Appendix

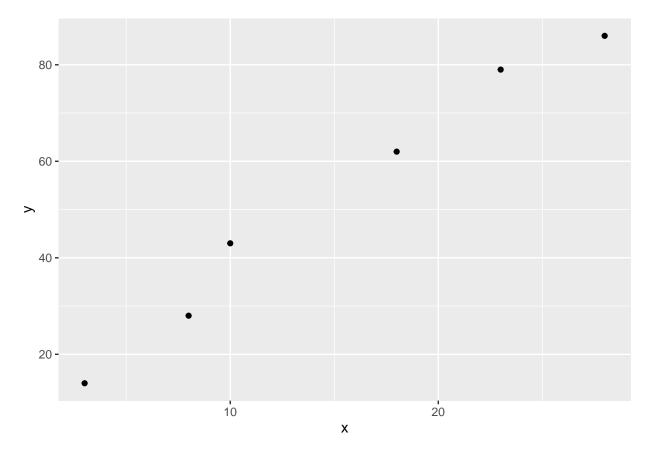
Jadon Fowler, STA 570 Section 1 Homework 10, 2023/05/02

```
library(car)
library(ggplot2)
library(dplyr)
library(ggfortify)
library(emmeans)
library(multcompView)
library(multcomp)
```

1.a.

```
# read in the data
p1.data <- data.frame(
    x = c( 3, 8, 10, 18, 23, 28),
    y = c(14, 28, 43, 62, 79, 86) )

# make a nice graph
ggplot(p1.data, aes(x=x, y=y)) +
    geom_point()</pre>
```



1.c.

```
p1.model <- lm(y ~ x, p1.data)
anova(p1.model)
## Analysis of Variance Table
##
## Response: y
##
            Df Sum Sq Mean Sq F value Pr(>F)
            1 4003.1 4003.1 193.27 0.0001552 ***
## x
## Residuals 4 82.9
                        20.7
## ---
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' ' 1
predict(p1.model)
##
            2
                  3
                        4
                             5
## 16.60 31.35 37.25 60.85 75.60 90.35
resid(p1.model)
            2
                 3
                       4
                             5
     1
## -2.60 -3.35 5.75 1.15 3.40 -4.35
summary(p1.model)
##
## Call:
## lm(formula = y ~ x, data = p1.data)
## Residuals:
##
      1
                 3
                      4
                             5
## -2.60 -3.35 5.75 1.15 3.40 -4.35
## Coefficients:
              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 7.7500 3.6855 2.103 0.103325
## x
                2.9500
                         0.2122 13.902 0.000155 ***
## ---
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' 1
## Residual standard error: 4.551 on 4 degrees of freedom
## Multiple R-squared: 0.9797, Adjusted R-squared: 0.9747
## F-statistic: 193.3 on 1 and 4 DF, p-value: 0.0001552
1.d.
# 'x' here is the slope CI
confint(p1.model)
                  2.5 %
                           97.5 %
## (Intercept) -2.482697 17.982697
              2.360849 3.539151
## x
```

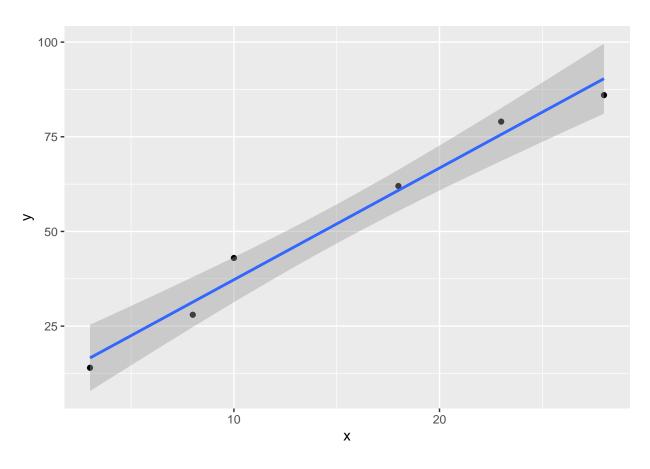
```
summary(p1.model)
```

```
##
## Call:
## lm(formula = y ~ x, data = p1.data)
## Residuals:
## 1 2
                 3
                       4
                             5
## -2.60 -3.35 5.75 1.15 3.40 -4.35
## Coefficients:
              Estimate Std. Error t value Pr(>|t|)
                       3.6855 2.103 0.103325
## (Intercept)
                7.7500
                2.9500
                          0.2122 13.902 0.000155 ***
## x
## ---
## Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' ' 1
## Residual standard error: 4.551 on 4 degrees of freedom
## Multiple R-squared: 0.9797, Adjusted R-squared: 0.9747
## F-statistic: 193.3 on 1 and 4 DF, \, p-value: 0.0001552
# e. p = 0.000155, we can reject the null hypothesis
# f. R^2 = 0.9797
# g. typical distance = stddev = 4.551
```

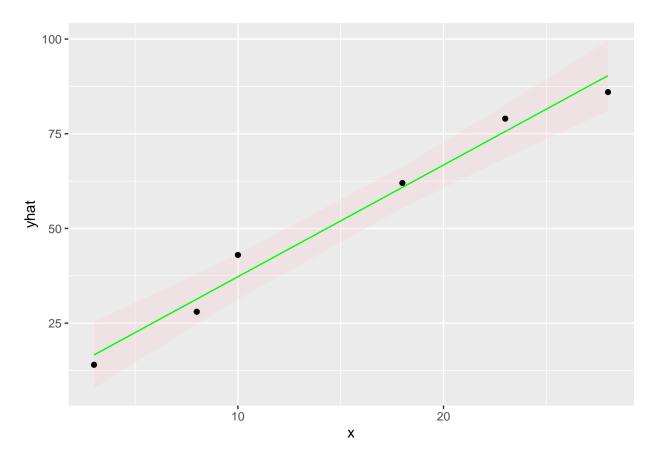
1.h.

```
# make a nice graph
ggplot(p1.data, aes(x=x, y=y)) +
geom_point() +
geom_smooth(method='lm')
```

```
## 'geom_smooth()' using formula = 'y ~ x'
```

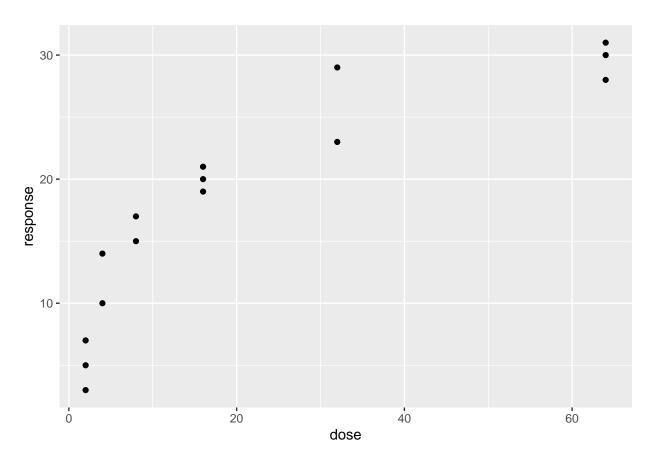


```
# Often I want to create the confidence region myself (perhaps to use a prediction
# interval instead of a confidence interval), and we could use the following code:
p1.data2 <- p1.data %>%
  mutate( yhat = predict(p1.model),
  lwr = predict(p1.model, interval='confidence')[,2],
  upr = predict(p1.model, interval='confidence')[,3] )
# make a nice graph
ggplot(p1.data2, aes(x=x)) +
geom_ribbon( aes(ymin=lwr, ymax=upr), fill='pink', alpha=.2 ) +
geom_line( aes( y=yhat), color='green' ) +
geom_point( aes( y=y ), color='black' )
```

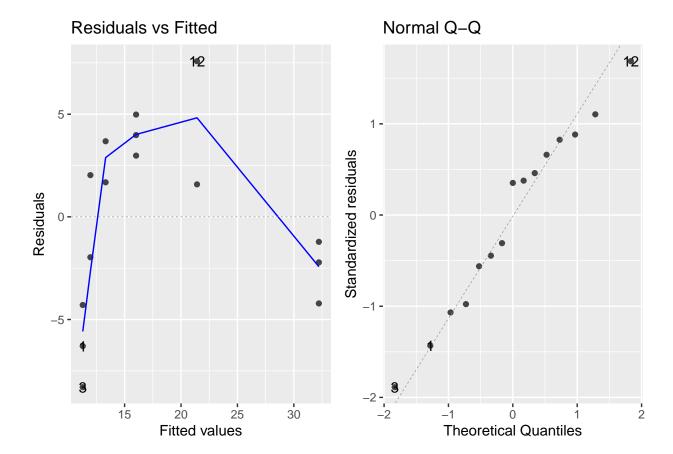


3.a.

```
drug.data <- data.frame(
  dose = c(2,2,4,4,8,8,16,16,16,32,32,64,64,64),
  response = c(5,7,3,10,14,15,17,20,21,19,23,29,28,31,30) )
ggplot(drug.data) +
  geom_point(aes(x=dose, y=response))</pre>
```

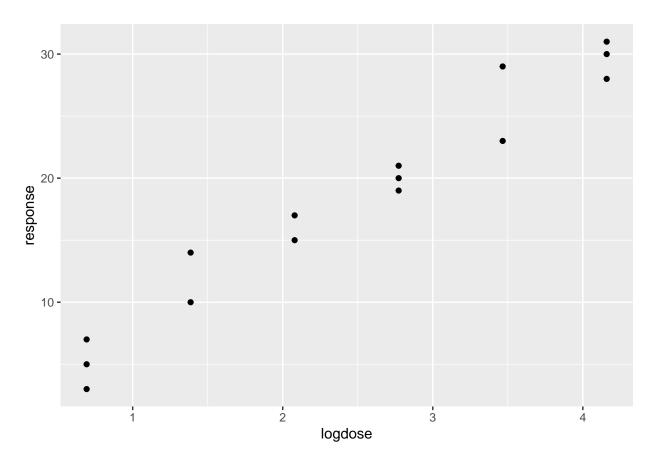


drug.model <- lm(response ~ dose, drug.data)
autoplot(drug.model, which=c(1,2))</pre>



3.b.

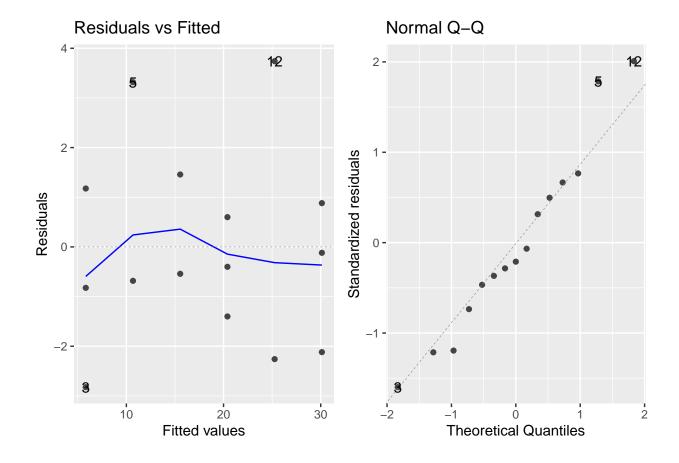
```
# i
drug.data <- drug.data %>% mutate(logdose = log(dose))
ggplot(drug.data) +
  geom_point(aes(x=logdose, y=response))
```



```
# A linear model seems appropriate

# ii
drug.model <- lm(response ~ logdose, drug.data)

# iii
autoplot(drug.model, which=c(1,2))</pre>
```



```
# The residuals have far less curvature, so the linear model seems appropriate.
# iv
shapiro.test(resid(drug.model))

##
## Shapiro-Wilk normality test
##
## data: resid(drug.model)
## W = 0.95469, p-value = 0.6011

# The model appears to be Normally Distributed

# v
# slope = 7

# vi
confint(drug.model)

##
## 2.5 % 97.5 %
```

(Intercept) -1.481133 3.411301

6.118344 7.901590

logdose