MA 354: Data Analysis I – Fall 2019
Homework 3:

Complete the following opportunities to use what we've talked about in class. These questions will be graded for correctness, communication and succinctness. Ensure you show your work and explain your logic in a legible and refined submission.

0. **Complete weekly diagnostics.**

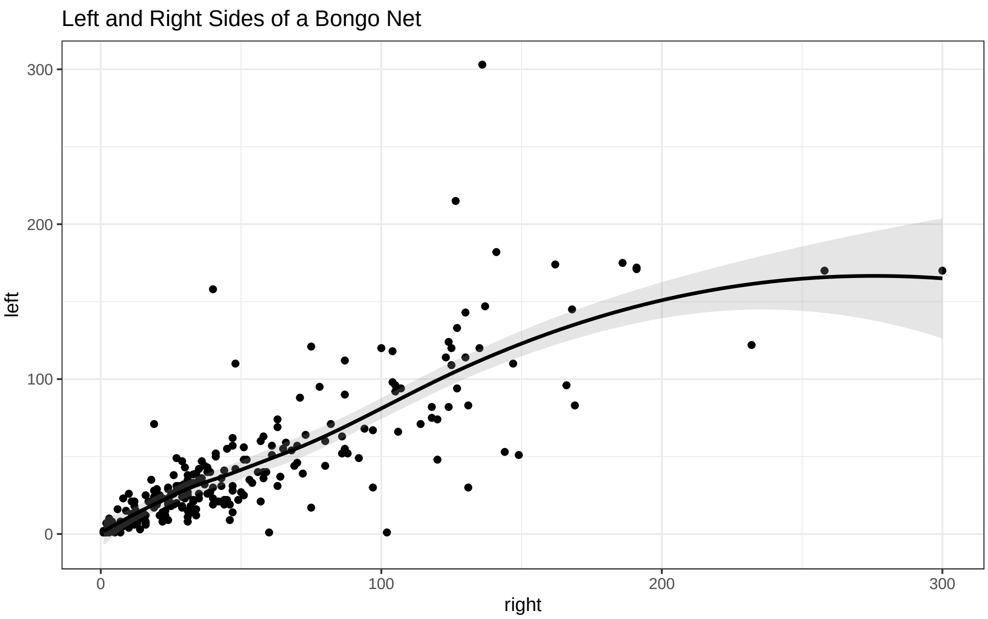
1. Plankton samples are typically collected using fine mesh nets towed from research vessels, and larval fish are removed then stored after sample preservation. Samples are frequently collected using the paired bongo net, which consists of two usually round net frames joined at a central point, and towed either obliquely or vertically through the water column. Mesopelagic fish families such as the Myctophidae are some of the most specious and abundant in the worlds oceans. We expect the number of Myctophidae in the left and right side of each net to be highly correlated, but we want to quantify this relationship.

   ? provide data on a total of 261 paired samples from the Gulf of Mexico. Myctophidae counts from the left and right sides of each bongo net are a result of over years (1987-2008) of sampling. We define X and Y to be the count of myctophid larvae in the left and right side of the bongo net, respectively.

   Research Question: Does the data we have confirm our expectation that the number of Myctophidae in the left and right side of each net tend to be highly correlated?

   The data can be loaded as follows. The data for the number of fish caught in the left and right net are in the columns labeled `Left` and `Right`, respectively.

```
> dat.bongo<-read.csv(file = "https://cipolli.com/students/data/BongoNetData.txt",
+                        header = TRUE,sep = ",")
>

> summary(dat.bongo$Left)

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   1.00   14.00   27.00   42.09   53.00  303.00

> summary(dat.bongo$Right)

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   1.00   18.00   33.00   50.07   66.00  300.00

> library(ggplot2)
> library(gridExtra)
> ggdat<-data.frame(left=dat.bongo$Left, right=dat.bongo$Right)
> ggplot(data=ggdat,aes(x = right, y= left))+
+   geom_point()+
+   geom_smooth(alpha=0.25,color="black",method="loess")+
+   theme_bw()+
+   ggtitle("Left and Right Sides of a Bongo Net")
```




```
> cor(dat.bongo$Left,dat.bongo$Right,method = "pearson")

[1] 0.8232054

> cor(dat.bongo$Left,dat.bongo$Right,method = "kendall")

[1] 0.7105615

> cor(dat.bongo$Left,dat.bongo$Right,method = "spearman")

[1] 0.8639953
```

**Would we want to use a kendall or a spearman's rank because the graph shows that the correlation isn't totally linear?

2. **(Working with Data)** Hepatitis C is a disease that affects the liver. The virus that causes hepatitis C is spread through blood or bodily fluids of an infected person. The virus is often difficult to diagnose because there are few unique symptoms. Those infected, however, sometimes experience jaundice – a condition that causes yellowing of the skin or eyes, as the liver is infected.

   Bracht et al. (2016) consider the human microfibrillar-associated protein 4, or MFAP4, and its role in disease-related tissue. Stage 0–no fibrosis; Stage 1–enlarged, fibrotic portal tracts; Stage 2–periportal fibrosis or portal-portal septa, but intact architecture; Stage 3–fibrosis with architectural distortion, but no obvious cirrhosis; and Stage 4–probable or definite cirrhosis.

   Previously, it has been shown that MFAP4 is a biomarker candidate for hepatic fibrosis and cirrhosis in hepatitis C patients. The analysis of Bracht et al. (2016) aimed to consider the ability of MFAP4 to differentiate between stages of the disease – fibrosis stages (0-2) and cirrhosis (3-4) based on the Scheuer scoring system.

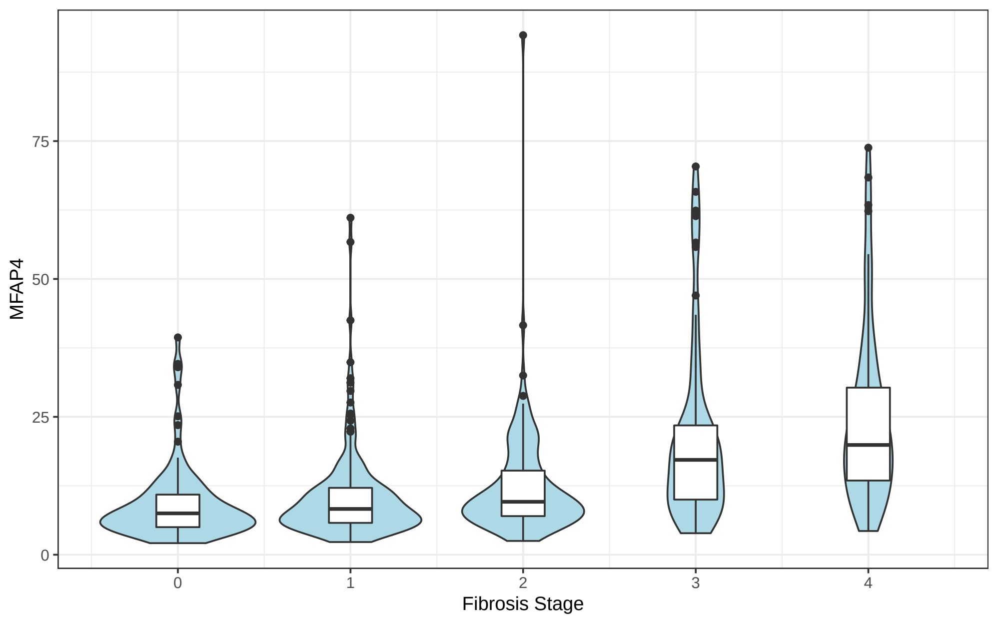
   Below, I load the data from the web.

```
> fn<-"http://cipolli.com/students/data/biomarker.csv"
> dat <- read.csv(file=fn, header=TRUE, sep=",")
> head(dat)
```

```
  Patient.ID Year.of.Birth Gender Date.of.sampling Fibrosis.Stage HCV.Genotype
1       1112          1958 female         2/1/2005              0            1
2       3403          1946 female        1/18/2005              2             
3       2841          1954 female         1/3/2005              3            1
4        654          1958   male         2/1/2005              3            1
5       2788          1960   male        12/9/2004              0            3
6       2242          1954 female        5/12/2004              0            1
  MFAP4.U.mL
1        5.1
2        5.3
3       12.9
4        6.2
5        3.3
6        7.5
```

In homework 0, you recreated Table 1 in https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4932744/. Now, recreate Table 2.

```
> ggdat<-data.frame(fibrosis=dat$Fibrosis.Stage, MFAP4=dat$MFAP4.U.mL)
> ggplot(data=ggdat,aes(x=fibrosis, y=MFAP4, group=fibrosis))+
+   geom_violin(fill="lightblue")+
+   geom_boxplot(width=0.25)+
+   theme_bw()+
+   xlab("Fibrosis Stage")+
+   ylab("MFAP4")
```




```
> dat.f<-ggdat
> dat.f$fibrosis<-as.factor(dat.f$fibrosis)
> dat.f$MFAP4<-as.factor(dat.f$MFAP4)
> anova(lm(dat$MFAP4.U.mL~dat$Fibrosis.Stage))

Analysis of Variance Table

Response: dat$MFAP4.U.mL
                    Df Sum Sq Mean Sq F value    Pr(>F)
```

```
dat$Fibrosis.Stage   1  13584 13583.9  112.67 < 2.2e-16 ***
Residuals          540  65102   120.6
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> anova(lm(MFAP4.U.mL~Fibrosis.Stage, data=dat))

Analysis of Variance Table

Response: MFAP4.U.mL
                Df Sum Sq Mean Sq F value    Pr(>F)
Fibrosis.Stage   1  13584 13583.9  112.67 < 2.2e-16 ***
Residuals      540  65102   120.6
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> TukeyHSD(aov(lm(dat$MFAP4.U.mL~as.factor(dat$Fibrosis.Stage)), conf.level = 0.95))

  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = lm(dat$MFAP4.U.mL ~ as.factor(dat$Fibrosis.Stage)), conf.level = 0.95)

$`as.factor(dat$Fibrosis.Stage)`
         diff        lwr       upr     p adj
1-0  1.301353 -2.4541799  5.056886 0.8777020
2-0  3.153807 -0.7991649  7.106778 0.1874077
3-0 11.741745  7.0240362 16.459454 0.0000000
4-0 15.388014 10.6703049 20.105722 0.0000000
2-1  1.852454 -1.5452808  5.250188 0.5679669
3-1 10.440392  6.1771314 14.703652 0.0000000
4-1 14.086660  9.8234000 18.349921 0.0000000
3-2  8.587938  4.1497688 13.026107 0.0000017
4-2 12.234207  7.7960375 16.672376 0.0000000
4-3  3.646269 -1.4848264  8.777364 0.2948449
```

Comparison	Difference	Lower Bound	Upper Bound	p value
F1-F0				
F2-F0				
F3-F0				
F4-F0				
F2-F1				
F3-F1				
F4-F1				
F3-F2				
F4-F2				
F4-F3				

Table 1: Results of the pairwise comparisons of individual hepatic fibrosis stages with respect to MFAP4 values after significant ANOVA result.

** Are the results I get different from the table because the table uses log MFAP4 values?

3. Complete the following parts. This will lead you through the simulation of data, fitting regression lines and evaluating the assumptions.

(a) Fit a model to the following simulated data. Make observations about the model equation and the Pearson correlation.

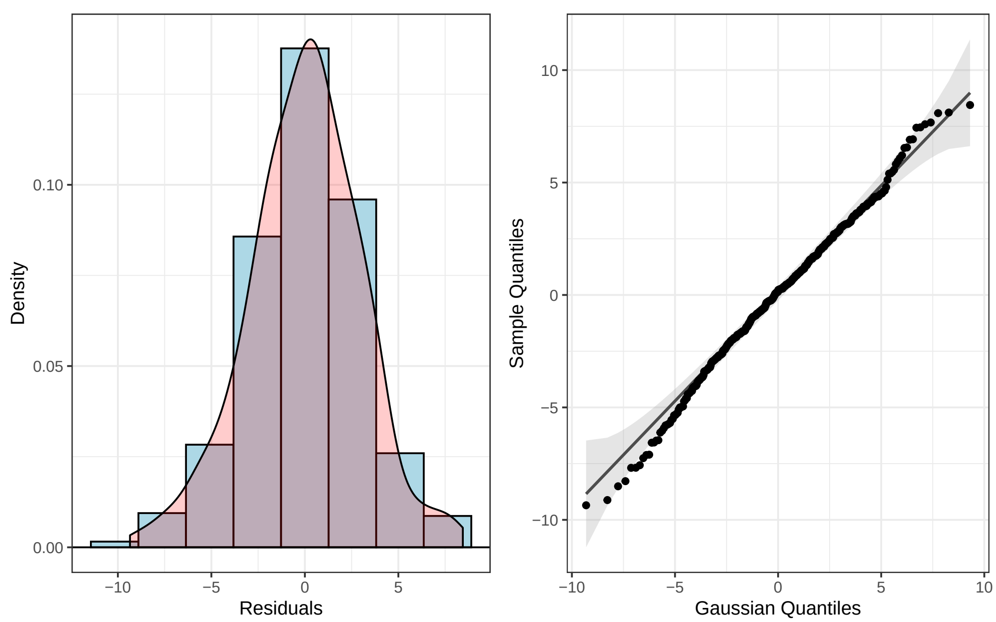
```
> n=500
> x<-sample(x = seq(0,5,0.01),size = n,replace = T)
> y<-5*x + 3
> plot(x,y)
> xy.mod<-lm(y~x)
> summary(xy.mod)

Call:
lm(formula = y ~ x)

Residuals:
       Min         1Q     Median         3Q        Max
-8.804e-14 -5.590e-16  1.810e-16  8.800e-16  3.788e-15

Coefficients:
             Estimate Std. Error   t value Pr(>|t|)
(Intercept) 3.000e+00  3.831e-16 7.831e+15   <2e-16 ***
x           5.000e+00  1.308e-16 3.822e+16   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.238e-15 on 498 degrees of freedom
Multiple R-squared:      1,        Adjusted R-squared:      1
F-statistic: 1.461e+33 on 1 and 498 DF,  p-value: < 2.2e-16

> cor(x,y, method = "pearson") #is the R squared the pearson correlation?
[1] 1
```

(b) Fit a model to the following simulated data, now with added Normal error. Make observations about the model equation and the Pearson correlation in relation to (a).

```
> e<-rnorm(n=n,mean=0,sd=3)
> y2<-5*x + 3 + e
> plot(x,y2)
> xy2.mod<-lm(y2~x)
> summary(xy2.mod)

Call:
lm(formula = y2 ~ x)

Residuals:
    Min      1Q  Median      3Q     Max
-9.3521 -1.8736  0.1815  2.0200  8.4481

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  2.88840    0.27288   10.59   <2e-16 ***
x            5.11015    0.09319   54.84   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 3.019 on 498 degrees of freedom
Multiple R-squared:  0.8579,        Adjusted R-squared:  0.8576
F-statistic:  3007 on 1 and 498 DF,  p-value: < 2.2e-16
```

(c) In the model of part (b), test for normality and constance of error terms. Note that we know both of these items to be true since we've taken $\epsilon \sim \mathrm{N}(\mu = 0, \sigma = 3)$.

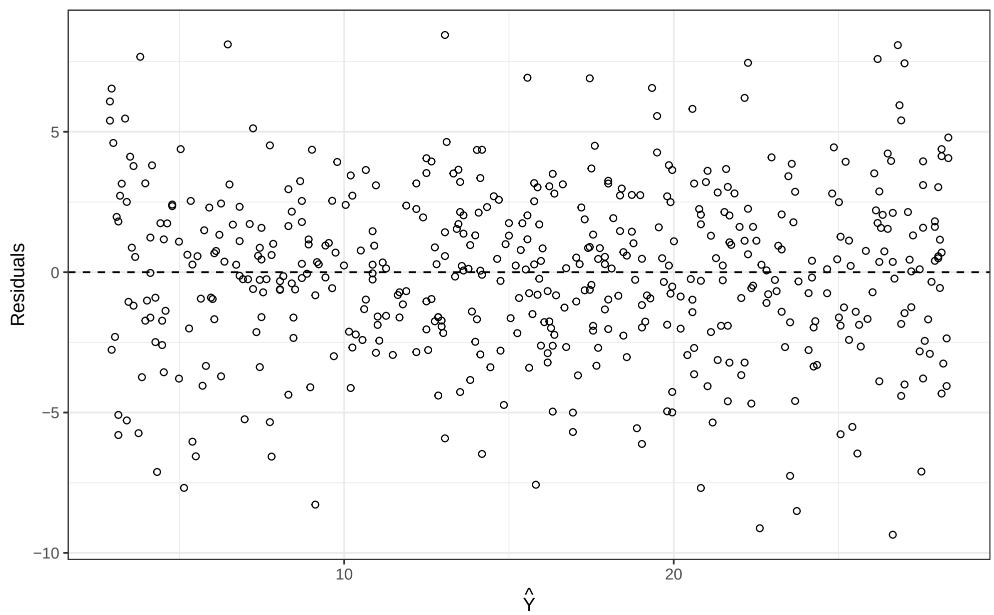
```
> #check for normality - plots residuals
> ggdat<-data.frame(residuals=xy2.mod$residuals)
> g1<-ggplot(data=ggdat,aes(x=residuals))+
+   geom_histogram(aes(y=..density..),
+                  fill="lightblue",color="black",bins=8)+
+   geom_hline(yintercept=0)+
+   geom_density(fill="red", alpha = 0.2)+
+   theme_bw()+
+   xlab("Residuals")+
+   ylab("Density")
> library("qqplotr")
> g2<-ggplot(data=ggdat,aes(sample=residuals))+
+   stat_qq_band(alpha=0.25) +
+   stat_qq_line() +
+   stat_qq_point() +
+   theme_bw()+
+   xlab("Gaussian Quantiles")+
+   ylab("Sample Quantiles")
> grid.arrange(g1,g2,ncol=2)
```




```
> sum(xy2.mod$residuals) #close to zero
```

```
[1] 8.312795e-15
```

```
> #check constance - plot residuals against fitted values
> ggdat<-data.frame(residuals=xy2.mod$residuals,
+                   fitted=xy2.mod$fitted.values)
> ggplot(data=ggdat, aes(x=fitted, y=residuals))+
+   geom_point(shape=1) +
+   geom_hline(yintercept=0, linetype="dashed")+
+   theme_bw()+
+   xlab(bquote(hat(Y)))+
+   ylab("Residuals")
```



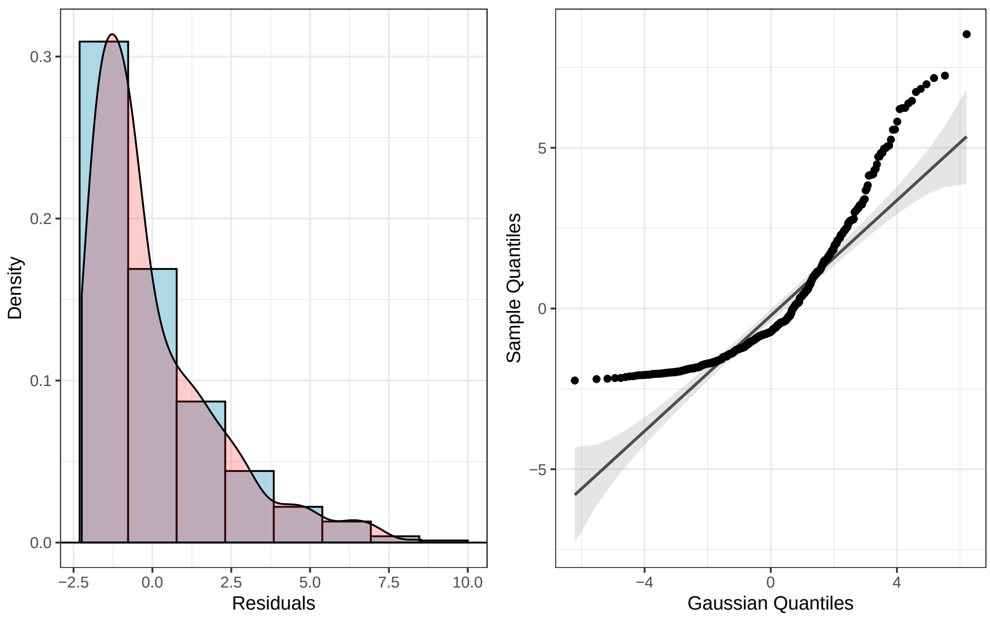
(d) Fit a model to the following simulated data, now with added exponential error. Make observations about the model equation and the Pearson correlation in relation to the model of part (b).

```
> e<-rexp(n=n,rate = 1/2)
> y3<-5*x + 3 + e
> plot(x,y3)

> xy3.mod<-lm(y3~x)
> summary(xy3.mod)

Call:
lm(formula = y3 ~ x)

Residuals:
    Min      1Q  Median      3Q     Max
-2.2405 -1.4410 -0.7256  0.9924  8.5343

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  5.26540    0.18206   28.92   <2e-16 ***
x            4.93482    0.06217   79.37   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 2.014 on 498 degrees of freedom
Multiple R-squared:  0.9267,       Adjusted R-squared:  0.9266
F-statistic:  6300 on 1 and 498 DF,  p-value: < 2.2e-16
```

(e) In the model of part (d), test for normality and constance of error terms. Note that we know that common variance is true but we've taken $\epsilon \sim \exp(\beta = 2)$.

```
> #check for normality - plots residuals
> ggdat<-data.frame(residuals=xy3.mod$residuals)
> g1<-ggplot(data=ggdat,aes(x=residuals))+
+   geom_histogram(aes(y=..density..),
+                  fill="lightblue",color="black",bins=8)+
+   geom_hline(yintercept=0)+
```

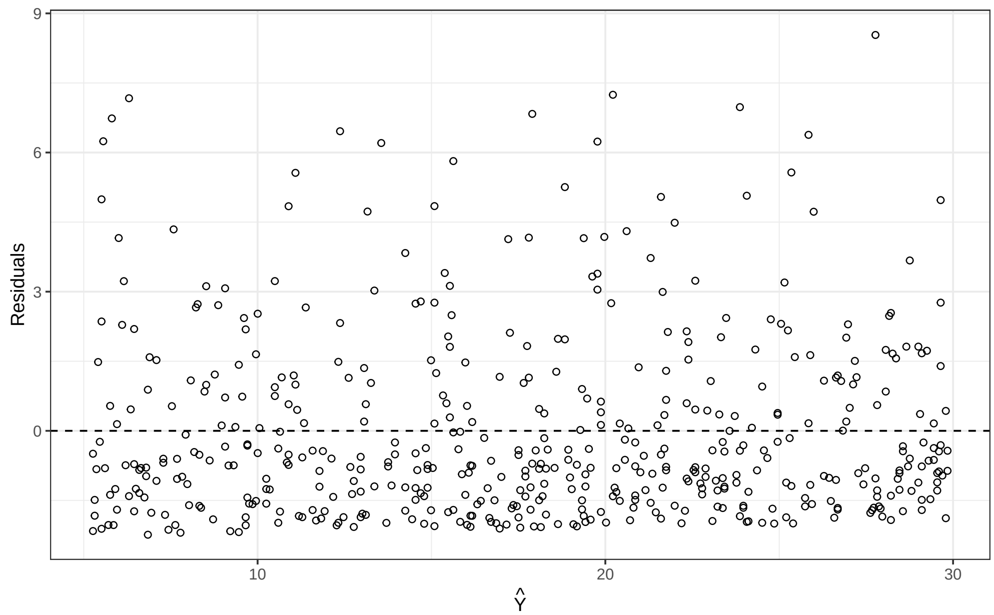
```
+   geom_density(fill="red", alpha = 0.2)+
+   theme_bw()+
+   xlab("Residuals")+
+   ylab("Density")
> library("qqplotr")
> g2<-ggplot(data=ggdat,aes(sample=residuals))+
+   stat_qq_band(alpha=0.25) +
+   stat_qq_line() +
+   stat_qq_point() +
+   theme_bw()+
+   xlab("Gaussian Quantiles")+
+   ylab("Sample Quantiles")
> grid.arrange(g1,g2,ncol=2)
```




```
> sum(xy3.mod$residuals) #close to zero
```

```
[1] -4.96686e-14
```

```
> #check constance - plot residuals against fitted values
> ggdat<-data.frame(residuals=xy3.mod$residuals,
+                   fitted=xy3.mod$fitted.values)
> ggplot(data=ggdat, aes(x=fitted, y=residuals))+
+   geom_point(shape=1) +
+   geom_hline(yintercept=0, linetype="dashed")+
+   theme_bw()+
+   xlab(bquote(hat(Y)))+
+   ylab("Residuals")
```



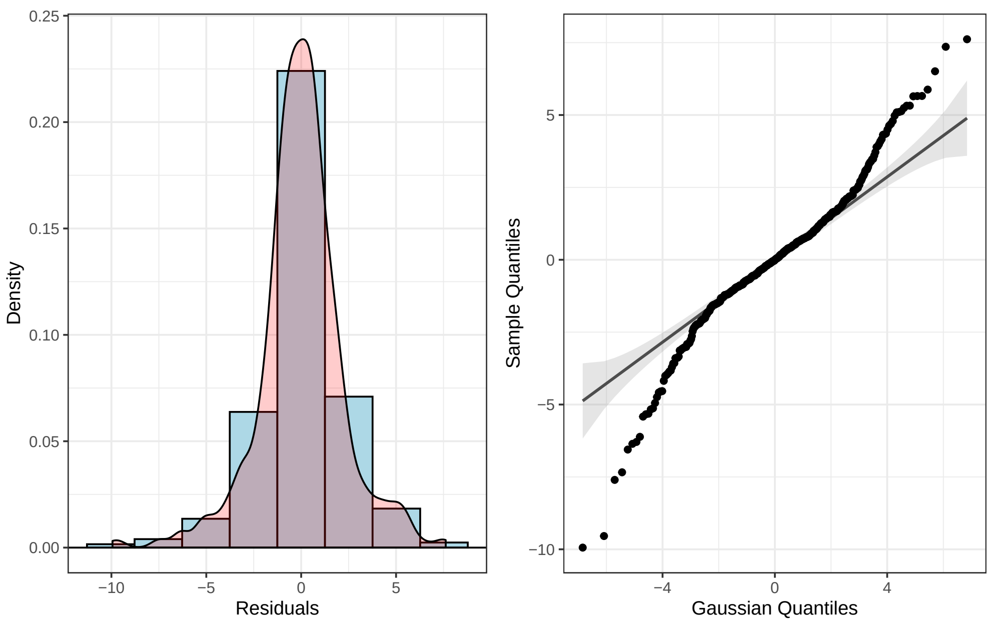
(f) Fit a model to the following simulated data, now with added Heteroskedastic normal error. Make observations about the model equation and the Pearson correlation in relation to the model of part (b).

```
> #order X to simulate non constant error
> x4<-x[order(x)]
> e<-rnorm(n=n,mean=0,sd=c(rep(1,n/2),rep(3,n/2)))
> y4<-5*x4 + 3 + e
> plot(x4,log(y4))

> x4y4.mod<-lm(y4~x4)
> summary(x4y4.mod)

Call:
lm(formula = y4 ~ x4)

Residuals:
    Min      1Q  Median      3Q     Max
-9.9412 -1.0581 -0.0021  1.0737  7.6170

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   2.9665     0.2006   14.79   <2e-16 ***
x4            5.0113     0.0685   73.16   <2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 2.219 on 498 degrees of freedom
Multiple R-squared:  0.9149,	Adjusted R-squared:  0.9147
F-statistic:  5352 on 1 and 498 DF,  p-value: < 2.2e-16
```

(g) In the model of part (f), test for normality and constance of error terms. Note that we know that normality of error terms is true, but $\epsilon \sim \mathrm{N}(\mu = 0, \sigma = 1)$ for $x < \widehat{m}$ and $\epsilon \sim \mathrm{N}(\mu = 0, \sigma = 3)$ for $x > \widehat{m}$.

```
> #check for normality - plots residuals
> ggdat<-data.frame(residuals=x4y4.mod$residuals)
```

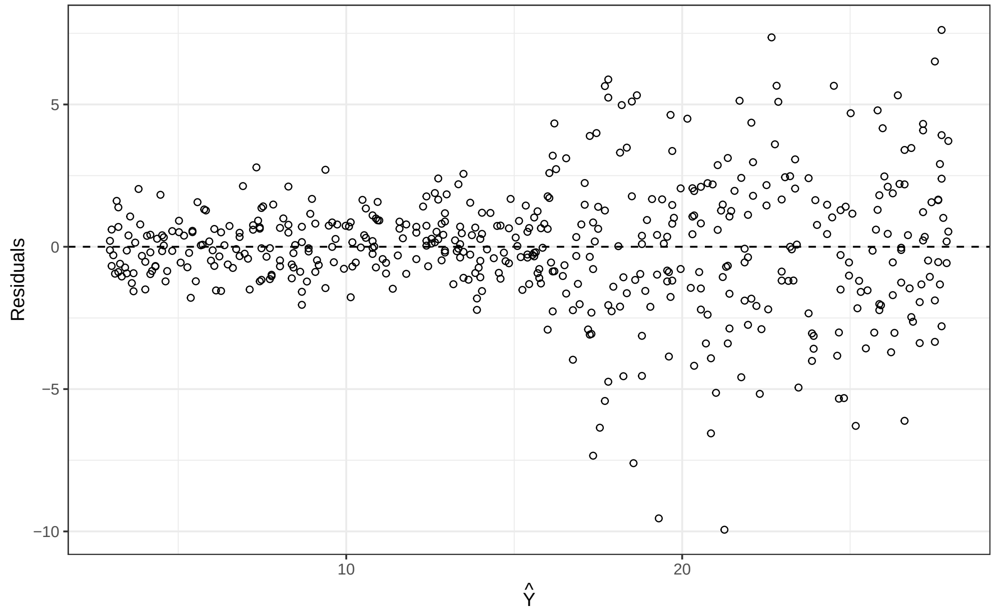
```
> g1<-ggplot(data=ggdat,aes(x=residuals))+
+   geom_histogram(aes(y=..density..),
+                  fill="lightblue",color="black",bins=8)+
+   geom_hline(yintercept=0)+
+   geom_density(fill="red", alpha = 0.2)+
+   theme_bw()+
+   xlab("Residuals")+
+   ylab("Density")
> library("qqplotr")
> g2<-ggplot(data=ggdat,aes(sample=residuals))+
+   stat_qq_band(alpha=0.25) +
+   stat_qq_line() +
+   stat_qq_point() +
+   theme_bw()+
+   xlab("Gaussian Quantiles")+
+   ylab("Sample Quantiles")
> grid.arrange(g1,g2,ncol=2)
```




```
> sum(x4y4.mod$residuals) #close to zero
```

```
[1] -8.09422e-15
```

```
> #check constance - plot residuals against fitted values
> ggdat<-data.frame(residuals=x4y4.mod$residuals,
+                   fitted=x4y4.mod$fitted.values)
> ggplot(data=ggdat, aes(x=fitted, y=residuals))+
+   geom_point(shape=1) +
+   geom_hline(yintercept=0, linetype="dashed")+
+   theme_bw()+
+   xlab(bquote(hat(Y)))+
+   ylab("Residuals")
```



4. Consider the following simulation. This looks intimidating, but it's a fairly simple exploration about what we'll talk about in class. This walks you through "seeing" what's going on in the background.

   (a) Plot the data simulated below. Assess the linear relationship.

   ```
   > set.seed(50)
   > x_1<-sample(x=seq(0,100,0.01),size=50,replace=TRUE)
   > e_1<-rnorm(n=50,mean=0,sd=5)
   > y_1<-3.5+2.1*x_1 + e_1

   > plot(x_1, y_1)
   ```

   i. Write out the population model.

   $$Y_i = \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + \epsilon$$

   ii. Fit the model based on the sample data and write out the sample model below.
   iii. Add the regression line to the plot in black, with lwd=2 and lty=3.
   iv. Check the assumptions of OLS for this model.
   v. Interpret the R^2 of the model.
   vi. Interpret the overall F test of the model. Report all 5 steps.
   vii. Interpret the coefficients of the model; are they what you would expect?

   (b) Now, let's add a bad datapoint to the data created in part (a).

   i. Plot the data simulated below; ensure to plot the Assess the linear relationship.

   ```
   > x_2<-c(x_1,100)
   > y_2<-c(y_1,25)
   ```

   ii. Fit the model based on the sample data and write out the sample model below.
   iii. Check the assumptions of OLS for this model.
   iv. Plot the data and regression lines from Questions 1-2. Add the regression line to the plot in red.
   v. Interpret the coefficients of the model; are they what you would expect?

   (c) Continue with the data from Question b.

   i. Plot the residuals of your model against x_2 as well as the residuals against predicted.

ii. Fit the appropriate model for estimating the weights for weighted least squares regression.
iii. Provide a summary of the weights. How does the weight for the observation (100,25) compare to the other observations?
iv. Use the weights from the previous part to fit a weighted least squares regression.
v. Check the assumptions of OLS for this model.
vi. Plot the data and regression lines from Questions 1-2. Add the regression line to the plot in blue.
vii. Interpret the coefficients of the model; are they what you would expect?

(d) Continue with the data from parts (b,c).

i. Fit a robust regression using Huber-weighted iterated reweighted least squares and write out the sample model below.
ii. Plot the data and regression lines from Questions 1-3. Add the regression line to the plot in purple.
iii. Interpret the coefficients of the model; are they what you would expect?

(e) Continue with the data from parts (b,c,d).

i. Fit a robust regression using Bisquare-weighted iterated reweighted least squares and write out the sample model below.
ii. Plot the data and regression lines from Questions 1-4. Add the regression line to the plot in purple.
iii. Interpret the coefficients of the model; are they what you would expect?

(f) Continue with the data from parts (b,c,d,e).

i. Fit a quantile regression and write out the sample model below.
ii. Plot the data and regression lines from Questions 1-5. Add the regression line to the plot in black
iii. Interpret the coefficients of the model; are they what you would expect?

(g) Reflect on parts (a-f).

i. Which model is "right"? If there's no one model that is "right", which one is "best"?
ii. Rerun your code for Questions 1-6, but change the original sample size from 50 to 1000. There's no need to redo all of the parts from those questions, but discuss the difference. Look at the graph of the data with all the fitted regression models and compare it to that from the original data.

5. **Case Study** The MASS package in `R` (Venables and Ripley, 2002) provides data about housing values in the Suburbs of Boston. The data provided is described below.

- **crim** – per capita crime rate by town.
- **zn** – proportion of residential land zoned for lots over 25,000 sq.ft.
- **indus** – proportion of non-retail business acres per town.
- **chas** – Charles River dummy variable (= 1 if tract bounds river; 0 otherwise).
- **nox** – nitrogen oxides concentration (parts per 10 million).
- **rm** – average number of rooms per dwelling.
- **age** – proportion of owner-occupied units built prior to 1940.
- **dis** – weighted mean of distances to five Boston employment centres.
- **rad** – index of accessibility to radial highways.
- **tax** – full-value property-tax rate per \$10,000.
- **ptratio** – pupil-teacher ratio by town.
- **black** – $1000(Bk - 0.63)^2$ where Bk is the proportion of blacks by town.

- **lstat** – lower status of the population (percent).
- **medv** – median value of owner-occupied homes in \$1000s.

You can load this data using

```
> #install.packages("MASS",repos = "http://cloud.r-project.org/")
> library(MASS)
> data(Boston)
```

Use your tools to build a regression model that predicts the median value of owner-occupied homes in \$1000s based on the other variables in the data set.

```
> mod<-lm(formula = medv ~ crim +. , data = Boston)
> summary(mod)

Call:
lm(formula = medv ~ crim + ., data = Boston)

Residuals:
    Min      1Q  Median      3Q     Max 
-15.595  -2.730  -0.518   1.777  26.199 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)    
(Intercept)  3.646e+01  5.103e+00   7.144 3.28e-12 ***
crim        -1.080e-01  3.286e-02  -3.287 0.001087 ** 
zn           4.642e-02  1.373e-02   3.382 0.000778 ***
indus        2.056e-02  6.150e-02   0.334 0.738288    
chas         2.687e+00  8.616e-01   3.118 0.001925 ** 
nox         -1.777e+01  3.820e+00  -4.651 4.25e-06 ***
rm           3.810e+00  4.179e-01   9.116  < 2e-16 ***
age          6.922e-04  1.321e-02   0.052 0.958229    
dis         -1.476e+00  1.995e-01  -7.398 6.01e-13 ***
rad          3.060e-01  6.635e-02   4.613 5.07e-06 ***
tax         -1.233e-02  3.760e-03  -3.280 0.001112 ** 
ptratio     -9.527e-01  1.308e-01  -7.283 1.31e-12 ***
black        9.312e-03  2.686e-03   3.467 0.000573 ***
lstat       -5.248e-01  5.072e-02 -10.347  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.745 on 492 degrees of freedom
Multiple R-squared:  0.7406,	Adjusted R-squared:  0.7338 
F-statistic: 108.1 on 13 and 492 DF,  p-value: < 2.2e-16

> #remove statistically insignificant variables
> mod1<-lm(formula = medv ~ crim + zn + chas + nox + rm + dis + rad + tax + ptratio + black + lstat
> summary(mod1)

Call:
lm(formula = medv ~ crim + zn + chas + nox + rm + dis + rad + 
    tax + ptratio + black + lstat, data = Boston)

Residuals:
     Min       1Q   Median       3Q      Max 
-15.5984  -2.7386  -0.5046   1.7273  26.2373 
```

```
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  36.341145   5.067492   7.171 2.73e-12 ***
crim         -0.108413   0.032779  -3.307 0.001010 **
zn            0.045845   0.013523   3.390 0.000754 ***
chas          2.718716   0.854240   3.183 0.001551 **
nox         -17.376023   3.535243  -4.915 1.21e-06 ***
rm            3.801579   0.406316   9.356  < 2e-16 ***
dis          -1.492711   0.185731  -8.037 6.84e-15 ***
rad           0.299608   0.063402   4.726 3.00e-06 ***
tax          -0.011778   0.003372  -3.493 0.000521 ***
ptratio      -0.946525   0.129066  -7.334 9.24e-13 ***
black         0.009291   0.002674   3.475 0.000557 ***
lstat        -0.522553   0.047424 -11.019  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.736 on 494 degrees of freedom
Multiple R-squared:  0.7406,	Adjusted R-squared:  0.7348
F-statistic: 128.2 on 11 and 494 DF,  p-value: < 2.2e-16

> summary(mod1)$r.squared

[1] 0.7405823
```

References

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