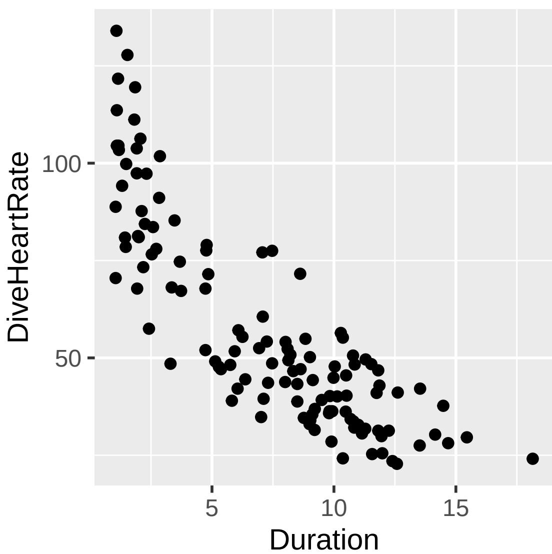
Polynomial Regression

Adapted from De Veaux, Velleman, and Bock

Emperor penguins can slow their heart rates while diving. Here's a plot showing 125 observations of penguin dives, with the duration of the penguin's dive on the horizontal axis and the penguin's heart rate on the vertical axis.

```r
library(readr) # for read_csv, which can read csv files from the internet
library(dplyr) # for data manipulation functions
library(ggplot2) # for making plots

penguins <- read_csv("http://www.evanlray.com/data/sdm4/Penguins.csv")

ggplot() +
  geom_point(data = penguins, mapping = aes(x = Duration, y = DiveHeartRate))
```



Linear Fit

Is a simple linear regression model good enough? Let's fit a model and look at some diagnostic plots to find out:

```r
slr_fit <- lm(DiveHeartRate ~ Duration, data = penguins)
summary(slr_fit)
```

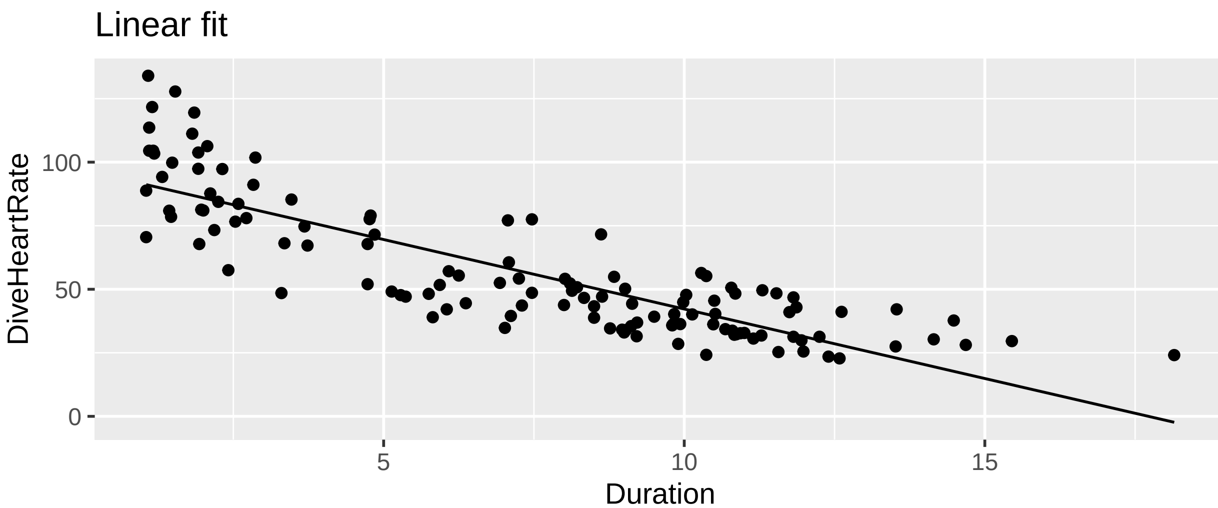
```
##
## Call:
## lm(formula = DiveHeartRate ~ Duration, data = penguins)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -30.358  -8.356  -2.933  10.770  43.022
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   96.902      2.601   37.26   <2e-16 ***
## Duration      -5.468      0.311  -17.58   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 14.11 on 123 degrees of freedom
## Multiple R-squared:  0.7153, Adjusted R-squared:  0.713
## F-statistic:   309 on 1 and 123 DF,  p-value: < 2.2e-16
```

1. Write down the model that we fit, for a single observation indexed by i.

2. Write down the model that we fit, for all observations using matrix notation.

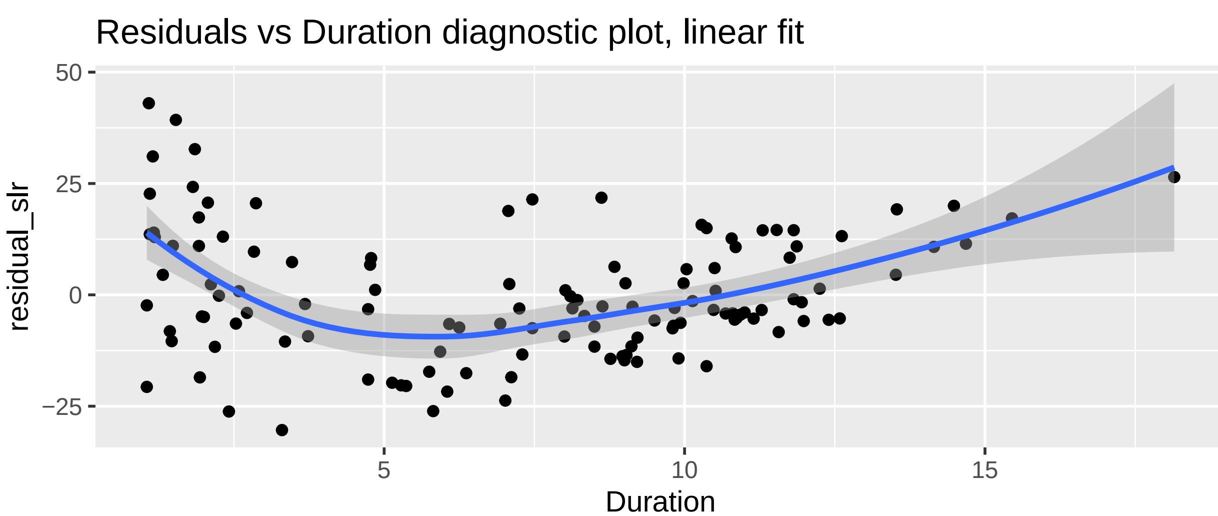
3. Write down the estimated equation for predicting dive heart rate as a function of dive duration, for a single observation indexed by i.

```r
predict_slr <- function(x) {
  predict(slr_fit, data.frame(Duration = x))
}

ggplot(data = penguins, mapping = aes(x = Duration, y = DiveHeartRate)) +
  geom_point() +
  stat_function(fun = predict_slr) +
  ggtitle("Linear fit")
```




```r
penguins <- penguins %>%
  mutate(
    residual_slr = residuals(slr_fit)
  )

ggplot(data = penguins, mapping = aes(x = Duration, y = residual_slr)) +
  geom_point() +
  geom_smooth() +
  ggtitle("Residuals vs Duration diagnostic plot, linear fit")
```

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



There is a clear trend in the residuals. Let's try fitting a parabola instead.

Quadratic Fit

Note the addition of `+ I(Duration^2)` in the model formula.

```r
quad_fit <- lm(DiveHeartRate ~ Duration + I(Duration^2), data = penguins)
summary(quad_fit)
```

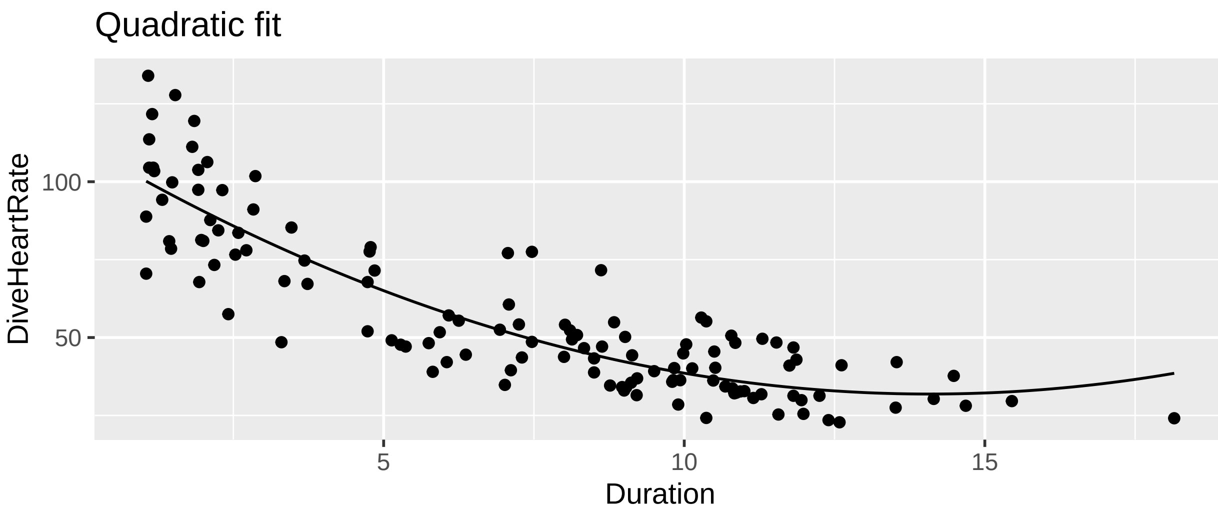
```
##
## Call:
## lm(formula = DiveHeartRate ~ Duration + I(Duration^2), data = penguins)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -30.115  -8.289  -1.567   8.016  34.187
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)   111.60991    3.32024  33.615  < 2e-16 ***
## Duration      -11.32555    0.99734 -11.356  < 2e-16 ***
## I(Duration^2)   0.40212    0.06585   6.107 1.25e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 12.4 on 122 degrees of freedom
## Multiple R-squared:  0.782,  Adjusted R-squared:  0.7784
## F-statistic: 218.8 on 2 and 122 DF,  p-value: < 2.2e-16
```

4. Write down the model that we fit

5. Write down the model that we fit, for all observations using matrix notation.

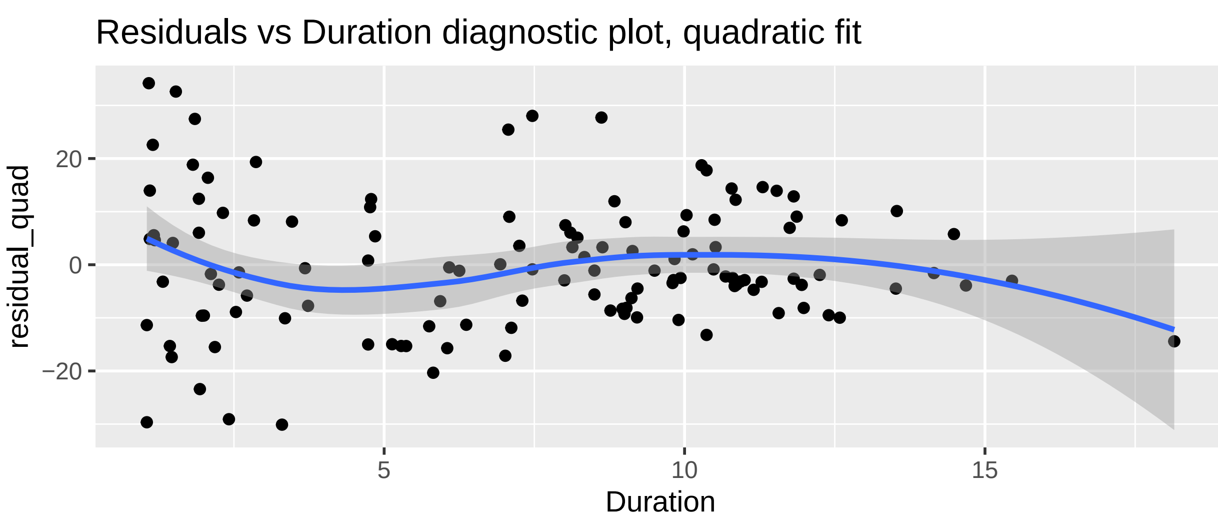
6. Write down the estimated equation for predicting dive heart rate as a function of dive duration.

```r
predict_quad <- function(x) {
  predict(quad_fit, data.frame(Duration = x))
}

ggplot(data = penguins, mapping = aes(x = Duration, y = DiveHeartRate)) +
  geom_point() +
  stat_function(fun = predict_quad) +
  ggtitle("Quadratic fit")
```




```r
penguins <- penguins %>%
  mutate(
    residual_quad = residuals(quad_fit)
  )

ggplot(data = penguins, mapping = aes(x = Duration, y = residual_quad)) +
  geom_point() +
  geom_smooth() +
  ggtitle("Residuals vs Duration diagnostic plot, quadratic fit")
```

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



Not as much of a trend... What happens if we fit a cubic polynomial?

Cubic Fit

```
cubic_fit <- lm(DiveHeartRate ~ Duration + I(Duration^2) + I(Duration^3), data = penguins)
summary(cubic_fit)
```

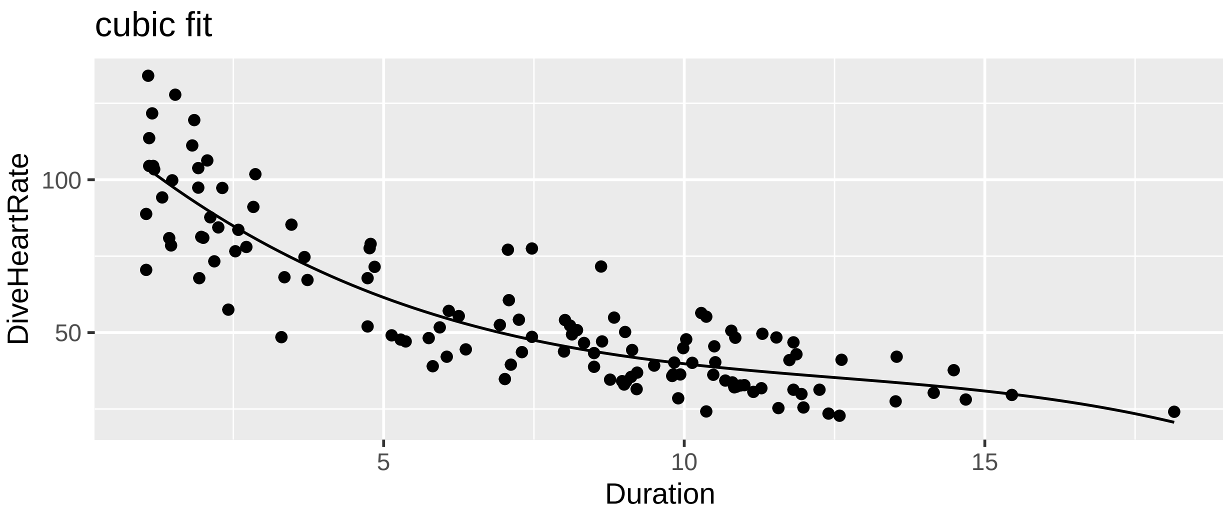
```
##
## Call:
## lm(formula = DiveHeartRate ~ Duration + I(Duration^2) + I(Duration^3),
##     data = penguins)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -33.458  -7.882  -1.752   7.109  30.710
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)   120.74815    4.97143  24.288  < 2e-16 ***
## Duration      -17.26431    2.63037  -6.563 1.38e-09 ***
## I(Duration^2)   1.24772    0.35363   3.528 0.000592 ***
## I(Duration^3)  -0.03308    0.01360  -2.432 0.016478 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 12.16 on 121 degrees of freedom
## Multiple R-squared:  0.7921, Adjusted R-squared:  0.787
## F-statistic: 153.7 on 3 and 121 DF,  p-value: < 2.2e-16
```

7. Write down the model that we fit

8. Write down the model that we fit, for all observations using matrix notation.

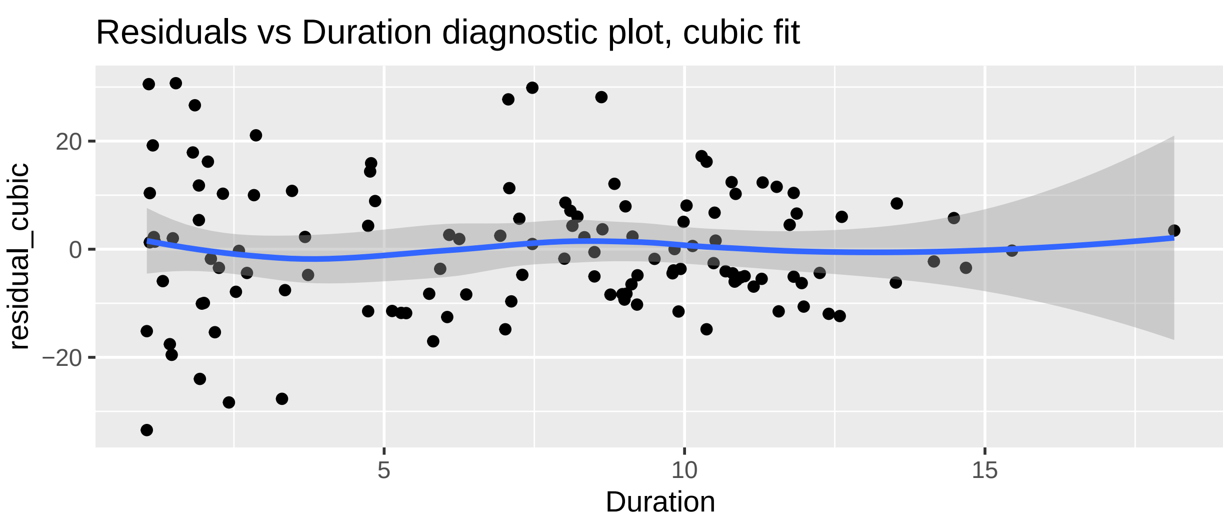
9. Write down the estimated equation for predicting dive heart rate as a function of dive duration.

```
predict_cubic <- function(x) {
  predict(cubic_fit, data.frame(Duration = x))
}

ggplot(data = penguins, mapping = aes(x = Duration, y = DiveHeartRate)) +
  geom_point() +
  stat_function(fun = predict_cubic) +
  ggtitle("cubic fit")
```




```
penguins <- penguins %>%
  mutate(
    residual_cubic = residuals(cubic_fit)
  )

ggplot(data = penguins, mapping = aes(x = Duration, y = residual_cubic)) +
  geom_point() +
  geom_smooth() +
  ggtitle("Residuals vs Duration diagnostic plot, cubic fit")
```

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



10. Does this residuals plot indicate the presence of further non-linearities not captured by our model?

11. Are there any other concerns raised by this residuals plot?

12. Suggest a strategy to address the concern you raised in question 11.

Note: we can also get the same model fit another way, using `poly()` instead of `I()`:

```r
cubic_fit <- lm(DiveHeartRate ~ poly(Duration, 3, raw = TRUE), data = penguins)
summary(cubic_fit)
```

```
##
## Call:
## lm(formula = DiveHeartRate ~ poly(Duration, 3, raw = TRUE), data = penguins)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -33.458  -7.882  -1.752   7.109  30.710
##
## Coefficients:
##                                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)                     120.74815    4.97143  24.288  < 2e-16 ***
## poly(Duration, 3, raw = TRUE)1 -17.26431    2.63037  -6.563 1.38e-09 ***
## poly(Duration, 3, raw = TRUE)2   1.24772    0.35363   3.528 0.000592 ***
## poly(Duration, 3, raw = TRUE)3  -0.03308    0.01360  -2.432 0.016478 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 12.16 on 121 degrees of freedom
## Multiple R-squared:  0.7921, Adjusted R-squared:  0.787
## F-statistic: 153.7 on 3 and 121 DF,  p-value: < 2.2e-16
```