.636e-03 -1.636e-03 -1.636e-03  7.277e-19 -1.63
## [2,]  8.781e-03  8.781e-03  8.781e-03  1.247e-16 -1.636e-03 -1.636e-03 -1.636e-03 -2.742e-16 -1.63
## [3,]  8.781e-03  8.781e-03  8.781e-03 -3.317e-16 -1.636e-03 -1.636e-03 -1.636e-03  2.735e-16 -1.63
## [4,]  2.204e-17 -2.691e-16  2.569e-16  1.659e-31  3.291e-16 -3.190e-16 -1.639e-16  7.409e-32  2.5
## [5,] -1.636e-03 -1.636e-03 -1.636e-03  4.232e-16  3.573e-03  3.573e-03  3.573e-03 -5.657e-17  3.57
## [6,] -1.636e-03 -1.636e-03 -1.636e-03 -4.185e-16  3.573e-03  3.573e-03  3.573e-03  2.413e-17  3.57
## [7,] -1.636e-03 -1.636e-03 -1.636e-03 -4.177e-16  3.573e-03  3.573e-03  3.573e-03  2.360e-16  3.57
## [8,]  1.396e-17 -1.009e-16  8.692e-17 -1.578e-32  1.206e-16 -8.094e-17  2.935e-17  8.808e-32 -1.1
## [9,] -1.636e-03 -1.636e-03 -1.636e-03  7.737e-16  3.573e-03  3.573e-03  3.573e-03 -2.168e-16  3.57
## [10,] -1.636e-03 -1.636e-03 -1.636e-03  2.207e-16  3.573e-03  3.573e-03  3.573e-03 -2.368e-16  3.57
## [11,] -1.636e-03 -1.636e-03 -1.636e-03 -5.684e-16  3.573e-03  3.573e-03  3.573e-03  2.501e-16  3.57
## [12,] -2.235e-19 -7.336e-17  7.359e-17  3.827e-31  3.676e-16 -3.392e-16 -3.443e-16 -1.869e-31  2.65
##           [,12]
## [1,]  8.043e-20
## [2,]  5.077e-17
## [3,] -5.085e-17
## [4,] -1.096e-31
## [5,] -1.185e-16
## [6,]  1.206e-16
## [7,]  6.287e-17
## [8,] -3.226e-32
## [9,] -1.585e-18
## [10,] -6.325e-17
## [11,] -7.020e-20
## [12,] -1.026e-31

H <- linkMatrix(model=model,v=v)
fX <- cbind(Xr%*%H, getZ(s,p))
A1 <- t(fX) %*% fX
A2 <- t(H)%*%Ar%*%H

# While A1 and A2 differ:

```

```

ginv(A1)[1:6,1:6]

##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
## [1,]  0.14611 -0.06222 -0.06222  0.08535 -0.03965 -0.03965
## [2,] -0.06222  0.14611 -0.06222 -0.03965  0.08535 -0.03965
## [3,] -0.06222 -0.06222  0.14611 -0.03965 -0.03965  0.08535
## [4,]  0.08535 -0.03965 -0.03965  0.25831 -0.11669 -0.11669
## [5,] -0.03965  0.08535 -0.03965 -0.11669  0.25831 -0.11669
## [6,] -0.03965 -0.03965  0.08535 -0.11669 -0.11669  0.25831

ginv(A2)

##           [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
## [1,]  0.13889 -0.06944 -0.06944  0.08333 -0.04167 -0.04167
## [2,] -0.06944  0.13889 -0.06944 -0.04167  0.08333 -0.04167
## [3,] -0.06944 -0.06944  0.13889 -0.04167 -0.04167  0.08333
## [4,]  0.08333 -0.04167 -0.04167  0.25000 -0.12500 -0.12500
## [5,] -0.04167  0.08333 -0.04167 -0.12500  0.25000 -0.12500
## [6,] -0.04167 -0.04167  0.08333 -0.12500 -0.12500  0.25000

max(abs(ginv(A1)[1:6,1:6]-ginv(A2)))

## [1] 0.008314

# The variances for the estimable contrasts are the same:

C <- matrix(0,nrow=15,ncol=1)
C[1:2,1] <- c(-1,1)
tdiff1 <- t(C)%*%ginv(A1)%*%C
tdiff2 <- t(C[1:6,])%*%ginv(A2)%*%C[1:6,]
tdiff1 - tdiff2

##           [,1]
## [1,] 1.665e-16

C <- matrix(0,nrow=6,ncol=1)
C[1:2,1] <- c(-1,1)
tdiff1 <- t(C)%*%ginv(A1)[1:6,1:6]%*%C
tdiff2 <- t(C)%*%ginv(A2)%*%C
tdiff1 - tdiff2

##           [,1]
## [1,] 1.665e-16

```

Definition 3.1 (Efficiency). If the difference of two treatments, each replicated r times, is estimated in an *ideal design* with residual variance σ^2 , the variance of the estimated difference $\bar{y}_A - \bar{y}_B$ is

$$V_I = \frac{2\sigma^2}{r}.$$

In a cross-over design the variance of a parameter estimates for A and B are given by the corresponding elements $\sigma^2 x_A$ and $\sigma^2 x_B$ of

$$\sigma^2(X^T X)^{-1}$$

with X the crossover design matrix. The variance of the difference is $\sigma^2(x_A + x_B - 2 * x_{AB})$ where x_{AB} is the element of $X^T X$ specifying the covariance of the two treatment parameter estimates. The efficiency is

$$E := \frac{V_I}{V_C} = \frac{2}{rx} \in [0, 1].$$

4 Random Subject Effects Model

See Jones and Kenward [2003], 5.3, page 213ff. The model stays the same

$$Y_{ijk} = \mu + \pi_j + \tau_{d[i,j]} + \lambda_{d[i,j-1]} + s_{ik} + e_{ijk},$$

but we also assume that the subject effects follow a normal distribution: $s_{ik} \sim \mathcal{N}(0, \sigma_s^2)$.

In matrix notation we have

$$Y = X\beta + Z\gamma + \varepsilon$$

with X and Z the fixed and random effects design matrices⁵, $\varepsilon \sim \mathcal{N}(0, \Sigma)$ and $\gamma \sim \mathcal{N}(0, D)$. Then⁶

$$\text{Var}(Y) = ZDZ^T + \Sigma.$$

For known $V := \text{Var}(Y) = ZDZ^T + \Sigma$ the MLE and BLUE is given by

$$\hat{\beta} = (X^t V^{-1} X)^{-1} X^t V^{-1} Y.$$

⁵Note that X and Z are different from the ...

⁶See for example [Lee et al., 2006, chapter 5].

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Table of Symbols

Sets

\mathbb{R}	set of real numbers
\mathbb{N}_0	set of natural numbers (including 0)
$\mathfrak{Pot}(X)$	power set of set X , i.e. the set of all subsets of X

Variables

v	number of treatments
p	number of periods
s	number of sequences
μ	intercept
π_j	period effect for period j
$\tau_{d[i,j]}$	direct treatment effect for treatment $d[i, j]$ in period j of sequence i
$\lambda_{d[i,j-1]}$	first-order carry-over effect (0 for $j-1=0$)
s_{ik}	k th subject effect on sequence i
e_{ijk}	random error with zero mean and variance σ^2

Functions

X'	transpose of matrix X
X^+	Moore-Penrose pseudoinverse of X
$\langle \cdot, \cdot \rangle$	standard direct product $\langle x, y \rangle = \sum_{j=1}^n x_j \cdot y_j$ for $x, y \in \mathbb{R}^n$
id_X	identity on X , i.e. $\text{id}_X : X \rightarrow X, x \mapsto x$

Other Symbols

$\mathcal{N}(\mu, \sigma^2)$	Normal distribution with mean μ and variance σ^2 .
$\mathcal{N}(\mu, \Sigma)$	Multivariate normal distribution with mean μ and covariance matrix Σ .