
**Obtaining, randomizing, exposing the confounding &
formulating mixed models for designs for comparative
experiments using R**
(with output and solutions)

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This document describes how to use functions from the R (R Core Team, 2024) packages `dae` (Brien, 2024b) and `odw` (Butler, 2022) to produce layouts for experiments and to check some of their properties. An introduction to the approach used in the document is given by Brien et al. (2023).

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Topic 0. Introduction for the workshop and the software to be used

0.1 Installed software

The following software should be installed on your computer:

- R (4.2.x or later preferable)
- RStudio
- Packages (you can check the version using the `packageVersion` function.)
 - `dae` (Version 3.2.24 or later from CRAN (<https://cran.at.r-project.org/package=dae/>) or <http://chris.brien.name/rpackages>)
 - `odw` (Version 2.1.4) from <https://mmade.org/optimaldesign/>)

0.2 Programme

08:30–09:30: Topic I. Concepts in experimental design & analysis: Experiment description, randomization by permutation based on the nesting and crossing, canonical analysis of a design and formulating allocation-based mixed models for orthogonal designs, including those with multiple errors.

09:30–10:30: Practical I. Orthogonal experimental design & analysis in R : using `dae` to generate orthogonal designs for experiments.

10:30–11:00: Refreshment break

11:00–12:00: Topic II. Nonorthogonal experimental design & analysis: Using the concepts in the context of balanced and unbalanced experiments; canonical efficiency factors and the alphabet of efficiency measures; the effects of covariates and missing observations.

12:00–13:00: Practical II. Nonorthogonal experimental design & analysis in R : using `dae` and `odw` to produce a range of nonorthogonal designs for experiments.

13:00–14:30: Lunch

14:00–15:30: Topic III. Miscellaneous topics in experimental design & analysis: systematic allocation, pseudoreplication, block-treatment interactions, experiments involving time, and nested factorials.

15:30–16:00: Refreshment break

16:00–17:00: Practical III. Miscellaneous topics in experimental design & analysis in R : further use of `dae` and `odw` related to the miscellaneous topics.

0.3 Packages and the functions to be used

0.3.1 dae

The package **dae** provides functions useful in the design and anova of experiments (Brien, 2024b). There are around 90 functions that fall into the following categories and those that will be used in this course are described:

1. Data

BIBDWheat.dat Data for a balanced incomplete block experiment.

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

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

Exp249.munit.des Systematic, main-unit 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
7. Miscellaneous functions.

0.3.2 odw

The package `odw` generates optimal experimental designs ([Butler, 2022](#)). It does this based on an *anticipated* mixed model and obtains a design that minimizes the average variance of pairwise differences (AVPD). It has more than 30 functions; the two primary functions for this course are as follows:

odw: Generates optimal designs for comparative experiments under a general linear mixed model.

odw.options: Sets or displays various options that affect the behaviour of `odw`.

Documentation for each of these functions is available from the user manual for the relevant package. In general this can be found in the `doc` subdirectory of the directory in which the package is installed or from the `help` for the function once the package has been installed. For the latter, to see the manual for package `foo`, enter `help(package="foo")` and click on the link [User guides, package vignettes and other documentation](#).

For `dae`, the manual is available via `vignette("dae-manual", package="dae")` and there are some notes that show how to use the functions that are available via `vignette("DesignNotes", package="dae")`.

0.4 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 random effects for each observation, sometimes referred to as random errors. 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 that specify a different effect for each observation are called identity terms and are underlined.

Topic I. Orthogonal experimental design & analysis in R

This class of experiments covers the orthogonal standard or textbook experiments, those that 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, an allocated set that is allocated to a recipient set. These two sets are also referred to as the units and treatments 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] '3.2.26'
```

I.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., 2023) for the RCBD is in Figure 1 and that for the LSqD is in Figure 2.

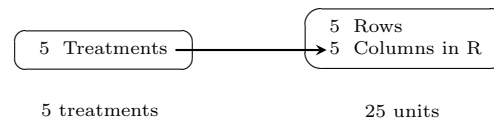


Figure 1: Factor-allocation diagram for an RCBD: treatments are allocated to units; the arrow indicates that the factor Treatments is randomized to Columns; Columns in R indicates that the Columns are considered to be nested within Rows for this randomization; R = Rows.

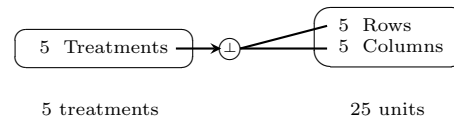


Figure 2: Factor-allocation diagram for an LSqD: treatments are allocated to units; the arrow indicates that the allocation is randomized; the \oplus at the end of the arrow indicates that an orthogonal design is used; the two lines from \oplus indicates that the Treatments are allocated to the combinations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

I.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) `recipient`, (iii) `nested.recipients`, 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 several ways of doing this.

Our 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, in these notes, 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:

```
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)

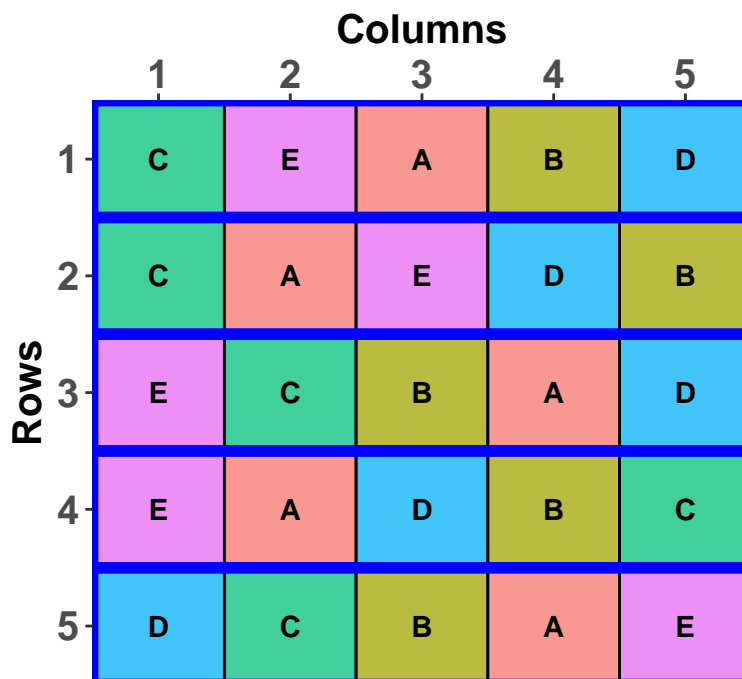
### Output the layout
RCBD.lay
```

| ## | 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.lay, labels = "Treatments", cellalpha = 0.75,
             blockdefinition = cbind(1,t))
```

Plot of Treatments



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 argument settings.

I.1.2 Produce the randomized layout for an LSqD

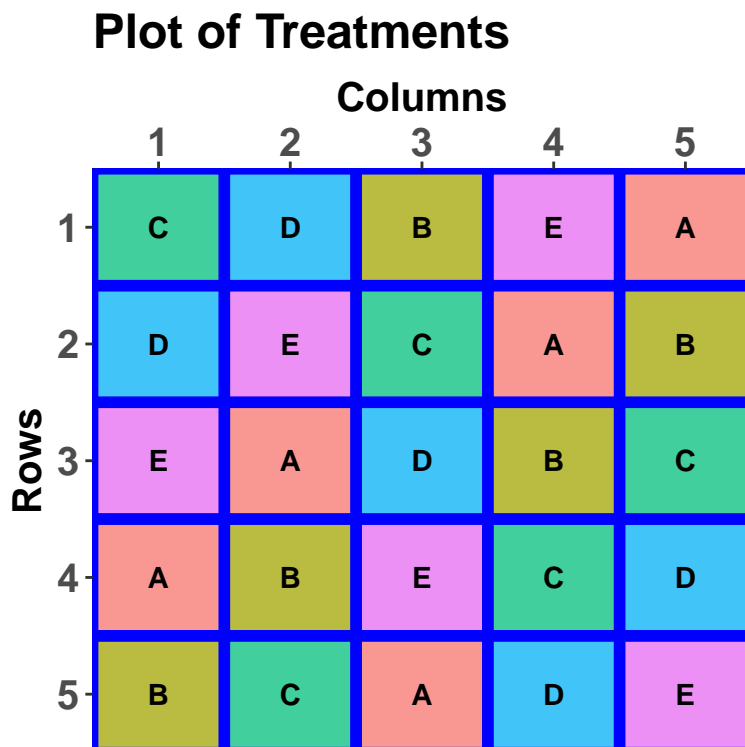
Use `designRandomize` to randomize the treatments according to an LSqD, having obtained the systematic design using `fac.gen` and `designLatinSqrSys`. For this design, Rows and Columns are crossed; there are no nested factors. Consequently, the `nested.recipients` argument is omitted so that `designRandomize` 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.lay <- designRandomize(allocated = LSqD.sys["Treatments"],
                           recipient = LSqD.sys[c("Rows", "Columns")],
                           seed      = 141)
### Output the layout
LSqD.lay
##      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))
```



I.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 (like skeleton-anova tables but produced from an eigenanalysis) 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`.

```
##### Get the 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 aeffericiency eeffericiency 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 aeffericiency eeffericiency 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
```

I.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 between the designs in the interpretation of these units 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.

I.2 Split-unit design for a pasture experiment from Kaps and Lamberson (2004)

Kaps and Lamberson (2004, p.344) describes a split-unit experiment that investigates the effects of four different pasture treatments and two mineral supplements on the milk yield of cows. The Pasture treatments are assigned to the main units formed from large plots using a randomized complete-block design with 3 blocks and the Mineral supplements are randomly assigned to the subunits (smaller plots) in each main unit. The factor-allocation diagram for the experiment is in Figure 3.

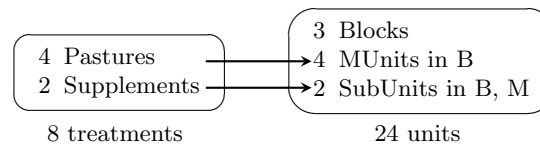


Figure 3: Factor-allocation diagram for a split-unit design: treatments are allocated to units; the arrows indicates that the factors Pastures and Supplements are randomized to MUnits and SubUnits, respectively; MUnits in B indicates that the MUnits are considered to be nested within Blocks for this randomization; SubUnits in B, M indicates that the SubUnits are considered to be nested within Blocks and MUnits for this randomization; B = Blocks, M = MUnits

I.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:

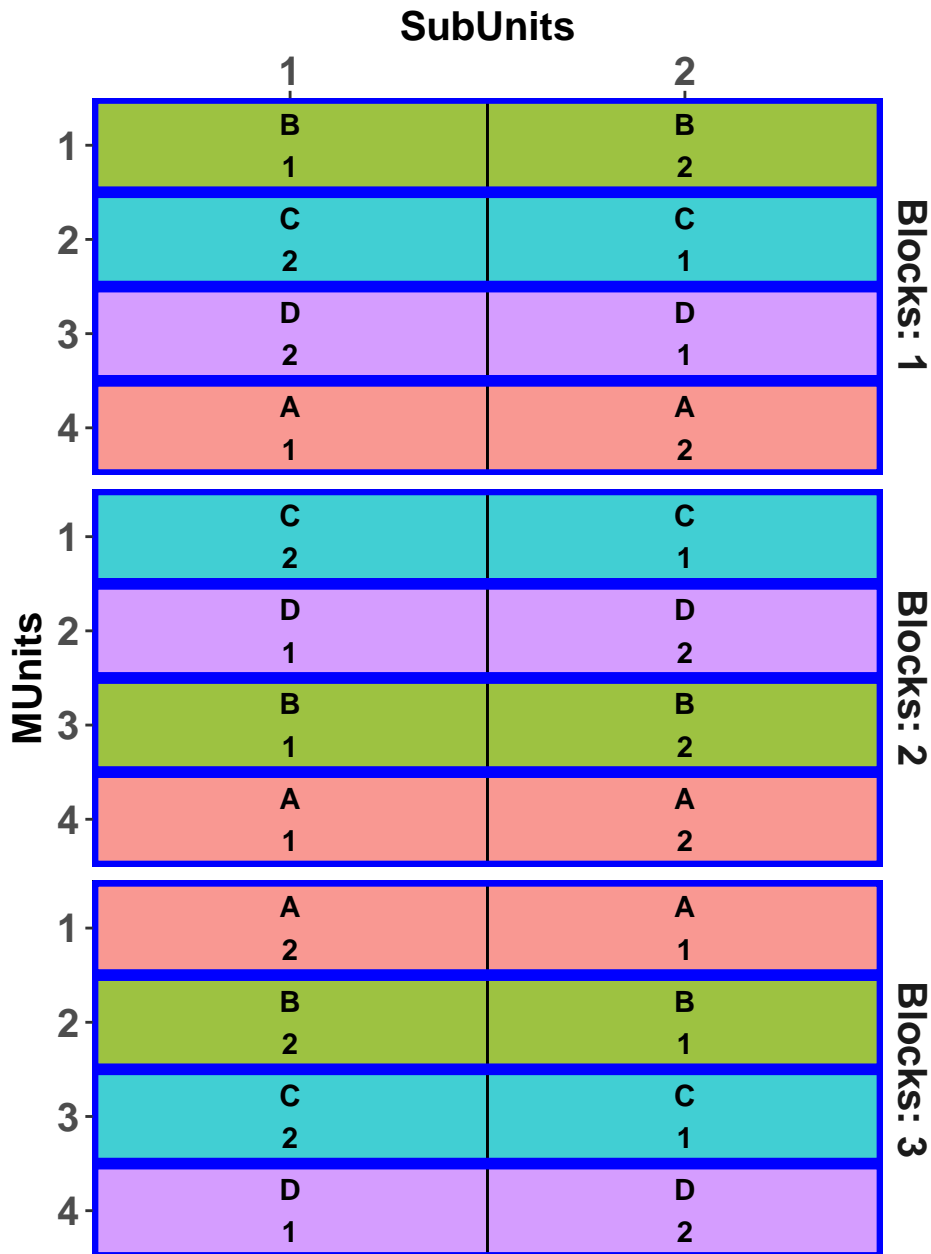
```
#### Set up the systematic design
Milk.sys <- cbind(fac.gen(list(Blocks=3, MUnits=4, SubUnits=2)),
                 fac.gen(list(Pastures=LETTERS[1:4],
                              Supplements=2), times=3))

#### Obtain the randomized layout
Milk.layout <- designRandomize(allocated = Milk.sys[c("Pastures", "Supplements")],
                              recipient = Milk.sys[c("Blocks", "MUnits", "SubUnits")],
                              nested.recipients = list(MUnits = "Blocks",
                                                         SubUnits = c("MUnits", "Blocks")),
                              seed = 580523)

#### Plot design produced with blue lines showing MainUnits, first combining Pastures and
#### Supplements so that they are plotted on 2 lines per cell
Milk.layout$Treatments <- with(Milk.layout, fac.combine(list(Pastures, Supplements),
                                                         combine.levels = TRUE, sep = "\n"))

designGGPlot(Milk.layout, labels = "Treatments",
             row.factors = c("Blocks", "MUnits"), column.factors = "SubUnits",
             cellfillcolour.column = "Pastures", cellalpha = 0.75,
             blockdefinition = rbind(c(1,2)))
```

Plot of Treatments



```
## Check its properties
Milk.canon <- designAnatomy(formulae = list(units = ~ Blocks/MUnits/SubUnits,
                                           trts  = ~ Pastures*Supplements),
                           grandMean = TRUE, data = Milk.lay)
summary(Milk.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 | 2 | | | | |
| ## | MUnits[Blocks] | 9 | Pastures | 3 | 1.0000 | 1 |
| ## | | | Residual | 6 | | |
| ## | SubUnits[Blocks:MUnits] | 12 | Supplements | 1 | 1.0000 | 1 |
| ## | | | Pastures#Supplements | 3 | 1.0000 | 1 |
| ## | | | Residual | 8 | | |

I.2.2 Questions

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

In the sense that the randomization of both Supplements and Pastures can be achieved with a single permutation of the units, in this case the SubUnits.

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

The initial allocation mixed model is $Pastures + Supplements + Pastures:Supplements \mid Blocks + Blocks:MUnits + Blocks:MUnits:SubUnits$. The initial allocation model is equivalent to a randomization model because all allocation was by randomization.

3. A factorial RCBD would involve randomizing the $3 \times 4 = 12$ treatments to the 12 subunits within each block. What is the effect on treatment comparisons of using the split-unit design as compared to a factorial RCBD?

The precision of the Pastures differences may be less than the precision of the Supplements differences, depending on the how much extra variability there is between MUnits as compared to the variability between SubUnits. If there is extra variation between the MUnits as compared to the SubUnit, then the Residual mean square for MUnits[Blocks] will be larger than that for SubUnits[Blocks:MUnits]. If a factorial RCBD had been used, the Residual mean square for Units[Blocks] would be the weighted average of the two Residual mean squares from the split-unit experiment, the weights being their 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-unit design. Consequently, the comparison between Supplements within Varieties will be more precise for the split-unit design.

I.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.

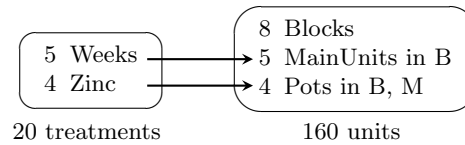


Figure 4: Factor-allocation diagram for a split-unit design: treatments are allocated to units; the arrows indicates that the factors Weeks and Zinc are randomized to MainUnits and Pots, respectively; MainUnits in B indicates that the MainUnits are considered to be nested within Blocks for this randomization;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

I.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

```

I.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 $Pots[Blocks:MainUnits]$.

I.4 Split-unit design with criss-cross design of the sub-units from Mead (1990)

Mead (1990, Example 14.1) describes an experiment to investigate the effects of grazing patterns on pasture composition. It is available in `dae` as `SPLGrass.dat`.

The design for the experiment is a split-unit design with a criss-cross or strip-unit design on the subunits. The main units are arranged in 3 Rows \times 3 Columns. Each main unit is split into 2 SubRows \times 2 SubColumns.

The factor Period, with levels 3, 9 and 18 days, is assigned to the main units using a 3 \times 3 Latin square. The two-level factors Spring and Summer are assigned to subunits using a criss-cross or strip-unit design that is randomized within each main unit; Spring is randomized to SubRows and Summer is randomized to SubColumns. The levels of each of Spring and Summer are two different grazing patterns in its season. The response variable is `Main.Grass`.

Use `data(SPLGrass.dat)` to load the design (and the data). Plot the design: create a factor `Treats` by combining the factors Period, Spring and Summer using `fac.combine` with the argument `combine.levels` set to `TRUE` and then use `designGGPlot` with `cellfillcolour.column` set to "Period" and `cellalpha` set to about 0.4. Also, investigate the properties of the design using `designAnatomy`.

```

#### Load the design
data("SPLGrass.dat")

#### Plot the design
SPLGrass.dat$Treats <- with(SPLGrass.dat,
                           fac.combine(list(Period, Spring, Summer), combine.levels = TRUE))
designGGPlot(SPLGrass.dat, labels = "Treats",

```

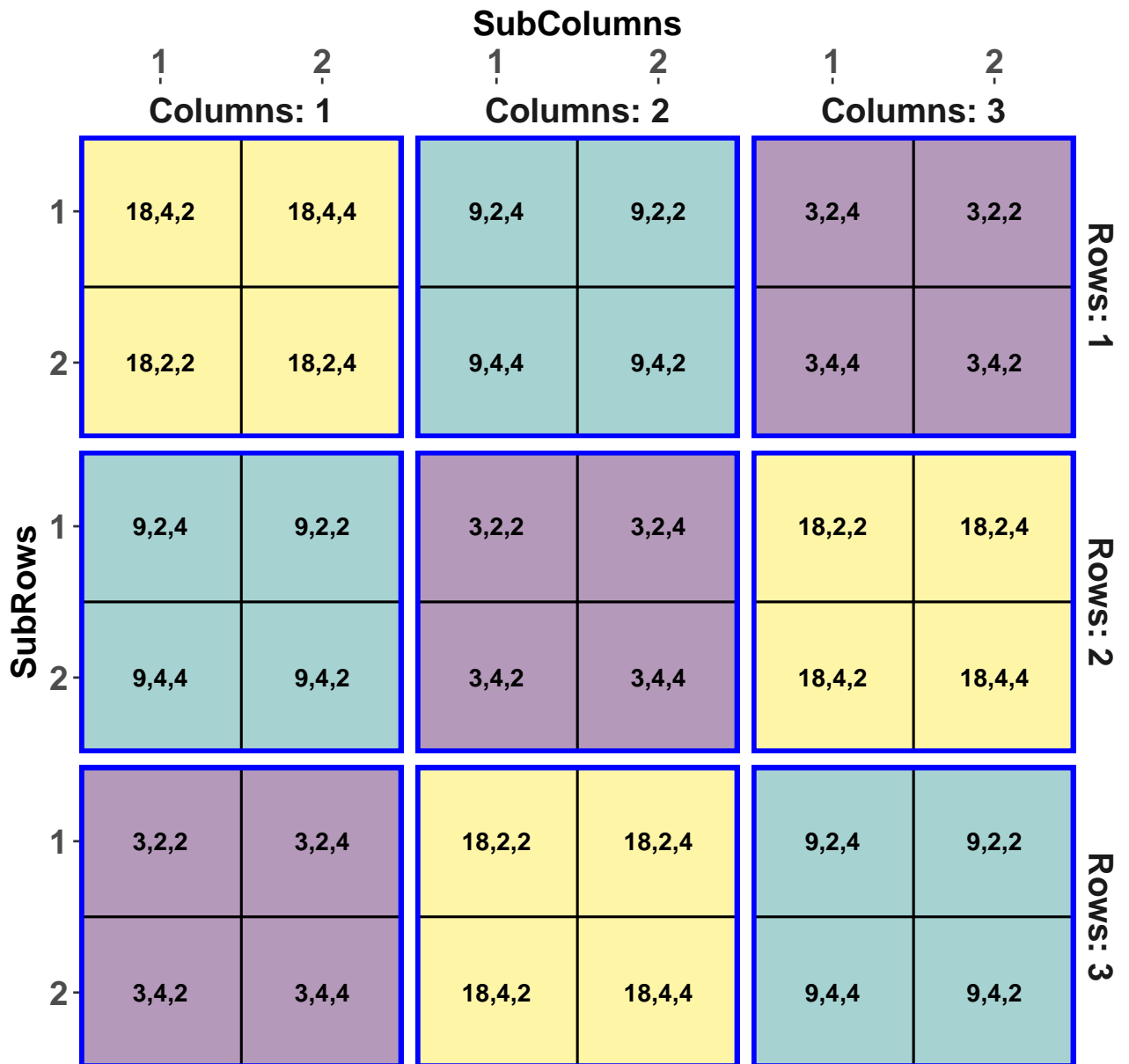


```

row.factors = c("Rows", "SubRows"), column.factors = c("Columns", "SubColumns"),
cellfillcolour.column = "Period", cellalpha = 0.4,
blockdefinition = cbind(2,2))

```

Plot of Treats



```

## Check its properties
Grass.canon <- designAnatomy(formulae = list(units = ~ (Rows*Columns)/(SubRows*SubColumns),
                                             trts = ~ Period*Spring*Summer),
                             grandMean = TRUE, data = SPLGrass.dat)
summary(Grass.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
## Rows              2
## Columns            2
## Rows#Columns      4 Period              2      1.0000      1
##                   Residual              2
## SubRows[Rows:Columns] 9 Spring              1      1.0000      1
##                   Period#Spring          2      1.0000      1
##                   Residual              6
## SubColumns[Rows:Columns] 9 Summer              1      1.0000      1
##                   Period#Summer          2      1.0000      1
##                   Residual              6
## SubRows#SubColumns[Rows:Columns] 9 Spring#Summer 1      1.0000      1
##                   Period#Spring#Summer 2      1.0000      1
##                   Residual              6
```

I.4.1 Questions

1. Describe the confounding that is inherent in this design.

Period is confounded with Rows#Columns; Spring and Period#Spring are confounded with SubRows[Rows:Columns], while Summer and Period#Summer are confounded with SubColumns[Rows:Columns]. Finally Spring#Summer and Period#Spring#Summer are confounded with SubRows#SubColumns[Rows:Columns].

2. Draw a factor-allocation diagram for this experiment.

You should have (i) a treatments panel with 3 Periods, 2 Spring and 2 Summers, (ii) a plots panel with 3 Rows, 3 Columns, 2 SubRows in R, C, 2 SubColumns in R, C. There should be an arrow from Periods to an orthogonal design symbol and two lines from the symbol to Rows and Columns, as well as arrows from Spring to SubRows and Summer to SubColumns.

3. What is the initial allocated mixed model for this design?

The initial allocation mixed model is $\text{Period} + \text{Spring} + \text{Period:Spring} + \text{Summer} + \text{Period:Summer} + \text{Spring:Summer} + \text{Spring:Summer} \mid \text{Rows} + \text{Columns} + \text{Rows:Columns} + \text{Rows:Columns:SubRows} + \text{Rows:Columns:SubColumns} + \text{Rows:Columns:SubRows:SubColumns}$. The initial allocation model is equivalent to a randomization model because the allocation was only by randomization.

I.5 A design for the petrol additives experiment

Box et al. (2005, Section 4.4) describe 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 for allocating the 4 Additives to the 32 tests, being the combinations of the 2 Occasions x 4 Drivers x 4 Cars. Make sure that a Latin square is used for each Occasion.

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.

```
## 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"),
```

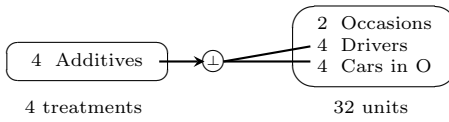
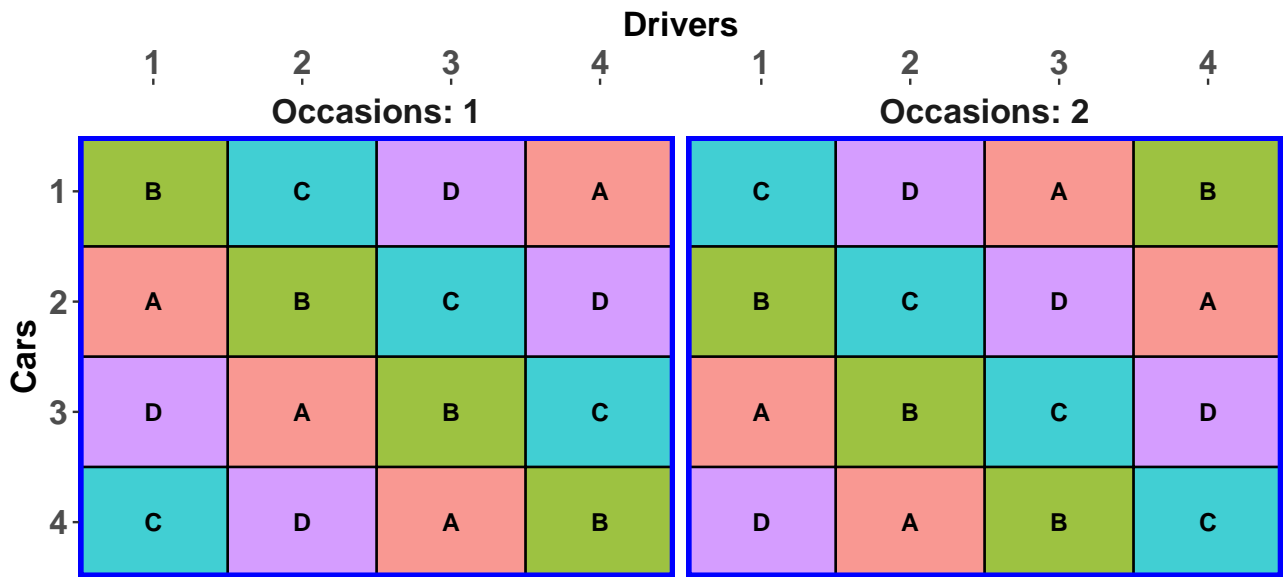


Figure 5: Factor-allocation diagram for repeated LSQDs: treatments are allocated to units; the arrow indicates that the allocation is randomized; the ‘⊕’ at the end of the arrow indicates that an orthogonal design is used; the two lines from ‘⊕’ indicates that the Additives are allocated to the combinations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

```
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
```

Secondly, 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.

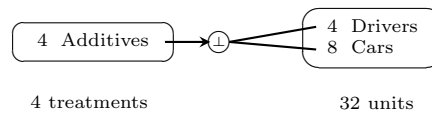
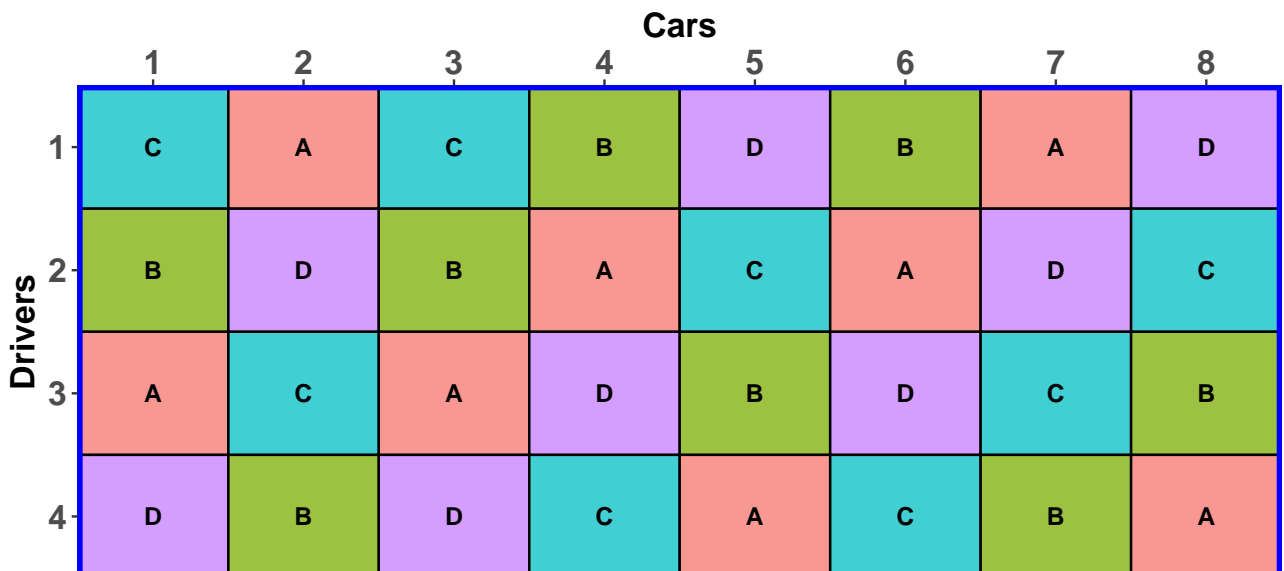


Figure 6: Factor-allocation diagram for repeated LSQDs: treatments are allocated to units; the arrow indicates that the allocation is randomized; the '⊥' at the end of the arrow indicates that an orthogonal design is used; the two lines from '⊥' indicates that the Additives are allocated to the combinations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

```
### 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),])
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 aeffericiency eeffericiency 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 aeffericiency eeffericiency 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
```

I.5.1 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).

Topic II. Nonorthogonal experimental design & analysis in R

This class of experiments covers the nonorthogonal standard or textbook experiments and these experiments must be single phase because they involve a single randomization. ?, Section 5 discuss the anatomy and its interpretation for a nonorthogonal, balanced experiment.

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

```
library(dae, quietly = TRUE)
library(odw)

## Loading required package: Matrix

packageVersion("odw")

## [1] '2.1.4'

options(width=100)
```

II.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 | | | | | Replicate 2 | | | | | Replicate 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.

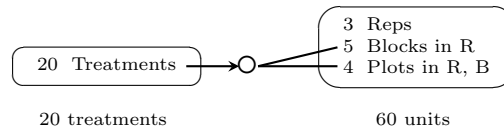


Figure 7: Factor-allocation diagram for the alpha design: treatments are allocated to units; the arrow indicates that the allocation is randomized; the ‘O’ at the end of the arrow indicates that a nonorthogonal design is used; the two lines from ‘O’ indicate that the Treatments are allocated to the combinations 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.

II.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.lay <- designRandomize(allocated = alpha.sys["Treats"],
                             recipient = alpha.sys[c("Reps", "Plots", "Blocks")],
                             nested.recipients = list(Blocks = "Reps",
                                                         Plots = c("Reps", "Blocks")),
                             seed = 918508)

alpha.lay <- with(alpha.lay, alpha.lay[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 (A), that is, to 0.7447 . In particular, $AVPD = 2/(rA)$.

```
AVPD <- designAmeasures(mat.Vpredicts(target = ~ Treats - 1,
                                     fixed = ~ Reps/Blocks,
                                     design = alpha.lay))[[1]]
Aeff <- summary(alpha.canon, which.criteria = "aeff")$decomp$aefficiency[4]
(measures <- c(AVPD, Aeff, 2/(3*Aeff)))

## [1] 0.8952381 0.7446809 0.8952381
```

II.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 $Treats \mid Reps + Reps:Blocks + Reps:Blocks:Plots$.

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, Reps 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 Reps (there is no Treats information between Reps).

II.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.

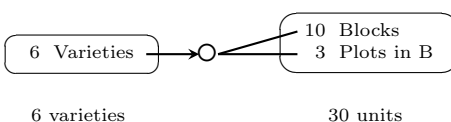


Figure 8: Factor-allocation diagram for the balanced incomplete-block design: treatments are allocated to units; the arrow indicates that the allocation is randomized; the ‘O’ at the end of the arrow indicates that a nonorthogonal design is used; the two lines from ‘O’ indicates that the Varieties are 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.

II.2.1 Load the design and check its 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.

Calculate the AVPD and check that $AVPD = 2/(rA)$

```
AVPD <- designAmeasures(mat.Vpredicts(target = ~ Varieties - 1,
                                     fixed = ~ Blocks,
                                     design = BIBDWheat.dat))[[1]]
Aeff <- summary(bibdwheat.canon, which.criteria = "aeff")$decomp$aefficiency[4]
(measures <- c(AVPD, Aeff, 2/(5*Aeff)))

## [1] 0.5 0.8 0.5
```

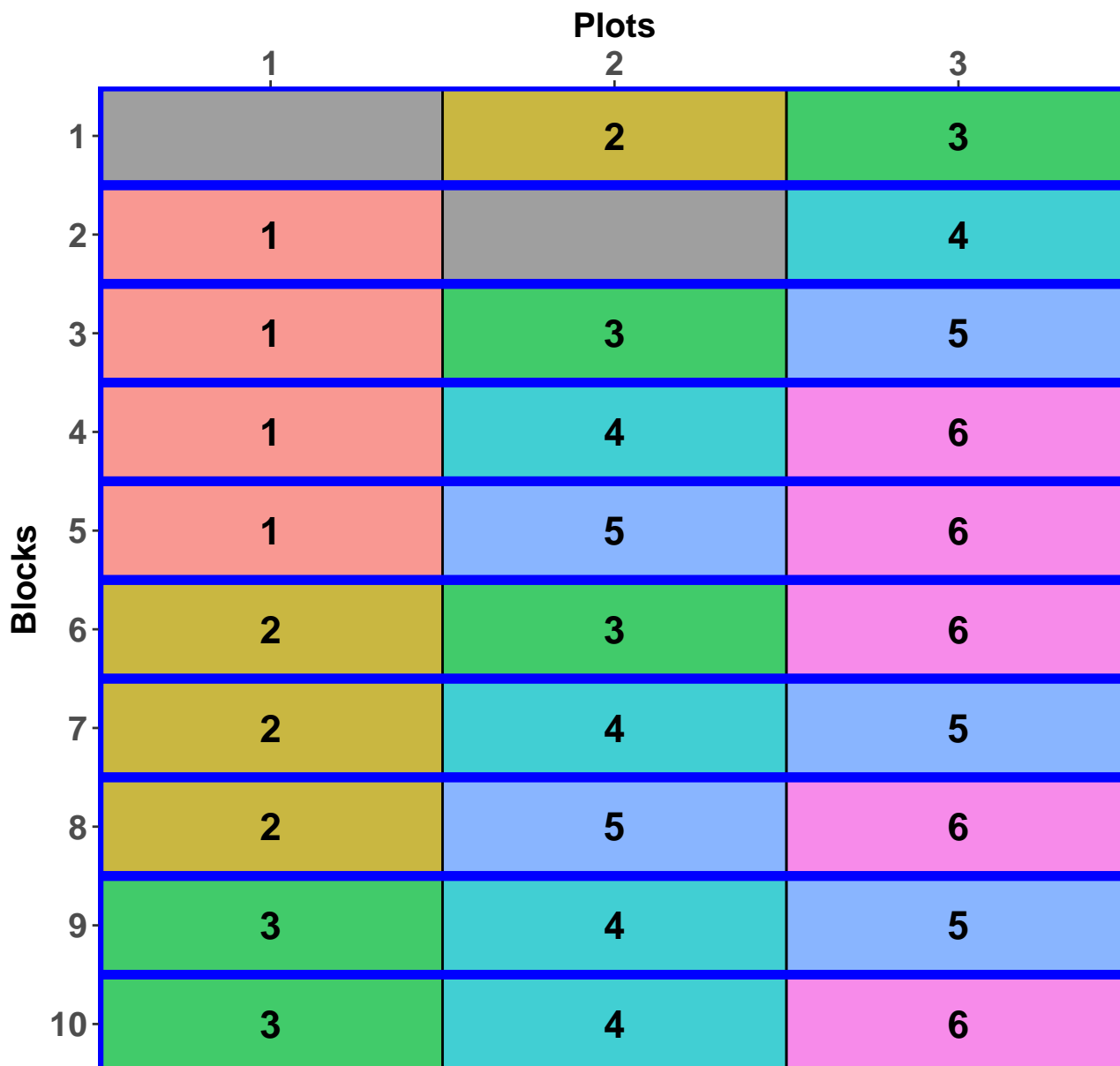
II.2.2 What if two observations are missing?

Set the two observations that are not the Control to missing and obtain the anatomy. The greatest effect is surprisingly on the comparison between the Control and New.

```
## Investigate the effect of two-missing observations
#+ "BIBDDet"
bibdwheat.Miss.dat <- BIBDWheat.dat
bibdwheat.Miss.dat$Varieties[c(1,5)] <- NA #different Blocks & Varieties
designGGPlot(bibdwheat.Miss.dat, labels = "Varieties",
            row.factors = "Blocks", column.factors = "Plots",
            cellalpha = 0.75, label.size = 6, blockdefinition = cbind(1,3))

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

Plot of Varieties



```
bibd wheat.Miss.canon <- designAnatomy(formulae = list(units = ~ Blocks/Plots,
                                                    trts = ~ Varieties),
                                     grandMean = TRUE, data = na.omit(bibd wheat.Miss.dat))
summary(bibd wheat.Miss.canon, which.criteria = c('aeff', 'xeff', 'eeff', 'order'))

##
##
## Summary table of the decomposition for units & trts (based on adjusted quantities)
##
## Source.units df1 Source.trts df2 aefficiency xeffecticiency eeffecticiency order
## Mean 1 Mean 1 1.0000 1.0000 1.0000 1
## Blocks 9 Varieties 5 0.1909 0.4365 0.1154 5
## Residual 4
```

```
## Plots[Blocks] 18 Varieties 5 0.7513 0.8846 0.5635 5
## Residual 13
##
## The design is not orthogonal
```

II.2.3 Questions

1. What is the value of efficiency for Varieties when confounded with Plots[Blocks] for the original 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. What is the effect of the missing values on the efficiency for Varieties when confounded with Plots[Blocks]?

There are now 5 different canonical efficiency factor ranging from 0.56 to 0.88 with an average of 0.75. This compares with all values equal to 0.80 for the full design.

II.3 A design with rows and columns for a Casuarina trial

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.

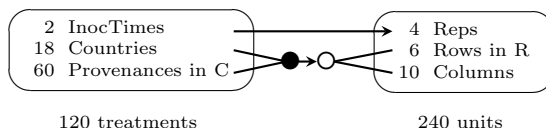


Figure 9: Factor-allocation diagram for the balanced lattice design: treatments are allocated to units; the arrows indicates that the allocations are randomized; the two lines leading to the ‘●’ indicate that it is the combinations of Countries and Provenances that is allocated; the ‘○’ at the end of the arrow from the ‘●’ 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.

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

##
##
## Summary table of the decomposition for units & trts (based on adjusted quantities)
##
## Source.units      df1 Source.trts      df2 aeffericiency eeffericiency 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              aeffericiency
## 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
## eeffericiency 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.

II.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.

II.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.

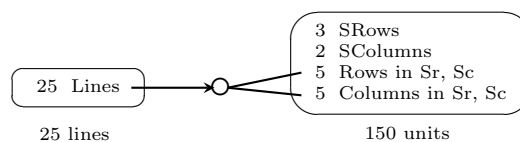


Figure 10: Factor-allocation diagram for the balanced lattice square design: treatments are allocated to units; the arrows indicates that the allocations are randomized; the ‘O’ at the end of the lower arrow indicates that a nonorthogonal design is used; the two lines from ‘O’ indicates that the Lines 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(up)erRows; Sc = S(up)erColumns.

In the lectures it was stated that, while the design is optimal for a fixed model, it is not optimal for a mixed model. In this exercise, a search will be made for a resolved design that is near-A-optimal under a mixed model.

II.4.1 Input the design and check the properties of the design

Use the following R code to input and extract the design, plot it and check its properties. The R package `asremlPlus` Brien (2024a) can be used to access the data set or it is available in an `rda` data file. Because we are going to use the design to produce a new design for another experiment, we rerandomize the design using the randomization appropriate to the balanced lattice square design. Being a valid randomization in that it corresponds to the randomization model, the properties of the design will be unchanged.

```
#'## 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"])

### Rerandomize the design for a new experiment
latt.lay <- designRandomize(allocated = latt.lay["Variety"],
                           recipient = latt.lay[c("SRows", "Rows", "SColumns", "Columns")],
                           nested.recipients = list(Rows = "SRows",
                                                       Columns = "SColumns"),
                           seed = 63146)

### Add row and column factors that have a unique level for each row and each column (needed for ar1)
latt.lay <- cbind(fac.gen(list(ARows = 10, AColumns = 15)), latt.lay)

### 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"),
             colour.values = cell.colours, cellalpha = 0.75, label.size = 6,
             blockdefinition = cbind(5,5))

```

Figure 1 displays a 5x15 grid of numbers, organized into two main sections: Rows: 1 and Rows: 2. Each section contains three 5x5 sub-grids, labeled SColumns: 1, SColumns: 2, and SColumns: 3. The columns are numbered 1 to 5, and the rows are numbered 1 to 5. The numbers are color-coded, with colors repeating in a 5x5 pattern across each sub-grid.

| | | SColumns: 1 | | | | | SColumns: 2 | | | | | SColumns: 3 | | | | |
|---------|---|-------------|----|----|----|----|-------------|----|----|----|----|-------------|----|----|----|----|
| | | 1 | 2 | 3 | 4 | 5 | 1 | 2 | 3 | 4 | 5 | 1 | 2 | 3 | 4 | 5 |
| Rows: 1 | 1 | 16 | 24 | 2 | 13 | 10 | 3 | 8 | 18 | 23 | 13 | 17 | 10 | 4 | 23 | 11 |
| | 2 | 4 | 7 | 15 | 21 | 18 | 5 | 10 | 20 | 25 | 15 | 1 | 19 | 13 | 7 | 25 |
| | 3 | 8 | 11 | 19 | 5 | 22 | 4 | 9 | 19 | 24 | 14 | 15 | 3 | 22 | 16 | 9 |
| | 4 | 25 | 3 | 6 | 17 | 14 | 2 | 7 | 17 | 22 | 12 | 8 | 21 | 20 | 14 | 2 |
| | 5 | 12 | 20 | 23 | 9 | 1 | 1 | 6 | 16 | 21 | 11 | 24 | 12 | 6 | 5 | 18 |
| Rows: 2 | 1 | 11 | 20 | 7 | 3 | 24 | 21 | 24 | 22 | 25 | 23 | 22 | 6 | 13 | 20 | 4 |
| | 2 | 5 | 9 | 21 | 17 | 13 | 16 | 19 | 17 | 20 | 18 | 3 | 12 | 19 | 21 | 10 |
| | 3 | 8 | 12 | 4 | 25 | 16 | 6 | 9 | 7 | 10 | 8 | 16 | 5 | 7 | 14 | 23 |
| | 4 | 22 | 1 | 18 | 14 | 10 | 11 | 14 | 12 | 15 | 13 | 15 | 24 | 1 | 8 | 17 |
| | 5 | 19 | 23 | 15 | 6 | 2 | 1 | 4 | 2 | 5 | 3 | 9 | 18 | 25 | 2 | 11 |

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```
## 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
```

II.4.2 Search for a near-A-optimal design

Use `odw` to search for a near-A-optimal design under a mixed model for a crossed row-column design with autocorrelations, as opposed to a nested row-column design with independent errors. In this case the "tabu+rw" search method is to be used. Further, the `odw` options are to be set to values that I have found by trail-and-error to be successful. The options are

P: the probability of accepting a non-improving design; the default is $P=0.005$.

localSearch: the number of steps in the random walk local search strategy of the "tabu+rw" search option; the default is 10000.

tabuStop: if the number of consecutive tabu loops with no change in the objective function exceeds `tabuStop`, then tabu optimization terminates (the default is 4).

```
##### Set odw options
maxit <- 25
search <- "tabu+rw"
odw.options(P = 0.10, localSearch = 10000, tabuStop = 100)
##### Set up the values of the variance components and autocorrelation for the random terms
params <- c(2.5, 1, 0.1, 0.1, 0.5, 1, 0.6, 0.4)
names(params) <- c("g.sRR", "g.sCC", "g.sRsCR", "g.sRsCC", "g.u", "g.aRaC", "rho.R", "rho.C")
##### Set the values in odw
Wheat.start <- odw(fixed = ~ SRows*SColumns + Variety,
                  random = ~ SRows:Rows + SColumns:Columns +
                           SRows:SColumns:(Rows + Columns) + units,
                  residual = ~ ar1(ARows):ar1(AColumns),
                  permute = ~ Variety, swap = ~ SRows:SColumns,
                  data = latt.layout, start.values = TRUE)
vp.table <- Wheat.start$vpparameters.table
vp.table$Value <- params
print(vp.table)

##                               Component Value
## 1                               SRows:Rows      2.5
## 2                               SColumns:Columns  1.0
## 3                               SRows:SColumns:Rows 0.1
## 4                               SRows:SColumns:Columns 0.1
## 5                               units      0.5
## 6                               ARows:AColumns!R      1.0
## 7                               ARows:AColumns!ARows!cor 0.6
## 8                               ARows:AColumns!AColumns!cor 0.4

##### Generate the near-A-optimal design
Wheat.odw <- odw(fixed = ~ SRows*SColumns + Variety,
                random = ~ SRows:Rows + SColumns:Columns +
                         SRows:SColumns:(Rows + Columns) + units,
```

```

    residual = ~ ar1(ARows):ar1(AColumns),
    permute = ~ Variety, swap = ~ SRows:SColumns,
    G.param = vp.table, R.param = vp.table,
    maxit = maxit, search = search,
    data = latt.lay)

## Sat May 18 00:13:25 2024
## Initial criterion = 0.385054 (25 A-equations; rank C 24)
## Criterion after 1000 initial random iterations: 0.375673
## Criterion after tabu loop 1 is 0.372568
## Criterion after tabu loop 2 is 0.372336
## Criterion after tabu loop 3 is 0.371981
## Criterion after tabu loop 4 is 0.371981
## Criterion after tabu loop 5 is 0.371938
## Criterion after tabu loop 6 is 0.371676
## Criterion after tabu loop 7 is 0.371676
## Criterion after tabu loop 8 is 0.371497
## Criterion after tabu loop 9 is 0.371102
## Criterion after tabu loop 10 is 0.370951
## Criterion after tabu loop 11 is 0.370951
## Criterion after tabu loop 12 is 0.370951
## Criterion after tabu loop 13 is 0.370951
## Criterion after tabu loop 14 is 0.370951
## Criterion after tabu loop 15 is 0.370951
## Criterion after tabu loop 16 is 0.370951
## Criterion after tabu loop 17 is 0.370951
## Criterion after tabu loop 18 is 0.370951
## Criterion after tabu loop 19 is 0.370951
## Criterion after tabu loop 20 is 0.370874
## Criterion after tabu loop 21 is 0.370874
## Criterion after tabu loop 22 is 0.370874
## Criterion after tabu loop 23 is 0.370874
## Criterion after tabu loop 24 is 0.370874
## Criterion after tabu loop 25 is 0.370874
## Hash table size 363
## Final criterion after 25 tabu+rw iterations: 0.370874
## Cleaning up: Sat May 18 00:13:29 2024

Wheat.lay <- Wheat.odw$design
Wheat.lay$unit <- factor(1:nrow(Wheat.lay))

```

Given that this is a spatial design, it cannot be now randomized. However, the initial design from which it was derived was randomized, thereby guarding against systematic patterns that might have been artefacts from a systematic input design.

II.4.3 Checking the properties of the designs

Now calculate the A-measure for the original lattice-square design and the near-optimal design produce by `odw`. Also, produce the anatomy for the near-optimal design.

```

##### Calculate the A-measure for the lattice square design under a mixed model
latt.lay$unit <- factor(1:nrow(latt.lay))
(A.latt <- designAmeasures(mat.Vpredicts(target = ~ Variety - 1,
                                           fixed = ~ SRows*SColumns - 1,

```

```

random = ~ SRows:Rows + SColumns:Columns +
          SRows:SColumns:(Rows + Columns) + unit - 1,
G       = as.list(params[1:5]),
R       = kronecker(mat.ar1(params["rho.R"], 10),
                    mat.ar1(params["rho.C"], 15)),
design = latt.lay))[[1]])

## [1] 0.3850544

##### Check the A-value for the near-optimal design
(A.wht <- designAmeasures(mat.Vpredicts(target = ~ Variety - 1,
fixed = ~ SRows*SColumns - 1,
random = ~ SRows:Rows + SColumns:Columns +
          SRows:SColumns:(Rows + Columns) + unit - 1,
G       = as.list(params[1:5]),
R       = kronecker(mat.ar1(params["rho.R"], 10),
                    mat.ar1(params["rho.C"], 15)),
design = Wheat.lay))[[1]])

## [1] 0.370874

(A.wht/A.latt)

## [1] 0.963173

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

##
##
## Summary table of the decomposition for units & trts (based on adjusted quantities)
##
## Source.units          df1 Source.trts df2 aeffectivity meffectivity xeffectivity eeffectivity
## Mean                  1 Mean          1      1.0000      1.0000      1.0000      1.0000
## SRows:SColumns        5
## Rows[SRows:SColumns] 24 Variety      24      0.0054      0.1667      0.4663      0.0003
## Columns[SRows:SColumns] 24 Variety    24      0.0012      0.1667      0.4886      0.0001
## Rows#Columns[SRows:SColumns] 96 Variety 24      0.6273      0.6667      0.9191      0.3789
##                      Residual      72
## order
## 1
##
## 24
## 24
## 24
##
##
## The design is not orthogonal

```

II.4.4 Questions

1. How do the AVPD values calculated by `odw` and those calculated using `designAmeasures` and `mat.Vpredicts` compare?

They are the same.

2. Summarize the differences between the original balanced lattice square design and the `odw` design. Is the increased precision of the `odw` design worthwhile?

The AVPD has decreased by around 3% and so the increase in precision is small. The lattice square design is balanced, the order of Lines always being one, and so all contrasts have equal variance. On the other hand, for the `odw` design, Lines has order 24, the same as the number of degrees of freedom. The values of the efficiencies range from 0.4249 to 0.9335 so that the variances of the contrast will vary. It seems that the balance of the lattice square design is not worth sacrificing for the minor increase in precision. However, this is for the values of the variance parameters used in the call to `odw`. It would be safest to conduct a study of the value obtained for a range of values for the variance parameters.

Topic III. Miscellaneous topics in experimental design & analysis in R

This section includes examples covering the recognition pseudoreplication, grazing trials 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)
library(odw)
packageVersion("odw")

## [1] '2.1.4'

options(width=100)
```

III.1 An animal feeding experiment

Suppose an animal scientist wants to investigate the effect on the weight gain of calves fed four different feed mixtures. They have four pens available for the experiment and they randomize the mixtures to these pens. Each pen has six calves and the weight gain of the each calf is obtained. The factor-allocation diagram for the experiment is in Figure 11.

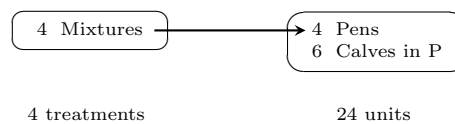


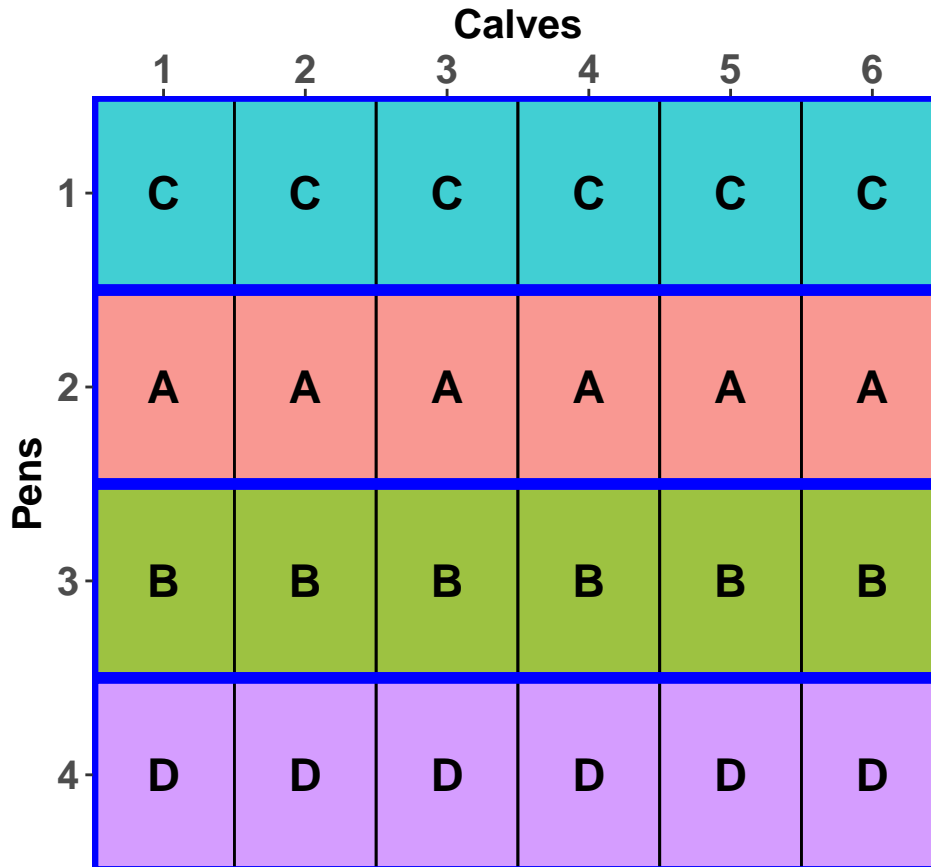
Figure 11: Factor-allocation diagram for the animal feeding experiment: treatments are allocated to units; the arrow indicates that the factor Mixtures is randomized to Pens; Calves in P indicates that the Calves are nested within Pens; P = Pens.

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

```
### Set up the systematic design and obtain the randomized layout
Feed.sys <- cbind(fac.gen(list(Pens=4, Calves=6)),
                  Mixtures = factor(rep(LETTERS[1:4], each=6)))
Feed.layout <- designRandomize(allocated = Feed.sys["Mixtures"],
                               recipient = Feed.sys[c("Pens", "Calves")],
                               nested.recipients = list(Calves = "Pens"),
                               seed = 872159)

### plot the design
designGGPlot(Feed.layout, labels = "Mixtures",
             row.factors = "Pens", column.factors = "Calves",
             cell.alpha = 0.75, label.size = 6, blockdefinition = cbind(1,6))
```

Plot of Mixtures



```
## Check its properties
Feed.canon <- designAnatomy(formulae = list(units = ~Pens/Calves,
                                             trts = ~Mixtures),
                             grandMean = TRUE, data = Feed.lay)

summary(Feed.canon)

##
##
## Summary table of the decomposition for units & trts
##
## Source.units df1 Source.trts df2 aeffecticiency eeffecticiency order
## Mean          1 Mean          1    1.0000    1.0000    1
## Pens          3 Mixtures       3    1.0000    1.0000    1
## Calves[Pens]  20
```

III.1.1 Questions

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

Because (i) Pens and Mixtures are alongside each other in the anova table, (ii) they both have 3 degrees of freedom, and (iii) the single canonical efficiency factor is one, then Pens and Mixtures are inextricably confounded. That is, the pseudoreplication has resulted in differences between Pens and between Mixtures being completely mixed up.

2. The randomization-based mixed model for the experiment is $\text{Mixtures} \mid \text{Pens} + \text{Pens:Calves}$. 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 Pens is confounded with Mixtures. A fit could be obtained by removing Pens from the random model. The problem is that a test of Mixtures would then be based on the ratio of variability in Mixtures differences to an estimate of the variance of Calves-within-Pens variability. This does not include Pens 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 Pens variability is included in the denominator of the F-statistic.

III.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 [I.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 aefficiency eefficiency 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
```

III.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.

III.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

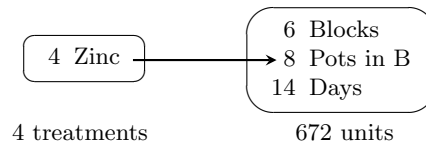


Figure 12: Factor-allocation diagram showing the treatments allocation to units for the longitudinal experiment that uses a generalized randomized block design: the arrow indicates that Zinc is allocated to Pots within B using randomization; B = Blocks.

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.layout <- cbind(with(longi.layout, fac.divide(Blocks,
                                                    factor.names = list(PPlanes = 2,
                                                                           QPositions = 3))),
                    with(longi.layout, fac.divide(Pots,
                                                    factor.names = list(Lanes = 2,
                                                                           Positions = 4))),
                    longi.layout)
longi.layout <- within(longi.layout,
                      {
```

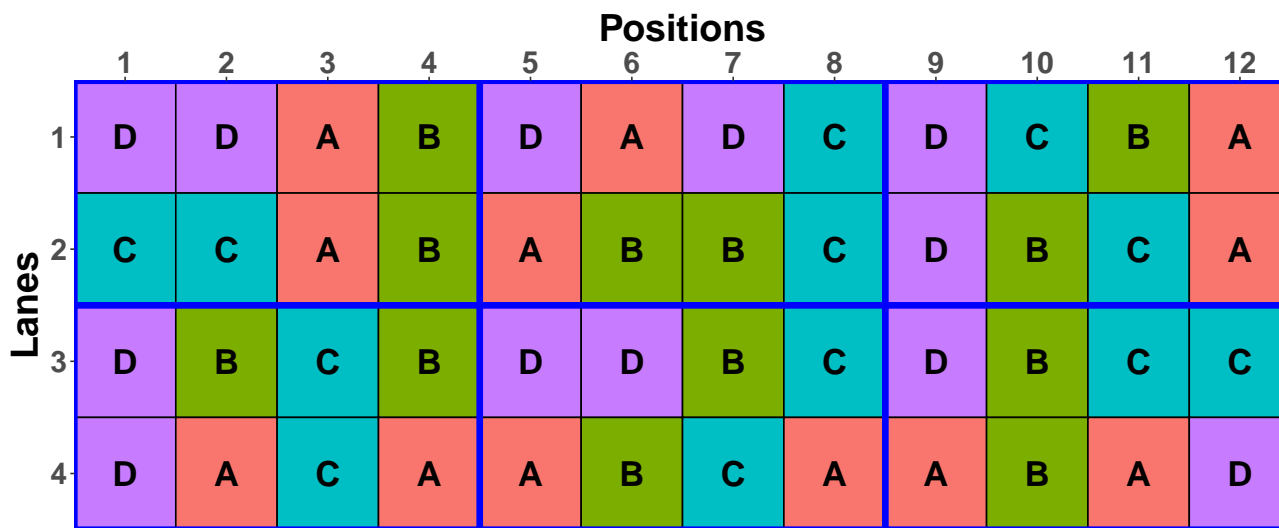


```

      Lanes <- fac.combine(list(PLanes, Lanes))
      Positions <- fac.combine(list(QPositions, Positions))
    })
longi.lay <- longi.lay[, -match(c("PLanes", "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 aefficiency 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 | | | |

III.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 I.3 and III.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.

III.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.

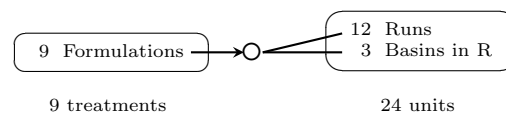


Figure 13: Factor-allocation diagram for the detergent experiment: treatments are allocated to units; the arrow indicates that the allocation is randomized; the ‘O’ at the end of the arrow indicates that a nonorthogonal design is used; the two lines from ‘O’ indicate that the Treatments are allocated to the combinations of 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.

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

III.4.1 Produce the randomized layout for the BIBD and check its properties

```

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

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 |

```

#### 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
```

III.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 aefficiency 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
```

III.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  aeffericiency 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 aeffericiency 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  aeffericiency order
## Bases  1 Additives              trts    1.0000      1
## Bases  1 ## Information remaining trts    1.0000      1
##
## The design is not orthogonal
```

III.4.4 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.

III.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"))))

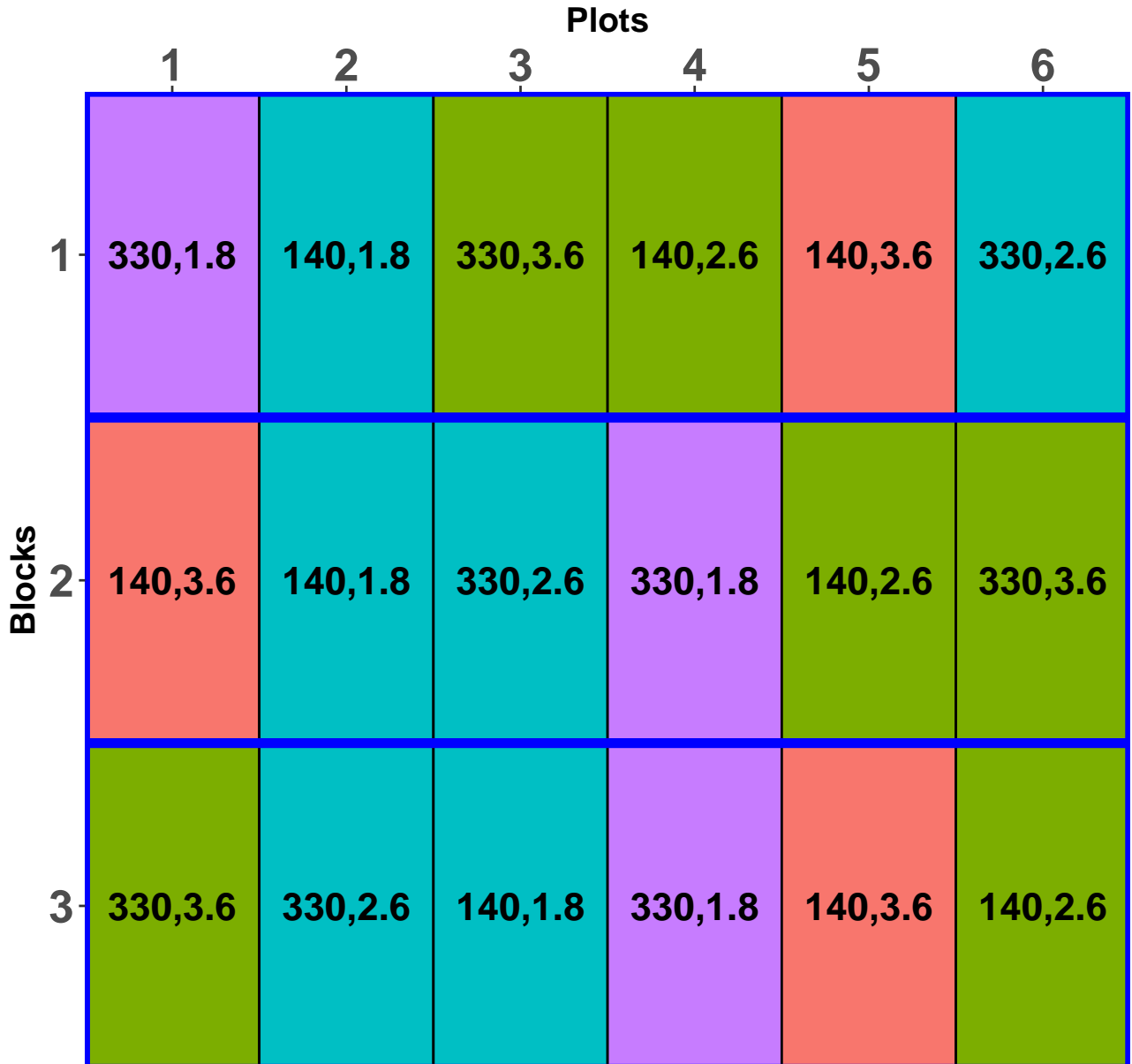
### Output the layout
RCBD.lay

##      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
```

III.5.1 Questions

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

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

III.6 A Control treatment for an incomplete-block design

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

Input the design.

```
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),
    labels = LETTERS[1:t]))
```

Randomize the design and check its properties

```
##### Randomize design according to the units 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          A
## 2         1     2          C
## 3         1     3          D
## 4         1     4          F
## 5         2     1          A
## 6         2     2          B
## 7         2     3          E
## 8         2     4          D
## 9         3     1          D
## 10        3     2          A
## 11        3     3          F
## 12        3     4          C
## 13        4     1          B
## 14        4     2          C
## 15        4     3          F
## 16        4     4          E
## 17        5     1          A
## 18        5     2          D
## 19        5     3          B
## 20        5     4          E
## 21        6     1          B
## 22        6     2          E
## 23        6     3          C
## 24        6     4          F

##### 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 odw design
PBIBD.lay$Control <- with(PBIBD.lay, fac.uselogical(Treatments == "A",
                                                    labels = c("Control", "rest")))
PBIBD.canon <- designAnatomy(formulae = list(units = ~ Blocks/Units,
                                             trts = ~ Control + Treatments),
                             grandMean = TRUE, data = PBIBD.lay)

## Warning in proj.2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Treatments[Control] and
## Control are partially aliased in Blocks
## Warning in proj.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 aeffectiveness xeffectiveness eeffectiveness 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 aeffectiveness xeffectiveness eeffectiveness 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 == "C",
                                                    labels = c("Control", "rest")))

#Rerun the designAnatomy and summary functions
```

Now use `odw`, to obtain a near-A-optimal under a fixed model using a randomization of the treatment to the plots within incomplete blocks for the initial design.

```
##### Initialize with a randomized layout
PBIBD.ini <- cbind(fac.gen(list(Blocks=b, Units=k)),
                  Treatments = factor(rep(1:t, times = b*k/t), labels = LETTERS[1:t]))
PBIBD.ini <- designRandomize(allocated = PBIBD.ini["Treatments"],
                             recipient = PBIBD.ini[c("Blocks", "Units")],
                             nested.recipients = list(Units = "Blocks"),
                             seed = 4794)

##### Get the odw design for fixed Blocks
PBIBD.odw <- odw(fixed = ~ Blocks + Treatments,
```

```

    permute = ~ Treatments,
    search   = "tabu", maxit = 25,
    data     = PBIBD.ini)

## Sat May 18 00:13:56 2024
## Initial criterion = 0.566667 (6 A-equations; rank C 5)
## Criterion after 1000 initial random iterations: 0.559487
## Criterion after tabu loop 1 is 0.559487
## Criterion after tabu loop 2 is 0.559487
## Criterion after tabu loop 3 is 0.559487
## Criterion after tabu loop 4 is 0.559487
## Criterion after tabu loop 5 is 0.559487
## Criterion after tabu loop 6 is 0.559487
## Criterion after tabu loop 7 is 0.559487
## Criterion after tabu loop 8 is 0.559487
## Criterion after tabu loop 9 is 0.559487
## Criterion after tabu loop 10 is 0.559487
## Criterion after tabu loop 11 is 0.559487
## Criterion after tabu loop 12 is 0.559487
## Criterion after tabu loop 13 is 0.559487
## Criterion after tabu loop 14 is 0.559487
## Criterion after tabu loop 15 is 0.559487
## Criterion after tabu loop 16 is 0.559487
## Criterion after tabu loop 17 is 0.559487
## Criterion after tabu loop 18 is 0.559487
## Criterion after tabu loop 19 is 0.559487
## Criterion after tabu loop 20 is 0.559487
## Criterion after tabu loop 21 is 0.559487
## Criterion after tabu loop 22 is 0.559487
## Criterion after tabu loop 23 is 0.559487
## Criterion after tabu loop 24 is 0.559487
## Criterion after tabu loop 25 is 0.559487
## Hash table size 3
## Final criterion after 25 tabu iterations: 0.559487
## Cleaning up: Sat May 18 00:13:56 2024

PBIBD.odw.lay <- PBIBD.odw$design

```

Randomize the design obtained using `odw` and check its properties

```

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

PBIBD.odw.lay

##      Blocks Units Treatments
## 1         1     1           C
## 2         1     2           F
## 3         1     3           D
## 4         1     4           A
## 5         2     1           F
## 6         2     2           B

```

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

#'### Check properties of the odw layout
PBIBD.odw.canon <- designAnatomy(formulae = list(units = ~ Blocks/Units,
                                                trts = ~ Treatments),
                                grandMean = TRUE, data = PBIBD.odw.lay)
summary(PBIBD.odw.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 Treatments    4      0.0937      0.1875      0.0625      2          0
##               Residual        1
## Units[Blocks] 18 Treatments    5      0.8937      1.0000      0.8125      3          1
##               Residual        13
##
##
## The design is not orthogonal
```

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.

2. How do the Cochran and Cox design and the design obtained with odw compare?

The aeffecticiency of the Cochran and Cox design is less than that for the odw design. However, the Cochran and Cox design has only two different efficiency factors (0.75 and 1) and has 3 orthogonal degrees of freedom. This compares with 3 efficiency factors and 1 orthogonal degree of freedom for the odw design. Sacrificing approximately 0.01 in aeffecticiency to have a design that is closer to balanced seems acceptable.

III.7 The Casuarina experiment (continued)

In Section II.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 among 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 Rows#Columns
## Warning in projs.2canon(CombinedSets$Q[[ntiers]], struct[[ktier]]$Q): Prov_China[Countries]
## and Countries are partially aliased in Rows#Columns
```



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

```

III.7.1 Questions

1. How does this analysis compare with that conducted in Section [II.3](#)?

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

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