Analysis of Covariance, ANCOVA

Self-test answers

SELF-TEST: Use **R** to find out the mean and standard deviation of both the participant's libido and that of their partner in the three groups.

The easiest way to get these values is to use the function *stat.desc()* from the package *pastecs;* **R** will output a host of useful descriptive statistics). Therefore, by combining *by()* and *stat.desc()*, we can get a table of descriptives for each group by executing:

```
Library(pastecs)

by(viagraData$libido, viagraData$dose, stat.desc, basic = F)

by(viagraData$partnerLibido, viagraData$dose, stat.desc, basic = F)
```

Note we load the *pastecs* packages first; then we get descriptives for **libido** and **partnerLibido** using two separate commands (we use *basic = F* to remove some of the descriptives that don't interest us, the 'F' is for 'False').
 To get the descriptives for the variabes overall, we just use *stat.desc()* alone:

```
stat.desc(viagraData$libido, basic = F)

stat.desc(viagraData$partnerLibido, basic = F)
```

Your output will look like this:

SELF-TEST: Convert the variable **dose** into a factor such that the values 1, 2 and 3 correspond to Placebo, Low Dose and High Dose respectively**.**
SELF-TEST: Run a hierarchical regression analysis with **Libido** as the outcome. In the first block enter partner's libido (**Partner_Libido**) as a predictor, and then in a second block enter both dummy variables (Forced entry)**.**

To convert **dose** to a factor execute:

```
viagraData$dose<-factor(viagraData$dose, levels = c(1:3), labels = c("Placebo", "Low Dose", "High Dose"))
```

To create the multiple regression models execute:

```
viagraModel.1<-lm(libido~partnerLibido, data = viagraData)
```

```
viagraModel.2<-update(viagraModel.1, .~. + dose)
```

To see these models, execute:

```
anova(viagraModel.1, viagraModel.2)
```

```
summary(viagraModel.1)
```

```
summary(viagraModel.2)
```

- Use *ggplot2* to produce boxplots for the Viagra data. Try to recreate Figure 11.4.

This task is actually quite tricky because the data are not in the correct format. The data are currently in wide format, but we need them in long format, so we create a new datafile called *restructuredData* that has the data in the correct format using the *melt()* function from the *shape* package:

```
restructuredData<-melt(viagraData, id = c("dose"), measured = c("libido", "partnerLibido"))
names(restructuredData)<-c("dose", "libido_type", "libido")
```

This dataframe now looks like this:

```
    dose    libido_type libido
1    1           libido     3
2    1           libido     2
3    1           libido     5
4    1           libido     2
5    1           libido     2
6    1           libido     2
7    1           libido     7
8    1           libido     2
9    1           libido     4
10   2           libido     7
11   2           libido     5
12   2           libido     3
13   2           libido     4
14   2           libido     4
15   2           libido     7
16   2           libido     5
17   2           libido     4
18   3           libido     9
19   3           libido     2
20   3           libido     6
21   3           libido     3
22   3           libido     4
23   3           libido     4
24   3           libido     4
25   3           libido     6
26   3           libido     4
27   3           libido     6
28   3           libido     2
29   3           libido     8
30   3           libido     5
31   1 partnerLibido     4
32   1 partnerLibido     1
33   1 partnerLibido     5
34   1 partnerLibido     1
35   1 partnerLibido     2
36   1 partnerLibido     2
37   1 partnerLibido     7
38   1 partnerLibido     4
39   1 partnerLibido     5
```

```
40    2 partnerLibido       5
41    2 partnerLibido       3
42    2 partnerLibido       1
43    2 partnerLibido       2
44    2 partnerLibido       2
45    2 partnerLibido       6
46    2 partnerLibido       4
47    2 partnerLibido       2
48    3 partnerLibido       1
49    3 partnerLibido       3
50    3 partnerLibido       5
51    3 partnerLibido       4
52    3 partnerLibido       3
53    3 partnerLibido       3
54    3 partnerLibido       2
55    3 partnerLibido       0
56    3 partnerLibido       1
57    3 partnerLibido       3
58    3 partnerLibido       0
59    3 partnerLibido       1
60    3 partnerLibido       0
```

Note how participants and partners libido are now stacked in a single column (called **libido**) and that a new variable (**libido_type**) has been created that indicates whether the libido score relates to the participant (0) or the Partner (1).

Finally, we obtain the graph by executing:

```
boxplot <- ggplot(restructuredData, aes(dose, libido))
```

```
boxplot + geom_boxplot() + facet_wrap(~libido_type) + labs(x = "Dose", y = "Libido")
```

- Conduct an ANOVA to test whether partner's libido (our covariate) is independent of the dose of Viagra (our independent variable).

We can do this by executing these commands:

```
checkIndependenceModel<-aov(partnerLibido ~ dose, data = viagraData)
```

```
summary(checkIndependenceModel)
```

- Plot a scatterplot of **partnerLibido** against **libido**.

We can get the scatterplot by executing:

```
scatter <- ggplot(viagraData, aes(partnerLibido, libido))
```

```
scatter + geom_point(size = 3) + geom_smooth(method = "lm", alpha = 0.1) + labs(x =
"Partner's Libido", y = "Participant's Libido")
```

- Run a one-way ANOVA to see whether the three groups differ in their levels of libido.

We can compute this model by executing:

```
anovaModel<-aov(libido ~ dose, data = viagraData)
```

```
summary(anovaModel)
```

- Use *ggplot2* to recreate Figure 11.3.

Unlike the previous plot, which required a radical restructuring of the data, this one is much easier because we can use the original dataframe. The graph is created by executing the following commands:

```
scatter <- ggplot(viagraData, aes(partnerLibido, libido, colour = dose))
```

```
scatter + geom_point(aes(shape = dose), size = 3) + geom_smooth(method = "lm",
aes(fill = dose), alpha = 0.1) + labs(x = "Partner's Libido", y = "Participant's
Libido")
```

- Use *ggplot2* to produce boxplots for the invisibility data. Try to recreate Figure 11.7.

This task again requires us to restructure the data. The data currently look like this:

```
      cloak mischief1 mischief2 id
1   No Cloak         4        11   1
2   No Cloak         5         7   2
3   No Cloak         8         8   3
4   No Cloak         6         7   4
5   No Cloak         6        10   5
6   No Cloak         4         7   6
7   No Cloak         3        11   7
8   No Cloak         6         7   8
9   No Cloak         7        11   9
10  No Cloak         1         6  10
11  No Cloak         8         8  11
12  No Cloak         2         7  12
13  No Cloak         5         8  13
14  No Cloak         6         9  14
15  No Cloak         2         9  15
16  No Cloak         5        10  16
17  No Cloak         0         6  17
18  No Cloak         4        10  18
19  No Cloak         5         9  19
20  No Cloak         5         8  20
21  No Cloak         2         7  21
22  No Cloak         3         7  22
23  No Cloak         5         9  23
24  No Cloak         7        12  24
25  No Cloak         5        10  25
26  No Cloak         7        10  26
27  No Cloak         4         9  27
28  No Cloak         4         9  28
29  No Cloak         4        11  29
30  No Cloak         1         9  30
31  No Cloak         3         8  31
32  No Cloak         3         6  32
33  No Cloak         5        12  33
34  No Cloak         4        10  34
35     Cloak         1        10  35
36     Cloak         7        10  36
37     Cloak         7         9  37
38     Cloak         6        12  38
39     Cloak         9        11  39
40     Cloak         5         5  40
41     Cloak         4        13  41
42     Cloak        10        12  42
43     Cloak         7        13  43
44     Cloak         7        10  44
45     Cloak         2        12  45
46     Cloak         2        12  46
47     Cloak         4        10  47
48     Cloak         6        12  48
49     Cloak         4        11  49
50     Cloak         6        11  50
51     Cloak         5        12  51
```

```
52    Cloak         1        7 52
53    Cloak         6        9 53
54    Cloak         3        8 54
55    Cloak         2       13 55
56    Cloak         4       10 56
57    Cloak         1        9 57
58    Cloak         2       10 58
59    Cloak         2        8 59
60    Cloak         3        8 60
61    Cloak         6       13 61
62    Cloak         1        6 62
63    Cloak         6       11 63
64    Cloak         6        9 64
65    Cloak         6        8 65
66    Cloak         5       11 66
67    Cloak         6       10 67
68    Cloak         1       10 68
69    Cloak         7        9 69
70    Cloak         6       13 70
71    Cloak         5        9 71
72    Cloak         7       12 72
73    Cloak         6       10 73
74    Cloak         4        9 74
75    Cloak         4       13 75
76    Cloak         7        9 76
77    Cloak         2       10 77
78    Cloak         3        8 78
79    Cloak         6       10 79
80    Cloak         0       10 80
```

The data are currently in wide format, but we need them in long format, so we create a new datafile called *restructuredData* that has the data in the correct format:

```
restructuredData<-melt(invisibilityData, id = c("cloak"), measured = c("mischief1",
"mischief2"))
names(restructuredData)<-c("cloak", "Time", "mischief")
```

The data now look like this:

```
       cloak      Time mischief
1   No Cloak mischief1        4
2   No Cloak mischief1        5
3   No Cloak mischief1        8
4   No Cloak mischief1        6
5   No Cloak mischief1        6
6   No Cloak mischief1        4
7   No Cloak mischief1        3
8   No Cloak mischief1        6
9   No Cloak mischief1        7
10  No Cloak mischief1        1
11  No Cloak mischief1        8
12  No Cloak mischief1        2
13  No Cloak mischief1        5
14  No Cloak mischief1        6
15  No Cloak mischief1        2
16  No Cloak mischief1        5
17  No Cloak mischief1        0
18  No Cloak mischief1        4
19  No Cloak mischief1        5
20  No Cloak mischief1        5
21  No Cloak mischief1        2
22  No Cloak mischief1        3
23  No Cloak mischief1        5
24  No Cloak mischief1        7
25  No Cloak mischief1        5
26  No Cloak mischief1        7
27  No Cloak mischief1        4
28  No Cloak mischief1        4
29  No Cloak mischief1        4
30  No Cloak mischief1        1
31  No Cloak mischief1        3
32  No Cloak mischief1        3
33  No Cloak mischief1        5
34  No Cloak mischief1        4
35     Cloak mischief1        1
36     Cloak mischief1        7
```

```
37        Cloak mischief1          7
38        Cloak mischief1          6
39        Cloak mischief1          9
40        Cloak mischief1          5
41        Cloak mischief1          4
42        Cloak mischief1         10
43        Cloak mischief1          7
44        Cloak mischief1          7
45        Cloak mischief1          2
46        Cloak mischief1          2
47        Cloak mischief1          4
48        Cloak mischief1          6
49        Cloak mischief1          4
50        Cloak mischief1          6
51        Cloak mischief1          5
52        Cloak mischief1          1
53        Cloak mischief1          6
54        Cloak mischief1          3
55        Cloak mischief1          2
56        Cloak mischief1          4
57        Cloak mischief1          1
58        Cloak mischief1          2
59        Cloak mischief1          2
60        Cloak mischief1          3
61        Cloak mischief1          6
62        Cloak mischief1          1
63        Cloak mischief1          6
64        Cloak mischief1          6
65        Cloak mischief1          6
66        Cloak mischief1          5
67        Cloak mischief1          6
68        Cloak mischief1          1
69        Cloak mischief1          7
70        Cloak mischief1          6
71        Cloak mischief1          5
72        Cloak mischief1          7
73        Cloak mischief1          6
74        Cloak mischief1          4
75        Cloak mischief1          4
76        Cloak mischief1          7
77        Cloak mischief1          2
78        Cloak mischief1          3
79        Cloak mischief1          6
80        Cloak mischief1          0
81  No Cloak mischief2         11
82  No Cloak mischief2          7
83  No Cloak mischief2          8
84  No Cloak mischief2          7
85  No Cloak mischief2         10
86  No Cloak mischief2          7
87  No Cloak mischief2         11
88  No Cloak mischief2          7
89  No Cloak mischief2         11
90  No Cloak mischief2          6
91  No Cloak mischief2          8
92  No Cloak mischief2          7
93  No Cloak mischief2          8
94  No Cloak mischief2          9
95  No Cloak mischief2          9
96  No Cloak mischief2         10
97  No Cloak mischief2          6
98  No Cloak mischief2         10
99  No Cloak mischief2          9
100 No Cloak mischief2          8
101 No Cloak mischief2          7
102 No Cloak mischief2          7
103 No Cloak mischief2          9
104 No Cloak mischief2         12
105 No Cloak mischief2         10
106 No Cloak mischief2         10
107 No Cloak mischief2          9
108 No Cloak mischief2          9
109 No Cloak mischief2         11
110 No Cloak mischief2          9
111 No Cloak mischief2          8
112 No Cloak mischief2          6
113 No Cloak mischief2         12
114 No Cloak mischief2         10
115       Cloak mischief2         10
```

```
116    Cloak mischief2        10
117    Cloak mischief2         9
118    Cloak mischief2        12
119    Cloak mischief2        11
120    Cloak mischief2         5
121    Cloak mischief2        13
122    Cloak mischief2        12
123    Cloak mischief2        13
124    Cloak mischief2        10
125    Cloak mischief2        12
126    Cloak mischief2        12
127    Cloak mischief2        10
128    Cloak mischief2        12
129    Cloak mischief2        11
130    Cloak mischief2        11
131    Cloak mischief2        12
132    Cloak mischief2         7
133    Cloak mischief2         9
134    Cloak mischief2         8
135    Cloak mischief2        13
136    Cloak mischief2        10
137    Cloak mischief2         9
138    Cloak mischief2        10
139    Cloak mischief2         8
140    Cloak mischief2         8
141    Cloak mischief2        13
142    Cloak mischief2         6
143    Cloak mischief2        11
144    Cloak mischief2         9
145    Cloak mischief2         8
146    Cloak mischief2        11
147    Cloak mischief2        10
148    Cloak mischief2        10
149    Cloak mischief2         9
150    Cloak mischief2        13
151    Cloak mischief2         9
152    Cloak mischief2        12
153    Cloak mischief2        10
154    Cloak mischief2         9
155    Cloak mischief2        13
156    Cloak mischief2         9
157    Cloak mischief2        10
158    Cloak mischief2         8
159    Cloak mischief2        10
160    Cloak mischief2        10
```

Finally, we obtain the graph by executing:

```
boxplot <- ggplot(restructuredData, aes(cloak, mischief))
```

```
boxplot + geom_boxplot() + facet_wrap(~Time) + labs(x = "Cloak of Invisibility", y =
"Number of Mischievous Acts")
```

- Create a standard ANCOVA model of these data. What conclusions can you draw?

First we want to do a Levene's test to see whether the variance in **mischief2** (the outcome) varies across groups that received the cloak or not (**cloak**), we can execute:

```
leveneTest(invisibilityData$mischief2, invisibilityData$cloak, center = median)
```

The output shows that Levene's test is very non-significant, $F(1, 78) = 0.03$, $p = .86$. This means that for these data the variances are very similar (hence the high probability value). The assumption of homogeneity of variance seems to be met.

```
Levene's Test for Homogeneity of Variance
      Df F value Pr(>F)
group  1  0.0307 0.8615
      78
```

Next we should check that the covariate is independent from the experimental manipulation. In this case, the proposed covariate is baseline mischief (**mischief1**), and we need to check that this variable was roughly equal across levels of our independent variable (**cloak**). We

can test this by running an ANOVA with **mischief1** as the outcome and **cloak** as the predictor:

```
checkIndependenceModel<-aov(mischief1 ~ cloak, data = invisibilityData)
```

```
summary(checkIndependenceModel)
```

```
summary.lm(checkIndependenceModel)
```

The main effect of **cloak** is not significant, $F(1, 78) = 0.14$, $p = .71$, which shows that the average level of mischief at baseline was roughly the same in the two experimental groups. This result means that it is appropriate to use baseline mischief as a covariate in the analysis.

```
            Df Sum Sq Mean Sq F value Pr(>F)
cloak        1   0.65  0.6537  0.1351 0.7142
Residuals   78 377.33  4.8376
```

To create the ANCOVA the model we execute:

```
invisibilityModel<-aov(mischief2~ mischief1 + cloak, data = invisibilityData)
```

```
Anova(invisibilityModel, type = "III")
```

Looking first at the significance values, it is clear that the covariate significantly predicts the dependent variable, because the significance value is less than .05. Therefore, the tendency for mischief after the experimental manipulation was influenced by their baseline tendency for mischief (as you might expect). What's more interesting is that when the effect of baseline mischief is removed, the effect of having a cloak of invisibility is significant (p is .001 which is less than .05).

```
Anova Table (Type III tests)

Response: mischief2
            Sum Sq Df  F value     Pr(>F)
(Intercept) 735.10  1 236.7522 < 2.2e-16 ***
mischief1    22.97  1   7.3985  0.008065 **
cloak        35.17  1  11.3259  0.001194 **
Residuals   239.08 77
```

We can get the adjusted means by executing:

```
adjustedMeans<-effect("cloak", invisibilityModel, se = TRUE)
```

```
summary(adjustedMeans)
```

```
adjustedMeans$se
```

The adjusted means (and their confidence intervals) show that there was significantly mode mischief in those with a cloak of invisibility than those who were just told that the cameras would be switched off.

```
cloak effect
cloak
No Cloak    Cloak
 8.79065 10.13300

 Lower 95 Percent Confidence Limits
cloak
No Cloak    Cloak
8.188603 9.615469

 Upper 95 Percent Confidence Limits
cloak
 No Cloak     Cloak
 9.392696 10.650527

> adjustedMeans$se
       81        82
0.3023456 0.2599009
```

To get the regression parameter for the covariate we can execute:

```
summary.lm(invisibilityModel)
```

If the *b*-value for the covariate is positive then it means that the covariate and the outcome variable have a positive relationship (as the covariate increases, so does the outcome). If the *b*-value is negative it means the opposite: that the covariate and the outcome variable have a negative relationship (as the covariate increases, the outcome decreases). For these data the *b*-value is positive (*b* = 0.25), indicating that as the natural tendency for mischief (baseline) increases so does the tendency for mischief after the experimental manipulation:

```
Coefficients:
               Estimate Std. Error t value Pr(>|t|)
(Intercept)     7.68342    0.49935  15.387  < 2e-16 ***
mischief1       0.24674    0.09071   2.720  0.00807 **
cloak[T.Cloak]  1.34235    0.39887   3.365  0.00119 **
```

We can look at the graphs of the model by executing:

```
plot(invisibilityModel)
```

The left plot does not show any substantial funneling (although the fitted line is not perfectly flat) which implies that the residuals are probably not heteroscedastic. The second plot (on the right) is a Q-Q plot, which tells us about the normality of residuals in the model. We want our residuals to be normally distributed which means that the dots on the graph should hover around the diagonal line. On ours, these is some deviation form the line.
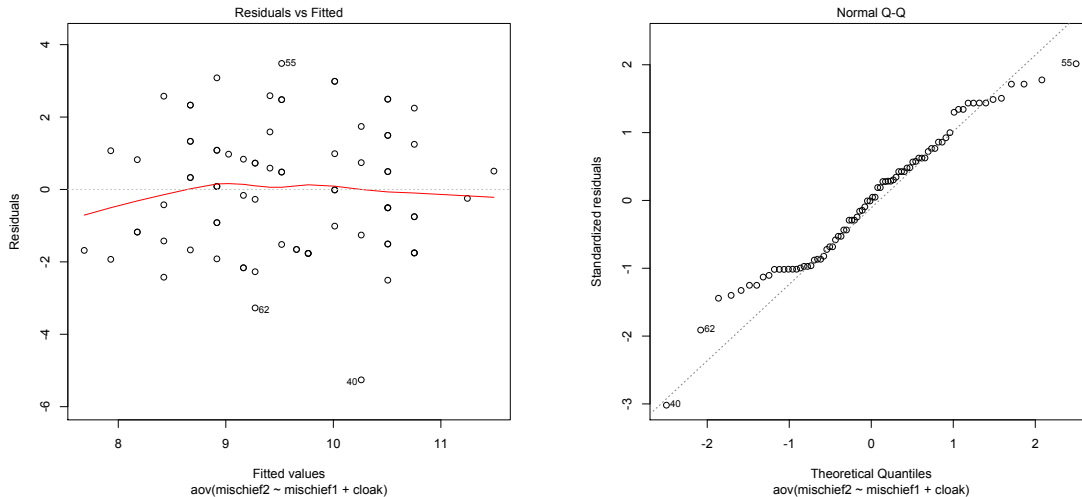
To test the assumption of homogeneity of regression slopes we execute:

```
hoRS<-update(invisibilityModel, .~. + mischief1:cloak)
```

```
Anova(hoRS, type = "III")
```

The output shows that the interaction between **cloak** and **mischief1** (the covariate) is not significant, which means that we can assume homogeneity of regression slopes.

```
Response: mischief2
                Sum Sq Df F value    Pr(>F)
(Intercept)    301.863  1 96.3849 3.681e-15 ***
mischief1       13.167  1  4.2044   0.04377 *
cloak           11.888  1  3.7958   0.05507 .
mischief1:cloak  1.060  1  0.3385   0.56244
Residuals      238.021 76
```

Labcoat Leni's Real Research

Space Invaders

Problem

Muris, P. et al. (2008). *Child Psychiatry and Human Development*, *39*, 469-480.

Anxious people tend to interpret ambiguous information in a negative way. For example, being highly anxious myself, if I overheard a student saying 'Andy Field's lectures are really *different*' I would assume that 'different' meant rubbish, but it could also mean 'refreshing' or 'innovative'. One current mystery is how these interpretational biases develop in children. Peter Muris and his colleagues addressed this issue in an ingenious study. Children did a task in which they imagined that they were astronauts who had discovered a new planet. Although the planet was similar to Earth, some things were different. They were given some scenarios about their time on the planet (e.g. 'On the street, you encounter a spaceman. He has a sort of toy handgun and he fires at you …') and the child had to decide which of two outcomes occurred. One outcome was positive ('You laugh: it is a water pistol and the weather is fine anyway') and the other negative ('Oops, this hurts! The pistol produces a red beam which burns your skin!'). After each response the child was told whether their choice was correct. Half of the children were *always* told that the negative interpretation was correct, and the reminder were told that the positive interpretation was correct.

Over 30 scenarios children were trained to interpret their experiences on the planet as negative or positive. Muris et al. then gave children a standard measure of interpretational biases in everyday life to see whether the training had created a bias to interpret things negatively. In doing so, they could ascertain whether children learn interpretational biases through feedback (e.g. from parents) about how to disambiguate ambiguous situations.

The data from this study are in the file **Muris et al. (2008).dat**. The independent variable is **Training** (positive or negative) and the outcome was the child's interpretational bias score (**Interpretational_Bias**)—a high score reflects a tendency to interpret situations negatively. It is important to factor in the **Age** and **Gender** of the child and also their natural anxiety level (which they measured with a standard questionnaire of child anxiety called the **SCARED**) because these things affect interpretational biases also. Labcoat Leni wants you to carry out a one-way ANCOVA on these data to see whether **Training** significantly affected children's **Interpretational_Bias** using **Age**, **Gender** and **SCARED** as covariates. What can you conclude?

Solution

First of all, load in the data:

```
murisData<-read.delim("Muris et al. (2008).dat", header = TRUE)
```

Next we can make the variable **Training** a factor, with two levels (Negative Training and Positive Training):

```
murisData$Training<-factor(murisData$Training, levels = c(1:2), labels = c("Negative Training", "Positive Training"))
```

We also need to make the **Gender** variable a factor, with two levels (boy and girl):

```
murisData$Gender<-factor(murisData$Gender, levels = c(1:2), labels = c("Boy", "Girl"))
```

We can now conduct a normal ANCOVA:

First we want to do a Levene's test to see whether the variance in **Interpretational_Bias** (the outcome) varies across the interaction of the variables; training (**Training**), age (**Age**), gender (**Gender**) and anxiety (**SCARED**) groups. To do this can execute:

```
leveneTest(murisData$Interpretational_Bias, interaction(murisData$Gender,
murisData$Age, murisData$SCARED, murisData$Training), center = median)
```

```
Levene's Test for Homogeneity of Variance
      Df F value Pr(>F)
group 62  0.1902      1
       7
```

The output shows that Levene's test is non-significant, $F(62, 7) = 0.19$, $p > .05$. This means that for these data the variances are very similar (hence the high probability value). The assumption of homogeneity of variance seems to be met.

Let's look at the ANOVA output before entering any of the covariates:

```
murisModel<-aov(Interpretational_Bias ~ Training, data = murisData)
summary(murisModel)

    Df Sum Sq Mean Sq F value   Pr(>F)
Training    1  25986 25986.4  11.747 0.001039 **
Residuals  68 150431  2212.2
```

The above output shows a significant effect of training on interpretational bias scores without taking the effects of age, gender or SCARED into account.

Next we should check that the covariates are independent from the experimental manipulation. In this case, the proposed covariates are **Age**, **Gender** and **SCARED** and we need to check that these variables were roughly equal across levels of our independent variable (**Training**). We can test this by running an ANOVA with **age**, **gender** and **SCARED** as the outcomes and **Training** as the predictor:

```
checkIndependenceModel.1<-aov(Age ~Training, data = murisData)
checkIndependenceModel.2<-aov(Gender ~Training, data = murisData)
checkIndependenceModel.3<-aov(SCARED ~Training, data = murisData)

summary(checkIndependenceModel.1)


           Df Sum Sq Mean Sq F value Pr(>F)
Training    1  0.525 0.52456  0.6677  0.4167
Residuals  68 53.418 0.78556

summary(checkIndependenceModel.2)


           Df  Sum Sq Mean Sq F value  Pr(>F)
Training    1  0.1311 0.13114  0.5138  0.4759
Residuals  68 17.3546 0.25521

summary(checkIndependenceModel.3)


           Df Sum Sq Mean Sq F value   Pr(>F)
Training    1   10.0   9.965  0.1021  0.7503
Residuals  68 6638.7  97.628
```

None of the main effects were significant, all ps > .05, which shows that the average level of all the covariates (Age, Gender and SCARED) were roughly the same in the two experimental groups. This result means that it is appropriate to use Age, Gender and SCARED as covariates in the analysis.

Next we can create the ANCOVA model. Remember that if we want to use Type III sums of squares, we have to set some orthogonal contrasts - even though it seems a little pointless as both of the categorical variables (**gender** and **training**) have only two groups- to do this we can execute:

```
contrasts(murisData$Gender)<-c(-1,1)
```

```
contrasts(murisData$Training)<-c(-1,1)
murisModel<-aov(Interpretational_Bias~SCARED + Age + Gender + Training, data =
 murisData)
Anova(murisModel, type = "III")
```

```
Response: Interpretational_Bias
            Sum Sq Df F value     Pr(>F)
(Intercept)  12296  1  7.4590 0.0081165 **
SCARED       26400  1 16.0157 0.0001636 ***
Age           2643  1  1.6036 0.2099092
Gender       11083  1  6.7236 0.0117414 *
Training     22129  1 13.4248 0.0005010 ***
Residuals   107147 65
```

We can see that even after partialling out the effects of age, gender and natural anxiety, the training had a significant effect on the subsequent bias score, $F(1, 65) = 13.42$, $p < .001$. In terms of the covariates, age did not significantly influence the acquisition of interpretational biases. However, both anxiety and gender did.

We can get the adjusted means by executing:

```
adjustedMeans<-effect("Training", murisModel, se = TRUE)
```

```
summary(adjustedMeans)
```

```
adjustedMeans$se
```

The adjusted means (and their confidence intervals) tell us that interpretational biases were stronger (higher) after negative training. This result is as expected. It seems then that giving children feedback that tells them to interpret ambiguous situations negatively does induce an interpretational bias that persists into everyday situations, which is an important step towards understanding how these biases develop.

```
 Training effect
 Training
 Negative Training Positive Training
        144.6175          108.5835

  Lower 95 Percent Confidence Limits
 Training
 Negative Training Positive Training
        130.61893          94.98436

  Upper 95 Percent Confidence Limits
 Training
 Negative Training Positive Training
        158.6160          122.1827
 adjustedMeans$se
 [1] 7.009296 6.809317
```

To get the regression parameter for the covariate we can execute:

```
summary.lm(murisModel)
```

If we look at the parameter estimates below, we can use the beta values to interpret the effects. For anxiety (**SCARED**), $b = 2.01$, which reflects a positive relationship. Therefore, as anxiety increases, the interpretational bias increases also (this is what you would expect because anxious children would be more likely to naturally interpret ambiguous situations in a negative way). If you draw a scatterplot of the relationship between **SCARED** and **Interpretational_Bias** you'll see a very nice positive relationship. For **Gender** (GenderGirl) $b = 26.12$, Therefore, girls show a stronger natural tendency to interpret ambiguous situations negatively. This is consistent with the anxiety literature, which shows that females are more likely to have anxiety disorders.

One important thing to remember is that although anxiety and gender naturally affected whether children interpreted ambiguous situations negatively, the training (the experiences on the alien planet) had an effect above and beyond these natural tendencies (in other words, the effects of training cannot be explained by gender of natural anxiety levels in the sample).

```
 Coefficients:
                        Estimate Std. Error t value Pr(>|t|)
```

```
(Intercept)                   168.6465    61.7499   2.731 0.008117 **
SCARED                          2.0071     0.5015   4.002 0.000164 ***
Age                            -7.2781     5.7473  -1.266 0.209909
GenderGirl                     26.1207    10.0736   2.593 0.011741 *
TrainingPositive Training     -36.0340     9.8346  -3.664 0.000501 ***
```

We can look at the graphs of the model by executing:

```
plot(murisModel)
```

The left plot does not show any substantial funneling (although the fitted line is not perfectly flat) which implies that the residuals are probably not heteroscedastic. The second plot (on the right) is a Q-Q plot, which tells us about the normality of residuals in the model. We want our residuals to be normally distributed which means that the dots on the graph should hover around the diagonal line. On ours, there is some slight deviation form the line.
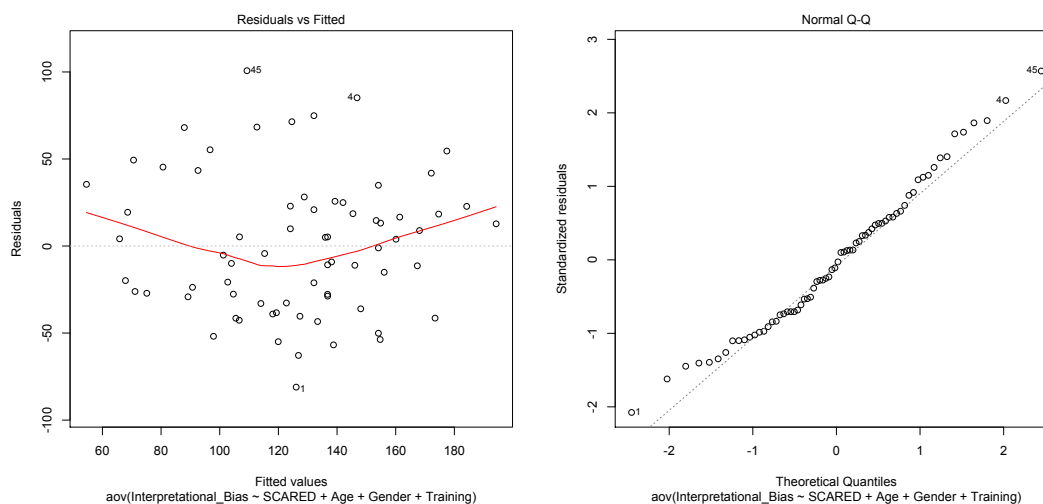
To test the assumption of homogeneity of regression slopes we execute:

```
hoRS<-update(murisModel, .~. + SCARED:Training + Age:Training + Gender:Training)

Anova(hoRS, type = "III")
```

The output shows that none of the interactions between the covariates and the predictor were significant, which means that we can assume homogeneity of regression slopes.

```
Anova Table (Type III tests)

Response: Interpretational_Bias
                Sum Sq Df F value    Pr(>F)
(Intercept)       3360  1  2.0880 0.1534996
SCARED           24432  1 15.1836 0.0002419 ***
Age               1004  1  0.6240 0.4325727
Gender            8307  1  5.1628 0.0265545 *
Training           440  1  0.2732 0.6030528
SCARED:Training   6366  1  3.9561 0.0511191 .
Age:Training       532  1  0.3307 0.5673025
Gender:Training      1  1  0.0004 0.9834079
Residuals        99763 62
```

Have a look at the original article to see how Muris et al. reported the results of this analysis – this can help you to see how you can report your own data from an ANCOVA. (One bit of good practice that you should note is that they report effect sizes from their analysis – as you will see from the book chapter this is an excellent thing to do).

Smart Alex's Solutions

Task 1

- Stalking is a very disruptive and upsetting (for the person being stalked) experience in which someone (the stalker) constantly harasses or obsesses about another person. It can take many forms, from sending intensely disturbing letters threatening to boil your cat if you don't reciprocate the stalker's undeniable love for you, to literally following you around your local area in a desperate attempt to see which CD you buy on a Saturday (as if it would be anything other than Fugazi!). A psychologist, who'd had enough of being stalked by people, decided to try two different therapies on different groups of stalkers (25 stalkers in each group—this variable is called **Group**). To the first group of stalkers he gave what he termed cruel-to-be-kind therapy. This therapy was based on punishment for stalking behaviours; in short, every time the stalkers followed him around, or sent him a letter, the psychologist attacked them with a cattle prod until they stopped their stalking behaviour. It was hoped that the stalkers would learn an aversive reaction to anything resembling stalking. The second therapy was psychodyshamic therapy, which is a recent development on Freud's psychodynamic therapy that acknowledges what a sham this kind of treatment is (so you could say it's based on Fraudian theory!). The stalkers were hypnotised and regressed into their childhood, the therapist would also discuss their penis (unless it was a woman, in which case they discussed their lack of penis), the penis of their father, their dog's penis, the penis of the cat down the road and anyone else's penis that sprang to mind. At the end of therapy, the psychologist measured the number of hours in the week that the stalker spent stalking their prey (this variable is called **stalk2**). Now, the therapist believed that the success of therapy might well depend on how bad the problem was to begin with, so before therapy the therapist measured the number of hours that the patient spent stalking as an indicator of how much of a stalker the person was (this variable is called **stalk1**). The data are in the file **Stalker.dat**. Analyse the effect of therapy on stalking behaviour after therapy, controlling for the amount of stalking behaviour before therapy.

The first thing we need to do is load in the data, so assuming you have set your working directory to where the **Stalker.dat** data are then we can execute the following command:

```
stalkerData<-read.delim("Stalker.dat", header = TRUE)
```

Next, we can set the variable **group** to be a factor, with two levels "Cruel to be Kind Therapy" and "Psychodyshamic Therapy":

```
stalkerData$group<-factor(stalkerData$group, levels = c(1:2), labels = c("Cruel to be Kind Therapy", "Psychodyshamic Therapy"))
```

Next, we could create some boxplots, but don't forget that we need to restructure the data first:

```
restructuredData<-melt(stalkerData, id = c("group"), measured = c("stalk1", "stalk2"))
names(restructuredData)<-c("group", "Time", "Stalk")
```

```
boxplot <- ggplot(restructuredData, aes(group, Stalk))
 boxplot + geom_boxplot() + facet_wrap(~Time) + labs(x = "Type of Therapy", y = "Number of Hours Spent Stalking")
```
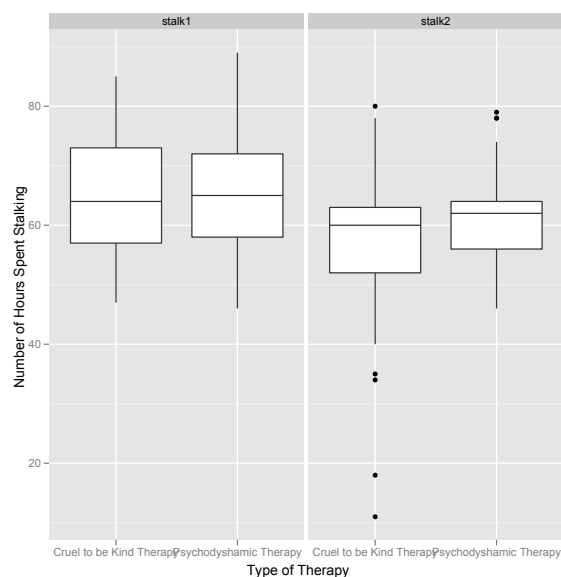
The boxplots show that the number of hours spent stalking were comparable at baseline (stalk1) and decreased in both groups. The whiskers show that the spread of scores is greater for the participants who received cruel to be kind therapy.

Let's have a look at the ANOVA when the covariate is not included by executing:

```
stalkerModel.1<-aov(stalk2~ group, data = stalkerData)
```

```
          Df Sum Sq Mean Sq F value  Pr(>F)
group      1  591.7  591.68  3.3309 0.07421
Residuals 48 8526.3  177.63
```

It is clear from the significance value that there is no difference in the hours spent stalking after therapy for the two therapy groups (p is .074, which is greater than .05). You should note that the total amount of variation to be explained (SS_T) was 9118 (591.68 + 8526.32), of which the experimental manipulation accounted for 591.68 units (SS_M), while 8526.32 were unexplained (SS_R).

We can now conduct a normal ANCOVA:

First we want to do a Levene's test to see whether the variance in **stalking behaviour** (the outcome) varies across the interaction of different groups experiencing different types of therapy (**group**) and the number of hours spent stalking before therapy (**stalk1**). To do this we can execute:

```
leveneTest(stalkerData$stalk2, interaction(stalkerData$group, stalkerData$stalk1),
center = median)
```

```
      Levene's Test for Homogeneity of Variance
      Df     F value    Pr(>F)
group 37 6.5752e+29 < 2.2e-16 ***
      12
```

  The output shows that Levene's test is significant, which means that for these data the variances are significantly different and the assumption of homogeneity of variance has been violated.

Next we should check that the covariate is independent from the experimental manipulation. In this case, the proposed covariate is baseline stalking behaviour (**stalk1**), and we need to check that this variable was roughly equal across levels of our independent variable (**group**). We can test this by running an ANOVA with **stalk1** as the outcome and **group** as the predictor:

```
checkIndependenceModel<-aov(stalk1 ~ group, data = stalkerData)
```

```
summary(checkIndependenceModel)
```

The main effect of **stalk1** is not significant, $F(1, 48) = 0.06$, $p = .80$, which shows that the average level of baseline stalking behaviour was roughly the same in the two experimental groups. This result means that it is appropriate to use baseline stalking behaviour as a covariate in the analysis.

```
           Df Sum Sq Mean Sq F value Pr(>F)
group       1    7.2    7.22  0.0624 0.8038
Residuals  48 5555.4  115.74
```

To create the ANCOVA model we execute:

```
contrasts(stalkerData$group)<-c(-1, 1)
stalkerModel.1<-aov(stalk2~stalk1 + group, data = stalkerData)
Anova(stalkerModel.1, type = "III")

Anova Table (Type III tests)

Response: stalk2
            Sum Sq Df F value    Pr(>F)
(Intercept)    0.1  1  0.0010   0.97505
stalk1      4414.6  1 50.4621 5.692e-09 ***
group        480.3  1  5.4898   0.02341 *
Residuals   4111.7 47
```

Looking first at the significance values in the ANCOVA output above, it is clear that the covariate significantly predicts the dependent variable, so the hours spent stalking after therapy depend on the extent of the initial problem (i.e. the hours spent stalking before therapy). More interesting is that when the effect of initial stalking behaviour is removed, the effect of therapy becomes significant (p has gone down from .074 to .023, which is less than .05).

We can get the adjusted means by executing:

```
adjustedMeans<-effect("group", stalkerModel.1, se = TRUE)
summary(adjustedMeans)
adjustedMeans$se

group effect
group
Cruel to be Kind Therapy    Psychodyshamic Therapy
             55.29875                     61.50125

Lower 95 Percent Confidence Limits
group
Cruel to be Kind Therapy    Psychodyshamic Therapy
             51.53426                     57.73677

Upper 95 Percent Confidence Limits
group
Cruel to be Kind Therapy    Psychodyshamic Therapy
             59.06323                     65.26574

adjustedMeans$se
[1] 1.871259 1.871259
```

To interpret the results of the main effect of therapy we need to look at adjusted means. These adjusted means are shown above. There are only two groups being compared in this example so we can conclude that the therapies had a significantly different effect on stalking behaviour; specifically, stalking behaviour was lower after the therapy involving the cattle prod compared to psychodyshamic therapy.

To get the regression parameter for the covariate we can execute:

```
summary.lm(stalkerModel.1)
```

If the *b*-value for the covariate is positive then it means that the covariate and the outcome variable have a positive relationship (as the covariate increases, so does the outcome). If the *b*-value is negative it means the opposite: that the covariate and the outcome variable have a negative relationship (as the covariate increases, the outcome decreases). For these data the *b*-value is positive (*b* = 0.89), indicating that as the natural tendency for stalking (baseline) increases so does the tendency for stalking behaviour after the experimental manipulation:

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   0.2606     8.2906   0.031   0.9751
stalk1        0.8914     0.1255   7.104 5.69e-09 ***
group1        3.1013     1.3236   2.343   0.0234 *
```

We can look at the graphs of the model by executing:

```
plot(stalkerModel.1)
```

The left plot shows some funneling, which implies that there is a chance that the residuals are heteroscedastic. The second plot (on the right) is a Q-Q plot, which tells us about the normality of residuals in the model. We want our residuals to be normally distributed which means that the dots on the graph should hover around the diagonal line. On ours, there is a fair amount of deviation form the line.
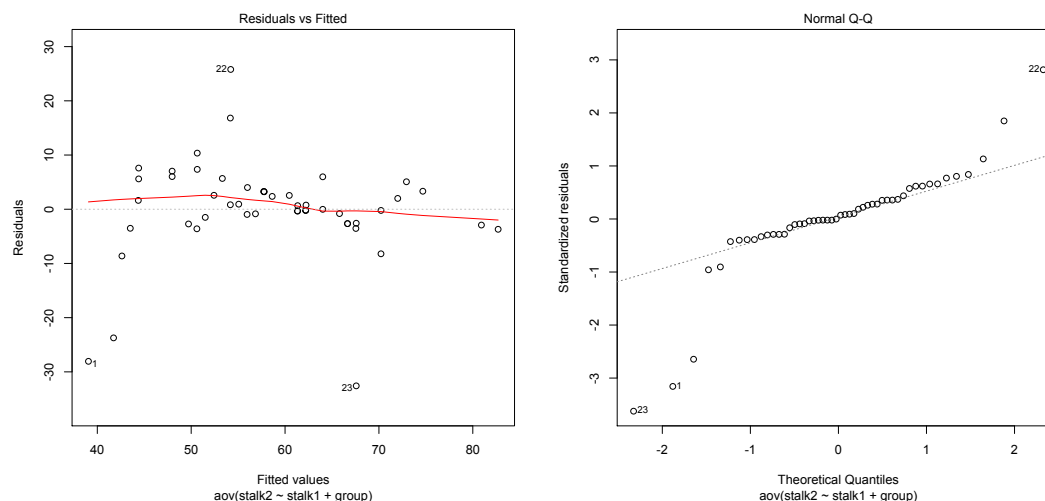
To test the assumption of homogeneity of regression slopes we execute:

```
hoRS<-update(stalkerModel.1, .~. + stalk1:group)
```

```
Anova(hoRS, type = "III")
```

The output shows that the interaction between **group** and **stalk1** (the covariate) is not significant, which means that we can assume homogeneity of regression slopes.

```
Response: stalk2
             Sum Sq Df F value     Pr(>F)
(Intercept)    71.3  1  0.8133     0.3719
stalk1       2798.7  1 31.9101 9.696e-07 ***
group         148.3  1  1.6912     0.1999
stalk1:group   77.3  1  0.8816     0.3527
Residuals    4034.4 46
```

Calculating the effect size

$$\text{Partial } \eta_{therapy}^2 = \frac{SS_{therapy}}{SS_{therapy} + SS_{Residual}}$$

$$=\frac{480.3}{480.3+4111.7}$$

$$= .10$$

This represents a medium to large effect. Therefore, the effect of a cattle prod compared to psychodyshamic therapy is a substantive finding. If going by the r guidelines (0.1 is a small effect, 0.3 a medium effect and 0.5 a large effect) then the equivalent guidelines for eta-squared would be the squareroot of these, i.e. .01 is a small effect, .09 a medium effect and .25 a large effect, and these should also be applicable to eta-squared (Levine & Hullett, 2002).

For the effect of the covariate, the error mean squares is the same, but the effect is much bigger (MS_M is 4414.60 rounded to 2 decimal places). If we place this value in the equation, we get the following:

$$\text{Partial } \eta_{stalk1}^2 = \frac{SS_{stalk1}}{SS_{stalk1} + SS_{Residual}}$$

$$=\frac{4414.6}{4414.6+4111.7}$$

$$= .52$$

This represents a very large effect, therefore, the relationship between initial stalking behaviour and the stalking behaviour after therapy is very strong indeed.

Interpreting and writing the result
The correct way to report the main finding would be:

```
      Levene's Test for Homogeneity of Variance
    Df      F value      Pr(>F)
group 37 6.5752e+29 < 2.2e-16 ***
     12
```

- ✓ Levene's test was significant, $F(37, 12) = 6.58e+29$, $p < .001$, indicating that the assumption of homogeneity of variance had been violated. The main effect of therapy was significant, $F(1, 47) = 5.49$, $p < .05$, partial $\eta^2 = .10$, indicating that the time spent stalking was lower after using a cattle prod ($M = 55.30$, $SE = 1.87$) compared to after psychodyshamic therapy ($M = 61.50$, $SE = 1.87$).
- ✓ The covariate was also significant, $F(1, 47) = 50.46$, $p < .001$, partial $\eta^2 = .52$, indicating that level of stalking before therapy had a significant effect on level of stalking after therapy (there was a positive relationship between these two variables). All significant values are reported at $p < .05$.

The second part of the question asks us to conduct a robust ANCOVA.

The main difficulty in running robust regression is getting the data into the right format. The functions for robust ANCOVA require us to create four variables, which I have labelled as follows in the functions:
- *covGrp1*: This variable contains scores for the covariate (**stalk1**) for the first group (in this case the 'Cruel to be Kind Therapy' group of the **group** variable).
- *dvGrp1*: This variable contains scores for the dependent variable/outcome (**stalk2**) for the first group (in this case the 'Cruel to be Kind Therapy' group of the **group** variable).
- *covGrp2*: This variable contains scores for the covariate (**stalk1**) for the second group (in this case the 'Psychodyshamic Therapy' group of the **group** variable).
- *dvGrp2*: This variable contains scores for the dependent variable/outcome (**stalk2**) for the second group (in this case the 'Psychodyshamic Therapy' group of the **group** variable).

To create these variables, we could start by splitting the dataframe into two new dataframes: one for the Cruel to be Kind Therapy group and the other for the Psychodyshamic Therapy group. We can achieve this by executing these commands:

```
CruelGroup<-subset(stalkerData, group=="Cruel to be Kind Therapy",)
```

```
PsychoGroup<-subset(stalkerData, group=="Psychodyshamic Therapy",)
```

Note that we have created two new dataframes (named *CruelGroup* and *PsychoGroup*). In both cases we have used the *subset()* function, specified the original dataframe (*stalkerData*), set a condition on which to select rows (this condition is that the value of the variable **group** is equal to "Cruel to be Kind Therapy" for the first dataframe and "Psychodyshamic Therapy" for the second).

We can now create the four variables by selecting the appropriate columns (i.e., variables) from these new dataframes. Execute these four commands:

```
covGrp1<- CruelGroup$stalk1
```

```
dvGrp1<- CruelGroup$stalk2
```

```
covGrp2<-PsychoGroup$stalk1
```

```
dvGrp2<-PsychoGroup$stalk2
```

Having created these variables, we can input them into the robust ANCOVA commands (note that I have also changed the number of bootstrap samples to 2000) and execute them:

```
ancova(covGrp1, dvGrp1, covGrp2, dvGrp2)
```

```
      X n1 n2        DIF      TEST        se     ci.low      ci.hi   p.value crit.val
[1,] 52 13 12 -4.347222 0.8928197 4.869093 -18.814099 10.119654 0.3881421 2.971165
[2,] 57 15 15 -5.000000 1.2850588 3.890873 -16.970348  6.970348 0.2265335 3.076520
[3,] 62 20 18 -1.250000 0.5761977 2.169394  -7.344261  4.844261 0.5706801 2.809199
[4,] 66 20 17 -1.287879 0.7065820 1.822688  -6.411654  3.835896 0.4877380 2.811109
[5,] 72 17 12 -1.568182 0.8827332 1.776507  -6.916134  3.779770 0.3947346 3.010374
```

```
ancboot(covGrp1, dvGrp1, covGrp2, dvGrp2, nboot = 2000)
```

```
      X n1 n2        DIF       TEST     ci.low     ci.hi p.value
[1,] 52 13 12 -4.347222 -0.8928197 -18.467487 9.773043  0.3950
[2,] 57 15 15 -5.000000 -1.2850588 -16.283447 6.283447  0.2370
[3,] 62 20 18 -1.250000 -0.5761977  -7.541196 5.041196  0.5600
[4,] 66 20 17 -1.287879 -0.7065820  -6.573636 3.997878  0.4900
[5,] 72 17 12 -1.568182 -0.8827332  -6.720014 3.583651  0.4085
```

```
$crit
[1] 2.899978
```

The output of the *ancova()* function and the *ancboot()* function can be interpreted in the same way. We can see that there are no significant differences between trimmed means for any of the 5 design points. In other words none of the groups differ significantly in their number of hours spent stalking (adjusted for baseline stalking behaviour). This suggests that type of therapy did not significantly effect the number of hours spent stalking.

Looking at the plot of the covariate plotted against the outcome variable below, we can see that the crosses are usually higher than the circles. This probably explains why we found no significant group differences in the robust analysis.
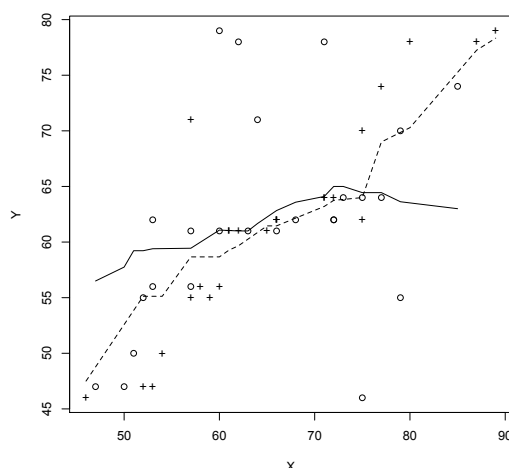
Task 2

- • A marketing manager for a certain well-known drinks manufacturer was interested in the therapeutic benefit of certain soft drinks for curing hangovers. He took 15 people out on the town one night and got them drunk. The next morning as they awoke, dehydrated and feeling as though they'd licked a camel's sandy feet clean with their tongue, he gave five of them water to drink, five of them Lucozade (in case this isn't sold outside of the UK, it's a very nice glucose-based drink) and the remaining five a leading brand of cola (this variable is called **drink**). He then measured how well they felt (on a scale from 0 = I feel like death to 10 = I feel really full of beans and healthy) two hours later (this variable is called **well**). He wanted to know which drink produced the greatest level of wellness. However, he realised it was important to control for how drunk the person got the night before, and so he measured this on a scale of 0 = as sober as a nun to 10 = flapping about like a haddock out of water on the floor in a puddle of their own vomit. The data are in the file **HangoverCure.dat**. Conduct an ANCOVA to see whether people felt better after different drinks when controlling for how drunk they were the night before.

First of all, load in the data:

```
hangoverData<-read.delim("HangoverCure.dat", header = TRUE)
```

Next we can make the variable **drink** a factor:

```
hangoverData$drink<-factor(hangoverData$drink, levels = c(1:3), labels = c("Water",
"Lucozade", "Cola"))
```

Conduct a one-way ANOVA without covariate:

```
hangoverModel<-aov(well~drink, data = hangoverData)
summary(hangoverModel)
```

```
            Df  Sum Sq Mean Sq F value Pr(>F)
drink        2  2.1333  1.0667  0.8205 0.4635
Residuals   12 15.6000  1.3000
```

The above output shows the ANOVA for these data when the covariate is not included. It is clear from the significance value that there are no differences in how well people feel when they have different drinks.

We can now conduct a normal ANCOVA:

First we want to do a Levene's test to see whether the variance in **well** (how well the person feels) varies across the interaction of different types of drinks (**drink**) and how drunk the person was the night before (**drunk**). To do this we can execute:

```
leveneTest(hangoverData$well, interaction(hangoverData$drink, hangoverData$drunk),
center = median)
```

The output shows that Levene's test is very non-significant, $F(10, 4) = 0.34$, $p = .92$. This means that for these data the variances are very similar (hence the high probability value). The assumption of homogeneity of variance seems to be met.

```
Levene's Test for Homogeneity of Variance
      Df F value Pr(>F)
group 10    0.34 0.9242
       4
```

Next we should check that the covariate is independent from the experimental manipulation. In this case, the proposed covariate is how drunk the person was the night before (**drunk**), and we need to check that this variable was roughly equal across levels of our independent variable (**drink**). We can test this by running an ANOVA with **drunk** as the outcome and **drink** as the predictor:

```
checkIndependenceModel<-aov(drunk ~ drink, data = hangoverData)

summary(checkIndependenceModel)
```

The main effect of **drunk** is non significant, $F(2, 12) = 1.35$, $p = .29$, which shows that the average level of drunkedness the night before was roughly the same in the three experimental groups. This result means that it is appropriate to use drunk as a covariate in the analysis.

```
          Df Sum Sq Mean Sq F value Pr(>F)
drink      2    8.4     4.2  1.3548 0.2948
Residuals 12   37.2     3.1
```

Next we can create the ANCOVA model and set some contrasts. As explained in the book chapter, **R** will set some contrasts by default, however these contrasts are not orthogonal and because we are using Type III sums of squares, this just won't do! We need to make sure that our contrasts *are* orthogonal otherwise the type III sums of squares will be screwed up. Therefore, we will set our own contrasts.
  I tend to find Lucozade to be the best cure of a hangover. To test this hypothesis, I have set the first contrast to compare drinking Lucozade to drinking Water and Cola (1, 2, -1) and the second contrast to compare Water to Cola (1, 0, -1).
  We can specify these contrasts by executing the following commands:

```
contrasts(hangoverData$drink)<-cbind(c(-1,2,-1), c(1,0,-1))
hangoverModel<-aov(well~drunk + drink, data = hangoverData)
Anova(hangoverModel, type="III")
```

  It is clear that the covariate significantly predicts the dependent variable, so the drunkenness of the person influenced how well they felt the next day. What's more interesting is that when the effect of drunkenness is removed, the effect of drink becomes significant (p is .041, which is less than .05).

```
Response: well
             Sum Sq Df  F value     Pr(>F)
(Intercept) 145.006  1 361.4557 9.197e-10 ***
drunk        11.187  1  27.8860   0.00026 ***
drink         3.464  2   4.3177   0.04130 *
Residuals     4.413 11
```

We can get the adjusted means by executing:

```
adjustedMeans<-effect("drink", hangoverModel, se = TRUE)
```

```
summary(adjustedMeans)

adjustedMeans$se
```

The adjusted means show that the significant ANCOVA reflects a difference between the water and the Lucozade groups. The cola and water groups appear to have fairly similar adjusted means indicating that cola is no better than water at helping your hangover.

```
drink effect
drink
   Water Lucozade      Cola
5.109677 6.238710 5.251613

 Lower 95 Percent Confidence Limits
drink
   Water Lucozade      Cola
4.484559 5.589003 4.587591

 Upper 95 Percent Confidence Limits
drink
   Water Lucozade      Cola
5.734796 6.888416 5.915635

adjustedMeans$se
[1] 0.2840176 0.2951889 0.3016933
```

To get the regression parameter for the covariate we can execute:

```
summary.lm(hangoverModel)
```

For these data the *b*-value is negative ($b = -0.55$), indicating that the more drunk a person was the night before, the less well they felt the next day. The output also shows the model parameters, which correspond to the contrasts that we specified for the variable **drink**. The first dummy variable (**drink1**) compares drinking Lucozade to drinking Water and Cola. The associated *t*-statistic is significant, indicating that the effect of Lucozade was significantly different from Cola and Water. Looking at the adjusted means, it seems that my hypothesis is supported, people felt significantly better after drinking Lucozade than the other two drinks.

  The second dummy variable (**drink2**) compares water and Cola, the associated *t*-statistic is non-significant (not surprising when looking at how similar the adjusted means are!), indicating that the effect of drinking Cola was not significantly different from drinking Water.

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  7.39785    0.38911  19.012  9.2e-10 ***
drunk       -0.54839    0.10385  -5.281  0.00026 ***
drink1       0.35269    0.12287   2.870  0.01523 *
drink2       0.07097    0.20976   0.338  0.74149
```

We can look at the graphs of the model by executing:

```
plot(hangoverModel)
```

The left plot does not show any substantial funneling (although the fitted line is nowhere near flat) which implies that the residuals are probably not heteroscedastic. The second plot (on the right) is a Q-Q plot, which tells us about the normality of residuals in the model. We want our residuals to be normally distributed which means that the dots on the graph should hover around the diagonal line. On ours, there is only very slight deviation form the line.
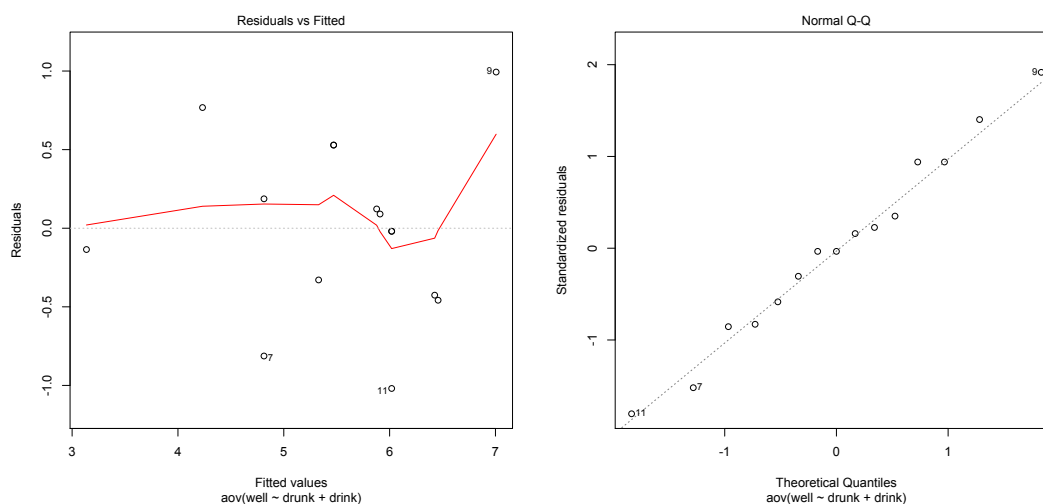
To test the assumption of homogeneity of regression slopes we execute:

```
hoRS<-update(hangoverModel, .~. + drunk:drink)
```

```
Anova(hoRS, type = "III")
```

The output shows that the interaction between **drink** and **drunk** (the covariate) is not significant, which means that we can assume homogeneity of regression slopes.

```
Anova Table (Type III tests)

Response: well
            Sum Sq Df  F value    Pr(>F)
(Intercept) 59.295  1 194.1961 2.134e-07 ***
drunk        5.216  1  17.0812  0.002548 **
drink        3.376  2   5.5278  0.027166 *
drunk:drink  1.665  2   2.7263  0.118668
Residuals    2.748  9
```

Calculating the effect size

We can calculate η^2 for the main effect of drink:

$$\text{Partial } \eta_{drink}^2 = \frac{SS_{drink}}{SS_{drink} + SS_{Residual}}$$

$$= \frac{3.46}{3.46 + 4.41}$$

$$= .44$$

We can also do the same for the covariate:

$$= \frac{11.187}{11.187 + 4.41}$$

$$= .72$$

We've got *t*-statistics for the comparisons between the cola and water groups and the cola and Lucozade groups. These *t*-statistics have $N-2$ degrees of freedom, where N is the total sample size (in this case 15). Therefore we get:

$$r_{\text{Lucozade vs. Water and Cola}} = \sqrt{\frac{2.872}{2.872 + 13}}$$

$$= .62$$

$$r_{\text{Water vs. Cola}} = \sqrt{\frac{0.342}{0.342 + 13}}$$

$$= .09$$

Interpreting and writing the result

We could report the main finding as:

- ✓ The covariate, drunkenness, was significantly related to the how ill the person felt the next day, $F(1, 11) = 27.89$, $p < .001$, $\eta^2 = .72$. There was also a significant effect of the type of drink on how well the person felt after controlling for how drunk they were the night before, $F(2, 11) = 4.32$, $p < .05$, $\eta^2 = .44$.

We can also report some contrasts:

- ✓ Planned contrasts revealed that having Lucozade significantly improved how well you felt compared to having cola or water, $t(13) = 2.87$, $p < .05$, $r = .62$, but having cola was no better than having water, $t(13) = 0.34$, ns, $r = .09$. We can conclude that cola and water have the same effects on hangovers but that Lucozade seems significantly better at curing hangovers than cola.

Task 3

- • The annual Elephant football (soccer) event in Nepal is the highlight of the elephant calendar. However, in recent years a heated argument has arisen between the African and Asian elephants. It started in 2010 when the president of the Asian Elephant Football Association (AEFA), an elephant named Boji, claimed that Asian elephants were more talented than their African counterparts. The head of the African Elephant Soccer Association (AESA), an elephant called Tunc, counteracted in a press statement that read 'I make it a matter of personal pride never to take seriously any remark made by something that looks like an enormous scrotum'. I was called in to settle things. I collected data from two types of elephants (**elephant**) over one season. For each elephant, I measured how many goals they scored in the season (**goals**) and how many years experience the elephant had (**experience**). The data are in **Elephant Football.dat**. Analyse the effect of the type of elephant on goal scoring, controlling for the amount of football experience the elephant has. Also try conducting a robust ANCOVA.

First of all, load in the data:

```
elephantData<-read.delim("Elephant Football.dat", header = TRUE)
```

Next we can make the variable **elephant** a factor, with two levels (Asian and African):

```
elephantData$elephant<-factor(elephantData$elephant, levels = c(1:2), labels =
c("Asian Elephant", "African Elephant"))
```

Lets create some boxplots of the data:

In this example, instead of restructuring the data, it makes more sense to create two boxplots, one plotting type of elephant against number of goals scored and one plotting type of elephant against number of years of football experience:

```
boxplot <- ggplot(elephantData, aes(elephant, goals))
boxplot + geom_boxplot() + labs(x = "Type of Elephant", y = "Number of Goals")
```
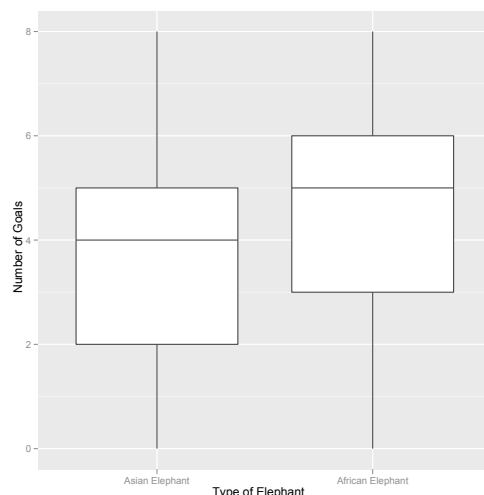
This boxplot suggests that African elephants scored more goals over the season than Asian elephants.

```
boxplot <- ggplot(elephantData, aes(elephant, experience))
boxplot + geom_boxplot() + labs(x = "Type of Elephant", y = "Football Experience
(Years)")
```
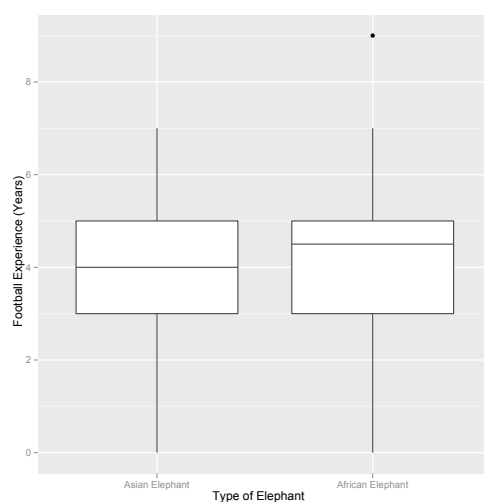

This boxplot suggests that the two types of elephant (Asian and African) had roughly the same number of years of football experience.

We can now conduct a normal ANCOVA:

First we want to do a Levene's test to see whether the variance in **goals** (the outcome) varies across the interaction between **elephant** and **experience**. To do this we can execute:

```
leveneTest(elephantData$goals, interaction(elephantData$elephant,
elephantData$experience), center = median)
```

The output shows that Levene's test is very non-significant, $F(16, 103) = 1.24$, $p = .25$. This means that for these data the variances are very similar (hence the high probability value). The assumption of homogeneity of variance seems to be met.

```
Levene's Test for Homogeneity of Variance
      Df F value Pr(>F)
group 16  1.2414 0.2504
      103
```

Next we should check that the covariate is independent from the experimental manipulation. In this case, the proposed covariate is number of years of prior football experience (**experience**), and we need to check that this variable was roughly equal across levels of our independent variable (**elephant**). We can test this by running an ANOVA with **experience** as the outcome and **elephant** as the predictor:

```
checkIndependenceModel<-aov(experience ~ elephant, data = elephantData)
```

```
summary(checkIndependenceModel)
```

```
summary.lm(checkIndependenceModel)
```

  The main effect of **experience** is not significant, $F(1, 118) = 1.38$, $p = .24$, which shows that the average level of experience was roughly the same in the two experimental groups. This confirms the boxplot above. This result means that it is appropriate to use experience as a covariate in the analysis.

```
           Df  Sum Sq Mean Sq F value Pr(>F)
elephant    1    4.03  4.0333  1.3838 0.2418
Residuals 118 343.93  2.9147
```

To create the ANCOVA model with orthogonal contrasts we execute:

```
contrasts(elephantData$elephant)<-c(-1, 1)
elephantModel<-aov(goals~ experience + elephant, data = elephantData)
Anova(elephantModel, type = "III")
```

Looking first at the significance values, it is clear that the covariate (experience) significantly predicts the dependent variable (goals), because the significance value (.002) is less than .05. Therefore, the number of goals scored by the different elephants was influenced by the number of years of football experience they had (as you might expect). What's more interesting is that when the effect of experience is removed, the effect of type of elephant is significant ($p = .004$ which is less than .05).

```
Anova Table (Type III tests)

Response: goals
            Sum Sq  Df F value    Pr(>F)
(Intercept) 131.70   1 40.4640 4.034e-09 ***
experience   32.32   1  9.9306  0.002065 **
elephant     27.95   1  8.5887  0.004069 **
Residuals   380.80 117
```

  We can get the adjusted means by executing:

```
adjustedMeans<-effect("elephant", elephantModel, se = TRUE)
```

```
summary(adjustedMeans)
```

```
adjustedMeans$se
```

 The adjusted means (and their confidence intervals) show that African elephants scored significantly more goals than Asian elephants.

```
elephant effect
elephant
  Asian Elephant   African Elephant
       3.589534           4.560466

 Lower 95 Percent Confidence Limits
elephant
  Asian Elephant African Elephant
       3.126929         4.097860

 Upper 95 Percent Confidence Limits
elephant
  Asian Elephant African Elephant
       4.052140         5.023071
adjustedMeans$se
     121        122
0.2335862 0.2335862
```

  To get the regression parameter for the covariate we can execute:

```
summary.lm(elephantModel)
```

If the *b*-value for the covariate is positive then it means that the covariate and the outcome variable have a positive relationship (as the covariate increases, so does the outcome). If the *b*-value is negative it means the opposite: that the covariate and the outcome variable have a negative relationship (as the covariate increases, the outcome decreases). For these data the *b*-value is positive (*b* = 0.31), indicating that as the level of experience increases so does the number of goals scored in the football season:

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  2.79259    0.43901   6.361 4.03e-09 ***
experience   0.30655    0.09728   3.151  0.00206 **
elephant1    0.48547    0.16565   2.931  0.00407 **
```

We can look at the graphs of the model by executing:

```
plot(elephantModel)
```

The left plot does not show any substantial funneling (although the fitted line is not perfectly flat), which implies that the residuals are probably not heteroscedastic. The second plot (on the right) is a Q-Q plot, which tells us about the normality of residuals in the model. We want our residuals to be normally distributed which means that the dots on the graph should hover around the diagonal line. On ours, there is only very slight deviation form the line.
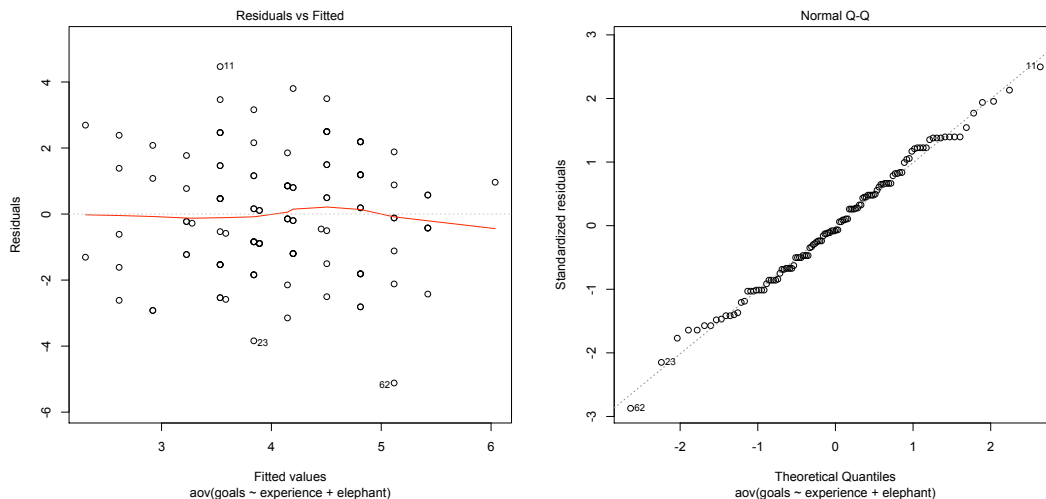
To test the assumption of homogeneity of regression slopes we execute:

```
hoRS<-update(elephantModel, .~. + experience:elephant)
```

```
Anova(hoRS, type = "III")
```

The output shows that the interaction between **elephant** and **experience** (the covariate) is not significant, which means that we can assume homogeneity of regression slopes.

```
Response: goals
                    Sum Sq  Df F value    Pr(>F)
(Intercept)          49.80   1 15.1756 0.0001643 ***
experience           13.06   1  3.9806 0.0483722 *
elephant              2.65   1  0.8082 0.3705086
experience:elephant   0.16   1  0.0477 0.8275456
Residuals           380.64 116
```

As such we do not need to conduct a robust ANCOVA. However, because the question asks us to conduct a robust ANCOVA we will do it anyway.

We need to get the data into the right format. For example, we need to create the four variables **covGrp1, dvGrp1, covGrp2, dvGrp2**. We could start by splitting the dataframe into two new dataframes: one for the Asian elephant group and one for the African elephant group. We can achieve this by executing these commands:

```
asian<-subset(elephantData, elephant=="Asian Elephant",)
african<-subset(elephantData, elephant=="African Elephant",)
```

We can now create the four variables by selecting the appropriate columns (i.e., variables) from these new dataframes. Execute these four commands:

```
covGrp1<-asian$experience
dvGrp1<-asian$goals
covGrp2<-african$experience
dvGrp2<-african$goals
```

Having created these variables, we can input them into the robust ANCOVA commands and execute them:

```
ancova(covGrp1, dvGrp1, covGrp2, dvGrp2)
```

```
[1] "NOTE: Confidence intervals are adjusted to control the probability"
[1] "of at least one Type I error."
[1] "But p-values are not"
$output
     X n1 n2        DIF     TEST        se    ci.low     ci.hi     p.value
[1,] 2 15 30 -1.277778 1.846494 0.6920022 -3.281135 0.7255791 0.08366899
[2,] 4 38 50 -1.066667 2.139515 0.4985554 -2.394075 0.2607418 0.03711825
[3,] 4 38 50 -1.066667 2.139515 0.4985554 -2.394075 0.2607418 0.03711825
[4,] 5 42 50 -1.092308 2.256915 0.4839827 -2.379391 0.1947753 0.02810398
[5,] 6 25 41 -1.333333 2.341798 0.5693630 -2.875131 0.2084640 0.02504472
     crit.val
[1,] 2.895015
[2,] 2.662510
[3,] 2.662510
[4,] 2.659358
[5,] 2.707934
```

```
ancboot(covGrp1, dvGrp1, covGrp2, dvGrp2, nboot = 2000)
```

```
[1] "Note: confidence intervals are adjusted to control FWE"
[1] "But p-values are not adjusted to control FWE"
[1] "Taking bootstrap samples. Please wait."
$output
     X n1 n2        DIF      TEST     ci.low     ci.hi p.value
[1,] 2 15 30 -1.277778 -1.846494 -3.234577 0.6790212  0.0855
[2,] 4 38 50 -1.066667 -2.139515 -2.476449 0.3431158  0.0440
[3,] 4 38 50 -1.066667 -2.139515 -2.476449 0.3431158  0.0335
[4,] 5 42 50 -1.092308 -2.256915 -2.460882 0.2762670  0.0320
[5,] 6 25 41 -1.333333 -2.341798 -2.943341 0.2766743  0.0300

$crit
[1] 2.827735
```

The output of the *ancova()* function and the *ancboot()* function can be interpreted in the same way. We can see that there are significant differences between trimmed means for 4 of the 5 design points. In other words in most cases the groups differ significantly in their mean number of goals scored (adjusted for number of years of football experience). We didn't get a significant difference for values of the covariate around 2 (the start of the 5 design points tested), which seems to suggest that being an African elephant increased the elephant's chances of scoring more goals in all elephant's except for those who had very limited football experience (2 years or less).

Looking at the plot of the covariate plotted against the outcome variable below, we can see that the circles are usually higher than the crosses. The one exception is when $X = 2$, where there is a cross at the highest point and a circle at the lowest point. This probably explains why we found no significant group differences at this design point in the robust analysis (it is the one point where it is not obvious that the circles are generally higher than the crosses.