Section 5.3 Fitting the ANOVA Model

Loaded needed packages

```
library(Stat2Data)
library(mosaic)

EXAMPLE 5.5 Seeing the leafhopper data as a sum of overlays

Create a dataframe for Leafhoppers and look at the structure of the data.

data("Leafhoppers")
```

```
data("Leafhoppers")
str(Leafhoppers)

## 'data.frame': 8 obs. of 3 variables:
## $ Dish: int 1 2 3 4 5 6 7 8

## $ Diet: Factor w/ 4 levels "Control", "Fructose",..: 1 1 4 4 3 3 2 2

## $ Days: num 2.3 1.7 3.6 4 2.9 2.7 2.1 2.3

Question 0: What is the overall or "grand"" average?

ybar=mean(Leafhoppers$Days)
ybar
```

[1] 2.7

Question 1: How far is each group average from the grand average?

```
GroupMeans=mean(Days~Diet,data=Leafhoppers)
GroupMeans
```

```
## Control Fructose Glucose Sucrose
## 2.0 2.2 2.8 3.8
```

```
GroupMeansDiff=GroupMeans-ybar
GroupMeansDiff
```

```
## Control Fructose Glucose Sucrose ## -0.7 -0.5 0.1 1.1
```

Question 2: How far is each response from its group average?

Residuals=Leafhoppers\$Days-GroupMeans[Leafhoppers\$Diet] Residuals

```
## Control Control Sucrose Sucrose Glucose Glucose Fructose Fructose ## 0.3 -0.3 -0.2 0.2 0.1 -0.1 -0.1 0.1
```

FIGURE 5.9 Leafhopper data as a sum of overlays

Put the pieces of the decomposition into a dataframe

```
Overlays=data.frame(Response=Leafhoppers$Days)
Overlays$GrandAverage=rep(ybar,8)
Overlays$TreatmentEffects=GroupMeansDiff[Leafhoppers$Diet]
Overlays$Residuals=Residuals
Overlays
```

##		Response	${\tt GrandAverage}$	${\tt TreatmentEffects}$	Residuals
##	1	2.3	2.7	-0.7	0.3
##	2	1.7	2.7	-0.7	-0.3
##	3	3.6	2.7	1.1	-0.2
##	4	4.0	2.7	1.1	0.2
##	5	2.9	2.7	0.1	0.1
##	6	2.7	2.7	0.1	-0.1
##	7	2.1	2.7	-0.5	-0.1
##	8	2.3	2.7	-0.5	0.1

EXAMPLE 5.6 Evaluating psychotherapy

Create a dataframe for **Undoing** and look at the structure of the data.

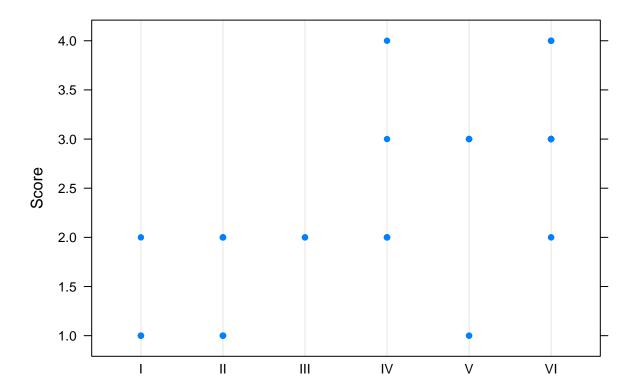
```
data(Undoing)
str(Undoing)
```

```
## 'data.frame': 44 obs. of 3 variables:
## $ Group : Factor w/ 6 levels "I","II","III",..: 1 1 1 1 2 2 2 2 2 2 ...
## $ Score : int 1 1 1 2 1 1 1 1 1 1 ...
## $ Symbol: int 1 1 1 1 0 0 0 0 0 ...
```

FIGURE 5.10 The Undoing data

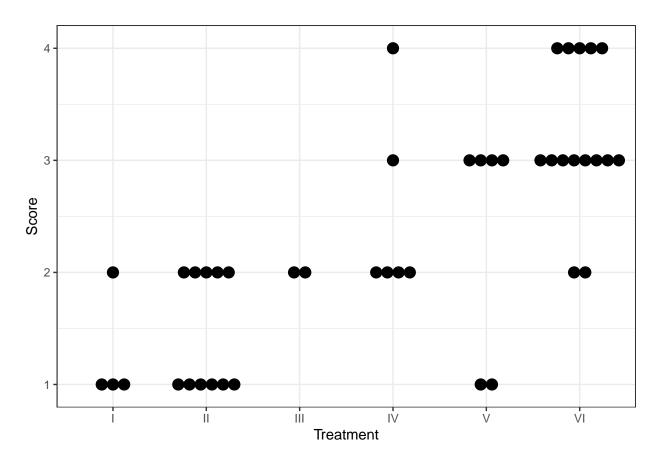
Note: There's some trouble if we use the generic dotplot() function, since multiple values are at the same point.

```
dotplot(Score~Group,data=Undoing)
```



A much better dotplot can be created with $\operatorname{ggplot}()$.

```
ggplot(Undoing, aes(x = Group, y = Score)) +
geom_dotplot(binaxis = "y", stackdir = "center", binwidth=0.1) +
labs(x="Treatment") +theme_bw()
```



Create a subset with just Groups I, III, and IV.

```
Undoing134=subset(Undoing,Group %in% c("I","III","IV"))
Undoing134$Group=factor(Undoing134$Group,levels=c("I","III","IV"))
Undoing134
```

```
##
      Group Score Symbol
## 1
           Ι
                 1
## 2
           Ι
                 1
                         1
## 3
           Ι
                 1
                         1
           Ι
                 2
## 4
                         1
                 2
## 16
                         1
         III
                 2
## 17
         III
                         1
                 2
## 18
          ΙV
                         1
                 2
## 19
          IV
                         1
## 20
                 2
          ΙV
                         1
                 2
## 21
          IV
                         1
                 3
## 22
          ΙV
                         1
## 23
          ΙV
                 4
```

Question 0: What is the overall or "grand" average?

```
ScoreMean=mean(Undoing134$Score)
ScoreMean
```

[1] 2

Question 1: How far is each group average from the grand average?

```
ScoreMeans=mean(Score~Group, data=Undoing134)
ScoreMeans
```

```
## I III IV
## 1.25 2.00 2.50
```

GroupEffects=ScoreMeans-ScoreMean
GroupEffects

```
## I III IV
## -0.75 0.00 0.50
```

Question 2: How far is each response from its group average?

UndoingResid=Undoing134\$Score-ScoreMeans[Undoing134\$Group] UndoingResid

FIGURE 5.11 Decomposition of the psychotherapy data

Put the pieces of the decomposition into a dataframe

```
UndoingDecomposition=data.frame(Response=Undoing134$Score)
UndoingDecomposition$GrandMean=rep(ScoreMean,12)
UndoingDecomposition$TreatmentEffects=GroupEffects[Undoing134$Group]
UndoingDecomposition$Residuals=UndoingResid
UndoingDecomposition
```

##		Response	${\tt GrandMean}$	${\tt TreatmentEffects}$	Residuals
##	1	1	2	-0.75	-0.25
##	2	1	2	-0.75	-0.25
##	3	1	2	-0.75	-0.25
##	4	2	2	-0.75	0.75
##	5	2	2	0.00	0.00
##	6	2	2	0.00	0.00
##	7	2	2	0.50	-0.50
##	8	2	2	0.50	-0.50
##	9	2	2	0.50	-0.50
##	10	2	2	0.50	-0.50
##	11	3	2	0.50	0.50
##	12	4	2	0.50	1.50

EXAMPLE 5.7 ANOVA table for the leafhoppers

Note: R's ANOVA table includes a P-value that is introduced in Section 5.4, but does not include a row for Total.

```
anovamodel=aov(Days~Diet,data=Leafhoppers)
summary(anovamodel)
##
              Df Sum Sq Mean Sq F value Pr(>F)
                   3.92 1.307 17.42 0.00925 **
## Diet
## Residuals
                   0.30
                          0.075
## ---
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' ' 1
EXAMPLE 5.8 ANOVA table for the psychotherapy data
summary(aov(Score~Group,data=Undoing134))
              Df Sum Sq Mean Sq F value Pr(>F)
##
               2 3.75 1.8750 3.971 0.0581 .
## Group
## Residuals
               9 4.25 0.4722
## ---
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' ' 1
Compute sums of squares for Leafhoppers
SSGroups=sum(Overlays$TreatmentEffects^2)
SSE=sum(Overlays$Residuals^2)
SSTotal=SSGroups+SSE
paste("SSGroups=",SSGroups)
## [1] "SSGroups= 3.92"
paste("SSE = ",SSE)
## [1] "SSE = 0.3"
paste("SSTotal=",SSTotal)
```

[1] "SSTotal= 4.22"