

# MTH 3220 Lab 4

Due Tue., Oct. 8

## 1 Part A: Multiple Comparisons after One-Factor ANOVA

### 1.1 Blood Coagulation Times Data Set (Cont'd from Lab 3)

After the null hypothesis is rejected in a one-factor ANOVA  $F$  test, *Tukey's multiple comparison procedure* can be used to decide *which* means differ from each other while holding the (overall) **familywise Type I error rate** at **0.05**.

The **coagulation times** (seconds) for samples of blood drawn from 24 animals receiving four different **diets, A, B, C, and D** from **Lab 3** are shown again below.

| Diet (Treatment) |    |    |    |
|------------------|----|----|----|
| A                | B  | C  | D  |
| 62               | 63 | 68 | 56 |
| 60               | 67 | 66 | 62 |
| 63               | 71 | 71 | 60 |
| 59               | 64 | 67 | 61 |
| 59               | 65 | 68 | 63 |
| 63               | 66 | 68 | 64 |
| 62               | 64 | 66 | 63 |
| 61               | 67 | 68 | 59 |

The data are in the file **blood.txt** *stacked* in the order in which the blood samples were drawn.

1. Save **blood.txt** and use `read.table()` (with `header = TRUE`) to read the data into a data frame called, say, `my.data`. **Hint:** Here is a little trick you can use:

```
# Select the file:
my.file <- file.choose()
# Look at the path name for the selected file:
my.file
# Read the data from the file:
my.data <- read.table(my.file, header = TRUE)
```

2. In **Lab 3**, you carried out a **one-factor ANOVA**:

```
my.anova <- aov(CoagTime ~ Diet, data = my.data)
summary(my.anova)

##           Df Sum Sq Mean Sq F value    Pr(>F)
```

```
## Diet      3  278.6   92.87   20.12 3.74e-07 ***
## Residuals 28  129.2    4.62
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The null hypothesis is rejected. We want to know *which* of the four diets differ in their mean coagulation times.

The function `TukeyHSD()` will carry out *Tukey's multiple comparison procedure*. Among its arguments are:

|                         |   |
|-------------------------|---|
| <code>x</code>          | an aov object   |
| <code>conf.level</code> | the confidence level for a confidence interval for the differences in population mean, with default value 0.95. |

Using your *aov* object `my.anova` from above, carry out *Tukey's multiple comparison procedure* by typing:

```
TukeyHSD(x = my.anova, conf.level = 0.95)
```