Data Mining - Regression Project

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Part 1: Dataset background

WHO dataset provided by the Global Health Observatory compiled on Kaggle from 2000-2015, the data-set related to life expectancy, health factors for 193 countries has been collected from the same WHO data repository website and its corresponding economic data was collected from United Nation website. Contains life expectancy precise to 10th of a year for each country by each year from 2000-2015 Features include economic, social, and health factors for each country for a total of 23 features 2,938 Observations After cleaning the data for my models Ihad 1,649 observations (NA's)

Part 2: Questions of Interest

Response Variable: Life Expectancy in Years What feature or combination of features best predicts a country's life expectancy? What types of factors influence life expectancy most? ex. social vs economic What regression models will best fit and accurately predict life expectancy?

Call Libraries

```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.3     v readr     2.1.4
## v forcats   1.0.0     v stringr   1.5.0
## v ggplot2   3.4.4     v tibble    3.2.1
## v lubridate 1.9.3     v tidyr     1.3.0
## v purrr     1.0.2
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become error
```

```
library(broom)
library(dplyr)
```

Importing the Data

```
life_df <- read.csv("life_data.csv")
str(life_df)
```

```
## 'data.frame':    2938 obs. of  22 variables:
##  $ Country                        : chr  "Afghanistan" "Afghanistan" "Afghanistan" "Afghanistan" ...
##  $ Year                           : int  2015 2014 2013 2012 2011 2010 2009 2008 2007 2006 ...
##  $ Status                         : chr  "Developing" "Developing" "Developing" "Developing" ...
##  $ Life.expectancy                : num  65 59.9 59.9 59.5 59.2 58.8 58.6 58.1 57.5 57.3 ...
##  $ Adult.Mortality                : int  263 271 268 272 275 279 281 287 295 295 ...
##  $ infant.deaths                  : int  62 64 66 69 71 74 77 80 82 84 ...
##  $ Alcohol                        : num  0.01 0.01 0.01 0.01 0.01 0.01 0.01 0.03 0.02 0.03 ...
##  $ percentage.expenditure         : num  71.3 73.5 73.2 78.2 7.1 ...
##  $ Hepatitis.B                    : int  65 62 64 67 68 66 63 64 63 64 ...
##  $ Measles                        : int  1154 492 430 2787 3013 1989 2861 1599 1141 1990 ...
##  $ BMI                            : num  19.1 18.6 18.1 17.6 17.2 16.7 16.2 15.7 15.2 14.7 ...
##  $ under.five.deaths              : int  83 86 89 93 97 102 106 110 113 116 ...
##  $ Polio                          : int  6 58 62 67 68 66 63 64 63 58 ...
##  $ Total.expenditure              : num  8.16 8.18 8.13 8.52 7.87 9.2 9.42 8.33 6.73 7.43 ...
##  $ Diphtheria                     : int  65 62 64 67 68 66 63 64 63 58 ...
##  $ HIV.AIDS                       : num  0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 ...
##  $ GDP                            : num  584.3 612.7 631.7 670 63.5 ...
##  $ Population                     : num  33736494 327582 31731688 3696958 2978599 ...
##  $ thinness..1.19.years           : num  17.2 17.5 17.7 17.9 18.2 18.4 18.6 18.8 19 19.2 ...
##  $ thinness.5.9.years             : num  17.3 17.5 17.7 18 18.2 18.4 18.7 18.9 19.1 19.3 ...
##  $ Income.composition.of.resources: num  0.479 0.476 0.47 0.463 0.454 0.448 0.434 0.433 0.415 0.405
##  $ Schooling                      : num  10.1 10 9.9 9.8 9.5 9.2 8.9 8.7 8.4 8.1 ...
```

Rename colnames to names easier to reference in future code

```
life_df <- life_df %>%
  rename("country" = "Country",
         "year" = "Year",
         "status" = "Status",
         "life_exp_yrs" = "Life.expectancy",
         "adult_mortality" = "Adult.Mortality",
         "infant_deaths" = "infant.deaths",
         "alcohol" = "Alcohol",
         "perc_expend" = "percentage.expenditure",
         "hep_b" = "Hepatitis.B",
         "measles" = "Measles",
         "bmi" = "BMI",
         "5yr_deaths" = "under.five.deaths",
         "polio" = "Polio",
         "tot_expend" = "Total.expenditure",
         "diphtheria" = "Diphtheria",
         "hiv_aids" = "HIV.AIDS",
         "gdp" = "GDP",
         "population" = "Population",
         "thin_1to19" = "thinness..1.19.years",
         "thin_5to9" = "thinness.5.9.years",
         "inc_comp_resources" = "Income.composition.of.resources",
         "schooling" = "Schooling"
         )
```

```
colnames(life_df)
```

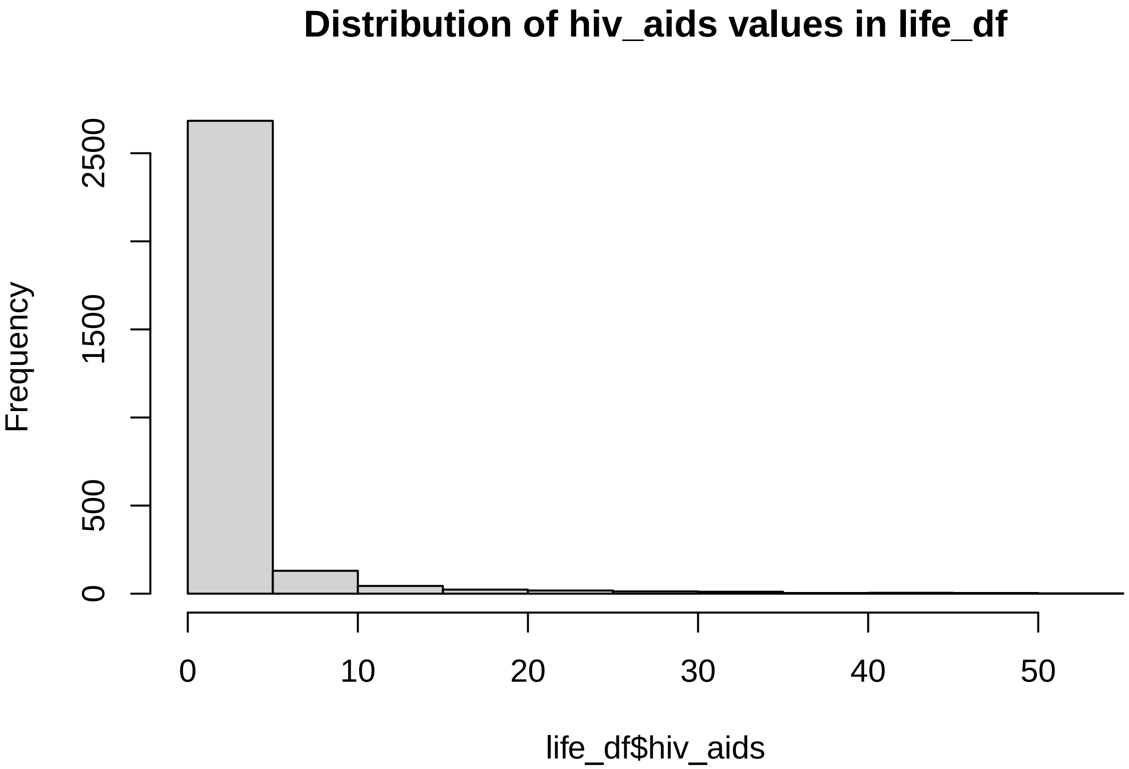
```
##  [1] "country"            "year"               "status"
##  [4] "life_exp_yrs"       "adult_mortality"    "infant_deaths"
##  [7] "alcohol"            "perc_expend"        "hep_b"
## [10] "measles"            "bmi"                "5yr_deaths"
## [13] "polio"              "tot_expend"         "diphtheria"
## [16] "hiv_aids"            "gdp"                 "population"
## [19] "thin_1to19"          "thin_5to9"           "inc_comp_resources"
## [22] "schooling"
```

The column names are now much easier to call for future code. Other than that the data is tidy, the only wrangling left to do is perhaps create a few more categorical variables since the data is light on categorical variables.

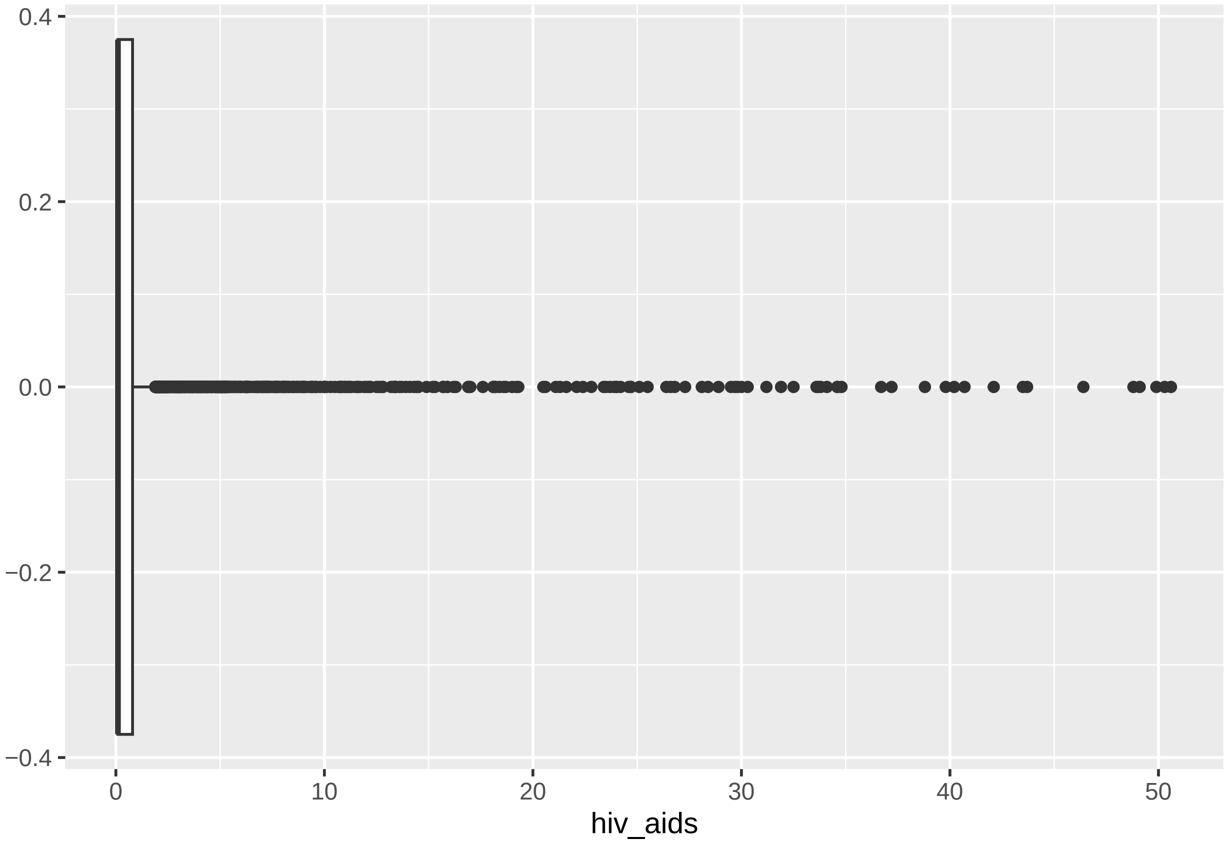
Creating another categorical variable from the hiv_aids column

The hiv_aids column looks like it is able to be split into two groups: significantly low and high hiv_aids deaths per 1000 people.

```
hist(life_df$hiv_aids,
     main = "Distribution of hiv_aids values in life_df")
```



```
ggplot(data = life_df, aes(hiv_aids))+
  geom_boxplot()
```



### Domain Information

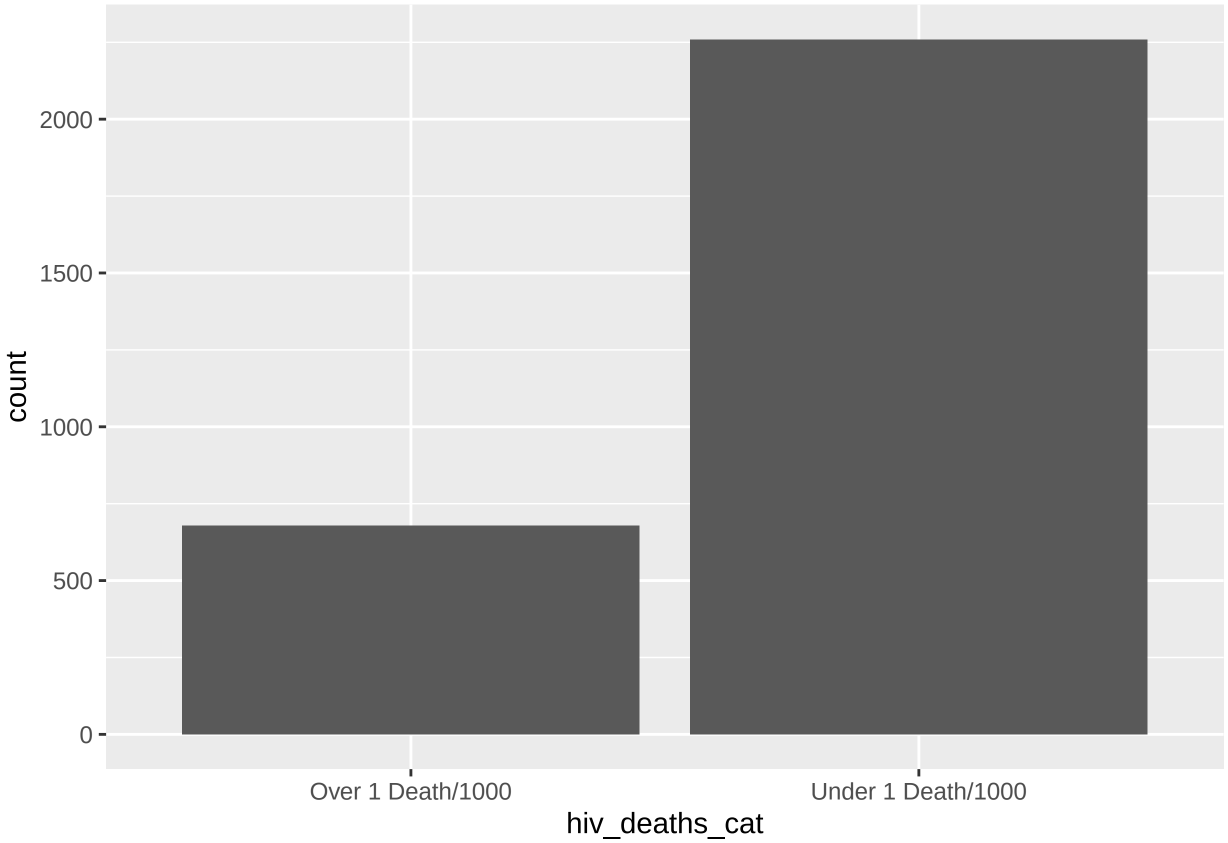
After some research, I was able to find reasonable numbers to create my bins from. In 2019, the world in data reports average levels across North America and Europe as approximately 1 deaths per 100,000 people (0.1 in my data). The study reports that higher levels of HIV deaths occur at 100 deaths per 100,000 which means for my data, high levels of hiv deaths would occur at 1 death per 1,000 people so 1 will be the cutoff for these bins.

```
life_df <- life_df %>%
  mutate(
    hiv_deaths_cat = case_when(
      hiv_aids < 1 ~ 'Under 1 Death/1000',
      TRUE ~ 'Over 1 Death/1000'
    )
  )
```

Used case_when() statements with mutate to create new categorical columns for bmi and hiv_deaths

Histogram of new column

```
ggplot(data = life_df, aes(x = hiv_deaths_cat))+
  geom_bar()
```



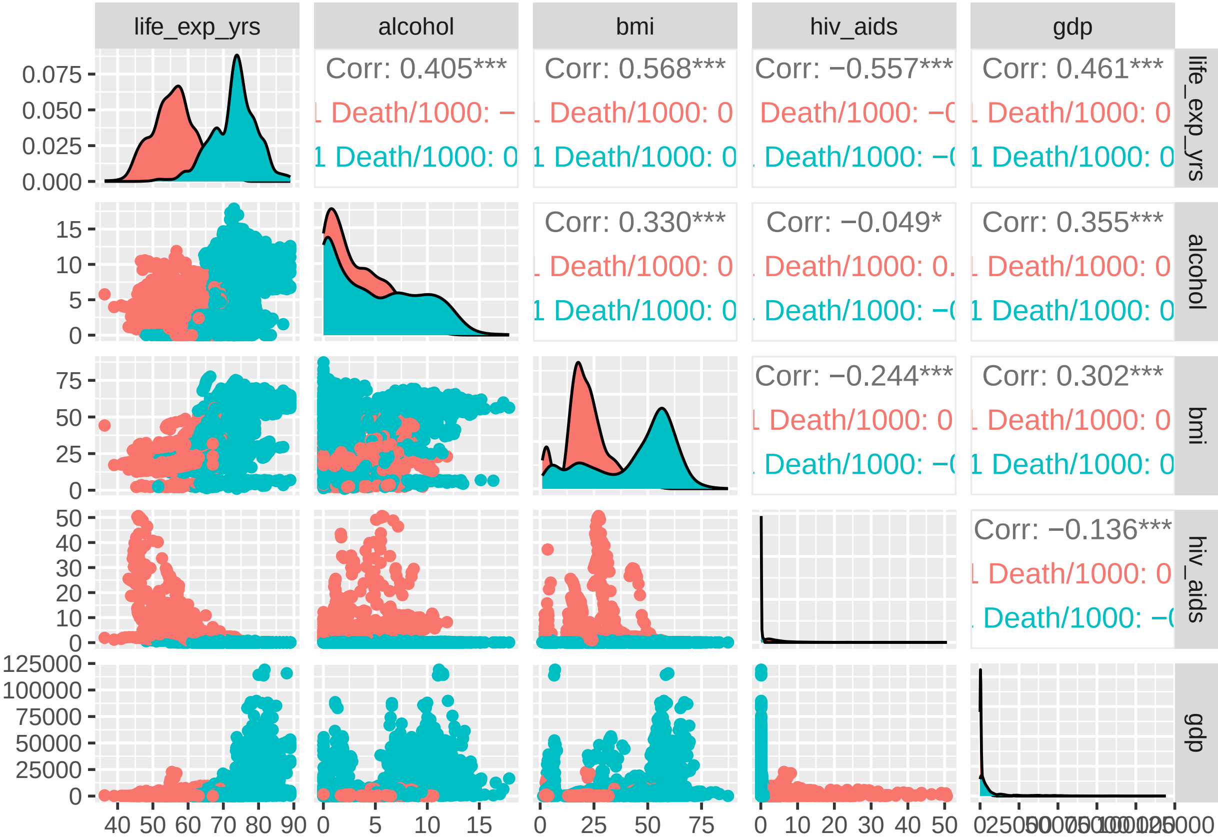
### Creating a BMI categorical variable I wanted to have one more categorical variable ready if needed in the future. Here are the official body mass index categories obtained from the CDC:

```
life_df <- life_df %>%
  mutate(bmi_cat = case_when(
    bmi <= 18.5 ~ "underweight",
    bmi <= 25 ~ "healthy",
    bmi <= 30 ~ "overweight",
    bmi <= 100 ~ "obese")
         )
```

Part 2: Linear Models

Step 0 - Pairs Plot

```
library(GGally)
life_df %>%
ggpairs(columns=c(4, 7, 11, 16, 17),
        ggplot2::aes(color = hiv_deaths_cat))
```



Looking at life expectancy using my hiv death category feature I can see there is definitely grouping Hiv_aids is non linear Mainly BMI is where I am going to start. I chose alcohol, bmi, hiv_aids, and gdp as they seemed to have the most effect on life expectancy.

Step 1 - Identifying Variables

Response:

'life_exp_yrs' - I am attempting to create a model that can accurately predict life expectancy given a selection of explanatory variables. The unit of this variable is years which is stored as a decimal accurate to 1 tenth of a year. Each record in the data is one country for a specific year, holding that country's average population life expectation.

Explanantory Numeric:

'bmi' - This is my first explanatory feature which is a record of a given country population's average BMI for that year. BMI is a calculation of body composition given height and weight.

Explanatory Categorical:

'hiv_deaths_cat' - This is my derived categorical variable which the creation of was explained in the data wrangling section. The levels of this variable are 'Under 1 Death/1000' and 'Over 1 Death/1000'.

Step 2 - Training and Testing Sets

Using a 70:30 split for my testing and training sets.

```r
dim(life_df) # 2938
```

```
## [1] 2938   24
```

```r
set.seed(123)

trainInd<-sample(1:2938, 2057)

life_df_train<-life_df[trainInd, ]
life_df_test<-life_df[-trainInd, ]
```

```r
dim(life_df_train)
```

```
## [1] 2057   24
```

```r
dim(life_df_test)
```

```
## [1] 881  24
```

Step 3 - Simple Linear Model

```r
life_mod1 <- lm(life_exp_yrs ~ bmi, data = life_df_train)
summary(life_mod1)
```

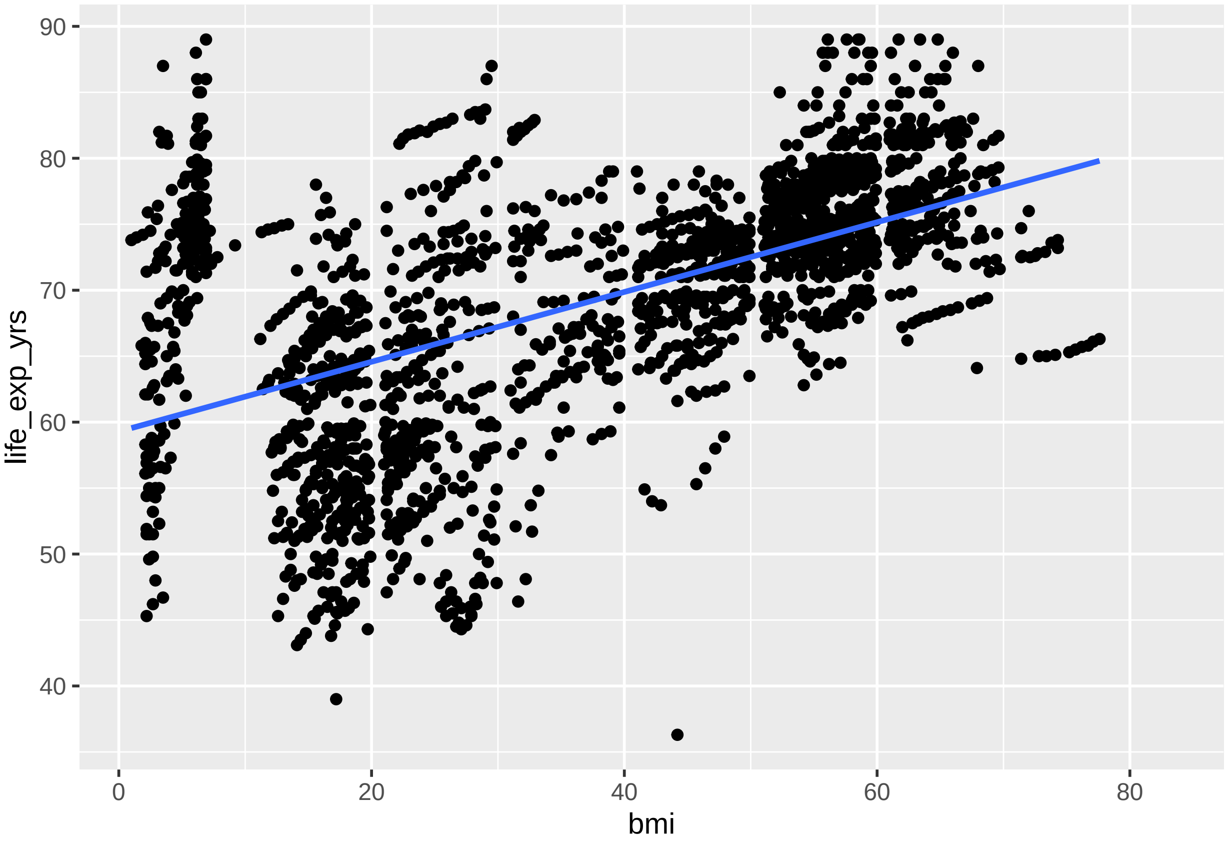
```
##
## Call:
## lm(formula = life_exp_yrs ~ bmi, data = life_df_train)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -34.676  -4.816   0.368   4.530  27.891
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 59.284322   0.377176  157.18   <2e-16 ***
## bmi          0.264514   0.008775   30.14   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.942 on 2029 degrees of freedom
##   (26 observations deleted due to missingness)
## Multiple R-squared:  0.3093, Adjusted R-squared:  0.309
## F-statistic: 908.7 on 1 and 2029 DF,  p-value: < 2.2e-16
```

Model: $\mathbf{Y = 59.284322 + 0.264514x}$

The relationship does appear to be significant; the p-value for bmi is significant at <2e-16. However the r-squared value shows the model does not account for much of the variability in the dataset.

Graphic

```r
ggplot(data = life_df_train, aes(x=bmi,y=life_exp_yrs))+
  geom_point()+
  geom_smooth(method = 'lm', se = FALSE)
```



I made a simple linear regression to help establish some sort of baseline so that I could fit the data to a graph, and used a 70/30 training to testing split to do so. The other models also follow the same testing to training split as well.

Step 4 - Parallel Slopes MLR Model

```
life_mod2 <- lm(life_exp_yrs ~ bmi + hiv_deaths_cat, data = life_df_train)
summary(life_mod2)
```

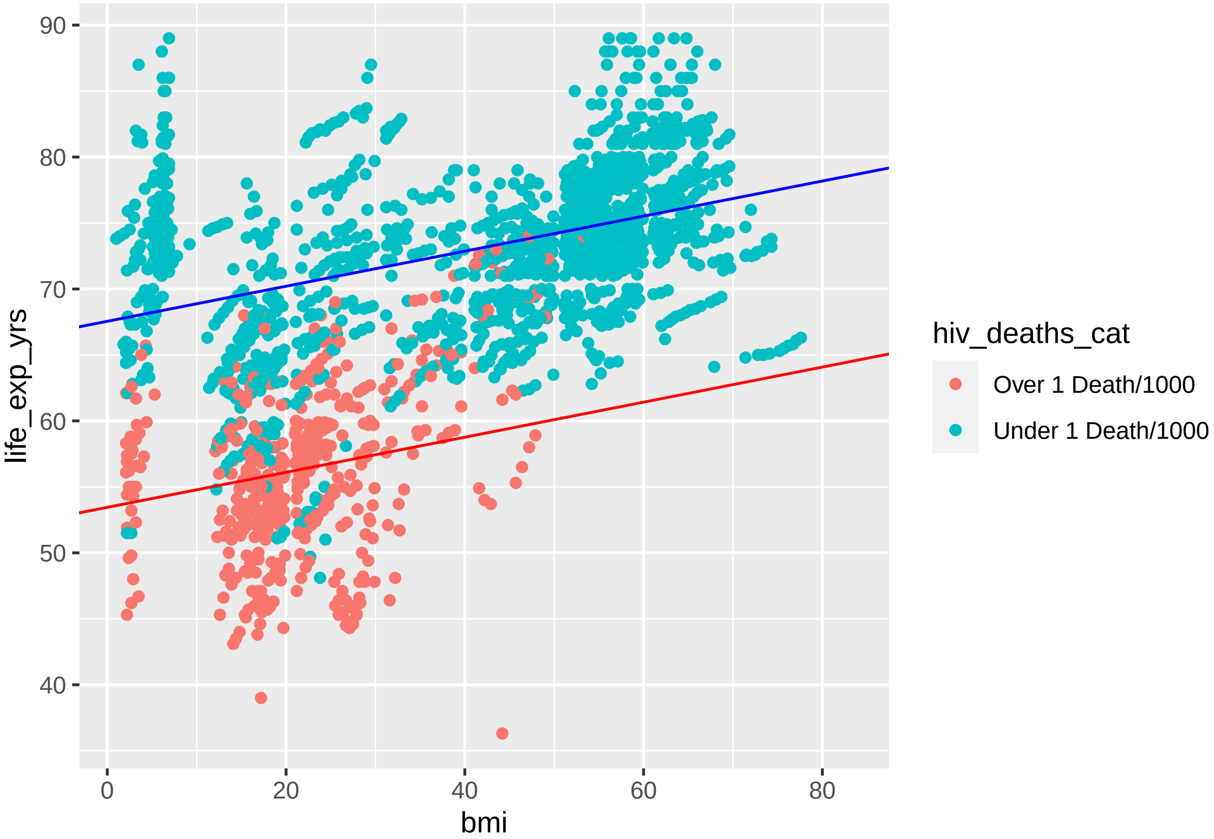
```
##
## Call:
## lm(formula = life_exp_yrs ~ bmi + hiv_deaths_cat, data = life_df_train)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -23.0213  -3.5461  -0.0837   3.7482  20.5330
##
## Coefficients:
##                                Estimate Std. Error t value Pr(>|t|)
## (Intercept)                   53.447460   0.314187  170.11   <2e-16 ***
## bmi                            0.132892   0.007263   18.30   <2e-16 ***
## hiv_deaths_catUnder 1 Death/1000 14.102622   0.345896   40.77   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.889 on 2028 degrees of freedom
##   (26 observations deleted due to missingness)
## Multiple R-squared:  0.6204, Adjusted R-squared:  0.6201
## F-statistic:  1658 on 2 and 2028 DF,  p-value: < 2.2e-16
```

Model for reference group (hiv_deaths_cat Over 1 Death/1000): Y = 53.447460 + 0.132892x

Model for alt group (hiv_deaths_cat Under 1 Death/1000): Y = (53.447460 + 14.102622) + 0.132892x

Graphic

```
ggplot(data = life_df_train, aes(x = bmi, y = life_exp_yrs, color = hiv_deaths_cat))+
  geom_point()+
  geom_abline(intercept=life_mod2$coefficients[1],
              slope = life_mod2$coefficients[2], color = "red")+
  geom_abline(intercept=life_mod2$coefficients[1] + life_mod2$coefficients[3],
              slope = life_mod2$coefficients[2], color = "blue")
```



RMSE = 5.476938, Adjusted R-squared = 0.6201 Took the simple linear regression a step further and subdivided the groups based on the hiv_death category After looking you can see parallel slopes did not accurately represent the subgroups as well as modeling with interaction did Interaction had slightly better ADJR2 and RMSE however the model still wasnt great at explaining variability in the data

Step 5 - MLR with Interaction

```
life_mod3 <- lm(life_exp_yrs ~ bmi * hiv_deaths_cat, data = life_df_train)
summary(life_mod3)
```

```
##
## Call:
```

```
## lm(formula = life_exp_yrs ~ bmi * hiv_deaths_cat, data = life_df_train)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -25.402  -3.456  -0.016   3.814  20.466
##
## Coefficients:
##                                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)                          51.14432    0.62851  81.374  < 2e-16 ***
## bmi                                   0.23885    0.02610   9.151  < 2e-16 ***
## hiv_deaths_catUnder 1 Death/1000     16.78394    0.72206  23.244  < 2e-16 ***
## bmi:hiv_deaths_catUnder 1 Death/1000 -0.11478    0.02716  -4.225 2.49e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.865 on 2027 degrees of freedom
##   (26 observations deleted due to missingness)
## Multiple R-squared:  0.6238, Adjusted R-squared:  0.6232
## F-statistic:  1120 on 3 and 2027 DF,  p-value: < 2.2e-16
```

Model for reference group (hiv_deaths_cat Over 1 Death/1000): Y = 51.14432 + 0.23885x

Model for alt group (hiv_deaths_cat Under 1 Death/1000): Y = (51.14432 + 16.78394) + (0.23885 - 0.11478)x

Graphic

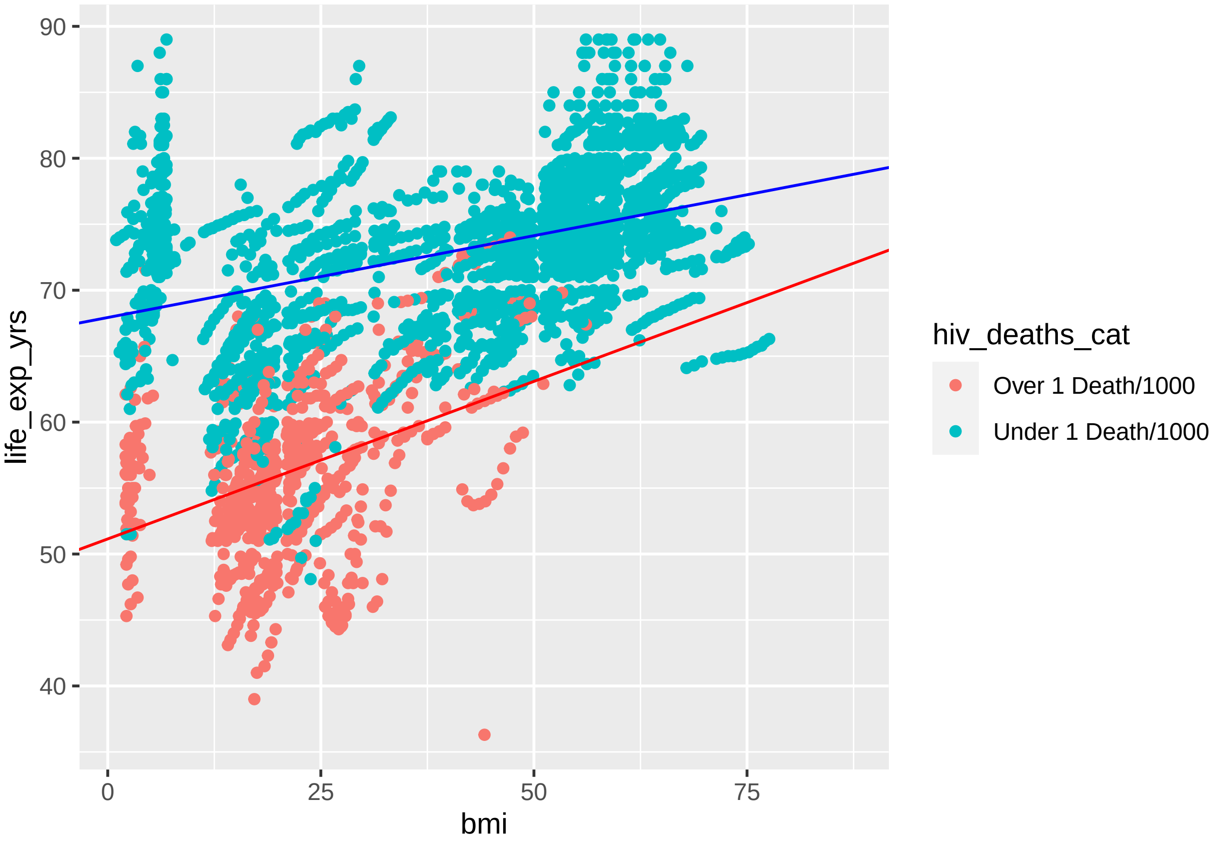
```
life_mod3$coefficients
```

```
##                          (Intercept)                                  bmi
##                           51.1443245                            0.2388523
##     hiv_deaths_catUnder 1 Death/1000 bmi:hiv_deaths_catUnder 1 Death/1000
##                           16.7839429                           -0.1147757
```

```
## Reference
mod3_yint_0<-life_mod3$coefficients[1]
mod3_slope_0<-life_mod3$coefficients[2]

## Alternative
mod3_yint_1<-mod3_yint_0 + life_mod3$coefficients[3]
mod3_slope_1<-mod3_slope_0 + life_mod3$coefficients[4]
```

```
ggplot(data=life_df, aes(x=bmi, y=life_exp_yrs, color=hiv_deaths_cat))+
  geom_point()+
  geom_abline(intercept=mod3_yint_0,
              slope=mod3_slope_0, color="red")+
  geom_abline(intercept=mod3_yint_1,
              slope=mod3_slope_1, color="blue")
```



RMSE = 5.425755, Adjusted R-Squared = 0.6232 Very similar to the one above as well.

Step 6 Prediction Tests

Mod 1

```
library(caret)
life_testPred1<-predict(life_mod1, life_df_test)

RMSE(life_testPred1, life_df_test$life_exp_yrs, na.rm = TRUE)
```

```
## [1] 7.501672
```

Mod 2

```
life_testPred2<-predict(life_mod2, life_df_test)
RMSE(life_testPred2, life_df_test$life_exp_yrs, na.rm = TRUE)
```

```
## [1] 5.476938
```

Mod 3

```
life_testPred3<-predict(life_mod3, life_df_test)
RMSE(life_testPred3, life_df_test$life_exp_yrs, na.rm = TRUE)
```

```
## [1] 5.425755
```

The model with the lowest RMSE is Model 3 (model with interaction between explanatory variables of ‘bmi’ and ‘hiv_deaths_cat’ columns).

After looking at all the differnet models that I created and interactions between explanatory variables that has the most significant relationship is bmi and hiv__deaths__cat which was the variable that I created which tells methat the variables that have the biggest effect on life expectancy on this dataset is the bmi of someone based on the classfications online and the hiv__deaths__cat which is from HIV, which looking at the dataset if 3rd world countries that do not have a lot of money have citizens with HIV or high BMI it is tougher for them to combat it especially HIV.