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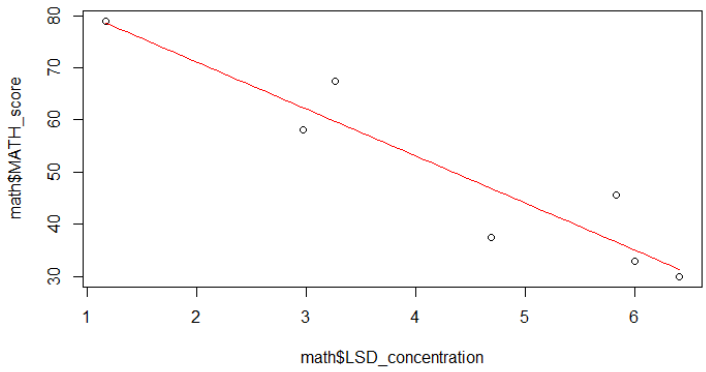
Stats
1/22/19

Homework 1

Question 1

```
> math<-read.csv("R/math_scores.csv")
> str(math)
'data.frame':  7 obs. of  2 variables:
 $ LSD_concentration: num  1.17 2.97 3.26 4.69 5.83 6 6.41
 $ MATH_score       : num  78.9 58.2 67.5 37.5 45.6 ...
> summary(math)
 LSD_concentration   MATH_score
 Min.   :1.170     Min.   :29.97
 1st Qu.:3.115     1st Qu.:35.20
 Median :4.690     Median :45.65
 Mean   :4.333     Mean   :50.09
 3rd Qu.:5.915     3rd Qu.:62.84
 Max.   :6.410     Max.   :78.93
> plot(math$MATH_score~math$LSD_concentration)
> mathmod<-lm(math$MATH_score~math$LSD_concentration)
> coef(mathmod)
           (Intercept) math$LSD_concentration
             89.123874                -9.009466
> curve(89.123874+-9.009466*x, add = T, col="red")
```

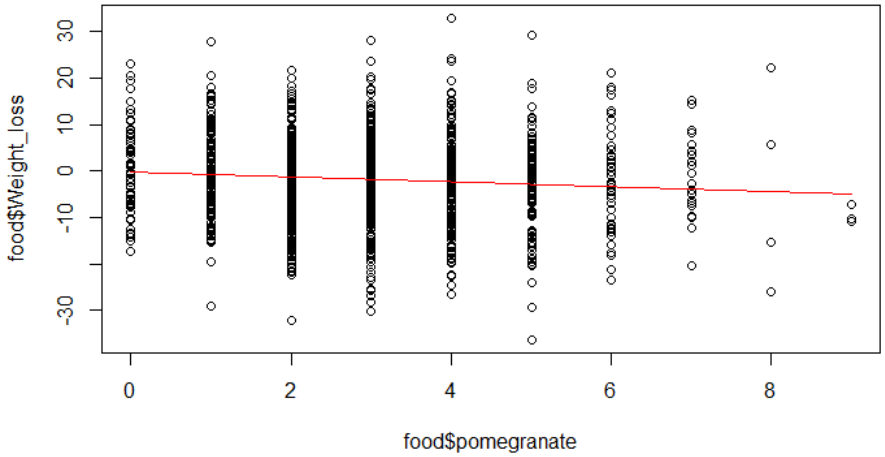



```
> confint(mathmod)
                              2.5 %     97.5 %
(Intercept)              71.00758 107.240169
math$LSD_concentration -12.87325  -5.145685
> a<-89.123874
> b<--9.009466
> yhat<-a+b*math$LSD_concentration
> SS<-sum((math$MATH_score-50.09)^2)
> RSS<-sum((math$MATH_score-yhat)^2)
> 1-(RSS/SS)
[1] 0.877835
```

A) To ensure a test score of over 85% you need a dosage of LSD that is equal or less than 0.4576. 85=89.123+-9.009(X)…. X=0.4576
B) The LSD dosage predicts math scores fairly well with a R^2=0.877.
C) The normal distribution may be inappropriate because the sample size is so small that it is difficult to determine if the data has a normal structure.

Question 2

```
> food<-read.csv("R/miracle_food.csv")
> str(food)
'data.frame':  1000 obs. of  2 variables:
 $ Weight_loss: num  -0.89 6.31 -30.21 -6.28 11.38 ...
 $ pomegranate: int  2 2 3 7 4 2 3 3 5 5 ...
> summary(food)
  Weight_loss       pomegranate
 Min.   :-36.240   Min.   :0.000
 1st Qu.: -8.570   1st Qu.:2.000
 Median : -1.650   Median :3.000
 Mean   : -1.724   Mean   :2.942
 3rd Qu.:  5.037   3rd Qu.:4.000
 Max.   : 32.890   Max.   :9.000
> plot(food$Weight_loss~food$pomegranate)
> foodmod<-lm(food$Weight_loss~food$pomegranate)
> coef(foodmod)
     (Intercept) food$pomegranate
      -0.1789802       -0.5251053
> curve(-0.17898+-0.52510*x, add = T, col="red")
```




```
> confint(foodmod)
                       2.5 %     97.5 %
(Intercept)       -1.408937  1.0509767
food$pomegranate -0.886420 -0.1637906
> m<--0.17898
> n<--0.52510
> yhat<-m+n*food$pomegranate
> SS<-sum((food$Weight_loss--1.724)^2)
> RSS<-sum((food$Weight_loss-yhat)^2)
> 1-(RSS/SS)
[1] 0.008083812
```

I do not agree with the claim that pomegranates helps with weight loss. The extremely low R^2 value (0.008) tells me that the model does a horrible job of predicting the data. Therefore, the amount of pomegranates eaten does not accurately predict weight loss.

Question 3

Function:

```
MAE<-function(y, yhat, n) {(1/n)*sum(abs(y-yhat))}
```

Math data:

RMSE:

```
> sqrt(mean((math$MATH_score-yhat)^2))
[1] 6.022355
```

R^2: 0.877835

MAE:

```
>MAE(y=math$MATH_score, yhat=89.123874+-9.009466*math$LSD_concentration, n=7)
[1] 4.890145
```

Food data:

RMSE:

```
> sqrt(mean((food$weight_loss-yhat)^2))
[1] 9.961044
```

R^2: 0.008083812

MAE:

```
>MAE(y=food$weight_loss, yhat=-0.17898+-0.52510*food$pomegranate, n=1000)
[1] 7.981461
```

The food data has a very high RMSE especially when you look at how small the slope is. Taking the MAE decreases the error a little bit, but still shows high variation from predicted points to actually observed data.

Question 4

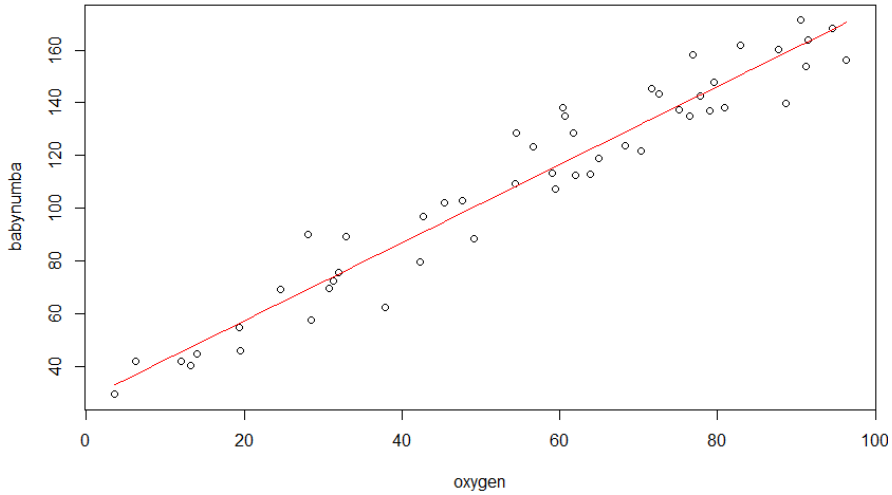
How does the level of oxygen in the water effect number of salmon offspring.

```
> oxygen<-runif(50, min=0, max=100)
> slope<-1.5
> intercept<-27

> babynumba<-rnorm(n=50, mean=intercept+slope*oxygen, sd=11)
> oxygen
 [1] 91.513178 82.921415 14.025232  6.186944 60.339769 30.766070 56.600732 94
.622946 88.660579 61.714800 64.949382
[12] 77.794945 28.458825 54.485391 12.010367 68.340633 58.992279 32.002447 63
.850225 28.016477 47.635212 54.331951
[23] 79.004674 87.721825 76.860253 71.680344  3.544301 80.895438 90.602979 37
.831771 19.394107 19.524388 70.366727
[34] 76.530286 31.317946 91.244335 79.575077 42.296468 45.402274 42.749988 32
.955032 72.535210 60.617658 59.452078
[45] 49.085682 24.537979 13.175931 96.371900 75.117814 61.982155
```

```
> babynumba
 [1] 164.01754 161.88521  44.67567  42.00623 138.08213  69.72432 123.43693 16
8.28017 139.75281 128.46999 118.87943
[12] 142.63865  57.61675 128.74246  42.01822 123.67976 113.54334  75.67099 11
2.91671  90.27277 102.92433 109.38802
[23] 136.93224 160.13431 158.11499 145.49042  29.45521 138.03383 171.28849  6
2.59388  54.83637  46.22218 121.86613
[34] 134.95248  72.50642 153.94686 147.73836  79.71988 102.19336  97.03057  8
9.45860 143.55504 135.03310 107.40421
[45]  88.69211  69.46224  40.34806 156.28155 137.38401 112.44494
> plot(babynumba~oxygen)
> model<-lm(babynumba~oxygen)
> coef(model)
(Intercept)      oxygen
  27.829322    1.479927

> curve(27.829322+1.4799*x, add=T, col="red")
```



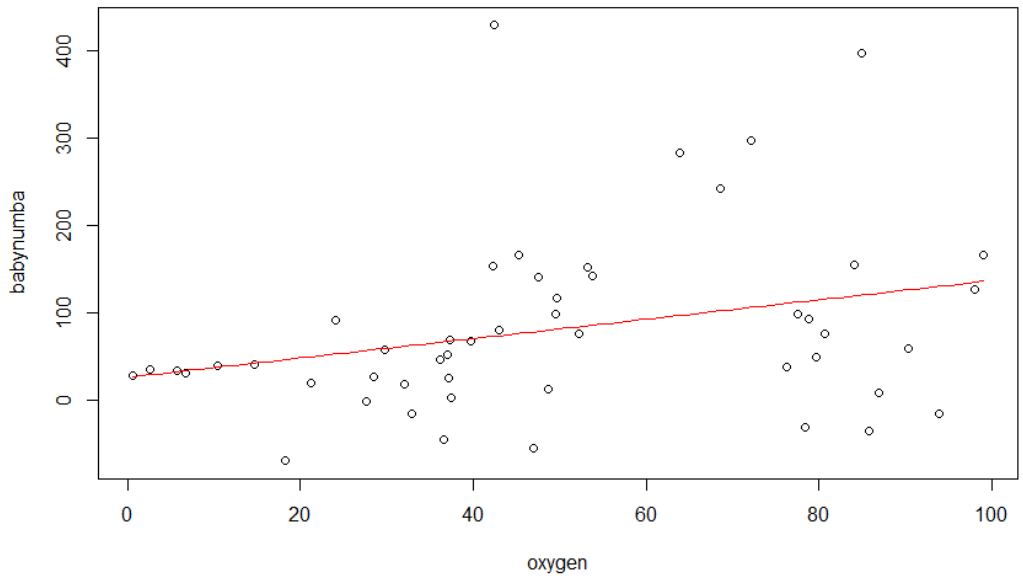
My estimates are extremely close to my set parameters.

Question 5

```
> oxygen<-runif(50, min=0, max=100)
>
> slope<-1.5
> intercept<-27
> sd<-(oxygen*2)
>
> babynumba<-rnorm(n=50, mean=intercept+slope*oxygen, sd)
>
> oxygen
 [1] 68.5905026 18.2767907 79.7402110 53.7840533 36.9795841 93.9449254 76.236
8807 42.2443310 43.0241601 85.8370586
[11] 37.1110472 52.1868965 45.3243309 14.7441561 21.2900886 99.0807190 42.454
7376 80.6264146 10.3413749 84.1171689
[21] 49.5465235 47.5817754 47.0207197 97.9896036 27.5865719 78.3505681 36.129
8476 78.8850430 32.0332619  0.5884682
[31] 63.9368161 90.3575582 37.5027739  5.7579422 24.0502437 36.5825688 72.124
8978  2.5668381 29.8082433 84.9902869
[41]  6.6890839 86.8893877 77.5981656 48.6108971 49.6832243 32.9304707 53.181
7149 28.4625526 39.7312838 37.3026041
```

```
> babynumba
 [1] 242.609474 -69.033102  50.335957 142.248821  52.385574 -15.586052  38.54
1274 153.372738  80.695223 -35.286654
[11]  26.458508  76.367237 166.549167  40.932470  19.655087 166.061261 429.38
3611  77.243707  39.714623 155.213390
[21]  99.581220 141.639133 -53.788295 126.914196  -1.053097 -30.844851  47.24
1508  93.007863  18.522905  28.855519
[31] 282.844938  59.484262   2.816173  33.980686  91.993027 -44.874966 297.53
2317  35.268772  58.287985 397.720713
[41]  32.099104   8.766778  99.406381  12.941841 117.059179 -14.333822 152.51
6832  26.776455  68.007161  69.205766
>
> plot(babynumba~oxygen)
>
> model<-lm(babynumba~oxygen)
>
> coef(model)
(Intercept)      oxygen
  26.776073    1.106902

> curve(26.776073+1.106902*x, add=T, col="red")
```



Lower oxygen levels seem to predict lower levels of salmon offspring. However, as oxygen levels increase this can either greatly reduce or greatly increase the number of salmon offspring. There appears to be something else interacting with the high level of oxygen to create this large variation in data.