Biomath 204 hw2

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Problem 1

Define $f(x) = x^2 - a, f'(x) = 2x$. According to newton's method, we have

$$x_{n+1} = x_n - \frac{f(x)}{f'(x)} = x_n - \frac{x_n^2 - a}{2x_n} = \frac{1}{2}(x_n - \frac{a}{x_n}).$$

```
newton <- function(f, fp, x) {
    tol = 1e-14
    xo = x
    xn = Inf
    iterations = 1
    for (i in 1:100) {
        xn = xo - f(xo) / fp(xo)
        if (abs(xn - xo) < tol) {
            break
        }
        # print(xn)
        # print(abs(xn - 12))
        xo = xn
        iterations = iterations + 1
    }

    if (iterations > 100) {
      error("Did not converge in 100 steps")
    }
    else {
      # print(iterations)
      return(xn)
    }
}

a = 144
test <- function(x) {return (x^2 - a)}
test_derivative <- function(x) {return (2*x)}
initial_guess = 2.34
newton(test, test_derivative, initial_guess)
```

```
## [1] 12
```

To show empiracally that this does converge to the desired quantity, I tested for the case $a = 144$, whose square root is 12. With initial guess 2.34, it took 8 steps to converge within tolerance of 10e-14. I never got the plots to work, but I can illustrate the same idea using numbers. For each iterations we have

$$x_1 = 31.93923, x_2 = 18.2239, x_3 = 13.0628, x_4 = 12.04324, x_5 = 12.00008, x_6 = x_7 = x_8 = 12$$

From this hint, we know that quadratic convergence implies $e_{n+1} \leq Ke_n^2 \iff K \geq \frac{e_{n+1}}{e_n^2}$ for some K and all

n. From the 7 terms above, the errors are

$$e_1 = 19.93923, e_2 = 6.223896, e_3 = 1.062805, e_4 = 0.0432355, e_5 = 7.760824e-05, e_6 = 2.509584e-10, e_7 = 0$$

and from this the first couple K's are:

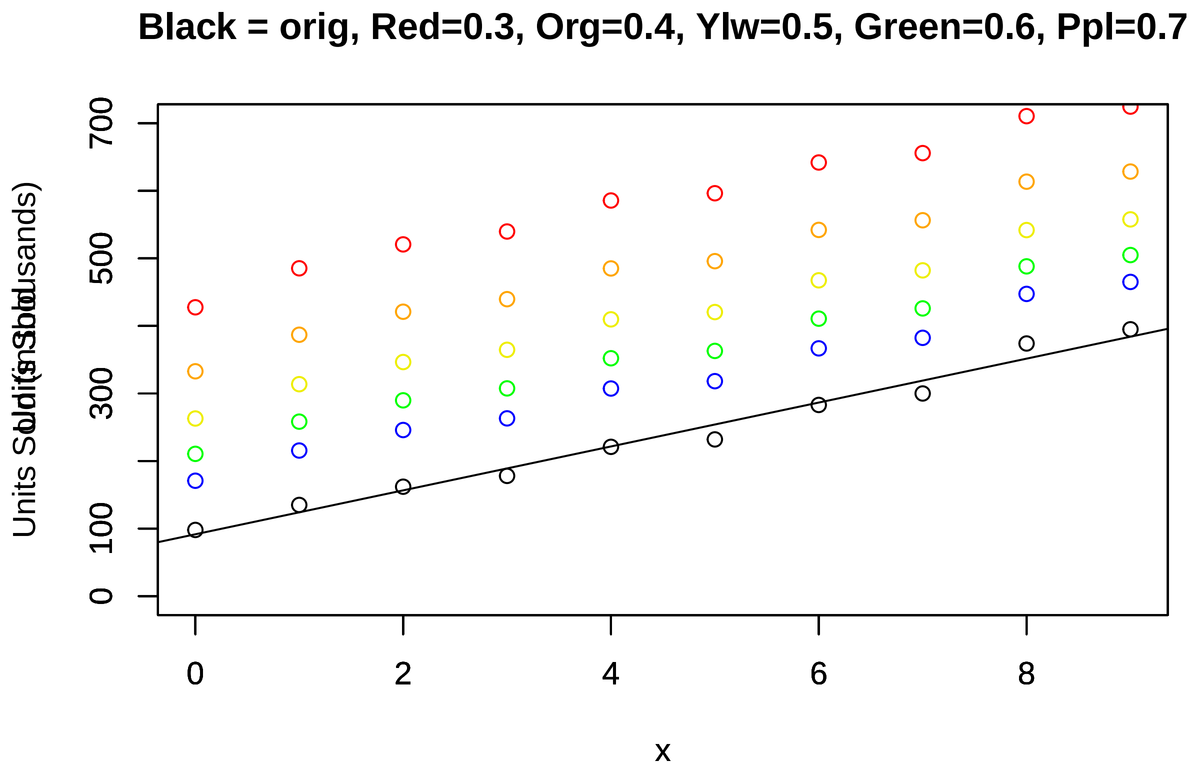
$$K_1 = 0.01565473, K_2 = 0.02743651, K_3 = 0.0382766, K_4 = 0.04151709, K_5 = 0.04166641$$

We observe that the K's eventually stabalize at around 0.042. In other words, we can pick $K = 0.05$ to satisfy $K \geq \frac{e_{n+1}}{e_n^2}$ for all n. i.e. we have quadratic convergence.

Problem 2

```r
library(MASS)
x = seq(0, 9, 1)
y = c(98, 135, 162, 178, 221, 232, 283, 300, 374, 395)
regl <- lm(y ~ x)
plot(x, y, ylim=c(0,700), ylab="Units Sold")
abline(regl)

g <- function(y) {
  n = length(y)
  output = 1
  for (num in y) {
    output = output * num^(1/n)
  }
  return(output)
}

z <- function(y, lambda, g) {
  output <- list()
  for (i in y) {
    z_i = (i^lambda - 1) / lambda / g^(lambda-1)
    # z_i = (i^lambda - 1) / lambda
    output <- append(output, z_i)
  }
  return(output)
}

num = g(y)
three = z(y, 0.3, num)
four = z(y, 0.4, num)
five = z(y, 0.5, num)
six = z(y, 0.6, num)
seven = z(y, 0.7, num)

par(new=TRUE)
plot(x, three, col="red", ylim=c(0,700), ylab="Units Sold (in thousands)", main="Black = orig, Red=0.3,
par(new=TRUE)
plot(x, four, col="orange", ylim=c(0,700), ylab="Units Sold")
par(new=TRUE)
plot(x, five, col="yellow2", ylim=c(0,700), ylab="Units Sold")
par(new=TRUE)
plot(x, six, col="green", ylim=c(0,700), ylab="Units Sold")
```

```r
par(new=TRUE)
plot(x, seven, col="blue", ylim=c(0,700), ylab="Units Sold")
```



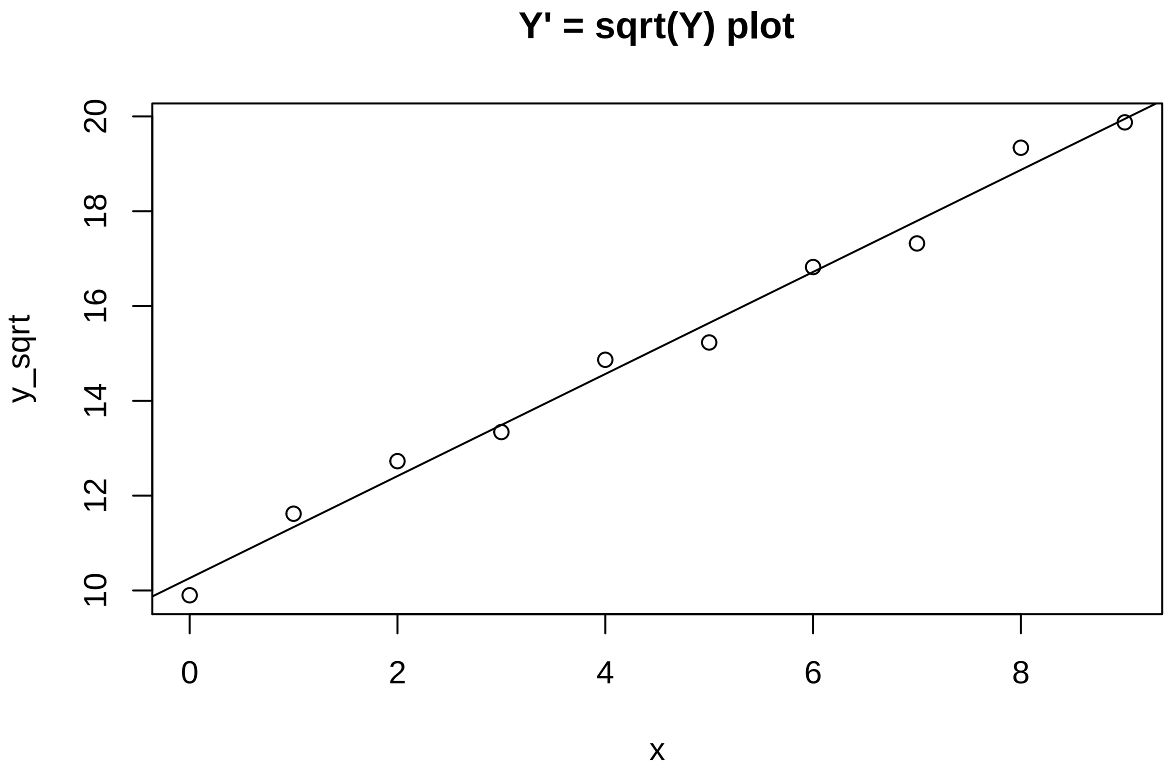

```r
# anova(lm(unlist(three) ~ x))
# anova(lm(unlist(four) ~ x))
# anova(lm(unlist(five) ~ x))
# anova(lm(unlist(six) ~ x))
# anova(lm(unlist(seven) ~ x))
```

It appears that the function, both before (black) and after box-cox transfer(red ~ blue) is quite linear. Here yellow line is the box cox transform with $\lambda = 0.5$. The SSE for each case can be computed by calling anova(lm(y ~ x)) as long as we converted the list element into a vector by unlisting them first. The SSE for the original = 1799, and the transformed ones have

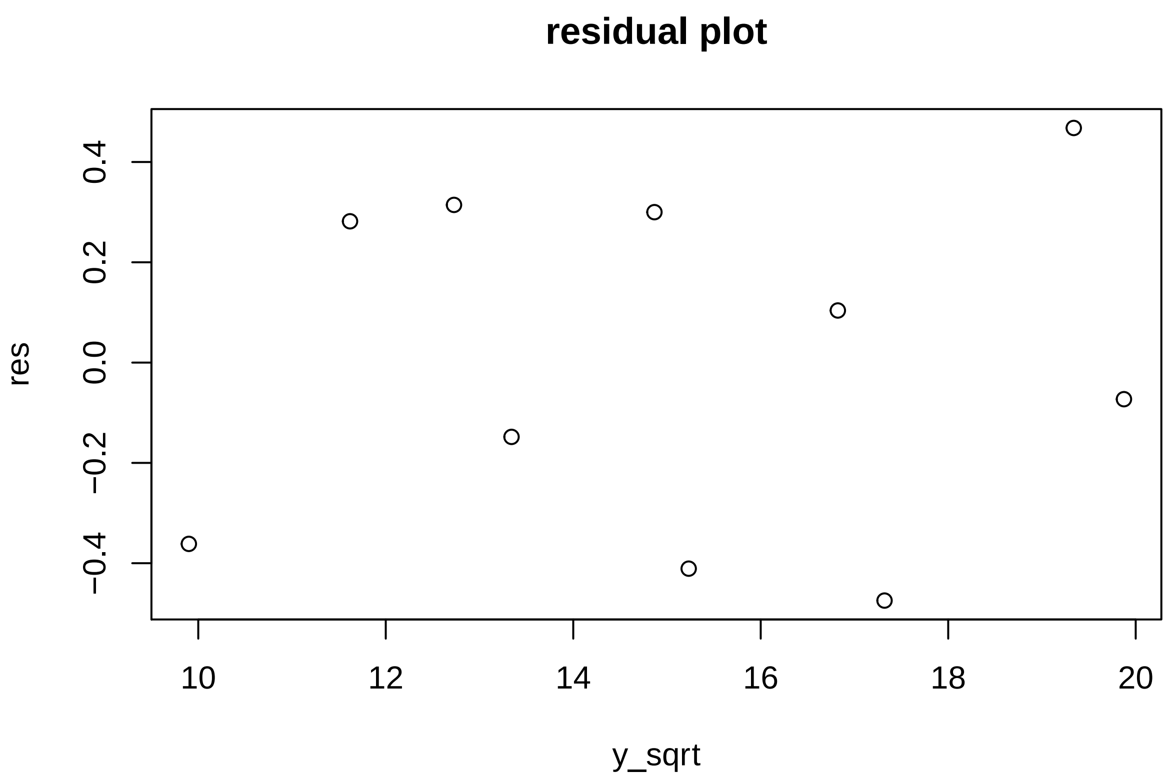
$$\text{SSE: } \lambda_{0.3} = 1100, \lambda_{0.4} = 968, \lambda_{0.5} = 916, \lambda_{0.6} = 942, \lambda_{0.7} = 1044$$

In particular this suggests that $\lambda = 0.5$ is the transform that minimizes the SSE.

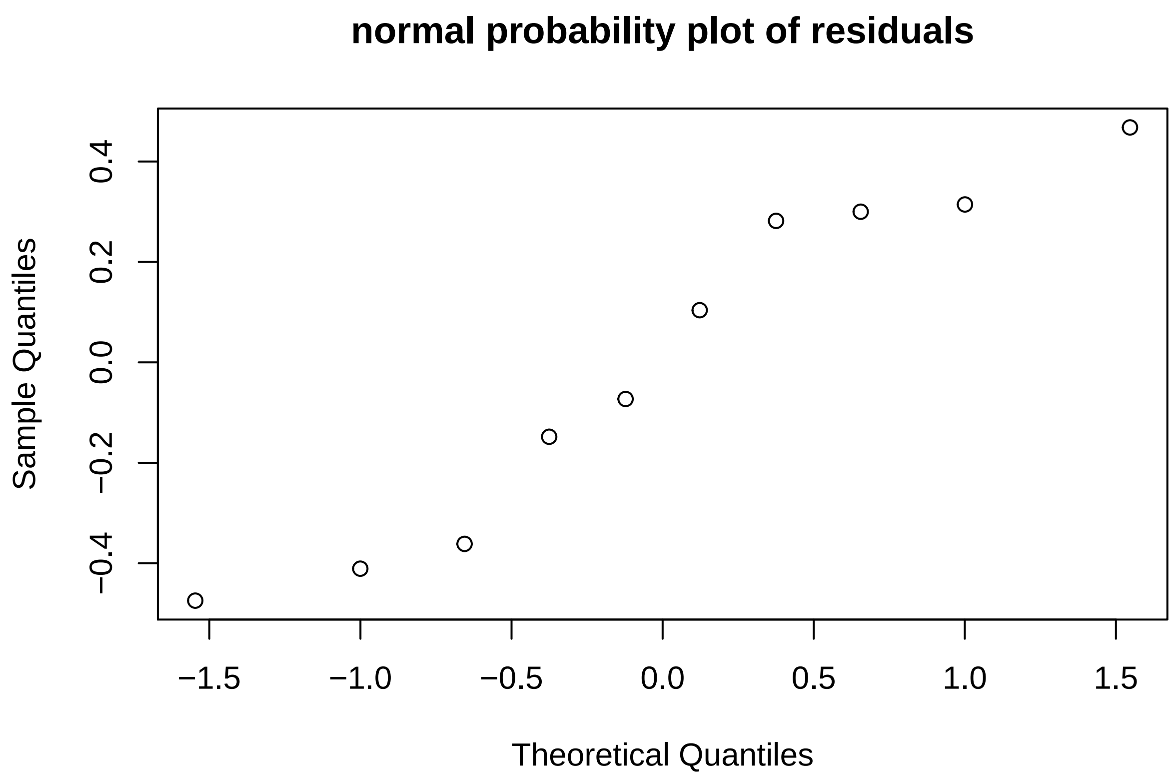
```r
x = seq(0, 9, 1)
y = c(98, 135, 162, 178, 221, 232, 283, 300, 374, 395)
y_sqrt = c(98^.5, 135^.5, 162^.5, 178^.5, 221^.5, 232^.5, 283^.5, 300^.5, 374^.5, 395^.5)

regl <- lm(y_sqrt ~ x)
plot(x, y_sqrt, main="Y' = sqrt(Y) plot")
abline(regl)
```




```r
res <- residuals(lm(y_sqrt ~ x))
plot(y_sqrt, res, main="residual plot")
```



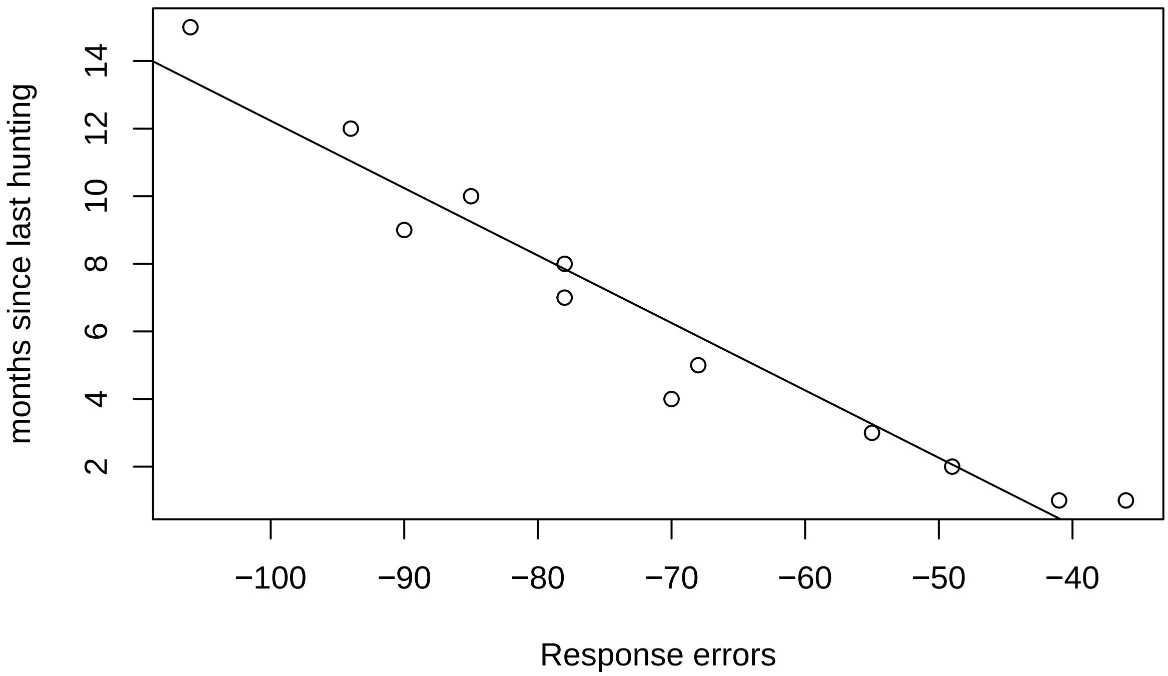

```r
qqnorm(res, main="normal probability plot of residuals")
```



Here the regression line appears to be a reasonably good fit to the transformed data, since it's linear. It appears that just plotting the residuals against the fitted values ($\sqrt{Y}$) does have have any indication that it's normally distributed. However graphing it in the normal probability plot, we see a rather straight line, indicating that it is almost normal.

Problem 3

```
mydata = read.table("ch03pr18.dat.txt")
x = mydata[1]
y = mydata[2]
regl <- lm(unlist(y) ~ unlist(x))
plot(unlist(x), unlist(y), xlab="Response errors", ylab="months since last hunting")
abline(regl)
```




```
#residuals(lm(unlist(mydata[2]) ~ unlist(mydata[1])))
```

Here the correlation between response errors and the months since last hinting is very linear, with correlation of -0.997. If we were to rescale this plot, I propose rescaling the Y axis (months since last hunting). This is because visually the scatter plot exhibits a somewhat inverse exponential behavior, with the left being higher than regression line and the right side approaching the x-axis. If we re-scale the Y-axis to decrease the left side (x-vales $-100 \sim -80$), we can make this plot more linear.

Problem 4