

December 2, 2019

The results below are generated from an R script.

```
# Analysis
# Scott Cohn + Ruja Kamblí

# Libraries -----

library(dplyr)
library(tidyverse) # duh.
library(ggplot2) # plotting
library(gridExtra) # plotting options
library(ggsci) # plot color palette
library(ggthemes) # Themes
library(bbplot) # plot style
library(readr) # import csv
library(lmtest) # BP test
library(scales) # Scale x-axis
library(MASS)
library(faraway) # Box-Cox transform / vif

# Colors
COLA <- c("#99d8c9", "#66c2a4", "#41ae76", "#238b45", "#005824")
COLB <- c("#4eb3d3", "#2b8cbe", "#0868ac", "#084081")

# Import Data -----
life_exp_full <- read_csv("data/life_exp_full.csv")

## Parsed with column specification:
## cols(
##   Country = col_character(),
##   'Birth Rate' = col_double(),
##   'Cancer Rate' = col_double(),
##   'Dengue Cases' = col_double(),
##   EPI = col_double(),
##   GDP = col_double(),
##   'Health Expenditure' = col_double(),
##   'Heart Disease Rate' = col_double(),
##   Population = col_double(),
##   Area = col_double(),
##   'Pop Density' = col_double(),
##   'Stroke Rate' = col_double(),
##   'Life Expectancy' = col_double()
## )

# Data Transformations -----
```

```

# Capitalize letters in Country var
# Not perfect, but good enough
simpleCap <- function(x) {
  s <- strsplit(x, " ")[[1]]
  paste(toupper(substring(s, 1,1)), substring(s, 2),
        sep = "", collapse = " ")
}

life_exp_full <- life_exp_full %>%
  mutate(Country = apply(life_exp_full, 1, simpleCap))

# Visualizations -----

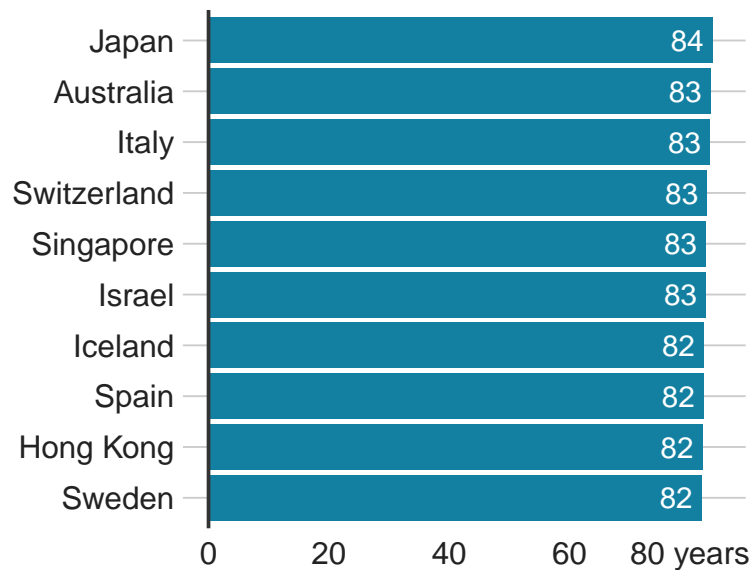
# Top 10 life exp by country
topten_lifeexp_country <- life_exp_full %>%
  arrange(desc(`Life Expectancy`)) %>%
  slice(1:10) %>%
  ggplot(aes(x = reorder(Country, `Life Expectancy`),
              y = `Life Expectancy`)) +
  geom_bar(stat = 'identity',
          fill = "#1380A1") +
  #scale_fill_d3() +
  coord_flip() +
  scale_y_continuous(
    limits = c(0, 85),
    breaks = seq(0, 80, by = 20),
    labels = c("0", "20", "40", "60", "80 years")
  ) +
  geom_hline(yintercept = 0,
            size = 1,
            color = "#333333") +
  geom_label(
    aes(label = round(`Life Expectancy`, 0)),
    hjust = 1,
    vjust = 0.5,
    colour = "white",
    fill = NA,
    label.size = NA,
    family = "Helvetica",
    size = 6
  ) +
  bbc_style() +
  labs(title = "Life Expectancy",
       subtitle = "Top 10 Countries")

# Save graph
finalise_plot(plot_name = topten_lifeexp_country,
              source = "Source: JNYH/Project Luther",
              save_filepath = "figures/topten_lifeexp_country.pdf",
              width_pixels = 640,
              height_pixels = 450)

```

Life Expectancy

Top 10 Countries



Source: JNYH/Project Luther

```
#logo_image_path = "placeholder.png")

# Bottom 10 life exp by country
# life_exp_full %>% drop_na(`Life Expectancy`) %>% nrow() = 201 rows w/out NA
bottomten_lifeexp_country <- life_exp_full %>%
  drop_na(`Life Expectancy`) %>%
  arrange(desc(`Life Expectancy`)) %>%
  slice(192:201) %>%
  ggplot(aes(x = reorder(Country, -`Life Expectancy`),
              y = `Life Expectancy`)) +
  geom_bar(stat = 'identity',
           fill = "#1380A1") +
  #scale_fill_d3() +
  coord_flip() +
  scale_y_continuous(
    limits = c(0, 85),
    breaks = seq(0, 80, by = 20),
    labels = c("0", "20", "40", "60", "80 years")
  ) +
  geom_hline(yintercept = 0,
             size = 1,
             color = "#333333") +
  geom_label(
    aes(label = round(`Life Expectancy`, 0)),
    hjust = 1,
    vjust = 0.5,
    colour = "white",
    fill = NA,
    label.size = NA,
```

```

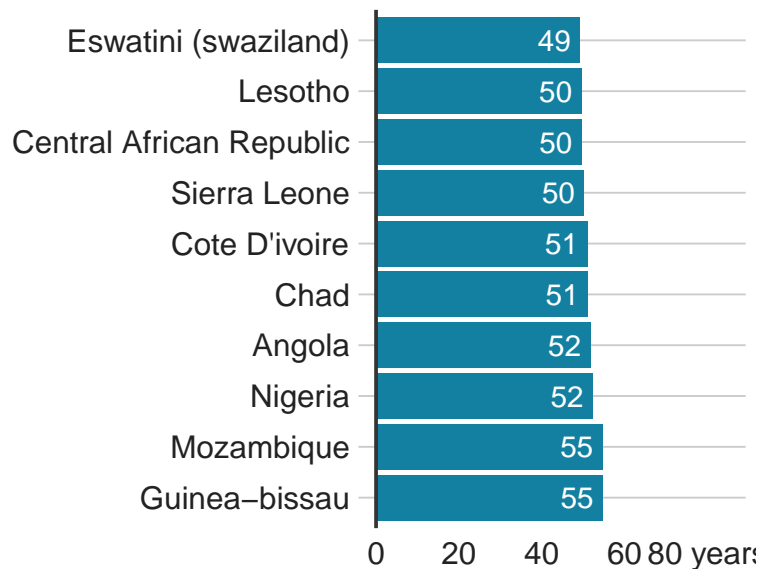
    family = "Helvetica",
    size = 6
  ) +
  bbc_style() +
  labs(title = "Life Expectancy",
        subtitle = "Bottom 10 Countries")

# Save graph
finalise_plot(plot_name = bottomten_lifeexp_country,
              source = "Source: JNYH/Project Luther",
              save_filepath = "figures/bottomten_lifeexp_country.pdf",
              width_pixels = 640,
              height_pixels = 450)

```

Life Expectancy

Bottom 10 Countries



Source: JNYH/Project Luther

```

#logo_image_path = "placeholder.png")

# Distribution of Life Expectancy, Histogram
lifeexp_distro <- life_exp_full %>%
  ggplot(aes(x = `Life Expectancy`)) +
  geom_histogram(binwidth = 5,
                 color = "white",
                 fill = "#1380A1") +
  geom_hline(yintercept = 0,
             size = 1,
             color = "#333333") +
  bbc_style() +
  scale_x_continuous(
    limits = c(40, 95),
    breaks = seq(40, 90, by = 10),

```

```

    labels = c("40", "50", "60", "70", "80", "90 years")
  ) +
  labs(title = "How life expectancy varies",
       subtitle = "Distribution of life expectancy")

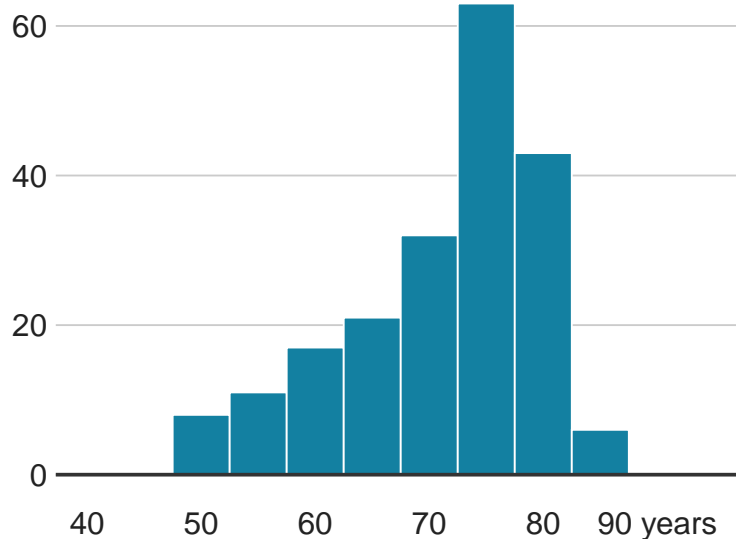
# Save graph
finalise_plot(plot_name = lifeexp_distro,
              source = "Source: JNYH/Project Luther",
              save_filepath = "figures/lifeexp_distro.pdf",
              width_pixels = 640,
              height_pixels = 450)

## Warning: Removed 47 rows containing non-finite values (stat_bin).
## Warning: Removed 2 rows containing missing values (geom_bar).

```

How life expectancy varies

Distribution of life expectancy



Source: JNYH/Project Luther

```

#logo_image_path = "placeholder.png")

# Life exp vs Birth Rate
life_exp_full %>%
  ggplot(aes(x = `Birth Rate`,
             y = `Life Expectancy`)) +
    xlab("Birth Rate per 1000 People") +
    ylab("Life Expectancy") +
    geom_point(color = "#1380A1") +
    geom_hline(yintercept = 0,
               size = 1,
               color = "#333333") +
    #scale_color_d3() +
    bbc_style() +
    #RK I tried labelling these axes multiple times,

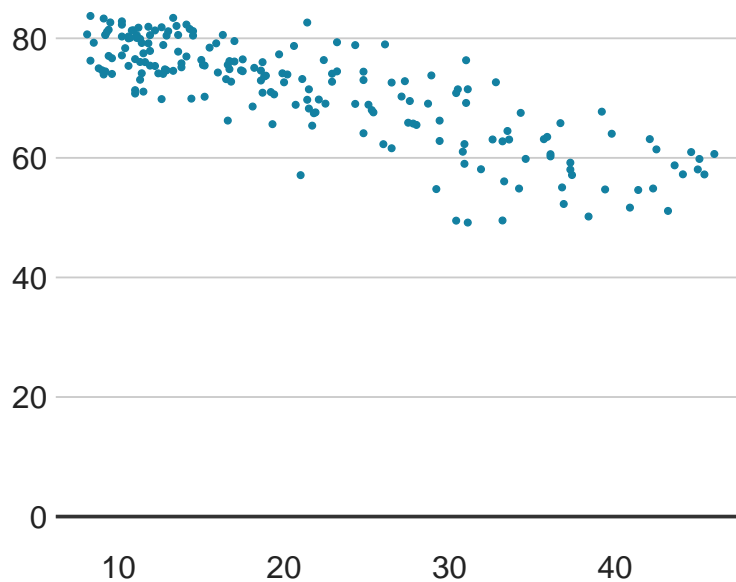
```

```
labs(title = "How long can we expect to live?",
      subtitle = "Birth Rate vs. Life Expectancy",
      ylab = "Life Expectancy",
      xlab = "Births Per 1000 People")
```

Warning: Removed 54 rows containing missing values (geom_point).

How long can we expect to live

Birth Rate vs. Life Expectancy

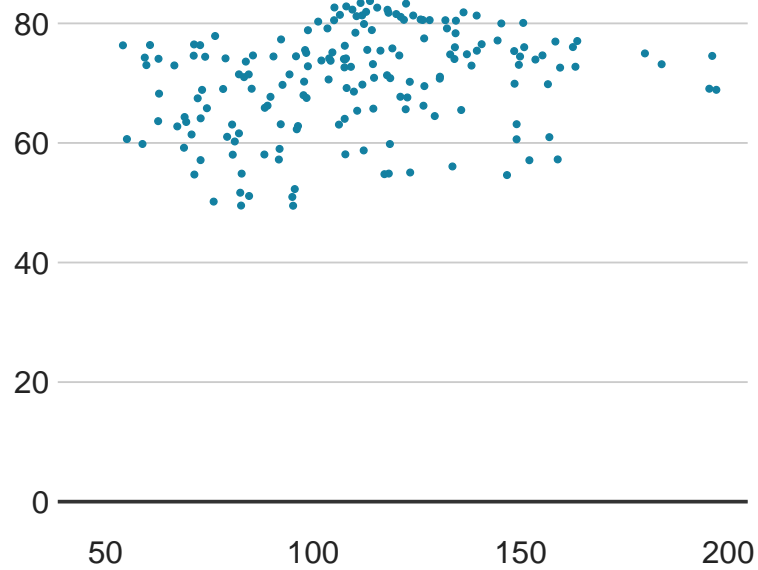


```
# Life vs Cancer
life_exp_full %>%
  ggplot(aes(x = `Cancer Rate`,
              y = `Life Expectancy`)) +
  geom_point(color = "#1380A1") +
  geom_hline(yintercept = 0,
             size = 1,
             colour = "#333333") +
  #scale_color_d3() +
  bbc_style() +
  labs(title = "How long do we expect to live?",
        subtitle = "Cancer Rate vs. Life Expectancy")
```

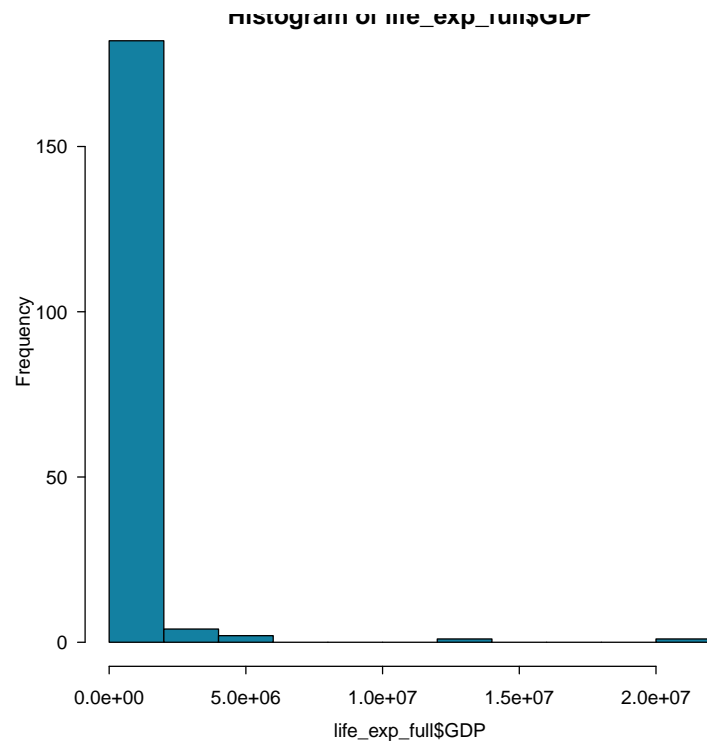
Warning: Removed 70 rows containing missing values (geom_point).

How long do we expect to live'

Cancer Rate vs. Life Expectancy



```
# GDP Distribution, Histogram  
hist(life_exp_full$GDP, col = "#1380A1")
```

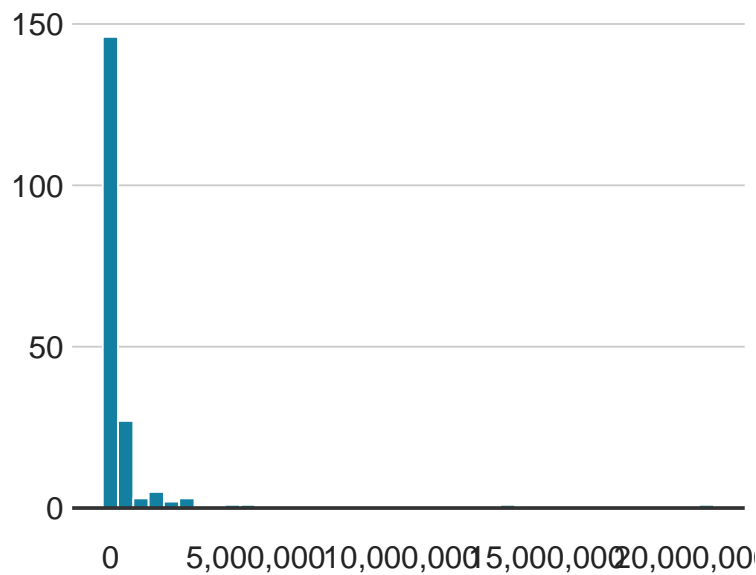


```
GDP_distro <- life_exp_full %>%
  ggplot(aes(x = GDP)) +
  geom_histogram(
    color = "white",
    fill = "#1380A1",
    na.rm = TRUE,
    bins = 40
  ) +
  geom_hline(yintercept = 0,
    size = 1,
    color = "#333333") +
  bbc_style() +
  scale_x_continuous(labels = scales::comma) +
  labs(title = "How GDP varies",
    subtitle = "Distribution of GDP (US $ Mil.)")

# Save graph
finalise_plot(plot_name = GDP_distro,
  source = "Source: JNYH/Project Luther",
  save_filepath = "figures/GDP_distro.pdf",
  width_pixels = 640,
  height_pixels = 450)
```

How GDP varies

Distribution of GDP (US \$ Mil.)



Source: JNYH/Project Luther

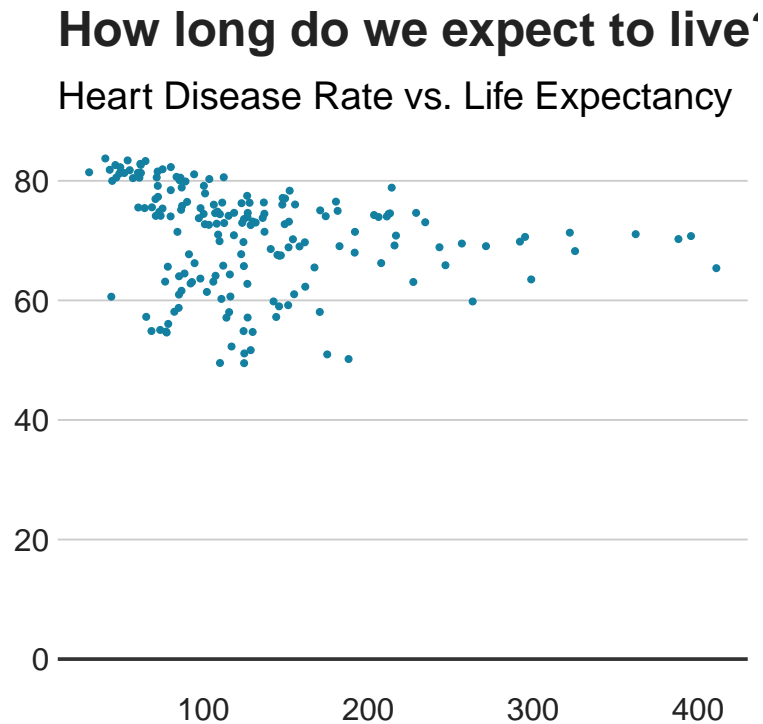
```
#logo_image_path = "placeholder.png")

# Life vs Heart Disease
life_exp_full %>%
  ggplot(aes(x = `Heart Disease Rate`,
    y = `Life Expectancy`)) +
```



```
geom_point(color = "#1380A1") +
geom_hline(yintercept = 0,
           size = 1,
           colour = "#333333") +
#scale_color_d3() +
bbc_style() +
labs(title = "How long do we expect to live?",
     subtitle = "Heart Disease Rate vs. Life Expectancy")

## Warning: Removed 70 rows containing missing values (geom_point).
```

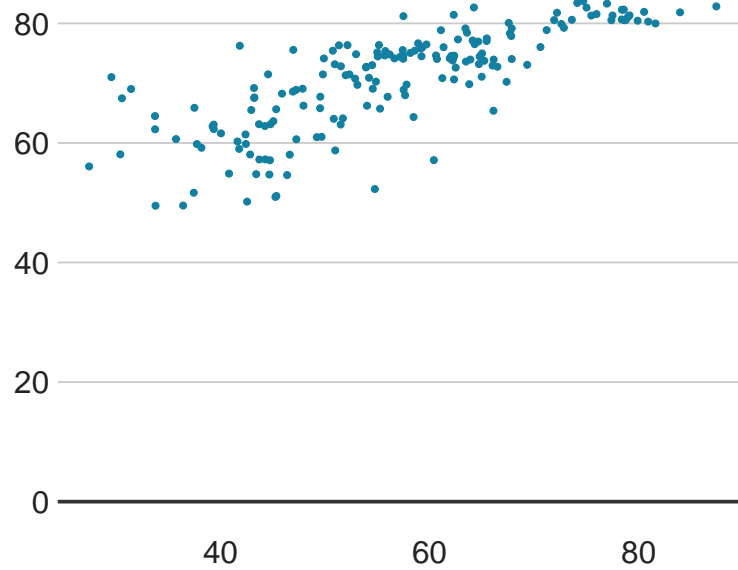


```
# Life vs EPI
life_exp_full %>%
  ggplot(aes(x = EPI,
             y = `Life Expectancy`)) +
  geom_point(color = "#1380A1") +
  geom_hline(yintercept = 0,
           size = 1,
           colour = "#333333") +
#scale_color_d3() +
bbc_style() +
labs(title = "How long do we expect to live?",
     subtitle = "EPI vs. Life Expectancy")

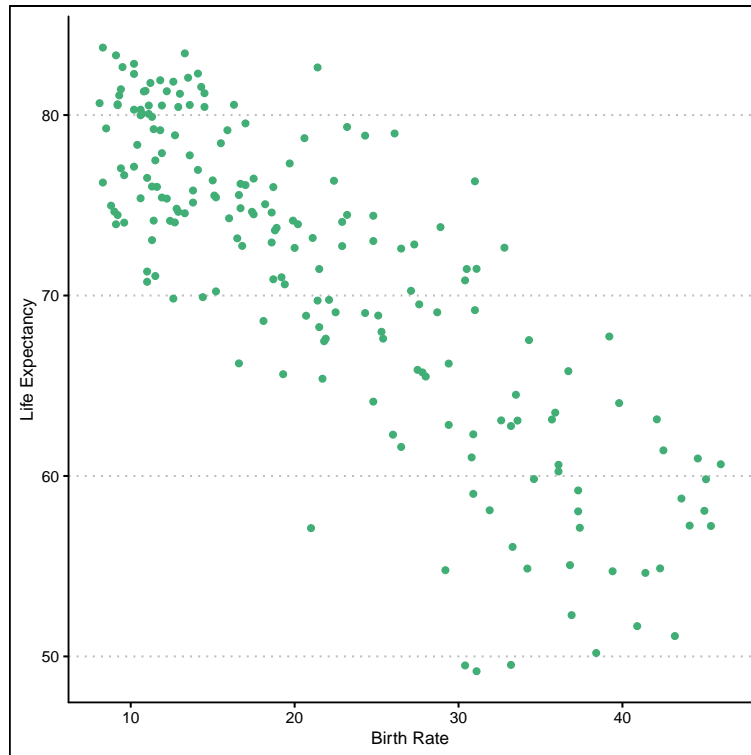
## Warning: Removed 73 rows containing missing values (geom_point).
```

How long do we expect to live'

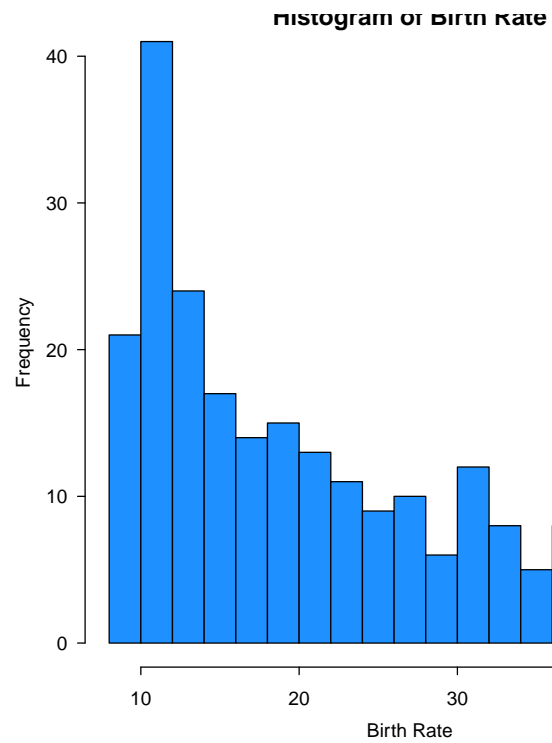
EPI vs. Life Expectancy



```
# Plot Variables v Life Expectancy -----  
  
# Birth  
life_exp_full %>%  
  ggplot() +  
  geom_point(  
    aes(y = `Life Expectancy`, x = `Birth Rate`),  
    color = COLA[3]) +  
  theme_clean()  
  
## Warning: Removed 54 rows containing missing values (geom_point).
```

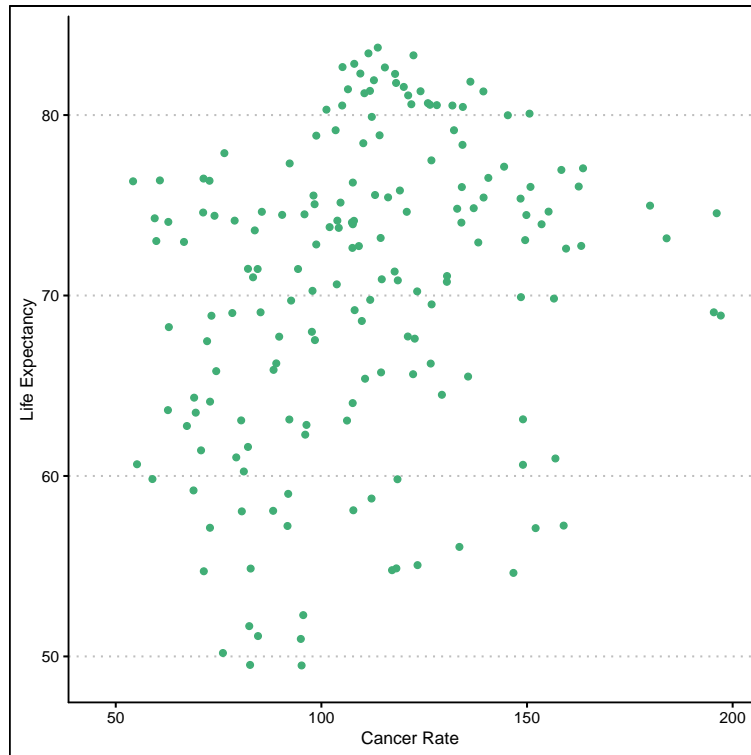


```
hist(life_exp_full$`Birth Rate`,
     xlab  = "Birth Rate",
     main  = "Histogram of Birth Rate",
     col   = "dodgerblue",
     border = "black",
     breaks = 20)
```

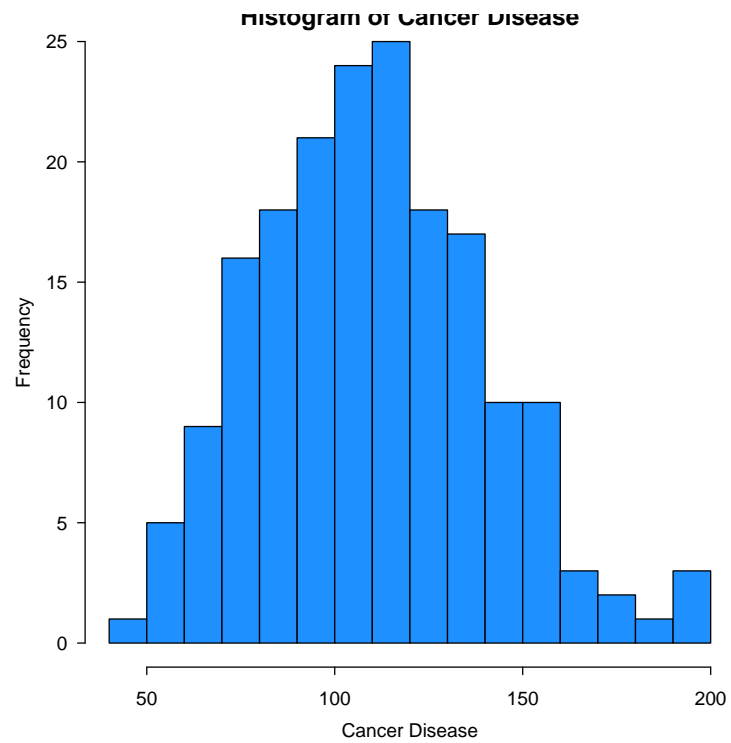


```
# Cancer
life_exp_full %>%
  ggplot() +
  geom_point(
    aes(y = `Life Expectancy`, x = `Cancer Rate`),
    color = COLA[3]) +
  theme_clean()

## Warning: Removed 70 rows containing missing values (geom_point).
```

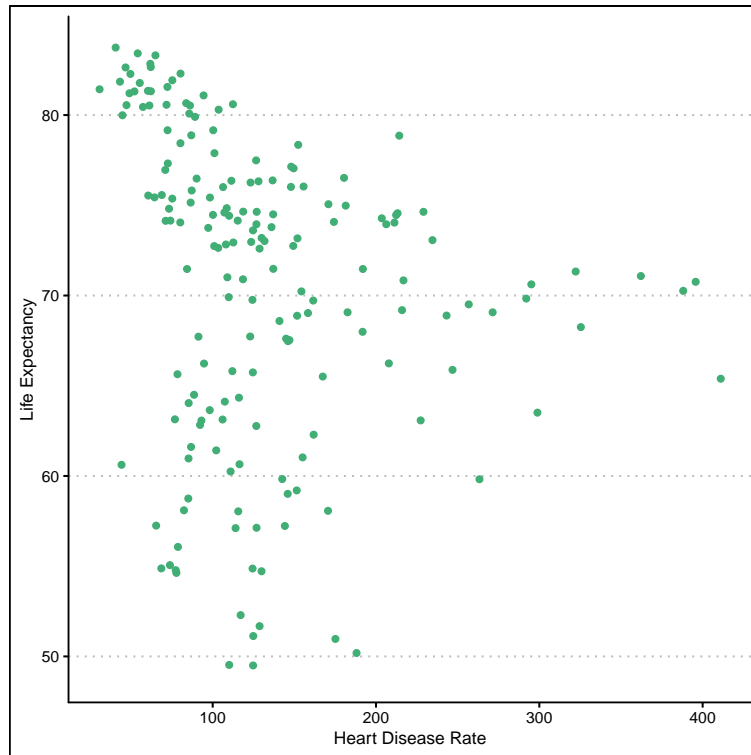


```
hist(life_exp_full$`Cancer Rate`,
     xlab  = "Cancer Disease",
     main  = "Histogram of Cancer Disease",
     col   = "dodgerblue",
     border = "black",
     breaks = 20)
```

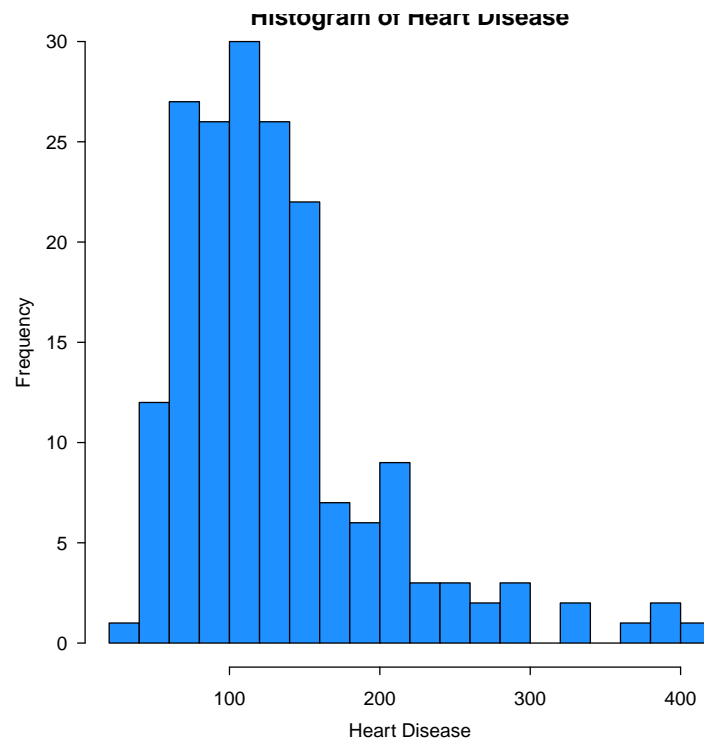


```
# Heart Disease
life_exp_full %>%
  ggplot() +
  geom_point(
    aes(y = `Life Expectancy`, x = `Heart Disease Rate`),
    color = COLA[3]) +
  theme_clean()

## Warning: Removed 70 rows containing missing values (geom_point).
```

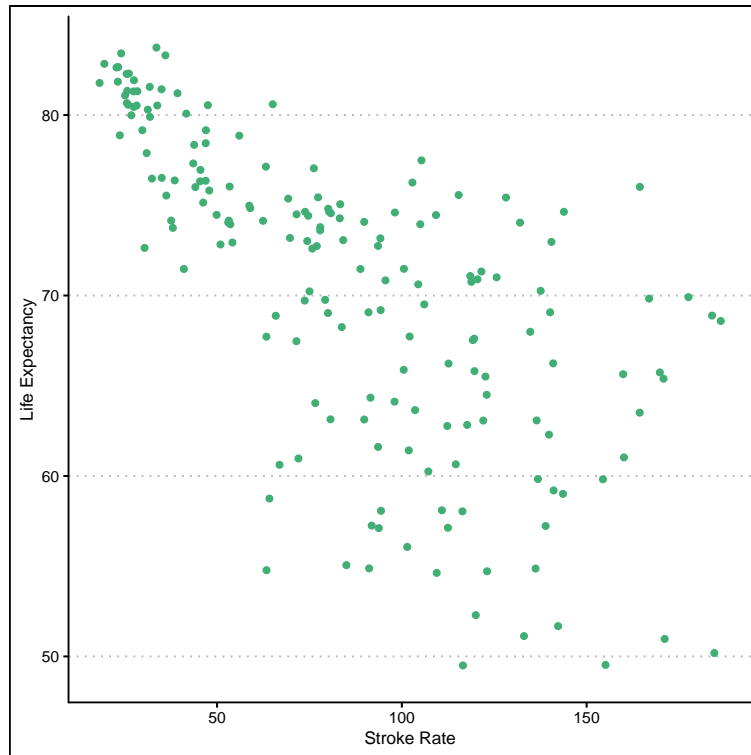


```
hist(life_exp_full$`Heart Disease Rate`,
     xlab  = "Heart Disease",
     main  = "Histogram of Heart Disease",
     col   = "dodgerblue",
     border = "black",
     breaks = 20)
```



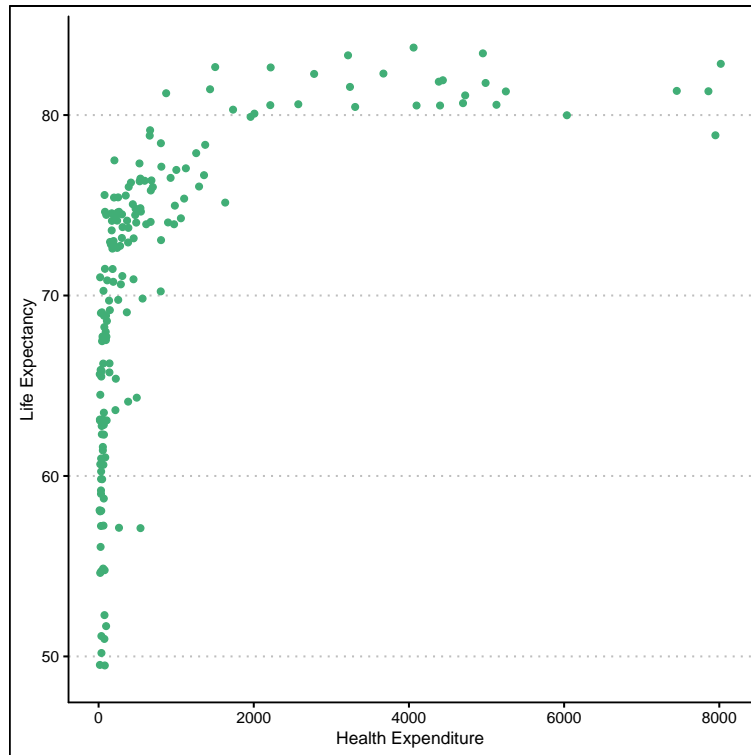
```
# Stroke
life_exp_full %>%
  ggplot() +
  geom_point(
    aes(y = `Life Expectancy`, x = `Stroke Rate`),
    color = COLA[3]) +
  theme_clean()

## Warning: Removed 70 rows containing missing values (geom_point).
```

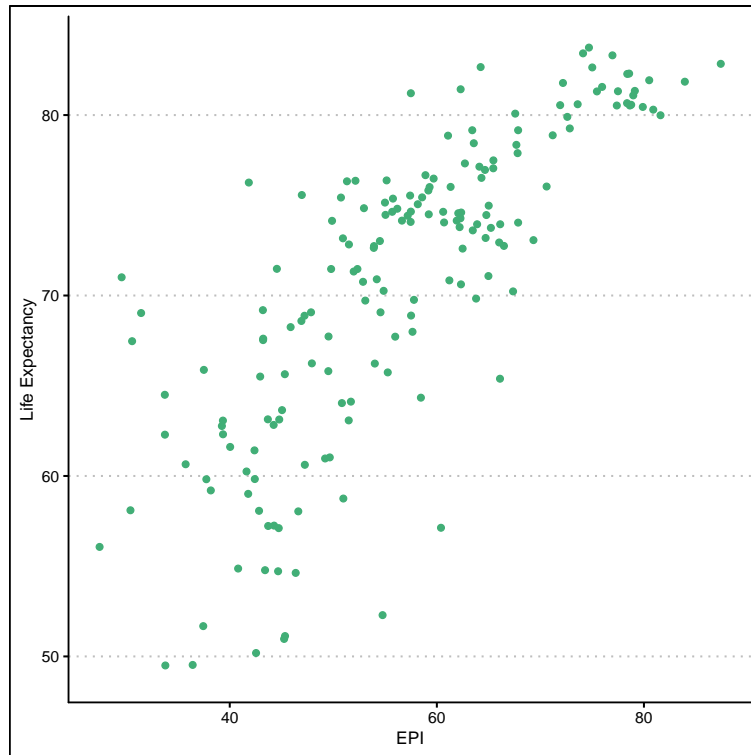
```
# Health Expenditure
life_exp_full %>%
  ggplot() +
  geom_point(
    aes(y = `Life Expectancy`, x = `Health Expenditure`),
    color = COLA[3]) +
  theme_clean()

## Warning: Removed 76 rows containing missing values (geom_point).
```



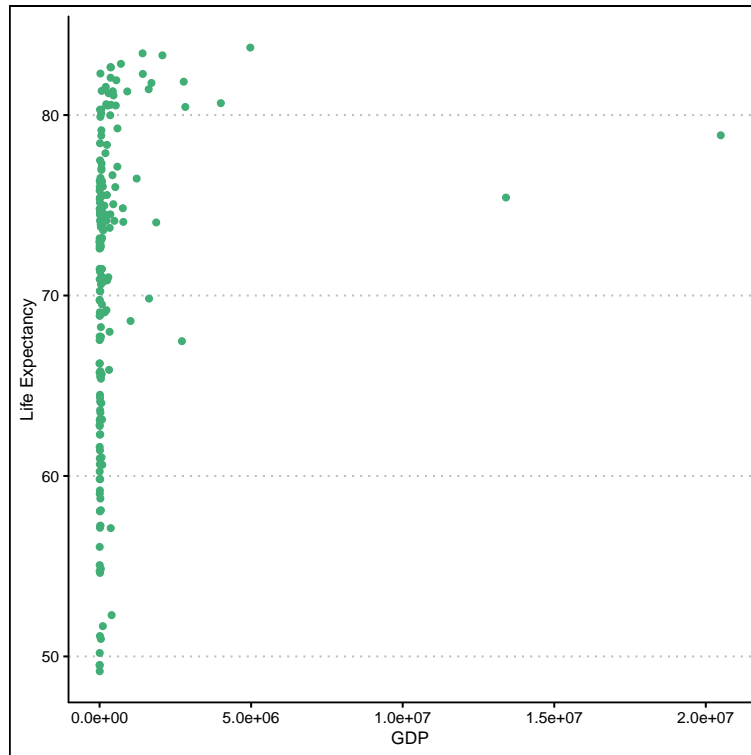
```
# EPI
life_exp_full %>%
  ggplot() +
  geom_point(
    aes(y = `Life Expectancy`, x = EPI),
    color = COLA[3]) +
  theme_clean()

## Warning: Removed 73 rows containing missing values (geom_point).
```



```
# GDP
life_exp_full %>%
  ggplot() +
  geom_point(
    aes(y = `Life Expectancy`, x = GDP),
    color = COLA[3]) +
  theme_clean()

## Warning: Removed 67 rows containing missing values (geom_point).
```



```
# Regressions -----

model_full <- lm(
  `Life Expectancy` ~ `Birth Rate` + `Cancer Rate` + `Heart Disease Rate` + `Stroke Rate` + `Health Exp
  data = life_exp_full
)

# Testing Model Fit -----

# compare model full and model reduced.
anova(model_red, model_full)

## Analysis of Variance Table
##
## Model 1: `Life Expectancy` ~ `Birth Rate` + `Stroke Rate` + `Health Expenditure` +
##      EPI + GDP
## Model 2: `Life Expectancy` ~ `Birth Rate` + `Cancer Rate` + `Heart Disease Rate` +
##      `Stroke Rate` + `Health Expenditure` + EPI + GDP
##   Res.Df    RSS Df Sum of Sq    F Pr(>F)
## 1      158 1995.2
## 2      156 1963.5  2    31.704 1.2594 0.2867

# F = 0.8399
# Pr(>F) = 0.5018
# Failed to reject H0: that removed var are zero.

# Diagnostic Checks - Model Full -----

# Model Summary and ANOVA
summary(model_full)
```

```
##
## Call:
## lm(formula = `Life Expectancy` ~ `Birth Rate` + `Cancer Rate` +
##     `Heart Disease Rate` + `Stroke Rate` + `Health Expenditure` +
##     EPI + GDP, data = life_exp_full)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -12.0296  -1.7375   0.0473   2.1224   7.1708
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    7.637e+01  2.958e+00  25.817 < 2e-16 ***
## `Birth Rate`   -4.243e-01  3.881e-02 -10.931 < 2e-16 ***
## `Cancer Rate`  -1.507e-02  1.017e-02  -1.482   0.140
## `Heart Disease Rate` 2.311e-03  5.156e-03   0.448   0.655
## `Stroke Rate`  -5.894e-02  1.051e-02  -5.607 9.13e-08 ***
## `Health Expenditure` -2.225e-04  2.687e-04  -0.828   0.409
## EPI            1.801e-01  4.050e-02   4.448 1.64e-05 ***
## GDP            9.325e-08  1.539e-07   0.606   0.546
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.548 on 156 degrees of freedom
## (84 observations deleted due to missingness)
## Multiple R-squared:  0.8326, Adjusted R-squared:  0.8251
## F-statistic: 110.8 on 7 and 156 DF,  p-value: < 2.2e-16

anova(model_full)

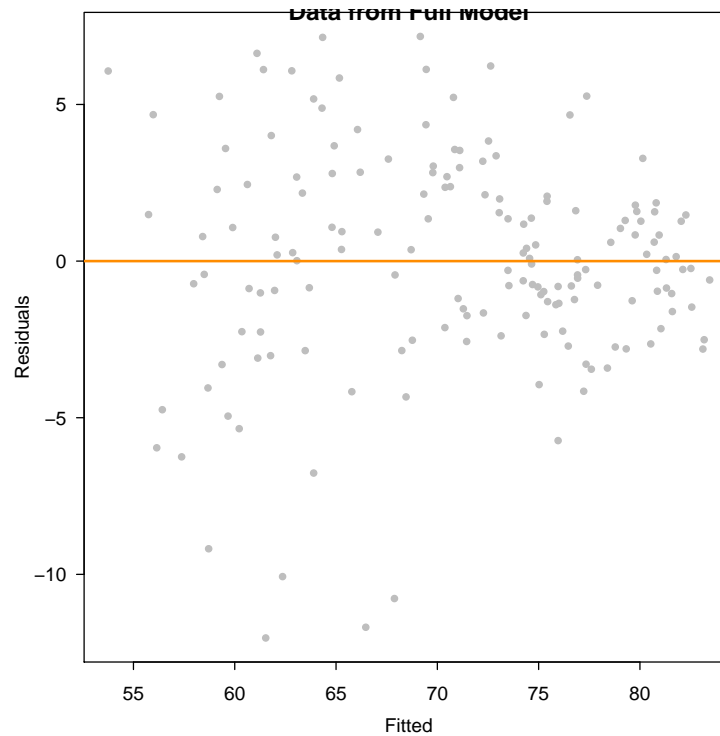
## Analysis of Variance Table
##
## Response: Life Expectancy
##              Df Sum Sq Mean Sq  F value    Pr(>F)
## `Birth Rate`    1 8213.0   8213.0 652.5242 < 2.2e-16 ***
## `Cancer Rate`    1   29.2    29.2   2.3207   0.12969
## `Heart Disease Rate` 1  276.2   276.2  21.9426 6.072e-06 ***
## `Stroke Rate`    1  950.8   950.8  75.5445 4.620e-15 ***
## `Health Expenditure` 1   45.0    45.0   3.5773  0.06043 .
## EPI              1  244.8   244.8  19.4518 1.914e-05 ***
## GDP              1    4.6     4.6   0.3669  0.54557
## Residuals       156 1963.5    12.6
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# 1 The regression function is linear (the relationship is linear).
# Yes
vif(model_full)

##           `Birth Rate`           `Cancer Rate` `Heart Disease Rate`           `Stroke Rate`
##           2.177726             1.214850         1.651303             2.617937
## `Health Expenditure`           EPI             GDP
##           2.712092             3.685143         1.226175

# 2 The error terms have a constant variance
```

```
# Fitted vs Residuals --- model_full
plot(fitted(model_full), resid(model_full), col = "grey", pch = 20,
     xlab = "Fitted", ylab = "Residuals", main = "Data from Full Model")
abline(h = 0, col = "darkorange", lwd = 2)
```



```
# Looks like it has a inverse parabolic shape

# 3 The error terms are independent (there is no relationship among the error terms).

# Breusch-Pagan Test for Homoskedasticity
bptest(model_full)

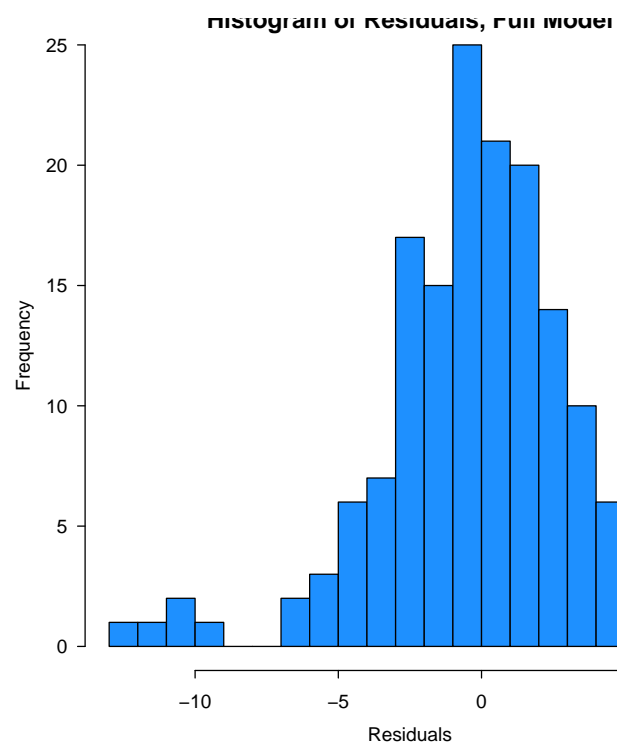
##
## studentized Breusch-Pagan test
##
## data: model_full
## BP = 20.003, df = 7, p-value = 0.005563

# For model_full we see a small p-value, so we reject the null hypothesis of
# homoskedasticity is rejected and heteroskedasticity assumed.
# The constant variance assumption is violated.
# This matches our findings with a fitted versus residuals plot.

# 4 The error terms are normally distributed

hist(resid(model_full),
     xlab = "Residuals",
     main = "Histogram of Residuals, Full Model",
```

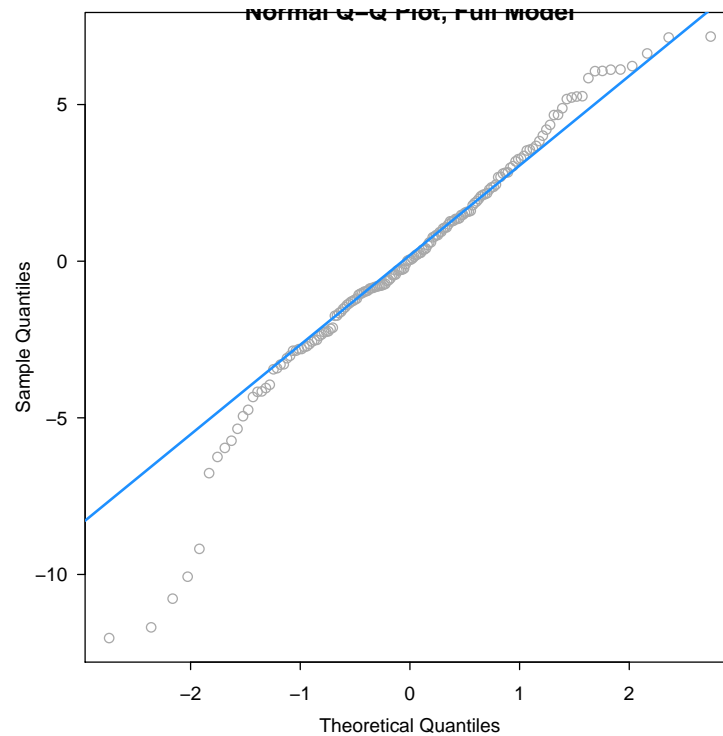
```
col    = "dodgerblue",  
border = "black",  
breaks = 20)
```



It does have a rough bell shape, however, it also has a semi-sharp peak.

Q-Q Plot

```
qqnorm(resid(model_full), main = "Normal Q-Q Plot, Full Model", col = "darkgrey")  
qqline(resid(model_full), col = "dodgerblue", lwd = 2)
```



```
# Deviates in smaller quantiles
# For Model Full, we have a suspect Q-Q plot.
# We would probably not believe the errors follow a normal distribution.

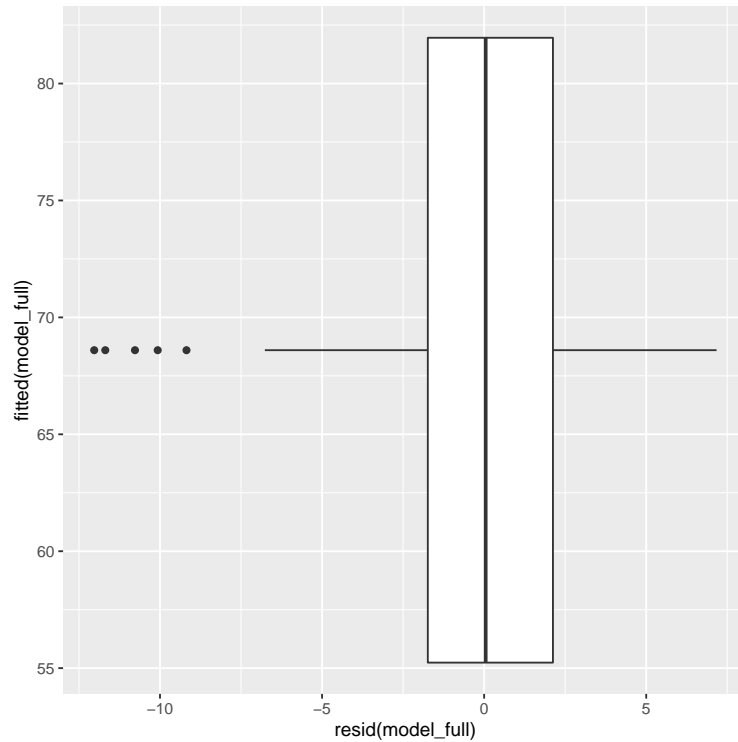
# Shapiro-Wilk Test
shapiro.test(resid(model_full))

##
##  Shapiro-Wilk normality test
##
## data:  resid(model_full)
## W = 0.96343, p-value = 0.0002576

# p = 7.152e-05
# A small p-value indicates we believe there is only a small probability
# the data could have been sampled from a normal distribution.

#RK 5 Outlier Check Via Boxplots- how should we deal with those outliers? Which countries are they?
outlierAssumption <- ggplot(model_full, aes(x=fitted(model_full), y=resid(model_full))) +
  geom_boxplot() +
  coord_flip()
outlierAssumption

## Warning: Continuous x aesthetic - did you forget aes(group=...)?
```

*# 6 There is no important predictor that have been omitted from the model
 # RK I think for this one since she's just looking for a logical explanation, we can say
 # that there very well maybe be other factors that are contributing to the life expectancy
 # of a country, but it is impossible to state them all. I'm going to put a better explanation
 # and possible alternative predictors in the actual paper.*

Diagnostic Checks - Model Reduced -----

Model Summary and ANOVA

summary(model_red)

##

Call:

lm(formula = `Life Expectancy` ~ `Birth Rate` + `Stroke Rate` +

`Health Expenditure` + EPI + GDP, data = model_full\$model)

##

Residuals:

##	Min	1Q	Median	3Q	Max
##	-12.0656	-1.8950	0.0142	2.1378	7.9142

##

##

Coefficients:

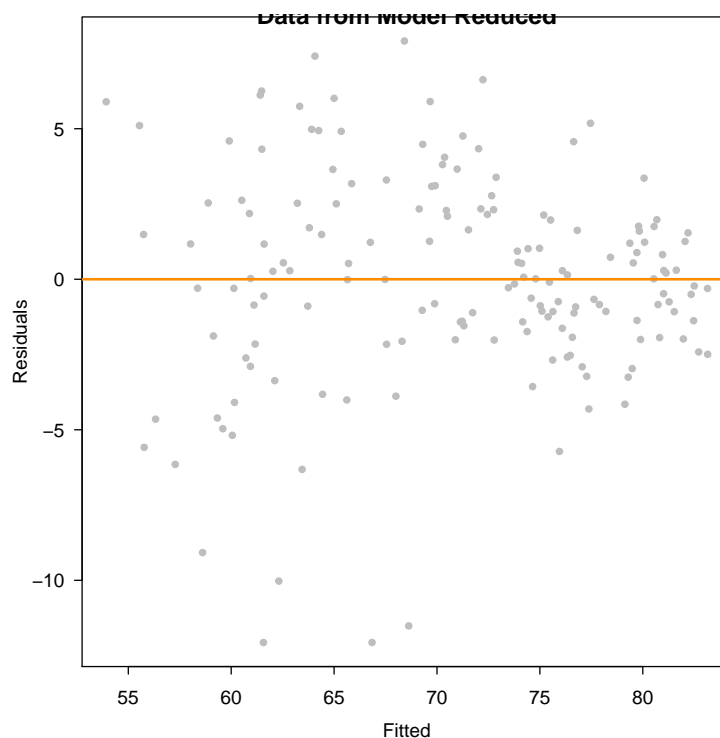
##		Estimate	Std. Error	t value	Pr(> t)
##	(Intercept)	7.523e+01	2.868e+00	26.228	< 2e-16 ***
##	`Birth Rate`	-4.158e-01	3.763e-02	-11.052	< 2e-16 ***
##	`Stroke Rate`	-5.863e-02	8.794e-03	-6.667	4.14e-10 ***
##	`Health Expenditure`	-2.300e-04	2.617e-04	-0.879	0.381
##	EPI	1.725e-01	3.872e-02	4.456	1.57e-05 ***
##	GDP	8.809e-08	1.542e-07	0.571	0.569

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.554 on 158 degrees of freedom
## Multiple R-squared:  0.8299, Adjusted R-squared:  0.8245
## F-statistic: 154.1 on 5 and 158 DF,  p-value: < 2.2e-16

anova(model_red)

## Analysis of Variance Table
##
## Response: Life Expectancy
##
##           Df Sum Sq Mean Sq  F value    Pr(>F)
## `Birth Rate`      1 8213.0   8213.0 650.3884 < 2.2e-16 ***
## `Stroke Rate`      1 1233.4   1233.4  97.6747 < 2.2e-16 ***
## `Health Expenditure` 1   34.0    34.0   2.6914  0.1029
## EPI                1  247.5   247.5  19.5972 1.776e-05 ***
## GDP                1    4.1    4.1   0.3265  0.5685
## Residuals        158 1995.2    12.6
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Fitted vs Residuals --- model_red
plot(fitted(model_red), resid(model_red), col = "grey", pch = 20,
     xlab = "Fitted", ylab = "Residuals", main = "Data from Model Reduced")
abline(h = 0, col = "darkorange", lwd = 2)
```



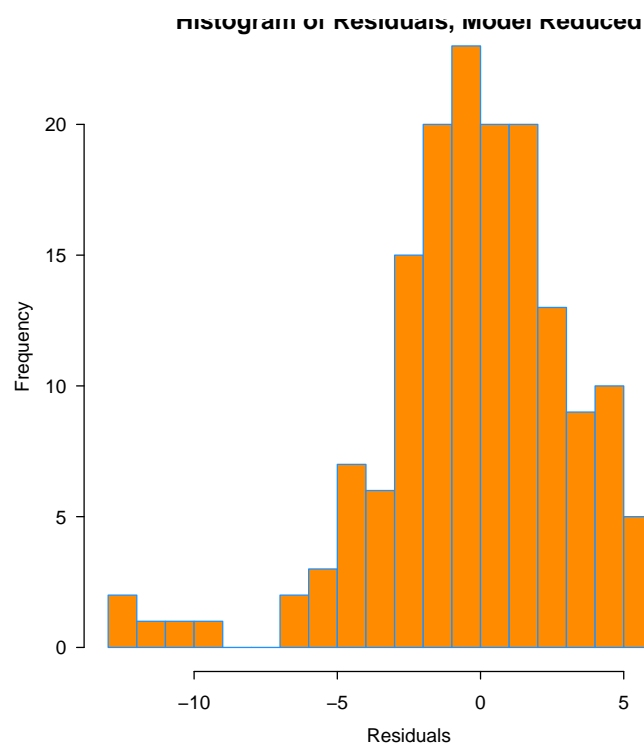
```
# Looks like it has a inverse parabolic shape

# Breusch-Pagan Test for Homoskedasticity
bptest(model_red)
```

```
##
## studentized Breusch-Pagan test
##
## data: model_red
## BP = 18.747, df = 5, p-value = 0.002142

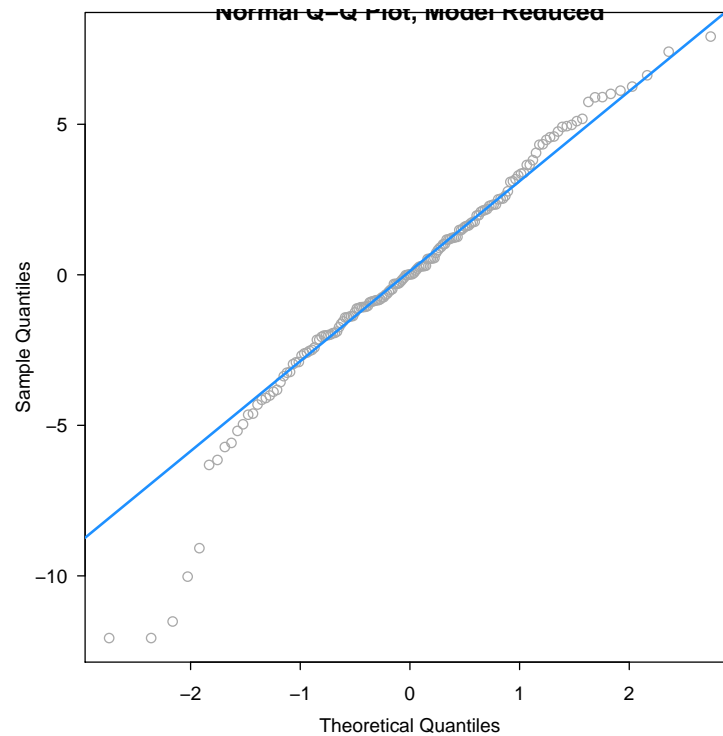
# For model_red we see a small p-value, so we reject the null of homoskedasticity.
# The constant variance assumption is violated.
# This matches our findings with a fitted versus residuals plot.

# Normality of errors
hist(resid(model_red),
     xlab = "Residuals",
     main = "Histogram of Residuals, Model Reduced",
     col = "darkorange",
     border = "dodgerblue",
     breaks = 20)
```



```
# It does have a rough bell shape, however, it also has a very sharp peak.

# Q-Q Plot
qqnorm(resid(model_red), main = "Normal Q-Q Plot, Model Reduced", col = "darkgrey")
qqline(resid(model_red), col = "dodgerblue", lwd = 2)
```



```
# Deviates in smaller quantiles
# For Model Reduced, we have a suspect Q-Q plot.
# We would probably not believe the errors follow a normal distribution.

# Shapiro-Wilk Test
shapiro.test(resid(model_red))

##
##  Shapiro-Wilk normality test
##
## data:  resid(model_red)
## W = 0.96242, p-value = 0.0002042

# p = 7.152e-05
# A small p-value indicates we believe there is only a small probability
# the data could have been sampled from a normal distribution.

# End of File -----
```

The R session information (including the OS info, R version and all packages used):

```
sessionInfo()

## R version 3.6.1 (2019-07-05)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Catalina 10.15.1
##
## Matrix products: default
## BLAS:   /System/Library/Frameworks/Accelerate.framework/Versions/A/Frameworks/vecLib.framework/Versions/A/
```

```
## LAPACK: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] faraway_1.0.7    MASS_7.3-51.4    scales_1.0.0     lmtest_0.9-37    zoo_1.8-6
## [6] bbplot_0.2       ggthemes_4.2.0   ggsci_2.9        gridExtra_2.3    forcats_0.4.0
## [11] stringr_1.4.0    purrr_0.3.3      readr_1.3.1      tidyr_1.0.0      tibble_2.1.3
## [16] ggplot2_3.2.1    tidyverse_1.2.1  dplyr_0.8.3      knitr_1.26
##
## loaded via a namespace (and not attached):
## [1] Rcpp_1.0.3        lubridate_1.7.4   lattice_0.20-38   png_0.1-7
## [5] statquotes_0.2.2  assertthat_0.2.1  zeallot_0.1.0     packrat_0.5.0
## [9] R6_2.4.1          cellranger_1.1.0  backports_1.1.5   evaluate_0.14
## [13] httr_1.4.0        highr_0.8         pillar_1.4.2      rlang_0.4.1
## [17] lazyeval_0.2.2    readxl_1.3.1      minqa_1.2.4       rstudioapi_0.10
## [21] nloptr_1.2.1      Matrix_1.2-17     labeling_0.3       splines_3.6.1
## [25] lme4_1.1-21       tidytext_0.2.1    tinytex_0.17      munsell_0.5.0
## [29] broom_0.5.2       compiler_3.6.1    janeaustenr_0.1.5 modelr_0.1.4
## [33] xfun_0.11         pkgconfig_2.0.3   tidyselect_0.2.5  ggpubr_0.2.4
## [37] crayon_1.3.4      withr_2.1.2       SnowballC_0.6.0   grid_3.6.1
## [41] nlme_3.1-140      jsonlite_1.6       gtable_0.3.0      lifecycle_0.1.0
## [45] magrittr_1.5      tokenizers_0.2.1  cli_1.1.0         stringi_1.4.3
## [49] ggsignif_0.6.0    xml2_1.2.0         ellipsis_0.3.0    generics_0.0.2
## [53] vctrs_0.2.0       cowplot_1.0.0     boot_1.3-22       wordcloud_2.6
## [57] RColorBrewer_1.1-2 tools_3.6.1        glue_1.3.1        hms_0.5.0
## [61] colorspace_1.4-1  rvest_0.3.4       haven_2.1.1
##
## Sys.time()
## [1] "2019-12-02 11:30:08 EST"
```