# MA50259: Statistical Design of Investigations

## Lab sheet 8: Generalised complete block design

In this practical you will continue to learn about blocked designs. In each question, describe in detail (mathematically or conceptually) what the code is doing. You may want to run the code and observe the result to aid your answer!

## Generalized Complete Block Design

A design with replicates of each treatment level within a block is called a generalized complete block design or GCB. Since there are replicate experimental units for each treatment in each block, it is possible (there are enough degrees of freedom left) to fit the model with interactions between blocks and treatment factors. The model is given by

$$y_{ijk} = \mu + b_i + \tau_j + (b\tau)_{ij} + \epsilon_{ijk}$$

where

- $b_i$ are the block effects

- $\tau_i$ are the treatment level effects

- $(b\tau)_{ij}$ are the effects of the interaction between blocks and treatment effects

- All $\epsilon_{ijk} \sim N(0, \sigma^2)$ and are independent

Load the data for this lab using the following command:

```
library(tidyverse)
 GCB<-"http://people.bath.ac.uk/kai21/MA50259/Data/GCB.txt" %>% read.table(header=TRUE)
```

1.

```
colnames(GCB)
```

```
## [1] "response"  "block"     "treatment"
```

```
GCB$block
```

```
##    [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 3 3 3 3 3 3
##   [38] 3 3 3 3 3 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5
##   [75] 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 8 8 8 8 8
##  [112] 8 8 8 8 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
```

```
GCB$treatment
```

```
##    [1] 1 1 1 1 1 1 2 2 2 2 2 2 3 3 3 3 3 3 1 1 1 1 1 2 2 2 2 2 3 3 3 3 3 3 1 1 1
##   [38] 2 2 2 3 3 3 3 3 1 1 1 1 1 2 2 2 2 2 3 3 3 3 3 3 1 1 1 1 1 2 2 2 2 2 3 3 3
##   [75] 3 1 1 1 1 1 2 2 2 2 2 3 3 3 3 3 3 1 1 1 1 1 2 2 2 2 2 3 3 3 3 3 3 1 1 1 1 2
##  [112] 2 2 2 2 3 3 3 3 3 1 1 1 1 1 2 2 2 2 2 3 3 3 3 3
```

```
GCB$block<-as.factor(GCB$block)
GCB$treatment<-as.factor(GCB$treatment)
```

2.

```r
inter<-interaction(GCB$block,GCB$treatment,sep=":")
```

3.

```r
X1<-model.matrix(~block-1,GCB)
X2<-model.matrix(~treatment-1,GCB)
X3<-model.matrix(~inter-1)
X<-cbind(1,X1,X2,X3)
```

4.

```r
G<-ginv(t(X)%*%X)
y<-GCB$response
n<-length(y)
resid<-y-X%*%G%*%t(X)%*%y
ssE<-t(resid)%*%resid %>% as.vector
ssE
```

```
## [1] 7340.752
```

5.

```r
X0<-cbind(1,X1,X2)
G0<-ginv(t(X0)%*%X0)
resid0<-y-X0%*%G0%*%t(X0)%*%y
ssE0<-t(resid0)%*%resid0 %>% as.vector
```

6.

```r
X00<-cbind(1,X1)
G00<-ginv(t(X00)%*%X00)
resid00<-y-X00%*%G00%*%t(X00)%*%y
ssE00<-t(resid00)%*%resid00 %>% as.vector
```

7.

```r
# which hypotheses are being tested?
df1<-(rankMatrix(X)-rankMatrix(X0)) %>% as.numeric
df2<-(n-rankMatrix(X)) %>% as.numeric
Fval<-((ssE0-ssE)/df1)/((ssE)/df2)
Fval
```

```
## [1] 2.166491
```

```r
p_value<-pf(Fval,df1,df2,lower.tail = FALSE)
p_value
```

```
## [1] 0.01017868
```

8.

```r
# which hypotheses are being tested?
df1<-(rankMatrix(X0)-rankMatrix(X00)) %>% as.numeric
df2<-(n-rankMatrix(X)) %>% as.numeric
Fval<-((ssE00-ssE0)/df1)/((ssE)/df2)
Fval
```

```
## [1] 12.68158
```

```
p_value<-pf(Fval,df1,df2,lower.tail = FALSE)
p_value
```

```
## [1] 1.129655e-05
```

9.

```
# which hypotheses are being tested
df1<-(rankMatrix(X0)-rankMatrix(X00)) %>% as.numeric
df2<-(rankMatrix(X)-rankMatrix(X0)) %>% as.numeric
Fval<-((ssE00-ssE0)/df1)/((ssE0-ssE)/df2);Fval
```

```
## [1] 5.85351
```

```
p_value<-pf(Fval,df1,df2,lower.tail = FALSE);p_value
```

```
## [1] 0.01236634
```

10.

```
# relate this  to the answers in questions 7,8,9
aov(response~block*treatment,GCB) %>% summary
```

```
##                  Df Sum Sq Mean Sq F value  Pr(>F)
## block             8 124741   15593 229.406  < 2e-16 ***
## treatment         2   1724     862  12.682 1.13e-05 ***
## block:treatment  16   2356     147   2.166   0.0102 *
## Residuals       108   7341      68
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

11.

```
# relate this command to the answers in questions 7,8,9
aov(response~ treatment + Error(block/treatment), data = GCB) %>% summary
```

```
##
## Error: block
##           Df Sum Sq Mean Sq F value Pr(>F)
## Residuals  8 124741   15593
##
## Error: block:treatment
##           Df Sum Sq Mean Sq F value Pr(>F)
## treatment  2   1724   862.0   5.854 0.0124 *
## Residuals 16   2356   147.3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Error: Within
##            Df Sum Sq Mean Sq F value Pr(>F)
## Residuals 108   7341   67.97
```

12.

```
# relate this command to the answers in questions 7,8,9
summary_GCB<-GCB%>%
group_by(block,treatment) %>% summarise(response = mean(response))
```

```
## `summarise()` has grouped output by 'block'. You can override using the `.groups` argument.
```

```
aov( response ~block+ treatment,summary_GCB) %>% summary
```

```
##              Df Sum Sq Mean Sq F value   Pr(>F)
## block         8  24948  3118.5 105.888 2.19e-12 ***
## treatment     2    345   172.4   5.854   0.0124 *
## Residuals    16    471    29.5
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

13. Provide code to simulate your own GCB design with $b = 9$ blocks, $t = 3$ treatment levels and $r = 5$ replicates within each block. Use the model described at the start of this lab.