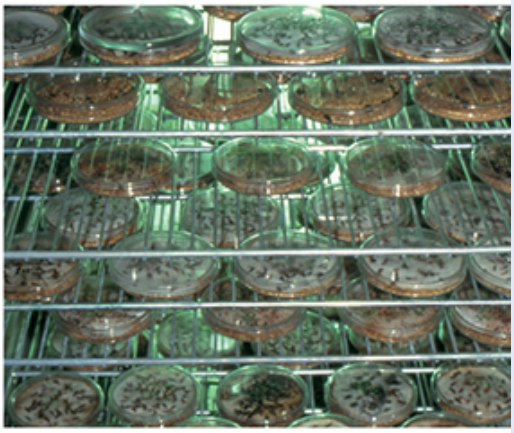
3RD EDITION

Experimental Design and Analysis for Tree Improvement



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Experimental Design and Analysis for tree Improvement using R

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Preface

This book contains R codes and tutorials from R package eda4treeR on **Experimental Design and Analysis for tree Improvement** by E.R. Williams, C.E. Harwood and A.C. Matheson.

The development version of R package eda4treeR can be installed from github as follows:

```
if (!require("remotes")) install.packages("remotes")
remotes::install_github("myaseen208/eda4treeR")
```

The stable version of R package eda4treeR can be installed from CRAN as follows:

```
install.packages("eda4treeR")
```

1Introduction

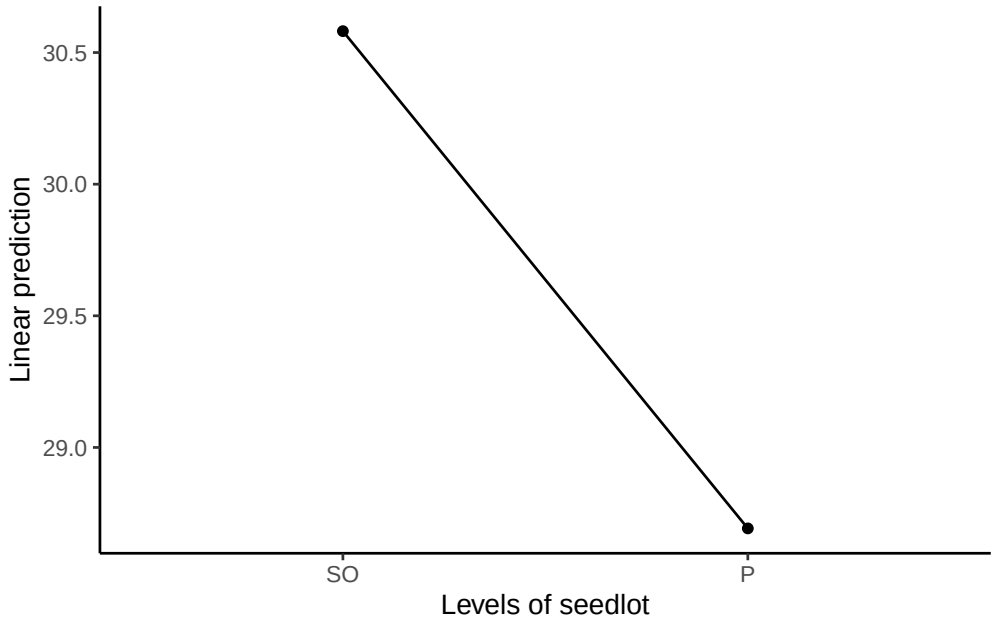
2Experimental Planning and Layout

2.1 Example 2.1 (Pg. 24)

Example 2.1 (Pg. 24)

A field trial was planted to compare a seedlot derived from a seed orchard (SO) with one collected from a routine plantation (P). There were eight plots of each seedlot, thinned at seven years of age. Tree diameters at breast height (*dbh*) were measured at 15 years and plot means calculated.

```
 library(car)

 library(dae)

 library(dplyr)

 library(emmeans)

 library(ggplot2)

 library(lmerTest)

 library(magrittr)

 library(predictmeans)

 data(DataExam2.1)

 # Pg. 22
 fmtab2.3  <- lm(formula = dbh ~ seedlot, data = DataExam2.1)

 # Pg. 23
 anova(fmtab2.3)
Analysis of Variance Table

Response: dbh
          Df Sum Sq Mean Sq F value  Pr(>F)
seedlot    1  14.27 14.2695  3.2531 0.09284 .
Residuals 14  61.41  4.3864
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

 # Pg. 23
 emmeans(object = fmtab2.3, specs = ~ seedlot)
 seedlot emmean   SE df lower.CL upper.CL
 SO         30.6 0.74 14     29.0     32.2
 P          28.7 0.74 14     27.1     30.3

Confidence level used: 0.95

 emmip(object = fmtab2.3, formula = ~ seedlot) +
   theme_classic()
```



2.2 Example 2.2 (Pg. 26)

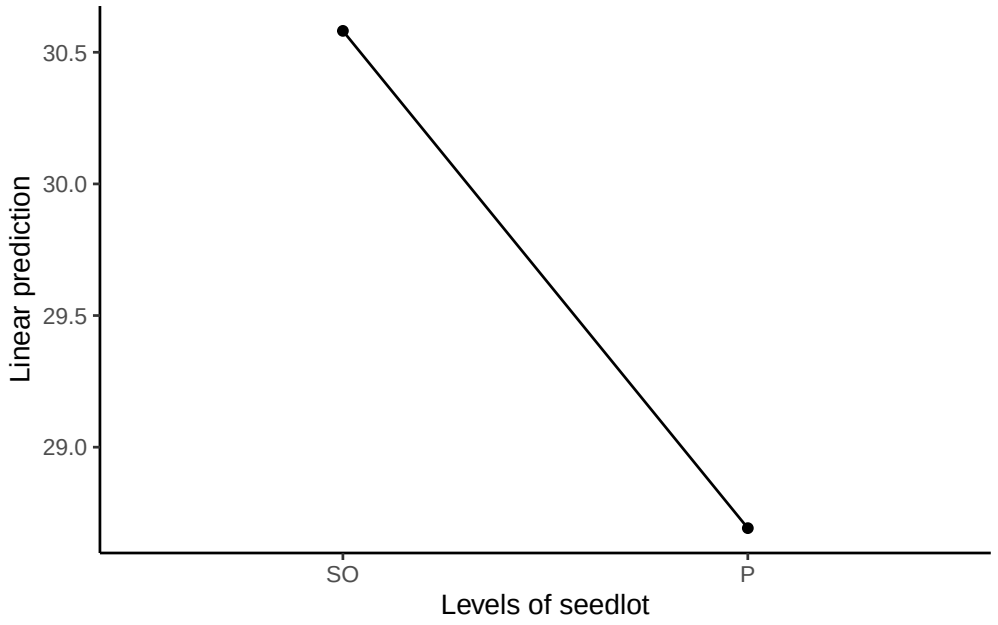
Example 2.2 (Pg. 26)

```
library(car)

library(dae)

library(dplyr)

library(emmeans)

library(ggplot2)

library(lmerTest)

library(magrittr)

library(predictmeans)

data(DataExam2.2)

# Pg. 24
fmtab2.5 <-
          lm(
             formula   = dbh ~ block + seedlot
           , data      = DataExam2.2
           )

# Pg. 26
anova(fmtab2.5)
Analysis of Variance Table

Response: dbh
```


```
          Df Sum Sq Mean Sq F value  Pr(>F)
block      7 48.867  6.9810  3.8959 0.04671 *
seedlot    1 14.270 14.2695  7.9635 0.02570 *
Residuals  7 12.543  1.7919
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Pg. 26
emmeans(object = fmtab2.5, specs = ~ seedlot)
seedlot emmean    SE df lower.CL upper.CL
SO        30.6 0.473  7     29.5     31.7
P         28.7 0.473  7     27.6     29.8

Results are averaged over the levels of: block
Confidence level used: 0.95
```

```
emmip(object = fmtab2.5, formula = ~ seedlot) +
  theme_classic()
```



3Data Collection and Pre-Processing

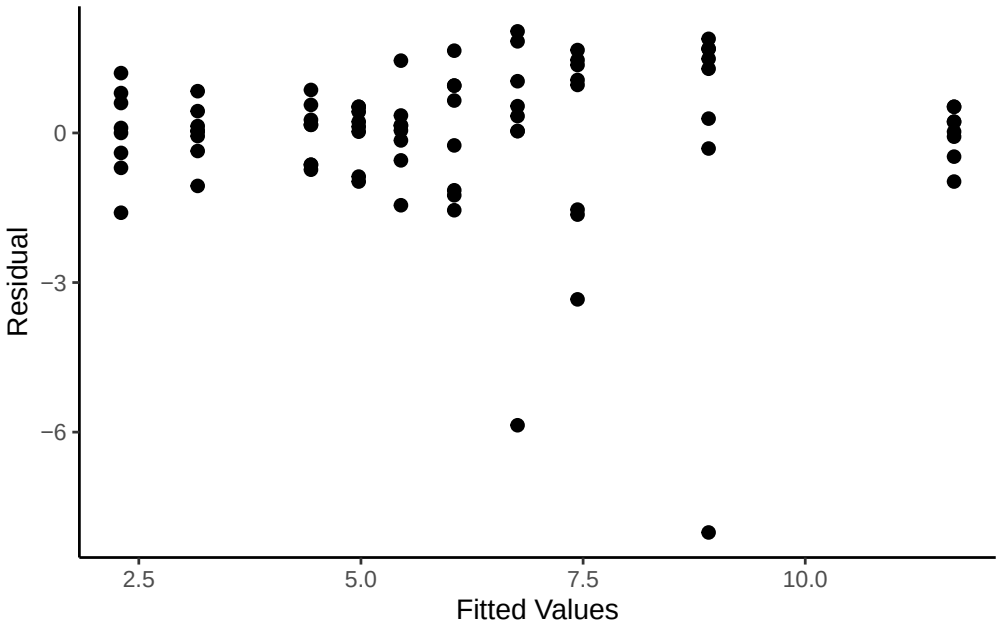
3.1 Example 3.1 (Pg. 30)

Example 3.1 (Pg. 30)

We illustrate the recommended layout for data sheets with one of the trials conducted by the Australian Centre for International Agricultural Research (ACIAR) in Queensland, Australia (Experiment 309). This was a species trial planted in 1985; survival was poor. For our example we will examine only part of the data from this experiment. Five of the species with good survival have been extracted at random, namely *Acacia*, *Angophora*, *Casuarina*, *Melaleuca* and *Petalostigma*.

```
library(car)

library(dae)

library(dplyr)

library(emmeans)

library(ggplot2)

library(lmerTest)

library(magrittr)

library(predictmeans)

library(supernova)

data(DataExam3.1)

# Pg. 28
fmtab3.3 <-
          lm(
              formula = ht ~ repl*seedlot
            , data    = DataExam3.1
             )

fmtab3.3ANOVA1 <-
  anova(fmtab3.3) %>%
  mutate(
  "F value" =
         c(
           anova(fmtab3.3)[1:2, 3]/anova(fmtab3.3)[3, 3]
         , anova(fmtab3.3)[3, 4]
         , NA
         )
          )

 # Pg. 33 (Table 3.3)
fmtab3.3ANOVA1 %>%
  mutate(
```


```
   "Pr(>F)"  =
        c(
          NA
        , pf(
             q    = fmtab3.3ANOVA1[2, 4]
           , df1  = fmtab3.3ANOVA1[2, 1]
           , df2  = fmtab3.3ANOVA1[3, 1], lower.tail = FALSE
            )
        , NA
        , NA
        )
        )
              Df  Sum Sq Mean Sq F value    Pr(>F)
repl           1   20.30  20.301  3.4197
seedlot        4 505.87 126.467 21.3035 0.005851 **
repl:seedlot   4  23.75   5.936  2.3663
Residuals     70 175.61   2.509
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

  # Pg. 33  (Table 3.3)
  emmeans(object  = fmtab3.3, specs = ~ seedlot)
 seedlot      emmean    SE df lower.CL upper.CL
 Acacia        10.29 0.396 70     9.50    11.08
 Angophora      7.10 0.396 70     6.31     7.89
 Casuarina      5.51 0.396 70     4.72     6.30
 Melaleuca      4.94 0.396 70     4.15     5.73
 Petalostigma   2.73 0.396 70     1.94     3.52

Results are averaged over the levels of: repl
Confidence level used: 0.95

  # Pg. 34  (Figure 3.2)
  ggplot(
     mapping = aes(
                   x = fitted.values(fmtab3.3)
                 , y = residuals(fmtab3.3)
                 )
                 ) +
  geom_point(size = 2) +
  labs(
     x = "Fitted Values"
   , y = "Residual"
    ) +
  theme_classic()
```




```
# Pg. 33 (Table 3.4)
DataExam3.1m <- DataExam3.1

DataExam3.1m[c(28, 51, 76), 5] <- NA

DataExam3.1m[c(28, 51, 76), 6] <- NA

fmtab3.4 <-
          lm(
              formula    = ht ~ repl*seedlot
            , data       = DataExam3.1m
            )

fmtab3.4ANOVA1 <-
  anova(fmtab3.4) %>%
  mutate(
      "F value" =
            c(
               anova(fmtab3.4)[1:2, 3]/anova(fmtab3.4)[3, 3]
             , anova(fmtab3.4)[3, 4]
             , NA
             )
             )

# Pg. 33 (Table 3.4)
fmtab3.4ANOVA1 %>%
  mutate(
  "Pr(>F)"   =
        c(
          NA
        , pf(
              q    = fmtab3.4ANOVA1[2, 4]
            , df1  = fmtab3.4ANOVA1[2, 1]
            , df2  = fmtab3.4ANOVA1[3, 1], lower.tail = FALSE
            )
        , NA
        , NA
        )
```


```
        )
             Df Sum Sq Mean Sq F value  Pr(>F)
repl          1  18.88  18.877 10.4201
seedlot       4 588.68 147.169 81.2367 0.00044 ***
repl:seedlot  4   7.25   1.812  2.4163
Residuals    67  50.23   0.750
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

  # Pg. 33  (Table 3.4)
  emmeans(object  = fmtab3.4, specs = ~ seedlot)
 seedlot      emmean    SE df lower.CL upper.CL
 Acacia        10.87 0.224 67    10.42    11.31
 Angophora      7.76 0.231 67     7.30     8.22
 Casuarina      5.51 0.216 67     5.08     5.94
 Melaleuca      4.94 0.216 67     4.51     5.38
 Petalostigma   2.73 0.216 67     2.30     3.16

Results are averaged over the levels of: repl
Confidence level used: 0.95
```

3.2 Example 3.1 (continued) (Pg. 34)

Example 3.1 (continued) (Pg. 34)

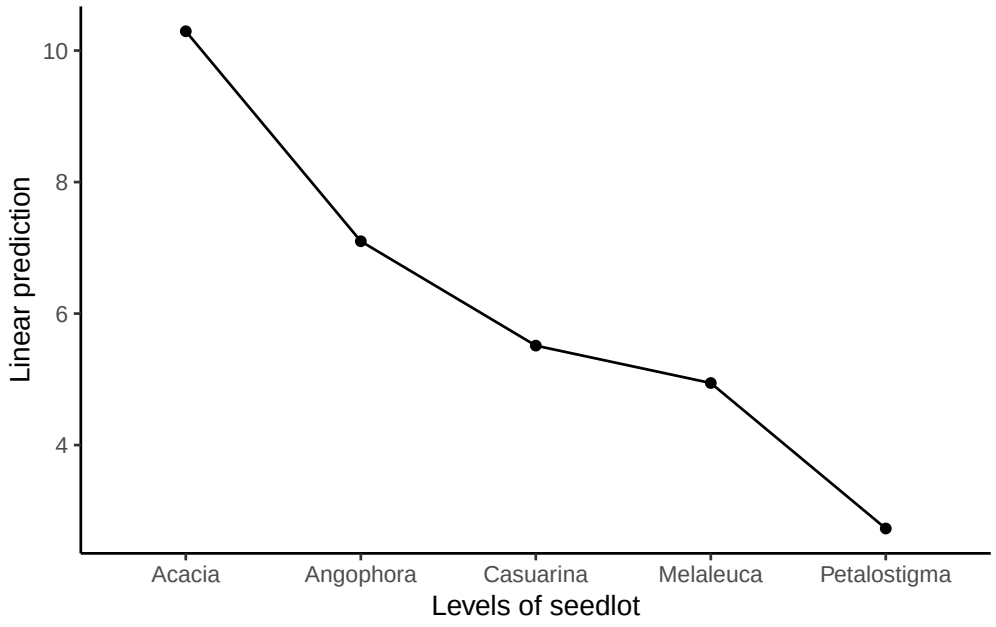
The analysis of variance table for *ht* is given below:

```
library(car)

library(dae)

library(dplyr)

library(emmeans)

library(ggplot2)

library(lmerTest)

library(magrittr)

library(predictmeans)

data(DataExam3.1.1)

# Pg. 36
fm3.8 <-
      lm(
         formula = ht ~ repl + seedlot
       , data    = DataExam3.1.1
        )

# Pg. 40
anova(fm3.8)
```


```
Analysis of Variance Table

Response: ht
          Df Sum Sq Mean Sq F value   Pr(>F)
repl       1  2.538  2.5376  3.4197 0.138108
seedlot    4 63.234 15.8084 21.3035 0.005851 **
Residuals  4  2.968  0.7421
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Pg. 40
emmeans(object = fm3.8, specs  = ~seedlot)
seedlot      emmean    SE df lower.CL upper.CL
Acacia        10.29 0.609  4     8.60    11.98
Angophora      7.10 0.609  4     5.41     8.79
Casuarina      5.51 0.609  4     3.82     7.20
Melaleuca      4.94 0.609  4     3.25     6.63
Petalostigma   2.73 0.609  4     1.04     4.42

Results are averaged over the levels of: repl
Confidence level used: 0.95
```

```
emmip(object = fm3.8, formula  = ~seedlot) +
 theme_classic()
```



4Experimental Design

4.1 Example 4.3 (Pg. 53)

Example 4.3 (Pg. 53)

Major seed distributors such as the Australian Tree Seed Centre (ATSC) routinely conduct seed viability tests so that, when seed is dispatched, the purchaser has an indication of the germination percentage of the seed. As part of the ATSC research program, a series of experiments was conducted in 1992 by Debbie Solomon on provenances of *Acacia mangium* to investigate methods of pre-treatment and loss of viability of stored seed. Each experiment involved six seedlots of *Acacia mangium* and four seed pre-treatments in a factorial design with three replicates.

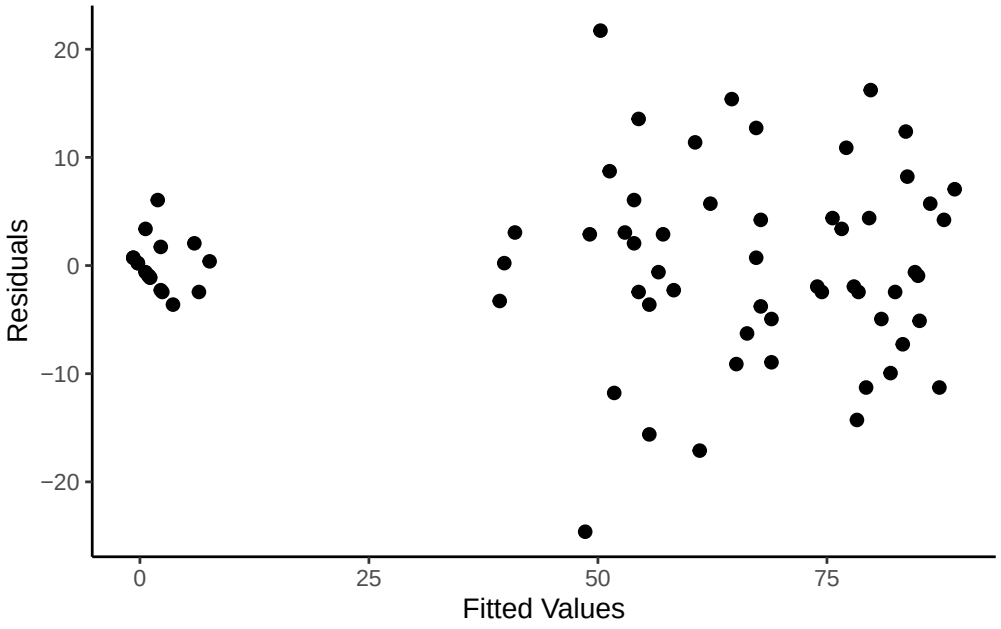
```
 library(car)

 library(dae)

 library(dplyr)

 library(emmeans)

 library(ggplot2)

 library(lmerTest)

 library(magrittr)

 library(predictmeans)

 data(DataExam4.3)

  # Pg. 50
  fm4.2    <-
    aov(
        formula =
        percent ~ repl + contcomp + seedlot +
                  treat/contcomp + contcomp/seedlot +
                  treat/contcomp/seedlot
      , data    = DataExam4.3
     )

  # Pg. 54
  anova(fm4.2)
Analysis of Variance Table

Response: percent
                      Df  Sum Sq Mean Sq  F value                Pr(>F)
repl                   2      35      18   0.1804             0.8355379
contcomp               1   58542   58542 601.5217 < 0.00000000000000022 ***
seedlot                5    2894     579   5.9481             0.0002538 ***
treat                  2    5300    2650  27.2295          0.00000001576 ***
contcomp:seedlot       5    1347     269   2.7682             0.0287571 *
```


```
contcomp:seedlot:treat 10    961       96    0.9876              0.4674993
Residuals              46   4477       97
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

  # Pg. 54
  model.tables(x = fm4.2, type = "means")
Tables of means
Grand mean

51.38889

 repl
        1     2     3
    52.33 50.67 51.17
rep 24.00 24.00 24.00

 contcomp
    Treated control
      67.85       2
rep   54.00      18

 seedlot
    18211 18212 18217 18248 18249 18265
       58 52.33    49 40.67 48.67 59.67
rep    12 12.00    12 12.00 12.00 12.00

 treat
     nick  bw&s control bw1min
    40.43 49.31   51.39  64.43
rep 18.00 18.00   18.00  18.00

 contcomp:seedlot
         seedlot
contcomp  18211 18212 18217 18248 18249 18265
  Treated 77.33 69.33 63.11 53.33 64.89 79.11
  rep      9.00  9.00  9.00  9.00  9.00  9.00
  control  0.00  1.33  6.67  2.67  0.00  1.33
  rep      3.00  3.00  3.00  3.00  3.00  3.00

 contcomp:seedlot:treat
, , treat = nick

         seedlot
contcomp  18211 18212 18217 18248 18249 18265
  Treated 65.33 54.67 57.33 40.00 49.33 74.67
  rep      3.00  3.00  3.00  3.00  3.00  3.00
  control
  rep      0.00  0.00  0.00  0.00  0.00  0.00

, , treat = bw&s

         seedlot
contcomp  18211 18212 18217 18248 18249 18265
  Treated 78.67 68.00 54.67 52.00 61.33 80.00
  rep      3.00  3.00  3.00  3.00  3.00  3.00
  control
  rep      0.00  0.00  0.00  0.00  0.00  0.00
```


```
, , treat = control

         seedlot
contcomp  18211 18212 18217 18248 18249 18265
  Treated
  rep      0.00  0.00  0.00  0.00  0.00  0.00
  control  0.00  1.33  6.67  2.67  0.00  1.33
  rep      3.00  3.00  3.00  3.00  3.00  3.00

, , treat = bw1min

         seedlot
contcomp  18211 18212 18217 18248 18249 18265
  Treated 88.00 85.33 77.33 68.00 84.00 82.67
  rep      3.00  3.00  3.00  3.00  3.00  3.00
  control
  rep      0.00  0.00  0.00  0.00  0.00  0.00


  emmeans(object = fm4.2, specs = ~ contcomp)
 contcomp emmean   SE df lower.CL upper.CL
 Treated    67.9 1.34 46    65.15    70.55
 control     2.0 2.33 46    -2.68     6.68

Results are averaged over the levels of: repl, seedlot, treat
Confidence level used: 0.95

  emmeans(object = fm4.2, specs = ~ seedlot)
 seedlot emmean   SE df lower.CL upper.CL
 18211     38.7 3.29 46     32.0     45.3
 18212     35.3 3.29 46     28.7     42.0
 18217     34.9 3.29 46     28.3     41.5
 18248     28.0 3.29 46     21.4     34.6
 18249     32.4 3.29 46     25.8     39.1
 18265     40.2 3.29 46     33.6     46.8

Results are averaged over the levels of: repl, treat, contcomp
Confidence level used: 0.95

  emmeans(object = fm4.2, specs = ~ contcomp + treat)
 treat   contcomp emmean   SE df lower.CL upper.CL
 nick    Treated    56.9 2.33 46    52.21    61.57
 bw&s    Treated    65.8 2.33 46    61.10    70.46
 bw1min  Treated    80.9 2.33 46    76.21    85.57
 control control     2.0 2.33 46    -2.68     6.68

Results are averaged over the levels of: repl, seedlot
Confidence level used: 0.95

  emmeans(object = fm4.2, specs = ~ contcomp + seedlot)
 contcomp seedlot emmean   SE df lower.CL upper.CL
 Treated  18211    77.33 3.29 46     70.7     84.0
 control  18211     0.00 5.70 46    -11.5     11.5
 Treated  18212    69.33 3.29 46     62.7     76.0
 control  18212     1.33 5.70 46    -10.1     12.8
 Treated  18217    63.11 3.29 46     56.5     69.7
 control  18217     6.67 5.70 46     -4.8     18.1
 Treated  18248    53.33 3.29 46     46.7     60.0
 control  18248     2.67 5.70 46     -8.8     14.1
```


```
 Treated   18249     64.89 3.29 46      58.3      71.5
 control   18249      0.00 5.70 46     -11.5      11.5
 Treated   18265     79.11 3.29 46      72.5      85.7
 control   18265      1.33 5.70 46     -10.1      12.8

Results are averaged over the levels of: repl, treat
Confidence level used: 0.95

  emmeans(object = fm4.2, specs = ~ contcomp + treat + seedlot)
 treat    contcomp seedlot emmean  SE df lower.CL upper.CL
 nick     Treated   18211    65.33 5.7 46     53.9     76.8
 bw&s     Treated   18211    78.67 5.7 46     67.2     90.1
 bw1min   Treated   18211    88.00 5.7 46     76.5     99.5
 control  control   18211     0.00 5.7 46    -11.5     11.5
 nick     Treated   18212    54.67 5.7 46     43.2     66.1
 bw&s     Treated   18212    68.00 5.7 46     56.5     79.5
 bw1min   Treated   18212    85.33 5.7 46     73.9     96.8
 control  control   18212     1.33 5.7 46    -10.1     12.8
 nick     Treated   18217    57.33 5.7 46     45.9     68.8
 bw&s     Treated   18217    54.67 5.7 46     43.2     66.1
 bw1min   Treated   18217    77.33 5.7 46     65.9     88.8
 control  control   18217     6.67 5.7 46     -4.8     18.1
 nick     Treated   18248    40.00 5.7 46     28.5     51.5
 bw&s     Treated   18248    52.00 5.7 46     40.5     63.5
 bw1min   Treated   18248    68.00 5.7 46     56.5     79.5
 control  control   18248     2.67 5.7 46     -8.8     14.1
 nick     Treated   18249    49.33 5.7 46     37.9     60.8
 bw&s     Treated   18249    61.33 5.7 46     49.9     72.8
 bw1min   Treated   18249    84.00 5.7 46     72.5     95.5
 control  control   18249     0.00 5.7 46    -11.5     11.5
 nick     Treated   18265    74.67 5.7 46     63.2     86.1
 bw&s     Treated   18265    80.00 5.7 46     68.5     91.5
 bw1min   Treated   18265    82.67 5.7 46     71.2     94.1
 control  control   18265     1.33 5.7 46    -10.1     12.8

Results are averaged over the levels of: repl
Confidence level used: 0.95

  DataExam4.3 %>%
    dplyr::group_by(treat, contcomp, seedlot) %>%
    dplyr::summarize(Mean = mean(percent))
# A tibble: 24 x 4
# Groups:   treat, contcomp [4]
   treat  contcomp seedlot  Mean
   <fct>  <fct>    <fct>   <dbl>
 1 nick   Treated  18211    65.3
 2 nick   Treated  18212    54.7
 3 nick   Treated  18217    57.3
 4 nick   Treated  18248    40
 5 nick   Treated  18249    49.3
 6 nick   Treated  18265    74.7
 7 bw&s   Treated  18211    78.7
 8 bw&s   Treated  18212    68
 9 bw&s   Treated  18217    54.7
10 bw&s   Treated  18248    52
# i 14 more rows

    RESFIT <-
           data.frame(
```


```
            residualvalue = residuals(fm4.2)
          , fittedvalue   = fitted.values(fm4.2)
          )

    ggplot(mapping = aes(
                           x = fitted.values(fm4.2)
                         , y = residuals(fm4.2))) +
    geom_point(size = 2) +
    labs(
        x = "Fitted Values"
      , y = "Residuals"
      ) +
      theme_classic()
```



Tip

Here the control pre-treatment was deleted.

```
library(car)

library(dae)

library(dplyr)

library(emmeans)

library(ggplot2)

library(lmerTest)

library(magrittr)

library(predictmeans)

data(DataExam4.3)

# Pg. 57
```


```
 fm4.4    <-
   aov(
       formula = percent ~ repl + treat*seedlot
     , data    = DataExam4.3 %>%
                  filter(treat != "control")
      )

  # Pg. 57
  anova(fm4.4)
Analysis of Variance Table

Response: percent
              Df Sum Sq Mean Sq F value      Pr(>F)
repl           2   64.6   32.30  0.2511   0.7793606
treat          2 5300.1 2650.07 20.6055 0.000001375 ***
seedlot        5 4148.1  829.63  6.4507   0.0002578 ***
treat:seedlot 10  961.2   96.12  0.7474   0.6759614
Residuals     34 4372.7  128.61
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

  model.tables(x = fm4.4, type = "means", se = TRUE)
Tables of means
Grand mean

67.85185

 repl
repl
    1     2     3
69.11 66.44 68.00

 treat
treat
  nick   bw&s bw1min
 56.89  65.78  80.89

 seedlot
seedlot
18211 18212 18217 18248 18249 18265
77.33 69.33 63.11 53.33 64.89 79.11

 treat:seedlot
        seedlot
treat    18211 18212 18217 18248 18249 18265
  nick   65.33 54.67 57.33 40.00 49.33 74.67
  bw&s   78.67 68.00 54.67 52.00 61.33 80.00
  bw1min 88.00 85.33 77.33 68.00 84.00 82.67

Standard errors for differences of means
         repl treat seedlot treat:seedlot
        3.780 3.780   5.346         9.260
replic.    18    18       9             3

  emmeans(object = fm4.4, specs = ~ treat)
 treat  emmean   SE df lower.CL upper.CL
 nick     56.9 2.67 34     51.5     62.3
 bw&s     65.8 2.67 34     60.3     71.2
 bw1min   80.9 2.67 34     75.5     86.3
```


```
Results are averaged over the levels of: repl, seedlot
Confidence level used: 0.95

  emmeans(object = fm4.4, specs = ~ seedlot)
 seedlot emmean   SE df lower.CL upper.CL
 18211     77.3 3.78 34     69.7     85.0
 18212     69.3 3.78 34     61.7     77.0
 18217     63.1 3.78 34     55.4     70.8
 18248     53.3 3.78 34     45.7     61.0
 18249     64.9 3.78 34     57.2     72.6
 18265     79.1 3.78 34     71.4     86.8

Results are averaged over the levels of: repl, treat
Confidence level used: 0.95

  emmeans(object = fm4.4, specs = ~ treat * seedlot)
 treat   seedlot emmean   SE df lower.CL upper.CL
 nick    18211     65.3 6.55 34     52.0     78.6
 bw&s    18211     78.7 6.55 34     65.4     92.0
 bw1min 18211     88.0 6.55 34     74.7    101.3
 nick    18212     54.7 6.55 34     41.4     68.0
 bw&s    18212     68.0 6.55 34     54.7     81.3
 bw1min 18212     85.3 6.55 34     72.0     98.6
 nick    18217     57.3 6.55 34     44.0     70.6
 bw&s    18217     54.7 6.55 34     41.4     68.0
 bw1min 18217     77.3 6.55 34     64.0     90.6
 nick    18248     40.0 6.55 34     26.7     53.3
 bw&s    18248     52.0 6.55 34     38.7     65.3
 bw1min 18248     68.0 6.55 34     54.7     81.3
 nick    18249     49.3 6.55 34     36.0     62.6
 bw&s    18249     61.3 6.55 34     48.0     74.6
 bw1min 18249     84.0 6.55 34     70.7     97.3
 nick    18265     74.7 6.55 34     61.4     88.0
 bw&s    18265     80.0 6.55 34     66.7     93.3
 bw1min 18265     82.7 6.55 34     69.4     96.0

Results are averaged over the levels of: repl
Confidence level used: 0.95
```

4.2 Example 4.4 (Pg. 61)

Example 4.4 (Pg. 61)

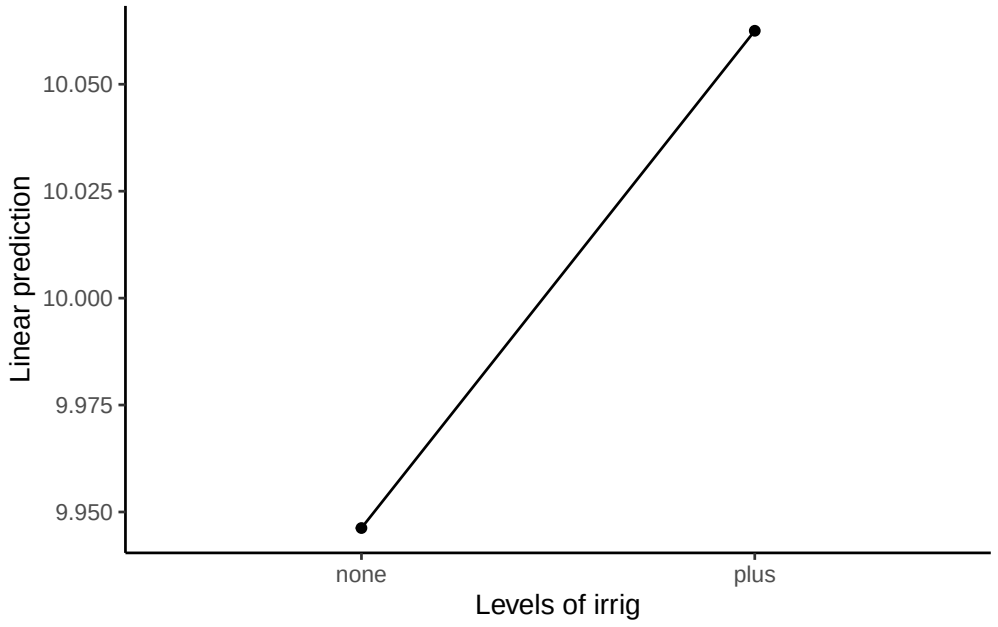
An experiment supported by the Shell Company was planted at Toolara Forest Reserve near Gympie, Queensland, in February 1987 to study the effects of irrigation and fertiliser on four seedlots of *Eucalyptus grandis*. Because of the difficulty in applying the irrigation and fertiliser treatments individually to each 7×6 plot of trees, the experiment was designed as a split-plot, with main-plot treatments, *irrig* and *fert*. There were two replicates of four main-plots each with four sub-plots.

```
library(car)
```


```
 library(dae)

 library(dplyr)

 library(emmeans)

 library(ggplot2)

 library(lmerTest)

 library(magrittr)

 library(predictmeans)

 data(DataExam4.4)

 # Pg. 58
 fm4.6    <-
   aov(
       formula = height ~ repl + irrig*fert*seedlot +
                          Error(repl/irrig:fert)
     , data    = DataExam4.4
     )

 # Pg. 61
  summary(fm4.6)

Error: repl
     Df Sum Sq Mean Sq
repl  1 0.7564  0.7564

Error: repl:irrig:fert
           Df Sum Sq Mean Sq F value  Pr(>F)
irrig       1    0.1     0.1   0.154   0.721
fert        1  590.6   590.6 841.110 0.00009 ***
irrig:fert  1    0.0     0.0   0.010   0.926
Residuals   3    2.1     0.7
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Error: Within
                   Df Sum Sq Mean Sq F value   Pr(>F)
seedlot             3  39.65  13.218  19.680 0.000063 ***
irrig:seedlot       3   1.11   0.370   0.551   0.6572
fert:seedlot        3   9.95   3.317   4.938   0.0185 *
irrig:fert:seedlot  3   1.74   0.579   0.862   0.4874
Residuals          12   8.06   0.672
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

 # Pg. 61
 model.tables(x = fm4.6, type = "means")
Tables of means
Grand mean

10.00437

 repl
repl
```


```
     1      2
10.158  9.851

 irrig
irrig
  none   plus
 9.946 10.062

 fert
fert
  none   plus
 5.708 14.301

 seedlot
seedlot
 Bulahdelah    Coffs SO Pomona pltn    Atherton
     10.178      11.404      10.149       8.287

 irrig:fert
      fert
irrig  none   plus
  none  5.635 14.257
  plus  5.781 14.344

 irrig:seedlot
      seedlot
irrig  Bulahdelah Coffs SO Pomona pltn Atherton
  none 10.060     11.647   10.055       8.022
  plus 10.295     11.160   10.242       8.552

 fert:seedlot
      seedlot
fert   Bulahdelah Coffs SO Pomona pltn Atherton
  none  5.687      6.790    5.410       4.945
  plus 14.667     16.017   14.887      11.630

 irrig:fert:seedlot
, , seedlot = Bulahdelah

      fert
irrig  none   plus
  none  5.275 14.845
  plus  6.100 14.490

, , seedlot = Coffs SO

      fert
irrig  none   plus
  none  7.125 16.170
  plus  6.455 15.865

, , seedlot = Pomona pltn

      fert
irrig  none   plus
  none  5.625 14.485
  plus  5.195 15.290

, , seedlot = Atherton
```

```
      fert
irrig  none   plus
  none  4.515 11.530
  plus  5.375 11.730


 # Pg. 61
 emmeans(object = fm4.6, specs = ~ irrig)
 irrig emmean  SE  df asymp.LCL asymp.UCL
 none    9.95 NaN NaN       NaN       NaN
 plus   10.06 NaN NaN       NaN       NaN

Results are averaged over the levels of: repl, fert, seedlot
Warning: EMMs are biased unless design is perfectly balanced
Confidence level used: 0.95

 emmip(object = fm4.6, formula  = ~ irrig) +
     theme_classic()
```



5 Analysis Across Sites

5.1 Example 5.1 (Pg. 68)

Example 5.1 (Pg. 68)

In 1985 species/provenance trials were laid out at six sites in Thailand as part of an ACIAR project extending over several years to investigate Australian multi-purpose tree species. The experimental design in each case was an RCB design with three replicates and the number of seedlots ranged from 30 to 42. Plots consisted of 5 × 5 trees with a 2m × 2m spacing. Plot summary files were constructed for the 24-month measurement according to the methods described in Chapter 3. Analyses were performed on the plot mean data at each site.

```
library(car)

library(dae)

library(dplyr)

library(emmeans)

library(ggplot2)

library(lmerTest)

library(magrittr)

library(predictmeans)

data(DataExam5.1)

# Pg.68
fm5.4 <-
      lm(
          formula = ht ~ site*seedlot
        , data    = DataExam5.1
        )

# Pg. 73
anova(fm5.4)
```

```
Analysis of Variance Table

Response: ht
             Df  Sum Sq Mean Sq F value Pr(>F)
site          3  919585  306528     NaN    NaN
seedlot      26 3176289  122165     NaN    NaN
site:seedlot 78  707957    9076     NaN    NaN
Residuals     0       0     NaN
```

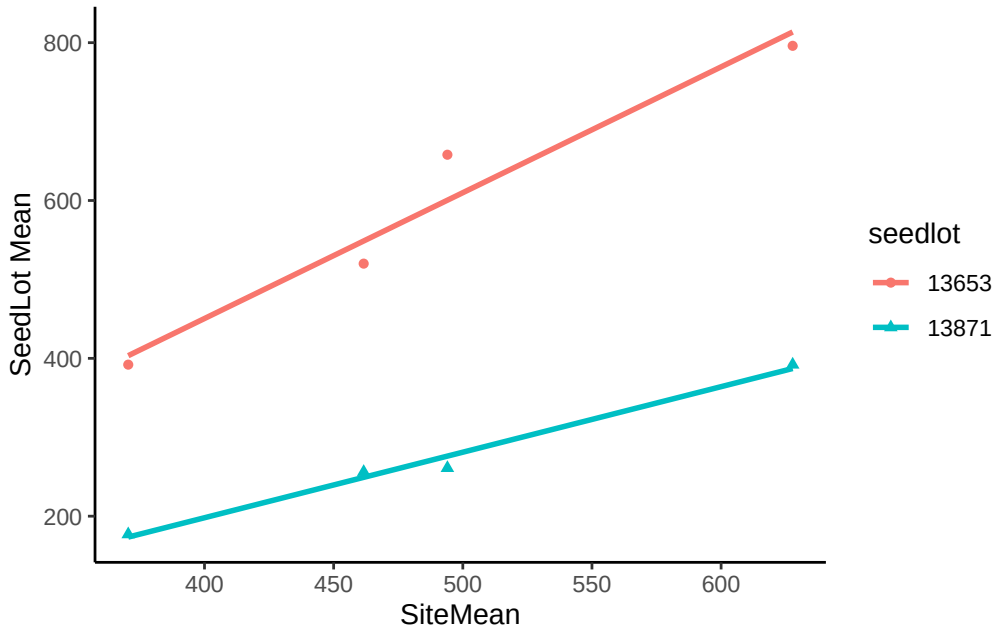
```
# Pg. 73
emmeans(object = fm5.4, specs = ~ site)
```

```
site       emmean  SE df lower.CL upper.CL
Ratchaburi    462 NaN  0      NaN      NaN
Sai Thong     628 NaN  0      NaN      NaN
```


```
 Si Sa Ket      494 NaN  0       NaN       NaN
 Sakaerat       370 NaN  0       NaN       NaN

Results are averaged over the levels of: seedlot
Confidence level used: 0.95

 emmeans(object = fm5.4, specs = ~ seedlot)
 seedlot emmean  SE df lower.CL upper.CL
 13877       365 NaN  0       NaN       NaN
 13866       353 NaN  0       NaN       NaN
 13689       559 NaN  0       NaN       NaN
 13688       546 NaN  0       NaN       NaN
 13861       627 NaN  0       NaN       NaN
 13854       628 NaN  0       NaN       NaN
 13684       660 NaN  0       NaN       NaN
 13864       422 NaN  0       NaN       NaN
 13863       586 NaN  0       NaN       NaN
 13683       770 NaN  0       NaN       NaN
 13681       695 NaN  0       NaN       NaN
 14175       438 NaN  0       NaN       NaN
 14660       521 NaN  0       NaN       NaN
 13653       592 NaN  0       NaN       NaN
 13846       440 NaN  0       NaN       NaN
 13621       384 NaN  0       NaN       NaN
 13871       272 NaN  0       NaN       NaN
 13519       422 NaN  0       NaN       NaN
 13514       369 NaN  0       NaN       NaN
 13148       273 NaN  0       NaN       NaN
 13990       282 NaN  0       NaN       NaN
 14537       780 NaN  0       NaN       NaN
 14106       772 NaN  0       NaN       NaN
 12013       616 NaN  0       NaN       NaN
 14130       422 NaN  0       NaN       NaN
 14485       123 NaN  0       NaN       NaN
 11935       273 NaN  0       NaN       NaN

Results are averaged over the levels of: site
Confidence level used: 0.95

 ANOVAfm5.4 <- anova(fm5.4)

 ANOVAfm5.4[4, 1:3] <- c(208, 208*1040, 1040)

 ANOVAfm5.4[3, 4]   <- ANOVAfm5.4[3, 3]/ANOVAfm5.4[4, 3]

 ANOVAfm5.4[3, 5]   <-
            pf(
               q        = ANOVAfm5.4[3, 4]
             , df1      = ANOVAfm5.4[3, 1]
             , df2      = ANOVAfm5.4[4, 1]
             , lower.tail = FALSE
            )

 # Pg. 73
 ANOVAfm5.4
Analysis of Variance Table

Response: ht
              Df  Sum Sq Mean Sq F value                Pr(>F)
```

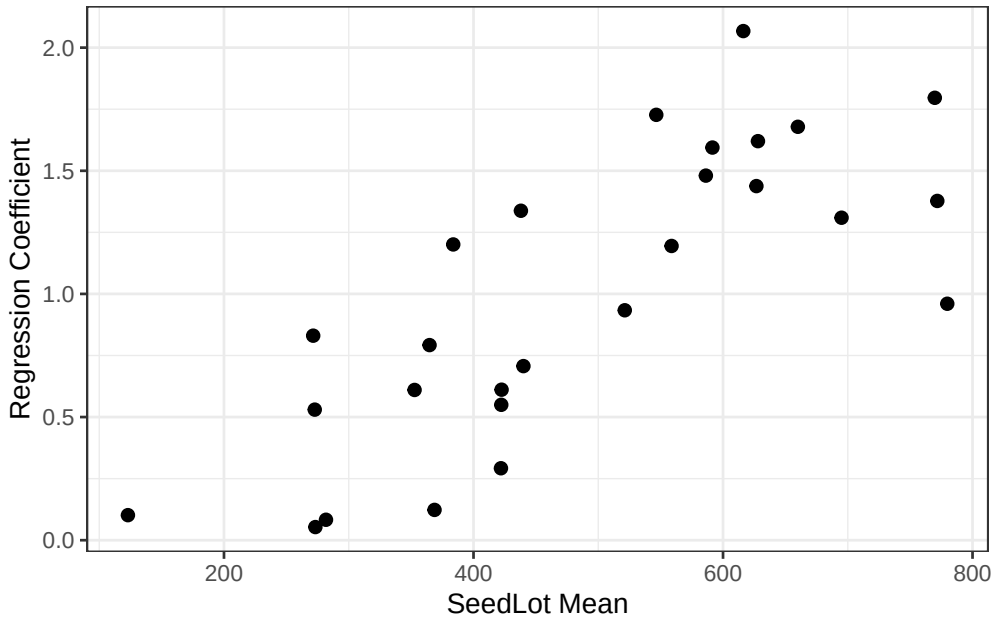

```
site            3  919585  306528     NaN                    NaN
seedlot        26 3176289  122165     NaN                    NaN
site:seedlot   78  707957    9076  8.7273 < 0.00000000000000022 ***
Residuals     208  216320    1040
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Pg. 80
DataExam5.1 %>%
  filter(seedlot %in% c("13653", "13871")) %>%
  ggplot(
    data = .
  , mapping = aes(
                   x      = sitemean
                 , y      = ht
                 , color  = seedlot
                 , shape  = seedlot
                 )
  ) +
  geom_point() +
  geom_smooth(
     method    = lm
   , se        = FALSE
   , fullrange = TRUE
   ) +
  theme_classic() +
  labs(
      x = "SiteMean"
    , y = "SeedLot Mean"
    )
```




```
Tab5.10 <-
  DataExam5.1 %>%
  summarise(Mean = mean(ht), .by = seedlot) %>%
  left_join(
     DataExam5.1 %>%
     nest_by(seedlot) %>%
     mutate(fm1 = list(lm(ht ~ sitemean, data = data))) %>%
```


```
      summarise(Slope = coef(fm1)[2])
   , by = "seedlot"
     )

 # Pg. 81
 Tab5.10
   seedlot   Mean      Slope
1    11935 272.75 0.53017435
2    14485 123.00 0.10170020
3    14130 422.25 0.54976906
4    12013 616.25 2.06723798
5    14106 771.75 1.37751724
6    14537 779.75 0.96012145
7    13990 281.75 0.08298796
8    13148 273.25 0.05333546
9    13514 368.75 0.12307233
10   13519 422.00 0.29211648
11   13871 271.50 0.83048203
12   13621 383.75 1.20085607
13   13846 440.00 0.70691001
14   13653 591.50 1.59434380
15   14660 521.25 0.93353990
16   14175 438.00 1.33770745
17   13681 695.00 1.30937837
18   13683 769.75 1.79629735
19   13863 586.25 1.48034730
20   13864 422.50 0.61113857
21   13684 660.00 1.67860570
22   13854 628.00 1.62026853
23   13861 626.75 1.43784662
24   13688 546.50 1.72717652
25   13689 558.75 1.19475332
26   13866 352.75 0.61009734
27   13877 364.75 0.79221858

 ggplot(data = Tab5.10, mapping = aes(x = Mean, y = Slope)) +
  geom_point(size = 2) +
  theme_bw() +
  labs(
      x = "SeedLot Mean"
    , y = "Regression Coefficient"
    )
```




```
DevSS1 <-
  DataExam5.1 %>%
  nest_by(seedlot) %>%
  mutate(fm1 = list(lm(ht ~ sitemean, data = data))) %>%
  summarise(SSE = anova(fm1)[2, 2]) %>%
  ungroup() %>%
  summarise(Dev = sum(SSE)) %>%
  as.numeric()

ANOVAfm5.4[2, 2]
[1] 3176289

length(levels(DataExam5.1$SeedLot))
[1] 0

ANOVAfm5.4.1 <-
  rbind(
   ANOVAfm5.4[1:3, ]
  , c(
      ANOVAfm5.4[2, 1]
    , ANOVAfm5.4[3, 2] - DevSS1
    , (ANOVAfm5.4[3, 2] - DevSS1)/ANOVAfm5.4[2, 1]
    , NA
    , NA
    )
  , c(
      ANOVAfm5.4[3, 1]-ANOVAfm5.4[2, 1]
    , DevSS1
    , DevSS1/(ANOVAfm5.4[3, 1]-ANOVAfm5.4[2, 1])
    , DevSS1/(ANOVAfm5.4[3, 1]-ANOVAfm5.4[2, 1])/ANOVAfm5.4[4, 3]
    , pf(
            q = DevSS1/(ANOVAfm5.4[3, 1]-ANOVAfm5.4[2, 1])/ANOVAfm5.4[4, 3]
          , df1 = ANOVAfm5.4[3, 1]-ANOVAfm5.4[2, 1]
          , df2 = ANOVAfm5.4[4, 1]
          , lower.tail = FALSE
          )
    )
  , ANOVAfm5.4[4, ]
```


```
  )

rownames(ANOVAfm5.4.1) <-
  c(
    "Site"
  , "seedlot"
  , "site:seedlot"
  , "  regressions"
  , "  deviations"
  , "Residuals"
  )

# Pg. 82
ANOVAfm5.4.1
```

```
Analysis of Variance Table

Response: ht
               Df  Sum Sq Mean Sq F value                  Pr(>F)
Site            3  919585  306528     NaN                     NaN
seedlot        26 3176289  122165     NaN                     NaN
site:seedlot   78  707957    9076  8.7273 < 0.00000000000000022 ***
  regressions  26  308503   11866
  deviations   52  399454    7682  7.3863 < 0.00000000000000022 ***
Residuals     208  216320    1040
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

5.2 Example 5.2 (Pg. 72)

Example 5.2 (Pg. 72)

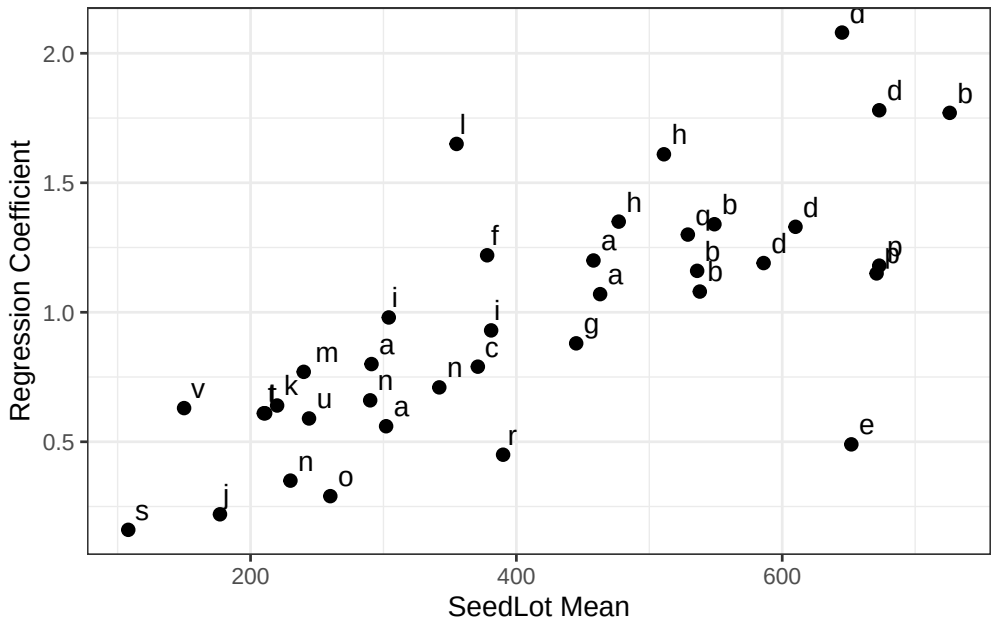
```
library(car)

library(dae)

library(dplyr)

library(emmeans)

library(ggplot2)

library(lmerTest)

library(magrittr)

library(predictmeans)

data(DataExam5.2)

# Pg. 75
fm5.7 <-
 lm(
     formula = ht ~ site*seedlot
   , data    = DataExam5.2
```


```
    )

 # Pg. 77
 anova(fm5.7)
Analysis of Variance Table

Response: ht
              Df  Sum Sq Mean Sq F value Pr(>F)
site           5 4157543  831509     NaN    NaN
seedlot       36 4425296  122925     NaN    NaN
site:seedlot 150 1351054    9007     NaN    NaN
Residuals      0       0     NaN

 fm5.9 <-
  lm(
      formula = ht ~ site*seedlot
    , data    = DataExam5.2
    )

 # Pg. 77
 anova(fm5.9)
Analysis of Variance Table

Response: ht
              Df  Sum Sq Mean Sq F value Pr(>F)
site           5 4157543  831509     NaN    NaN
seedlot       36 4425296  122925     NaN    NaN
site:seedlot 150 1351054    9007     NaN    NaN
Residuals      0       0     NaN

 ANOVAfm5.9 <- anova(fm5.9)

 ANOVAfm5.9[4, 1:3] <- c(384, 384*964, 964)

 ANOVAfm5.9[3, 4]   <- ANOVAfm5.9[3, 3]/ANOVAfm5.9[4, 3]

 ANOVAfm5.9[3, 5]   <-
     pf(
         q = ANOVAfm5.9[3, 4]
     , df1 = ANOVAfm5.9[3, 1]
     , df2 = ANOVAfm5.9[4, 1]
     , lower.tail = FALSE
     )

 # Pg. 77
 ANOVAfm5.9
Analysis of Variance Table

Response: ht
              Df  Sum Sq Mean Sq F value                  Pr(>F)
site           5 4157543  831509     NaN                     NaN
seedlot       36 4425296  122925     NaN                     NaN
site:seedlot 150 1351054    9007  9.3434 < 0.00000000000000022 ***
Residuals    384  370176     964
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

 Tab5.14 <-
   DataExam5.2 %>%
```


```
   summarise(
        Mean = round(mean(ht, na.rm = TRUE), 0)
      , .by  = seedlot
      ) %>%
    left_join(
       DataExam5.2 %>%
       nest_by(seedlot) %>%
       mutate(fm2 = list(lm(ht ~ sitemean, data = data))) %>%
       summarise(Slope = round(coef(fm2)[2], 2))
     , by = "seedlot"
      ) %>%
   as.data.frame()

 # Pg. 81
 Tab5.14
   seedlot Mean Slope
1    13877  291  0.80
2    13866  302  0.56
3    13689  463  1.07
4    13688  458  1.20
5    13861  538  1.08
6    13854  536  1.16
7    13686  726  1.77
8    13684  549  1.34
9    13864  371  0.79
10   13863  586  1.19
11   13683  673  1.78
12   13681  610  1.33
13   13680  645  2.08
14   14623  652  0.49
15   14175  378  1.22
16   14660  445  0.88
17   13691  511  1.61
18   13653  477  1.35
19   13846  381  0.93
20   13621  304  0.98
21   14176  177  0.22
22   13871  220  0.64
23   14622  355  1.65
24   13876  240  0.77
25   13519  342  0.71
26   13514  290  0.66
27   13148  230  0.35
28   13990  260  0.29
29   14537  671  1.15
30   14106  673  1.18
31   12013  529  1.30
32   14130  390  0.45
33   14485  108  0.16
34   14166  210  0.61
35   11935  211  0.61
36   14170  244  0.59
37   14152  150  0.63

 DevSS2 <-
   DataExam5.2 %>%
   nest_by(seedlot) %>%
   mutate(fm2 = list(lm(ht ~ sitemean, data = data))) %>%
   summarise(SSE = anova(fm2)[2, 2]) %>%
```


```
  ungroup() %>%
  summarise(Dev = sum(SSE)) %>%
  as.numeric()

ANOVAfm5.9.1 <-
  rbind(
     ANOVAfm5.9[1:3, ]
   , c(
        ANOVAfm5.9[2, 1]
      , ANOVAfm5.9[3, 2] - DevSS2
      , (ANOVAfm5.9[3, 2] - DevSS2)/ANOVAfm5.9[2, 1]
      , NA
      , NA
      )
   , c(
        ANOVAfm5.9[3, 1]-ANOVAfm5.9[2, 1]
      , DevSS2
      , DevSS2/(ANOVAfm5.9[3, 1]-ANOVAfm5.9[2, 1])
      , DevSS2/(ANOVAfm5.9[3, 1]-ANOVAfm5.9[2, 1])/ANOVAfm5.9[4, 3]
      , pf(
             q = DevSS2/(ANOVAfm5.9[3, 1]-ANOVAfm5.9[2, 1])/ANOVAfm5.9[4, 3]
           , df1 = ANOVAfm5.9[3, 1]-ANOVAfm5.9[2, 1]
           , df2 = ANOVAfm5.9[4, 1]
           , lower.tail = FALSE
           )
      )
   , ANOVAfm5.9[4, ]
  )

rownames(ANOVAfm5.9.1) <-
  c(
     "site"
   , "seedlot"
   , "site:seedlot"
   , "  regressions"
   , "  deviations"
   , "Residuals"
   )

# Pg. 82
ANOVAfm5.9.1
Analysis of Variance Table

Response: ht
               Df  Sum Sq Mean Sq F value                 Pr(>F)
site            5 4157543  831509     NaN                    NaN
seedlot        36 4425296  122925     NaN                    NaN
site:seedlot  150 1351054    9007  9.3434 < 0.00000000000000022 ***
  regressions  36  703203   19533
  deviations  114  647851    5683  5.8951 < 0.00000000000000022 ***
Residuals     384  370176     964
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Code <-
  c(
    "a","a","a","a","b","b","b","b"
  , "c","d","d","d","d","e","f","g"
  , "h","h","i","i","j","k","l","m"
```


```
 ,"n","n","n","o","p","p","q","r"
 , "s","t","t","u","v"
 )

Tab5.14$Code <- Code

ggplot(
   data = Tab5.14
 , mapping = aes(x = Mean, y = Slope)
 ) +
 geom_point(size = 2) +
 geom_text(
    mapping = aes(label = Code)
  , hjust   = -0.5
  , vjust   = -0.5
 ) +
 theme_bw() +
 labs(
     x = "SeedLot Mean"
   , y = "Regression Coefficient"
   )
```



6 Variance Components and Genetics Concepts

6.1 Example 6.2 (Pg. 90)

Example 6.2 (Pg. 90)

A progeny trial of *Acacia mangium* was planted at Segaluid, Sabah, by the Sabah Forest Research Centre in 1994. The trial was designed to test 48 open-pollinated families collected from natural provenances in Papua New Guinea (PNG, 41 families) and far north Queensland (five families) and two families of the land race that had developed in Sabah after introduction of *A. mangium* in the 1960s. Based on the results of many previous trials (Harwood & Williams 1992), it was expected that the Sabah and Queensland families would perform more poorly than those from PNG. The trial was set out as an RCB design with four replicates each containing 48 five-tree plots. Spacing was 3m × 3m between trees, and an external perimeter row surrounded the trial. Diameter at breast height (*dbh*) and height (*ht*) measurements were taken in 1997, 36 months after planting.

```
library(car)

library(dae)

library(dplyr)

library(emmeans)

library(ggplot2)

library(lmerTest)

library(magrittr)

library(predictmeans)

data(DataExam6.2)

DataExam6.2.1 <-
    DataExam6.2 %>%
    filter(Province == "PNG")

# Pg. 94
fm6.3 <-
     lm(
          formula = Dbh.mean ~ Replication + Family
        , data    = DataExam6.2.1
       )

b    <- anova(fm6.3)

HM       <- function(x){length(x)/sum(1/x)}
```


```
w       <- HM(DataExam6.2.1$Dbh.count)

S2      <- b[["Mean Sq"]][length(b[["Mean Sq"]])]

Sigma2t <- mean(DataExam6.2.1$Dbh.variance)

sigma2m <- S2-(Sigma2t/w)

fm6.3.1 <-
  lmer(
      formula = Dbh.mean ~ 1 + Replication + (1|Family)
    , data    = DataExam6.2.1
    , REML    = TRUE
    )

# Pg. 104
# summary(fm6.3.1)
varcomp(fm6.3.1)
                     vcov     SE  2.5 % 97.5 %
Family.(Intercept) 0.2584 0.1286 0.0538 0.5767
residual           1.1667 0.1506 0.8954 1.4774

sigma2f <- 0.2584

h2 <- (sigma2f/(0.3))/(Sigma2t + sigma2m + sigma2f)

cbind(hmean = w, Sigma2t, sigma2m, sigma2f, h2)
       hmean   Sigma2t   sigma2m sigma2f        h2
[1,] 4.408602 3.920732 0.2773606  0.2584 0.1932761

fm6.4 <-
  lm(
      formula = Dbh.mean ~ Replication+Family
    , data    = DataExam6.2
     )

b    <- anova(fm6.4)

HM      <- function(x){length(x)/sum(1/x)}

w       <- HM(DataExam6.2$Dbh.count)

S2      <- b[["Mean Sq"]][length(b[["Mean Sq"]])]

Sigma2t <- mean(DataExam6.2$Dbh.variance)

sigma2m <- S2-(Sigma2t/w)

fm6.4.1 <-
 lmer(
   formula = Dbh.mean ~ 1 + Replication + Province + (1|Family)
 , data    = DataExam6.2
 , REML    = TRUE
    )

# Pg. 107
varcomp(fm6.4.1)
                     vcov     SE  2.5 % 97.5 %
Family.(Intercept) 0.3514 0.1358 0.1203 0.6361
```


```
residual            1.0951 0.1304 0.8584 1.3634

 sigma2f <- 0.3514

 h2 <- (sigma2f/(0.3))/(Sigma2t+sigma2m+sigma2f)

 cbind(hmean = w, Sigma2t, sigma2m, sigma2f, h2)
        hmean   Sigma2t   sigma2m sigma2f        h2
[1,] 4.451314 3.860156 0.227873   0.3514 0.2638477

 fm6.7.1 <-
  lmer(
    formula = Dbh.mean ~ 1+Replication+(1|Family)
  , data    = DataExam6.2.1
  , REML = TRUE
  )

 # Pg. 116
 varcomp(fm6.7.1)
                      vcov     SE  2.5 % 97.5 %
Family.(Intercept) 0.2584 0.1286 0.0538 0.5767
residual           1.1667 0.1506 0.8954 1.4774

 sigma2f[1] <- 0.2584

 fm6.7.2<-
  lmer(
    formula = Ht.mean ~ 1 + Replication + (1|Family)
  , data    = DataExam6.2.1
  , REML    = TRUE
    )

 # Pg. 116
 varcomp(fm6.7.2)
                      vcov     SE  2.5 % 97.5 %
Family.(Intercept) 0.2711 0.1243 0.0743 0.5794
residual           1.0549 0.1362 0.8097 1.3359

 sigma2f[2] <- 0.2711

 fm6.7.3 <-
  lmer(
    formula = Sum.means ~ 1 + Replication + (1|Family)
  , data    = DataExam6.2.1
  , REML    = TRUE
  , control = lmerControl()
  )

 # Pg. 116
 varcomp(fm6.7.3)
                      vcov     SE  2.5 % 97.5 %
Family.(Intercept) 0.8729 0.3907 0.2553 1.8421
residual           3.2428 0.4186 2.4888 4.1063

 sigma2f[3] <- 0.873

 sigma2xy   <- 0.5*(sigma2f[3]-sigma2f[1]-sigma2f[2])

 GenCorr <- sigma2xy/sqrt(sigma2f[1]*sigma2f[2])
```


```
 cbind(
      S2x = sigma2f[1]
    , S2y = sigma2f[2]
    , S2.x.plus.y = sigma2f[3]
    , GenCorr
    )
         S2x    S2y S2.x.plus.y   GenCorr
[1,] 0.2584 0.2711        0.873 0.6489119
```

7Incomplete Block Designs

8Analysis of Generalized Lattice Designs

8.1 Example 8.1 (Pg. 139)

Example 8.1 (Pg. 139)

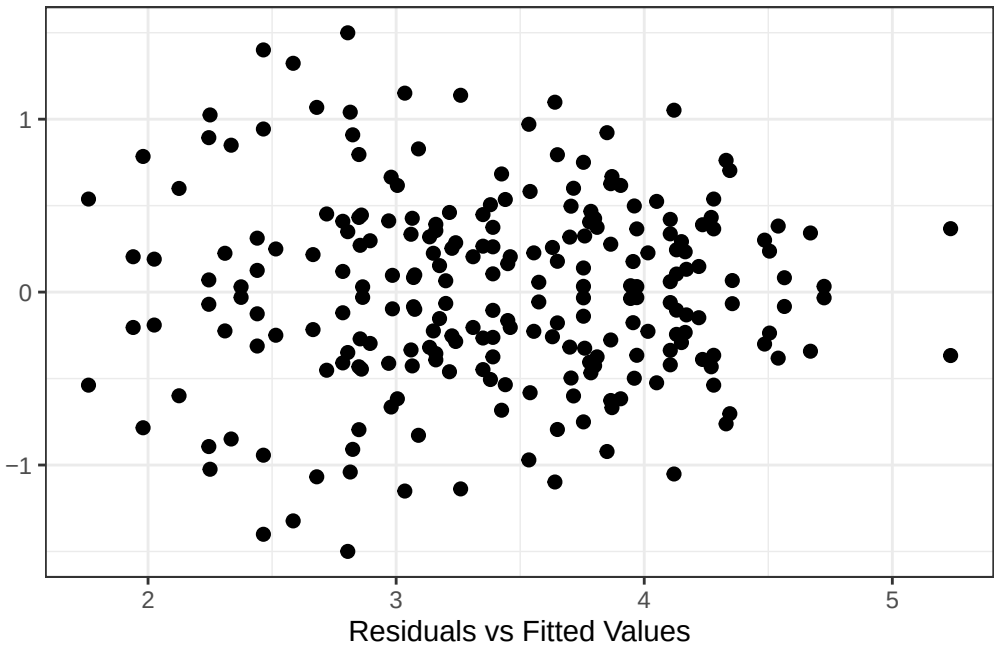
In the early 1990s Khongsak Pinyopusarerk of CSIRO Forestry and Forest Products initiated a far-reaching study of *Casuarina equisetifolia*. This is a nitrogen-fixing tree of considerable social, economic and environmental importance in tropical/subtropical littoral zones of Asia, the Pacific and Africa. Provenance collections were obtained from 18 countries and, with this material, more than 40 trials were laid out in 20 countries. The number of seedlots included in each trial varied, depending on the suitability and size of the planting sites for the available material. One of the trials, in Weipa, northern Queensland, contained all the available seedlots and is the example used here.

```
library(car)

library(dae)

library(dplyr)

library(emmeans)

library(ggplot2)

library(lmerTest)

library(magrittr)

library(predictmeans)

data(DataExam8.1)

# Pg. 141
fm8.4 <-
  aov(
    formula = dbh ~ inoc + Error(repl/inoc) +
                    inoc*country*prov
  , data    = DataExam8.1
    )

# Pg. 150
summary(fm8.4)

Error: repl
          Df Sum Sq Mean Sq F value Pr(>F)
inoc       1 11.542  11.542   11.46 0.0773 .
Residuals  2  2.014   1.007
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Error: Within
              Df Sum Sq Mean Sq F value       Pr(>F)
```


```
country        17  54.62   3.213   5.305 0.0000000159 ***
prov           41  18.61   0.454   0.749         0.854
inoc:country   17  10.07   0.592   0.978         0.487
inoc:prov      41  21.46   0.523   0.864         0.698
Residuals     116  70.26   0.606
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

 # Pg. 150
 model.tables(x = fm8.4, type = "means")
Tables of means
Grand mean

3.40411

 inoc
    7 weeks  1 week
      3.625   3.183
rep 118.000 118.000

 country
     India Vietnam  Egypt  Kenya   Fiji Thailand Malaysia Philippines Australia
     3.575   3.276  2.498  3.491  2.612    3.841    4.031       3.612     2.631
rep 24.000  20.000 12.000 32.000 12.000   16.000   36.000      12.000    16.000
     PNG Solomon Is. Mauritius Sri Lanka  Guam  China Puerto Rico Vanuatu Benin
    3.65        3.699     3.122     3.243 2.342  3.686       3.345   2.762 3.342
rep 4.00        8.000     4.000    12.000 4.000 12.000       4.000   4.000 4.000

 prov
        1     2    3    4     5     6     7     8    10    11   12   13    14
    2.623 4.013 3.71 3.27 3.404 3.093 3.701 3.541 3.371 3.301 3.18 3.37 3.404
rep 4.000 4.000 4.00 4.00 4.000 4.000 4.000 4.000 4.000 4.000 4.00 4.00 4.000
       15    16    17    18    19    20    21    22    23    24    25    26    27
    3.595 3.43 3.275 3.085 3.66 3.382 3.235 3.46 3.08 3.555 3.918 3.648 3.43
rep 4.000 4.00 4.000 4.000 4.00 4.000 4.000 4.00 4.00 4.000 4.000 4.000 4.00
       28    29    30    31    32    33    34    35    36    37    38   39    40
    2.905 3.708 3.196 3.761 3.416 3.178 2.958 3.636 3.376 3.404 3.252 3.15 3.81
rep 4.000 4.000 4.000 4.000 4.000 4.000 4.000 4.000 4.000 4.000 4.000 4.00 4.00
       41    42    45   46    47    48    50    51    52    53    54   55    56
    3.195 3.613 3.518 2.76 3.733 3.605 3.404 3.685 3.235 3.755 3.605 2.74 3.662
rep 4.000 4.000 4.000 4.00 4.000 4.000 4.000 4.000 4.000 4.000 4.000 4.00 4.000
       57    58    59    60    61    62    63
    3.408 3.404 3.404 3.528 3.178 3.506 3.418
rep 4.000 4.000 4.000 4.000 4.000 4.000 4.000

 inoc:country
          country
inoc       India  Vietnam Egypt  Kenya  Fiji   Thailand Malaysia Philippines
  7 weeks  3.672  3.443   2.747  3.609  2.955  3.611    4.502    3.558
  rep     12.000 10.000   6.000 16.000  6.000  8.000   18.000    6.000
  1 week   3.477  3.110   2.250  3.373  2.268  4.071    3.559    3.665
  rep     12.000 10.000   6.000 16.000  6.000  8.000   18.000    6.000
          country
inoc       Australia PNG    Solomon Is. Mauritius Sri Lanka Guam   China
  7 weeks  2.959     3.850  4.200       3.390     3.695     2.245  4.030
  rep      8.000     2.000  4.000       2.000     6.000     2.000  6.000
  1 week   2.304     3.450  3.197       2.855     2.792     2.440  3.342
  rep      8.000     2.000  4.000       2.000     6.000     2.000  6.000
          country
```


```
inoc       Puerto Rico Vanuatu Benin
  7 weeks   3.540        2.720   3.870
  rep       2.000        2.000   2.000
  1 week    3.150        2.805   2.815
  rep       2.000        2.000   2.000

 inoc:prov
          prov
inoc       1     2     3     4     5     6     7     8     10    11    12
  7 weeks 2.427 4.682 3.757 3.637 3.625 3.540 4.100 3.774 3.559 3.544 3.135
  rep     2.000 2.819 3.344 3.664 2.904 3.183 2.646 3.301 3.308 3.183 3.058
  1 week  2.819 3.344 3.664 2.904 3.183 2.646 3.301 3.308 3.183 3.058 3.225
  rep     2.427 4.682 3.757 3.637 3.625 3.540 4.100 3.774 3.559 3.544 3.135
          prov
inoc       13    14    15    16    17    18    19    20    21    22    23
  7 weeks 3.845 3.625 4.104 4.119 3.604 3.114 3.509 3.304 3.591 3.801 3.276
  rep     3.225 2.895 3.183 3.085 2.740 2.945 3.055 3.810 3.460 2.880 3.120
  1 week  2.895 3.183 3.085 2.740 2.945 3.055 3.810 3.460 2.880 3.120 2.885
  rep     3.845 3.625 4.104 4.119 3.604 3.114 3.509 3.304 3.591 3.801 3.276
          prov
inoc       24    25    26    27    28    29    30    31    32    33    34
  7 weeks 3.021 3.976 4.286 4.186 2.866 3.663 2.988 3.793 4.358 3.343 3.468
  rep     2.885 4.090 3.860 3.010 2.675 2.945 3.754 3.404 3.729 2.474 3.014
  1 week  4.090 3.860 3.010 2.675 2.945 3.754 3.404 3.729 2.474 3.014 2.449
  rep     3.021 3.976 4.286 4.186 2.866 3.663 2.988 3.793 4.358 3.343 3.468
          prov
inoc       35    36    37    38    39    40    41    42    45    46    47
  7 weeks 3.848 3.688 3.625 3.772 3.132 3.972 3.545 3.705 3.439 2.599 4.119
  rep     2.449 3.424 3.064 3.183 2.733 3.168 3.648 2.845 3.520 3.597 2.922
  1 week  3.424 3.064 3.183 2.733 3.168 3.648 2.845 3.520 3.597 2.922 3.347
  rep     3.848 3.688 3.625 3.772 3.132 3.972 3.545 3.705 3.439 2.599 4.119
          prov
inoc       48    50    51    52    53    54    55    56    57    58    59
  7 weeks 4.344 3.625 4.137 4.152 4.047 3.167 2.622 3.895 3.478 3.625 3.625
  rep     3.347 2.867 3.183 3.233 2.318 3.463 4.043 2.858 3.430 3.339 3.183
  1 week  2.867 3.183 3.233 2.318 3.463 4.043 2.858 3.430 3.339 3.183 3.183
  rep     4.344 3.625 4.137 4.152 4.047 3.167 2.622 3.895 3.478 3.625 3.625
          prov
inoc       60    61    62    63
  7 weeks 3.685 3.630 3.560 3.235
  rep     3.183 3.371 2.726 3.451
  1 week  3.371 2.726 3.451 3.601
  rep     3.685 3.630 3.560 3.235

 RESFit <-
     data.frame(
       fittedvalue    = fitted.aovlist(fm8.4)
     , residualvalue = proj(fm8.4)$Within[,"Residuals"]
     )

 ggplot(
    data     =  RESFit
  , mapping = aes(x = fittedvalue, y = residualvalue)
  ) +
 geom_point(size = 2) +
 labs(
    x = "Residuals vs Fitted Values"
  , y = ""
  ) +
```

```
theme_bw()
```



Residuals vs Fitted Values

```
# Pg. 153
fm8.6 <-
 aov(
   formula = terms(
                   dbh ~ inoc + repl + col +
                         repl:row + repl:col +
                         prov + inoc:prov
                   , keep.order = TRUE
                   )
  , data    = DataExam8.1
  )

 summary(fm8.6)
             Df Sum Sq Mean Sq F value               Pr(>F)
inoc          1  11.54  11.542  48.054         0.00000000327 ***
repl          2   2.01   1.007   4.193              0.019746 *
col           9  65.24   7.249  30.182 < 0.0000000000000002 ***
repl:row     20  16.59   0.830   3.454              0.000105 ***
repl:col     27  16.41   0.608   2.530              0.001443 **
prov         58  53.89   0.929   3.869         0.00000026687 ***
inoc:prov    58   8.47   0.146   0.608              0.970544
Residuals    60  14.41   0.240
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

8.2 Example 8.1 (continued) (Pg. 147)

Example 8.1 (continued) (Pg. 147)

```
 library(car)

 library(dae)

 library(dplyr)

 library(emmeans)

 library(ggplot2)

 library(lmerTest)

 library(magrittr)

 library(predictmeans)

 data(DataExam8.1)

 # Pg. 155
 fm8.8 <-
  lmerTest::lmer(
      formula = dbh ~ 1 + repl + col + prov +
                      (1|repl:row) + (1|repl:col)
    , data    = DataExam8.1
    , REML    = TRUE
    )

 # Pg. 157
 #\dontrun{
 varcomp(fm8.8)
                       vcov     SE  2.5 % 97.5 %
repl:col.(Intercept) 0.0459 0.0262 0.0000 0.0565
repl:row.(Intercept) 0.0640 0.0294 0.0210 0.1161
residual             0.1951 0.0253 0.1126 0.1782

 #}

 anova(fm8.8)
Type III Analysis of Variance Table with Satterthwaite's method
     Sum Sq Mean Sq NumDF   DenDF F value              Pr(>F)
repl  2.581 0.86023     3  21.257  4.4082             0.01469 *
col  24.874 2.76378     9  23.705 14.1627 0.00000015112494790 ***
prov 55.433 0.95574    58 136.623  4.8976 0.00000000000001306 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

 anova(fm8.8, ddf = "Kenward-Roger")
Type III Analysis of Variance Table with Kenward-Roger's method
     Sum Sq Mean Sq NumDF   DenDF F value              Pr(>F)
repl  2.580 0.86016     3  22.622  4.4078              0.0139 *
col  24.824 2.75827     9  22.947 14.1337 0.0000002097637857 ***
prov 54.795 0.94473    58 133.852  4.8396 0.0000000000000283 ***
---
```


```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

 predictmeans(model = fm8.8, modelterm = "repl")
```

```
$`Predicted Means`
repl
     1      2      3      4
3.7543 3.1269 3.2128 3.5023

$`Standard Error of Means`
All means have the same SE
                   0.13629

$`Standard Error of Differences`
  Max.SED   Min.SED  Aveg.SED
0.1927495 0.1927423 0.1927472

$LSD
 Max.LSD  Min.LSD Aveg.LSD
 0.39910  0.39909  0.39910
attr(,"Significant level")
[1] 0.05
attr(,"Degree of freedom")
[1] 22.62

$mean_table
  repl   Mean       SE      Df LL(95%) UL(95%)
1    1 3.7543 0.13629 22.6214  3.4721  4.0365
2    2 3.1269 0.13629 22.6214  2.8447  3.4091
3    3 3.2128 0.13629 22.6214  2.9306  3.4950
4    4 3.5023 0.13629 22.6214  3.2201  3.7845


 predictmeans(model = fm8.8, modelterm = "col")
```

```
$`Predicted Means`
col
     1      2      3      4      5      6      7      8      9     10
3.5053 3.4996 3.8509 3.8280 3.5947 3.7829 3.3059 3.5158 3.1776 1.9301

$`Standard Error of Means`
col
      1       2       3       4       5       6       7       8       9      10
0.15496 0.15649 0.15493 0.15494 0.15490 0.15721 0.15479 0.15699 0.15485 0.15648

$`Standard Error of Differences`
  Max.SED   Min.SED  Aveg.SED
0.2132295 0.2061223 0.2086161

$LSD
 Max.LSD  Min.LSD Aveg.LSD
 0.43742  0.42284  0.42796
attr(,"Significant level")
[1] 0.05
attr(,"Degree of freedom")
[1] 27.12

$mean_table
   col    Mean       SE       Df LL(95%) UL(95%)
```


```
1     1 3.5053 0.15496 27.11736  3.1874  3.8232
2     2 3.4996 0.15649 27.11736  3.1786  3.8207
3     3 3.8509 0.15493 27.11736  3.5330  4.1687
4     4 3.8280 0.15494 27.11736  3.5101  4.1458
5     5 3.5947 0.15490 27.11736  3.2769  3.9125
6     6 3.7829 0.15721 27.11736  3.4604  4.1054
7     7 3.3059 0.15479 27.11736  2.9883  3.6234
8     8 3.5158 0.15699 27.11736  3.1938  3.8379
9     9 3.1776 0.15485 27.11736  2.8599  3.4952
10   10 1.9301 0.15648 27.11736  1.6091  2.2511


 predictmeans(model = fm8.8, modelterm = "prov")
```

```
$`Predicted Means`
prov
     1      2      3      4      5      6      7      8      10     11     12
2.4222 3.1425 2.8646 2.2599 3.7189 3.5445 3.9474 2.7469 2.6459 2.0497 2.7497
    13     14     15     16     17     18     19     20     21     22     23
2.9833 2.6534 3.4459 3.9209 3.4294 3.3624 3.6540 3.3685 3.2210 3.3315 3.2453
    24     25     26     27     28     29     30     31     32     33     34
3.6933 3.8460 3.5233 3.5271 3.1001 3.8997 3.5447 4.1294 4.2755 3.7429 3.8890
    35     36     37     38     39     40     41     42     45     46     47
4.1179 3.8526 3.4538 3.0379 3.5306 3.7412 3.7422 3.8765 4.2126 3.4660 4.4688
    48     50     51     52     53     54     55     56     57     58     59
3.7503 2.5571 3.4571 3.3227 3.5926 3.5337 2.7157 2.7702 3.9805 2.9968 3.3978
    60     61     62     63
3.0115 3.2238 3.2814 3.5751

$`Standard Error of Means`
prov
      1       2       3       4       5       6       7       8       10      11
0.25362 0.25446 0.25278 0.25443 0.25423 0.25588 0.25420 0.25338 0.25417 0.25259
     12      13      14      15      16      17      18      19      20      21
0.25306 0.25436 0.25259 0.25232 0.25502 0.25319 0.25340 0.25309 0.25294 0.25204
     22      23      24      25      26      27      28      29      30      31
0.25350 0.25355 0.25358 0.25316 0.25289 0.25294 0.25291 0.25341 0.25254 0.25330
     32      33      34      35      36      37      38      39      40      41
0.25377 0.25387 0.25510 0.25347 0.25351 0.25352 0.25416 0.25393 0.25450 0.25416
     42      45      46      47      48      50      51      52      53      54
0.25303 0.25257 0.25323 0.25316 0.25356 0.25354 0.25372 0.25361 0.25237 0.25321
     55      56      57      58      59      60      61      62      63
0.25374 0.25639 0.25173 0.25319 0.25250 0.25303 0.25378 0.25266 0.25500

$`Standard Error of Differences`
  Max.SED   Min.SED  Aveg.SED
0.3591712 0.3326719 0.3482665

$LSD
 Max.LSD  Min.LSD Aveg.LSD
 0.70924  0.65691  0.68770
attr(,"Significant level")
[1] 0.05
attr(,"Degree of freedom")
[1] 162.73

$mean_table
   prov    Mean       SE       Df LL(95%) UL(95%)
1     1 2.4222 0.25362 162.7269  1.9214  2.9230
```

2	2	3.1425	0.25446	162.7269	2.6401	3.6450
3	3	2.8646	0.25278	162.7269	2.3655	3.3638
4	4	2.2599	0.25443	162.7269	1.7575	2.7623
5	5	3.7189	0.25423	162.7269	3.2169	4.2209
6	6	3.5445	0.25588	162.7269	3.0392	4.0498
7	7	3.9474	0.25420	162.7269	3.4454	4.4493
8	8	2.7469	0.25338	162.7269	2.2466	3.2473
9	10	2.6459	0.25417	162.7269	2.1440	3.1478
10	11	2.0497	0.25259	162.7269	1.5509	2.5485
11	12	2.7497	0.25306	162.7269	2.2500	3.2494
12	13	2.9833	0.25436	162.7269	2.4810	3.4855
13	14	2.6534	0.25259	162.7269	2.1546	3.1522
14	15	3.4459	0.25232	162.7269	2.9476	3.9441
15	16	3.9209	0.25502	162.7269	3.4173	4.4245
16	17	3.4294	0.25319	162.7269	2.9294	3.9293
17	18	3.3624	0.25340	162.7269	2.8620	3.8628
18	19	3.6540	0.25309	162.7269	3.1543	4.1538
19	20	3.3685	0.25294	162.7269	2.8690	3.8680
20	21	3.2210	0.25204	162.7269	2.7234	3.7187
21	22	3.3315	0.25350	162.7269	2.8310	3.8321
22	23	3.2453	0.25355	162.7269	2.7447	3.7460
23	24	3.6933	0.25358	162.7269	3.1926	4.1941
24	25	3.8460	0.25316	162.7269	3.3461	4.3459
25	26	3.5233	0.25289	162.7269	3.0239	4.0227
26	27	3.5271	0.25294	162.7269	3.0276	4.0265
27	28	3.1001	0.25291	162.7269	2.6007	3.5996
28	29	3.8997	0.25341	162.7269	3.3993	4.4001
29	30	3.5447	0.25254	162.7269	3.0460	4.0434
30	31	4.1294	0.25330	162.7269	3.6293	4.6296
31	32	4.2755	0.25377	162.7269	3.7744	4.7766
32	33	3.7429	0.25387	162.7269	3.2416	4.2442
33	34	3.8890	0.25510	162.7269	3.3853	4.3928
34	35	4.1179	0.25347	162.7269	3.6174	4.6185
35	36	3.8526	0.25351	162.7269	3.3520	4.3532
36	37	3.4538	0.25352	162.7269	2.9532	3.9544
37	38	3.0379	0.25416	162.7269	2.5360	3.5398
38	39	3.5306	0.25393	162.7269	3.0291	4.0320
39	40	3.7412	0.25450	162.7269	3.2386	4.2437
40	41	3.7422	0.25416	162.7269	3.2403	4.2440
41	42	3.8765	0.25303	162.7269	3.3769	4.3761
42	45	4.2126	0.25257	162.7269	3.7139	4.7114
43	46	3.4660	0.25323	162.7269	2.9660	3.9661
44	47	4.4688	0.25316	162.7269	3.9689	4.9687
45	48	3.7503	0.25356	162.7269	3.2496	4.2510
46	50	2.5571	0.25354	162.7269	2.0564	3.0577
47	51	3.4571	0.25372	162.7269	2.9561	3.9582
48	52	3.3227	0.25361	162.7269	2.8219	3.8235
49	53	3.5926	0.25237	162.7269	3.0943	4.0910
50	54	3.5337	0.25321	162.7269	3.0337	4.0337
51	55	2.7157	0.25374	162.7269	2.2146	3.2167
52	56	2.7702	0.25639	162.7269	2.2640	3.2765
53	57	3.9805	0.25173	162.7269	3.4834	4.4776
54	58	2.9968	0.25319	162.7269	2.4968	3.4968
55	59	3.3978	0.25250	162.7269	2.8992	3.8963
56	60	3.0115	0.25303	162.7269	2.5118	3.5112
57	61	3.2238	0.25378	162.7269	2.7227	3.7250
58	62	3.2814	0.25266	162.7269	2.7825	3.7803
59	63	3.5751	0.25500	162.7269	3.0716	4.0787


```
  # Pg. 161
   RCB1 <-
         aov(dbh ~ prov + repl, data = DataExam8.1)

   RCB  <-
         emmeans(RCB1,  specs = "prov") %>%
         as_tibble()

   Mixed <-
           emmeans(fm8.8, specs = "prov") %>%
           as_tibble()

   table8.9 <-
       left_join(
          x      = RCB
        , y      = Mixed
        , by     = "prov"
        , suffix = c(".RCBD", ".Mixed")
        )

   print(table8.9)
# A tibble: 59 x 11
   prov  emmean.RCBD SE.RCBD df.RCBD lower.CL.RCBD upper.CL.RCBD emmean.Mixed
   <fct>       <dbl>   <dbl>   <dbl>         <dbl>         <dbl>         <dbl>
 1 1            1.85   0.382     174          1.10          2.60          2.42
 2 2            3.24   0.382     174          2.49          3.99          3.14
 3 3            2.94   0.382     174          2.18          3.69          2.86
 4 4            2.50   0.382     174          1.74          3.25          2.26
 5 5            3.34   0.382     174          2.59          4.10          3.72
 6 6            3.37   0.382     174          2.62          4.13          3.54
 7 7            3.98   0.382     174          3.23          4.74          3.95
 8 8            2.63   0.382     174          1.88          3.39          2.75
 9 10           2.47   0.382     174          1.71          3.22          2.65
10 11           2.40   0.382     174          1.64          3.15          2.05
# i 49 more rows
# i 4 more variables: SE.Mixed <dbl>, df.Mixed <dbl>, lower.CL.Mixed <dbl>,
#   upper.CL.Mixed <dbl>
```

8.3 Example 8.1 (continued) (Pg. 155)

Example 8.1 (continued) (Pg. 155)

```
library(car)

library(dae)

library(dplyr)

library(emmeans)

library(ggplot2)

library(lmerTest)
```


```
library(magrittr)

library(predictmeans)

data(DataExam8.1)

# Pg. 167
fm8.11 <-
  aov(
       formula = dbh ~ country + country:prov
     , data    = DataExam8.1
      )

  b <- anova(fm8.11)

  Res <- length(b[["Sum Sq"]])

  df  <- 119

  MSS <- 0.1951

  b[["Df"]][Res] <- df

  b[["Sum Sq"]][Res] <- MSS*df

  b[["Mean Sq"]][Res] <- b[["Sum Sq"]][Res]/b[["Df"]][Res]

  b[["F value"]][1:Res-1] <-
            b[["Mean Sq"]][1:Res-1]/b[["Mean Sq"]][Res]

  b[["Pr(>F)"]][Res-1] <-
     df(
       b[["F value"]][Res-1]
     , b[["Df"]][Res-1]
     , b[["Df"]][Res]
     )

  b
Analysis of Variance Table

Response: dbh
              Df Sum Sq Mean Sq F value         Pr(>F)
country       17 54.619  3.2129  16.468 0.00000001235 ***
country:prov  41 18.606  0.4538   2.326       0.001502 **
Residuals    119 23.217  0.1951
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

  emmeans(fm8.11, specs = "country")
 country     emmean    SE  df lower.CL upper.CL
 India         3.57 0.165 177     3.25     3.90
 Vietnam       3.28 0.181 177     2.92     3.63
 Egypt         2.50 0.233 177     2.04     2.96
 Kenya         3.49 0.143 177     3.21     3.77
 Fiji          2.61 0.233 177     2.15     3.07
 Thailand      3.84 0.202 177     3.44     4.24
 Malaysia      4.03 0.135 177     3.77     4.30
 Philippines   3.61 0.233 177     3.15     4.07
```


```
 Australia      2.63 0.202 177      2.23      3.03
 PNG            3.65 0.404 177      2.85      4.45
 Solomon Is.    3.70 0.285 177      3.14      4.26
 Mauritius      3.12 0.404 177      2.33      3.92
 Sri Lanka      3.24 0.233 177      2.78      3.70
 Guam           2.34 0.404 177      1.55      3.14
 China          3.69 0.233 177      3.23      4.15
 Puerto Rico    3.35 0.404 177      2.55      4.14
 Vanuatu        2.76 0.404 177      1.97      3.56
 Benin          3.34 0.404 177      2.55      4.14

Results are averaged over the levels of: prov
Confidence level used: 0.95
```

8.4 Example 8.2 (Pg. 157)

Example 8.2 (Pg. 157)

In Example 7.1 we discussed a Eucalyptus clone trial conducted in Vietnam and described the experimental layout. The trial tested 56 hybrid clones of the interspecific hybrid combination *E. urophylla* × *E. pellita* (UP). These candidates had been selected from progeny trials of control-pollinated hybrid families; here we ignore the parental origins of the different UP clones.

```
library(car)

library(dae)

library(dplyr)

library(emmeans)

library(ggplot2)

library(lmerTest)

library(magrittr)

library(predictmeans)

data(DataExam8.2)

# Pg.
fm8.2  <-
  lmerTest::lmer(
    formula = dbh ~ repl + column +
                    contcompf + contcompf:standard +
                    (1|repl:row) + (1|repl:column) +
                    (1|contcompv:clone)
  , data    = DataExam8.2
    )

#\dontrun{
varcomp(fm8.2)
```


```
                                vcov     SE  2.5 % 97.5 %
contcompv:clone.(Intercept) 0.4950 0.1126 0.3057 0.7422
repl:row.(Intercept)        0.0802 0.0351 0.0173 0.1458
repl:column.(Intercept)     0.0529 0.0326 0.0000 0.0783
residual                    0.3992 0.0435 0.3245 0.5024

 #}
 anova(fm8.2)
Type III Analysis of Variance Table with Satterthwaite's method
                   Sum Sq Mean Sq NumDF   DenDF F value          Pr(>F)
repl               3.2720  0.8180     4  26.467  2.0489       0.1162606
column             3.1018  0.6204     5  19.545  1.5539       0.2194719
contcompf          5.3203  5.3203     1  54.905 13.3265       0.0005845 ***
contcompf:standard 20.6587  6.8862     3 207.152 17.2488 0.0000000004896 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

 Anova(fm8.2, type = "II", test.statistic = "Chisq")
Analysis of Deviance Table (Type II Wald chisquare tests)

Response: dbh
                    Chisq Df Pr(>Chisq)
repl                8.1957  4    0.08467 .
column              7.7694  5    0.16941
contcompf           4.6841  1    0.03044 *
contcompf:standard 51.7463  3  3.392e-11 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

 predictmeans(model = fm8.2, modelterm = "repl")
```

```
$`Predicted Means`
repl
     1      2      3      4      5
7.8926 8.2070 8.3429 8.4604 8.5464

$`Standard Error of Means`
repl
      1       2       3       4       5
0.33123 0.33126 0.32992 0.32992 0.32992

$`Standard Error of Differences`
  Max.SED   Min.SED  Aveg.SED
0.2239675 0.2167320 0.2196681

$LSD
 Max.LSD  Min.LSD Aveg.LSD
 0.44792  0.43345  0.43932
attr(,"Significant level")
[1] 0.05
attr(,"Degree of freedom")
[1] 60.56

$mean_table
  repl    Mean       SE       Df LL(95%) UL(95%)
1    1 7.8926 0.33123 60.55892  7.2302  8.5551
2    2 8.2070 0.33126 60.55892  7.5445  8.8695
3    3 8.3429 0.32992 60.55892  7.6831  9.0027
4    4 8.4604 0.32992 60.55892  7.8006  9.1202
```

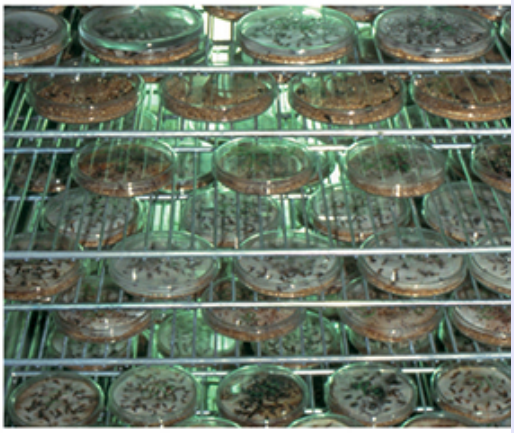

```
5     5 8.5464 0.32992 60.55892  7.8866  9.2062


 predictmeans(model = fm8.2, modelterm = "column")
```

```
$`Predicted Means`
column
     1      2      3      4      5      6
8.2214 8.4708 8.3779 7.9721 7.8166 8.7141

$`Standard Error of Means`
column
      1       2       3       4       5       6
0.31662 0.39168 0.39315 0.26648 0.26646 0.31653

$`Standard Error of Differences`
  Max.SED   Min.SED  Aveg.SED
0.2714760 0.2102583 0.2373610

$LSD
 Max.LSD  Min.LSD Aveg.LSD
 0.54250  0.42017  0.47433
attr(,"Significant level")
[1] 0.05
attr(,"Degree of freedom")
[1] 62.99

$mean_table
  column    Mean       SE       Df LL(95%) UL(95%)
1      1 8.2214 0.31662 62.99437  7.5887  8.8542
2      2 8.4708 0.39168 62.99437  7.6881  9.2535
3      3 8.3779 0.39315 62.99437  7.5923  9.1636
4      4 7.9721 0.26648 62.99437  7.4396  8.5047
5      5 7.8166 0.26646 62.99437  7.2841  8.3491
6      6 8.7141 0.31653 62.99437  8.0816  9.3467


 emmeans(object = fm8.2, specs = ~contcompf|standard)
contcompf = 1, standard = 0:
 emmean    SE   df lower.CL upper.CL
   8.91 0.117 65.9     8.67     9.14

contcompf = 0, standard = UG323:
 emmean    SE   df lower.CL upper.CL
   8.97 0.770 55.6     7.43    10.51

contcompf = 0, standard = U6:
 emmean    SE   df lower.CL upper.CL
   6.55 0.770 55.5     5.01     8.10

contcompf = 0, standard = PN14:
 emmean    SE   df lower.CL upper.CL
   7.70 0.771 55.8     6.16     9.25

contcompf = 0, standard = SSOseed:
 emmean    SE   df lower.CL upper.CL
   6.08 0.770 55.5     4.54     7.63

Results are averaged over the levels of: repl, column
```


```
Degrees-of-freedom method: kenward-roger
Confidence level used: 0.95
```

3RD EDITION

Experimental Design and Analysis for Tree Improvement



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