

Homework 3
MTH 4230, Spring 2020

Due Wednesday, Feb. 19

Chapter in Book	Problems
2	2.29*, 2.30, 2.31, 2.32
3	3.8 (skip part <i>e</i>)**, 3.15, 3.16 (skip part <i>b</i>)

* For Problem 2.29, Part *a*, after reading the **Muscle mass** data into R using `read.table()`, you can obtain the residuals $Y_i - \hat{Y}_i$ and the deviations of fitted values away from the mean $\hat{Y}_i - \bar{Y}$ by typing something like this:

```
> my.reg <- lm(mass ~ age, data = my.data)
> my.resids <- my.reg$residuals
> my.yhatdevs <- my.reg$fitted.values - mean(my.data$mass)
```

Then you can plot them using `plot()`. Don't forget to use the same scales via the `xlim` and `ylim` arguments to `plot()`.

** In Problem 3.8 Part *d*, for the correlation test for normality of the errors, you can mimic the following R code, then use Table B.6:

```
> my.reg <- lm(crime ~ diplomas)
> my.pts <- qqnorm(my.reg$res) # Makes a normal probability
                              # (or 'quantile-quantile')
                              # plot and saves the x and y
                              # coordinates of the plotted
                              # points in my.pts (a list).

> cor(my.pts$x, my.pts$y)      # my.pts$x stores the ex-
                              # pected values of the or-
                              # dered residuals under
                              # normality ('theoretical,
                              # quantiles') and my.pts$y
                              # stores the ordered re-
                              # siduals ('sample quan-
                              # tiles').
```