
Notes on the use of dae for design

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1 Introduction

The R ([R Core Team, 2024](#)) package **dae** ([Brien, 2024b](#)) provides functions useful in the design and anova of experiments. This document describes how to use some of them to produce layouts for experiments and to check some of their properties. [Brien et al. \(2023\)](#) provide a general discussion of a paradigm for designing experiments that utilizes **dae** functions.

1.1 Functions to be used

The functions in **dae** fall into the following categories and those that will be covered in this document are listed and described:

1. Data

BIBDWheat.dat Data for a balanced incomplete block experiment.

Casuarina.dat Data for an experiment with rows and columns from [Williams et al. \(2002\)](#).

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

Exp249.mplot.des Systematic, main-plot design for an experiment to be run in a greenhouse.

Fac4Proc.dat Data for a 2^4 factorial experiment.

LatticeSquare_t49.des A Lattice square design for 49 treatments.

McIntyreTMV.dat The design and data from [McIntyre \(1955\)](#) two-phase experiment.

Oats.dat Data for an experiment to investigate nitrogen response of 3 oats varieties from [Yates \(1937\)](#).

Sensory3Phase.dat Data for the three-phase sensory evaluation experiment in [Brien and Payne \(1999\)](#).

Sensory3PhaseShort.dat Data for the three-phase sensory evaluation experiment in [Brien and Payne \(1999\)](#), but with short factor names.

SPLGrass.dat Data for an experiment to investigate the effects of grazing patterns on pasture composition.

2. Factor manipulation functions

fac.gen: Generate all combinations of several factors and, optionally, replicate them.

fac.recast: Recasts a factor by modifying the values in the factor vector and/or the levels attribute, possibly combining some levels into a single level.

fac.uselogical: Forms a two-level factor from a logical object.

fac.combine: Combines several factors into one.

fac.divide: Divides a factor into several separate factors.

fac.multinested: Creates several factors, one for each level of a nesting.fac and each of whose values are either generated within those of the level of nesting.fac or using the values of a nested.fac.

fac.nested: Creates a factor, the nested factor, whose values are generated within those of a nesting factor.

3. Design functions

designAnatomy: Given the layout for a design, obtain its anatomy via the canonical analysis of its projectors to show the confounding and aliasing inherent in the design.

designLatinSqrSys: Generate a systematic plan for a Latin Square design.

designBlocksGGPlot: Adds block boundaries to a plot produced by designGGPlot.

designGGPlot: A graphical representation of an experimental design based on labels stored in a `data.frame` using `ggplot2`.

designRandomize: Takes a systematic design and randomizes it according to the nesting (and crossing) relationships between the recipient(unit) factors for the randomization.

no.reps: Computes the number of replicates for an experiment.

summary.pcanon: Summarizes the anatomy of a design, being the decomposition of the sample space based on its canonical analysis, as produced by `designAnatomy`. The table produced includes the degrees of freedom and summary statistics of the canonical efficiency factors.

efficiencies.pcanon: Extracts the canonical efficiency factors from a `pcanon.object` produced by `designAnatomy`.

4. ANOVA functions

5. Matrix functions

6. Projector and canonical efficiency functions

efficiencies.pcanon: Produces a list containing the canonical efficiency factors for the joint decomposition of two or more sets of projectors (Brien and Bailey, 2009) obtained using `designAnatomy`.

7. Miscellaneous functions.

Documentation for these functions is available from the user manual via `vignette("dae-manual", package="dae")` and there are some notes that show how to use some of them in `vignette("DesignNotes", package="dae")`.

1.2 The paradigm

Fundamental to the approach in this document, and to using the functions described, is that a single allocation involves allocating a set of *allocated* factors to a set of *recipient* factors. In many designs, this allocation is achieved by randomization. However, sometimes there is systematic allocation or restricted allocation. Brien et al. (2023) provide a detailed discussion of the underlying paradigm.

1.3 Notation used for mixed models

The general form for a mixed model is:

$$\mathbf{Y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u} + \mathbf{e},$$

where $\boldsymbol{\beta}$ is the vector of fixed parameters, \mathbf{u} is the vector of random effects, and \mathbf{e} is the vector of residuals corresponding to each observation. The matrices \mathbf{X} and \mathbf{Z} are the design matrices for the fixed and random effects, respectively. Generally, \mathbf{X} and $\boldsymbol{\beta}$ are conformably partitioned so that there is a separate submatrix and subvector for each fixed term. Similarly, \mathbf{Z} and \mathbf{u} are conformably partitioned according to the random terms.

A mixed model is expressed in symbolic form by list of the fixed terms, followed by a '|', and then a list of the random terms. Terms contributing to the residuals are underlined.

2 Single-allocation orthogonal design in R

This class of experiments covers the orthogonal standard or textbook experiments and these experiments must be single phase because they involve a single randomization, in the sense that the randomization can be achieved with a single permutation. Hence there will be two sets of factors, or tiers, one set being allocated to the other set. In `designRandomize`, these are referred to as the allocated and recipient sets of factors. They are also called the unit and treatment factors, respectively.

Firstly, initialize by loading the `dae` library. Also check the version that is loaded.

```
library(dae)

## Loading required package: ggplot2

packageVersion("dae")

## [1] '3.2.24'
```

2.1 Two potential designs for a 5×5 grid of plots (Brien et al., 2023, Section 2)

Suppose an experiment to investigate five treatments is to be conducted on 25 plots, the 25 plots being arranged in a 5×5 grid. Two possible designs are a randomized complete-block design (RCBD) or a Latin square design (LSqD). The factor-allocation diagram (Brien et al., 2011) for the RCBD is in Figure 1 and that for the LSqD is in Figure 2.

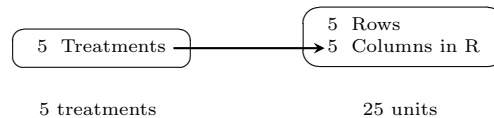


Figure 1: Factor-allocation diagram for an RCBD: treatments are allocated to units; the arrow indicates that the factor Treatments is randomized to Columns; Columns in R indicates that the Columns are considered to be nested within Rows for this randomization; R = Rows.

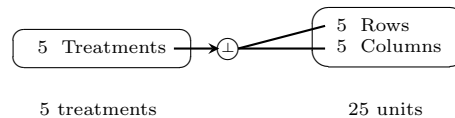


Figure 2: Factor-allocation diagram for an LSqD: treatments are allocated to units; the arrow indicates that the allocation is randomized; the '⊥' at the end of the arrow indicates that an orthogonal design is used; the two lines from '⊥' indicates that the Treatments are allocated to the combinations of Rows and Columns using the design.

2.1.1 Produce the randomized layout for an RCBD

Use `designRandomize` to randomize the treatments according to an RCBD. The arguments to `designRandomize` that need to be set are (i) `allocated`, (ii) `nested.recipients`, (iii) `recipient`, and optionally, (iv) `seed`. The allocated factors are also referred to as treatment factors and the recipient factors as block or unit factors. A systematic arrangement of the allocated factors, corresponding to the values of the recipient factors, needs to be supplied and there are a number of ways of doing this.

In these notes, the general approach is to set up a systematic design in a `data.frame` to separate this aspect of constructing a design from the randomizing of a design. The naming convention used is that the name of the `data.frame` containing the systematic design ends in `.sys`. This `data.frame` should contain the values of both the recipient and the allocated **factors**, the latter in a systematic order that is appropriate for the design. The `dae` function `fac.gen` will be used to generate the values of the recipient **factors** in standard order and often will also be used to generate the values of the allocated **factors**.

Then the allocated and recipient factors are supplied to `designRandomize` by subsetting the columns of the `data.frames` to just the appropriate factors for each argument. Note that the Treatments could also be supplied as a factor and the recipient factors can be specified directly to the `recipient` argument as a `list`, e.g. `list(Rows=b, Columns=t)`. A `data.frame` containing the recipient and randomized allocated factors is produced and the name for the `data.frame` with the randomized layout will end in `.lay`.

The randomization is controlled by `nested.recipients`: nested recipient factors are permuted within those factors that nest them. Only the nesting is specified: it is assumed that if two factors are not nested then they must be crossed. So for this example, given that the `nested.recipients` has Columns nested within Rows, the randomized layout is obtained by permuting (i) Rows and (ii) Columns within Rows. Then the permuted Rows and Columns and the systematic Treatments are sorted so that Rows and Columns are in standard order.

In this example, the allocated factor is Treatments, with 5 levels, and the recipient factors are Rows and Columns, both with 5 levels. Suppose that Rows are to form the blocks.

Use the following R code to obtain and display the layout:

```
### Obtain the randomized layout
b <- 5
t <- 5

### Set up a systematic design
RCBD.sys <- cbind(fac.gen(generate = list(Rows=b, Columns=t)),
                  fac.gen(generate = list(Treatments = LETTERS[1:t]),
                          times = b))

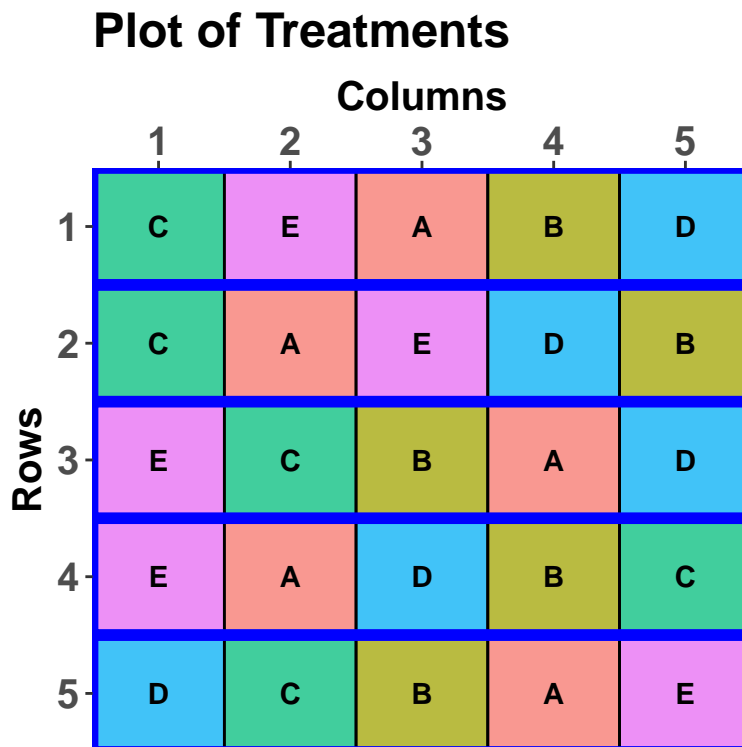
### Obtain the randomized layout
RCBD.lay <- designRandomize(allocated = RCBD.sys["Treatments"],
                           recipient  = RCBD.sys[c("Rows", "Columns")],
                           nested.recipients = list(Columns = "Rows"),
                           seed        = 1134)

### Output the layout
RCBD.lay
```

##	Rows	Columns	Treatments
## 1	1	1	C
## 2	1	2	E
## 3	1	3	A
## 4	1	4	B
## 5	1	5	D
## 6	2	1	C
## 7	2	2	A
## 8	2	3	E
## 9	2	4	D
## 10	2	5	B
## 11	3	1	E
## 12	3	2	C
## 13	3	3	B
## 14	3	4	A
## 15	3	5	D
## 16	4	1	E
## 17	4	2	A
## 18	4	3	D
## 19	4	4	B
## 20	4	5	C
## 21	5	1	D
## 22	5	2	C
## 23	5	3	B

```
## 24      5      4      A
## 25      5      5      E

### Plot the layout
designGGPlot(RCBD.layout, labels = "Treatments", cellalpha = 0.75,
             blockdefinition = cbind(1,t))
```



The function `fac.gen` is from the package `dae` and generates the factors in the `list` in standard order with the specified numbers of levels or the levels in supplied character or numeric vectors. The `seed` is specified to ensure that the same design is produced whenever `designRandomize` is run with these arguments.

2.1.2 Produce the randomized layout for an LSqD

Use `designRandomize` to randomize the treatments according to an LSqD, having obtained the systematic design using `fac.gen` and `designLatinSqrSys`. For this design, Rows and Columns are crossed; there are no nested factors. Consequently, the `nested.recipients` argument is omitted and `designRandomize` assumes that the recipient factors are crossed. The layout can be obtained using the following R code:

```
b <- 5
t <- 5
### Set up a systematic design
LSqD.sys <- cbind(fac.gen(list(Rows=b, Columns=t)),
                  Treatments = factor(designLatinSqrSys(t), labels = LETTERS[1:t]))
### Obtain the randomized layout
LSqD.layout <- designRandomize(allocated = LSqD.sys["Treatments"],
                              recipient = LSqD.sys[c("Rows", "Columns")],
                              seed      = 141)

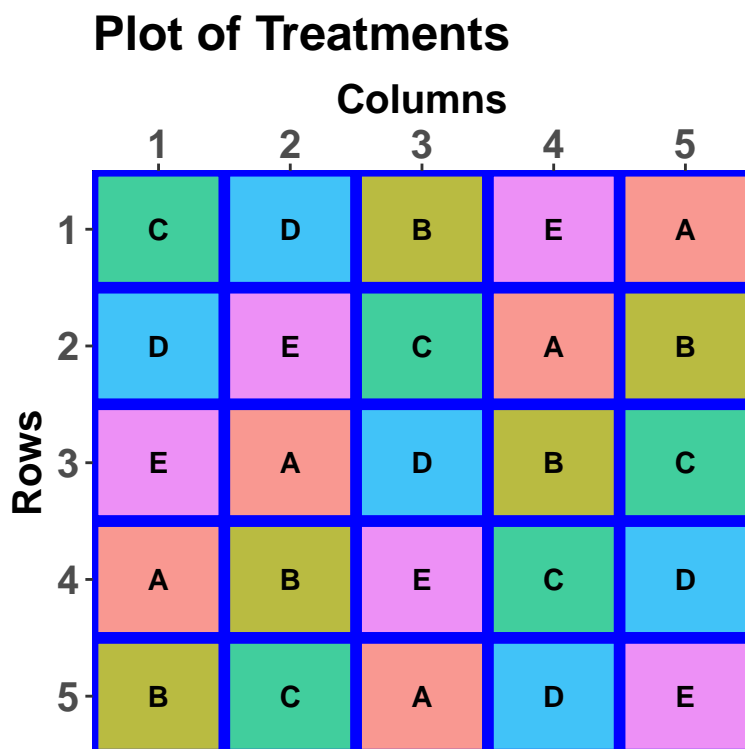
### Output the layout
LSqD.layout

##      Rows Columns Treatments
```



```
## 1 1 1 C
## 2 1 2 D
## 3 1 3 B
## 4 1 4 E
## 5 1 5 A
## 6 2 1 D
## 7 2 2 E
## 8 2 3 C
## 9 2 4 A
## 10 2 5 B
## 11 3 1 E
## 12 3 2 A
## 13 3 3 D
## 14 3 4 B
## 15 3 5 C
## 16 4 1 A
## 17 4 2 B
## 18 4 3 E
## 19 4 4 C
## 20 4 5 D
## 21 5 1 B
## 22 5 2 C
## 23 5 3 A
## 24 5 4 D
## 25 5 5 E

# Plot the layout
designGGPlot(LSqD.lay, labels = "Treatments", cellalpha = 0.75,
             blockdefinition = cbind(1,1))
```



2.1.3 Check the properties of the designs

The properties of the designs can be investigated using `designAnatomy`.

Because these experiments involve a single randomization, they are two-tiered. That is, there are just two sets of factors involved in the randomization. As we have seen, the first set of factors is the set of allocated (treatment) factors and the second set is the set of recipient (unit) factors. Further there will be a set of projectors associated with each tier and `designAnatomy` is used to do an eigenanalysis of the relationships between the two sets of projectors. The sets of projectors are specified to `designAnatomy` via model `formulae`, the formula for the recipient factors coming first in the `list` for `formulae`.

For both the RCBD and LSqD the two sets of factors are (i) {Rows, Columns} and (ii) {Treatments}. What differs between the two designs is the nesting/crossing relationship between Rows and Columns and this will be expressed in the `formulae`.

Use the commands given below to produce the anatomies (a type of skeleton-anova table) for the RCBD and LSqD that have been obtained. Note that the 'Mean' source has been omitted from these tables, but can be included using `grandMean = TRUE` when calling `designAnatomy`.

```
#'## Anatomy for the RCBD
RCBD.canon <- designAnatomy(formulae = list(units = ~ Rows/Columns,
                                           trts = ~ Treatments),
                           grandMean = TRUE, data = RCBD.lay)

summary(RCBD.canon)

##
##
## Summary table of the decomposition for units & trts
##
## Source.units df1 Source.trts df2 aefficiency eefficiency order
## Mean        1 Mean        1      1.0000      1.0000      1
## Rows         4
## Columns[Rows] 20 Treatments  4      1.0000      1.0000      1
##              Residual    16

#'## Anatomy for the LSqD
LSqD.canon <- designAnatomy(formulae = list(units = ~ Rows*Columns,
                                           trts = ~ Treatments),
                           grandMean = TRUE, data = LSqD.lay)

summary(LSqD.canon)

##
##
## Summary table of the decomposition for units & trts
##
## Source.units df1 Source.trts df2 aefficiency eefficiency order
## Mean        1 Mean        1      1.0000      1.0000      1
## Rows         4
## Columns       4
## Rows#Columns 16 Treatments  4      1.0000      1.0000      1
##              Residual    12
```

Get the mixed-model terms for the analysis by rerunning the `summary` function with the `labels.swap` argument set to `TRUE`.

```
#'## Term-based anatomy for the RCBD
summary(RCBD.canon, labels.swap = TRUE)

##
```

```
##
## Summary table of the decomposition for units & trts
##
##   Term.units    df1 Term.trts    df2 aefficiency eefficiency order
##   Mean           1 Mean           1      1.0000      1.0000      1
##   Rows           4
##   Rows:Columns   20 Treatments     4      1.0000      1.0000      1
##                      Residual     16

#'## Term-based anatomy for the LSqD
summary(LSqD.canon, labels.swap = TRUE)

##
##
## Summary table of the decomposition for units & trts
##
##   Term.units    df1 Term.trts    df2 aefficiency eefficiency order
##   Mean           1 Mean           1      1.0000      1.0000      1
##   Rows           4
##   Columns        4
##   Rows:Columns   16 Treatments     4      1.0000      1.0000      1
##                      Residual     12
```

2.1.4 Questions

1. What is the advantage of specifying a **seed** in **designRandomize**?

It means that the design can be reproduced in subsequent executions of the R script.

2. With what unit source is Treatments confounded in these designs and what is the difference in the interpretation of these sources?

Treatments is confounded with the term Rows:Columns. For the RCBD, Treatments is confounded with the source Columns[Rows]. For the LSqD, Treatments is confounded with the source Rows#Columns. The source Columns[Rows] reflects the differences between Rows within Columns; Rows#Columns is the interaction of Rows-and-Columns and reflects how the differences between Rows (Columns) vary between Columns (Rows).

3. What would determine which of these two designs is used for a particular experiment?

In a discussion with the researcher, it needs to be determined whether overall Column differences can be ruled out. If they can, then the RCBD should be used; otherwise, the LSqD would be used.

2.2 Split-plot from [Yates \(1937\)](#) (See also [Brien et al., 2023](#), Section 4.1)

[Yates \(1937\)](#) describes a split-plot experiment that investigates the effects of three varieties of oats and four levels of Nitrogen fertilizer. The varieties are assigned to the main plots using a randomized complete-block design with 6 blocks and the nitrogen levels are randomly assigned to the subplots in each main plot. The factor-allocation diagram for the experiment is in [Figure 3](#).

2.2.1 Produce the randomized experimental layout

Use **fac.gen** to obtain a systematic layout and then **designRandomize** to obtain a randomized layout for this experiment. Check the properties of the design, as illustrated in the following R code:

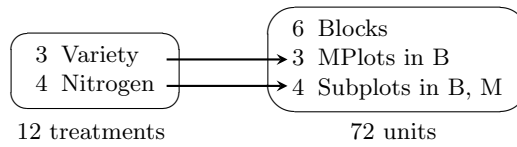


Figure 3: Factor-allocation diagram for a split-plot design: treatments are allocated to units; the arrows indicates that the factors Variety and Nitrogen are randomized to MPlots and Subplots, respectively; MPlots in B indicates that the MPlots are considered to be nested within Blocks for this randomization; Subplots in B, M indicates that the Subplots are considered to be nested within Blocks and MPlots for this randomization; B = Blocks, M = MPlots

```

Oats.sys <- cbind(fac.gen(list(Blocks=6, MPlots=3, SubPlots=4)),
                  fac.gen(list(Variety=c("Victory", "Golden Rain", "Marvellous"),
                                Nitrogen=c(0,0.2,0.4,0.6)), times=6))
Oats.lay <- designRandomize(allocated = Oats.sys[c("Variety", "Nitrogen")],
                           recipient = Oats.sys[c("Blocks", "MPlots", "SubPlots")],
                           nested.recipients = list(MPlots = "Blocks",
                                                    SubPlots = c("MPlots", "Blocks")),
                           seed = 235805)

#### Display design produced
Oats.lay

##   Blocks MPlots SubPlots   Variety Nitrogen
## 1      1      1      1  Marvellous    0.4
## 2      1      1      2  Marvellous    0
## 3      1      1      3  Marvellous    0.2
## 4      1      1      4  Marvellous    0.6
## 5      1      2      1    Victory    0
## 6      1      2      2    Victory    0.2
## 7      1      2      3    Victory    0.6
## 8      1      2      4    Victory    0.4
## 9      1      3      1 Golden Rain    0.2
## 10     1      3      2 Golden Rain    0.4
## 11     1      3      3 Golden Rain    0.6
## 12     1      3      4 Golden Rain    0
## 13     2      1      1  Marvellous    0.4
## 14     2      1      2  Marvellous    0.2
## 15     2      1      3  Marvellous    0
## 16     2      1      4  Marvellous    0.6
## 17     2      2      1    Victory    0.2
## 18     2      2      2    Victory    0
## 19     2      2      3    Victory    0.6
## 20     2      2      4    Victory    0.4
## 21     2      3      1 Golden Rain    0.6
## 22     2      3      2 Golden Rain    0.4
## 23     2      3      3 Golden Rain    0.2
## 24     2      3      4 Golden Rain    0
## 25     3      1      1 Golden Rain    0.2
## 26     3      1      2 Golden Rain    0.6
## 27     3      1      3 Golden Rain    0.4
## 28     3      1      4 Golden Rain    0
## 29     3      2      1  Marvellous    0.4
## 30     3      2      2  Marvellous    0.6
## 31     3      2      3  Marvellous    0

```

```
## 32      3      2      4 Marvellous      0.2
## 33      3      3      1      Victory      0.4
## 34      3      3      2      Victory      0.2
## 35      3      3      3      Victory      0
## 36      3      3      4      Victory      0.6
## 37      4      1      1 Marvellous      0
## 38      4      1      2 Marvellous      0.4
## 39      4      1      3 Marvellous      0.2
## 40      4      1      4 Marvellous      0.6
## 41      4      2      1 Golden Rain      0.2
## 42      4      2      2 Golden Rain      0.6
## 43      4      2      3 Golden Rain      0.4
## 44      4      2      4 Golden Rain      0
## 45      4      3      1      Victory      0.4
## 46      4      3      2      Victory      0
## 47      4      3      3      Victory      0.6
## 48      4      3      4      Victory      0.2
## 49      5      1      1 Golden Rain      0.2
## 50      5      1      2 Golden Rain      0
## 51      5      1      3 Golden Rain      0.6
## 52      5      1      4 Golden Rain      0.4
## 53      5      2      1 Marvellous      0
## 54      5      2      2 Marvellous      0.2
## 55      5      2      3 Marvellous      0.6
## 56      5      2      4 Marvellous      0.4
## 57      5      3      1      Victory      0.4
## 58      5      3      2      Victory      0.2
## 59      5      3      3      Victory      0.6
## 60      5      3      4      Victory      0
## 61      6      1      1 Marvellous      0
## 62      6      1      2 Marvellous      0.6
## 63      6      1      3 Marvellous      0.4
## 64      6      1      4 Marvellous      0.2
## 65      6      2      1      Victory      0.4
## 66      6      2      2      Victory      0.2
## 67      6      2      3      Victory      0
## 68      6      2      4      Victory      0.6
## 69      6      3      1 Golden Rain      0.6
## 70      6      3      2 Golden Rain      0.2
## 71      6      3      3 Golden Rain      0.4
## 72      6      3      4 Golden Rain      0

### Check its properties
Oats.canon <- designAnatomy(formulae = list(units = ~ Blocks/MPlots/SubPlots,
                                           trts = ~ Variety*Nitrogen),
                           grandMean = TRUE, data = Oats.lay)
summary(Oats.canon, which.criteria = c("aeff", "order"))

##
##
## Summary table of the decomposition for units & trts
##
## Source.units      df1 Source.trts      df2 aefficiency order
## Mean              1 Mean              1      1.0000      1
```

```
## Blocks 5
## MPlots[Blocks] 12 Variety 2 1.0000 1
## Residual 10
## SubPlots[Blocks:MPlots] 54 Nitrogen 3 1.0000 1
## Variety#Nitrogen 6 1.0000 1
## Residual 45
```

2.2.2 Analysis of variance (anova) for the Yields

After reading in the data, use the `aov` function to produce the anova as shown below. Note the use of the `Error` function to produce two Residual lines, one each for Wplots and Subplots (Note the change from MPlots to Wplots).

```
#### Read in data for actual experiment
data("Oats.dat")

#### Analyse by anova
oats.aov <- aov(Yield ~ Nitrogen*Variety +
               Error(Blocks/Wplots/Subplots), data=Oats.dat)
summary(oats.aov)

##
## Error: Blocks
##      Df Sum Sq Mean Sq F value Pr(>F)
## Residuals  5  15875    3175
##
## Error: Blocks:Wplots
##      Df Sum Sq Mean Sq F value Pr(>F)
## Variety   2   1786   893.2   1.485  0.272
## Residuals 10   6013   601.3
##
## Error: Blocks:Wplots:Subplots
##      Df Sum Sq Mean Sq F value Pr(>F)
## Nitrogen   3  20021   6674  37.686 2.46e-12 ***
## Nitrogen:Variety  6    322    54   0.303   0.932
## Residuals   45   7969    177
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The anova table shown here is the same as the anatomy, but in a different format.

2.2.3 Questions

1. In what sense does this design involve a single randomization?

In the sense that the randomization of both Nitrogen and Variety can be achieved with a single permutation of the units, the subplots.

2. What is the initial allocated mixed model for this design? Is it equivalent to a randomization model?

The initial allocation mixed model is $\text{Variety} + \text{Nitrogen} + \text{Variety}^{\wedge}\text{Nitrogen} \mid \text{Blocks} + \text{Blocks}^{\wedge}\text{MPlots} + \text{Blocks}^{\wedge}\text{MPlots}^{\wedge}\text{SubPlots}$. The initial allocation model is equivalent to a randomization model because the allocation was a randomization.

3. A factorial RCBD would involve randomizing the $3 \times 4 = 12$ treatments to the 12 subplots within each block. What has been achieved in using the split-plot design as compared to a factorial RCBD?

The precision of the Variety differences has been sacrificed to increase the precision of the Nitrogen differences. This is the case because the Residual mean square for $MPlots[Blocks]$ is substantially larger than that for $Subplots[Blocks \times MPlots]$. If a factorial RCBD had been used, the Residual mean square for $Plots[Blocks]$ would be the weighted average of the two Residual mean squares from the split-plot experiment, the weight being the Residual degrees of freedom. That is, the value of the Residual mean square for the factorial RCBD would be between the values for the two Residual mean squares for the split-plot design.

2.3 Split-unit design for an experiment in which time is randomized (Brien et al., 2023, Section 4.1)

A design is required for a conventional greenhouse experiment to investigate Zinc effects on plants of a medic species. A response over five weeks is to be measured, but the measurement of the response requires destructive harvesting of the plants. It is to involve four levels of Zinc and there are to be eight replicates of the Zinc-Weeks combinations. The Weeks are assigned to the main units, formed from 4 pots, using a randomized complete-block design with 8 blocks and the Zinc levels are randomly assigned to the pots in each main unit. The factor-allocation diagram for the experiment is in Figure 4.

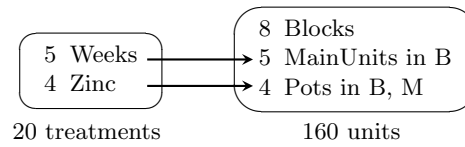


Figure 4: Factor-allocation diagram for a split-plot design: treatments are allocated to units; the arrows indicates that the factors Weeks and Zinc are randomized to MainUnits and Pots, respectively; MainUnits in B indicates that the MainUnits are considered to be nested within Blocks for this randomization; Pots in B, M indicates that the Pots are considered to be nested within Blocks and MainUnits for this randomization; B = Blocks, M = MainUnits

2.3.1 Produce the randomized experimental layout

Use `fac.gen` to obtain a systematic layout and then `designRandomize` to obtain a randomized layout for this experiment. Check the properties of the design, as illustrated in the R code below. Note that this experiment has the additional requirement that the design be located in the greenhouse.

```
### Set up the systematic design
SUD.sys <- cbind(fac.gen(list(Blocks = 8, MainUnits = 5, Pots = 4)),
                fac.gen(list(Weeks = LETTERS[1:5], Zinc = 4), times = 8))

### Obtain the randomized layout
SUD.lay <- designRandomize(allocated = SUD.sys[c("Zinc", "Weeks")],
                          recipient   = SUD.sys[c("Blocks", "MainUnits", "Pots")],
                          nested.recipients = list(MainUnits = "Blocks",
                                                    Pots = c("MainUnits", "Blocks")),
                          seed = 3116)

### Locate the design in the glasshouse and plot
SUD.lay <- cbind(SUD.lay,
                with(SUD.lay, fac.divide(Pots, list(PLane = 2, PPosn = 2))),
                with(SUD.lay, fac.divide(Blocks, list(BLane = 2, BPosn = 4))))
SUD.lay <- within(SUD.lay,
{
  Lanes <- fac.combine(list(BLane, PLane))
  Positions <- fac.combine(list(BPosn, MainUnits, PPosn))
  Treatments <- fac.combine(list(Weeks, Zinc), combine.levels = TRUE)
})
```

```

SUD.lay <- SUD.lay[c("Lanes", "Positions", "Blocks", "MainUnits", "Pots",
                    "Zinc", "Weeks", "Treatments")]
designGGPlot(SUD.lay, labels = "Treatments", label.size = 5,
             row.factors = "Positions", column.factors = "Lanes",
             cellfillcolour.column = "Weeks",
             title = NULL, title.size = 18, axis.text.size = 15,
             blockdefinition = cbind(10,2))

```


		Lanes			
		1	2	3	4
1		E,2	E,4	A,2	A,3
2		E,1	E,3	A,1	A,4
3		D,3	D,4	B,3	B,4
4		D,1	D,2	B,1	B,2
5		C,3	C,1	E,3	E,2
6		C,2	C,4	E,4	E,1
7		B,2	B,1	D,4	D,2
8		B,3	B,4	D,1	D,3
9		A,3	A,4	C,4	C,3
10		A,1	A,2	C,1	C,2
11		B,4	B,2	B,2	B,1
12		B,3	B,1	B,4	B,3
13		E,3	E,1	D,2	D,1
14		E,2	E,4	D,4	D,3
15		D,3	D,1	E,3	E,4
16		D,2	D,4	E,1	E,2
17		A,4	A,1	C,1	C,2
18		A,3	A,2	C,4	C,3
19		C,2	C,3	A,3	A,4
20		C,4	C,1	A,2	A,1
21		C,4	C,2	B,3	B,2
22		C,3	C,1	B,1	B,4
23		D,1	D,3	C,1	C,3
24		D,4	D,2	C,4	C,2
25		A,4	A,1	A,1	A,3
26		A,2	A,3	A,4	A,2
27		B,4	B,2	E,1	E,4
28		B,1	B,3	E,2	E,3
29		E,2	E,4	D,4	D,1
30		E,1	E,3	D,3	D,2
31		C,3	C,4	C,3	C,4
32		C,2	C,1	C,1	C,2
33		A,4	A,2	A,3	A,4
34		A,3	A,1	A,1	A,2
35		B,3	B,1	D,1	D,3
36		B,4	B,2	D,2	D,4
37		D,3	D,4	B,3	B,4
38		D,2	D,1	B,1	B,2
39		E,4	E,1	E,2	E,1
40		E,2	E,3	E,3	E,4

```

#### Check its properties
SUD.canon <- designAnatomy(formulae = list(units = ~ Blocks/MainUnits/Pots,
                                           trts = ~ Zinc*Weeks),
                           grandMean = TRUE, data = SUD.lay)

summary(SUD.canon)

##
##
## Summary table of the decomposition for units & trts
##
## Source.units      df1 Source.trts df2 aefficiency eefficiency order
## Mean              1 Mean          1      1.0000      1.0000      1
## Blocks            7
## MainUnits[Blocks] 32 Weeks         4      1.0000      1.0000      1
##                   Residual       28
## Pots[Blocks:MainUnits] 120 Zinc       3      1.0000      1.0000      1
##                   Zinc#Weeks    12      1.0000      1.0000      1
##                   Residual     105

```

2.3.2 Questions

1. What is the initial allocated mixed model for this design? Is it equivalent to a randomization model?

The initial allocation mixed model is $Weeks + Zinc + Weeks:Zinc \mid Blocks + Blocks:MainUnits + Blocks:MainUnits:Pots$. The initial allocation model is equivalent to a randomization model because all allocation was by randomization.

2. In general terms, how are the two Residual mean squares expected to compare in magnitude?

It is expected that the Residual mean squares for $MainUnits[Blocks]$ will be greater than the Residual mean squares for $Pots[Blocks:MainUnits]$.

2.4 A design for a petrol additives experiment

Box et al. (2005, Section 4.4) describes a car emission experiment that investigates 4 additives. It involves 4 cars being driven by 4 drivers. Here we investigate increasing the replication by repeating the experiment on two occasions. Suppose that the 4 cars differ between occasions.

In a `data.frame` called `LSRepeat.sys`, generate a systematic design using two 4×4 Latin squares to for allocating the 4 Additives to the 32 tests, being the combinations of the 2 Occasions x 4 Drivers x 4 Cars.

Now a comparison is made of two different ways of randomizing this design. Firstly, we retain the factors Occasions, Drivers and Cars from the systematic design. The factor-allocation diagram is in Figure 5.

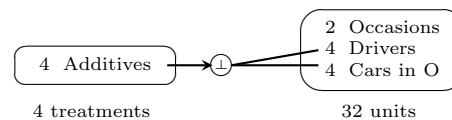


Figure 5: Factor-allocation diagram for repeated LSQDs: treatments are allocated to units; the arrow indicates that the allocation is randomized; the \oplus at the end of the arrow indicates that an orthogonal design is used; the two lines from \oplus indicates that the Additives are allocated to the combinations of Drivers and Cars within Occasions using the design.

```

#### Obtain a randomized layout with Cars nested within Occasions
LSRepeat2b.lay <- designRandomize(allocated = LSRepeat.sys["Additives"],
                                recipient   = LSRepeat.sys[c("Occasions", "Drivers",
                                                             "Cars")],

```

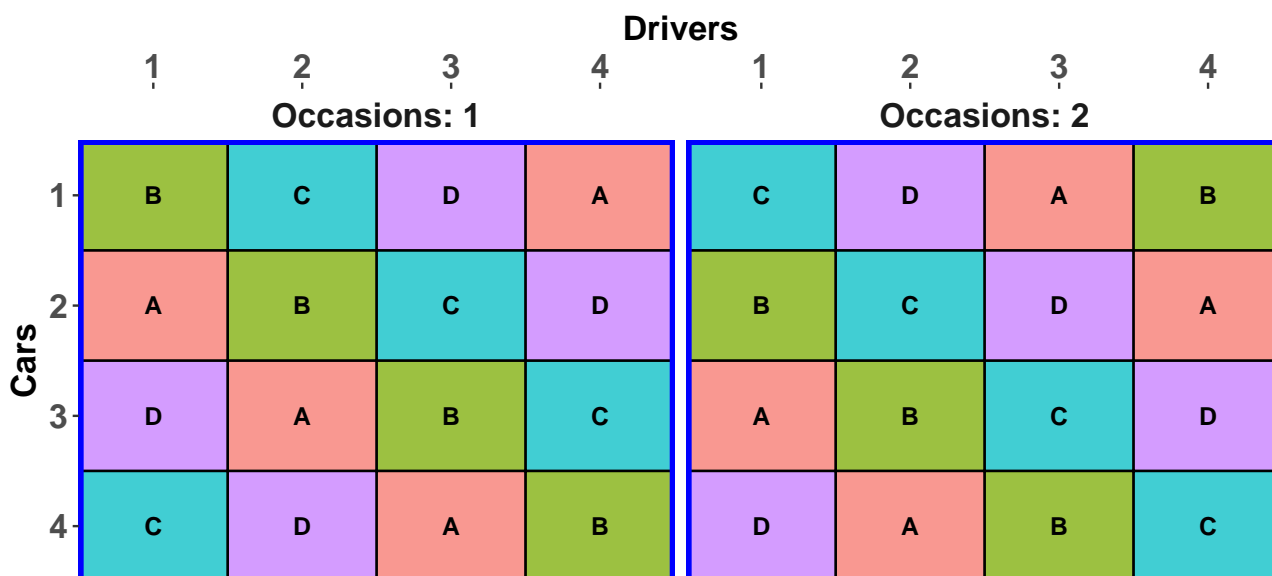
```

nested.recipients = list(Cars="Occasions"),
seed               = 194)

### Plot the layout
designGGPlot(LSRepeat2b.lay, row.factors = "Cars", column.factors = c("Occasions", "Drivers"),
            labels = "Additives", cellalpha = 0.75, blockdefinition = cbind(4,4))

```

Plot of Additives



```

### Get the anatomy of the layout
LSRepeat2b.canon <- designAnatomy(formulae = list(units = ~ (Occasions/Cars)*Drivers,
                                                trts = ~ Additives),
                                grandMean = TRUE, data = LSRepeat2b.lay)

summary(LSRepeat2b.canon)

##
##
## Summary table of the decomposition for units & trts
##
## Source.units      df1 Source.trts df2 aefficiency eefficiency order
## Mean              1 Mean          1    1.0000    1.0000    1
## Occasions         1
## Cars[Occasions]   6
## Drivers           3
## Occasions#Drivers 3
## Cars#Drivers[Occasions] 18 Additives 3    1.0000    1.0000    1
## Residual          15

```

Now we use only Drivers and Cars to do the randomization, but still attempt to include Occasions in the analysis. The new factor-allocation diagram is in Figure 6.

```

### Obtain a randomized layout
LSRepeat.D8.sys <- LSRepeat.sys
LSRepeat.D8.sys$Cars <- with(LSRepeat.D8.sys, fac.combine(list(Occasions, Cars)))
LSRepeat.D8.sys <- with(LSRepeat.D8.sys, LSRepeat.D8.sys[order(Drivers,Cars),])

```

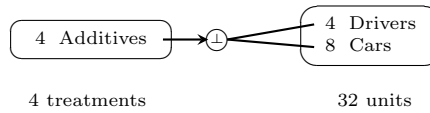
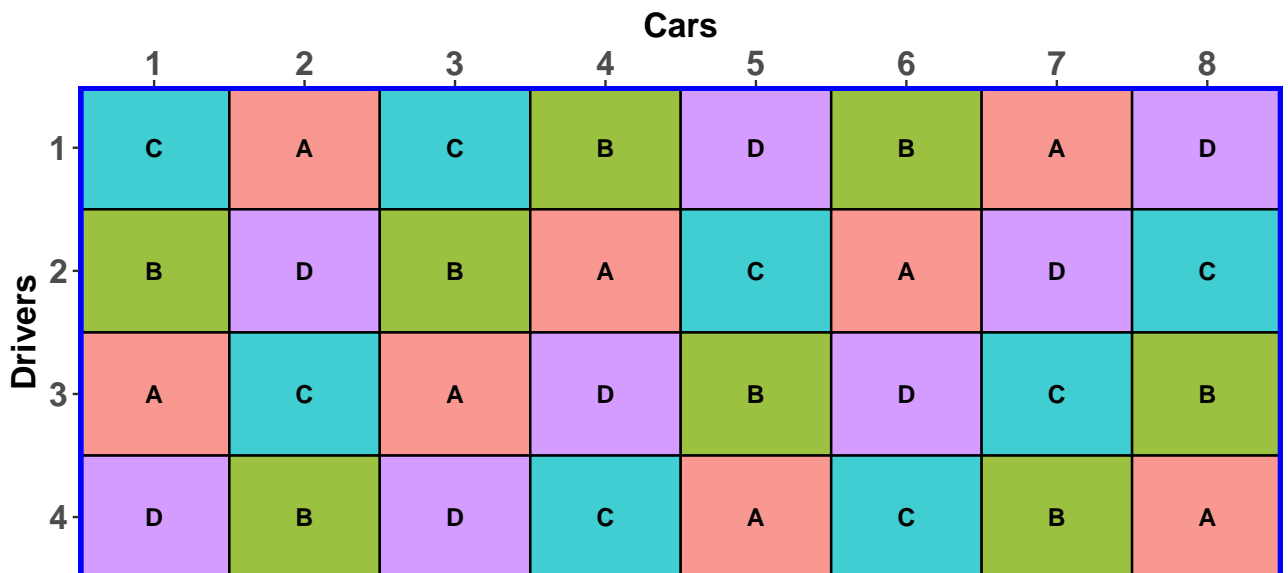


Figure 6: Factor-allocation diagram for repeated LSQDs: treatments are allocated to units; the arrow indicates that the allocation is randomized; the '⊕' at the end of the arrow indicates that an orthogonal design is used; the two lines from '⊕' indicates that the Additives are allocated to the combinations of Drivers and Cars using the design.

```
LSRepeat2b.D8.lay <- designRandomize(allocated = LSRepeat.D8.sys["Additives"],
                                     recipient = LSRepeat.D8.sys[c("Drivers", "Cars")],
                                     seed       = 149)

### Plot the layout
designGGPlot(LSRepeat2b.D8.lay, row.factors = "Drivers", column.factors = "Cars",
            labels = "Additives", cellfillcolour.column = "Additives",
            cellalpha = 0.75, blockdefinition = cbind(4,8))
```

Plot of Additives



```
### Get the Anatomy of the layout
LSRepeat2.D8.canon <- designAnatomy(formulae = list(units = ~ Drivers*Cars,
                                                    trts = ~ Additives),
                                    grandMean = TRUE, data = LSRepeat2b.D8.lay)

summary(LSRepeat2.D8.canon)

##
##
## Summary table of the decomposition for units & trts
##
## Source.units df1 Source.trts df2 aefficiency eefficiency order
## Mean          1 Mean          1    1.0000    1.0000    1
## Drivers         3
## Cars            7
## Drivers#Cars   21 Additives    3    1.0000    1.0000    1
```

```
##                               Residual      18

#'## Add Occasions to the analysis
LSRepeat2b.D8.lay$Occasions <- fac.recast(LSRepeat2b.D8.lay$Cars,
                                         newlevels = rep(1:2, each=4))

LSRepeat2b.D8.lay

##      Drivers Cars Additives Occasions
## 1         1    1          C         1
## 2         1    2          A         1
## 3         1    3          C         1
## 4         1    4          B         1
## 5         1    5          D         2
## 6         1    6          B         2
## 7         1    7          A         2
## 8         1    8          D         2
## 9         2    1          B         1
## 10        2    2          D         1
## 11        2    3          B         1
## 12        2    4          A         1
## 13        2    5          C         2
## 14        2    6          A         2
## 15        2    7          D         2
## 16        2    8          C         2
## 17        3    1          A         1
## 18        3    2          C         1
## 19        3    3          A         1
## 20        3    4          D         1
## 21        3    5          B         2
## 22        3    6          D         2
## 23        3    7          C         2
## 24        3    8          B         2
## 25        4    1          D         1
## 26        4    2          B         1
## 27        4    3          D         1
## 28        4    4          C         1
## 29        4    5          A         2
## 30        4    6          C         2
## 31        4    7          B         2
## 32        4    8          A         2

LSRepeat2b.D8.canon <- designAnatomy(formulae = list(units = ~ (Occasions + Cars)*Drivers,
                                                    trts = ~ Additives),
                                     grandMean = TRUE, data = LSRepeat2b.D8.lay)

summary(LSRepeat2b.D8.canon)

##
##
## Summary table of the decomposition for units & trts (based on adjusted quantities)
##
## Source.units      df1 Source.trts df2 aefficiency eefficiency order
## Mean              1 Mean          1      1.0000      1.0000      1
## Occasions          1
## Cars[Occasions]    6
## Drivers             3
```

```
## Occasions#Drivers      3 Additives      3      0.1500      0.1250      2
## Cars#Drivers[Occasions] 18 Additives      3      0.8289      0.7500      2
##                               Residual      15
##
## The design is not orthogonal
```

2.4.1 Questions

1. The Residual degrees of freedom for a single 4×4 Latin square are 6. Has the use of two 4×4 Latin squares had the desired effect of increasing the Residual df? What other advantage does the use of two Latin squares have over the use of a single Latin square?

Yes, the Residual df have been increased from 6 to 15. Using two Latin squares doubles the replication as compared to a single Latin square, thereby increasing the precision of the experiment by decreasing the standard error of differences between pairs of Additive means.

2. What is the difference between the two randomizations?

For the first randomization, the Additives are randomized to the Cars within Occasions so that each Driver does all 4 Additives in the 4 Cars in an Occasion. The design is said to be resolved. This does not happen with the randomization based on only Drivers and Cars.

3. How do the two anatomies that include Occasions differ?

The first anatomy is orthogonal and does not have any information about Additives confounded with Cars#Drivers[Occasions]. On the other hand, the second anatomy, based on the layout where Occasions was not included in the randomization, is not orthogonal. Additives information is partially confounded with both Occasions#Drivers and Cars#Drivers[Occasions].

4. What effect does including Occasions#Drivers have on the anatomy?

Including Occasions#Drivers reduces the Residual DF by 3 (from 18 to 15).

3 Single-allocation, nonorthogonal design in R

This class of experiments covers the nonorthogonal standard or textbook experiments. [Brien et al. \(2023, Section 5\)](#) discuss the anatomy and its interpretation for a nonorthogonal, balanced experiment.

3.1 Twenty treatments in an alpha design

The following table gives an alpha design for 20 treatments, taken from [Williams et al. \(2002, p.128\)](#). The design has 3 replicates, each of which contains 5 blocks of 4 plots. It is a resolved design in that each replicate contains a complete set of the treatments.

Table 1: Unrandomized alpha design for 20 treatments

Block	Replicate														
	1					2					3				
	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5
	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5
	6	7	8	9	10	7	8	9	10	6	8	9	10	6	7
	11	12	13	14	15	13	14	15	11	12	15	11	12	13	14
	16	17	18	19	20	19	20	16	17	18	17	18	19	20	16

The factor-allocation diagram for the experiment is in Figure 7.

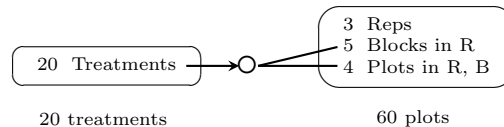


Figure 7: Factor-allocation diagram for the alpha design: treatments are allocated to units; the arrow indicates that the allocation is randomized; the ‘O’ at the end of the arrow indicates that a nonorthogonal design is used; the two lines from ‘O’ indicate that the Treatments are allocated to the combinations of Blocks and Plots using the design; Blocks in R indicates that the Blocks are considered to be nested within Reps for this randomization; Plots in R, B indicates that the Plots are considered to be nested within Reps and Blocks for this randomization; R = Reps; B = Blocks.

3.1.1 Produce the randomized layout for the alpha design and check its properties

Use `designRandomize` to obtain the randomized layout and `designAnatomy` to check its properties.

```
#### Set up the systematic design
# Note that Treatments has been entered by rows within a replicate
alpha.sys <- cbind(fac.gen(list(Reps=3, Plots=4, Blocks=5)),
  Treats = factor(c(1:20,
    1:5, 7:10, 6, 13:15, 11, 12, 19, 20, 16:18,
    1:5, 8:10, 6, 7, 15, 11:14, 17:20, 16)))

#### Obtain the randomized layout
alpha.layout <- designRandomize(allocated = alpha.sys["Treats"],
  recipient = alpha.sys[c("Reps", "Plots", "Blocks")],
  nested.recipients = list(Blocks = "Reps",
    Plots = c("Reps", "Blocks")),
  seed = 918508)
alpha.layout <- with(alpha.layout, alpha.layout[order(Reps, Blocks, Plots), ])

#### Check its properties
```

```

alpha.canon <- designAnatomy(formulae      = list(units = ~ Reps/Blocks/Plots,
                                                trts  = ~ Treats),
                             which.criteria = "all",
                             grandMean     = TRUE, data = alpha.lay)
summary(alpha.canon, which.criteria = "all")

##
##
## Summary table of the decomposition for units & trts (based on adjusted quantities)
##
## Source.units      df1 Source.trts df2 aefficiency eefficiency mefficiency sefficiency xefficiency
## Mean              1 Mean          1      1.0000      1.0000      1.0000      0.0000      1.0000
## Reps              2
## Blocks[Reps]      12 Treats        12      0.2778      0.1667      0.3333      0.0152      0.4167
## Plots[Reps:Blocks] 45 Treats        19      0.7447      0.5833      0.7895      0.0365      1.0000
##                   Residual        26
## order dforthog
##      1         1
##
##      2         0
##      3         7
##
##
## The design is not orthogonal

```

The summary table shows us a number of summary statistics calculated from the canonical efficiency factors. They are:

aefficiency: the harmonic mean of the nonzero canonical efficiency factors.

mefficiency: the mean of the nonzero canonical efficiency factors.

eefficiency: the minimum of the nonzero canonical efficiency factors.

sefficiency: the variance of the nonzero canonical efficiency factors.

xefficiency: the maximum of the nonzero canonical efficiency factors.

order: the order of balance and is the number of unique nonzero canonical efficiency factors.

dforthog: the number of canonical efficiency factors that are equal to one.

For this example it can be seen that (i) an average 74.47%, as measured by the harmonic mean, or 78.95%, as measured by the arithmetic mean, of the information about Treats is confounded with the differences between plots within the reps-blocks combinations and (ii) there are 3 different efficiency factors associated with the 19 Treats degrees of freedom estimated from Plots[Reps:Blocks], the smallest of which is 0.5833 and 7 of which are one. In this case, where the treatments are equally replicated, it can be concluded that the mean variance of a normalized treatment contrast is inversely proportional to the harmonic mean of the canonical efficiency factors, that is, to 0.7447.

Get the mixed-model terms for the analysis by rerunning the summary function with the `labels.swap` argument set to `TRUE`.

```

#'## Obtain the terms for the design
summary(alpha.canon, which.criteria = "all", labels.swap = TRUE)

##
##

```



```
## Summary table of the decomposition for units & trts (based on adjusted quantities)
##
##   Term.units      df1 Term.trts df2 aefficiency eefficiency mefficiency sefficiency xefficiency
##   Mean            1 Mean      1      1.0000      1.0000      1.0000      0.0000      1.0000
##   Reps            2
##   Reps:Blocks     12 Treats     12      0.2778      0.1667      0.3333      0.0152      0.4167
##   Reps:Blocks:Plots 45 Treats     19      0.7447      0.5833      0.7895      0.0365      1.0000
##                               Residual  26
##   order dforthog
##       1         1
##
##       2         0
##       3         7
##
##
## The design is not orthogonal
```

3.1.2 Questions

1. What is the randomization-based mixed model for this experiment?

The trts term (Source.trts) provides the fixed term and the units terms (Source.units) provide the random terms. Hence, the symbolic, randomization-based, mixed model is $Treats \mid Reps + Repls \wedge Blocks + Repls \wedge Blocks \wedge Plots$.

2. In a mixed-model analysis, which unit terms might you fit as fixed terms? Why?

Reps is a definite candidate for the following reasons. Firstly, Repls has only two degrees of freedom and it will be difficult to estimate a variance component for it. Secondly, one does not want to estimate Treats from Repls (there is no Treats information between Repls).

3.2 Balanced incomplete-block design from Joshi (1987)

Joshi (1987) gives an experiment to investigate six varieties of wheat that employs a balanced incomplete-block design with 10 blocks, each consisting of three plots. The factor-allocation diagram for the experiment is in Figure 8.

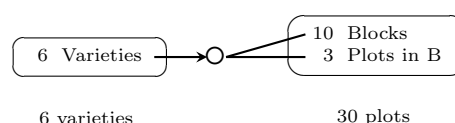


Figure 8: Factor-allocation diagram for the balanced incomplete-block design: treatments are allocated to units; the arrow indicates that the allocation is randomized; the 'O' at the end of the arrow indicates that a nonorthogonal design is used; the two lines from 'O' indicates that the Varieties are allocated to the combinations of Blocks and Plots using the design; Plots in B indicates that the Plots are considered to be nested within Blocks for this randomization; B = Blocks.

3.2.1 Input the Yields and check properties of the design

Use the following R code to input the data for the experiment and check its properties.

```
#### Input the design and data
data("BIBDWheat.dat")

#### Check the properties of the design
```

```

bibdwheat.canon <- designAnatomy(formulae = list(units = ~ Blocks/Plots,
                                                trts = ~ Varieties),
                                grandMean = TRUE, data = BIBDWheat.dat)

summary(bibdwheat.canon)

##
##
## Summary table of the decomposition for units & trts (based on adjusted quantities)
##
## Source.units df1 Source.trts df2 aefficiency eefficiency order
## Mean 1 Mean 1 1.0000 1.0000 1
## Blocks 9 Varieties 5 0.2000 0.2000 1
## Residual 4
## Plots[Blocks] 20 Varieties 5 0.8000 0.8000 1
## Residual 15
##
## The design is not orthogonal

```

From this it is clear that 80% of the information about Varieties is available from the Plots[Blocks] source; that is, 80% of the Varieties information is confounded with differences between plots within blocks. Of course, the remaining 20% is confounded with Blocks.

3.2.2 Anova for the Yields

```

##### Perform an anova
summary(aov(Yield ~ Varieties + Error(Blocks/Plots), data = BIBDWheat.dat))

##
## Error: Blocks
##          Df Sum Sq Mean Sq F value Pr(>F)
## Varieties  5  196.6   39.32   0.582  0.718
## Residuals  4  270.4   67.59
##
## Error: Blocks:Plots
##          Df Sum Sq Mean Sq F value Pr(>F)
## Varieties  5 1156.4  231.29   4.021 0.0163 *
## Residuals 15  862.9   57.53
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

3.2.3 Questions

1. What is the value of xefficiency for Varieties when confounded with Plots[Blocks] for this design? Why?
It is 0.80 because there is only the one value for the canonical efficiency factor between these two sources
2. How many nonzero eigenvalues does $\mathbf{Q}_V \mathbf{Q}_{BP} \mathbf{Q}_V$ have?
It has 5 nonzero eigenvalues because there is 5 df of Varieties confounded with Plots[Blocks].

3.3 A design with rows and columns from Williams (2002)

[Williams et al. \(2002, p.144\)](#) provide an example of a tree experiment that investigated differences between 60 provenances of a species of Casuarina tree, these provenances coming from 18 countries; the trees were inoculated prior to planting at two different times. The design used was a split-unit design comprised of four rectangles

each of six rows by ten columns; the rectangles are located next to each other so that they are contiguous along the rows. The two inoculation times were randomized to the rectangles (main units). The provenances were randomized to the subunits using a resolved, latinized, row-column design, the rectangles forming replicates of the Provenances. The latinization was by columns and was necessary because differences between Columns (across Reps) was anticipated; it served to avoid multiple occurrences of a provenance in a column. At 30 months, diameter at breast height (Dbh) was measured.

The factor-allocation diagram for the experiment is in Figure 9.

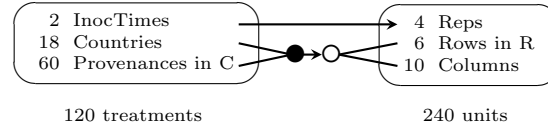


Figure 9: Factor-allocation diagram for the row-and-column design: treatments are allocated to units; the arrows indicates that the allocations are randomized; the two lines leading to the '●' indicate that it is the combinations of Countries and Provenances that is allocated; the '○' at the end of the lower arrow indicates that a nonorthogonal design is used; the two lines from '○' indicates that the Countries and Provenances are allocated to the combinations of Rows and Columns using the design; Rows in B indicates that the Rows are considered to be nested within Reps for this randomization; R = Reps.

3.3.1 Input the design and check the properties of the design

Use the following R code to input the design and check its properties.

```
### Input the design
data("Casuarina.dat")
### Check the properties of the design
Casuarina.canon <- designAnatomy(formulae = list(units = ~ (Reps/Rows)*Columns,
trts = ~ InocTime*(Countries+Provenances)),
grandMean = TRUE, data = Casuarina.dat)

## Warning in proj2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Provenances[Countries]
## and Countries are partially aliased in Rows[Reps]
## Warning in proj2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Provenances[Countries]
## and Countries are partially aliased in Rows#Columns
## Warning in proj2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Provenances[Countries]
## and Countries are partially aliased in Rows#Columns[Reps]
## Warning in proj2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): InocTime#Countries and
## Countries are partially aliased in Rows#Columns[Reps]
## Warning in proj2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): InocTime#Countries and
## Provenances[Countries] are partially aliased in Rows#Columns[Reps]
## Warning in proj2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): InocTime#Provenances[Countries]
## and Countries are partially aliased in Rows#Columns[Reps]
## Warning in proj2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): InocTime#Provenances[Countries]
## and Provenances[Countries] are partially aliased in Rows#Columns[Reps]
## Warning in proj2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): InocTime#Provenances[Countries]
## and InocTime#Countries are partially aliased in Rows#Columns[Reps]

summary(Casuarina.canon, which = c("aeff", "eeff", "order", "dforth"))

##
##
## Summary table of the decomposition for units & trts (based on adjusted quantities)
##
## Source.units      df1 Source.trts      df2 aefficiency eefficiency order dforthog
## Mean              1 Mean              1      1.0000      1.0000      1          1
```

```

## Reps          3 InocTime          1      1.0000      1.0000      1      1
## Residual          2
## Rows[Reps]     20 Countries        17      0.0145      0.0018     17      0
## Provenances[Countries]      3      0.1622      0.1326      3      0
## Columns        9 Countries        9      0.0137      0.0028      9      0
## Reps#Columns   27 Countries        17      0.0134      0.0012     17      0
## Provenances[Countries]     10      0.2320      0.1596     10      0
## Rows#Columns[Reps] 180 Countries   17      0.7611      0.5588     17      0
## Provenances[Countries]    42      0.6851      0.3429     42      0
## InocTime#Countries      17      0.6808      0.4735     17      0
## InocTime#Provenances[Countries] 42      0.5516      0.2009     42      0
## Residual          62
##
## Table of information (partially) aliased with previous sources derived from the same formula
##
## Source          df Alias          In          aefficiency
## Provenances[Countries] 17 Countries Rows[Reps]      1.0000
## Provenances[Countries] 17 Countries Reps#Columns    1.0000
## Provenances[Countries] 17 Countries Rows#Columns[Reps] 0.0178
## InocTime#Countries      17 Countries Rows#Columns[Reps] 0.0001
## InocTime#Countries      17 Provenances[Countries] Rows#Columns[Reps] 0.0222
## InocTime#Provenances[Countries] 17 Countries Rows#Columns[Reps] 0.0222
## InocTime#Provenances[Countries] 42 Provenances[Countries] Rows#Columns[Reps] 0.0000
## InocTime#Provenances[Countries] 17 InocTime#Countries Rows#Columns[Reps] 0.0178
## eefficiency order dforthog
##      1.0000      1      17
##      1.0000      1      17
##      0.0025     17      0
##      0.0000     17      0
##      0.0042     17      0
##      0.0042     17      0
##      0.0000     42      0
##      0.0025     17      0
##
## The design is not orthogonal

```

Firstly, note that **designAnatomy** has automatically detected that Provenances is nested within Countries, even though Provenances has 60 unique levels: the sources for these two terms are Countries and Provenances[Countries] and these have 17 and 42 degrees of freedom when estimated from Rows # Columns[Reps], respectively. The total of these degrees of freedom is 59, one less than the number of Provenances, as expected.

Secondly, the partial aliasing evident in this design reflects a lack of (structure) balance between the treatment sources within each units source. This is an undesirable, but unavoidable, feature of the design for this experiment.

3.3.2 Questions

1. What is it about the design that makes it resolved for Provenances?

Each Rep contains all 60 Provenances once and only once, i.e. a complete replicate of the Provenances.

2. What is the disadvantage of allocating InocTimes to Reps?

There are only two Residual degrees of freedom for testing for the main effect for InocTimes.

3.4 A resolved design for the wheat experiment that is near-A-optimal under a mixed model

Gilmour et al. (1995) provides an example of a wheat experiment for 25 Varieties in which a balanced lattice square design was employed, it being a resolved row-column design.

The factor-allocation diagram for the experiment is in Figure 10.

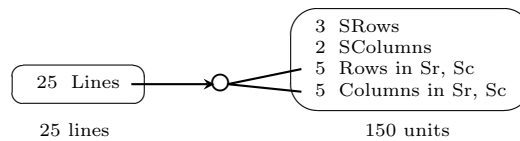


Figure 10: Factor-allocation diagram for the balanced lattice square design: treatments are allocated to units; the arrows indicates that the allocations are randomized; the ‘O’ at the end of the lower arrow indicates that a nonorthogonal design is used; the two lines from ‘O’ indicates that the Lines are allocated to the combinations of Rows and Columns using the design; Rows (Columns) in Sr, Sc indicates that the Rows (Columns) are considered to be nested within SRows and SColumns for this randomization; Sr = S(uper)Rows; Sc = S(uper)Columns.

3.4.1 Input the design and check the properties of the design

The design is available in the Wheat data set in the asremlPlus package (Brien, 2024a). Use the following R code to input the design, plot it and check its properties.

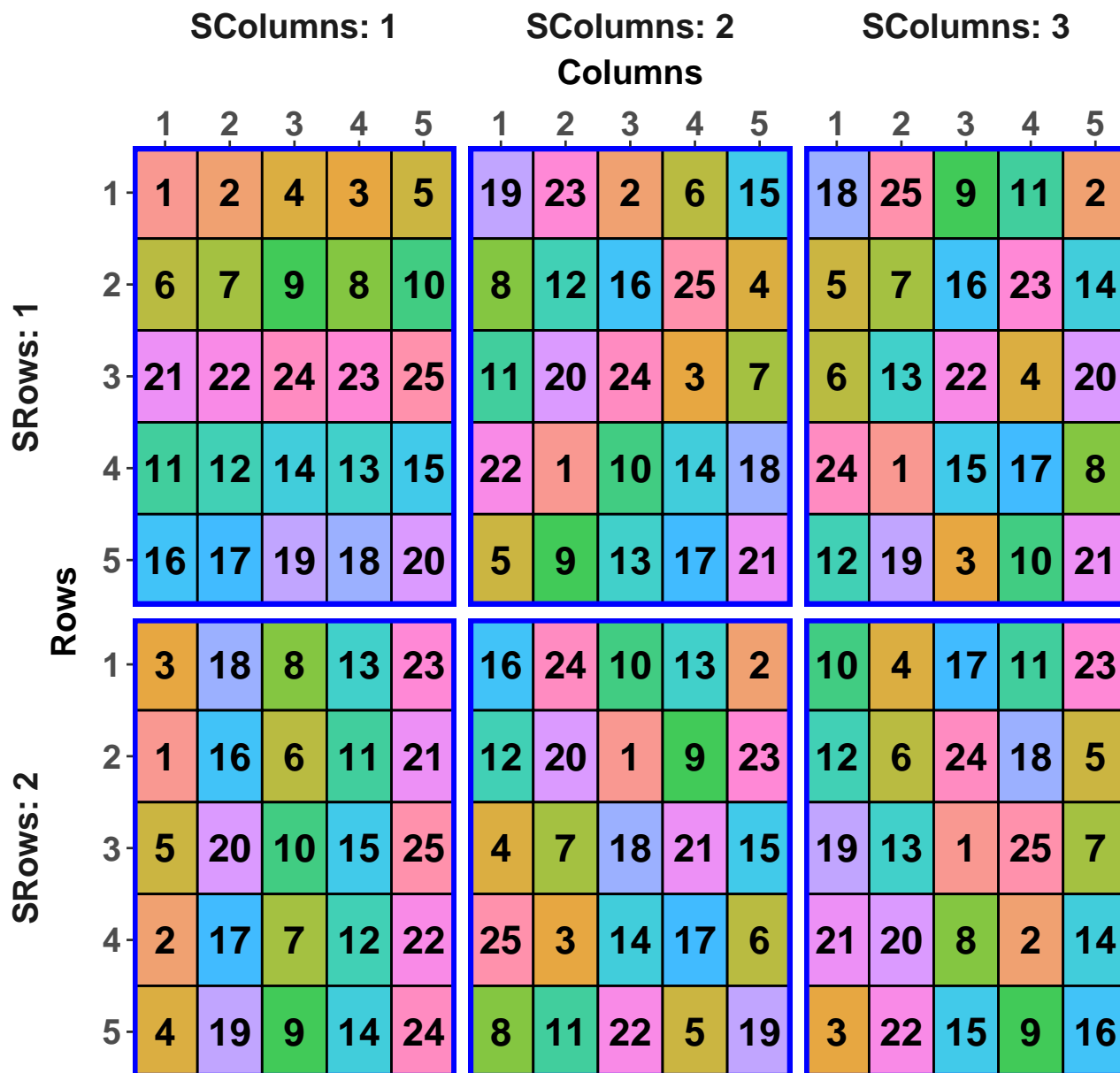
```
### Get the design
library(asremlPlus)

## ASReML-R needs to be loaded if the mixed-model functions are to be used.
##
## ASReML-R is available from VSNi. Please visit http://www.vsnr.co.uk/ for more information.

data(Wheat.dat)
latt.lay <- cbind(fac.gen(list(SRows = 2, Rows = 5, SColumns = 3, Columns = 5)),
                  Wheat.dat["Variety"])

### Plot the design
#+ "LattDesign"
library(scales)
cell.colours <- hue_pal()(25)
designGGPlot(latt.lay, labels = "Variety",
             row.factors = c("SRows", "Rows"), column.factors = c("SColumns", "Columns"),
             facetstrips.switch = "y", facetstrips.placement = "outside.title",
             colour.values = cell.colours, cellalpha = 0.75, label.size = 6,
             blockdefinition = cbind(5,5))
```

Plot of Variety



```
## Check the properties of the design
latt.canon <- designAnatomy(formulae = list(units = ~ (SRows:SColumns)/(Rows*Columns),
                                           trts = ~ Variety),
                           grandMean = TRUE, data = latt.lay)
summary(latt.canon, which.criteria = c("aeff", "order"))

##
##
## Summary table of the decomposition for units & trts (based on adjusted quantities)
##
## Source.units          df1 Source.trts df2 aefficiency order
## Mean                  1 Mean          1    1.0000      1
## SRows:SColumns        5
```

```
## Rows[SRows:SColumns]      24 Variety      24      0.1667      1
## Columns[SRows:SColumns]    24 Variety      24      0.1667      1
## Rows#Columns[SRows:SColumns] 96 Variety      24      0.6667      1
##                               Residual      72
##
## The design is not orthogonal
```

4 Miscellaneous experimental design topics in R

This section includes examples showing the effects of missing values, recognizing pseudoreplication and the use of nested factorials.

Firstly, initialize by loading the libraries that will be used and setting the output width.

```
library(dae, quietly = TRUE)
options(width=100)
```

4.1 An environmental experiment

Suppose an environmental scientist wants to investigate the effect on the biomass of burning areas of natural vegetation. There are available two areas separated by several kilometres for use in the investigation. It is only possible to either burn or not burn an entire area. The area to be burnt is randomly selected and the other area is to be left unburnt as a control. Further, 30 locations in each area are to be randomly sampled and the biomass measured at each location. The factor-allocation diagram for the experiment is in Figure 11.

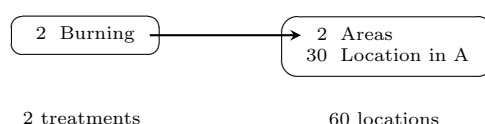


Figure 11: Factor-allocation diagram for the environmental experiment: treatments are allocated to locations; the arrow indicates that the factor Burning is randomized to Areas; Locations in A indicates that the Locations are considered to be nested within Areas; A = Areas.

Obtain the randomized layout for this experiment and check its properties.

```
### Obtain the randomized layout
Burn.sys <- cbind(fac.gen(list(Areas=2, Locations=30)),
                  Burn = factor(rep(c("Burn", "NoBurn"), each=30)))
Burn.lay <- designRandomize(allocated = Burn.sys["Burn"],
                           recipient  = Burn.sys[c("Areas", "Locations")],
                           nested.recipients = list(Locations = "Areas"),
                           seed       = 872159)

### plot the design
designGGPlot(Burn.lay, labels = "Burn", row.factors = "Locations", column.factors = "Areas")
```


Plot of Burn

		Areas	
		1	2
Locations	1	Burn	NoBurn
	2	Burn	NoBurn
	3	Burn	NoBurn
	4	Burn	NoBurn
	5	Burn	NoBurn
	6	Burn	NoBurn
	7	Burn	NoBurn
	8	Burn	NoBurn
	9	Burn	NoBurn
	10	Burn	NoBurn
	11	Burn	NoBurn
	12	Burn	NoBurn
	13	Burn	NoBurn
	14	Burn	NoBurn
	15	Burn	NoBurn
	16	Burn	NoBurn
	17	Burn	NoBurn
	18	Burn	NoBurn
	19	Burn	NoBurn
	20	Burn	NoBurn
	21	Burn	NoBurn
	22	Burn	NoBurn
	23	Burn	NoBurn
	24	Burn	NoBurn
	25	Burn	NoBurn
	26	Burn	NoBurn
	27	Burn	NoBurn
	28	Burn	NoBurn
	29	Burn	NoBurn
	30	Burn	NoBurn

```
## Check its properties
Burn.canon <- designAnatomy(formulae = list(units = ~Areas/Locations,
                                           trts = ~Burn),
                           grandMean = TRUE, data = Burn.lay)

summary(Burn.canon)

##
##
## Summary table of the decomposition for units & trts
##
## Source.units    df1 Source.trts df2 aefficiency eefficiency order
## Mean           1 Mean          1    1.0000    1.0000    1
## Areas          1 Burn          1    1.0000    1.0000    1
```

4.1.1 Questions

1. How is the pseudo-replication involved in this experiment manifested in the anatomy? (Brien et al. (2023, Section 4.3) discuss the issues associated with pseudoreplication.)

Because (i) Areas and Burn are alongside each other in the anova table, (ii) they both have 1 degree of freedom, and (iii) the single canonical efficiency factor is one, then Areas and Burn are completely confounded. That is, the pseudoreplication has resulted in differences between Areas and between Burns being inextricably mixed up.

2. The randomization-based mixed model for the experiment is $\text{Burn} \mid \text{Areas} + \text{Areas:Locations}$. What difficulties do you anticipate in attempting to fit this model? How could the model be modified so that a fit can be obtained? Brien and Demétrio (2009) call models formed by removing terms to enable a fit to be achieved ‘models of convenience’. What dangers do you foresee in basing conclusions on the fitted model of convenience?

There will be a singularity in the model because Areas is confounded with Burn. A fit could be obtained by removing Areas from the random model. The problem is that a test of Burn would then be based on the ratio of variability in Burn differences to an estimate of the variance of Locations-within-Areas variability. This does not include Areas variability and so the denominator is likely to be underestimated; p-values based from this test are likely to be too small and significant differences are more likely to be declared where there are none as compared to when an estimate of Areas variability is included in the denominator of the F-statistic.

4.2 Block-treatment interactions for an experiment in which time is randomized (Brien et al., 2023, Section 4.1)

The properties of a split-unit design have been examined in Section 2.3 for an experiment in which the effects on Zinc over five weeks were investigated. In that investigation, the terms in the initial allocation model were considered. Here the properties of a homogeneous model with block-treatment interactions are checked. If you have not saved the design, reconstruct it as shown below; otherwise, use the saved design. Then, obtain the anatomy to establish its properties.

```
##### Set up the systematic design
SUD.sys <- cbind(fac.gen(list(Blocks = 8, MainUnits = 5, Pots = 4)),
               fac.gen(list(Weeks = LETTERS[1:5], Zinc = 4), times = 8))

##### Obtain the randomized layout
SUD.layout <- designRandomize(allocated = SUD.sys[c("Zinc", "Weeks")],
                             recipient = SUD.sys[c("Blocks", "MainUnits", "Pots")],
                             nested.recipients = list(MainUnits = "Blocks",
                                                       Pots = c("MainUnits", "Blocks")),
                             seed = 3116)

##### Check its properties
SUD.BT.canon <- designAnatomy(formulae = list(units = ~ Blocks/MainUnits/Pots,
                                             trts = ~ Blocks*Zinc*Weeks),
                             grandMean = TRUE, data = SUD.layout)

summary(SUD.BT.canon)

##
##
## Summary table of the decomposition for units & trts
```

```
##
## Source.units      df1 Source.trts      df2 aeffericiency eeffericiency order
## Mean              1 Mean              1      1.0000      1.0000      1
## Blocks            7 Blocks            7      1.0000      1.0000      1
## MainUnits[Blocks] 32 Weeks            4      1.0000      1.0000      1
##                   Blocks#Weeks        28      1.0000      1.0000      1
## Pots[Blocks:MainUnits] 120 Zinc        3      1.0000      1.0000      1
##                   Blocks#Zinc          21      1.0000      1.0000      1
##                   Zinc#Weeks           12      1.0000      1.0000      1
##                   Blocks#Zinc#Weeks    84      1.0000      1.0000      1
```

4.2.1 Questions

1. What do you conclude from the anatomy about the estimability of terms?

It is not possible to separately estimate MainUnits[Blocks] and Blocks#Weeks. It is also not possible to separately estimate Pots[Blocks:MainUnits] and Blocks#Zinc#Weeks.

2. How might you change the design so that the block-treatment interactions are separately estimable?

Employ a generalized randomized block design (GRBD) for the main-unit design to randomize the Weeks.

4.3 A longitudinal greenhouse experiment that uses a generalized randomized block design (GRBD) (Brien et al., 2023, Section 4.2)

Consider an experiment in a glasshouse that has equipment to automatically image plants daily, the images being processed to produce a measure related to plant biomass. Suppose that the experiment to investigate the effects of four levels of Zinc on medic plants is to be run in this glasshouse and that the plants are to be imaged over 14 Days. It is to involve 12 replicates and the experimental area can accommodate 48 pots in grid of four lanes by 12 positions, each pot having a single plant. Previous experience is that the differences between pots in the same lane separated by more than two pots are likely to be larger than between those separated by no more than two pots. Also, pots in the front pair of lanes are likely to differ from pots in the back pair of lanes. That is, Blocks consisting of eight pots arranged in two lanes by four positions are likely to be relatively homogeneous. Further, suppose that it is thought that the response to Zinc may differ between the Blocks. As Brien et al. (2023, Section 3.2) conclude, a GRBD is a suitable design for this experiment.

The factor allocation diagram for this experiment is given in Figure 12

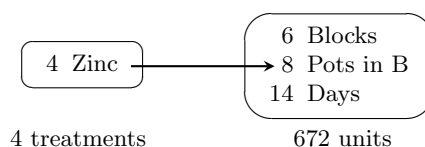


Figure 12: Factor-allocation diagram showing the treatments allocation to units for the longitudinal experiment that uses a generalized randomized block design: the arrow indicates that Zinc is allocated to Pots within B using randomization; B = Blocks.

Obtain the randomized layout for this longitudinal experiment.

```
##### Construct a systematic design
longi.sys <- cbind(fac.gen(list(Blocks = 6, Pots = 8, Days = 14)),
                  fac.gen(list(Zinc = LETTERS[1:4]), times = 12, each = 14))

##### Obtain the randomized layout
longi.layout <- designRandomize(allocated = longi.sys["Zinc"],
                                recipient   = longi.sys[c("Blocks", "Pots", "Days")],
                                nested.recipients = list(Pots = "Blocks"),
```

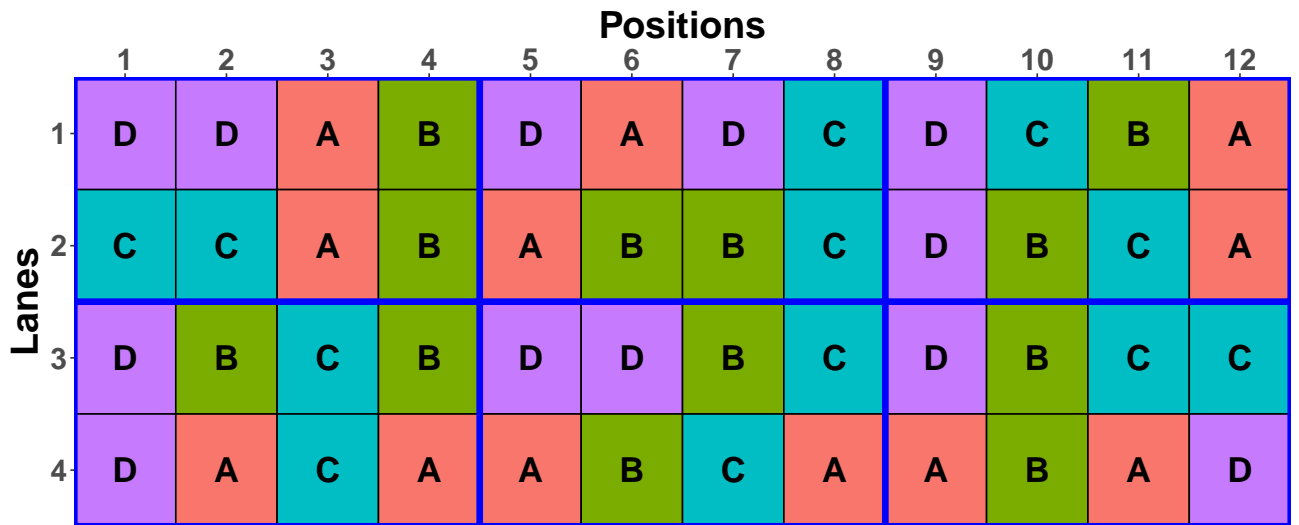
```

seed = 5733)

### Add factors for Lane and Position
longi.lay <- cbind(with(longi.lay, fac.divide(Blocks,
                                             factor.names = list(Panes = 2,
                                                                    QPositions = 3))),
                  with(longi.lay, fac.divide(Pots,
                                             factor.names = list(Lanes = 2,
                                                                    Positions = 4))),
                  longi.lay)
longi.lay <- within(longi.lay,
{
  Lanes <- fac.combine(list(Panes, Lanes))
  Positions <- fac.combine(list(QPositions, Positions))
})
longi.lay <- longi.lay[, -match(c("Panes", "QPositions"), names(longi.lay))]

### Plot the layout
designGGPlot(subset(longi.lay, Days == "1"),
             row.factors = "Lanes", column.factors = "Positions",
             labels = "Zinc", label.size = 8,
             title = NULL, title.size = 25, axis.text.size = 20,
             blockdefinition = cbind(2,4))

```



The homogeneous allocation model given by [Brien et al. \(2023, Section 4.2\)](#) is:

$$\text{Mean} + \text{Z} + \text{D} + \text{Z} \wedge \text{D} \quad | \quad \text{Mean} + \text{B} + \text{B} \wedge \text{Z} + \text{B} \wedge \text{P} + \text{B} \wedge \text{D} + \text{B} \wedge \text{Z} \wedge \text{D} + \text{B} \wedge \text{P} \wedge \text{D}.$$

Check the properties of the layout corresponding to the homogeneous allocation model using an anatomy.

```

longi.BZD.canon <- designAnatomy(formulae = list(units = ~ (Blocks/Pots)*Days,
                                                trtblks = ~ Blocks*Zinc*Days),
                                grandMean = TRUE, data = longi.lay)
summary(longi.BZD.canon)

##

```

```
##
## Summary table of the decomposition for units & trtblks
##
## Source.units      df1 Source.trtblks    df2 aeffericiency eefficiency order
## Mean              1 Mean              1    1.0000      1.0000      1
## Blocks            5 Blocks            5    1.0000      1.0000      1
## Pots[Blocks]      42 Zinc              3    1.0000      1.0000      1
##                   Blocks#Zinc          15    1.0000      1.0000      1
##                   Residual            24
## Days              13 Days              13    1.0000      1.0000      1
## Blocks#Days        65 Blocks#Days        65    1.0000      1.0000      1
## Pots#Days[Blocks] 546 Zinc#Days          39    1.0000      1.0000      1
##                   Blocks#Zinc#Days     195    1.0000      1.0000      1
##                   Residual            312
```

4.3.1 Questions

1. What are the block-treatments interactions in this experiment? Are they all estimable?

They are Blocks#Zinc, Zinc#Days and Blocks#Zinc#Days. All of these block-treatments interactions are estimable.

2. How do the properties of the longitudinal experiment differ from those of the experiment in which Weeks are randomized (Sections 2.3 and 4.2)?

The fundamental difference is that Weeks are randomized, whereas Days are not allocated; Days are potential recipient factors. This affects the nature of the inference possible for terms involving Weeks and Days. In particular, randomization cannot be used as the basis of the inference for terms involving Days, whereas it can for terms involving Weeks.

4.4 A detergent experiment

Mead et al. (2012) describe an experiment to investigate nine detergent formulations that were compared by washing plates one at a time until they were clean. There were only 3 basins available at any one time and so a BIBD with 12 blocks was used to assign formulations to washing instances. Each basin has a different operator who washed at the same rate at each time of washing. The response is the number of plates washed before the foam disappears.

The treatments involve two bases, four additive amounts and a control; they are:

1. base I + three parts additive
2. base I + two parts additive
3. base I + one part additive
4. base I
5. base II + three parts additive
6. base II + two parts additive
7. base II + one part additive
8. base II
9. Control

The factor-allocation diagram for the experiment is in Figure 13.

The systematic incomplete-block design is shown in Table 2.

4.4.1 Produce the randomized layout for the BIBD and check its properties

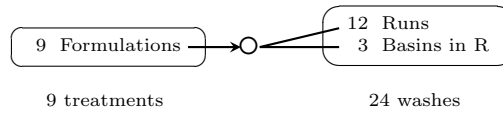


Figure 13: Factor-allocation diagram for the detergent experiment: treatments are allocated to washes; the arrow indicates that the allocation is randomized; the ‘O’ at the end of the arrow indicates that a nonorthogonal design is used; the two lines from ‘O’ indicate that the Treatments are allocated to the combinations of Runs and Basins using the design; Basins in R indicates that the Basins are considered to be nested within Runs for this randomization; R = Runs.

Table 2: Systematic balanced incomplete-block design for 9 treatments in blocks of 3

Run	Basin		
	1	2	3
1	1	2	3
2	4	5	6
3	7	8	9
4	1	4	7
5	2	5	8
6	3	6	9
7	1	5	9
8	2	6	7
9	3	4	8
10	1	6	8
11	2	4	9
12	3	5	7

```

b <- 12
k <- 3
t <- 9

### Input the systematic design and randomize
BIBD.sys <- cbind(fac.gen(list(Runs = b, Basins = k)),
                  Formulations = factor(c(1:9,
                                          1, 4, 7,
                                          2, 5, 8,
                                          3, 6, 9,
                                          1, 5, 9,
                                          2, 6, 7,
                                          3, 4, 8,
                                          1, 6, 8,
                                          2, 4, 9,
                                          3, 5, 7))))

### Randomize the systematic design
BIBD.lay <- designRandomize(allocated = BIBD.sys["Formulations"],
                           recipient = BIBD.sys[c("Runs", "Basins")],
                           nested.recipients = list(Basins = "Runs"),
                           seed = 64686)

#### Check properties of the BIBD
BIBD.canon <- designAnatomy(formulae = list(units = ~ Runs/Basins,
                                             trts = ~ Formulations),

```

```

grandMean = TRUE, data = BIBD.lay)
summary(BIBD.canon, which.criteria = c('aeff', 'order'))

##
##
## Summary table of the decomposition for units & trts (based on adjusted quantities)
##
## Source.units df1 Source.trts df2 aeffericiency order
## Mean 1 Mean 1 1.0000 1
## Runs 11 Formulations 8 0.2500 1
## Residual 3
## Basins[Runs] 24 Formulations 8 0.7500 1
## Residual 16
##
## The design is not orthogonal

```

4.4.2 Add nested factors and check the decomposition using them

```

BIBD.lay <- within(BIBD.lay,
{
  Types <- fac.uselogical(Formulations == "9", labels = c("Control", "New"))
  Bases <- fac.recast(Formulations,
    newlevels = c(rep(c("I", "II"), each = 4), "Control"))
  Additives <- fac.recast(Formulations,
    newlevels = c(rep(c("four", "three", "two", "none"),
      times = 2), "Control"))
})

BIBD.nest.canon <- designAnatomy(formulae = list(units = ~ Runs/Basins,
  trts = ~ Types/(Bases*Additives)),
  grandMean = TRUE, data = BIBD.lay)
summary(BIBD.nest.canon, which.criteria = c('aeff', 'order'))

##
##
## Summary table of the decomposition for units & trts (based on adjusted quantities)
##
## Source.units df1 Source.trts df2 aeffericiency order
## Mean 1 Mean 1 1.0000 1
## Runs 11 Types 1 0.2500 1
## Bases[Types] 1 0.2500 1
## Additives[Types] 3 0.2500 1
## Bases#Additives[Types] 3 0.2500 1
## Residual 3
## Basins[Runs] 24 Types 1 0.7500 1
## Bases[Types] 1 0.7500 1
## Additives[Types] 3 0.7500 1
## Bases#Additives[Types] 3 0.7500 1
## Residual 16
##
## The design is not orthogonal

```

4.4.3 Leave out Types and try decomposition with Bases and Additives in both orders

```
BIBD.nest2.canon <- designAnatomy(formulae = list(units = ~ Runs/Basins,
                                                trts = ~ Bases*Additives),
                                grandMean = TRUE, data = BIBD.lay)
summary(BIBD.nest2.canon, which.criteria = c('aeff', 'order'))

##
##
## Summary table of the decomposition for units & trts (based on adjusted quantities)
##
## Source.units df1 Source.trts      df2 aefficiency order
## Mean          1 Mean              1    1.0000      1
## Runs          11 Bases              2    0.2500      1
##               Additives            3    0.2500      1
##               Bases#Additives      3    0.2500      1
##               Residual              3
## Basins[Runs]  24 Bases              2    0.7500      1
##               Additives            3    0.7500      1
##               Bases#Additives      3    0.7500      1
##               Residual             16
##
## Table of information (partially) aliased with previous sources derived from the same formula
##
## Source    df Alias              In  aefficiency order
## Additives 1 Bases              trts    1.0000      1
## Additives 3 ## Information remaining trts    1.0000      1
##
## The design is not orthogonal

BIBD.nest2.canon <- designAnatomy(formulae = list(units = ~ Runs/Basins,
                                                trts = ~ Additives*Bases),
                                grandMean = TRUE, data = BIBD.lay)
summary(BIBD.nest2.canon, which.criteria = c('aeff', 'order'))

##
##
## Summary table of the decomposition for units & trts (based on adjusted quantities)
##
## Source.units df1 Source.trts      df2 aefficiency order
## Mean          1 Mean              1    1.0000      1
## Runs          11 Additives          4    0.2500      1
##               Bases                1    0.2500      1
##               Additives#Bases      3    0.2500      1
##               Residual              3
## Basins[Runs]  24 Additives          4    0.7500      1
##               Bases                1    0.7500      1
##               Additives#Bases      3    0.7500      1
##               Residual             16
##
## Table of information (partially) aliased with previous sources derived from the same formula
##
## Source df Alias              In  aefficiency order
## Bases  1 Additives          trts    1.0000      1
```



```
## Bases 1 ## Information remaining trts 1.0000 1
##
## The design is not orthogonal
```

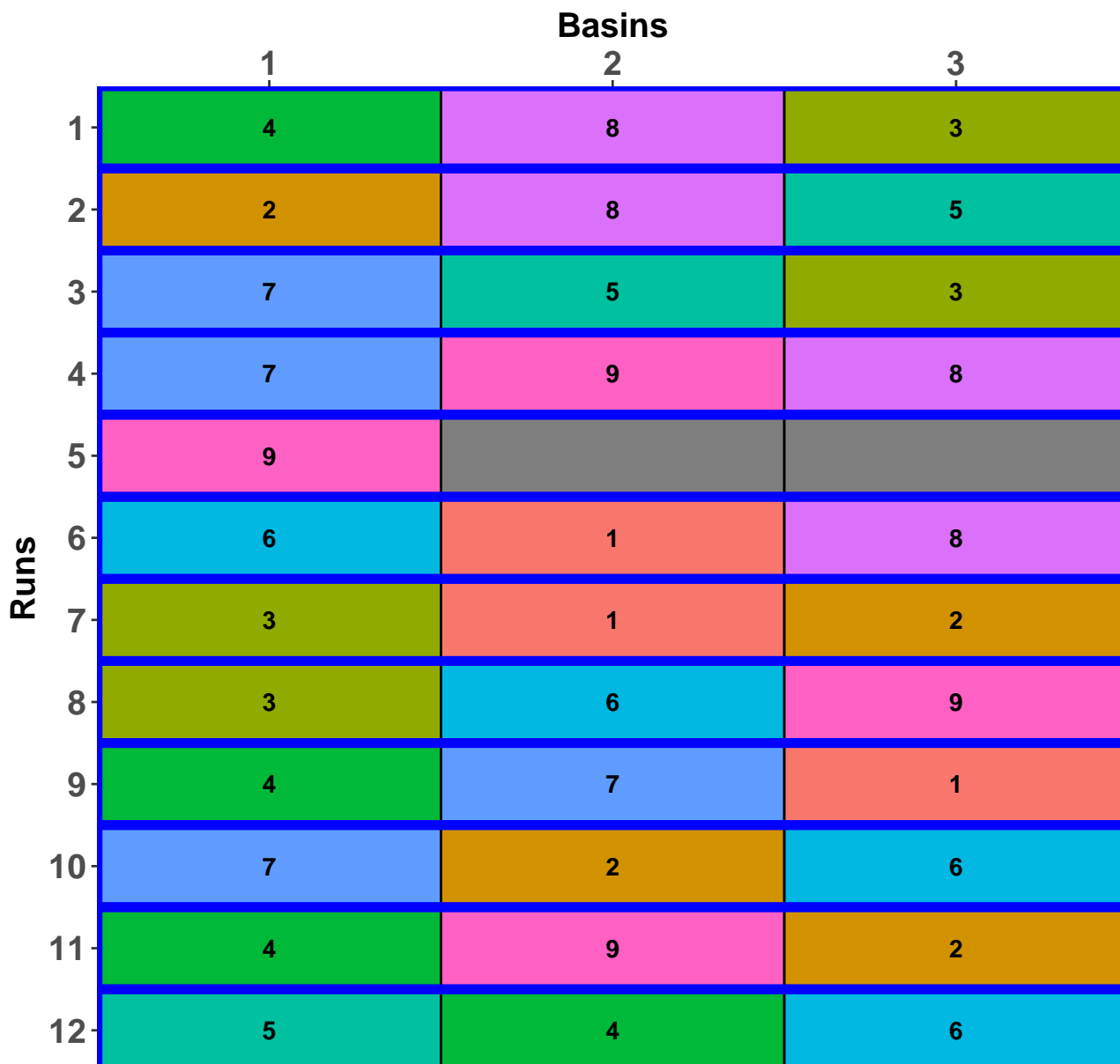
4.4.4 What if two observations are missing?

Two observations that are not the Control are set to missing and the anatomy obtained. The greatest effect is surprisingly on the comparison between the Control and New.

```
## Investigate the effect of two-missing observations
#+ "BIBDDet"
BIBD.Miss.lay <- BIBD.lay
BIBD.Miss.lay$Formulations[c(14,15)] <- NA
designGGPlot(BIBD.Miss.lay, labels = "Formulations",
             row.factors = "Runs", column.factors = "Basins",
             blockdefinition = rbind(c(1,3)))

## Warning: Removed 2 rows containing missing values ('geom_text()').
```

Plot of Formulations



```
BIBD.Miss.canon <- designAnatomy(formulae = list(units = ~ Runs/Basins,
                                                trts = ~ Types/(Bases*Additives)),
                                grandMean = TRUE, data = na.omit(BIBD.Miss.lay))

## Warning in projs.2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Additives[Types] and
Types are partially aliased in Runs
## Warning in projs.2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Bases#Additives[Types]
and Bases[Types] are partially aliased in Runs
## Warning in projs.2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Additives[Types] and
Types are partially aliased in Basins[Runs]
## Warning in projs.2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Bases#Additives[Types]
and Bases[Types] are partially aliased in Basins[Runs]
```

```
summary(BIBD.Miss.canon, which.criteria = c('aeff', 'order'))
```

```
##
##
## Summary table of the decomposition for units & trts (based on adjusted quantities)
##
## Source.units df1 Source.trts          df2 aefficiency order
## Mean          1 Mean          1          1.0000      1
## Runs          11 Types          1          0.4333      1
##              Bases[Types]      1          0.2667      1
##              Additives[Types]   3          0.1899      2
##              Bases#Additives[Types] 3          0.2679      2
##              Residual           3
## Basins[Runs]  22 Types          1          0.5667      1
##              Bases[Types]      1          0.7333      1
##              Additives[Types]   3          0.7759      2
##              Bases#Additives[Types] 3          0.7258      2
##              Residual           14
##
## Table of information (partially) aliased with previous sources derived from the same formula
##
## Source          df Alias          In          aefficiency order
## Additives[Types] 1 Types          Runs          0.1453      1
## Bases#Additives[Types] 1 Bases[Types] Runs          0.0132      1
## Additives[Types] 1 Types          Basins[Runs]  0.0196      1
## Bases#Additives[Types] 1 Bases[Types] Basins[Runs]  0.0022      1
##
## The design is not orthogonal
```

4.4.5 Questions

1. What do you conclude about the properties of the design both without and with the nested factors?

Without the nested factors, the BIBD is balanced. It retains this balance when Formulations is partitioned using the nested factors. This is to be expected with a balanced design because all Formulations contrasts have the same efficiency. The intrablock efficiency factor is 0.75, which is acceptable

2. What is the effect of removing the Types factor?

The one df for Types is included with the main effect fitted immediately after Types. Clearly the Types factor needs to be separated out before fitting the other factors to remove this arbitrariness in composition of sources.

3. What is the advantage of using nested factors for this experiment?

It enables the main effects and interactions of Bases and Additives to be explored.

4. Is there any reason to think that a row-column design might be better than a block design for this experiment?

There would be if the same three operators are used for each Run, and there is reason to believe that systematic differences between the operators. A row-column design would reduce the influence of these differences on the precision of the experiment.

4.5 An experiment to investigate the effects of spraying Sultana grapes

[Clingeffer et al. \(1977\)](#) report an experiment to investigate the effects of tractor speed and spray pressure on the quality of dried sultanas. The response was the lightness of the dried sultanas which is measured using a

Hunterlab D25 L colour difference meter. Lighter sultanas are considered to be of better quality and these will have a higher lightness measurement (L). There were three tractor speeds and two spray pressures resulting in 6 treatment combinations which were applied to 6 plots, each consisting of 12 vines, using a randomized complete-block design with three blocks. However, these 6 treatment combinations resulted in only 4 rates of spray application as indicated in the following table.

Table 3: Application rates for the sprayer experiment

Pressure (kPa)	Tractor speed (km hr ⁻¹)		
	3.6	2.6	1.8
140	2090	2930	4120
330	2930	4120	5770

That is, there are 4 different rates of application, two of which have different combinations of Tractor speed and Spray pressure. So, a factor, Rates, with four levels is set up to compare the means of the four rates and then separate nested factors for each rate are generated.

We set up the RCBD for Speed and Pressure then derive the Rate factors.

```

b <- 3
t <- 6
### Construct a systematic layout
RCBD.sys <- cbind(fac.gen(generate = list(Blocks=b, Plots=t)),
                  fac.gen(generate = list(Pressure = c("140", "330"),
                                          Speed = c("3.6", "2.6", "1.8")), times = b))

### Obtain the randomized layout
RCBD.lay <- designRandomize(allocated = RCBD.sys[c("Pressure", "Speed")],
                           recipient = RCBD.sys[c("Blocks", "Plots")],
                           nested.recipients = list(Plots = "Blocks"),
                           seed = 353441)

### Add nested factors
RCBD.lay <- within(RCBD.lay,
{
  Treatments <- fac.combine(list(Pressure, Speed), combine.levels = TRUE)
  Rates <- fac.recast(Treatments,
                     newlevels = c("2090", "2930", "4120",
                                   "2930", "4120", "5770"))
})
RCBD.lay <- with(RCBD.lay, cbind(RCBD.lay,
                                fac.multinested(nesting.fac = Rates,
                                                nested.fac = Treatments,
                                                fac.prefix = "Rate")))

### Output the layout
RCBD.lay

##   Blocks Plots Pressure Speed Rates Treatments Rate2090 Rate2930 Rate4120 Rate5770
## 1     1     1     330    1.8  5770   330,1.8      rest      rest      rest  330,1.8
## 2     1     2     140    1.8  4120   140,1.8      rest      rest  140,1.8      rest
## 3     1     3     330    3.6  2930   330,3.6      rest  330,3.6      rest      rest
## 4     1     4     140    2.6  2930   140,2.6      rest  140,2.6      rest      rest
## 5     1     5     140    3.6  2090   140,3.6  140,3.6      rest      rest      rest

```

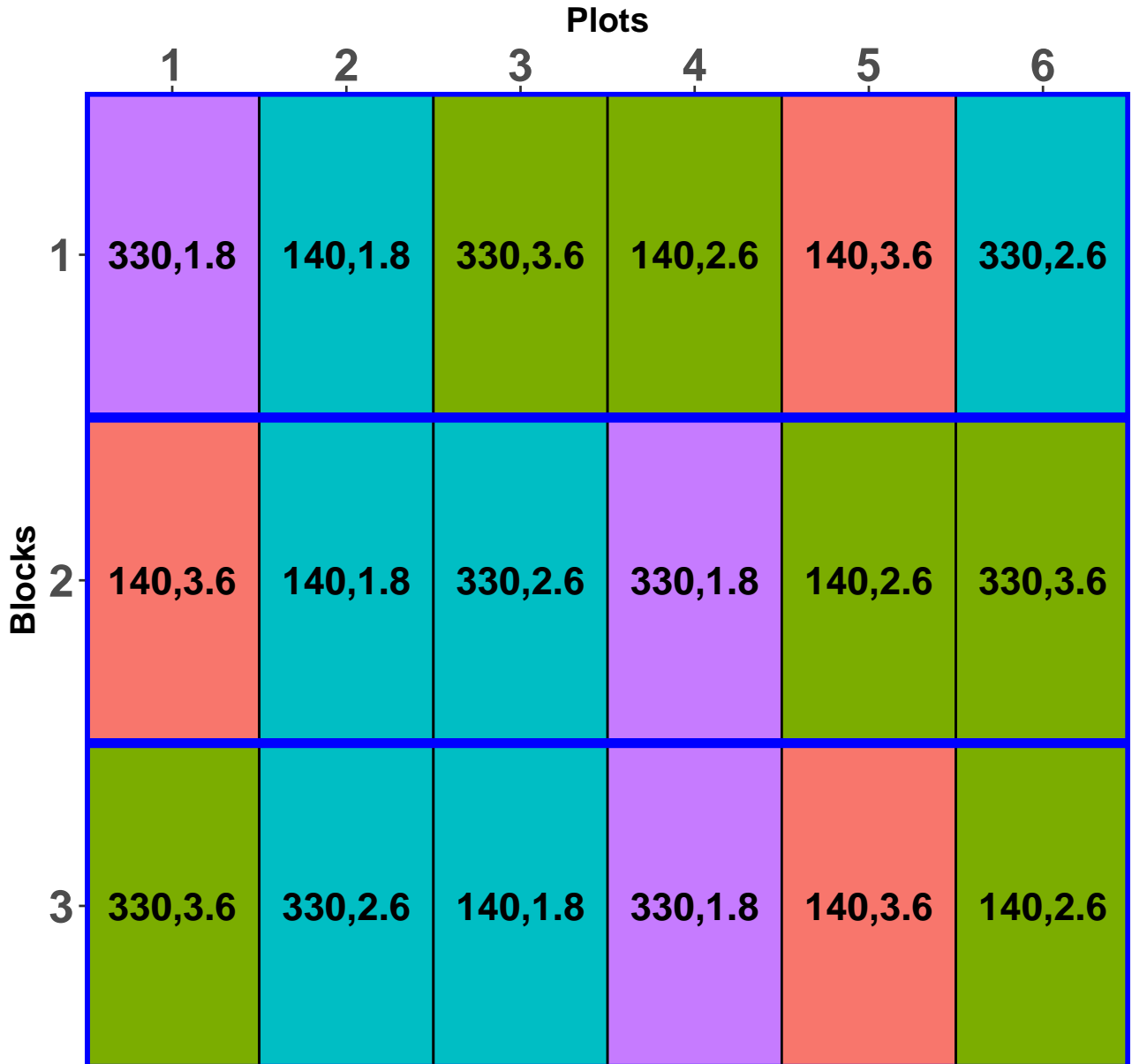
## 6	1	6	330	2.6	4120	330,2.6	rest	rest	330,2.6	rest
## 7	2	1	140	3.6	2090	140,3.6	140,3.6	rest	rest	rest
## 8	2	2	140	1.8	4120	140,1.8	rest	rest	140,1.8	rest
## 9	2	3	330	2.6	4120	330,2.6	rest	rest	330,2.6	rest
## 10	2	4	330	1.8	5770	330,1.8	rest	rest	rest	330,1.8
## 11	2	5	140	2.6	2930	140,2.6	rest	140,2.6	rest	rest
## 12	2	6	330	3.6	2930	330,3.6	rest	330,3.6	rest	rest
## 13	3	1	330	3.6	2930	330,3.6	rest	330,3.6	rest	rest
## 14	3	2	330	2.6	4120	330,2.6	rest	rest	330,2.6	rest
## 15	3	3	140	1.8	4120	140,1.8	rest	rest	140,1.8	rest
## 16	3	4	330	1.8	5770	330,1.8	rest	rest	rest	330,1.8
## 17	3	5	140	3.6	2090	140,3.6	140,3.6	rest	rest	rest
## 18	3	6	140	2.6	2930	140,2.6	rest	140,2.6	rest	rest

```
## Plot the layout
```

```
#+ "RCBDSpray_v1"
```

```
designGGPlot(RCBD.lay, labels = "Treatments",
             cellfillcolour.column = "Rates",
             row.factors = "Blocks", column.factors = "Plots",
             axis.text.size = 20, label.size = 6,
             title = "Plot of Treatments (coloured for Rates)",
             blockdefinition = cbind(1,t))
```

Plot of Treatments (coloured for Rates)



Now check the properties of the design with the nested factors.

```
RCBD.canon <- designAnatomy(formulae = list(units = ~ Blocks/Plots,
                                           trts  = ~ Rates/(Rate2090 + Rate2930 + Rate4120 +
                                                         Rate5770)),
                           grandMean = TRUE, data = RCBD.lay)

## Warning in porthogonalize.list(projectors = Q, formula = formula, keep.order = keep.order,
## : Rates:Rate2090 is aliased with previous terms in the formula and has been removed
## Warning in porthogonalize.list(projectors = Q, formula = formula, keep.order = keep.order,
## : Rates:Rate5770 is aliased with previous terms in the formula and has been removed

summary(RCBD.canon, which.criteria = "aeff")
```

```
##
##
## Summary table of the decomposition for units & trts (based on adjusted quantities)
##
## Source.units df1 Source.trts df2 aeffericiency
## Mean 1 Mean 1 1.0000
## Blocks 2
## Plots[Blocks] 15 Rates 3 1.0000
## Rate2930[Rates] 1 1.0000
## Rate4120[Rates] 1 1.0000
## Residual 10
##
## Table of information (partially) aliased with previous sources derived from the same formula
##
## Source df Alias In aeffericiency
## Rates:Rate2090 3 Rates trts 1.0000
## Rates:Rate2090 0 ## Aliased trts 1.0000
## Rates:Rate5770 3 Rates trts 1.0000
## Rates:Rate5770 0 ## Aliased trts 1.0000
```

4.5.1 Questions

1. What is the prior allocation model for this design?

The initial allocation mixed model is $\text{Pressure} + \text{Speed} + \text{Pressure}:\text{Speed} \mid \text{Blocks} + \underline{\text{Blocks}:\text{Plots}}$. The fixed model is reparameterized to be based on Rates terms: $\text{Rates} + \text{Rates}:\text{Rates2930} + \text{Rates}:\text{Rates4120} \mid \text{Blocks} + \underline{\text{Blocks}:\text{Plots}}$. The fixed model can also be specified simply as $\text{Rates} + \text{Rates2930} + \text{Rates4120}$.

2. How does the prior allocation model differ from the randomization model for this design?

Only in its parameterization of the fixed model, although Blocks might also be moved to the fixed model.

3. Why are terms involving Rate2090 and Rate5770 not included in the prior allocation model?

Because there is only one combination of Pressure and Speed for each of these Rates so that, as shown in the Table of aliasing accompanying the Summary table for the anatomy, both Rate2090 and Rate5770 are aliased with Rates.

4.6 A Control treatment for an incomplete-block design

An incomplete-block design for 6 treatments in 6 blocks of size 4 is obtained from [Cochran and Cox \(1957, p. 379\)](#).

```
b <- 6
k <- 4
t <- 6

##### Input the systematic design and randomize
PBIBD.sys <- cbind(fac.gen(list(Blocks = b, Units = k)),
                   Treatments = factor(c(1,4,2,5,
                                         2,5,3,6,
                                         3,6,1,4,
                                         4,1,5,2,
                                         5,2,6,3,
                                         6,3,4,1))))
```

Randomize the design and check its properties

```
##### Randomize design according to the plots structure
PBIBD.lay <- designRandomize(allocated = PBIBD.sys["Treatments"],
                             recipient = PBIBD.sys[c("Blocks", "Units")],
                             nested.recipients = list(Units = "Blocks"),
                             seed = 65460)

PBIBD.lay

##      Blocks Units Treatments
## 1         1     1           1
## 2         1     2           3
## 3         1     3           4
## 4         1     4           6
## 5         2     1           1
## 6         2     2           2
## 7         2     3           5
## 8         2     4           4
## 9         3     1           4
## 10        3     2           1
## 11        3     3           6
## 12        3     4           3
## 13        4     1           2
## 14        4     2           3
## 15        4     3           6
## 16        4     4           5
## 17        5     1           1
## 18        5     2           4
## 19        5     3           2
## 20        5     4           5
## 21        6     1           2
## 22        6     2           5
## 23        6     3           3
## 24        6     4           6

##### Check properties of the od layout
PBIBD.canon <- designAnatomy(formulae = list(units = ~ Blocks/Units,
                                              trts = ~ Treatments),
                             grandMean = TRUE, data = PBIBD.lay)
summary(PBIBD.canon, which.criteria = c('aeff', 'xeff', 'eeff', 'order', 'dforth'))

##
##
## Summary table of the decomposition for units & trts (based on adjusted quantities)
##
## Source.units  df1 Source.trts df2 aefficiency xefficiency eefficiency order dforthog
## Mean          1 Mean          1    1.0000    1.0000    1.0000    1          1
## Blocks         5 Treatments    2    0.2500    0.2500    0.2500    1          0
##               Residual        3
## Units[Blocks] 18 Treatments    5    0.8824    1.0000    0.7500    2          3
##               Residual        13
##
## The design is not orthogonal
```

Investigate the effect of designating a treatment to be a Control and including a Control factor in the fixed

model. It is noted that, in this case at least, it does not matter which treatment is designated to be the control.

```
##### Investigate a Control contrast (say treatment 1) for the od design
PBIBD.lay$Control <- with(PBIBD.lay, fac.uselogical(Treatments == 1,
                                                    labels = c("Control", "rest")))
PBIBD.canon <- designAnatomy(formulae = list(units = ~ Blocks/Units,
                                           trts = ~ Control + Treatments),
                             grandMean = TRUE, data = PBIBD.lay)

## Warning in projs.2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Treatments[Control] and
## Control are partially aliased in Blocks
## Warning in projs.2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Treatments[Control] and
## Control are partially aliased in Units[Blocks]

summary(PBIBD.canon, which.criteria = c('aeff', 'xeff', 'eeff', 'order', 'dforthog'))

##
##
## Summary table of the decomposition for units & trts (based on adjusted quantities)
##
## Source.units df1 Source.trts df2 aeffecticiency xeffecticiency eeffecticiency order dforthog
## Mean 1 Mean 1 1.0000 1.0000 1.0000 1 1
## Blocks 5 Control 1 0.1000 0.1000 0.1000 1 0
## Treatments[Control] 1 0.2500 0.2500 0.2500 1 0
## Residual 3
## Units[Blocks] 18 Control 1 0.9000 0.9000 0.9000 1 0
## Treatments[Control] 4 0.8824 1.0000 0.7500 3 2
## Residual 13
##
## Table of information (partially) aliased with previous sources derived from the same formula
##
## Source df Alias In aeffecticiency xeffecticiency eeffecticiency order dforthog
## Treatments[Control] 1 Control Blocks 1.0000 1.0000 1.0000 1 1
## Treatments[Control] 1 Control Units[Blocks] 0.0196 0.0196 0.0196 1 0
##
## The design is not orthogonal

##### Try other treatments
PBIBD.lay$Control <- with(PBIBD.lay, fac.uselogical(Treatments == "3",
                                                    labels = c("Control", "rest")))
#Rerun the designAnatomy and summary functions
```

1. Why must the Control source be balanced?

Because it has a single degree of freedom and so there can only be one value for the single efficiency factor.

4.7 The Casuarina experiment (continued)

In Section 3.3 an exploration was made of the properties of the split-unit design for an experiment to investigate the differences between 60 provenances of a species of Casuarina tree, these provenances coming from 18 countries; the trees were inoculated prior to planting at two different times.

The experiment involves nested factors in that the provenances came from 12 countries so that the factor Provenances is nested within Countries. Here we investigate a model that has separate terms for each country that model differences between provenances from each country. Use the `dae` function `fac.multinested` to generate the individual nested factors for each country.

```

### Input the design
data(Casuarina.dat)
### Add the nested factors
Casuarina.dat <- cbind(Casuarina.dat,
                      with(Casuarina.dat, fac.multinested(nesting.fac = Countries,
                                                          nested.fac = Provenances,
                                                          fac.prefix = "Prov_"))))

```

This example has two difficulties that need to be dealt with. Firstly, a number of Countries contribute only one Provenance and terms for differences amongst provenances from those countries are superfluous. Secondly, because of the large number of terms and considerable nonorthogonality in the design, it is difficult to get a full decomposition. To overcome this, the following measures are taken:

- Leave out nested terms for countries with only a single provenance;
- Reduce the tolerances on testing for idempotency using the function `set.daeTolerance`;
- Do not attempt to partition the `InocTimes#Provenances[Countries]` interaction.

```

### Produce a list of Countries that have one than Provenance and construct the trts formula
fac.names <- paste0("Prov_", levels(Casuarina.dat$Countries))
no.prov <- unlist(lapply(Casuarina.dat[fac.names], function(fac) length(levels(fac[1]))-1))
(multProv <- names(no.prov[no.prov > 1]))

## [1] "Prov_Australia" "Prov_China" "Prov_Egypt" "Prov_Fiji" "Prov_India"
## [6] "Prov_Kenya" "Prov_Malaysia" "Prov_Phillipines" "Prov_SolomomIs" "Prov_SriLanka"
## [11] "Prov_Thailand" "Prov_Vanuatu" "Prov_Vietnam"

trts.form <- as.formula(paste0("~ Countries/(",
                              paste0(multProv, collapse = "+"),
                              ")+InocTime/Countries/Provenances"))

(trts.form)

## ~Countries/(Prov_Australia + Prov_China + Prov_Egypt + Prov_Fiji +
## Prov_India + Prov_Kenya + Prov_Malaysia + Prov_Phillipines +
## Prov_SolomomIs + Prov_SriLanka + Prov_Thailand + Prov_Vanuatu +
## Prov_Vietnam) + InocTime/Countries/Provenances

### Check the properties of the design
set.daeTolerance(1e-05)
Casuarina.canon <- designAnatomy(formulae = list(units = ~ (Reps/Rows)*Columns,
                                                trts = trts.form),
                                keep.order = TRUE,
                                grandMean = TRUE,
                                data = Casuarina.dat)

## Warning in projs.2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Prov_Australia[Countries]
## and Countries are partially aliased in Rows[Reps]
## Warning in projs.2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Prov_Australia[Countries]
## and Countries are partially aliased in Reps#Columns
## Warning in projs.2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Prov_China[Countries]
## and Countries are partially aliased in Reps#Columns
## Warning in projs.2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Prov_China[Countries]
## and Prov_Australia[Countries] are partially aliased in Reps#Columns

```

[illegible]

[illegible]


```
## Warning in projS.2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): InocTime#Provenances[Countries]
and Countries#InocTime are partially aliased in Rows#Columns[Reps]
```

```
summary(Casuarina.canon, which = c("aeff", "eeff", "order", "dforth"))
```

```
##
```

```
##
```

```
## Summary table of the decomposition for units & trts (based on adjusted quantities)
```

```
##
```

Source.units	df1	Source.trts	df2	aefficiency	eefficiency	order	dforthog
Mean	1	Mean	1	1.0000	1.0000	1	1
Reps	3	InocTime	1	1.0000	1.0000	1	1
		Residual	2				
Rows[Reps]	20	Countries	17	0.0145	0.0018	17	0
		Prov_Australia[Countries]	3	0.0001	0.0000	3	0
Columns	9	Countries	9	0.0137	0.0028	9	0
Reps#Columns	27	Countries	17	0.0134	0.0012	17	0
		Prov_Australia[Countries]	3	0.0522	0.0350	3	0
		Prov_China[Countries]	1	0.0318	0.0318	1	0
		Prov_Egypt[Countries]	2	0.0044	0.0023	2	0
		Prov_Fiji[Countries]	2	0.0041	0.0021	2	0
		Prov_India[Countries]	2	0.0705	0.0566	2	0
Rows#Columns[Reps]	180	Countries	17	0.7611	0.5588	17	0
		Prov_Australia[Countries]	3	0.7259	0.6874	3	0
		Prov_China[Countries]	2	0.7260	0.6771	2	0
		Prov_Egypt[Countries]	2	0.7346	0.7309	2	0
		Prov_Fiji[Countries]	2	0.7314	0.6754	2	0
		Prov_India[Countries]	5	0.7097	0.6231	5	0
		Prov_Kenya[Countries]	7	0.7128	0.6269	7	0
		Prov_Malaysia[Countries]	8	0.7120	0.5745	8	0
		Prov_Phillipines[Countries]	2	0.6736	0.6704	2	0
		Prov_SolomomIs[Countries]	1	0.6838	0.6838	1	0
		Prov_SriLanka[Countries]	2	0.7220	0.6759	2	0
		Prov_Thailand[Countries]	3	0.7069	0.6701	3	0
		Prov_Vanuatu[Countries]	1	0.7297	0.7297	1	0
		Prov_Vietnam[Countries]	4	0.6975	0.6281	4	0
		Countries#InocTime	17	0.6808	0.4735	17	0
		InocTime#Provenances[Countries]	42	0.5516	0.2009	42	0
		Residual	62				

```
##
```

```
## Table of information (partially) aliased with previous sources derived from the same formula
```

```
##
```

Source	df	Alias	In	aefficiency
Prov_Australia[Countries]	3	Countries	Rows[Reps]	0.9251
Prov_Australia[Countries]	3	Countries	Reps#Columns	0.5010
Prov_China[Countries]	2	Countries	Reps#Columns	0.6772
Prov_China[Countries]	2	Prov_Australia[Countries]	Reps#Columns	0.0597
Prov_Egypt[Countries]	2	Countries	Reps#Columns	0.7933
Prov_Fiji[Countries]	2	Countries	Reps#Columns	0.4978
Prov_Fiji[Countries]	2	Prov_Australia[Countries]	Reps#Columns	0.0028
Prov_Fiji[Countries]	2	Prov_Egypt[Countries]	Reps#Columns	0.0645
Prov_India[Countries]	5	Countries	Reps#Columns	0.3421
Prov_India[Countries]	3	Prov_Australia[Countries]	Reps#Columns	0.1025
Prov_India[Countries]	2	Prov_China[Countries]	Reps#Columns	0.0613

##	Prov_India[Countries]	2	Prov_Egypt[Countries]	Reps#Columns	0.0173
##	Prov_India[Countries]	2	Prov_Fiji[Countries]	Reps#Columns	0.0321
##	Prov_Australia[Countries]	3	Countries	Rows#Columns[Reps]	0.0161
##	Prov_China[Countries]	2	Countries	Rows#Columns[Reps]	0.0178
##	Prov_China[Countries]	2	Prov_Australia[Countries]	Rows#Columns[Reps]	0.0003
##	Prov_Egypt[Countries]	2	Countries	Rows#Columns[Reps]	0.0245
##	Prov_Egypt[Countries]	2	Prov_China[Countries]	Rows#Columns[Reps]	0.0028
##	Prov_Fiji[Countries]	2	Countries	Rows#Columns[Reps]	0.0110
##	Prov_Fiji[Countries]	2	Prov_Australia[Countries]	Rows#Columns[Reps]	0.0007
##	Prov_Fiji[Countries]	2	Prov_Egypt[Countries]	Rows#Columns[Reps]	0.0005
##	Prov_India[Countries]	5	Countries	Rows#Columns[Reps]	0.0115
##	Prov_India[Countries]	3	Prov_Australia[Countries]	Rows#Columns[Reps]	0.0040
##	Prov_India[Countries]	2	Prov_China[Countries]	Rows#Columns[Reps]	0.0036
##	Prov_India[Countries]	2	Prov_Egypt[Countries]	Rows#Columns[Reps]	0.0014
##	Prov_India[Countries]	2	Prov_Fiji[Countries]	Rows#Columns[Reps]	0.0042
##	Prov_Kenya[Countries]	7	Countries	Rows#Columns[Reps]	0.0083
##	Prov_Kenya[Countries]	3	Prov_Australia[Countries]	Rows#Columns[Reps]	0.0102
##	Prov_Kenya[Countries]	2	Prov_China[Countries]	Rows#Columns[Reps]	0.0082
##	Prov_Kenya[Countries]	2	Prov_Egypt[Countries]	Rows#Columns[Reps]	0.0065
##	Prov_Kenya[Countries]	2	Prov_Fiji[Countries]	Rows#Columns[Reps]	0.0035
##	Prov_Kenya[Countries]	5	Prov_India[Countries]	Rows#Columns[Reps]	0.0015
##	Prov_Malaysia[Countries]	8	Countries	Rows#Columns[Reps]	0.0068
##	Prov_Malaysia[Countries]	3	Prov_Australia[Countries]	Rows#Columns[Reps]	0.0058
##	Prov_Malaysia[Countries]	2	Prov_China[Countries]	Rows#Columns[Reps]	0.0093
##	Prov_Malaysia[Countries]	2	Prov_Egypt[Countries]	Rows#Columns[Reps]	0.0079
##	Prov_Malaysia[Countries]	2	Prov_Fiji[Countries]	Rows#Columns[Reps]	0.0088
##	Prov_Malaysia[Countries]	5	Prov_India[Countries]	Rows#Columns[Reps]	0.0077
##	Prov_Malaysia[Countries]	7	Prov_Kenya[Countries]	Rows#Columns[Reps]	0.0005
##	Prov_Phillipines[Countries]	2	Countries	Rows#Columns[Reps]	0.0199
##	Prov_Phillipines[Countries]	2	Prov_Australia[Countries]	Rows#Columns[Reps]	0.0018
##	Prov_Phillipines[Countries]	2	Prov_China[Countries]	Rows#Columns[Reps]	0.0033
##	Prov_Phillipines[Countries]	2	Prov_Egypt[Countries]	Rows#Columns[Reps]	0.0017
##	Prov_Phillipines[Countries]	2	Prov_India[Countries]	Rows#Columns[Reps]	0.0116
##	Prov_Phillipines[Countries]	2	Prov_Kenya[Countries]	Rows#Columns[Reps]	0.0030
##	Prov_Phillipines[Countries]	2	Prov_Malaysia[Countries]	Rows#Columns[Reps]	0.0090
##	Prov_SolomomIs[Countries]	1	Countries	Rows#Columns[Reps]	0.0244
##	Prov_SolomomIs[Countries]	1	Prov_Kenya[Countries]	Rows#Columns[Reps]	0.0103
##	Prov_SolomomIs[Countries]	1	Prov_Malaysia[Countries]	Rows#Columns[Reps]	0.0108
##	Prov_SriLanka[Countries]	2	Countries	Rows#Columns[Reps]	0.0192
##	Prov_SriLanka[Countries]	2	Prov_Australia[Countries]	Rows#Columns[Reps]	0.0020
##	Prov_SriLanka[Countries]	2	Prov_China[Countries]	Rows#Columns[Reps]	0.0062
##	Prov_SriLanka[Countries]	2	Prov_Egypt[Countries]	Rows#Columns[Reps]	0.0017
##	Prov_SriLanka[Countries]	2	Prov_Kenya[Countries]	Rows#Columns[Reps]	0.0079
##	Prov_SriLanka[Countries]	2	Prov_Malaysia[Countries]	Rows#Columns[Reps]	0.0027
##	Prov_Thailand[Countries]	3	Countries	Rows#Columns[Reps]	0.0109
##	Prov_Thailand[Countries]	3	Prov_Australia[Countries]	Rows#Columns[Reps]	0.0000
##	Prov_Thailand[Countries]	2	Prov_China[Countries]	Rows#Columns[Reps]	0.0003
##	Prov_Thailand[Countries]	2	Prov_Egypt[Countries]	Rows#Columns[Reps]	0.0024
##	Prov_Thailand[Countries]	2	Prov_Fiji[Countries]	Rows#Columns[Reps]	0.0065
##	Prov_Thailand[Countries]	3	Prov_India[Countries]	Rows#Columns[Reps]	0.0014
##	Prov_Thailand[Countries]	3	Prov_Kenya[Countries]	Rows#Columns[Reps]	0.0059
##	Prov_Thailand[Countries]	3	Prov_Malaysia[Countries]	Rows#Columns[Reps]	0.0021
##	Prov_Thailand[Countries]	2	Prov_Phillipines[Countries]	Rows#Columns[Reps]	0.0019

##	Prov_Vanuatu[Countries]	1	Countries	Rows#Columns[Reps]	0.0185
##	Prov_Vanuatu[Countries]	1	Prov_China[Countries]	Rows#Columns[Reps]	0.0107
##	Prov_Vanuatu[Countries]	1	Prov_India[Countries]	Rows#Columns[Reps]	0.0070
##	Prov_Vanuatu[Countries]	1	Prov_Kenya[Countries]	Rows#Columns[Reps]	0.0103
##	Prov_Vanuatu[Countries]	1	Prov_Malaysia[Countries]	Rows#Columns[Reps]	0.0044
##	Prov_Vanuatu[Countries]	1	Prov_SriLanka[Countries]	Rows#Columns[Reps]	0.0072
##	Prov_Vietnam[Countries]	4	Countries	Rows#Columns[Reps]	0.0144
##	Prov_Vietnam[Countries]	3	Prov_Australia[Countries]	Rows#Columns[Reps]	0.0021
##	Prov_Vietnam[Countries]	2	Prov_China[Countries]	Rows#Columns[Reps]	0.0028
##	Prov_Vietnam[Countries]	2	Prov_Egypt[Countries]	Rows#Columns[Reps]	0.0025
##	Prov_Vietnam[Countries]	4	Prov_India[Countries]	Rows#Columns[Reps]	0.0017
##	Prov_Vietnam[Countries]	4	Prov_Kenya[Countries]	Rows#Columns[Reps]	0.0031
##	Prov_Vietnam[Countries]	4	Prov_Malaysia[Countries]	Rows#Columns[Reps]	0.0019
##	Prov_Vietnam[Countries]	2	Prov_Phillipines[Countries]	Rows#Columns[Reps]	0.0061
##	Prov_Vietnam[Countries]	2	Prov_SriLanka[Countries]	Rows#Columns[Reps]	0.0080
##	Prov_Vietnam[Countries]	3	Prov_Thailand[Countries]	Rows#Columns[Reps]	0.0005
##	Countries#InocTime	17	Countries	Rows#Columns[Reps]	0.0001
##	Countries#InocTime	3	Prov_Australia[Countries]	Rows#Columns[Reps]	0.0147
##	Countries#InocTime	2	Prov_China[Countries]	Rows#Columns[Reps]	0.0186
##	Countries#InocTime	2	Prov_Egypt[Countries]	Rows#Columns[Reps]	0.0182
##	Countries#InocTime	2	Prov_Fiji[Countries]	Rows#Columns[Reps]	0.0085
##	Countries#InocTime	5	Prov_India[Countries]	Rows#Columns[Reps]	0.0114
##	Countries#InocTime	7	Prov_Kenya[Countries]	Rows#Columns[Reps]	0.0095
##	Countries#InocTime	8	Prov_Malaysia[Countries]	Rows#Columns[Reps]	0.0100
##	Countries#InocTime	2	Prov_Phillipines[Countries]	Rows#Columns[Reps]	0.0263
##	Countries#InocTime	1	Prov_SolomomIs[Countries]	Rows#Columns[Reps]	0.0198
##	Countries#InocTime	2	Prov_SriLanka[Countries]	Rows#Columns[Reps]	0.0126
##	Countries#InocTime	3	Prov_Thailand[Countries]	Rows#Columns[Reps]	0.0211
##	Countries#InocTime	1	Prov_Vanuatu[Countries]	Rows#Columns[Reps]	0.0099
##	Countries#InocTime	4	Prov_Vietnam[Countries]	Rows#Columns[Reps]	0.0162
##	InocTime#Provenances[Countries]	17	Countries	Rows#Columns[Reps]	0.0222
##	InocTime#Provenances[Countries]	3	Prov_Australia[Countries]	Rows#Columns[Reps]	0.0647
##	InocTime#Provenances[Countries]	2	Prov_China[Countries]	Rows#Columns[Reps]	0.0604
##	InocTime#Provenances[Countries]	2	Prov_Egypt[Countries]	Rows#Columns[Reps]	0.0636
##	InocTime#Provenances[Countries]	2	Prov_Fiji[Countries]	Rows#Columns[Reps]	0.0779
##	InocTime#Provenances[Countries]	5	Prov_India[Countries]	Rows#Columns[Reps]	0.0693
##	InocTime#Provenances[Countries]	7	Prov_Kenya[Countries]	Rows#Columns[Reps]	0.0528
##	InocTime#Provenances[Countries]	8	Prov_Malaysia[Countries]	Rows#Columns[Reps]	0.0488
##	InocTime#Provenances[Countries]	2	Prov_Phillipines[Countries]	Rows#Columns[Reps]	0.0750
##	InocTime#Provenances[Countries]	1	Prov_SolomomIs[Countries]	Rows#Columns[Reps]	0.0579
##	InocTime#Provenances[Countries]	2	Prov_SriLanka[Countries]	Rows#Columns[Reps]	0.0502
##	InocTime#Provenances[Countries]	3	Prov_Thailand[Countries]	Rows#Columns[Reps]	0.0720
##	InocTime#Provenances[Countries]	1	Prov_Vanuatu[Countries]	Rows#Columns[Reps]	0.0442
##	InocTime#Provenances[Countries]	4	Prov_Vietnam[Countries]	Rows#Columns[Reps]	0.0527
##	InocTime#Provenances[Countries]	17	Countries#InocTime	Rows#Columns[Reps]	0.0178
##	eefficiency order dforthog				
##	0.8435	3	0		
##	0.3667	3	0		
##	0.5119	2	1		
##	0.0349	2	0		
##	0.6920	2	0		
##	0.3561	2	0		
##	0.0014	2	0		

##	0.0514	2	0
##	0.1666	5	0
##	0.0708	3	0
##	0.0356	2	0
##	0.0092	2	0
##	0.0174	2	0
##	0.0113	3	0
##	0.0120	2	0
##	0.0002	2	0
##	0.0229	2	0
##	0.0020	2	0
##	0.0063	2	0
##	0.0004	2	0
##	0.0002	2	0
##	0.0040	5	0
##	0.0018	3	0
##	0.0021	2	0
##	0.0008	2	0
##	0.0026	2	0
##	0.0025	7	0
##	0.0059	3	0
##	0.0059	2	0
##	0.0043	2	0
##	0.0023	2	0
##	0.0004	5	0
##	0.0017	8	0
##	0.0033	3	0
##	0.0063	2	0
##	0.0058	2	0
##	0.0066	2	0
##	0.0033	5	0
##	0.0001	7	0
##	0.0162	2	0
##	0.0009	2	0
##	0.0022	2	0
##	0.0010	2	0
##	0.0088	2	0
##	0.0017	2	0
##	0.0065	2	0
##	0.0244	1	0
##	0.0103	1	0
##	0.0108	1	0
##	0.0161	2	0
##	0.0015	2	0
##	0.0039	2	0
##	0.0010	2	0
##	0.0067	2	0
##	0.0014	2	0
##	0.0063	3	0
##	0.0000	3	0
##	0.0001	2	0
##	0.0016	2	0
##	0.0059	2	0

```

##      0.0006      3      0
##      0.0034      3      0
##      0.0009      3      0
##      0.0010      2      0
##      0.0185      1      0
##      0.0107      1      0
##      0.0070      1      0
##      0.0103      1      0
##      0.0044      1      0
##      0.0072      1      0
##      0.0067      4      0
##      0.0009      3      0
##      0.0020      2      0
##      0.0019      2      0
##      0.0007      4      0
##      0.0012      4      0
##      0.0007      4      0
##      0.0053      2      0
##      0.0053      2      0
##      0.0002      3      0
##      0.0000     17      0
##      0.0090      3      0
##      0.0138      2      0
##      0.0148      2      0
##      0.0052      2      0
##      0.0038      5      0
##      0.0027      7      0
##      0.0026      8      0
##      0.0208      2      0
##      0.0198      1      0
##      0.0073      2      0
##      0.0153      3      0
##      0.0099      1      0
##      0.0102      4      0
##      0.0042     17      0
##      0.0497      3      0
##      0.0515      2      0
##      0.0489      2      0
##      0.0598      2      0
##      0.0395      5      0
##      0.0273      7      0
##      0.0228      8      0
##      0.0626      2      0
##      0.0579      1      0
##      0.0426      2      0
##      0.0501      3      0
##      0.0442      1      0
##      0.0348      4      0
##      0.0025     17      0
##
## The design is not orthogonal

```

4.7.1 Questions

1. How does this analysis compare with that conducted in Section 3.3?

The 42 df for Provenances[Countries] has been split into the differences between provenances for each country. Otherwise, the decompositions are the same.

5 Multiphase experiments in R

This class of experiments differs from those previously presented in that they often employ two or more randomizations or allocations, each to a different type of unit. As a result, there will be three or more sets of factors, or tiers, to deal with; further, when there are three sets of factors, three formula will need to be supplied to `designAnatomy`.

5.1 Athletic examples based on Brien et al. (2011)

Brien et al. (2011) give several designs for an athletic experiment that illustrate the basic principles to be employed in designing multiphase experiments. Here designs for two different multiphase scenarios are considered, both being based on a first-phase that is the testing phase and employs a split-unit design.

5.1.1 A standard single-phase athlete training experiment

First, a split-unit design is generated for an experiment in which the performance of an athlete when subject to nine different training conditions is tested. The nine training conditions are the combinations of three surfaces and three intensities of training. Also, assume that the prime interest is in surface differences, with intensities included to observe the surfaces over a range of intensities. The experiment is to involve 12 athletes, three per month for four consecutive months; each athlete undergoes three tests. The heart rate of the athlete is to be taken immediately upon completion of a test.

A split-plot design is to be employed for the experiment: the three intensities are randomized to the three athletes in each month and the three surfaces are randomized to the three tests that each athlete is to undergo. The factor-allocation diagram is shown in Figure 14. Generate a randomized layout for the experiment.

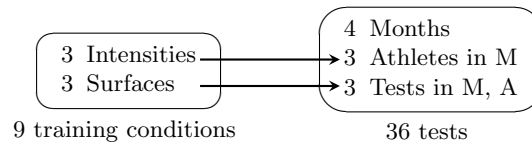


Figure 14: Factor-allocation diagram for the standard athlete training experiment: training conditions are randomized to tests; the two left-hand arrows indicate that the levels of Intensities and Surfaces are randomized to Athletes and Tests, respectively; M = Months; A = Athletes.

```
#'## Phase 1: Construct a systematic layout and generate a randomized layout for the first phase
split.sys <- cbind(fac.gen(list(Months = 4, Athletes = 3, Tests = 3)),
                  fac.gen(list(Intensities = LETTERS[1:3], Surfaces = 3),
                            times = 4))
split.lay <- designRandomize(allocated = split.sys[c("Intensities", "Surfaces")],
                             recipient = split.sys[c("Months", "Athletes", "Tests")],
                             nested.recipients = list(Athletes = "Months",
                                                         Tests = c("Months", "Athletes")),
                             seed = 2598)

split.lay
```

##	Months	Athletes	Tests	Intensities	Surfaces
## 1	1	1	1	B	3
## 2	1	1	2	B	2
## 3	1	1	3	B	1
## 4	1	2	1	C	2
## 5	1	2	2	C	1
## 6	1	2	3	C	3
## 7	1	3	1	A	1
## 8	1	3	2	A	2

```

## 9      1      3      3      A      3
## 10     2      1      1      B      1
## 11     2      1      2      B      2
## 12     2      1      3      B      3
## 13     2      2      1      A      3
## 14     2      2      2      A      2
## 15     2      2      3      A      1
## 16     2      3      1      C      1
## 17     2      3      2      C      3
## 18     2      3      3      C      2
## 19     3      1      1      B      1
## 20     3      1      2      B      3
## 21     3      1      3      B      2
## 22     3      2      1      C      2
## 23     3      2      2      C      3
## 24     3      2      3      C      1
## 25     3      3      1      A      2
## 26     3      3      2      A      3
## 27     3      3      3      A      1
## 28     4      1      1      A      3
## 29     4      1      2      A      2
## 30     4      1      3      A      1
## 31     4      2      1      B      1
## 32     4      2      2      B      2
## 33     4      2      3      B      3
## 34     4      3      1      C      1
## 35     4      3      2      C      3
## 36     4      3      3      C      2

### Get anatomy to check properties of the design
split.canon <- designAnatomy(formulae = list(tests = ~ Months/Athletes/Tests,
                                             cond = ~ Intensities*Surfaces),
                             grandMean = TRUE, data = split.lay)
summary(split.canon, which.criteria="none")

##
##
## Summary table of the decomposition for tests & cond
##
## Source.tests      df1 Source.cond      df2
## Mean              1 Mean              1
## Months            3
## Athletes[Months]  8 Intensities        2
##                   Residual            6
## Tests[Months:Athletes] 24 Surfaces        2
##                   Intensities#Surfaces  4
##                   Residual            18

### Plot the design
#+ "SplitDes_v2"
split.lay <- within(split.lay,
                    Conditions <- fac.combine(list(Intensities, Surfaces),
                                             combine.levels = TRUE))
plt <- designGGPlot(split.lay, labels = "Conditions",

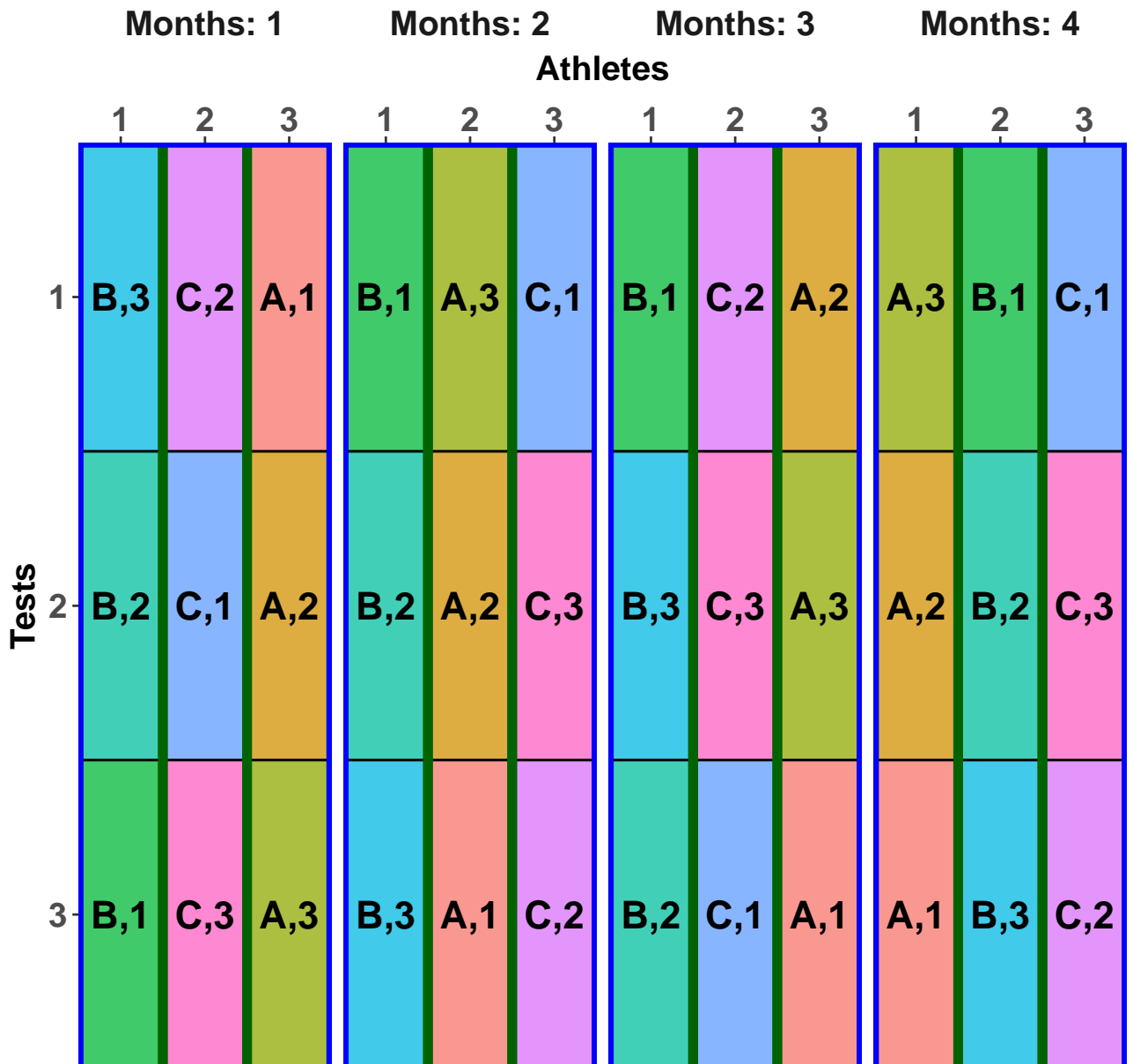
```

```

row.factors = "Tests", column.factors = c("Months", "Athletes"),
cellalpha = 0.75, label.size = 6,
blockdefinition = rbind(c(3,1)), blocklinecolour = "darkgreen",
printPlot = FALSE)
designBlocksGGPlot(plt, nrows = 3, ncolums = 3, blockdefinition = rbind(c(3,3)),
facetstrips.placement = "outside.title")

```

Plot of Conditions



Question

1. Why was a split-plot design chosen for this experiment?

Because it is likely that variation between tests within an athlete will be smaller than variation between

athletes within a month. Hence, because the prime interest is in Surfaces, they are assigned to tests within an athlete and will have better precision than Intensities, which have been assigned to the more variable athletes within a month.

5.1.2 A simple two-phase athlete training experiment

Suppose that, in addition to heart rate taken immediately upon completion of a test, the free haemoglobin is to be measured using blood specimens taken from the athletes after each test and transported to the laboratory for analysis. That is, a second laboratory phase is required to obtain the new response. In this phase, because the specimens become available monthly, the batch of specimens for one month are to be processed, in a random order, before those for the next month are available. The factor-allocation diagram for this experiment is in Figure 15, the dashed line indicating that Months are systematically allocated to Batches. The randomizations in this diagram are composed (Brien and Bailey, 2006) and is one of the two types of randomizations in a chain (Bailey and Brien, 2016). This means that the second-phase randomization only need to consider how the tests factors are to be assigned to locations; training conditions can be ignored in determining the second-phase design.

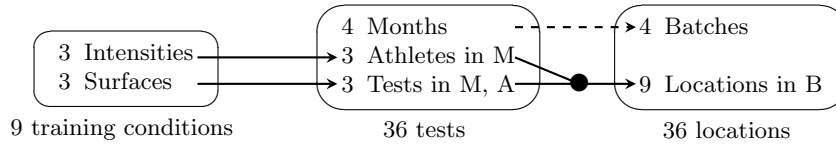


Figure 15: Factor-allocation diagram for the two-phase athlete training experiment: training conditions are randomized to tests and tests are allocated to locations; the two left-hand arrows indicate that the levels of Intensities and Surfaces are randomized to Athletes and Tests, respectively; the dashed arrow indicates that Months are systematically allocated to Batches; the '●' indicates that the combinations of the levels of Athletes and Tests are randomized to the Locations; M = Months; A = Athletes; B = Batches.

Using the following R code, obtain a layout for the second phase and check the properties of the layout. In doing this, the first-phase layout is randomized. However, because Months is not randomized to Batches, the argument `except` in `designRandomize` is used to effect the systematic allocation.

```
## Generate a layout for a simple two-phase athlete training experiment
#
### Phase 1 - the split-plot design that has already been generated.
### Phase 2 - randomize tests (and training conditions) to locations,
###           but Months assigned systematically to Batches
###           so except Batches from the randomization
eg1.lay <- designRandomize(allocated = split.lay,
                           recipient  = list(Batches = 4, Locations = 9),
                           nested.recipients = list(Locations = "Batches"),
                           except      = "Batches",
                           seed       = 71230)

eg1.lay
```

##	Batches	Locations	Months	Athletes	Tests	Intensities	Surfaces	Conditions
## 1	1	1	1	2	3	C	3	C,3
## 2	1	2	1	1	2	B	2	B,2
## 3	1	3	1	2	2	C	1	C,1
## 4	1	4	1	3	1	A	1	A,1
## 5	1	5	1	3	2	A	2	A,2
## 6	1	6	1	1	1	B	3	B,3
## 7	1	7	1	2	1	C	2	C,2
## 8	1	8	1	1	3	B	1	B,1
## 9	1	9	1	3	3	A	3	A,3
## 10	2	1	2	3	1	C	1	C,1
## 11	2	2	2	2	2	A	2	A,2

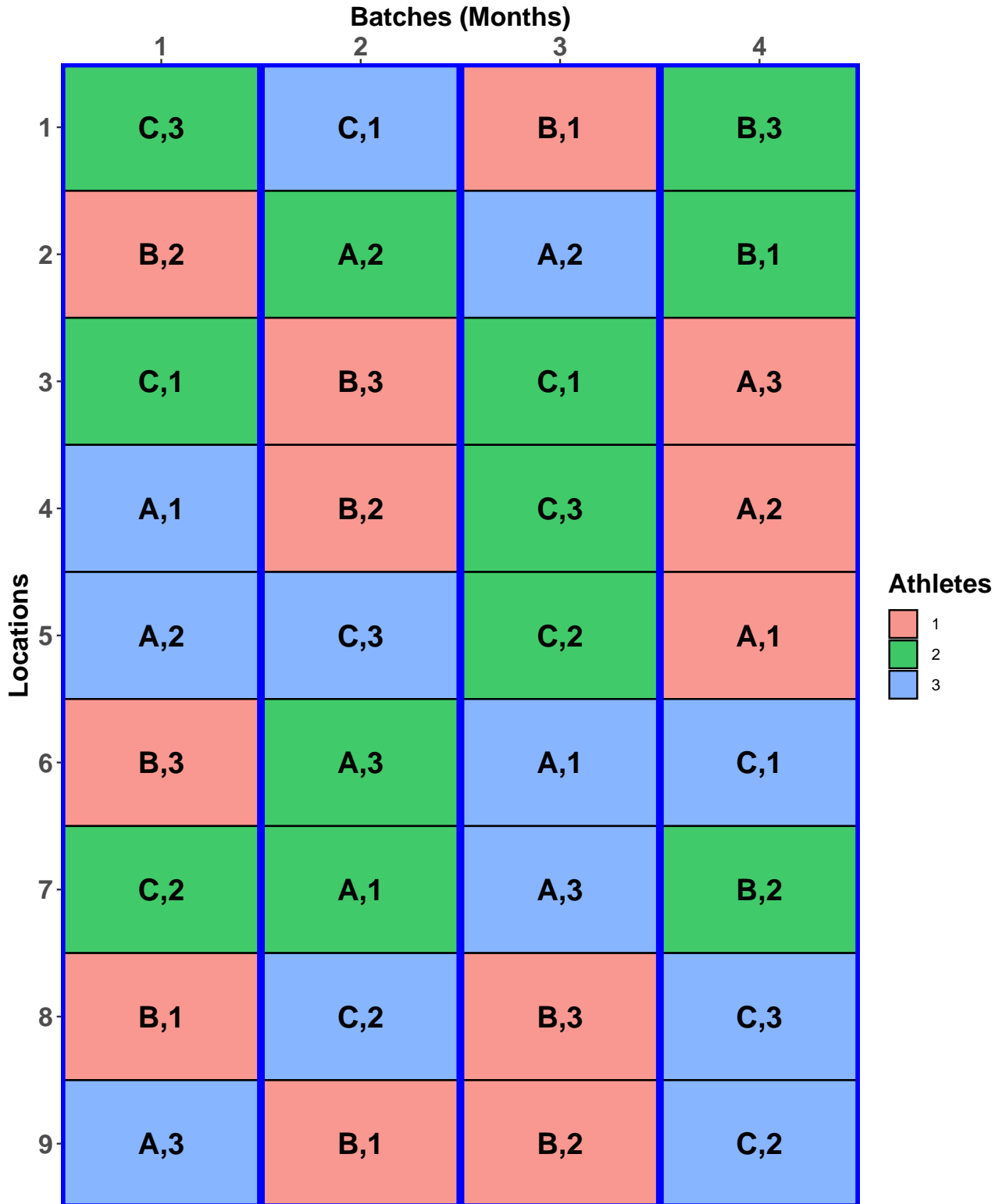
## 12	2	3	2	1	3	B	3	B,3
## 13	2	4	2	1	2	B	2	B,2
## 14	2	5	2	3	2	C	3	C,3
## 15	2	6	2	2	1	A	3	A,3
## 16	2	7	2	2	3	A	1	A,1
## 17	2	8	2	3	3	C	2	C,2
## 18	2	9	2	1	1	B	1	B,1
## 19	3	1	3	1	1	B	1	B,1
## 20	3	2	3	3	1	A	2	A,2
## 21	3	3	3	2	3	C	1	C,1
## 22	3	4	3	2	2	C	3	C,3
## 23	3	5	3	2	1	C	2	C,2
## 24	3	6	3	3	3	A	1	A,1
## 25	3	7	3	3	2	A	3	A,3
## 26	3	8	3	1	2	B	3	B,3
## 27	3	9	3	1	3	B	2	B,2
## 28	4	1	4	2	3	B	3	B,3
## 29	4	2	4	2	1	B	1	B,1
## 30	4	3	4	1	1	A	3	A,3
## 31	4	4	4	1	2	A	2	A,2
## 32	4	5	4	1	3	A	1	A,1
## 33	4	6	4	3	1	C	1	C,1
## 34	4	7	4	2	2	B	2	B,2
## 35	4	8	4	3	2	C	3	C,3
## 36	4	9	4	3	3	C	2	C,2

```

##'## Plot the layout
##+ Athlete_eg1lay
eg1.lay$Conditions <- with(eg1.lay, fac.combine(list(Intensities, Surfaces),
                                                    combine=TRUE, sep=","))
designGGPlot(eg1.lay, labels = "Conditions",
             row.factors = "Locations", column.factors = "Batches",
             cellfillcolour.column = "Athletes", cellalpha = 0.75, label.size = 6,
             title = "Randomized Intensities-Surfaces combinations",
             blockdefinition = rbind(c(9,1)),
             ggplotFuncs = list(xlab("Batches (Months)",
                                     theme(legend.position = "right"))))

```

Randomized Intensities–Surfaces combinations



Check the properties of the design.

```

#### Check properties of the design
eg1.canon <- designAnatomy(formulae = list(locs = ~ Batches/Locations,
                                           tests = ~ Months/Athletes/Tests,
                                           cond = ~ Intensities*Surfaces),
                          grandMean = TRUE, data = eg1.lay)
summary(eg1.canon, which.criteria="none")

##
##
## Summary table of the decomposition for locs, tests & cond
##
## Source.locs      df1 Source.tests      df2 Source.cond      df3
## Mean            1 Mean            1 Mean            1
## Batches          3 Months          3
## Locations[Batches] 32 Athletes[Months] 8 Intensities      2
##                                     Residual        6
##                                     Tests[Months:Athletes] 24 Surfaces          2
##                                     Intensities#Surfaces 4
##                                     Residual          18

```

Questions

1. What would be the allocation-based mixed model for this experiment, an allocation-based mixed model having the same terms as the randomization-based mixed model that would apply if all the allocations had been made by randomizing. Do you anticipate any problem in fitting it?

The allocation-based mixed model is formed by treating all training-conditions factors as fixed and the remaining factors as random. Hence, the symbolic mixed model is $\text{Intensities} + \text{Surfaces} + \text{Intensities} \wedge \text{Surfaces} \mid \text{Months} + \text{Months} \wedge \text{Athletes} + \text{Months} \wedge \text{Athletes} \wedge \text{Tests} + \text{Batches} + \text{Batches} \wedge \text{Locations}$. The problem in fitting it would be that Months and Batches are confounded so that the variance model is singular.

2. Compare the units for the two phases in this experiment?

A unit in the first phase is a test conducted on an athlete in a particular month; in the second phase, a unit is a location of a test within a batch. That is, the unit in the first phase is an athlete's test and in the second phase is a blood specimen in a lab location.

3. What are the outcomes for the two phases for this experiment?

The outcome for the first phase is the heart rate for a test and a blood specimen from the test; the outcome for the second phase, is the free haemoglobin measured at a location.

5.1.3 Allowing for lab processing order in the athletic training example

Brien (2017) discusses a design, and its properties, that differs in the second phase from that described in Section 5.1.2: it assumes that lab processing order within a batch is important and so the second phase now requires a row-column design. However, one cannot consider a design for just Months, Athletes and Tests and ignore Intensities and Surfaces, as was done in the previous design. Indeed prime consideration needs to be given to Intensities and Surfaces. That is, a suitable cross-phase design for allocating Intensities and Surfaces to Batches and Locations is needed. However, the second-phase design that allocates Months, Athletes and Tests to Batches and Locations has to be considered in that it must account for the split-unit nature of the first-phase design.

For the second-phase design, the Months are associated with Batches. Then each triple of consecutive locations in a batch are associated with a single athlete, one of those for the month associated with the batch. This leaves tests to be assigned to locations within triples. Thus, the cross-phase design will need to allocate efficiently an intensity to a location triple and surface to the locations within a triple.

The cross-phase design is a balanced factorial design (Hinkelmann and Kempthorne, 2005, Section 12.5) and can be constructed using two extended Latin squares (ELS) as follows:

1. A 3×4 ELS, formed from a 3×3 Latin square by repeating one of its columns, will be used to allocate Intensities to the 3 Locations triples \times 4 Months.
2. A 3×4 ELS will be used to allocate Surfaces to the 3 Locations \times 4 Months within a triple; the same ELS is used for the three triples.
3. To ensure no repeat Intensities-Surfaces combinations for a Location, the two Batches to which the repeated columns of the ELS for Intensities are assigned must be different from the two Batches to which repeated columns of the ELS for Surfaces are assigned.

The factor-allocation diagram, for this design, is in Figure 16. In this diagram, the training conditions and tests panels are surrounded by a dashed rectangle and lines go from the training conditions sources to the lines from the test sources. This indicates that the result of the allocation in the first phase needs to be explicitly taken into account in the second-phase allocation. The randomizations involved have been called a randomized-inclusive randomizations (Brien and Bailey, 2006) and are one of the two types of randomizations in a chain (Bailey and Brien, 2016). Because Batches and Locations are crossed, the second phase randomization is achieved by independently permuting the Batches and Locations. A design with the same properties had been previously constructed by Rosemary Bailey (pers. comm.).

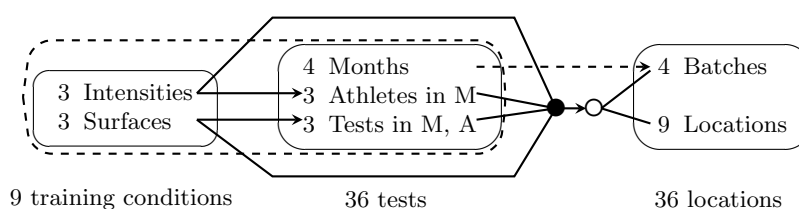


Figure 16: Factor-allocation diagram for the two-phase athlete training experiment with a row-column design for the second phase: training conditions are randomized to tests, then training conditions and tests are randomized to locations; the ‘●’ indicates that the observed combinations of the levels of Intensities, Surfaces, Athletes and Tests are randomized to locations; the ‘○’ indicates that a nonorthogonal design was used in this randomization to the combinations of the levels of Batches and Locations; the dashed arrow indicates that Months were systematically allocated to Batches; the dashed oval indicates that all factors from the first phase form a pseudotest and all are actively involved in determining the allocation to locations; M = Months and A = Athletes.

Use the following R code to obtain a layout for the new second phase design.

```
##### Generate a systematic cross-phase design for Intensities and Surfaces
#' It is based on (i) an extended Latin square (ELS) for allocating Intensities to
#' Locations triples x Batches and (ii) the same ELS for each triple, the ELSD being used to
#' allocate Surfaces to the three Locations within each triple by four Batches.
#' The Batches to which the repeated columns of the ELSD for Intensities are assigned must be
#' different from the Batches to which repeated columns of the ELSD for Surfaces are assigned.
#+ Athlete_eg2sys_v3

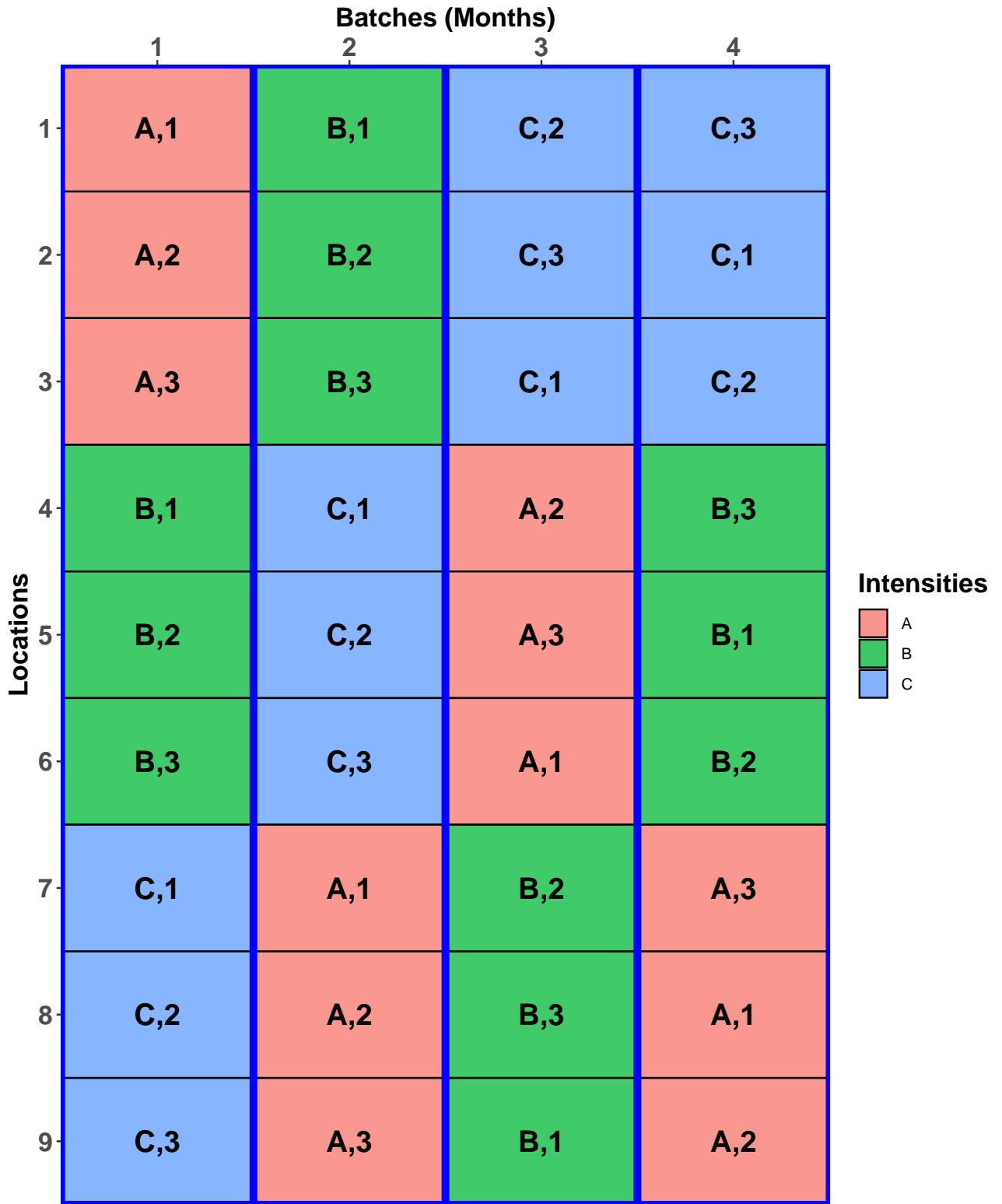
eg2.phx.sys <- cbind(fac.gen(list(Batches = 4, Locations = 9)),
                    data.frame(Intensities = factor(rep(c(designLatinSqrSys(3), c(3,2,1)),
                                                         each = 3), labels = LETTERS[1:3]),
                               Surfaces = factor(c(rep(1:3, times = 3),
                                                     rep(1:3, times = 3),
                                                     rep(c(2,3,1), times = 3),
                                                     rep(c(3,1,2), times = 3))))))

eg2.phx.sys$Conditions <- with(eg2.phx.sys, fac.combine(list(Intensities, Surfaces),
                                                         combine.levels = TRUE))

designGGPlot(eg2.phx.sys, labels = "Conditions",
            row.factors = "Locations", column.factors = "Batches",
            cellfillcolour.column = "Intensities", cellalpha = 0.75, label.size = 6,
            title = "Intensities-Surfaces for systematic cross-phase design",
            blockdefinition = rbind(c(9,1)),
```

```
ggplotFuns = list(xlab("Batches (Months)",
                      theme(legend.position = "right")))
```

Intensities–Surfaces for systematic cross–phase design

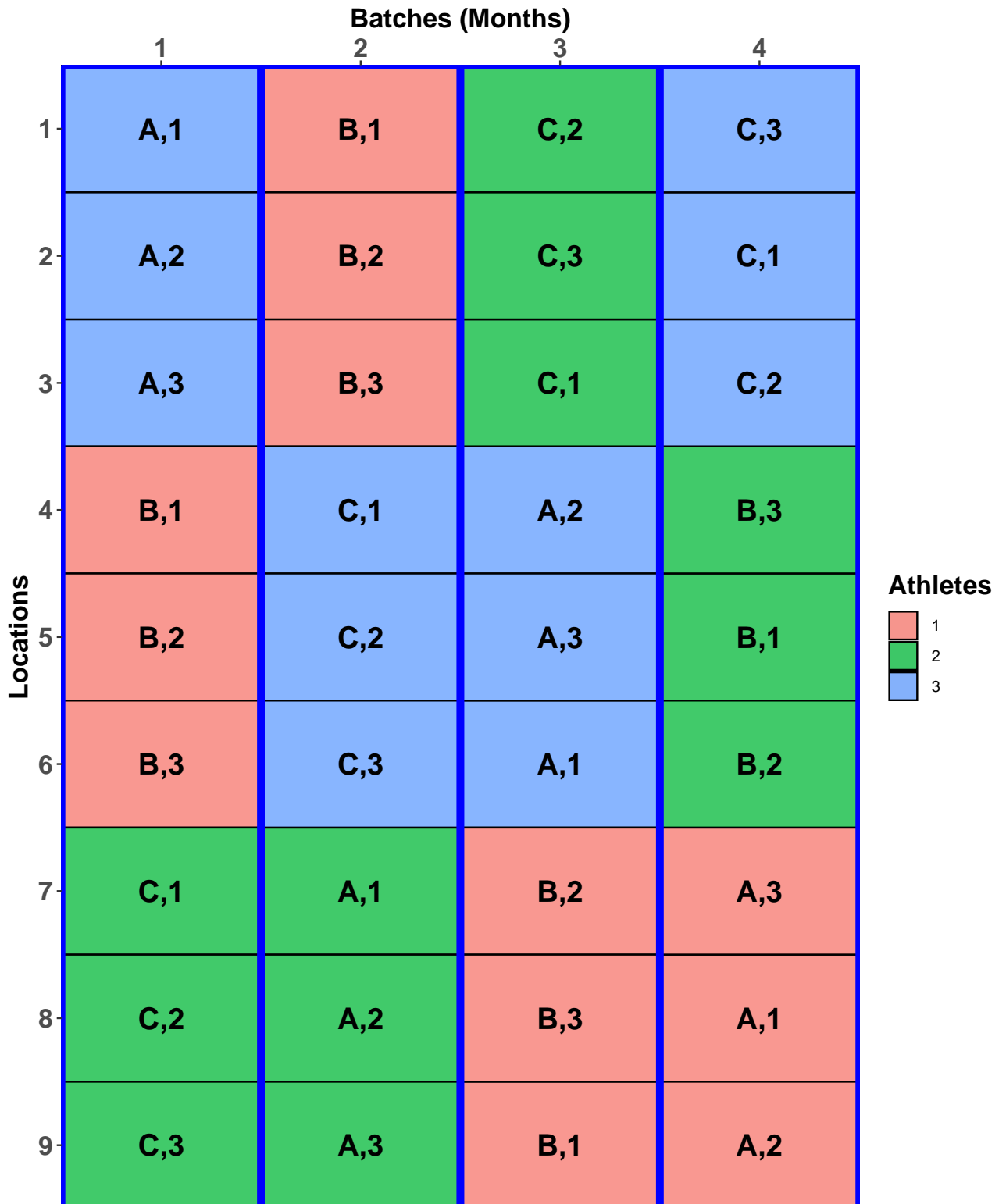



```

### Second phase design
### Generate a systematic two-phase design by bringing in first-phase recipient factors
eg2.phx.sys$Months <- eg2.phx.sys$Batches
eg2.sys <- merge(split.lay, eg2.phx.sys) #merge on common factors Months, Intensities & Surfaces
designGGPlot(eg2.sys, labels = "Conditions",
             row.factors = "Locations", column.factors = "Batches",
             cellfillcolour.column = "Athletes", cellalpha = 0.75, label.size = 6,
             title = "Intensities-Surfaces for systematic two-phase design",
             blockdefinition = rbind(c(9,1)),
             ggplotFuns = list(xlab("Batches (Months)"),
                               theme(legend.position = "right")))

```

Intensities–Surfaces for systematic two–phase design



```
#'## Allocate the second phase
eg2.lay <- designRandomize(allocated = eg2.sys[c("Months", "Athletes", "Tests",
```



```

                                "Intensities", "Surfaces"]],
recipient = eg2.sys[c("Batches", "Locations")],
except    = "Batches",
seed      = 243526)

head(eg2.lay)

##   Batches Locations Months Athletes Tests Intensities Surfaces
## 1      1         1       1        3     2           A         2
## 2      1         2       1        2     1           C         2
## 3      1         3       1        3     3           A         3
## 4      1         4       1        2     2           C         1
## 5      1         5       1        3     1           A         1
## 6      1         6       1        1     2           B         2

#'## Plot the layout
#+ Athlete_eg2lay_v3
eg2.lay$Conditions <- with(eg2.lay, fac.combine(list(Intensities, Surfaces),
                                                    combine=TRUE, sep=","))

designGGPlot(eg2.lay, labels = "Conditions",
             row.factors = "Locations", column.factors = "Batches",
             cellfillcolour.column = "Athletes", cellalpha = 0.75, label.size = 6,
             title = "Randomized Intensities-Surfaces combinations",
             blockdefinition = rbind(c(9,1)),
             ggplotFuns = list(xlab("Batches (Months)",
                                   theme(legend.position = "right"))))

```

Randomized Intensities–Surfaces combinations

		Batches (Months)			
		1	2	3	4
Locations	1	A,2	B,2	C,3	C,1
	2	C,2	A,2	B,3	A,1
	3	A,3	B,3	C,1	C,2
	4	C,1	A,1	B,2	A,3
	5	A,1	B,1	C,2	C,3
	6	B,2	C,2	A,3	B,1
	7	C,3	A,3	B,1	A,2
	8	B,1	C,1	A,2	B,3
	9	B,3	C,3	A,1	B,2

Athletes

1
2
3

Check the properties of the design.

```

#### Check properties of the design
eg2.canon <- designAnatomy(formulae = list(locs = ~ Batches*Locations,
                                           tests = ~ Months/Athletes/Tests,
                                           cond = ~ Intensities*Surfaces),
                           grandMean = TRUE, data = eg2.lay)
summary(eg2.canon, which.criteria = c("aefficiency", "order"))

##
##
## Summary table of the decomposition for locs, tests & cond (based on adjusted quantities)
##
## Source.locs      df1 Source.tests      df2 Source.cond      df3 aefficiency order
## Mean            1 Mean            1 Mean            1      1.0000      1
## Batches          3 Months          3      1.0000      1
## Locations        8 Athletes[Months]  2 Intensities      2      0.0625      1
##                  Tests[Months:Athletes] 6 Surfaces        2      0.0625      1
##                  Intensities#Surfaces  4      0.2500      1
## Batches#Locations 24 Athletes[Months]  6 Intensities      2      0.9375      1
##                  Residual            4      1.0000      1
##                  Tests[Months:Athletes] 18 Surfaces        2      0.9375      1
##                  Intensities#Surfaces  4      0.7500      1
##                  Residual            12      1.0000      1
##
## The design is not orthogonal

```

It is clear that Athletes[Months] and Tests[Months:Athletes] are not orthogonal to Locations and Batches#Locations, because the former sources are confounded with both of the latter sources. To examine the nature of the nonorthogonality, the anatomy for just the tests and locations tiers is obtained.

```

#### Examine the nonorthogonality between locations and tests
eg2.locstests.canon <- designAnatomy(formulae = list(locs = ~ Batches*Locations,
                                                    tests = ~ Months/Athletes/Tests),
                                     grandMean = TRUE, data = eg2.lay)
summary(eg2.locstests.canon, which.criteria = c("aefficiency", "order"))

##
##
## Summary table of the decomposition for locs & tests
##
## Source.locs      df1 Source.tests      df2 aefficiency order
## Mean            1 Mean            1      1.0000      1
## Batches          3 Months          3      1.0000      1
## Locations        8 Athletes[Months]  2      1.0000      1
##                  Tests[Months:Athletes] 6      1.0000      1
## Batches#Locations 24 Athletes[Months]  6      1.0000      1
##                  Tests[Months:Athletes] 18      1.0000      1

```

Questions

1. What do you conclude about the confounding of Athletes[Months] and Tests[Months:Athletes] with Locations?

Since all efficiency factors are one, it is concluded that the 8 degrees of freedom for Athletes[Months] has been split into two orthogonal parts, one with 2 degrees of freedom which is confounded with Batches and the other

with 6 degrees of freedom which is confounded with *Batches:Locations*. The source *Tests[Months:Athletes]* has been similarly partitioned.

2. Are the designs proposed for this experiment first-order balanced?

The design is first-order balanced, because the order of the efficiency factors is one for all confounded sources.

3. What has been the cost of allowing for order of processing in the lab? Is the cost acceptable? Why?

*The cost has been that some information about *Athletes[Months]*, along with *Intensities*, and some information about *Tests[Months:Athletes]*, along with *Surfaces* and *Intensities#Surfaces*, has been confounded with *Locations*. The cost is acceptable, because the amount of information lost on the main effects is only 6.25% and on the interaction is 25%. The latter will be recovered in a REML-based mixed model analysis. However, the Residual degrees of freedom for *Athletes[Months]* has been reduced from 6 to 4 and for *Tests[Months:Athletes]* from 18 to 14. While the latter is unlikely to be seriously deleterious, the former is of concern.*

5.2 McIntyre's (1955) two-phase example

McIntyre (1955) reports an investigation of the effect of four light intensities on the synthesis of tobacco mosaic virus in leaves of tobacco *Nicotiana tabacum* var. Hickory Pryor. It is a two-phase experiment: the first phase is a treatment phase, in which the four light treatments are randomized to the tobacco leaves, and the second phase is an assay phase, in which the tobacco leaves are randomized to the half-leaves of assay plants.

In the first phase, four successive leaves at defined positions on the stem were taken from each of eight plants of comparable age and vigour that had been inoculated with the virus. Arbitrarily grouping the plants into two sets of four, the four treatments were applied to the leaves, which had been separated from the plants and were sustained by flotation on distilled water, in a Latin square design for each set with tobacco plants as columns and leaf positions as rows; see Figure 18.

In the second phase, virus content of each tobacco leaf was assayed by expressing sap and inoculating half leaves of the assay plants, *Datura stramonium*, on which countable lesions would appear. Lots of eight sap samples were formed from pairs of tobacco plants, the pairs being comprised of a plant from each set in the treatment phase. The eight samples from a lot were assigned to four assay plants using one of four 4×4 Graeco-Latin square designs, with the leaves from a single tobacco plant assigned using one of the alphabets and the second tobacco plant using the other (see Figure 19). Actually, this design is a semi-Latin square (Bailey, 1992).

The factor-allocation diagram for the experiment is in Figure 17. Unfortunately, the randomization for this experiment was not described by McIntyre (1955). Because there are multiple squares in both phases, there are several possible randomizations depending on the effects anticipated as possible in the experiment. As shown by the nesting relations in the factor-allocation diagram, I have assumed that randomization to NicPlant was within Sets and to Posn was across Sets. Similarly, I have assumed that randomization to DatPlant was within Lot and to AssPosn across Lot. In the factor-allocation diagram, N_1 is a factor for the pairs of tobacco plants formed by taking a plant from each set in the first phase.

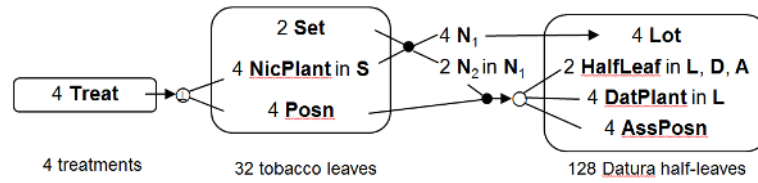


Figure 17: Factor-allocation diagram for McIntyre's (1955) two-phase experiment: treatments are randomized to tobacco leaves and tobacco leaves are randomized to Datura half-leaves; the arrow to the '⊥', the '⊥' and the two lines from the '⊥' indicate that Treat is randomized to the combinations of NicPlant and Posn using an orthogonal design; N_1 is a pseudofactor indexing the pairs of tobacco plants formed by taking a plant from each set in the first phase and N_2 is a pseudofactor indexing the tobacco plants within the pairs formed by taking a plant from each set in the first phase; N_1 is randomized to Lot in the second phase; the combinations of N_2 and Posn is randomized to the combinations of HalfLeaf, DatPlant and AssPosn using a nonorthogonal design, the latter indicated by the 'O'; S = Set; L = Lot; D = DatPlant; A = AssPosn.

Figure 18: Layout for the first phase of McIntyre's (1955) experiment[†]

		Nicotiana Plants							
		1	2	3	4	1	2	3	4
Leaf	Position					Leaf	Position		
1		a	b	c	d			a	b
		1	5	9	13			17	21
2		b	a	d	c			c	d
		2	6	10	14			18	22
3		c	d	a	b			d	c
		3	7	11	15			19	23
4		d	c	b	a			b	a
		4	8	12	16			20	24
								25	29
								26	30
								27	31
								28	32

[†]The letter in each cell refers to the light intensity to be applied to the unit and the number to the unit.

5.2.1 Check the properties of the randomized layout

Load the data and use `designAnatomy` to check the properties of the design.

```
### Load data
data("McIntyreTMV.dat")
### Check properties of the design
TMV.canon <- designAnatomy(formulae = list(assay = ~ ((Lot/DatPlant)*AssPosn)/HalfLeaf,
                                           test = ~ (Set/NicPlant)*Posn,
                                           trt = ~ Treat),
                           grandMean = TRUE, data = McIntyreTMV.dat)
summary(TMV.canon, which.criteria=c("aeff", "ord"))

##
##
## Summary table of the decomposition for assay, test & trt (based on adjusted quantities)
##
## Source.assay      df1 Source.test      df2 Source.trt df3 aefficiency order
## Mean             1 Mean             1 Mean         1      1.0000      1
## Lot              3 NicPlant[Set]      3              1.0000      1
```

Figure 19: Layout for the second phase of McIntyre's (1955) experiment[†]

		<i>Datura</i> Plants									
		1	2	3	4			5	6	7	8
Assay Leaf	Position					Assay Leaf	Position				
1		1 17	2 20	3 18	4 19			5 23	6 22	7 24	8 21
2		2 18	1 19	4 17	3 20			8 22	7 23	6 21	5 24
3		3 19	4 18	1 20	2 17			7 21	8 24	5 22	6 23
4		4 20	3 17	2 19	1 18			6 24	5 21	8 23	7 22

		<i>Datura</i> Plants									
		9	10	11	12			13	14	15	16
Assay Leaf	Position					Assay Leaf	Position				
1		9 28	10 25	11 27	12 26			13 30	14 31	15 29	16 32
2		10 27	9 26	12 28	11 25			16 31	15 30	14 32	13 29
3		11 26	12 27	9 25	10 28			15 32	16 29	13 31	14 30
4		12 25	11 28	10 26	9 27			14 29	13 32	16 30	15 31

[†]The numbers in the cell refer to the units from the first phase (tobacco leaves) to be assigned to the two half-leaves of the assay plant; they are in standard order for Set, then NicPlant followed by Position.

```

## DatPlant[Lot] 12
## AssPosn 3
## Lot#AssPosn 9
## DatPlant#AssPosn[Lot] 36 Posn 3 0.5000 1
## Set#Posn 3 0.5000 1
## NicPlant#Posn[Set] 18 Treat 3 0.5000 1
## Residual 15 0.5000 1
## Residual 12
## HalfLeaf[Lot:DatPlant:AssPosn] 64 Set 1 1.0000 1
## NicPlant[Set] 3 1.0000 1
## Posn 3 0.5000 1
## Set#Posn 3 0.5000 1
## NicPlant#Posn[Set] 18 Treat 3 0.5000 1
## Residual 15 0.5000 1
## Residual 36
##
## The design is not orthogonal

```

5.2.2 Questions

1. Is the variance matrix for this experiment based on two sets of terms that are orthogonal?

The variance matrix for this experiment is based on the factors in the tobacco leaves and Datura half-leaves tiers. The terms derived from the factors in these two tiers are not orthogonal. In particular, Set#Posn and NicPlant#Posn[Set] are partially confounded with both DatPlant#AssPosn[Lot] and HalfLeaf[Lot:DatPlant:AssPosn].

2. What are the advantages and disadvantages of a mixed-model analysis of the data from this experiment, as opposed to an anova?

The advantage of a mixed-model analysis is that combined estimates will be provided for Set#Posn, NicPlant#Posn[Set], and Treat. The disadvantages are (i) that not all random terms are well-estimated, some having small degrees of freedom, and cause problems in fitting the model, and (ii) the Wald F-statistics are only approximately distributed as F-distributions. On the other hand, an anova is not applicable because of the nonorthogonality between the sets of terms making up the variance matrix; at least some F-ratios will not be independently distributed.

5.3 A Plant Accelerator experiment with a split-unit design

This experiment involves the investigation of 75 wheat lines, of which 73 are Nested Association Mapping (NAM) wheat lines and the other two are two check lines, Scout and Gladius. It was conducted in 2014 in the Plant Accelerator, a facility in Adelaide with 4 Smarthouses. A Smarthouse is a large greenhouse with two areas within it: (i) a Table area at the southern end and (ii) a Conveyor area at the northern end — see Figure 20. The conveyor system has the capability of automatically moving and imaging around 500 pots per day. There are air conditioners placed down the western side of the Smarthouse, which creates a trend from west to east. Further, there is a north-south trend due to changes in light intensity (Brien et al., 2013).

The experiment involves two phases: the table and conveyor phases. The table phase is the establishment phase in which plants are germinated in pots on the tables where they undergo an early growth stage. In the conveyor phase, having placed the pots in carts on the conveyor system, the plants are automatically imaged and watered daily, being moved to a processing station by the conveyor system for this.

This experiment has a single plant per pot and these will be arranged in a 24×22 grid in both phases: 24 columns \times 22 locations in the table phase and 24 lanes \times 22 (2–23) positions, as shown in Figure 20. However, the 24 columns in the table phase run east-west and the 24 lanes in the conveyor phase run north-south. Because there are systematic trends in both phases to be accounted for in the analysis, the same layout will be used

in both phases, but the table layout will be rotated clockwise through 90°. That is, Locations 1–22 will be in Positions 2–23, respectively, and the Column will be placed in the Lane with the same number.

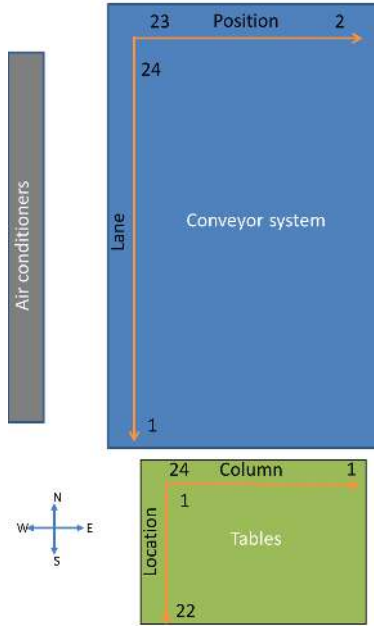


Figure 20: Schematic of Smarthouse for the Plant Accelerator experiment

The design employed for the experiment is a split-unit design in which two consecutive pots/carts form a main unit. The main-unit design uses a blocked design with rows and columns generated with DiGger (Coombes, 2009). It assigns Lines to main units, the Lines being unequally replicated; Scout and Gladius each occur on 12 main units (24 carts), 21 randomly-selected NAM lines each occur on 4 main units (8 carts) and the remaining 52 NAM lines each occur on 3 main units (6 carts). The subunit design merely randomizes Salt (0 mM NaCl, 100 mM NaCl) to the two carts in each main unit.

In the main-unit design, the blocks are, in the table phase, 6 Groups of 4 Columns and, in the conveyor phase, 6 Zones of 4 Rows (lanes). However, while the generated design is based on crossed rows and columns, it is known from past experience that, while there are differences between Zones, there are not differences between Rows within Zones (Brien et al., 2013) and none are anticipated between Columns within Groups on the tables. The columns of the main-unit design are indexed by 11 Pairs in the table phase and 11 MainPosns in the conveyor phase. The design generated with DiGger (Coombes, 2009) will be rerandomized so that the Lines are randomized to 4 Columns within each Groups-Pairs combination and the 11 sets of Lines assigned by DiGger to the 11 Pairs will be rerandomized to Pairs. The factor-allocation diagram is shown in Figure 21.

5.3.1 Produce the layout

Use the following instructions to load the main-unit design produced with DiGger and check its properties using designAnatomy.

```
#'## Load the main-unit design - it has Lines in row-column order
data("Exp249.munit.des")
Exp249.munit.des$Blocks <- factor(rep(1:6, each = 44))

#'## Check its properties
Exp249.munit.canon <- designAnatomy(formulae = list(cart = ~ (Blocks/Rows)*Cols,
                                                    treat = ~ Lines),
                                    grandMean = TRUE, data = Exp249.munit.des)
```

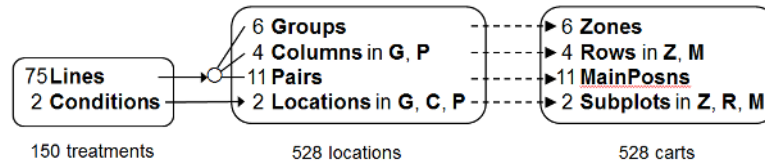



Figure 21: Factor-allocation diagram for the Plant Accelerator experiment: treatments are randomized to locations and locations are allocated to cars; the arrow to the ‘O’, the ‘O’ and the three lines from the ‘O’ indicate that Lines is randomized to the combinations of Groups, Columns and Pairs using a nonorthogonal design; the arrow from Conditions to Locations indicates that Conditions were randomized to Locations; the dashed arrows between the two panels on the right hand side indicate that the factors indexing locations were systematically assigned to those indexing the carts; G = Groups; P = Pairs; C = Columns; Z = Zones; M = MainPosns; R = Rows.

```
summary(Exp249.munit.canon)

##
##
## Summary table of the decomposition for cart & treat (based on adjusted quantities)
##
## Source.cart      df1 Source.treat df2 aeffericiency eeffericiency order
## Mean            1 Mean           1    1.0000    1.0000    1
## Blocks          5 Lines           5    0.1498    0.1422    5
## Rows[Blocks]    18 Lines          18    0.2685    0.1813   18
## Cols            10 Lines           10    0.2102    0.1769   10
## Blocks#Cols     50 Lines           50    0.1154    0.0142   50
## Rows#Cols[Blocks] 180 Lines        74    0.5816    0.2088   74
##                Residual          106
##
## The design is not orthogonal
```

Expand main-unit design to produce the split-unit design, including a three-level factor Checks that compares Scout, Gladius and the mean of the NAM lines. Perhaps, produce a plot of the allocation of the Lines.

```
#### Expand design to rerandomize lines and to assign salt treatments to locations
Exp249.alloc <- with(Exp249.munit.des,
  data.frame(Lines = factor(rep(Lines, each=2), levels=1:75),
    Checks = fac.recast(rep(Lines, each=2),
      newlevels=c(rep(3, 73), 1, 2),
      levels.order = c(3,1,2),
      newlabels = c("NAM","Scout","Gladius")),
    Salt = factor(rep(1:2, times=264),
      labels = c('0 NaCl','100 NaCl'))))
Exp249.recip <- fac.gen(list(Groups = 6, Cols = 4, Pairs = 11, Locations = 2))
Exp249.nest <- list(Cols = c("Groups", "Pairs"),
  Locations = c("Groups", "Cols", "Pairs"))
Exp249.lay <- designRandomize(allocated = Exp249.alloc,
  recipient = Exp249.recip,
  nested.recipients = Exp249.nest,
  seed = 51412)

#### Add second-phase factors
#### (to which the first-phase factors have been systematically allocated)
```

```
Exp249.lay <- cbind(fac.gen(list(Lanes = 24, Positions = 2:23)),
  fac.gen(list(Zones = 6, Rows = 4, MainPosn = 11, Subunits = 2)),
  Exp249.lay)

### Plot the assignment of Lines in the second-phase design - or see file that includes the output
Exp249.lay$Replication <- fac.recast(Exp249.lay$Lines,
  newlevels = rep(1:3, c(21,52,2)))
designGGPlot(Exp249.lay, labels = "Lines", cellfillcolour.column = "Replication",
  colour.values = c("lightblue", "grey", "lightgreen"),
  row.factors = "Lanes", column.factors = "Positions",
  title = "Layout of Lines for optimized design",
  reverse.x = TRUE, reverse.y = FALSE, blockdefinition = cbind(4,22))
```

Layout of Lines for optimized design

		Positions																					
		23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	3	2
Lanes	24	11	11	7	7	17	17	3	3	50	50	39	39	71	71	18	18	74	74	10	10	75	75
	23	75	75	69	69	24	24	67	67	28	28	4	4	74	74	45	45	13	13	51	51	31	31
	22	26	26	20	20	35	35	12	12	44	44	52	52	68	68	38	38	61	61	41	41	55	55
	21	2	2	22	22	9	9	30	30	36	36	58	58	27	27	72	72	16	16	57	57	8	8
	20	41	41	64	64	43	43	75	75	48	48	30	30	13	13	70	70	19	19	47	47	12	12
	19	34	34	74	74	40	40	6	6	31	31	2	2	62	62	21	21	53	53	59	59	29	29
	18	20	20	5	5	50	50	68	68	14	14	45	45	8	8	55	55	11	11	75	75	15	15
	17	44	44	26	26	72	72	60	60	73	73	16	16	1	1	74	74	33	33	46	46	51	51
	16	54	54	60	60	21	21	61	61	63	63	48	48	34	34	75	75	75	75	50	50	33	33
	15	37	37	53	53	18	18	65	65	59	59	74	74	49	49	23	23	8	8	58	58	32	32
	14	45	45	6	6	42	42	4	4	15	15	57	57	7	7	69	69	2	2	72	72	17	17
	13	74	74	66	66	3	3	24	24	19	19	14	14	73	73	11	11	39	39	35	35	13	13
	12	10	10	44	44	5	5	8	8	1	1	43	43	39	39	60	60	28	28	29	29	26	26
	11	65	65	42	42	70	70	27	27	18	18	75	75	54	54	9	9	6	6	67	67	74	74
	10	19	19	40	40	33	33	46	46	24	24	37	37	14	14	16	16	23	23	64	64	25	25
	9	71	71	75	75	15	15	66	66	12	12	56	56	38	38	58	58	22	22	74	74	57	57
	8	56	56	55	55	29	29	13	13	47	47	5	5	20	20	68	68	43	43	32	32	49	49
	7	25	25	1	1	75	75	18	18	9	9	27	27	41	41	31	31	17	17	65	65	54	54
	6	21	21	75	75	7	7	62	62	2	2	6	6	36	36	52	52	10	10	23	23	63	63
	5	61	61	4	4	74	74	74	74	42	42	3	3	64	64	73	73	40	40	71	71	11	11
	4	4	4	37	37	25	25	47	47	10	10	62	62	15	15	49	49	20	20	16	16	14	14
	3	69	69	48	48	56	56	9	9	74	74	51	51	5	5	7	7	67	67	53	53	46	46
	2	12	12	52	52	30	30	59	59	38	38	19	19	75	75	66	66	21	21	36	36	22	22
	1	70	70	32	32	34	34	17	17	75	75	63	63	35	35	28	28	1	1	74	74	3	3

5.3.2 Check the properties of the design

The maximal allocation-based mixed model is $(\text{Checks} + \text{Lines}) * \text{Salt} \mid (\text{Zones} * \text{MainPosn}) / \text{Rows} / \text{Subunits} + (\text{Groups} * \text{Pairs}) / \text{Cols} / \text{Locations}$, with Checks nested within Lines. Use the `designAnatomy` to check the properties of the design for an analysis of data from an experiment based on this design.

```
## Check design properties
Exp249.canon <- designAnatomy(formulae = list(carts = ~ (Zones*MainPosn)/Rows/Subunits,
                                             tables = ~ (Groups*Pairs)/Cols/Locations,
                                             treats = ~ (Checks + Lines) * Salt),
                             grandMean = TRUE, data = Exp249.lay)

## Warning in projs.2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Lines[Checks] and Checks
## are partially aliased in MainPosn&Pairs
## Warning in projs.2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Lines[Checks] and Checks
## are partially aliased in Zones#MainPosn&Groups#Pairs
## Warning in projs.2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Lines[Checks] and Checks
## are partially aliased in Rows[Zones:MainPosn]&Cols[Groups:Pairs]
```

```
summary(Exp249.canon)

##
##
## Summary table of the decomposition for carts, tables & treats (based on adjusted quantities)
##
## Source.carts      df1 Source.tables      df2 Source.treats      df3
## Mean              1 Mean              1 Mean              1
## Zones              5 Groups              5 Lines[Checks]      5
## MainPosn           10 Pairs              10 Checks          2
##                   Lines[Checks]          8
## Zones#MainPosn     50 Groups#Pairs        50 Checks          2
##                   Lines[Checks]          48
## Rows[Zones:MainPosn] 198 Cols[Groups:Pairs] 198 Checks          2
##                   Lines[Checks]          72
##                   Residual              124
## Subunits[Zones:MainPosn:Rows] 264 Locations[Groups:Pairs:Cols] 264 Salt              1
##                   Checks#Salt            2
##                   Lines#Salt[Checks]      72
##                   Residual              189
##
## aefficiency eefficiency order
##      1.0000      1.0000      1
##      0.1498      0.1422      5
##      0.0033      0.0031      2
##      0.2094      0.1809      8
##      0.2111      0.2049      2
##      0.1142      0.0145     48
##      0.7854      0.7792      2
##      0.6640      0.2632     66
##      1.0000      1.0000      1
##      1.0000      1.0000      1
##      1.0000      1.0000      1
##      1.0000      1.0000      1
```

```
##      1.0000      1.0000      1
##
## Table of information (partially) aliased with previous sources derived from the same formula
##
## Source      df Alias  In      aefficiency eefficiency order
## Lines[Checks] 2 Checks MainPosn&Pairs      1.0000      1.0000      1
## Lines[Checks] 2 Checks Zones#MainPosn&Groups#Pairs      1.0000      1.0000      1
## Lines[Checks] 2 Checks Rows[Zones:MainPosn]&Cols[Groups:Pairs]      0.0944      0.0785      2
##
## The design is not orthogonal
```

Because, there is a one-to-one correspondence between the tables and carts sources, omit the tables formula and rerun — it will make the anova table more readable.

```
#### Check design properties, with tables omitted
Exp249.canon <- designAnatomy(formulae = list(carts = ~ (Zones*MainPosn)/Rows/Subunits,
                                             treats = ~ (Checks + Lines) * Salt),
                              grandMean = TRUE, data = Exp249.lay)

## Warning in projs.2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Lines[Checks] and Checks
## are partially aliased in MainPosn
## Warning in projs.2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Lines[Checks] and Checks
## are partially aliased in Zones#MainPosn
## Warning in projs.2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Lines[Checks] and Checks
## are partially aliased in Rows[Zones:MainPosn]

summary(Exp249.canon)

##
##
## Summary table of the decomposition for carts & treats (based on adjusted quantities)
##
## Source.carts      df1 Source.treats      df2 aefficiency eefficiency order
## Mean              1 Mean              1      1.0000      1.0000      1
## Zones              5 Lines[Checks]      5      0.1498      0.1422      5
## MainPosn           10 Checks              2      0.0033      0.0031      2
##                   Lines[Checks]      8      0.2094      0.1809      8
## Zones#MainPosn     50 Checks              2      0.2111      0.2049      2
##                   Lines[Checks]     48      0.1142      0.0145     48
## Rows[Zones:MainPosn] 198 Checks              2      0.7854      0.7792      2
##                   Lines[Checks]     72      0.6640      0.2632     66
##                   Residual          124
## Subunits[Zones:MainPosn:Rows] 264 Salt              1      1.0000      1.0000      1
##                   Checks#Salt        2      1.0000      1.0000      1
##                   Lines#Salt[Checks] 72      1.0000      1.0000      1
##                   Residual          189
##
## Table of information (partially) aliased with previous sources derived from the same formula
##
## Source      df Alias  In      aefficiency eefficiency order
## Lines[Checks] 2 Checks MainPosn      1.0000      1.0000      1
## Lines[Checks] 2 Checks Zones#MainPosn      1.0000      1.0000      1
## Lines[Checks] 2 Checks Rows[Zones:MainPosn]      0.0944      0.0785      2
##
## The design is not orthogonal
```

5.3.3 Examine the properties of the design for an alternative analysis

However, rather than fit the allocation-based model, because it is known from past experience that once a linear trend for MainPosn has been fitted there are no deviations from this trend, the term `xMainPosn` is used to fit the trend; the term `xMainPosn` is a centred, linear covariate for MainPosn. Use the `designAnatomy` to check the properties of the design for an analysis based on a modified model, in which MainPosn in the random model has been replaced by `xMainPosn` in the fixed model, `Zones#MainPosn` has been omitted and `Rows[Zones:MainPosn]` has been replaced by `Mainunits[Zones]`.

```
### Add factors and variates for new analysis
Exp249.lay <- within(Exp249.lay,
  { xMainPosn <- as.numfac(MainPosn)
    xMainPosn <- -(xMainPosn - mean(xMainPosn))
    Mainunits <- fac.combine(list(Rows,MainPosn))
  })

head(Exp249.lay)
```

##	Lanes	Positions	Zones	Rows	MainPosn	Subunits	Groups	Cols	Pairs	Locations	Lines	Checks	Salt
## 1	1	2	1	1	1	1	1	1	1	1	3	NAM 100	NaCl
## 2	1	3	1	1	1	2	1	1	1	2	3	NAM 0	NaCl
## 3	1	4	1	1	2	1	1	1	2	1	74	Scout 100	NaCl
## 4	1	5	1	1	2	2	1	1	2	2	74	Scout 0	NaCl
## 5	1	6	1	1	3	1	1	1	3	1	1	NAM 100	NaCl
## 6	1	7	1	1	3	2	1	1	3	2	1	NAM 0	NaCl

```
## Replication Mainunits xMainPosn
## 1 1 1 5
## 2 1 1 5
## 3 3 2 4
## 4 3 2 4
## 5 1 3 3
## 6 1 3 3

### Check properties if only linear trend fitted
set.daeTolerance(element.tol = 1e-06)
Exp249.canon <- designAnatomy(formulae = list(cart = ~ Zones/Mainunits/Subunits,
  treat = ~ xMainPosn +
    (Checks + Lines) * Salt),
  grandMean = TRUE, data = Exp249.lay)

summary(Exp249.canon)
```

##	Source.cart	df1	Source.treat	df2	aefficiency	eefficiency	order
##	Mean	1	Mean	1	1.0000	1.0000	1
##	Zones	5	Lines[Checks]	5	0.1500	0.1426	5
##	Mainunits[Zones]	258	xMainPosn	1	1.0000	1.0000	1
##			Checks	2	1.0000	1.0000	1
##			Lines[Checks]	72	0.9879	0.8437	6
##			Residual	183			
##	Subunits[Zones:Mainunits]	264	Salt	1	1.0000	1.0000	1
##			Checks#Salt	2	1.0000	1.0000	1
##			Lines#Salt[Checks]	72	1.0000	1.0000	1
##			Residual	189			

```
##
## Table of information (partially) aliased with previous sources derived from the same formula
##
## Source          df Alias          In      aefficiency eefficiency order
## Checks          1 xMainPosn      treat    0.0010      0.0010      1
## Checks          2 ## Information remaining treat    0.9995      0.9990      2
## Lines[Checks]    1 xMainPosn      treat    0.2139      0.2139      1
## Lines[Checks]    1 Checks        treat    0.0003      0.0003      1
## Lines[Checks]   72 ## Information remaining treat    0.9962      0.7859      2
##
## The design is not orthogonal
```

The Table of (partial) aliasing shows that all `treat-` sources are partially aliased with `\verbxMainPosn=`, although they are not far from being orthogonal.

We have been able to check what information is available about Lines and Salt after adjustment for the linear trend. In practice, a spline term might be needed to account for nonlinearity in the trend.

5.3.4 Questions

1. What advantages accrue from randomizing Lines within Groups[^]Pairs (Zones[^]MainPosn) as compared to the original DiGger design, in which they are randomized to Cols within Groups (Lanes within Zones) and to Pairs (MainPosn)?

The anatomy for the DiGger design shows us that all 74 degrees of freedom are estimable in Rows#Cols[Blocks] with average efficiency 0.582 and minimum efficiency 0.209. Compared to this, the anatomy for the rerandomized design shows that the NAM lines are estimable from Rows[Zones:MainPosn], the source equivalent to Rows#Cols[Blocks], with average efficiency 0.664 and minimum efficiency 0.263. Also, the Residual degrees of freedom for Rows#Cols[Blocks] have increased from 106 degrees of freedom in the original design to 124 degrees of freedom for Rows[Zones:MainPosn] in the rerandomized design. That is, one can expect the estimation of the Lines predictions and their standard errors to be more precise for the rerandomized design.

2. What effect does the use of a linear trend, as opposed to a set of effects, have on the analysis?

The efficiency for Lines has increased further so that the minimum is now 0.844 and the Residual degrees of freedom for Rows[Zones:MainPosn] now stands at 183. This allows one to consider ignoring information not estimable from Rows[Zones:MainPosn], while predictions will be adjusted for the trend across MainPosn.

5.4 Two-phase, wheat experiment with 49 lines

The first, or field, phase of a wheat trial for 49 lines is laid out as an RCBD with four blocks. The produce from the field trial is processed in the second, or laboratory, phase and the design employed is a balanced lattice square for 49 treatments that involves 4 replicates each consisting of a 7×7 square. In the laboratory phase there are four intervals each of which consists of 7 runs of a machine. In a run, samples are processed at seven consecutive times. This experiment is Example 2.2 from [Bailey and Brien \(2016\)](#), where its anova with expected mean squares is given. Its factor-allocation diagram is in Figure 22.

5.4.1 Produce randomized layout for both phases and check its properties

```
#'## Generate a layout for the field phase
field.sys <- cbind(fac.gen(list(Blocks = 4, Plots = 49)),
                  fac.gen(list(Lines = 49), times=4))
field.layout <- designRandomize(allocated = field.sys["Lines"],
                                recipient   = field.sys[c("Blocks", "Plots")],
                                nested.recipients = list(Plots = "Blocks"),
```

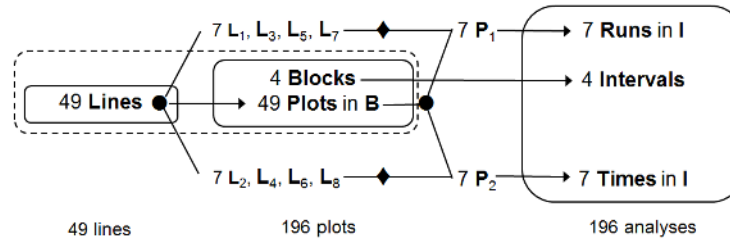


Figure 22: Factor-allocation diagram for the two-phase wheat variety experiment: lines are randomized to plots, then lines and plots are randomized to analyses; the arrow for Lines to Plots indicates that Lines are randomized to Plots; similarly, Blocks are randomized to intervals; L_1, L_3, L_5 and L_7 are pseudofactors that group the Lines for randomization to Runs and L_2, L_4, L_6 and L_8 are pseudofactors that group the Lines for randomization to Times; the two ‘♦’ symbols indicate that the pseudofactors for Lines determine the pseudofactors P_1 and P_2 for assigning Plots to Runs and Times, respectively; B = Blocks; I = Intervals.

```

seed = 82522)

head(field.lay)

##   Blocks Plots Lines
## 1      1      1   48
## 2      1      2   10
## 3      1      3   23
## 4      1      4   31
## 5      1      5   36
## 6      1      6   11

### Generate laboratory phase
#### Load a systematic balanced lattice square
data("LatticeSquare_t49.des")
#### Form systematic design
#### Add Intervals to field layout, merge the data frames and sort into lab phase order
field.lay$Intervals <- field.lay$Blocks
lab.alloc <- merge(LatticeSquare_t49.des, field.lay)
lab.alloc <- with(lab.alloc, lab.alloc[order(Intervals, Runs, Times),])
lab.alloc <- lab.alloc[c("Blocks", "Plots", "Lines")] #Reduce columns in lab.alloc
#### Randomize the design
lab.lay <- designRandomize(allocated = lab.alloc,
                           recipient  = list(Intervals = 4, Runs = 7, Times = 7),
                           nested.recipients = list(Runs = "Intervals",
                                                       Times = "Intervals"),
                           seed       = 141797)

head(lab.lay)

##   Intervals Runs Times Blocks Plots Lines
## 1      1      1      1      4      41      1
## 2      1      1      2      4      43      49
## 3      1      1      3      4      36      25
## 4      1      1      4      4      13       9
## 5      1      1      5      4      10      33
## 6      1      1      6      4      44      41

### Plot the design to show the allocation of Blocks, Plots and Lines in the lab phase
lab.lay$FieldFactors <- with(lab.lay, fac.combine(list(Blocks, Plots, Lines),

```

```

                                combine.levels = TRUE))
designGGPlot(lab.lay, labels = "FieldFactors",
             row.factors = c("Intervals", "Runs"), column.factors = "Times",
             facetstrips.switch = "x", facetstrips.placement = "outside.title",
             title = "Allocation of Blocks, Plots and Lines in the lab phase",
             cellalpha = 0.75, blockdefinition = cbind(7, 7))

```

Allocation of Blocks, Plots and Lines in the lab phase

		Times								
		1	2	3	4	5	6	7		
Runs	Intervals: 1	1	4,41,1	4,43,49	4,36,25	4,13,9	4,10,33	4,44,41	4,29,17	
		2	4,5,46	4,14,38	4,35,21	4,47,5	4,45,22	4,24,30	4,19,13	
		3	4,33,31	4,17,23	4,18,6	4,3,39	4,20,14	4,37,15	4,49,47	
		4	4,40,27	4,23,19	4,26,44	4,28,35	4,46,3	4,7,11	4,9,36	
		5	4,42,16	4,34,8	4,2,40	4,1,24	4,39,48	4,30,7	4,31,32	
		6	4,12,12	4,22,4	4,21,29	4,6,20	4,32,37	4,48,45	4,4,28	
		7	4,16,42	4,38,34	4,8,10	4,15,43	4,11,18	4,27,26	4,25,2	
	Intervals: 2	1	2,23,17	2,26,40	2,34,27	2,17,14	2,30,43	2,27,4	2,11,30	
		2	2,4,42	2,22,9	2,8,45	2,28,32	2,6,19	2,16,22	2,19,6	
		3	2,7,29	2,38,3	2,35,39	2,36,26	2,9,13	2,15,16	2,10,49	
		4	2,32,48	2,40,15	2,31,2	2,33,38	2,44,25	2,1,35	2,18,12	
		5	2,3,11	2,45,34	2,2,21	2,29,1	2,13,37	2,46,47	2,42,24	
		6	2,24,5	2,21,28	2,39,8	2,5,44	2,25,31	2,20,41	2,12,18	
		7	2,14,23	2,37,46	2,47,33	2,49,20	2,48,7	2,41,10	2,43,36	
	Intervals: 3	1	3,24,17	3,20,39	3,6,7	3,30,44	3,17,12	3,27,34	3,35,22	
		2	3,1,8	3,14,30	3,34,47	3,22,42	3,21,3	3,15,25	3,19,20	
		3	3,10,6	3,13,28	3,23,38	3,36,33	3,43,43	3,4,16	3,49,11	
		4	3,28,35	3,7,1	3,31,18	3,5,13	3,2,23	3,46,45	3,3,40	
		5	3,26,46	3,18,19	3,29,29	3,32,24	3,37,41	3,11,14	3,38,2	
		6	3,8,26	3,40,48	3,39,9	3,12,4	3,33,21	3,48,36	3,16,31	
		7	3,42,37	3,25,10	3,47,27	3,9,15	3,44,32	3,41,5	3,45,49	
	Intervals: 4	1	1,40,1	1,10,43	1,38,8	1,34,15	1,13,29	1,5,36	1,27,22	
		2	1,24,6	1,1,48	1,32,13	1,14,20	1,19,34	1,23,41	1,45,27	
		3	1,35,5	1,49,47	1,9,12	1,29,19	1,31,33	1,8,40	1,43,26	
		4	1,20,4	1,15,46	1,6,11	1,7,18	1,22,32	1,42,39	1,48,25	
		5	1,12,7	1,39,49	1,44,14	1,18,21	1,37,35	1,28,42	1,16,28	
		6	1,30,2	1,47,44	1,33,9	1,36,16	1,11,30	1,17,37	1,3,23	
		7	1,41,3	1,26,45	1,2,10	1,46,17	1,4,31	1,25,38	1,21,24	

```

#### Check properties of the design
wheat.canon <- designAnatomy(formulae = list(lab    = ~ Intervals/(Runs*Times),
                                             field  = ~ Blocks/Plots,
                                             treats = ~ Lines),
                             grandMean = TRUE, data = lab.lay)

```



```
summary(wheat.canon, which.criteria =c("aefficiency", "order"))

##
##
## Summary table of the decomposition for lab, field & treats (based on adjusted quantities)
##
## Source.lab          df1 Source.field  df2 Source.treats df3 aefficiency order
## Mean                1 Mean          1 Mean          1      1.0000      1
## Intervals           3 Blocks         3              1.0000      1
## Runs[Intervals]     24 Plots[Blocks] 24 Lines        24      0.2500      1
## Times[Intervals]    24 Plots[Blocks] 24 Lines        24      0.2500      1
## Runs#Times[Intervals] 144 Plots[Blocks] 144 Lines       48      0.7500      1
##                      Residual        96      1.0000      1
##
## The design is not orthogonal
```

Given, the nonorthogonality of Blocks:Plots evident in the anatomy, redo the table with just the lab and field tiers to investigate.

```
#'## Check confounding of field sources with lab sources
wheat.labfield.canon <- designAnatomy(formulae = list(lab = ~ Intervals/(Runs*Times),
                                                    field = ~ Blocks/Plots),
                                     grandMean = TRUE, data = lab.lay)
summary(wheat.labfield.canon, which.criteria =c("aefficiency", "order"))

##
##
## Summary table of the decomposition for lab & field
##
## Source.lab          df1 Source.field  df2 aefficiency order
## Mean                1 Mean          1      1.0000      1
## Intervals           3 Blocks         3      1.0000      1
## Runs[Intervals]     24 Plots[Blocks] 24      1.0000      1
## Times[Intervals]    24 Plots[Blocks] 24      1.0000      1
## Runs#Times[Intervals] 144 Plots[Blocks] 144      1.0000      1
```

5.4.2 Question

1. Is the variance matrix for this experiment based on two sets of terms that are orthogonal?

Because all plots sources are confounded orthogonally with analyses sources, the variance matrix is indeed based on two sets of terms that are orthogonal.

5.5 Elaborate, two-phase, sensory experiment

[Brien and Payne \(1999\)](#) describe a two-phase sensory experiment, of which the first, or field, phase is a viticultural experiment and the second, or evaluation, phase involves the assessment of wine made from the produce of the first phase plots. In the field phase, two adjacent Youden squares are used to assign trellis treatments to the plots, a plot being a row-column combination within a square. Each plot is divided into two halfplots and two methods of pruning assigned at random to them. In the second phase, the halfplots from the field phase are randomized, using two Latin squares and an extended Youden design, to glasses in positions on a table for evaluation by judges. This experiment is Example 1.2 from [Bailey and Brien \(2016\)](#), where its anova, along with expected mean squares, is given. Its factor-allocation diagram is in Figure 23.

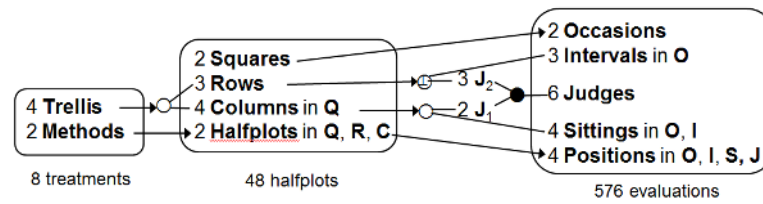


Figure 23: Factor-allocation diagram for the two-phase sensory experiment: treatments are randomized to halfplots, which are, in turn, randomized to evaluations; the arrow to the ‘O’, the ‘O’ and the two lines from the ‘O’ indicate that Trellis is randomized to the combinations of Rows and Columns using a nonorthogonal design; the single arrow between Methods and Halfplots indicates that Methods is randomized to Halfplots; the single arrows between the two right hand panels indicate that Squares are randomized to Occasions and Halfplots are randomized to Positions; J_1 and J_2 are two pseudofactors on Judges that split them into two sets of three; the Rows are randomized to the combinations of Intervals and J_2 using an orthogonal design, as indicated by the ‘ \oplus ’, and Columns are randomized to the combinations of J_1 and Sittings using a nonorthogonal design, as indicated by the ‘O’; Q = Squares; R = Rows; C = Columns; O = Occasions; I = Intervals; S = Sittings; J = Judges.

5.5.1 Check the properties of the randomized layout

Load the layout and use `designAnatomy` to check the properties of the design.

```
### Load the layout
data("Sensory3PhaseShort.dat")

### Examine the properties of the design
sensory.canon <- designAnatomy(formulae = list(eval = ~((Occ/Int/Sit)*Jud)/Posn,
                                             field = ~(Row*(Sqr/Col))/Hplot,
                                             treats = ~Trel*Meth),
                              grandMean = TRUE, data = Sensory3PhaseShort.dat)
summary(sensory.canon, which.criteria = c("aefficiency", "order"))

##
##
## Summary table of the decomposition for eval, field & treats (based on adjusted quantities)
##
## Source.eval      df1 Source.field      df2 Source.treats df3 aefficiency order
## Mean            1 Mean              1 Mean          1      1.0000      1
## Occ             1 Sqr                1              1.0000      1
## Int[Occ]         4
## Sit[Occ:Int]     18 Col[Sqr]          6 Trel          3      0.0370      1
## Residual         12              3      0.3333      1
## Jud              5
## Occ#Jud          5
## Int#Jud[Occ]     20 Row              2              1.0000      1
## Row#Sqr          2              1.0000      1
## Residual         16
## Sit#Jud[Occ:Int] 90 Col[Sqr]          6 Trel          3      0.0741      1
## Residual         3      0.6667      1
## Row#Col[Sqr]     12 Trel          3      0.8889      1
## Residual         9      1.0000      1
## Residual         72
## Posn[Occ:Int:Sit:Jud] 432 Hplot[Row:Sqr:Col] 24 Meth          1      1.0000      1
```

```
##                               Trel#Meth      3      1.0000      1
##                               Residual      20      1.0000      1
##                               Residual      408
##
## The design is not orthogonal
```

Note that 1/3 of Sqr:Col is partially confounded with Occ:Int:Sit and 2/3 with Occ:Int:Sit:Jud. Also, 1/9 of Trel is partially confounded with Sqr:Col and 8/9 with Row:Sqr:Col. The canonical efficiency factor for Trel in the two Sqr:Col sources is obtained by multiplying the canonical efficiency of 1/9 for Trel with that for the particular Sqr:Col source, yielding canonical efficiencies of 1/27 and 2/27.

5.5.2 Questions

1. Which is the nonorthogonal source amongst the field sources (`Source.field`) and what is its interblock and intrablock efficiency factors?

The only nonorthogonal field source is Sqr.Col. Its interblock efficiency factor is 1/3 and its intrablock efficiency factor is 2/3.

2. How would an intrablock analysis be achieved using, say, regression software?

To achieve an intrablock analysis requires careful specification of the order of fitting terms; a nonorthogonal source should not be estimated until after all nonorthogonal terms with which it is confounded, except the last, have been estimated. For this experiment, terms should be fitted in the following order:

$$\text{Occ*Jud} + \text{Row} + \text{Occ:Int}/(\text{Int} + \text{Sit}) + \text{Sqr.Col} + \text{Trel} + \text{Row:Sqr:Col} + \text{Occ:Int:Sit:Jud} + \text{Meth} + \text{Trel:Meth} + \text{Row:Sqr:Col:Hplot}.$$

This will leave a Residual that corresponds to Occ:Int:Sit:Jud:Posn.

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