

Lab 4

MTH 3220

October 24, 2017

1 Part A: Two-Factor ANOVA (Additive and Interaction Models)

1.1 Memory Data Set

The file **memory.txt** contains data from an experiment to test the effects of two factors, level of reinforcement (none or verbal) and time of isolation (20, 40, or 60 minutes), on students' abilities to recall information. The response variable is a score on a test that assesses a student's ability to recall items.

1. Use `read.table()` (with `header = TRUE`) to read the data from the **memory.txt** file into a *data frame* in R. Attach the data.
2. Using the data from the **memory.txt** file, carry out a two-factor ANOVA using the *additive* model to decide if either of the two factors (reinforcement and isolation) have any effect on the scores, e.g.:

```
memaov1 <- aov(Score ~ Reinforcement + Isolation)
summary(memaov1)
```

3. Oops! We should've checked for an interaction first. Load the package `lattice` by running the following:

```
library(lattice)
```

Then make an interaction plot using `xyplot` from the `lattice` package, e.g.:

```
xyplot(Score ~ Isolation, groups = Reinforcement, type = "a")
```

4. Now carry out a two-factor ANOVA using the *interaction* model by replacing the plus sign in the previous model with an asterisk:

```
memaov2 <- aov(Score ~ Reinforcement * Isolation)
summary(memaov2)
```

5. Extract the residuals and fitted values from your ANOVA model by running something like the following, where the ANOVA output from the previous problem is assumed to be called `memaov2`:

```
memres <- memaov2$residuals
memfit <- memaov2$fitted.values
```

6. Make a normal probability plot of the residuals to check the normality assumption on the interaction model:

```
qqnorm(memres)
qqline(memres)
```

7. Make a plot of the residuals (y axis) versus the fitted values (x axis) to check the homoskedasticity assumption on the interaction model:

```
plot(memfit, memres)
abline(h = 0)
```

2 Part B: Three-Factor ANOVA

2.1 Electrical Stimulation of Muscles Data Set

Muscles that have lost connections to nerve fibers are said to be *denervated*. Motor nerve transmissions to denervated muscles are decreased or nonexistent, leading loss of muscle tissue (or *muscle wasting*).

A number of experiments have suggested that electrical stimulation may be helpful in preventing the wasting away of denervated muscles.

A factorial experiment on rats was conducted to learn something about the best type of current and the most effective method of treatment. The factors and their levels are shown below:

Factor <i>A</i>	Factor <i>B</i>	Factor <i>C</i>
Number of treatment periods daily	Length of treatment (minutes)	Type of current
1	1	Galvanic
3	2	Faradic
6	3	60 cycle alternating
	5	25 cycle alternating

Treatments were started on the third day after denervation and continued for 11 consecutive days. There were 48 different combinations of methods of treatments ($IKK = 3 * 4 * 4 = 48$), each of which was applied to two rats, using 96 rats in all.

The rats' muscles were denervated by the removal of a small part of the sciatic nerve from the gastrocnemius-soleus (calf) muscle on one side. The weights of the denervated muscles were measured at the end of the experiment. Since this depends on the size of the animal, the weight of the corresponding unaffected muscle on the other side was also measured for use as a reference, or control.

Data from the experiment are contained in the file **muscles.txt**.

1. Use `read.table()` to read the data into a *data frame* in R (note that the file has a header row) and call the object **muscles**.
2. Create a new variable, call it **PctCh**, containing the percent change in muscle weights, i.e.

$$\text{Percent Change} = \frac{\text{Denervated Wt} - \text{Normal Wt}}{\text{Normal Wt}}$$

by running this (assuming data are in data frame called **muscles**):

```
PctCh <- (muscles$NormalWt - muscles$DenervedWt)/muscles$NormalWt
```

Insert the variable **PctCh** into the *data frame* containing the rest of the data, e.g.

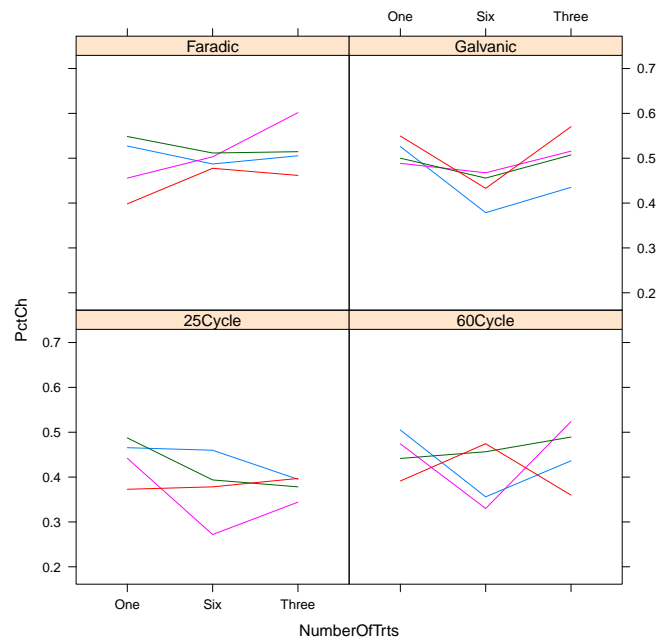
```
muscles$PctCh <- PctCh
```

and now attach the data frame **muscles** to the environment.

3. We want to check for a three-factor interaction graphically by making four separate interaction plots of **NumberOfTrts** and **TrtLength**, one plot for each **TypeOfCurrent**. Use `xyplot` in the package **lattice** as follows:

```
xyplot(PctCh ~ NumberOfTrts | TypeOfCurrent,
       groups = TrtLength, type = "a")
```

so that your plot looks like this (note: may have different layout in RStudio Plots viewer):



- Carry out a three-factor ANOVA, with `PctCh` as the response and `NumberOfTrts`, `TrtLength`, and `TypeOfCurrent` as the factors. Fit the *full model* (with all interaction terms) using `aov()`.