M12 Group Work: Simple Linear Regression for TAs

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```r
library(tidyverse)
```

```
## -- Attaching packages -------------------------------------- tidyverse 1.3.1 --

## v ggplot2 3.4.4      v purrr   1.0.2
## v tibble  3.2.1      v dplyr   1.1.3
## v tidyr   1.3.0      v stringr 1.5.1
## v readr   2.1.2      v forcats 0.5.1

## -- Conflicts ----------------------------------------- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```r
library(readxl)
library(car)
```

```
## Loading required package: carData

##
## Attaching package: 'car'

## The following object is masked from 'package:dplyr':
##
##     recode

## The following object is masked from 'package:purrr':
##
##     some
```
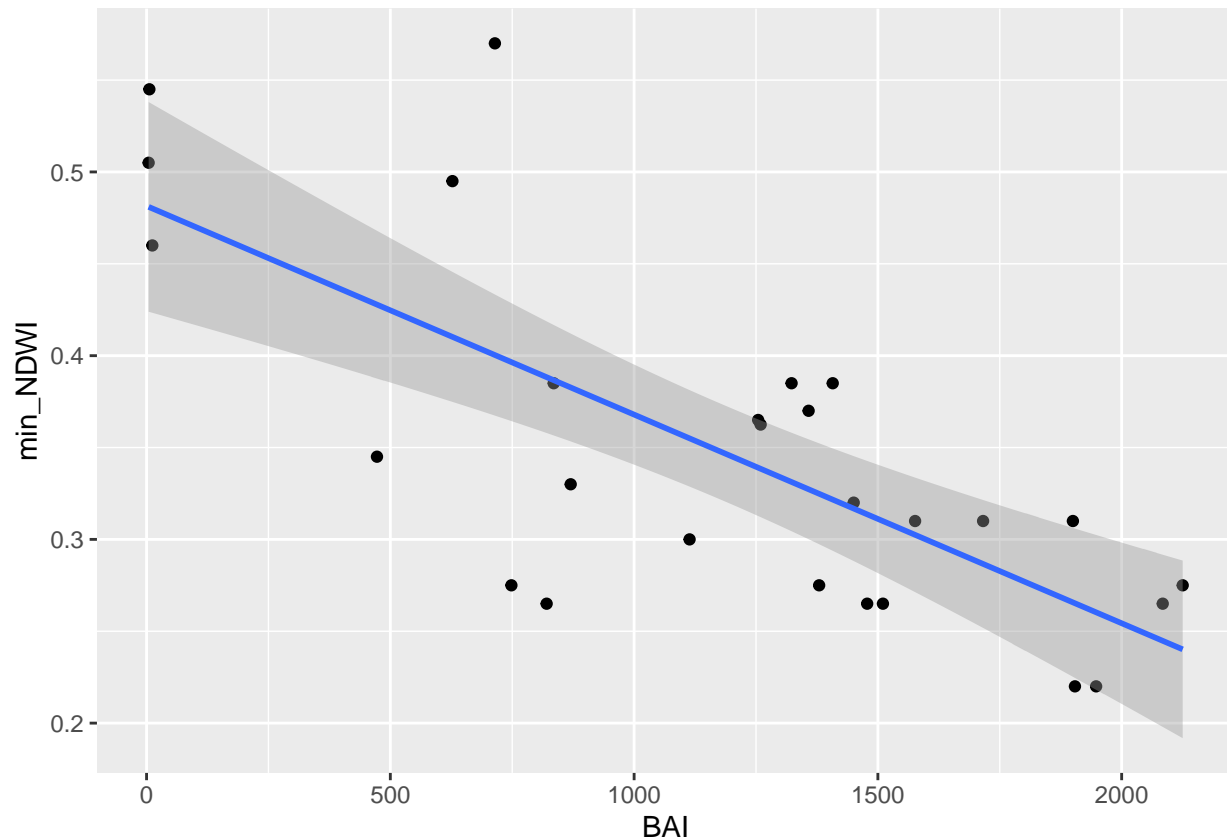
#Load data

```r
BAI_NDWI <- read_xlsx("PIRU_BAI.xlsx")
```

#This makes a plot with our regression line.

```r
ggplot(BAI_NDWI) +
  aes(x = BAI, y = min_NDWI) +
  geom_point() +
  theme(legend.position = "none") +
  stat_smooth(method = "lm", formula = y ~ x, geom = "smooth")
```

#this simply creates a 'model' for our regression model #This is the main think we are looking at!

```
model <- lm(BAI~ min_NDWI, data = BAI_NDWI)
summary(model)
```

```
##
## Call:
## lm(formula = BAI ~ min_NDWI, data = BAI_NDWI)
##
## Residuals:
##     Min      1Q Median      3Q     Max
## -777.4 -263.6  138.9  302.8  599.4
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   2835.1      315.7   8.981 2.68e-09 ***
## min_NDWI     -4761.5      877.7  -5.425 1.25e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 426.4 on 25 degrees of freedom
## Multiple R-squared:  0.5407, Adjusted R-squared:  0.5223
## F-statistic: 29.43 on 1 and 25 DF,  p-value: 1.246e-05
```

##the Breusch-Pagan test to assess homoscedasticity

```r
ncvTest(model)
```

```
## Non-constant Variance Score Test
## Variance formula: ~ fitted.values
## Chisquare = 0.005762692, Df = 1, p = 0.93949
```

#get list of residuals to nest normality

```r
res <- resid(model)
shapiro.test(res)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  res
## W = 0.94094, p-value = 0.1285
```