

# Section 1

MANE 6313

## Subsection 1

Week 10, Module F

# Student Learning Outcome

- Select an appropriate experimental design with one or more factors,
- Select an appropriate model with one or more factors,
- Evaluate statistical analyses of experimental designs,
- Assess the model adequacy of any experimental design, and
- Interpret model results.

# Module Learning Outcome

*Analyze a one-quarter fraction using R.*

# Quarter Fraction Example – Problem 8.11 (Textbook 9th edition)

**8.11** An article in *Industrial and Engineering Chemistry* (“More on Planning Experiments to Increase Research Efficiency,” 1970, pp. 60–65) uses a  $2^{5-2}$  design to investigate the effect of  $A$  = condensation temperature,  $B$  = amount of material 1,  $C$  = solvent volume,  $D$  = condensation time, and  $E$  = amount of material 2 on yield. The results obtained are as follows:

$$\begin{array}{llll} e = 23.2 & ad = 16.9 & cd = 23.8 & bde = 16.8 \\ ab = 15.5 & bc = 16.2 & ace = 23.4 & abcde = 18.1 \end{array}$$

- Verify that the design generators used were  $I = ACE$  and  $I = BDE$ .
- Write down the complete defining relation and the aliases for this design.
- Estimate the main effects.
- Prepare an analysis of variance table. Verify that the  $AB$  and  $AD$  interactions are available to use as error.

(e) Plot the residuals versus the fitted values. Also plot the residuals versus the

## FrF2 Generators

### **generators**

There are ``log2(nruns)`` base factors the full factorial of which spans the design (e.g. 3 for 8 runs). The generators specify how the remaining factors are to be allocated to interactions of these.

``generators`` can be

a list of vectors with position numbers of base factors (e.g. `c(1,3,4)` stands for the interaction between first, third and fourth base factor)

a vector of character representations of these interactions, e.g. "ACD" stands for the same interaction as above

a vector of columns numbers in Yates order (e.g. 13 stands for ACD). Note that the columns 1, 2, 4, 8, etc., i.e. all powers of 2, are reserved for the base factors and cannot be used for assigning additional factors, because the design would become a resolution II design. For looking up which column number stands for which interaction, type e.g. ``names(Yates)[1:15]`` for a 16 run design.

In all cases, preceding the respective entry with a minus sign (e.g. `-c(1,3,4)`, `"-ACD"`, `-13`) implies that the levels of the respective column are reversed. WARNING: Minus signs do not cause an error, but neither have an effect in case of automatic assignment of split-plot designs or hard-to-change columns.

Figure 2: FrF2 Generators Documentation

## Incorrect Generators

```
105 > ```{r}  
106 library(FrF2)  
107 p8_11.design2 <- FrF2(8,gen=c("ACE","BDE"),randomize=FALSE)  
108 summary(p8_11.design2)  
109 > ```
```

```
Error in gen.check(k, generators) :  
All generators must contain integer numbers from 1 to 3  
or letters from A to C only.
```

[Show Traceback](#)

Figure 3: Incorrect Generators

# Change of Variables

## Design Generators

$$I = ACE \rightarrow A = A^2CE \rightarrow A = CE$$

$$I = BDE \rightarrow B = B^2DE \rightarrow B = DE$$

Create full factorial in CDE and A & B using design generators

$a'$ ↑ <u>C</u>	$b'$ ↑ <u>D</u>	$c'$ ↑ <u>E</u>	$d' = a'c'$	$e' = b'c'$	<u>trt</u>
-	-	-	+	+	ab
+	-	-	-	+	bc
-	+	-	+	-	ad
+	+	-	-	-	cd
-	-	+	-	-	e
+	-	+	+	-	ace
-	+	+	-	+	bde



## Correct FrF2 Design

```

112 > {}
113 library(FrF2)
114 p8_11.design3 <- FrF2(8,factor.names=list(Solvent=c("-", "+"),condTime=c("-", "+"),Material2=c("-", "+"),
condTemp=c("-", "+"),Material1=c("-", "+")),generators=c("AC", "BC"),randomize=FALSE)
115 summary(p8_11.design3)
116 >

```

					data.frame	data.frame
					2 x 5	8 x 5
Solvent (C)	condTime (D)	Material2 (E)	condTemp (A)	Material1 (B)	trt	y
<fctr>	<fctr>	<fctr>	<fctr>	<fctr>		
1 -	-	-	+	+	ab	15.5
2 +	-	-	-	+	bc	16.2
3 -	+	-	+	-	ad	16.9
4 +	+	-	-	-	cd	23.8
5 -	-	+	-	-	e	23.2
6 +	-	+	+	-	ace	23.4
7 -	+	+	-	+	bde	16.8
8 +	+	+	+	+	abcde	18.1

8 rows

Figure 5: Correct FrF2 Design

# Design Details

```

112 ~```{r}
113 library(FrF2)
114 p8_11.design3 <- FrF2(8, factor.names=list(Solvent=c("-", "+"), condTime=c("-", "+"), Material2=c("-", "+"),
115   condTemp=c("-", "+"), Material1=c("-", "+")), generators=c("AC", "BC"), randomize=FALSE)
116 ~```

```

R Console

data.frame  
2 x 5

data.frame  
8 x 5

"+")), generators = c("AC", "BC"), randomize = FALSE)

Experimental design of type FrF2.generators

8 runs

Factor settings (scale ends):

Design generating information:

\$legend

[1] A=Solvent B=condTime C=Material2 D=condTemp E=Material1

\$generators

[1] D=AC E=BC

Alias structure:

\$main

[1] A=CD B=CE C=AD=BE D=AC E=BC

\$fi2

[1] AB=DE AE=BD

# Add Response Variable

```

118 ~ ````{r}
119 library(FrF2)
120 y2 <- c(15.5,16.2,16.9,23.8,23.2,23.4,16.8,18.1)
121 p8_11.design3 <- add.response(p8_11.design3,y2)
122 summary(p8_11.design3)
123 ~ ````

```

R Console

data.frame  
2 x 5

data.frame  
8 x 6

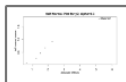
	Solvent <fctr>	condTime <fctr>	Material2 <fctr>	condTemp <fctr>	Material1 <fctr>	y2 <dbl>
1	-	-	-	+	+	15.5
2	+	-	-	-	+	16.2
3	-	+	-	+	-	16.9
4	+	+	-	-	-	23.8
5	-	-	+	-	-	23.2
6	+	-	+	+	-	23.4
7	-	+	+	-	+	16.8
8	+	+	+	+	+	18.1

8 rows

Figure 7: Adding Response Variable

# Half Normal Plot

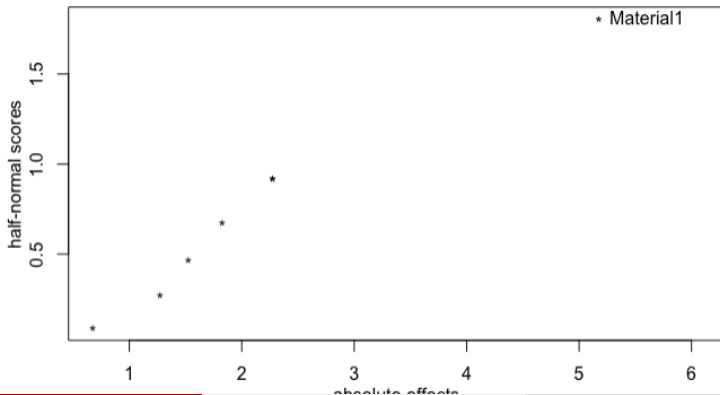
```
125 ~~~~{r}  
126 # Daniel Plot  
127 DanielPlot(p8_11.design3, half=TRUE, response='y2', alpha=0.3)  
128 ~~~~
```



estimated critical values are available for all  
families, and conservative ones

R Console

Half Normal Plot for y2, alpha=0.3



## First Model

```
130 ~ ````{r}  
131 p8_11.model1 <- aov(y2~Material1,data=p8_11.design3)  
132 summary(p8_11.model1)  
133 ~ ````
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Material1	1	53.56	53.56	8.883	0.0246 *
Residuals	6	36.18	6.03		

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Figure 9: First Model

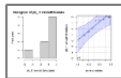
# Residual Analysis: Normality Assumption

```

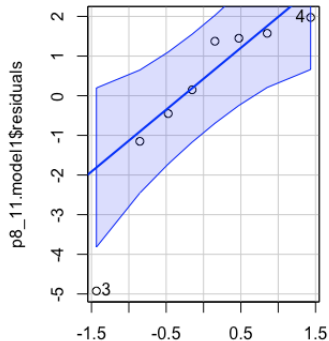
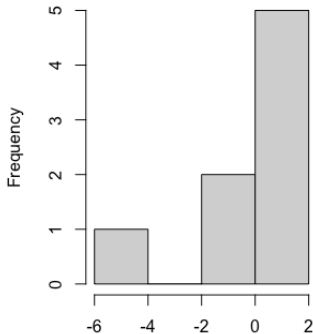
135 ~~~{r}
136 par(mfrow=c(1,2))
137 hist(p8_11.model1$residuals)
138 library(car)
139 qqPlot(p8_11.model1$residuals)
140 ~~~

```

R Console

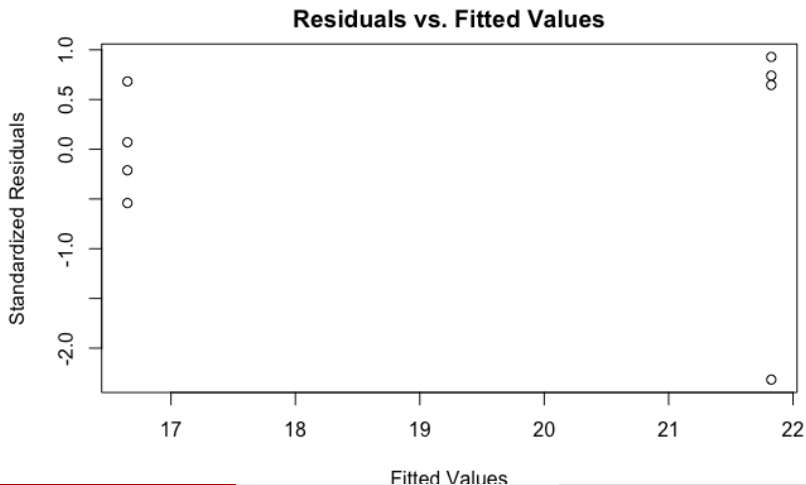


Histogram of p8\_11.model1\$residuals



## Residuals vs. Fitted Values

```
142 ~ ```{r}  
143 p8_11.stdRes <- rstandard(p8_11.model1)  
144 plot(p8_11.model1$fitted.values,p8_11.stdRes,xlab="Fitted Values",ylab="Standardized  
145 ~ Residuals", main="Residuals vs. Fitted Values")
```



## Residuals vs. Factor A

```

154 - ```{r}
155 # Create Data Frame with all residual information
156 residuals.df <- data.frame(p8_11.stdRes,p8_11.model1$fitted.values,p8_11.design3$Solvent,p8_11.design3$condTime,p8_11.design3$Material2,p8_11.design3$condTemp,p8_11.design3$Material1)
157 summary(residuals.df)
158 #
159 library(ggplot2)
160 ggplot(residuals.df,aes(x=p8_11.design3$Solvent,y=p8_11.stdRes)) +
161   geom_dotplot(binaxis='y',stackdir='center') +
162   labs(x="Solvent",y="Standard Residuals",title="Solvent vs. Residuals Plot")
163 - ```

```



[38;5;232mBin width defaults to 1/30 of the range of the data. Pick better value with 'binwidth'. [39m

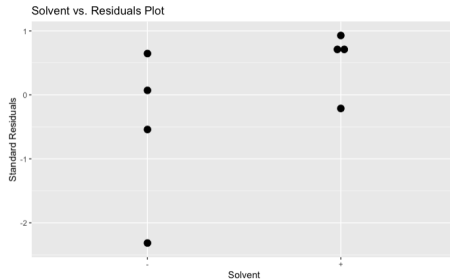


Figure 12: Residuals vs. Factor A



## Residuals vs. Factor B

```
166 > `r`{r warning=FALSE,message=FALSE}  
167 ggplot(residuals.df,aes(x=p8_11.design3$condTime,y=p8_11.stdRes)) +  
168   geom_dotplot(binaxis='y',stackdir='center') +  
169   labs(x="Condensation Time",y="Standard Residuals",title="Condensation Time vs. Residuals Plot")  
170 > `r`
```

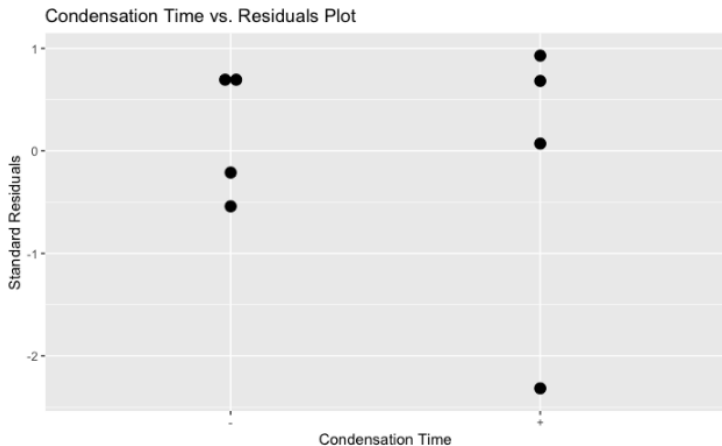
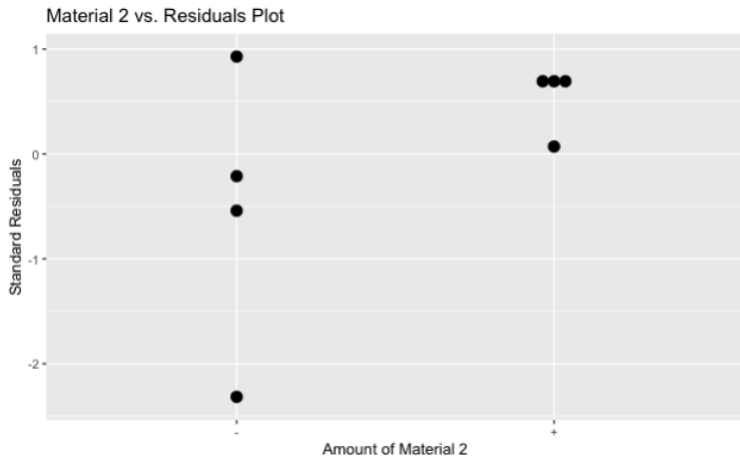


Figure 13: Residuals vs. Factor B

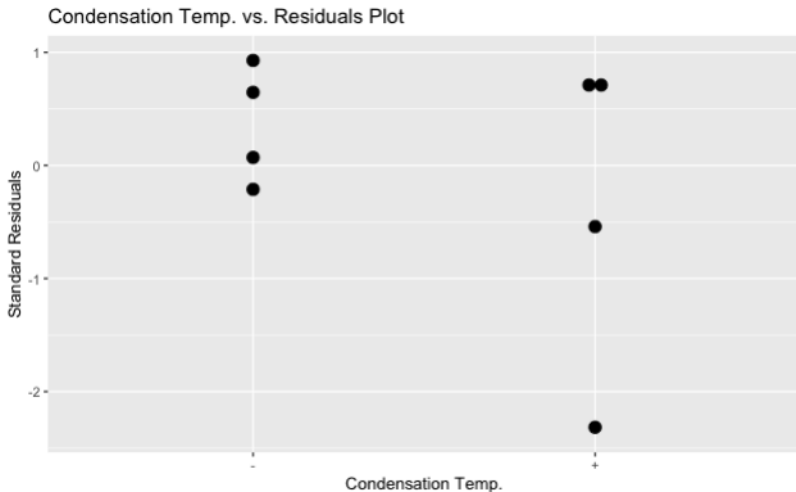
## Residuals vs. Factor C

```
172 > ```{r message=FALSE}  
173 ggplot(residuals.df,aes(x=p8_11.design3$Material2,y=p8_11.stdRes)) +  
174   geom_dotplot(binaxis='y',stackdir='center') +  
175   labs(x="Amount of Material 2",y="Standard Residuals",title="Material 2 vs. Residuals Plot")  
176 > ```
```



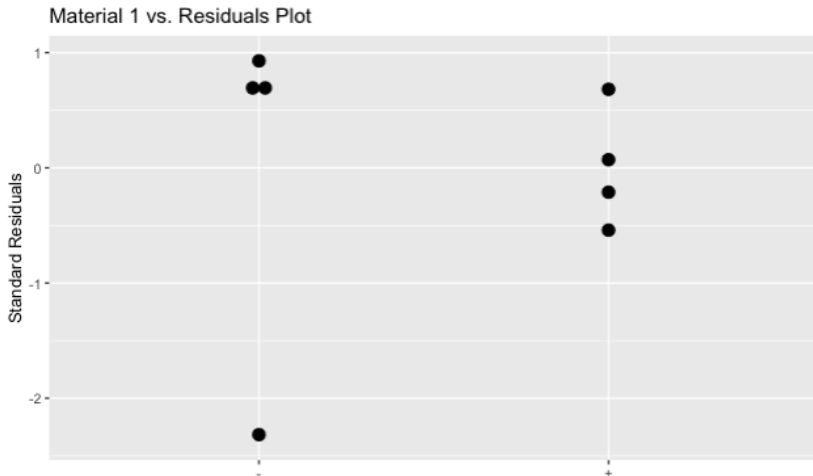
## Residuals vs. Factor D

```
178 ~ ```{r message=FALSE}  
179 ggplot(residuals.df,aes(x=p8_11.design3$condTemp,y=p8_11.stdRes)) +  
180   geom_dotplot(binaxis='y',stackdir='center') +  
181   labs(x="Condensation Temp.",y="Standard Residuals",title="Condensation Temp. vs. Residuals Plot")  
182 ~ ```
```



## Residuals vs. Factor E

```
184 > ```{r message=FALSE}  
185 p_e <- ggplot(residuals.df,aes(x=p8_11.design3$Material1,y=p8_11.stdRes)) +  
186   geom_dotplot(binaxis='y',stackdir='center') +  
187   labs(x="Amount of Material 1",y="Standard Residuals",title="Material 1 vs. Residuals Plot")  
188 p_e  
189 > ```
```



## Standardized Residuals

```
191 ▾ ```{r}  
192   p8_11.stdRes  
193 ▴ ```|
```

1	2	3	4	5	6	7	8
-0.5407837	-0.2116110	-2.3159648	0.9287371	0.6465892	0.7406385	0.0705370	0.6818577

Figure 17: Standardized Residuals