

Section 1

MANE 6313

Subsection 1

Week 14, Module B

Student Learning Outcome

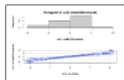
- Select an appropriate experimental design with one or more factors,
- Select an appropriate model with one or more factors,
- Evaluate statistical analyses of experimental designs,
- Assess the model adequacy of any experimental design, and
- Interpret model results.

Module Learning Outcome

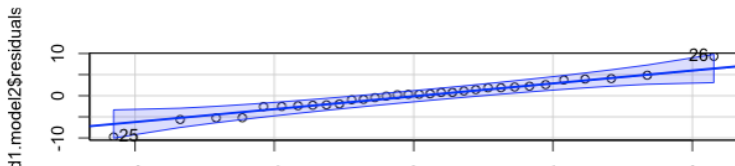
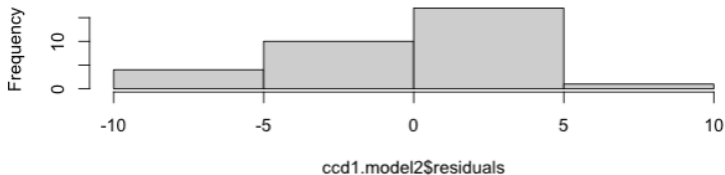
Appraise Model Assumptions Using Residual Analysis

Normality Assumption

```
28 ~~~{r}  
29 par(mfrow=c(2,1))  
30 hist(ccd1.model2$residuals)  
31 library(car)  
32 qqPlot(ccd1.model2$residuals)  
33 ~~~
```



Histogram of ccd1.model2\$residuals



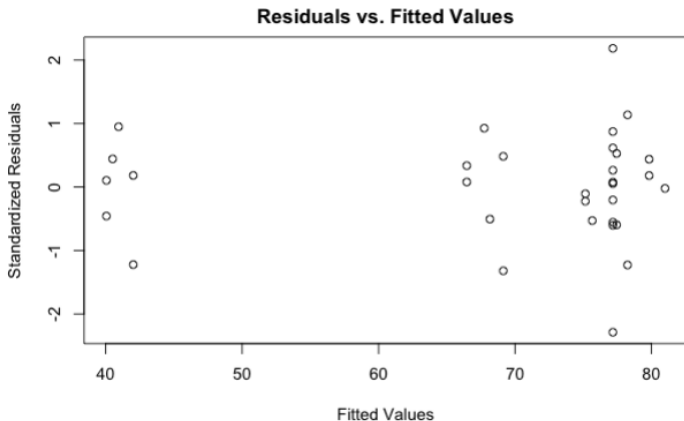
Standardized Residuals

- Your instructor could not make `rstandard()` function work with residuals from `rsm()` model
- The code to create standardized residuals is shown below

```
rmse.model2 <- sqrt(sum(ccd1.model2$residuals^2)/ccd1.model2$N)
model2.stdres <- ccd1.model2$residuals/rmse.model2
```

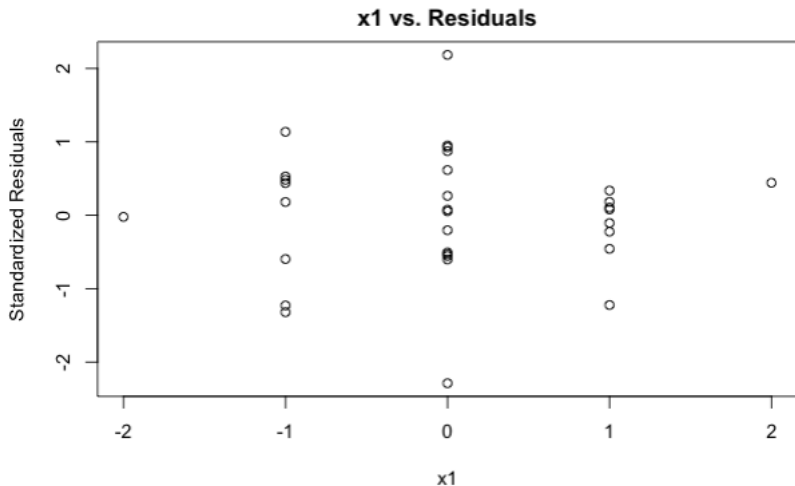
Residuals vs. Fitted Values

```
43 ~~~{r}  
44 plot(ccd1.model2$fitted.values,model2.stdres[,xlab="Fitted Values",ylab="Standardized Residuals",main="Residuals vs.  
Fitted Values")  
45 ~~~
```



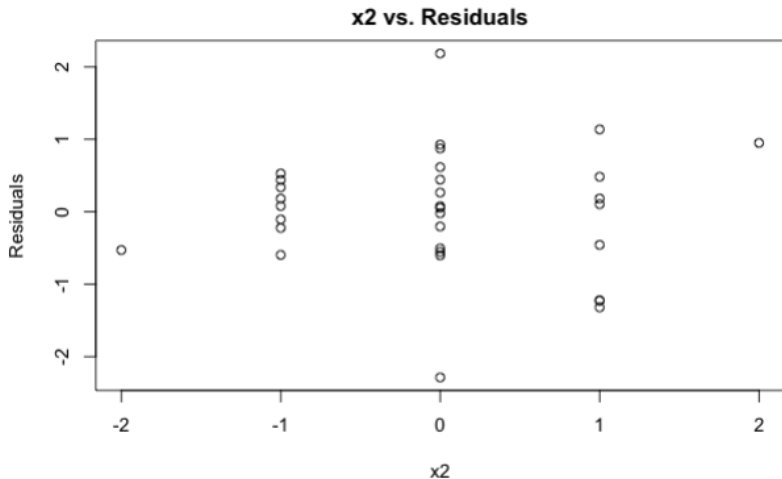
Residuals vs. x1

```
47 > ``{r}  
48 plot(ccd1.df$x1,model2.stdres,xlab="x1",ylab="Standardized Residuals",main="x1 vs. Residuals")  
49 > ``
```



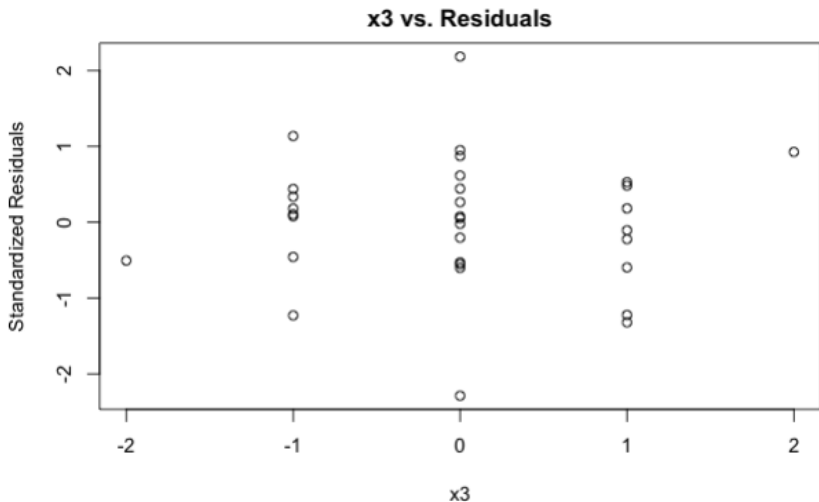
Residuals vs. x_2

```
51 > {r}  
52 plot(ccd1.df$x2,model2.stdres,xlab="x2",ylab="Standardized Residuals",main="x2 vs. Residuals")  
53 >
```



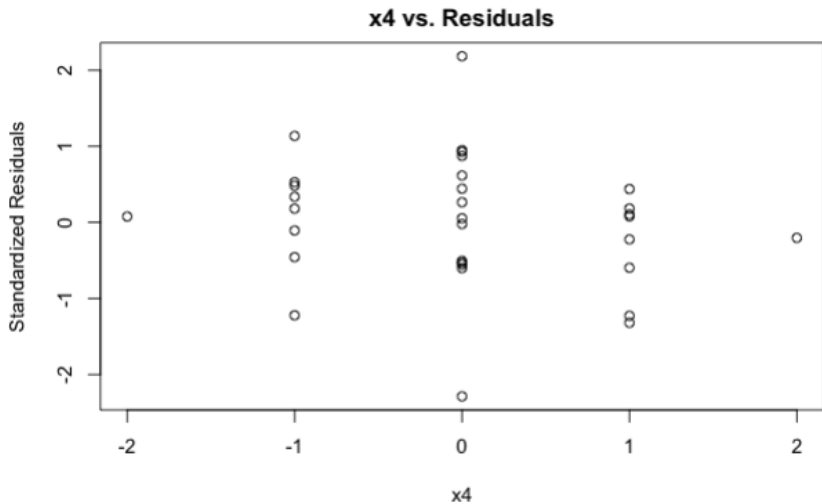
Residuals vs. x3

```
56 > {{r}}  
57 plot(ccd1.df$x3,model2.stdres,xlab="x3",ylab="Standardized Residuals",main="x3 vs. Residuals")  
58 > {{r}}
```



Residuals vs. x4

```
60 > ``{r}  
61 plot(ccd1.df$x4,model2.stdres,xlab="x4",ylab="Standardized Residuals",main="x4 vs. Residuals")  
62 > ``
```



Residuals vs. x5

```
64 > {{r}}  
65 plot(ccd1.df$x5,model2.stdres,xlab="x5",ylab="Standardized Residuals",main="x5 vs. Residuals")  
66 > {{r}}
```

