Homework 6 - AGST 5014

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1. With the data set below, answer: (another resource on IBD: Chapter 14 - http://users.stat.umn.edu/~gary/book/fcdae.pdf) a) Is this a balanced or partially balanced design?

```
data("taste", package = "daewr")
str(taste)
```

```
## 'data.frame':    24 obs. of  3 variables:
##  $ panelist: Factor w/ 12 levels "1","2","3","4",..: 1 2 3 4 5 6 7 8 9 10 ...
##  $ recipe  : Factor w/ 4 levels "A","B","C","D": 1 1 1 2 2 3 1 1 1 2 ...
##  $ score   : num  5 7 5 6 6 8 6 5 4 7 ...
```

```
table(taste$panelist)
```

```
##
##  1  2  3  4  5  6  7  8  9 10 11 12
##  2  2  2  2  2  2  2  2  2  2  2  2
```

We have 12 different panelists, and each one tasted recipes 2 times.
Each panelist is a block.

```
table(taste$recipe)
```

```
##
## A B C D
## 6 6 6 6
```

We have 4 different recipes, and each one was tasted 6 times.

```
with(taste, table(panelist, recipe))
```

```
##         recipe
## panelist A B C D
##       1  1 1 0 0
##       2  1 0 1 0
##       3  1 0 0 1
##       4  0 1 1 0
##       5  0 1 0 1
##       6  0 0 1 1
##       7  1 1 0 0
```

```
##       8  1 0 1 0
##       9  1 0 0 1
##       10 0 1 1 0
##       11 0 1 0 1
##       12 0 0 1 1
```

Some panelists didn't prove all the 4 recipes, so this is a **incomplete block design**.
Now we have to check whether is balanced or partially balanced.

We already know each recipe occurred 6 times, but how many times each treatment pair within blocks occurred?
If we check all possible pair combination (AB, AC, AD, BC, BD, CD) within blocks, all of them occurred two times, $\lambda = 2$. This means we have a Balanced Incomplete Block (BIB) design.

b) Run both, the intra-block and inter-block analysis on it.

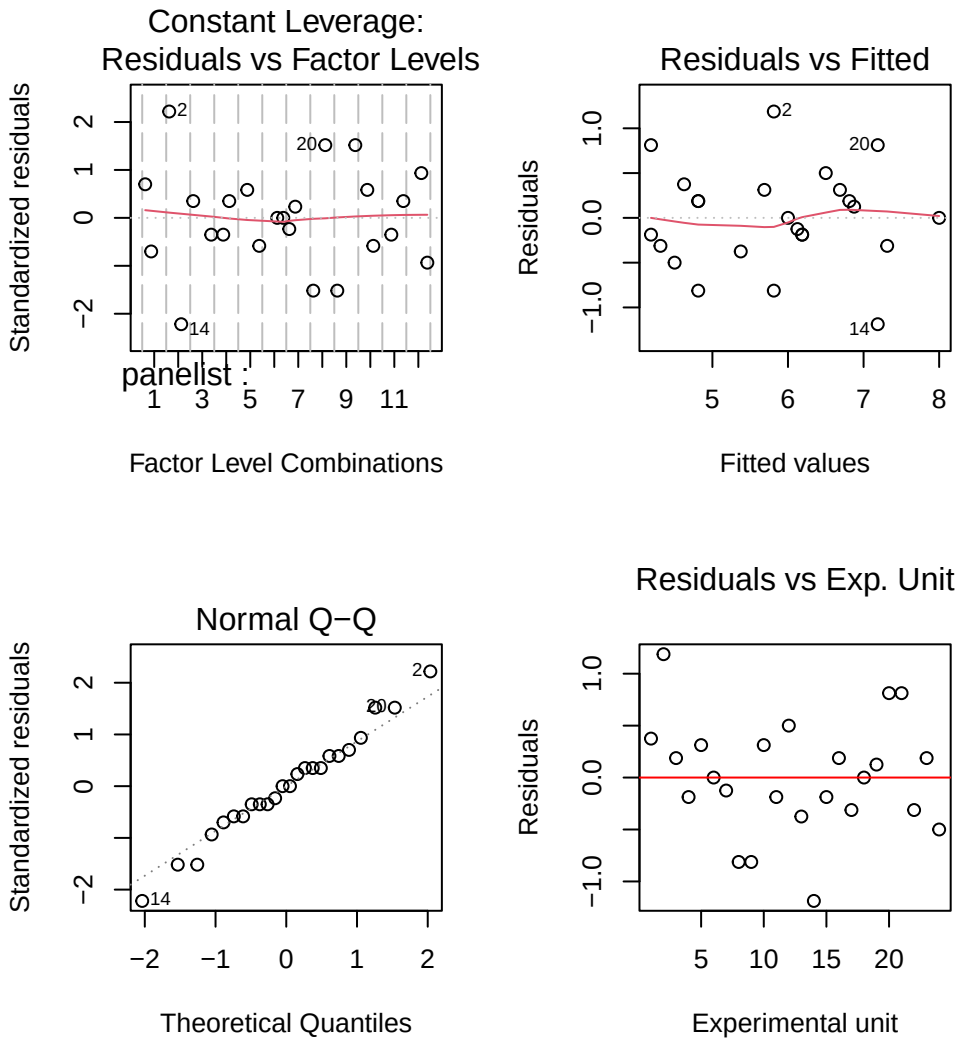
For intra-block analysis, the block must be fixed.
As we have an incomplete block design, we should use Type III sum of squares (or using Type I but being sure the block term comes first)

```
fit1 <- lm(score ~ panelist + recipe, data = taste, contrasts = list(recipe = contr.sum))
car::Anova(fit1, type = 'III')
```

```
## Anova Table (Type III tests)
##
## Response: score
##             Sum Sq Df F value    Pr(>F)
## (Intercept) 44.444  1 58.1818 3.232e-05 ***
## panelist     7.458 11  0.8876   0.58110
## recipe       9.125  3  3.9818   0.04649 *
## Residuals    6.875  9
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The recipe is significant, using a significance level of $\alpha = 0.05$.

```
par(mfrow = c(2, 2))
plot(fit1, which = 5)
plot(fit1, which = 1)
plot(fit1, which = 2)
plot(residuals(fit1) ~ rownames(taste), main = 'Residuals vs Exp. Unit',
     font.main = 1, data = taste, xlab = 'Experimental unit', ylab = 'Residuals')
abline(h = 0, col = 'red')
```



Seems we have homogeneity of variance across levels and also constant variability in residuals vs fitted plot. The residuals are normally distributed. The residuals vs exp. unit plot seems to have an horizontal pattern too.

```
emmeans::emmeans(fit1, pairwise ~ recipe, adjust = 'Tukey')
```

```
## $emmeans
##  recipe emmean    SE df lower.CL upper.CL
##  A        5.46 0.418  9     4.51     6.40
##  B        6.21 0.418  9     5.26     7.15
##  C        6.83 0.418  9     5.89     7.78
##  D        4.83 0.418  9     3.89     5.78
##
## Results are averaged over the levels of: panelist
## Confidence level used: 0.95
##
## $contrasts
```

```
##  contrast estimate    SE df t.ratio p.value
##  A - B      -0.750 0.618  9  -1.214  0.6342
##  A - C      -1.375 0.618  9  -2.225  0.1882
##  A - D       0.625 0.618  9   1.011  0.7472
##  B - C      -0.625 0.618  9  -1.011  0.7472
##  B - D       1.375 0.618  9   2.225  0.1882
##  C - D       2.000 0.618  9   3.236  0.0421
##
## Results are averaged over the levels of: panelist
## P value adjustment: tukey method for comparing a family of 4 estimates
```

The C recipe has slighly higher score than D (p-value < 0.05), but all the other pairwise comparions aren't significant.

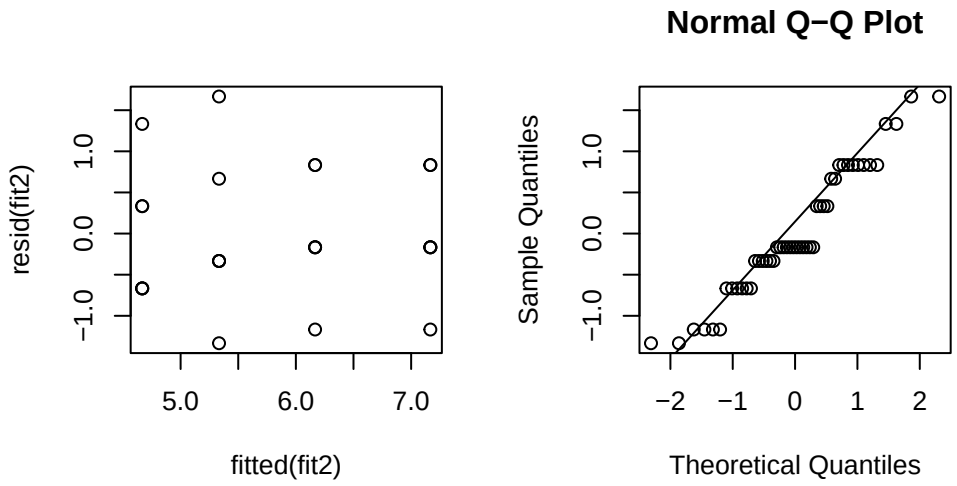
For the inter-block analysis, the block should be random.

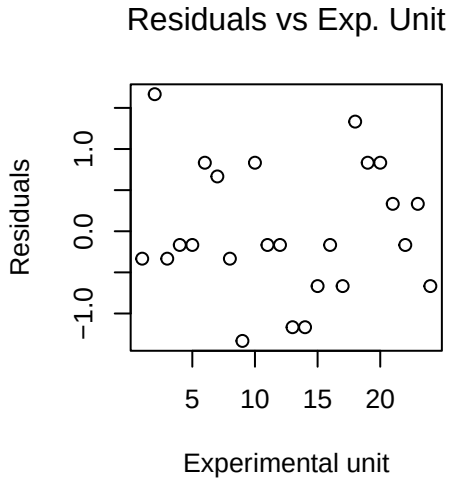
```
library(nlme)
fit2 <- lme(
  score ~ recipe,
  random = ~ 1 | panelist,
  data = taste
)
anova(fit2)
```

```
##             numDF denDF   F-value p-value
## (Intercept)     1    11 1139.5349  <.0001
## recipe          3     9    9.7674  0.0034
```

Again, now using a mixed model, the recipe is significant using a significance level of $\alpha = 0.05$.

```
par(mfrow = c(2, 2))
plot(resid(fit2) ~ fitted(fit2))
qqnorm(fit2$residuals)
qqline(fit2$residuals)
plot(residuals(fit2) ~ rownames(taste), main = 'Residuals vs Exp. Unit',
     font.main = 1, data = taste, xlab = 'Experimental unit', ylab = 'Residuals')
```





Seems the residuals are still good and the model adequate, although the QQ-normal plot was better in the fixed model.

```
emmeans::emmeans(fit2, pairwise ~ recipe, adjust = 'Tukey')
```

```
## $emmeans
##  recipe emmean    SE df lower.CL upper.CL
##  A        5.33 0.346 11     4.57     6.09
##  B        6.17 0.346  9     5.38     6.95
##  C        7.17 0.346  9     6.38     7.95
##  D        4.67 0.346  9     3.88     5.45
##
## Degrees-of-freedom method: containment
## Confidence level used: 0.95
##
## $contrasts
##  contrast estimate    SE df t.ratio p.value
```

```
##  A - B      -0.833 0.489  9  -1.705  0.3750
##  A - C      -1.833 0.489  9  -3.751  0.0195
##  A - D       0.667 0.489  9   1.364  0.5494
##  B - C      -1.000 0.489  9  -2.046  0.2412
##  B - D       1.500 0.489  9   3.069  0.0541
##  C - D       2.500 0.489  9   5.115  0.0029
##
## Degrees-of-freedom method: containment
## P value adjustment: tukey method for comparing a family of 4 estimates
```

The expected marginal means are somewhat different from the fixed block model. For the C recipe, in this mixed model the EMM is 7.17, whereas for the fixed model it was 6.83.

For this mixed model, the recipe C is still significantly higher than D, but now the difference is 2.5, whereas in the fixed model it was 2.0. Now, the recipe C is also significantly higher than A, using significance level of $\alpha = 0.05$.

2. With the data set below, answer:.

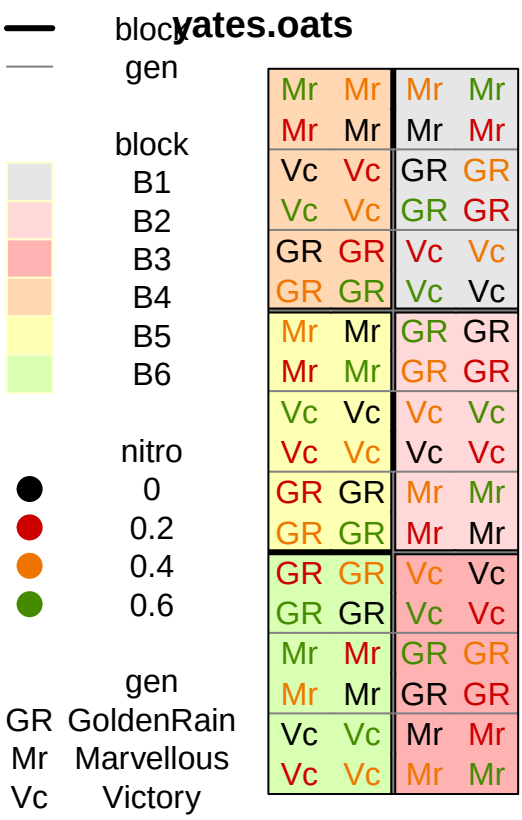
```
data(oats, package = "MASS")
?oats
str(oats)
```

```
## 'data.frame':    72 obs. of  4 variables:
##  $ B: Factor w/ 6 levels "I","II","III",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ V: Factor w/ 3 levels "Golden.rain",..: 3 3 3 3 1 1 1 1 2 2 ...
##  $ N: Factor w/ 4 levels "0.0cwt","0.2cwt",..: 1 2 3 4 1 2 3 4 1 2 ...
##  $ Y: int  111 130 157 174 117 114 161 141 105 140 ...
```

a) What design was used in the following experiment?
It's a split-plot design.
The varieties were applied to the **main** plots, whereas manurial treatments were applied in the **sub-plots**.

This same experiment is available in the `agridat` package, but without rows and columns information. For the sake of plotting for better visualize the experiment, let's check it:

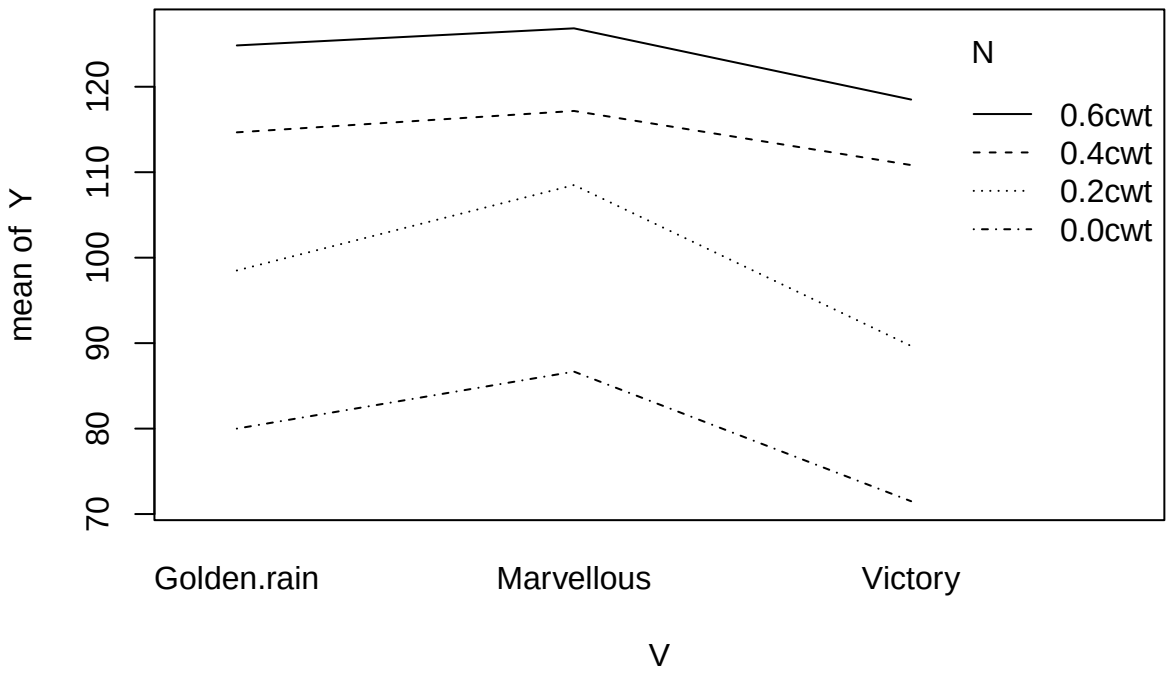
```
library(agridat)
library(desplot)
desplot(yates.oats, block ~ col+row,
        col=nitro, text=gen, cex=1, aspect=511/176,
        out1=block, out2=gen,
        out2.gpar=list(col = "gray50", lwd = 1, lty = 1))
```



The main plot is the variety (or genotype), and within this main plot we have sub-plots comprising all the 4 possible levels of manurial treatment level. The blocks form 3 main plots.

b) Run the appropriate analysis using both ANOVA and REML.

```
with(oats, interaction.plot(x.factor = V,
                            trace.factor = N,
                            response = Y))
```



Seems we don't have interaction between varieties and nitrogen doses because the lines are quite parallel.

Let's do ANOVA.
We have to add a error strata because in split-plot designs we have two error terms: one for the main-plot and another for the sub-plots.
When using block as random, the whole-plot error is `B + B:V` (not the Residual term as usual).

```
oats.random.block <- aov(Y ~ N * V + Error(B/V), data = oats)  # or Error(B + B:V)
oats.random.block
```

```
##
## Call:
## aov(formula = Y ~ N * V + Error(B/V), data = oats)
##
## Grand Mean: 103.9722
##
## Stratum 1: B
##
## Terms:
##                 Residuals
## Sum of Squares   15875.28
## Deg. of Freedom         5
##
## Residual standard error: 56.34763
##
## Stratum 2: B:V
##
```

```
## Terms:
##                         V Residuals
## Sum of Squares  1786.361  6013.306
## Deg. of Freedom        2        10
##
## Residual standard error: 24.52204
## 6 out of 8 effects not estimable
## Estimated effects may be unbalanced
##
## Stratum 3: Within
##
## Terms:
##                         N      N:V Residuals
## Sum of Squares  20020.50   321.75   7968.75
## Deg. of Freedom        3        6        45
##
## Residual standard error: 13.30727
## Estimated effects may be unbalanced
```

3. Design an experiment and present both the design and the layout (field map) for the following experiments:

a) To evaluate the effect of fertilization scheme and strawberry variety on fruit mass. Assume you have a 32 EU's available. The experiment consists of 8 different plots of land, 2 fertilization schemes, and 4 varieties.

b) An experiment to evaluate wine flavor. There are 42 brands of wine and 14 panelists.