Appendix

2022-12-05

Appendix A: Data Cleaning

https://www.kaggle.com/datasets/kumarajarshi/life-expectancy-who

```
library(tidyverse)
library(skimr)
library(GGally)
library(readr)
library(car)
library(broom)
library(leaps)
library(gt)
```

```
df <- read_csv("/Users/christinalopez/Desktop/STAT510_F22/datasets/Life.csv")

df <- df |>
  rename(country = Country,
         year = Year,
         status = Status,
         life = `Life expectancy`,
         mort = `Adult Mortality`,
         inf = `infant deaths`,
         alc = Alcohol,
         exp.p = `percentage expenditure`,
         hep = `Hepatitis B`,
         meas = Measles,
         bmi = BMI,
         under5 = `under-five deaths`,
         polio = Polio,
         exp.t = `Total expenditure`,
         dip = Diphtheria,
         hiv = `HIV/AIDS`,
         gdp = GDP,
         pop = Population,
         thin1.19 = `thinness  1-19 years`,
         thin5.9 = `thinness 5-9 years`,
         comp = `Income composition of resources`,
         school = Schooling) |>
  mutate(year = factor(year))
head(df)
```

```
## # A tibble: 6 x 22
##   country    year  status  life  mort   inf   alc exp.p   hep  meas   bmi under5
##   <chr>      <fct> <chr>  <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>  <dbl>
## 1 Afghanist~ 2015  Devel~  65     263    62  0.01 71.3     65  1154  19.1     83
## 2 Afghanist~ 2014  Devel~  59.9   271    64  0.01 73.5     62   492  18.6     86
```

```
## 3 Afghanist~ 2013  Devel~  59.9   268    66  0.01 73.2     64   430  18.1     89
## 4 Afghanist~ 2012  Devel~  59.5   272    69  0.01 78.2     67  2787  17.6     93
## 5 Afghanist~ 2011  Devel~  59.2   275    71  0.01  7.10    68  3013  17.2     97
## 6 Afghanist~ 2010  Devel~  58.8   279    74  0.01 79.7     66  1989  16.7    102
## # ... with 10 more variables: polio <dbl>, exp.t <dbl>, dip <dbl>, hiv <dbl>,
## #   gdp <dbl>, pop <dbl>, thin1.19 <dbl>, thin5.9 <dbl>, comp <dbl>,
## #   school <dbl>
```

Appendix B: Exploratory Data Analysis

B.1: Skim

```
skim_without_charts(df)
```

Table 1: Data summary

Name	df
Number of rows	2938
Number of columns	22
Column type frequency:	
character	2
factor	1
numeric	19
Group variables	None

Variable type: character

skim_variable	n_missing	complete_rate	min	max	empty	n_unique	whitespace
country	0	1	4	52	0	193	0
status	0	1	9	10	0	2	0

Variable type: factor

skim_variable	n_missing	complete_rate	ordered	n_unique	top_counts
year	0	1	FALSE	16	201: 193, 200: 183, 200: 183, 200: 183

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100
life	10	1.00	69.22	9.52	36.30	63.10	72.10	75.70	8.900000e+01
mort	10	1.00	164.80	124.29	1.00	74.00	144.00	228.00	7.230000e+02
inf	0	1.00	30.30	117.93	0.00	0.00	3.00	22.00	1.800000e+03
alc	194	0.93	4.60	4.05	0.01	0.88	3.76	7.70	1.787000e+01
exp.p	0	1.00	738.25	1987.91	0.00	4.69	64.91	441.53	1.947991e+04
hep	553	0.81	80.94	25.07	1.00	77.00	92.00	97.00	9.900000e+01
meas	0	1.00	2419.59	11467.27	0.00	0.00	17.00	360.25	2.121830e+05

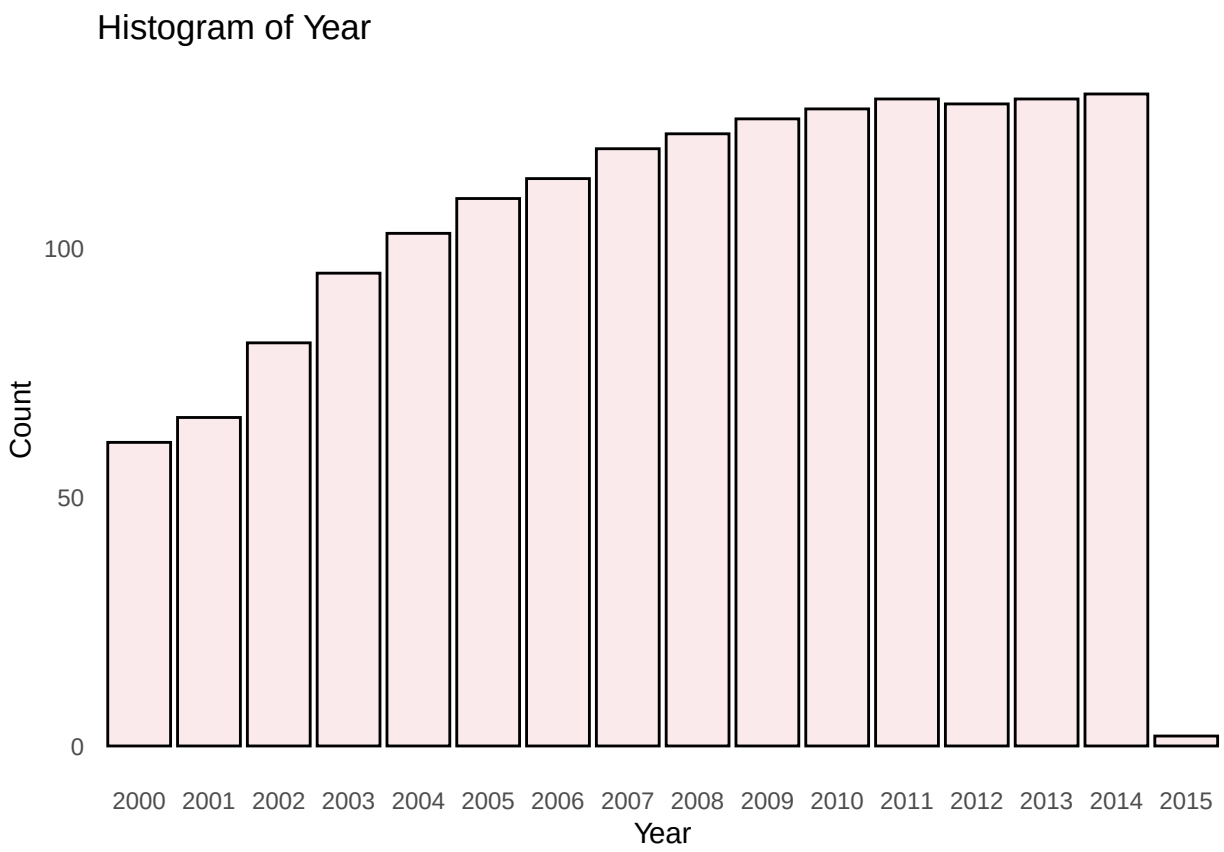
skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100
bmi	34	0.99	38.32	20.04	1.00	19.30	43.50	56.20	8.730000e+01
under5	0	1.00	42.04	160.45	0.00	0.00	4.00	28.00	2.500000e+03
polio	19	0.99	82.55	23.43	3.00	78.00	93.00	97.00	9.900000e+01
exp.t	226	0.92	5.94	2.50	0.37	4.26	5.76	7.49	1.760000e+01
dip	19	0.99	82.32	23.72	2.00	78.00	93.00	97.00	9.900000e+01
hiv	0	1.00	1.74	5.08	0.10	0.10	0.10	0.80	5.060000e+01
gdp	448	0.85	7483.16	14270.17	1.68	463.94	1766.95	5910.81	1.191727e+05
pop	652	0.78	12753375.12	61012096.51	34.00	195793.25	1386542.00	7420359.00	1.293859e+09
thin1.19	34	0.99	4.84	4.42	0.10	1.60	3.30	7.20	2.770000e+01
thin5.9	34	0.99	4.87	4.51	0.10	1.50	3.30	7.20	2.860000e+01
comp	167	0.94	0.63	0.21	0.00	0.49	0.68	0.78	9.500000e-01
school	163	0.94	11.99	3.36	0.00	10.10	12.30	14.30	2.070000e+01

There are a lot of missing values for some variables, so the first thing we want to do is drop NA's from the data set. Next, we will explore the data while dropping NA's.

```
common_theme =   theme_minimal() +
  theme(panel.grid.minor.y = element_blank(),
        panel.grid.minor.x = element_blank(),
        panel.grid.major.y = element_blank(),
        panel.grid.major.x = element_blank())
```

B.2: Year

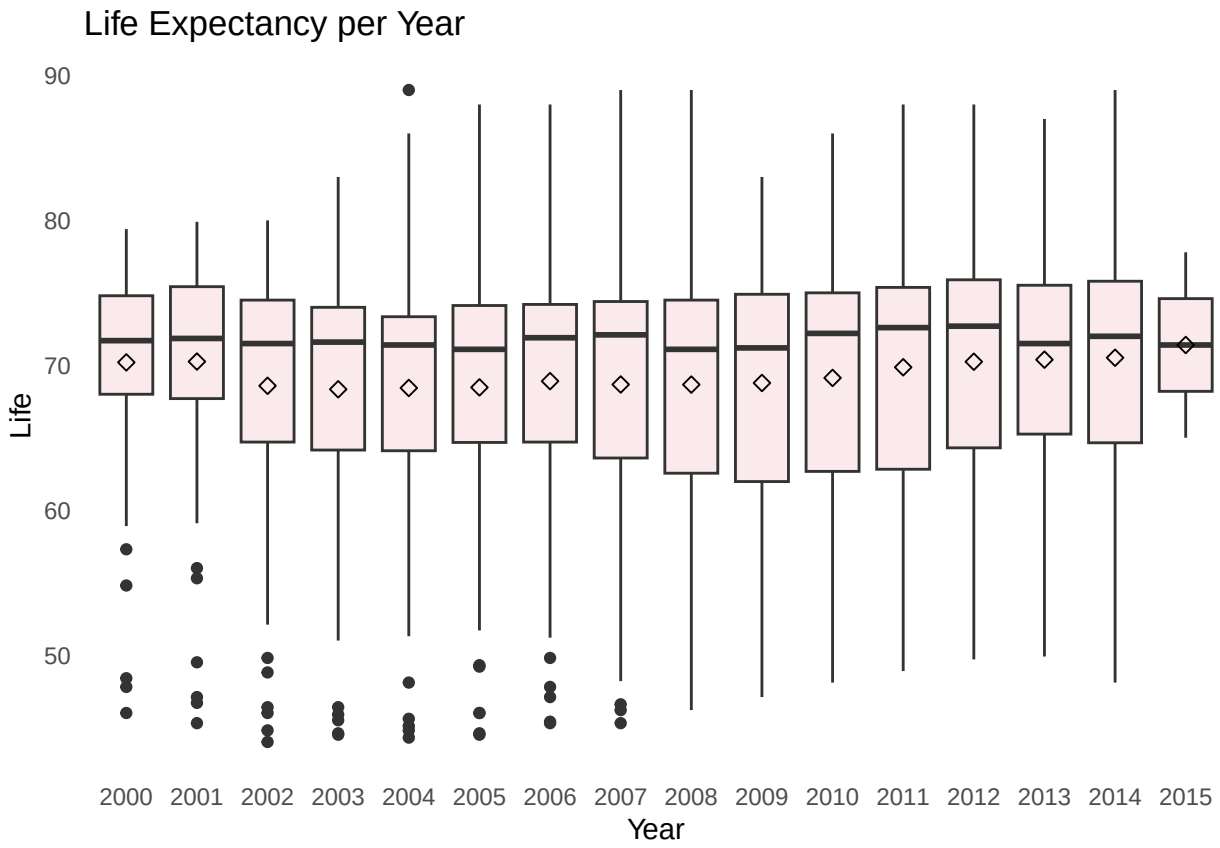
```
df |>
  drop_na() |>
  ggplot(aes(x = year)) +
  geom_histogram(stat = "count", fill = "#FBEAEB", color = "black") +
  labs(x = "Year", y = "Count", title = "Histogram of Year") +
  common_theme
```



Each year has progressively more data per year when null values are excluded. After 2011, the count flattens out. 2015 is not complete, so it should be excluded.

```
df |>
  drop_na() |>
ggplot(mapping = aes(x = year, y = life)) +
  geom_boxplot(fill = "#FBEAEB") +
  stat_summary(fun.y=mean, geom="point", shape=23, size=2) +
  labs(x = "Year", y = "Life", title = "Life Expectancy per Year") +
  common_theme
```

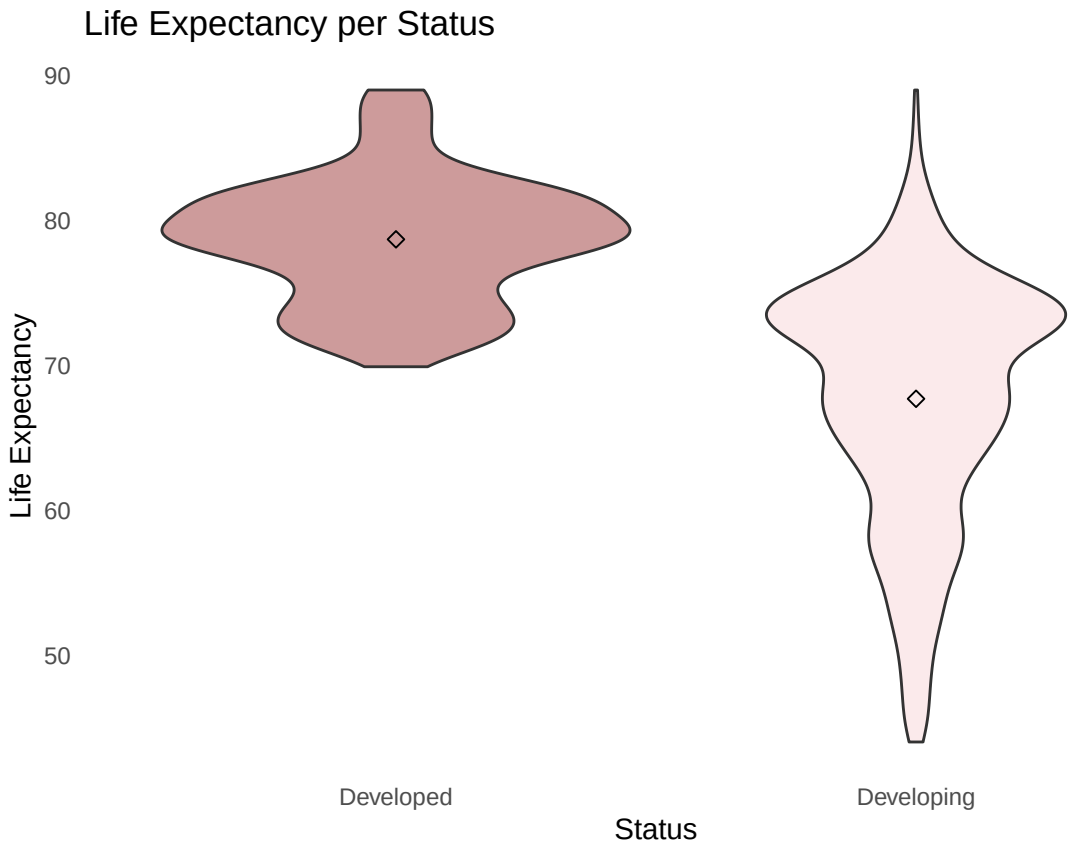
```
## Warning: The `fun.y` argument of `stat_summary()` is deprecated as of ggplot2 3.3.0.
## i Please use the `fun` argument instead.
```



The data should be subset for a recent year, to be most applicable. 2014 is the most recent year with complete data. The boxplot is similar to other recent years, so there is no concern with choosing 2014 as our year to subset the data.

B.3: Status

```
df |>
  drop_na() |>
ggplot(aes(status, life, fill = status)) +
  geom_violin() +
  stat_summary(fun.y=mean, geom="point", shape=23, size=2) +
  scale_fill_manual(values = c("rosybrown3", "#FBEAEB")) +
  labs(x = "Status", y = "Life Expectancy", title = "Life Expectancy per Status") +
  common_theme + theme(legend.position = "none")
```



There is a wider range of life expectancy in developing countries. Also, the research interest is in understanding how some developing can have higher life expectancy than others. As such, the data with be further subset by filtering for developing countries only.

B.4: Subset

```
df1 <- df |>
  filter(year %in% "2014",
         status %in% "Developing") |>
  select(-country, -year, -status) |>
  drop_na()

head(df1)
```

```
## # A tibble: 6 x 19
##    life  mort   inf   alc exp.p   hep  meas   bmi under5 polio exp.t   dip   hiv
##   <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>  <dbl> <dbl> <dbl> <dbl> <dbl>
## 1  59.9   271    64  0.01  73.5    62   492  18.6     86    58  8.18    62   0.1
## 2  77.5     8     0  4.51 429.     98     0  57.2      1    98  5.88    98   0.1
## 3  75.4    11    21  0.01  54.2    95     0  58.4     24    95  7.21    95   0.1
## 4  51.7   348    67  8.33  24.0    64 11699  22.7    101    68  3.31    64   2
## 5  76.2   118     8  7.93 847.     94     1  62.2      9    92  4.79    94   0.1
## 6  74.6    12     1  3.91 296.     93    13  54.1      1    95  4.48    93   0.1
## # ... with 6 more variables: gdp <dbl>, pop <dbl>, thin1.19 <dbl>,
## #   thin5.9 <dbl>, comp <dbl>, school <dbl>
```

```
skim_without_charts(df1)
```

Table 5: Data summary

Name	df1
Number of rows	112
Number of columns	19
Column type frequency:	
numeric	19
Group variables	None

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100
life	0	1	68.74	7.80	48.10	62.98	69.60	74.62	8.800000e+01
mort	0	1	174.47	111.86	2.00	109.50	156.50	242.75	5.220000e+02
inf	0	1	33.30	107.60	0.00	1.00	5.50	25.50	9.570000e+02
alc	0	1	2.23	3.23	0.01	0.01	0.01	4.12	1.394000e+01
exp.p	0	1	471.47	885.33	0.44	43.33	145.74	618.03	6.739680e+03
hep	0	1	80.54	24.17	2.00	77.00	89.00	96.00	9.900000e+01
meas	0	1	2376.57	10614.90	0.00	0.00	8.50	326.50	7.956300e+04
bmi	0	1	38.23	19.91	2.00	22.70	35.35	57.12	7.710000e+01
under5	0	1	44.60	141.09	0.00	1.00	6.50	36.75	1.200000e+03
polio	0	1	81.45	22.00	8.00	75.75	91.00	96.00	9.900000e+01
exp.t	0	1	5.82	2.38	1.21	4.34	5.66	7.22	1.373000e+01
dip	0	1	81.86	22.99	2.00	77.75	91.00	96.25	9.900000e+01
hiv	0	1	0.93	1.66	0.10	0.10	0.20	0.70	9.400000e+00
gdp	0	1	4382.11	6704.13	25.45	528.15	1665.99	5551.47	4.295524e+04
pop	0	1	25640759.09	125975736.58	41.00	288257.25	1458733.50	13813606.25	1.293859e+09
thin1.19	0	1	5.22	4.53	0.10	1.90	4.15	7.03	2.680000e+01
thin5.9	0	1	5.50	4.64	0.10	1.90	5.20	7.32	2.740000e+01
comp	0	1	0.64	0.14	0.34	0.51	0.66	0.74	9.100000e-01
school	0	1	12.07	2.42	5.30	10.38	12.35	13.60	1.730000e+01

There are 112 observations in our subset of data to analyze. All variables are now numeric because we have filtered to 1 value each for 2 of the categorical variables (year and status). Country was dropped for most of our analysis because each data point represents one country, so it's not useful in setting up regression.

Appendix C: Which developing countries had the highest life expectancy in 2014?

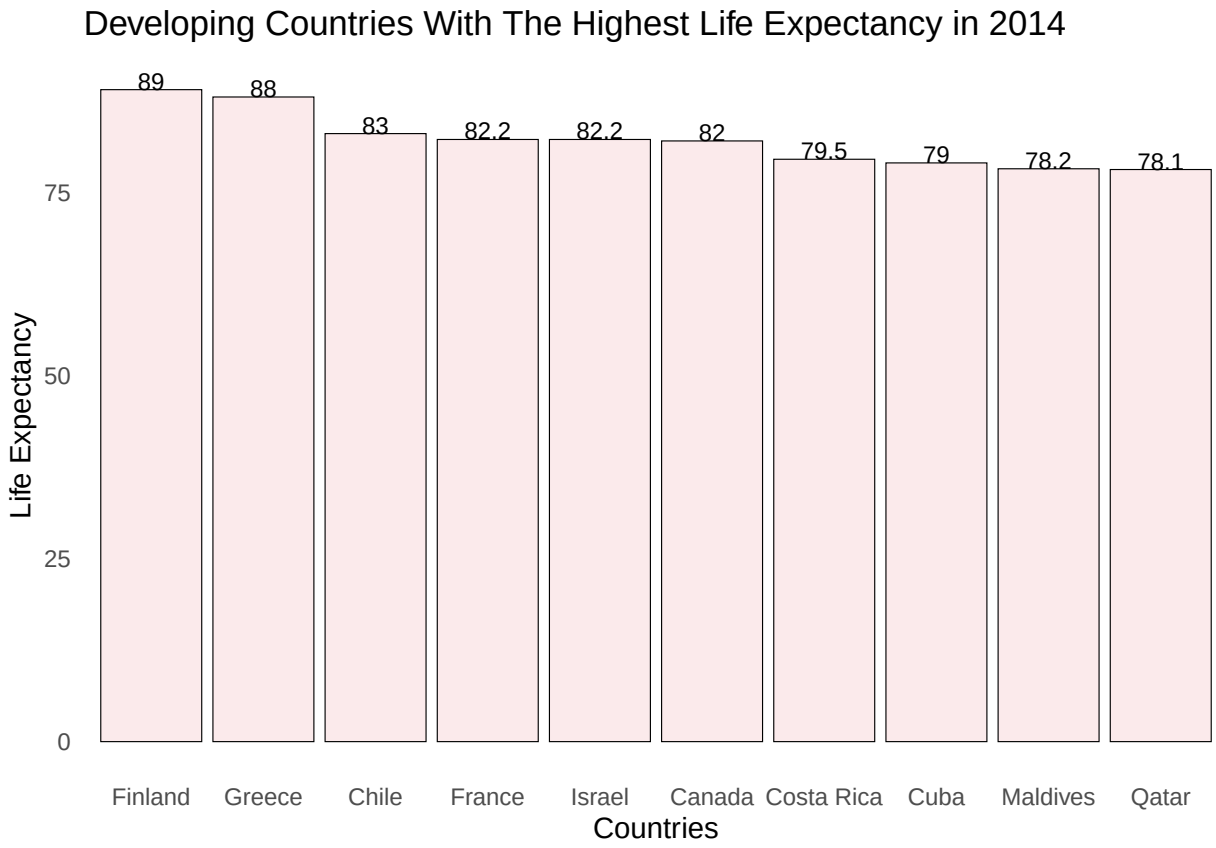
Bring country back into the data set for visualizations:

```
df2 <- df  |>
  filter(year %in% "2014",
         status %in% "Developing") |>
  select(life, mort, exp.t, hiv, comp, country) |>
  drop_na()
```

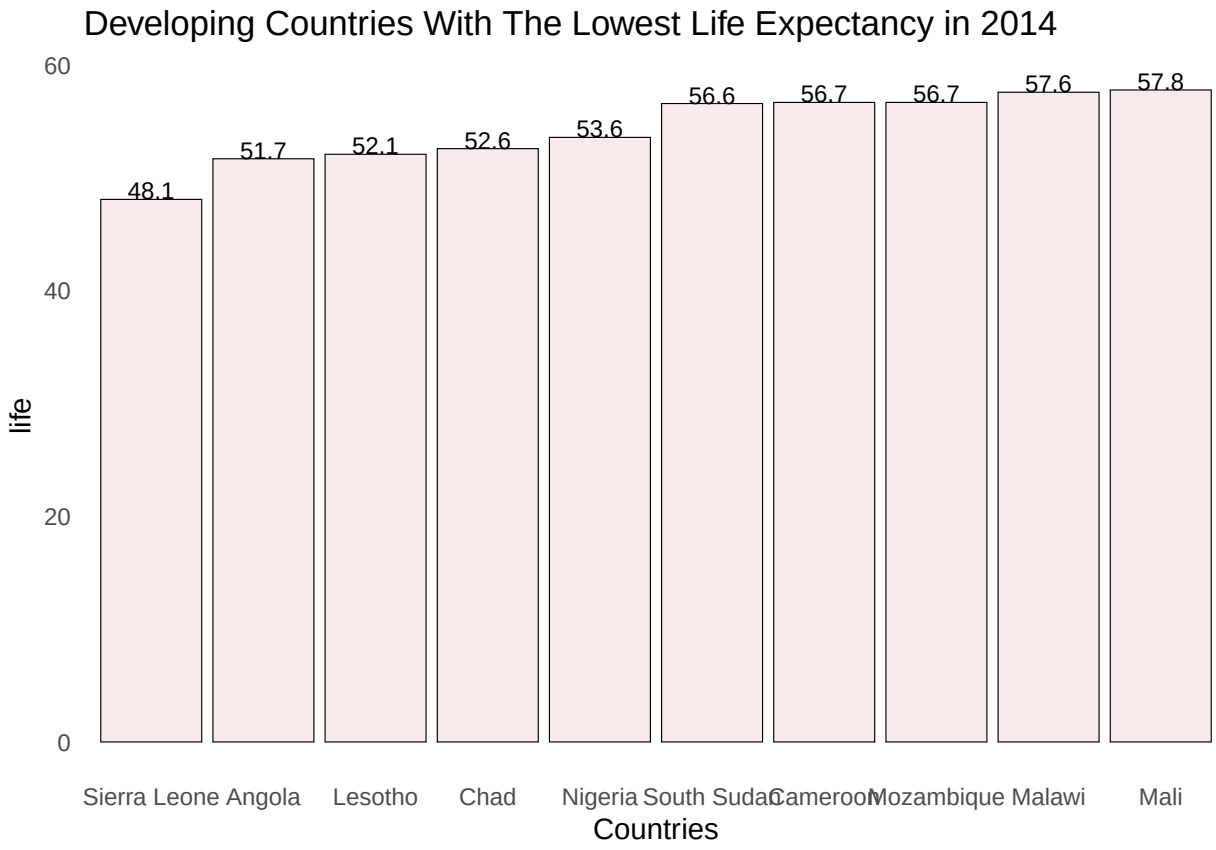
Top and bottom countries:

```
df2 |>
  arrange(desc(life)) |>
  head(10) |>
  ggplot(aes(x = reorder(country,-life), y = life)) +
  geom_bar(stat = "identity", fill = "#FBEAEB", color = "black", size = 0.2) +
  geom_text(aes(label=life), vjust=0, color="black", size=3) +
  labs(x = "Countries", y = "Life Expectancy",
       title = "Developing Countries With The Highest Life Expectancy in 2014") +
  common_theme
```

```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
```




```
df2 |>
  arrange(life) |>
  head(10) |>
  ggplot(aes(x = reorder(country,life), y = life)) +
  geom_bar(stat = "identity", fill = "#FBEAEB", color = "black", size = 0.2) +
  geom_text(aes(label=life), vjust=0, color="black", size=3) +
  labs(x = "Countries",
       title = "Developing Countries With The Lowest Life Expectancy in 2014") +
  common_theme
```



Appendix D: Which variables best predict life expectancy?

D.1 Stepwise Regression Variable Selection

```
n = nrow(df1)
mod0 = lm(life ~ 1, data = df1)
mod.all = lm(life ~., data = df1)
step(mod0, scope = list(lower = mod0, upper = mod.all))
```

```
## Start:  AIC=461.2
## life ~ 1
##
##             Df Sum of Sq    RSS    AIC
## + comp       1    5072.3 1685.7 307.68
## + school     1    3921.8 2836.3 365.96
## + mort       1    3868.9 2889.2 368.03
## + hiv        1    2721.6 4036.4 405.48
## + bmi        1    2219.4 4538.7 418.61
## + gdp        1    1805.1 4953.0 428.40
## + exp.p      1    1487.9 5270.1 435.35
## + alc        1    1321.4 5436.6 438.83
## + thin5.9    1     888.0 5870.1 447.42
## + thin1.19   1     779.6 5978.4 449.47
## + polio      1     682.6 6075.5 451.27
## + dip        1     501.9 6256.2 454.56
## + hep        1     408.7 6349.3 456.21
```

```
## + exp.t     1     359.2 6398.9 457.08
## + under5    1     279.0 6479.1 458.48
## + inf       1     198.6 6559.5 459.86
## <none>                  6758.1 461.20
## + meas      1       0.5 6757.5 463.19
## + pop       1       0.0 6758.1 463.20
##
## Step:  AIC=307.68
## life ~ comp
##
##            Df Sum of Sq    RSS    AIC
## + mort      1     517.6 1168.1 268.60
## + hiv       1     485.2 1200.5 271.67
## + exp.t     1      66.6 1619.1 305.17
## + hep       1      43.2 1642.5 306.77
## + polio     1      42.6 1643.1 306.82
## <none>                  1685.7 307.68
## + dip       1      22.7 1663.0 308.16
## + alc       1      17.1 1668.7 308.54
## + under5    1      13.7 1672.0 308.77
## + school    1      12.0 1673.8 308.89
## + exp.p     1       8.2 1677.5 309.14
## + inf       1       7.6 1678.1 309.18
## + bmi       1       1.8 1684.0 309.57
## + thin1.19  1       1.7 1684.1 309.57
## + meas      1       1.0 1684.8 309.62
## + pop       1       0.6 1685.1 309.64
## + thin5.9   1       0.1 1685.7 309.68
## + gdp       1       0.0 1685.7 309.68
## - comp      1    5072.3 6758.1 461.20
##
## Step:  AIC=268.6
## life ~ comp + mort
##
##            Df Sum of Sq    RSS    AIC
## + hiv       1    145.15 1023.0 255.74
## + exp.t     1     90.67 1077.5 261.55
## + exp.p     1     37.23 1130.9 266.97
## + hep       1     21.56 1146.6 268.51
## <none>                  1168.1 268.60
## + dip       1     18.10 1150.0 268.85
## + gdp       1     13.40 1154.7 269.31
## + polio     1      9.47 1158.7 269.69
## + bmi       1      7.96 1160.2 269.83
## + under5    1      6.61 1161.5 269.97
## + alc       1      4.15 1164.0 270.20
## + thin5.9   1      3.84 1164.3 270.23
## + inf       1      3.81 1164.3 270.23
## + thin1.19  1      1.18 1166.9 270.49
## + pop       1      0.49 1167.6 270.55
## + school    1      0.06 1168.1 270.60
## + meas      1      0.03 1168.1 270.60
## - mort      1    517.63 1685.8 307.68
## - comp      1   1721.08 2889.2 368.03
```

```
##
## Step:  AIC=255.74
## life ~ comp + mort + hiv
##
##            Df Sum of Sq     RSS    AIC
## + exp.t     1     87.80  935.17 247.69
## + exp.p     1     44.60  978.37 252.75
## <none>                   1022.97 255.74
## + gdp       1     18.00 1004.97 255.75
## + hep       1     15.16 1007.81 256.07
## + dip       1     14.49 1008.48 256.14
## + under5    1      9.56 1013.41 256.69
## + thin5.9   1      9.10 1013.87 256.74
## + inf       1      6.77 1016.20 257.00
## + bmi       1      4.10 1018.88 257.29
## + thin1.19  1      3.43 1019.54 257.36
## + polio     1      2.65 1020.32 257.45
## + meas      1      2.42 1020.55 257.48
## + alc       1      1.81 1021.16 257.54
## + school    1      0.59 1022.38 257.68
## + pop       1      0.09 1022.88 257.73
## - hiv       1    145.15 1168.12 268.60
## - mort      1    177.57 1200.55 271.67
## - comp      1   1612.58 2635.55 359.73
##
## Step:  AIC=247.69
## life ~ comp + mort + hiv + exp.t
##
##            Df Sum of Sq     RSS    AIC
## <none>                   935.17 247.69
## + exp.p     1     12.75  922.42 248.15
## + hep       1      8.33  926.85 248.69
## + dip       1      7.12  928.05 248.83
## + bmi       1      4.06  931.12 249.20
## + under5    1      3.81  931.37 249.23
## + gdp       1      2.80  932.37 249.35
## + thin5.9   1      2.60  932.58 249.38
## + inf       1      2.16  933.01 249.43
## + school    1      1.04  934.14 249.57
## + thin1.19  1      0.99  934.18 249.57
## + alc       1      0.63  934.54 249.61
## + meas      1      0.45  934.73 249.64
## + pop       1      0.14  935.03 249.67
## + polio     1      0.01  935.17 249.69
## - exp.t     1     87.80 1022.97 255.74
## - hiv       1    142.28 1077.45 261.55
## - mort      1    191.52 1126.70 266.56
## - comp      1   1461.68 2396.85 351.10
##
## Call:
## lm(formula = life ~ comp + mort + hiv + exp.t, data = df1)
##
## Coefficients:
```

```
## (Intercept)         comp         mort          hiv        exp.t
##    48.47452     34.50445     -0.01754     -0.89398      0.37833
```

The variables selected by the AIC workflow are comp, mort, hiv, exp.t

```
mod.aic <- lm(life ~ comp + mort + hiv + exp.t, data = df1)
summary(mod.aic)
```

```
##
## Call:
## lm(formula = life ~ comp + mort + hiv + exp.t, data = df1)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -10.918  -1.702   0.069   1.881   7.823
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 48.474517   2.122438  22.839  < 2e-16 ***
## comp        34.504450   2.668108  12.932  < 2e-16 ***
## mort        -0.017539   0.003747  -4.681  8.4e-06 ***
## hiv         -0.893979   0.221573  -4.035 0.000103 ***
## exp.t        0.378334   0.119368   3.169 0.001992 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.956 on 107 degrees of freedom
## Multiple R-squared:  0.8616, Adjusted R-squared:  0.8564
## F-statistic: 166.6 on 4 and 107 DF,  p-value: < 2.2e-16
```

R-squared for the AIC model is 0.8616, so 86% of variation is explained by the AIC model.

D.2 Best Subset Regression Variable Selection

```
xmat = df1 |>
select(-life) |>
select_if(is.numeric)
dim(xmat)
```

```
## [1] 112  18
```

There are 18 numeric variables up for selection

```
mod = regsubsets(xmat, df1$life, nvmax = 18)
summary.mod = summary(mod)
summary.mod$which
```

```
##   (Intercept)  mort   inf   alc exp.p   hep  meas   bmi under5 polio exp.t
## 1        TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE  FALSE FALSE FALSE
## 2        TRUE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE  FALSE FALSE FALSE
## 3        TRUE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE  FALSE FALSE FALSE
## 4        TRUE  TRUE FALSE FALSE FALSE FALSE FALSE FALSE  FALSE FALSE  TRUE
## 5        TRUE  TRUE FALSE FALSE  TRUE FALSE FALSE FALSE  FALSE FALSE  TRUE
## 6        TRUE  TRUE  TRUE FALSE FALSE FALSE FALSE FALSE   TRUE FALSE  TRUE
## 7        TRUE  TRUE  TRUE FALSE  TRUE FALSE FALSE FALSE   TRUE FALSE  TRUE
## 8        TRUE  TRUE  TRUE FALSE  TRUE FALSE FALSE FALSE   TRUE FALSE  TRUE
## 9        TRUE  TRUE  TRUE FALSE  TRUE  TRUE FALSE FALSE   TRUE FALSE  TRUE
```

```
## 10        TRUE  TRUE  TRUE FALSE  TRUE  TRUE FALSE FALSE   TRUE FALSE  TRUE
## 11        TRUE  TRUE  TRUE FALSE  TRUE  TRUE FALSE FALSE   TRUE FALSE  TRUE
## 12        TRUE  TRUE  TRUE FALSE  TRUE  TRUE  TRUE FALSE   TRUE FALSE  TRUE
## 13        TRUE  TRUE  TRUE FALSE  TRUE  TRUE  TRUE FALSE   TRUE  TRUE  TRUE
## 14        TRUE  TRUE  TRUE FALSE  TRUE  TRUE  TRUE FALSE   TRUE  TRUE  TRUE
## 15        TRUE  TRUE  TRUE FALSE  TRUE  TRUE  TRUE  TRUE   TRUE  TRUE  TRUE
## 16        TRUE  TRUE  TRUE FALSE  TRUE  TRUE  TRUE  TRUE   TRUE  TRUE  TRUE
## 17        TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE   TRUE  TRUE  TRUE
## 18        TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE   TRUE  TRUE  TRUE
##      dip   hiv   gdp   pop thin1.19 thin5.9 comp school
## 1  FALSE FALSE FALSE FALSE    FALSE   FALSE TRUE  FALSE
## 2  FALSE FALSE FALSE FALSE    FALSE   FALSE TRUE  FALSE
## 3  FALSE  TRUE FALSE FALSE    FALSE   FALSE TRUE  FALSE
## 4  FALSE  TRUE FALSE FALSE    FALSE   FALSE TRUE  FALSE
## 5  FALSE  TRUE FALSE FALSE    FALSE   FALSE TRUE  FALSE
## 6  FALSE  TRUE FALSE FALSE    FALSE   FALSE TRUE  FALSE
## 7  FALSE  TRUE FALSE FALSE    FALSE   FALSE TRUE  FALSE
## 8  FALSE  TRUE  TRUE FALSE    FALSE   FALSE TRUE  FALSE
## 9  FALSE  TRUE  TRUE FALSE    FALSE   FALSE TRUE  FALSE
## 10 FALSE  TRUE  TRUE FALSE     TRUE   FALSE TRUE  FALSE
## 11 FALSE  TRUE  TRUE  TRUE     TRUE   FALSE TRUE  FALSE
## 12 FALSE  TRUE  TRUE  TRUE     TRUE   FALSE TRUE  FALSE
## 13 FALSE  TRUE  TRUE  TRUE     TRUE   FALSE TRUE  FALSE
## 14 FALSE  TRUE  TRUE  TRUE     TRUE   FALSE TRUE   TRUE
## 15 FALSE  TRUE  TRUE  TRUE     TRUE    TRUE TRUE  FALSE
## 16 FALSE  TRUE  TRUE  TRUE     TRUE    TRUE TRUE   TRUE
## 17 FALSE  TRUE  TRUE  TRUE     TRUE    TRUE TRUE   TRUE
## 18  TRUE  TRUE  TRUE  TRUE     TRUE    TRUE TRUE   TRUE
```

```
summary.mod$rsq #check R^2
```

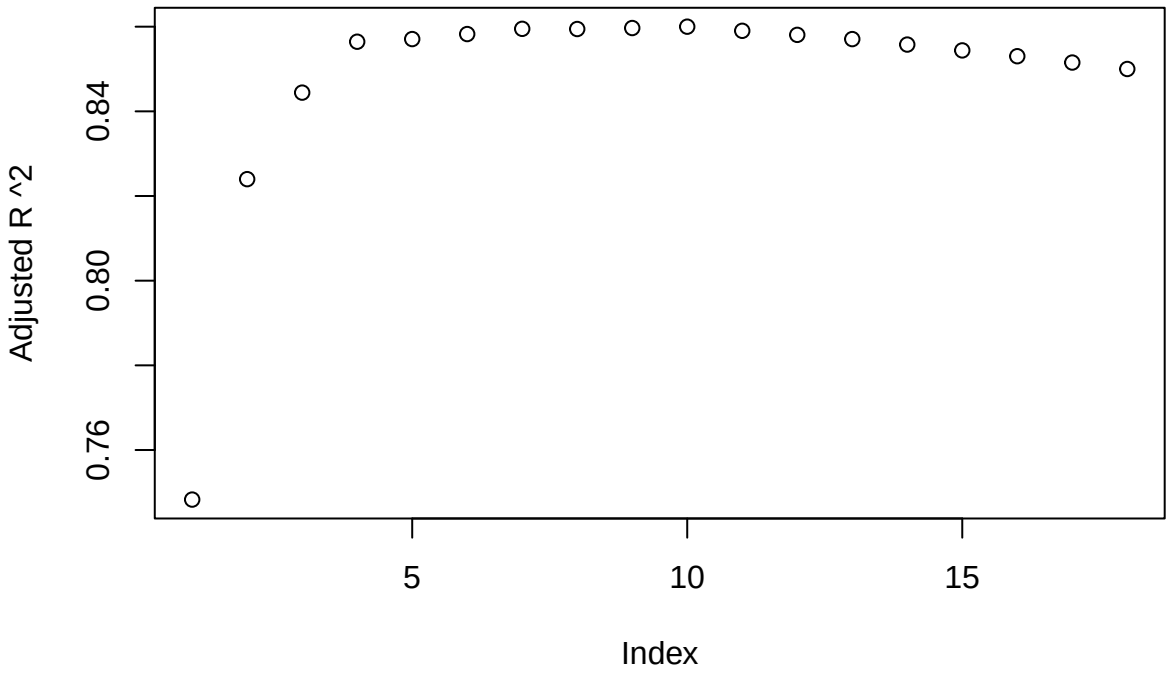
```
##  [1] 0.7505579 0.8271519 0.8486295 0.8616211 0.8635083 0.8659193 0.8683494
##  [8] 0.8695786 0.8710567 0.8726119 0.8729950 0.8734140 0.8738031 0.8739667
## [15] 0.8740737 0.8742070 0.8742664 0.8743277
```

R-squared levels out at the model with 4 predictors

```
summary.mod$adjr2 #check adjusted R^2
```

```
##  [1] 0.7482903 0.8239804 0.8444247 0.8564480 0.8570700 0.8582575 0.8594883
##  [8] 0.8594488 0.8596793 0.8599992 0.8590245 0.8580702 0.8570627 0.8557764
## [15] 0.8543977 0.8530208 0.8515274 0.8500041
```

```
`Adjusted R ^2` <- summary.mod$adjr2
plot(`Adjusted R ^2`)
```

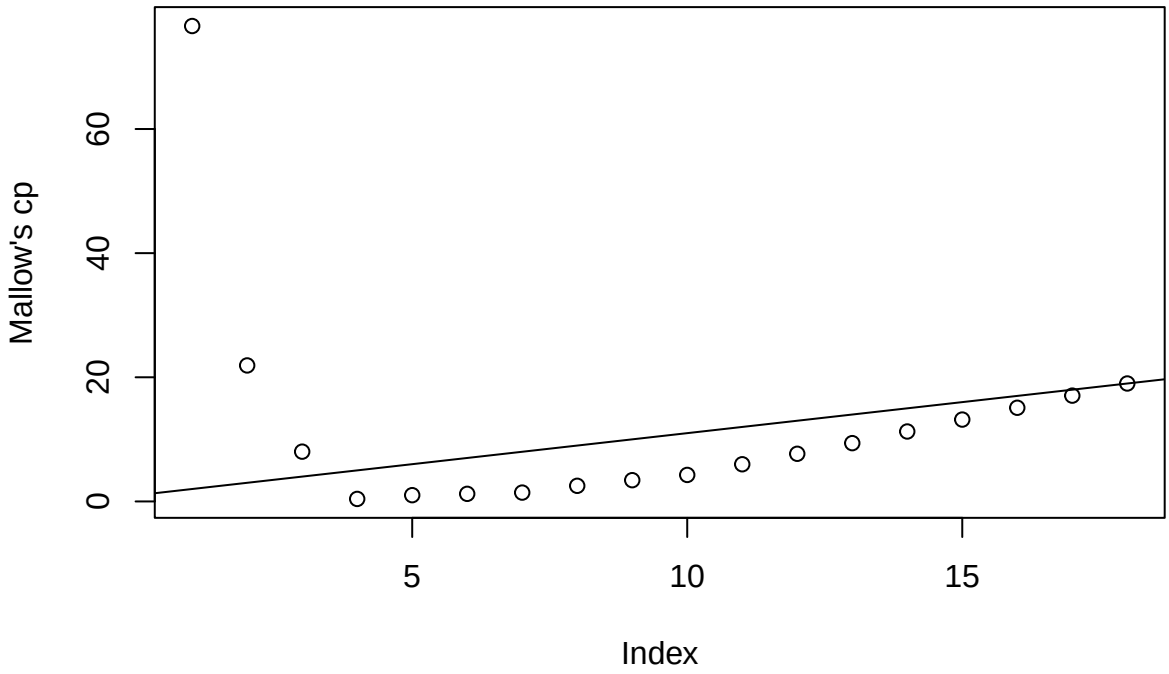


Adjusted R-squared levels out at the model with 4 predictors

```
summary.mod$cp
```

```
##  [1] 76.5921736 21.9110780  8.0172448  0.4031971  1.0066214  1.2224209
##  [7]  1.4241162  2.5144551  3.4206729  4.2697585  5.9862349  7.6762262
## [13]  9.3882377 11.2671548 13.1880066 15.0893862 17.0453657 19.0000000
```

```
`Mallow's cp` <- summary.mod$cp
plot(`Mallow's cp`)
abline(1,1)
```



The model with 4 variables is the simplest model with a Cp value (0.403) lower than p (19). The model with

4 variables includes comp, mort, hiv, and exp.t. So the model selected by best subset regression is the same as the model selected by stepwise regression.

Appendix E: Are there interactions between variables used to predict life expectancy?

E.1 Check interactions

```
add1(mod.aic, ~.+comp*mort+comp*hiv+comp*exp.t, test = 'F')
```

```
## Single term additions
##
## Model:
## life ~ comp + mort + hiv + exp.t
##           Df Sum of Sq    RSS    AIC F value   Pr(>F)
## <none>                  935.17 247.69
## comp:mort   1    11.548 923.63 248.30  1.3253 0.252230
## comp:hiv    1    89.125 846.05 238.47 11.1663 0.001151 **
## comp:exp.t  1    70.193 864.98 240.95  8.6019 0.004116 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

E.2 Update model

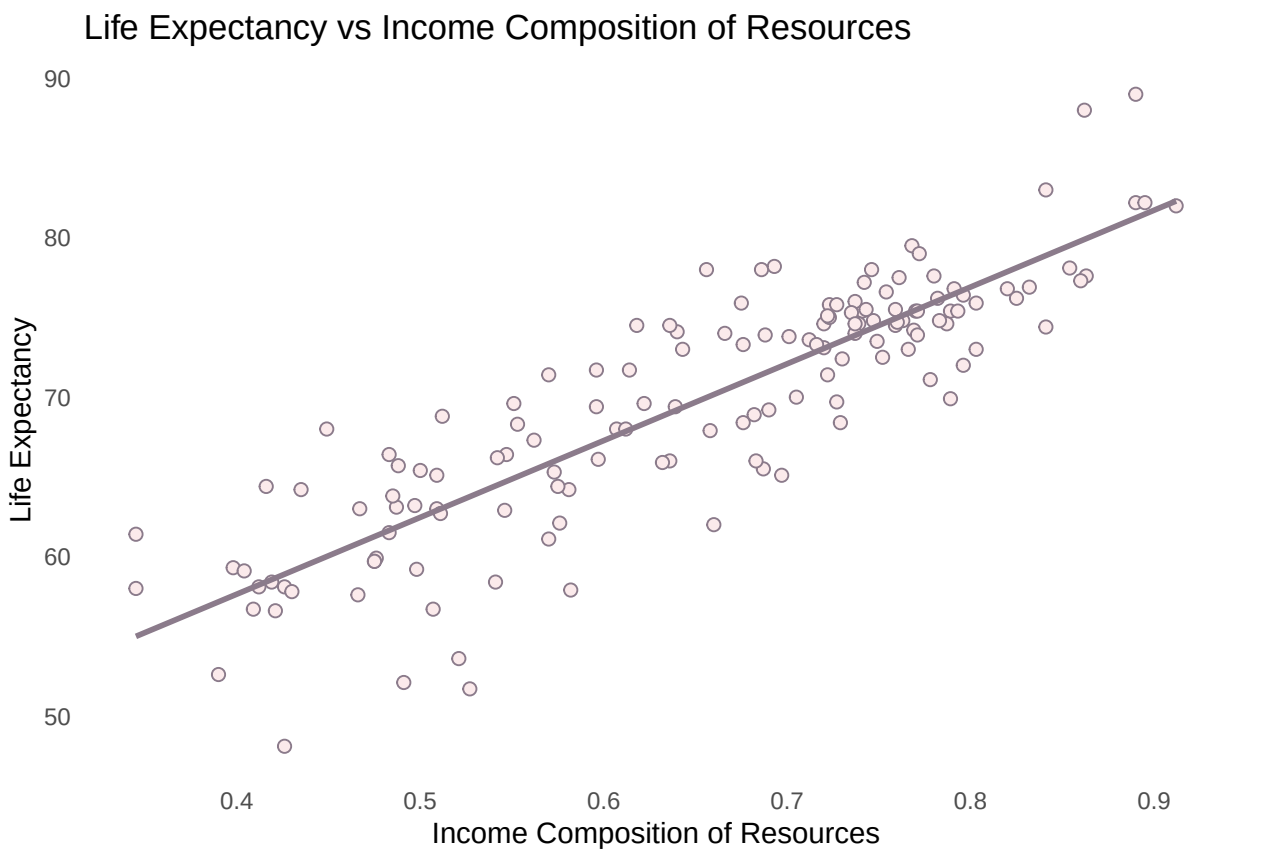
```
mod = update(mod.aic, ~.+comp:exp.t+comp:hiv)
summary(mod)
```

```
##
## Call:
## lm(formula = life ~ comp + mort + hiv + exp.t + comp:exp.t +
##     comp:hiv, data = df1)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -8.4418 -1.6289  0.1997  1.8930  6.0646
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 54.239712   3.547274  15.291  < 2e-16 ***
## comp        25.258188   5.367988   4.705 7.76e-06 ***
## mort        -0.017148   0.003489  -4.915 3.29e-06 ***
## hiv          2.436576   1.096983   2.221  0.02849 *
## exp.t       -0.946437   0.503578  -1.879  0.06296 .
## comp:exp.t   2.085222   0.773651   2.695  0.00819 **
## comp:hiv    -6.470091   2.069247  -3.127  0.00229 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.745 on 105 degrees of freedom
## Multiple R-squared:  0.8829, Adjusted R-squared:  0.8762
## F-statistic:   132 on 6 and 105 DF,  p-value: < 2.2e-16
```

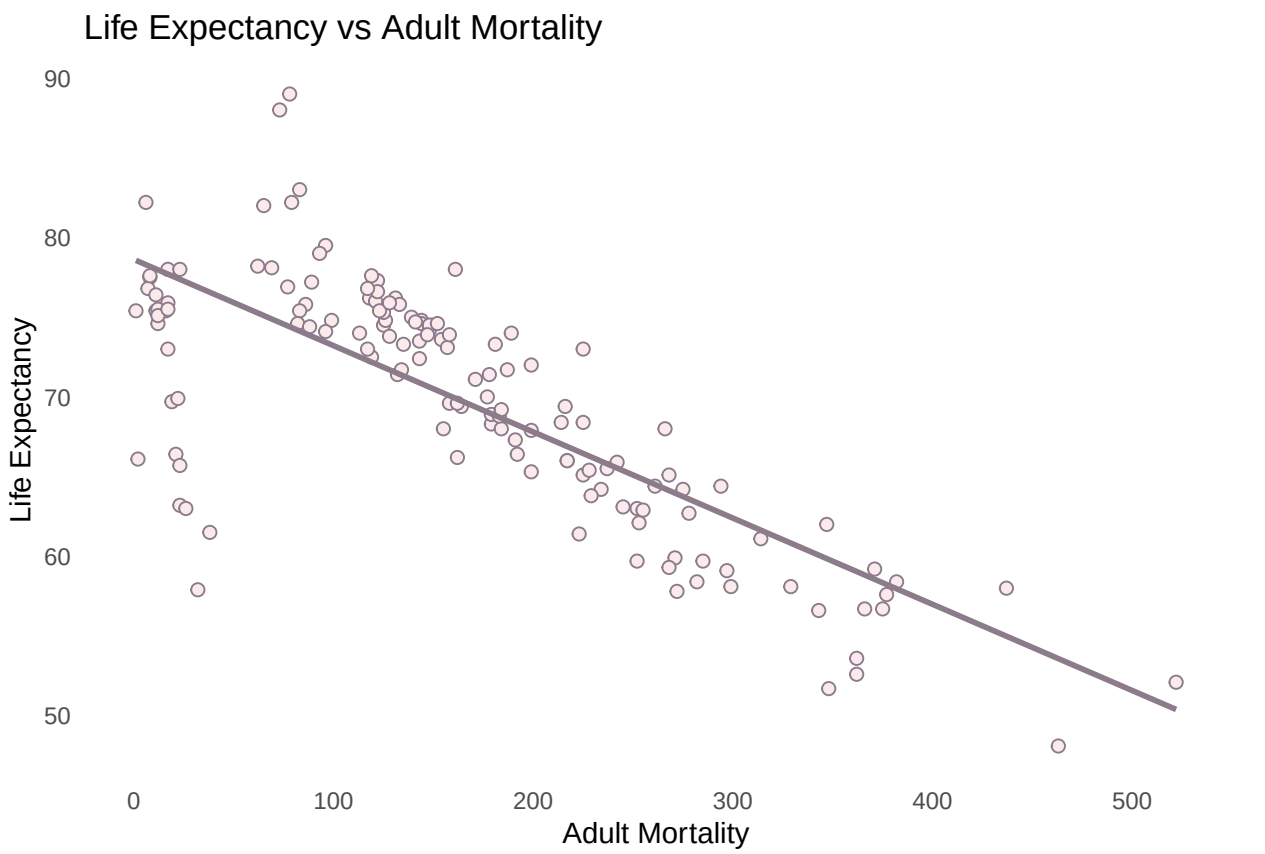
E.3 Model assumptions

Check linearity:

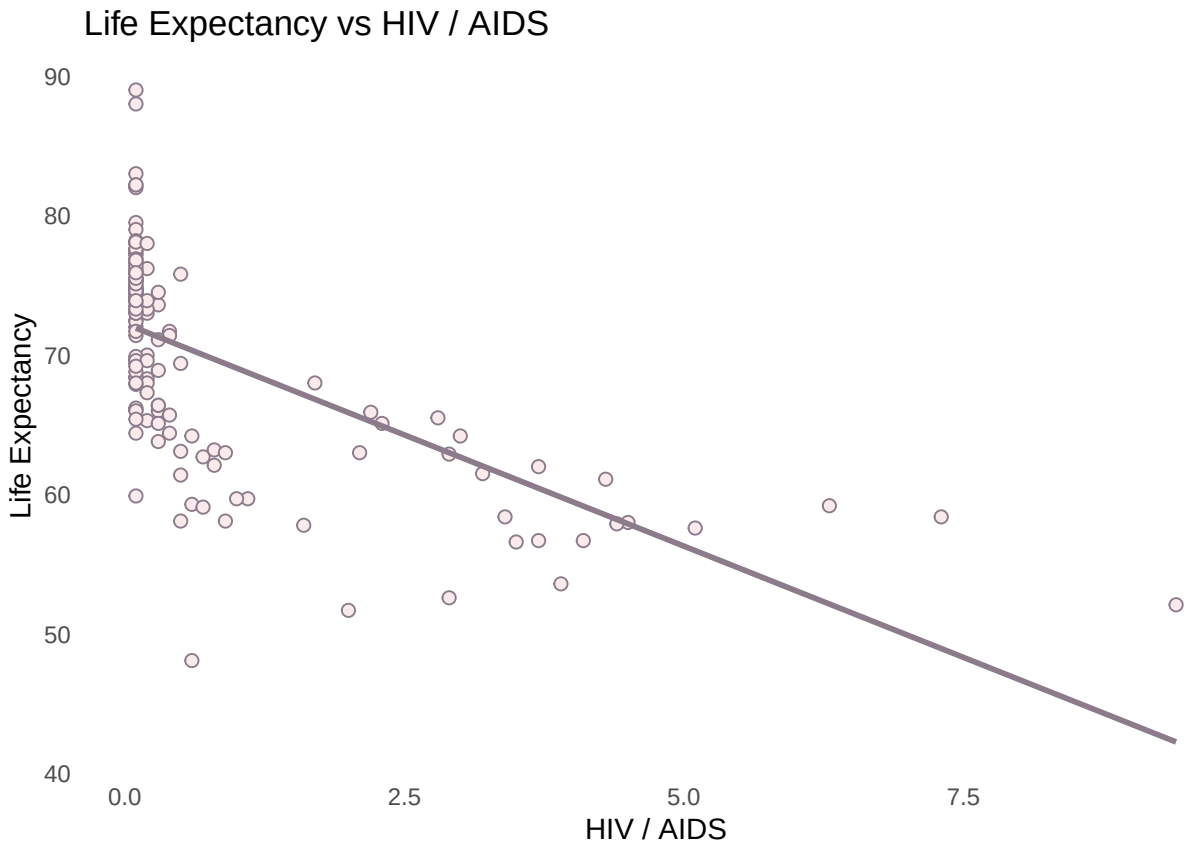
```
df2 |>
  ggplot(aes(x = comp, y = life, label = country)) +
  geom_point(shape = 21, color = "thistle4", fill = "#FBEAEB", size = 2) +
  geom_smooth(method = "lm", se = FALSE, color = "thistle4") +
  labs(x = "Income Composition of Resources", y = "Life Expectancy",
       title = "Life Expectancy vs Income Composition of Resources") +
  common_theme
```



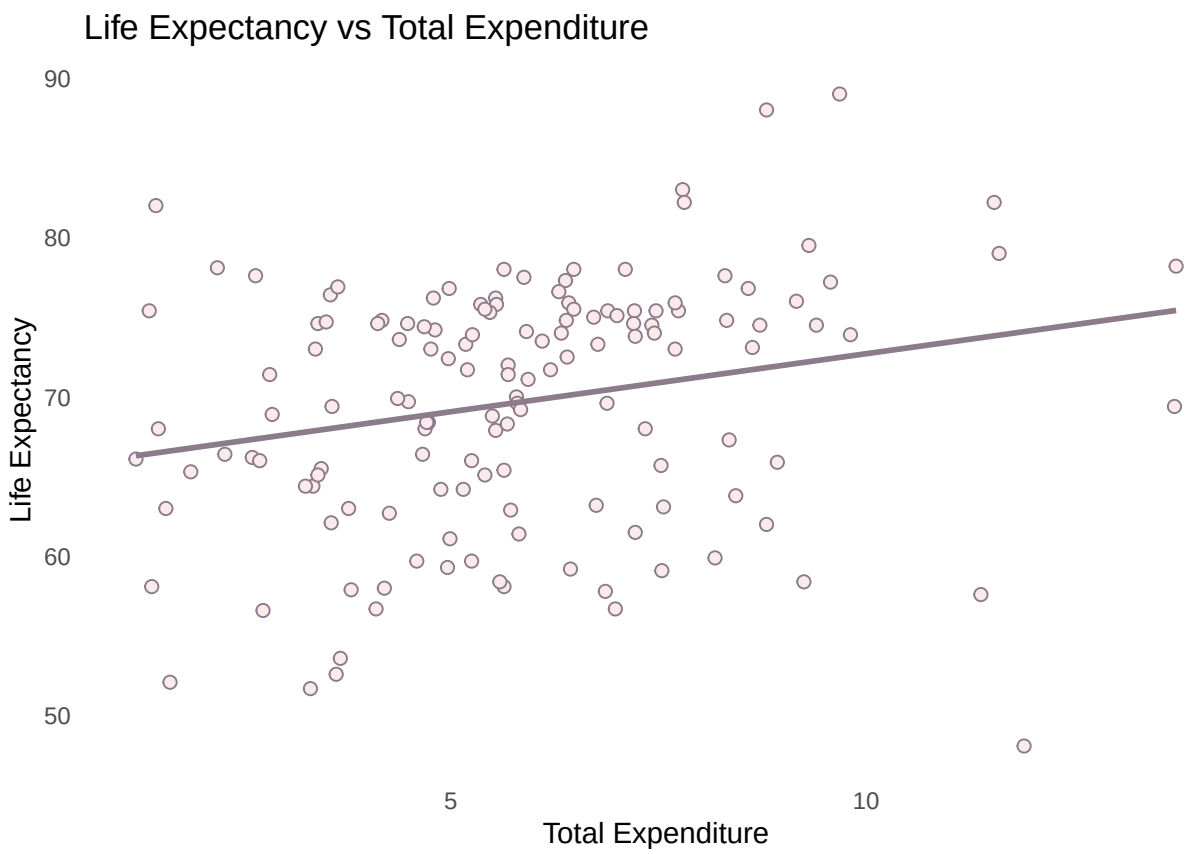

```
df2 |>
  ggplot(aes(x = mort, y = life, label = country)) +
  geom_point(shape = 21, color = "thistle4", fill = "#FBEAEB", size = 2) +
  geom_smooth(method = "lm", se = FALSE, color = "thistle4") +
  labs(x = "Adult Mortality", y = "Life Expectancy",
       title = "Life Expectancy vs Adult Mortality") +
  common_theme
```




```
df2 |>
  ggplot(aes(x = hiv, y = life, label = country)) +
  geom_point(shape = 21, color = "thistle4", fill = "#FBEAEB", size = 2) +
  geom_smooth(method = "lm", se = FALSE, color = "thistle4") +
  labs(x = "HIV / AIDS", y = "Life Expectancy", title = "Life Expectancy vs HIV / AIDS") +
  common_theme
```

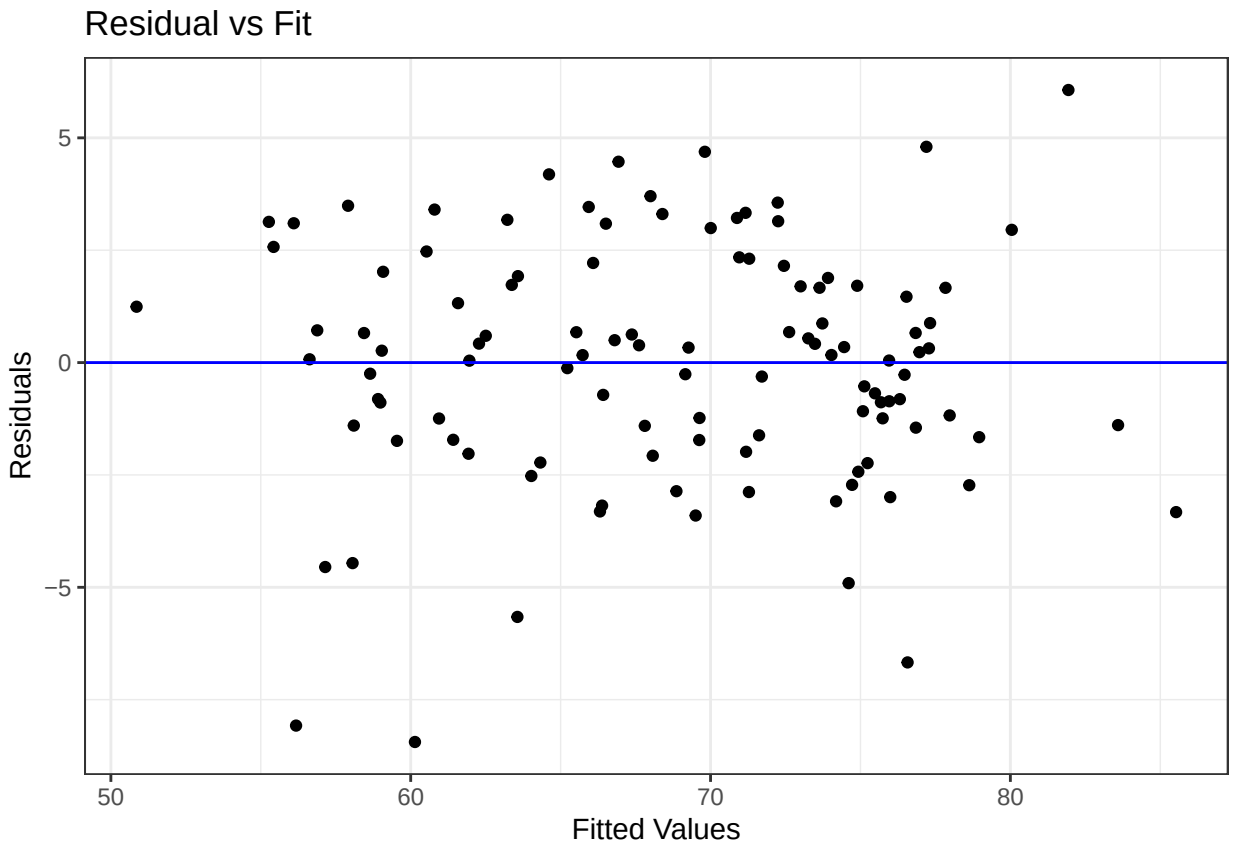



```
df2 |>
  ggplot(aes(x = exp.t, y = life, label = country)) +
  geom_point(shape = 21, color = "thistle4", fill = "#FBEAEB", size = 2) +
  geom_smooth(method = "lm", se = FALSE, color = "thistle4") +
  labs(x = "Total Expenditure", y = "Life Expectancy",
       title = "Life Expectancy vs Total Expenditure") +
  common_theme
```



Check variance and linearity:

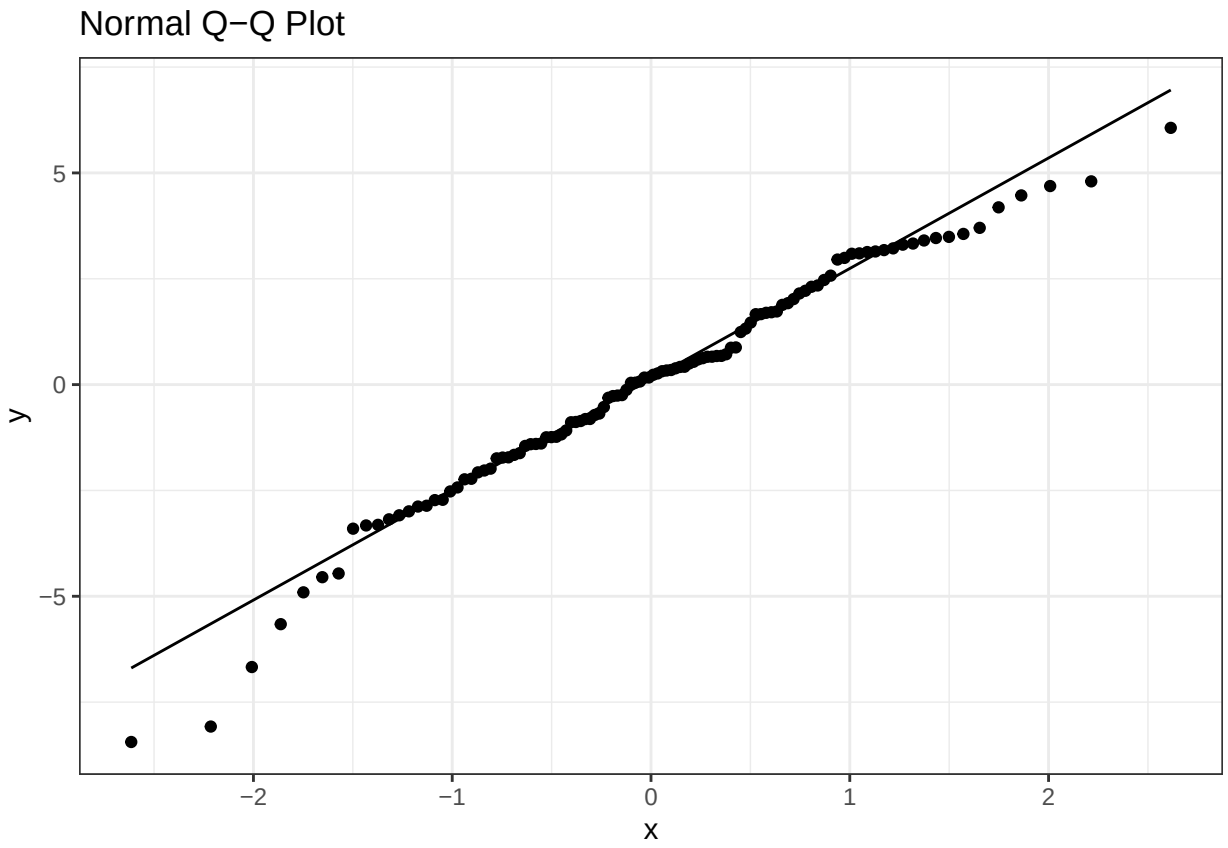
```
model.table = augment(mod)
ggplot(model.table, aes(x = .fitted, y = .resid)) +
  geom_point() +
  geom_hline(yintercept = 0, colour = 'blue') +
  labs(x = 'Fitted Values', y = 'Residuals') +
  ggtitle('Residual vs Fit') +
  theme_bw()
```



There are no issues with the variance or linearity assumption.

Check normality:

```
ggplot(model.table, aes(sample = .resid)) +
  stat_qq() +
  stat_qq_line() +
  ggtitle('Normal Q-Q Plot') +
  theme_bw()
```



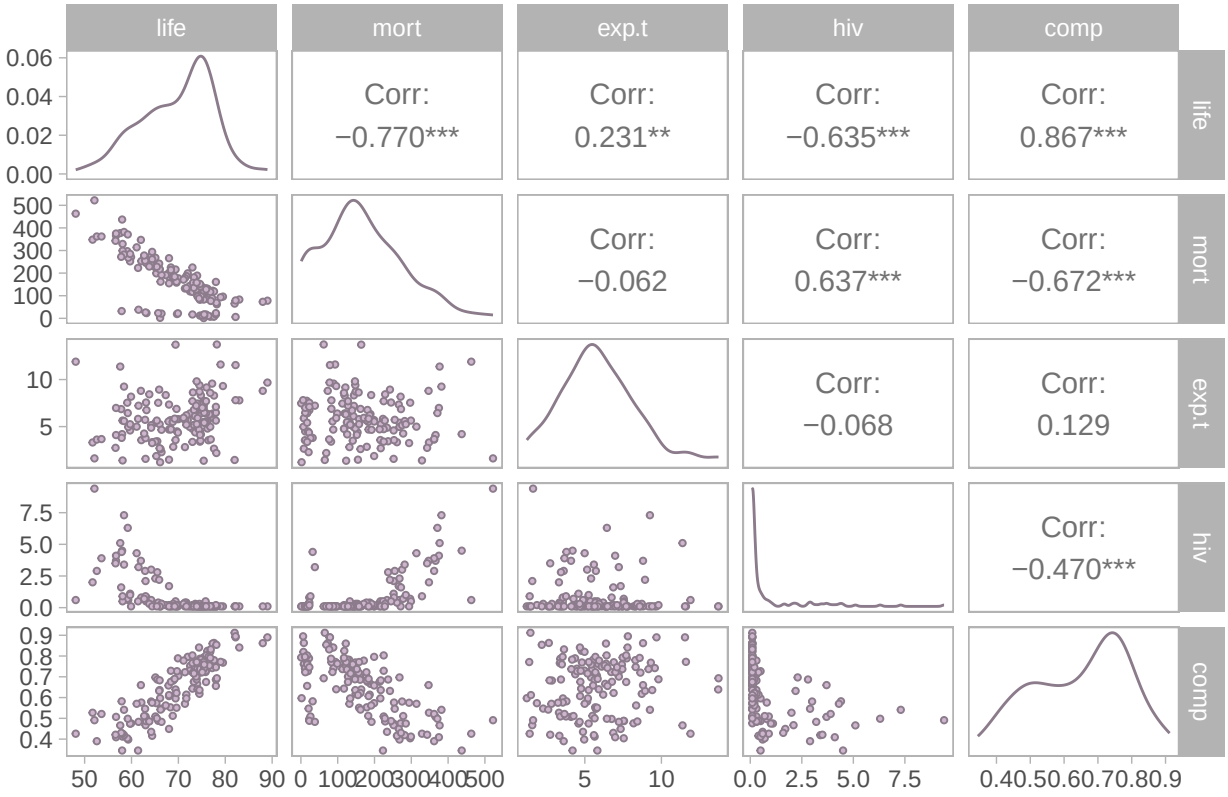

```
shapiro.test(resid(mod))
```

```
##
##  Shapiro-Wilk normality test
##
## data:  resid(mod)
## W = 0.97829, p-value = 0.06495
```

Appendix F: Are the predictors positive or negatively correlated to life expectancy?

```
df2 |>
  select(-country) |>
  ggpairs(
    lower = list(continuous = wrap("points", shape = 21, fill = "thistle3",
                                   color = "thistle4", size = 0.8)),
    diag = list(continuous = wrap("densityDiag", color = "thistle4")),
    title = "Scatterplot Matrix for Life Expectancy Model") +
  theme_light() +  theme(panel.grid.minor.y = element_blank(),
        panel.grid.minor.x = element_blank(),
        panel.grid.major.y = element_blank(),
        panel.grid.major.x = element_blank())
```

Scatterplot Matrix for Life Expectancy Model



Appendix G: Make a 95% point prediction for the life expectancy of a country with predictor values as the mean response of each predictor.

```
new <- df2 |>
  summarize(mort = mean(mort),
            hiv = mean(hiv),
            comp = mean(comp),
            exp.t = mean(exp.t)) |>
  data.frame()

pi = predict(mod, new, interval = "prediction", level = 0.95)
pi
```

```
##        fit      lwr      upr
## 1 68.79102 63.31005 74.27199
```

Appendix H: Summary Table

```
df2 |>
  select(country, life, mort,hiv,comp,exp.t) |>
  rename("Country" = country, "Life" = life, "Mort" = mort,
         "Comp" = comp, "Exp.T" = exp.t) |>
  arrange(desc(Life)) |>
```

```
head(10) |>
gt(rowname_col = "Country") |>
tab_header(title = md("Summary of **Life Expectancy**")) |>
tab_stubhead(label = md("Country"))
```

Summary of **Life Expectancy**

Country	Life	Mort	hiv	Comp	Exp.T
Finland	89.0	78	0.1	0.890	9.68
Greece	88.0	73	0.1	0.862	8.80
Chile	83.0	83	0.1	0.841	7.79
France	82.2	79	0.1	0.890	11.54
Israel	82.2	6	0.1	0.895	7.81
Canada	82.0	65	0.1	0.912	1.45
Costa Rica	79.5	96	0.1	0.768	9.31
Cuba	79.0	93	0.1	0.772	11.60
Maldives	78.2	62	0.1	0.693	13.73
Qatar	78.1	69	0.1	0.854	2.19