Quality of Life by Country: A Clustering Analysis

Katherine M. Prioli

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Abstract

Example abstract text

Background

The Centers for Disease Control and Prevention (CDC) has recently issued a report indicating that life expectancy in the United States has decreased in 2017 as compared to 2016, with the overwhelming majority of deaths caused by heart disease and cancer, arguably preventable illnesses (Murphy et al. (2018)). Given that the United States has the world's largest economy, this decline in life expectancy is particularly concerning, and indicates that national wealth may not be predictive of citizens' longevity (The World Bank (2018)).

As the world's economies trend toward globalism, there is increasing interest in understanding how these nations compare on key quality of life (QoL) factors, including but not limted to life expectancy. Several organizations report on QoL measures as they evolve, including among others the World Economic Forum (WEF), World Health Organization (WHO), and the United Nations Development Programme. The QoL measures reported by these bodies can be either unidimensional values or compound scores calculated from several factors of interest.

The objective of this analysis is to explore key QoL indicators by country, with particular focus on how the United States ranks, through a series of visualizations and *k*-means clustering analyses.

Methods

This analysis included country-level QoL indicators as described in Table 1.

Table 1. Country-Level QoL measures.

Measure	Single or Compound	Description	Source
Gross Domestic Product (GDP)	Single	Valued in $US 2018	@worldbank__gdp
Infant mortality rate	Single	Number of infant deaths per 1,000 live births	@who__infantmort
Life expectancy at birth	Single	Expected life at birth, both genders	@who__life
Life expectancy at sixty	Single	Expected remaining life years at age 60, both genders	@who__life
Human Development Index (HDI)	Compound	Developmental level, scale of 0:1	@un__dvlpt__HDIdesc
Human Development Index (HDI)	Compound	Developmental category, four levels (low, medium, high, very high)	@un__dvlpt__HDIdesc
Social Progress Index	Compound	Social progress level, scaled from 0:100 and comprising three broad categories: basic human needs (e.g., nutrition, safety), foundations of wellbeing (e.g., basic knowledge, environmental quality), and opportunity (e.g., personal rights, freedoms)	@socialprog__desc
Global Gender Gap Index	Compound	Gender equality index, scaled from 0:1, based on measurements of gender-related gaps in such dimensions as economic participation, level of education, health and survival, and political offices held	@wef__gender__desc
World Happiness Score	Compound	Happiness score, scaled from 0:10, based on several factors including per-capita GDP, healthy life expectancy, social support, freedoms, and perception of corruption	@whr

Data for these measures was obtained for calendar year 2016 in `.csv` or `.xls(x)` formats. Additionally, dataframe containing country identifiers (full names and three-letter codes) was generated from the `countrycode` library to facilitate merging the datafiles into one dataframe.

Wrangling and Exploration

Each country-level datafile was imported, wrangled as needed, then tested against the dataframe containing country identifiers via `anti_join()` to identify mismatches. Mismatching country names were manually recoded for each datafile, then all datafiles were merged using serial `lef_join()` statements. Countries with wholly missing data were excluded. The resulting dataframe, titled `alldata`, is presented in Table 2.

Table 2. `alldata` dataframe contents.

Source	Variable Name	Description
Social Progress Imperative (2018)	SPI	Social Progress Index value (scale of 0:100)
The World Bank (2018)	GDP_USD_2018	2016 Gross Domestic Product (valued in $US 2018)
The United Nations Development Programme (2018)	HDIrank	Human Development Index ranking
The United Nations Development Programme (2018)	HDIindex	HDI index value (scale of 0:1)
The United Nations Development Programme (2018)	HDI_cat	HDI index category (5 levels)
Helliwell, Layard, and Sachs (2018)	happiness	World Happiness Score (scale of 0:10)
World Economic Forum (2016)	genderequality_index	Gender Equality Index (scale of 0:1)
World Health Organization (2018b)	infantmort	Infant mortality rate
World Health Organization (2018a)	birth_MF	Life expectancy at birth, males & females
World Health Organization (2018a)	sixty_MF	Life expectancy at 60 years, males & females

At least one univariate visualization was generated for each variable in `alldata` via `ggplot()`, and a correlation matrix was produced to investigate pairwise relationshps between continuous variables. Next, a series of ordered country-as-factor bivariate visualizations were created to explore the top and bottom 20 countries by ranking within each variable.

k-Means Clustering

To assess how the United States compares to the rest of the world, a series of k-means cluster analyses was carried out. K-means clustering is described elsewhere; briefly, given bivariate data and a desired number k groups, this classification algorithm classifies the points in the two-dimensional plane to minimize the total within-cluster variation for all clusters (James et al. (2013)). This is an iterative process that works by establishing k centroids, classifying each point by which centroid is closest, then moving the centroids to the center of their corrresponding clusters, and repeating the process. Iteration terminates when the centroids no longer move, and the classification established in this terminal iteraton is the clustering.

The Human Development Index categorizes the world's countries into four developmental levels (low, medium, high, and very high); thus k-means clustering analysis was performed assuming 4 clusters. Missing values were excluded to ensure the clustering algorithm would run, and a function was written to subset the clustering dataset (named `clusterdata`) to the variables of interest for each k-means analysis. On each output plot, the United States was identified by an enlarged `geom_point()`.

Results

Loading libraries

```
library(tidyverse)
library(readxl)         # For importing .xls(x) datasets
library(lazyeval)       # For renaming columns in function
library(countrycode)    # For establishing uniform country identifiers
library(ggthemr)        # For prettifying output
```

```r
library(gridExtra)       # For grid.arrange()
library(grid)            # For textGrob() to annotate grid.arrange() elements
library(kableExtra)      # For nicer output tables
library(GGally)          # For ggpairs() correlation matrix

ggthemr("fresh")
```

Establishing a crosswalk for country names and 3-letter codes

```r
countries_full <- codelist_panel %>%
  select(country.name.en, year, genc3c, iso3c, wb_api3c) %>%
  group_by(country.name.en) %>%
  mutate(maxyr = max(year)) %>%
  ungroup %>%
  mutate(maxyr = case_when(
    maxyr == year ~ 1,
    TRUE ~ 0
  )) %>%
  filter(maxyr == 1) %>%
  select(-maxyr) %>%
  distinct()

countries_full <- countries_full %>%
  mutate(country3 = case_when(
    iso3c == genc3c & iso3c == wb_api3c ~ iso3c,
    is.na(iso3c) == FALSE ~ iso3c,
    is.na(iso3c) == TRUE & is.na(genc3c) == FALSE ~ genc3c,
    is.na(iso3c) == TRUE & is.na(genc3c) == TRUE & is.na(wb_api3c) == FALSE ~ wb_api3c
  )) %>%
  rename(country = country.name.en) %>%
  arrange(country)

countries <- countries_full %>%
  select(country, country3)
```

Importing and wrangling each data file, and standardizing country names

Each datafile was imported and wrangled to subset to the variable(s) of interest for 2016. Next, country identifiers in each dataset were compared to the `countries` table, and a `mutate()` statement was used to correct mismatches. In the interest of brevity, these steps are demonstrated for the Human Development Index (HDI) data below.

First, importing and wrangling the HDI data:

```r
# Importing raw data

HDIraw <- read_xlsx("data/HDIdata2018.xlsx", sheet = "Table 2")

# Selecting columns of interest

HDIdata <- HDIraw %>%
  select(1:2, X__14)

# Assigning sensible column names

HDIcolnm <- c(HDIdata[[3,1]], HDIdata[[3,2]], HDIdata[[4,3]])
colnames(HDIdata) <- HDIcolnm

# Determining boundaries for human development levels in the data
# and using these to create one dataframe for each level

vhhd_st <- which(HDIdata$Country == "VERY HIGH HUMAN DEVELOPMENT") + 1
vhhd_end <- which(HDIdata$Country == "HIGH HUMAN DEVELOPMENT") - 1

hhd_st <- which(HDIdata$Country == "HIGH HUMAN DEVELOPMENT") + 1
hhd_end <- which(HDIdata$Country == "MEDIUM HUMAN DEVELOPMENT") - 1

mhd_st <- which(HDIdata$Country == "MEDIUM HUMAN DEVELOPMENT") + 1
mhd_end <- which(HDIdata$Country == "LOW HUMAN DEVELOPMENT") - 1

lhd_st <- which(HDIdata$Country == "LOW HUMAN DEVELOPMENT") + 1
lhd_end <- which(HDIdata$Country == "OTHER COUNTRIES OR TERRITORIES") - 1

oth_st <- which(HDIdata$Country == "OTHER COUNTRIES OR TERRITORIES") + 1
oth_end <- which(HDIdata$Country == "Human development groups") - 2

HDI_vhhd <- HDIdata %>%
  slice(vhhd_st:vhhd_end) %>%
  mutate(HDI_cat = "Very High")

HDI_hhd <- HDIdata %>%
  slice(hhd_st:hhd_end) %>%
  mutate(HDI_cat = "High")

HDI_mhd <- HDIdata %>%
  slice(mhd_st:mhd_end) %>%
  mutate(HDI_cat = "Medium")

HDI_lhd <- HDIdata %>%
  slice(lhd_st:lhd_end) %>%
  mutate(HDI_cat = "Low")

HDI_oth <- HDIdata %>%
  slice(oth_st:oth_end) %>%
  mutate(HDI_cat = NA)

# Combining the dataframes into one

HDIdata <- bind_rows(HDI_vhhd, HDI_hhd, HDI_mhd, HDI_lhd, HDI_oth) %>%
  rename(HDIrank = `HDI rank`) %>%
  rename(country = Country) %>%
  rename(HDIindex = `2016`) %>%
  mutate(HDI_cat = factor(HDI_cat, levels = c("Low", "Medium", "High", "Very High"))) %>%
  mutate(HDIrank = case_when(
    HDIrank == ".." ~ as.numeric(NA),
    TRUE ~ as.numeric(HDIrank)
  )) %>%
  mutate(HDIindex = case_when(
    HDIindex == ".." ~ as.numeric(NA),
    TRUE ~ as.numeric(HDIindex)
  ))
HDIdata <- HDIdata[c(2, 1, 3:4)]
```

Next, standardizing country names by using `anti_join()` to see which countries in `HDIdata` don't have a match in the `countries` dataframe, and correcting those for which an inexact match exists:

```r
HDIanti <- HDIdata %>%
  anti_join(countries, by = "country") %>%
  select(country) %>%
  arrange(country)
dim(HDIanti)
```

```
## [1] 28  1
```

There are 28 countries in `HDIdata` without an exact match in `countries`. Correcting using `mutate()`:

```
HDIdata <- HDIdata %>%
  mutate(country = case_when(
    country == "Antigua and Barbuda"                       ~ "Antigua & Barbuda",
    country == "Bolivia (Plurinational State of)"          ~ "Bolivia",
    country == "Bosnia and Herzegovina"                    ~ "Bosnia & Herzegovina",
    country == "Brunei Darussalam"                         ~ "Brunei",
    country == "Cabo Verde"                                ~ "Cape Verde",
    country == "Congo"                                     ~ "Congo - Brazzaville",
    country == "Congo (Democratic Republic of the)"        ~ "Congo - Kinshasa",
    country == "Eswatini (Kingdom of)"                     ~ "Swaziland",
    country == "Hong Kong, China (SAR)"                    ~ "Hong Kong SAR China",
    country == "Iran (Islamic Republic of)"                ~ "Iran",
    country == "Korea (Democratic People's Rep. of)"       ~ "North Korea",
    country == "Korea (Republic of)"                       ~ "South Korea",
    country == "Lao People's Democratic Republic"          ~ "Laos",
    country == "Moldova (Republic of)"                     ~ "Moldova",
    country == "Myanmar"                                   ~ "Myanmar (Burma)",
    country == "Palestine, State of"                       ~ "Palestinian Territories",
    country == "Russian Federation"                        ~ "Russia",
    country == "Saint Kitts and Nevis"                     ~ "St. Kitts & Nevis",
    country == "Saint Lucia"                               ~ "St. Lucia",
    country == "Saint Vincent and the Grenadines"          ~ "St. Vincent & Grenadines",
    country == "Syrian Arab Republic"                      ~ "Syria",
    country == "Tanzania (United Republic of)"             ~ "Tanzania",
    country == "The former Yugoslav Republic of Macedonia" ~ "Macedonia",
    country == "Trinidad and Tobago"                       ~ "Trinidad & Tobago",
    country == "Venezuela (Bolivarian Republic of)"        ~ "Venezuela",
    country == "Viet Nam"                                  ~ "Vietnam",
    country == "Côte d'Ivoire"                             ~ as.character(NA),   # UTC-8
    country == "Sao Tome and Principe"                     ~ as.character(NA),   # conflicts
    TRUE                                                   ~ as.character(country)
  )) %>%
  filter(!is.na(country))

HDIanti <- HDIdata %>%
  anti_join(countries, by = "country") %>%
  select(country) %>%
  arrange(country)
dim(HDIanti)
```

```
## [1] 0 1
```

Now there are no countries in `HDIdata` without an exact match in `countries`.

This process of importing, wrangling, and testing against the `countries` dataframe was largely the same for all other datasets of interest, with minor differences depending on the native structure of the data. Again, for brevity, those steps are not shown here, but are available on the project GitHub site (Prioli 2018).

Combining individual data files into one dataframe

All datasets were merged into a single dataframe using serial `join()` statements, and the resulting dataset was filtered to omit countries without data.

```
joindata_1 <- full_join(countries, HDIdata, by = "country")
joindata_2 <- left_join(joindata_1, SPIdata, by = "country3")
```

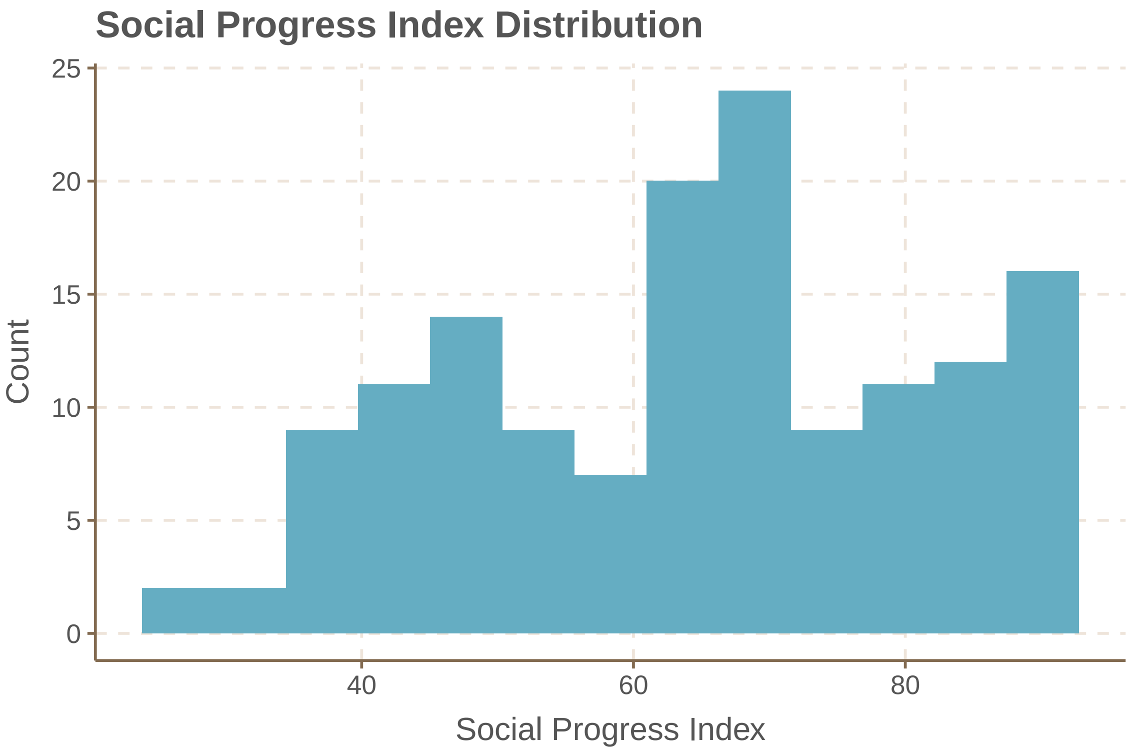
```r
joindata_3 <- left_join(joindata_2, WHRdata, by = "country")
joindata_4 <- left_join(joindata_3, genderdata, by = "country")
joindata_5 <- left_join(joindata_4, infantmortdata, by = "country")
joindata_6 <- left_join(joindata_5, lifeexpdata, by = "country")
joindata_7 <- left_join(joindata_6, GDPdata, by = "country3")

joinsub <- joindata_7 %>%
  arrange(country) %>%
  mutate(exclude_flag = case_when(
    is.na(HDIrank) == TRUE &
      is.na(HDIindex) == TRUE &
      is.na(HDI_cat) == TRUE &
      is.na(SPI) == TRUE &
      is.na(happiness) == TRUE &
      is.na(genderequality_index) == TRUE &
      is.na(infantmort) == TRUE &
      is.na(birth_MF) == TRUE &
      is.na(sixty_MF) == TRUE &
      is.na(GDP_USD_2018) == TRUE             ~ TRUE,
    TRUE                                      ~ FALSE
  )) %>%
  filter(exclude_flag == FALSE) %>%
  select(-exclude_flag)

alldata <- joinsub %>%
  mutate(country = factor(country)) %>%
  mutate(country3 = factor(country3)) %>%
  mutate(US = case_when(
    country == "United States" ~ "US",
    TRUE                       ~ "Non US"
  )) %>%
  mutate(color = case_when(
    country == "United States" ~ "red",
    TRUE                       ~ "#545454"
  ))

alldata <- alldata[c(1:2, 13:14, 6, 12, 3:5, 7:11)]

len <- dim(alldata)[[1]]

# write_csv(alldata, paste0("data/alldata_", lubridate::today(),".csv"))  # Uncomment to export data
```

Visualizations

Univariate and sensible bivariate analyses were generated to explore the data.

Exploring the Social Progress Index data:

```r
SPI_hist <- ggplot(data = alldata, aes(x = SPI)) +
  geom_histogram(bins = ceiling(sqrt(len - sum(is.na(alldata$SPI))))) +
  xlab("Social Progress Index") +
  ylab("Count") +
  ggtitle("Social Progress Index Distribution")
SPI_hist
```

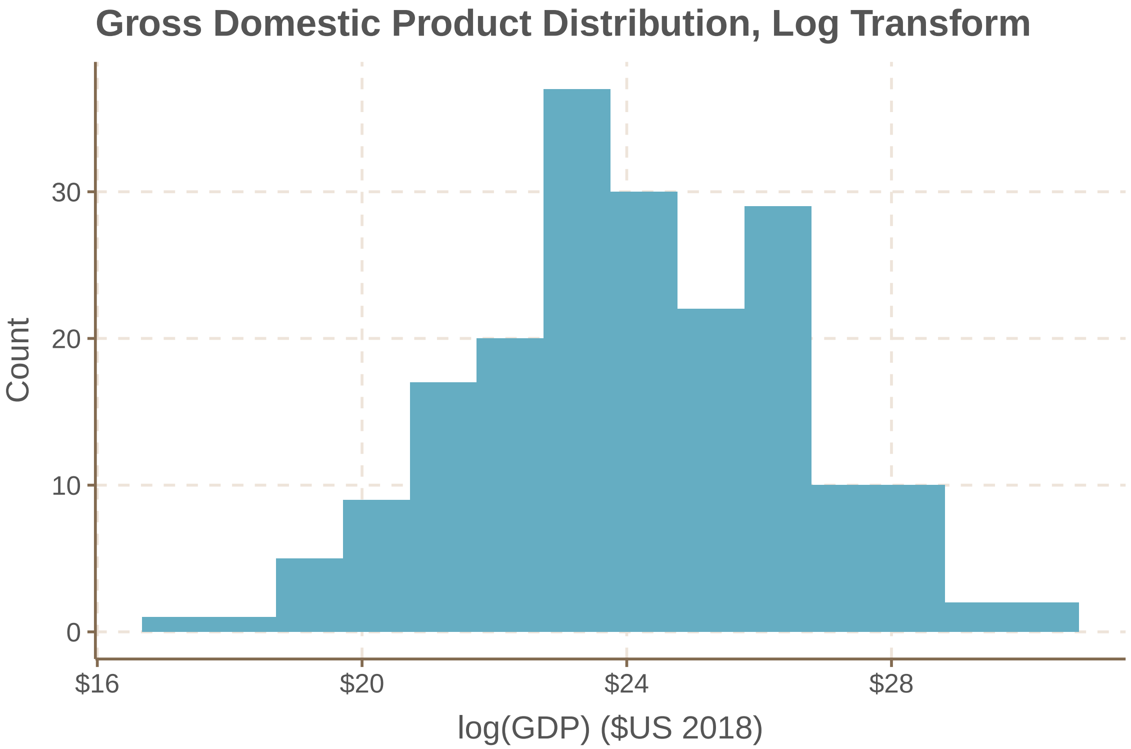


Next, exploring GDP by summary statistics:

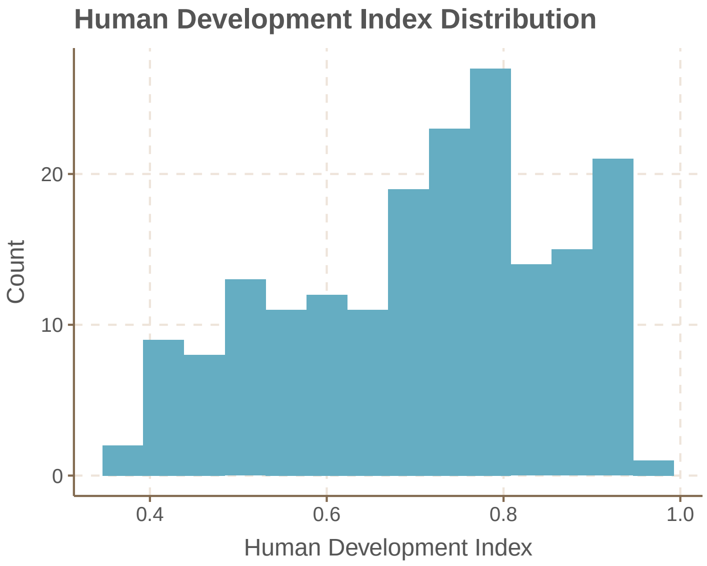
```
GDPsumm <- broom::tidy(round(summary(alldata$GDP_USD_2018 / 1000000), digits = 4)) %>%
  kable(format = "markdown")
GDPsumm
```

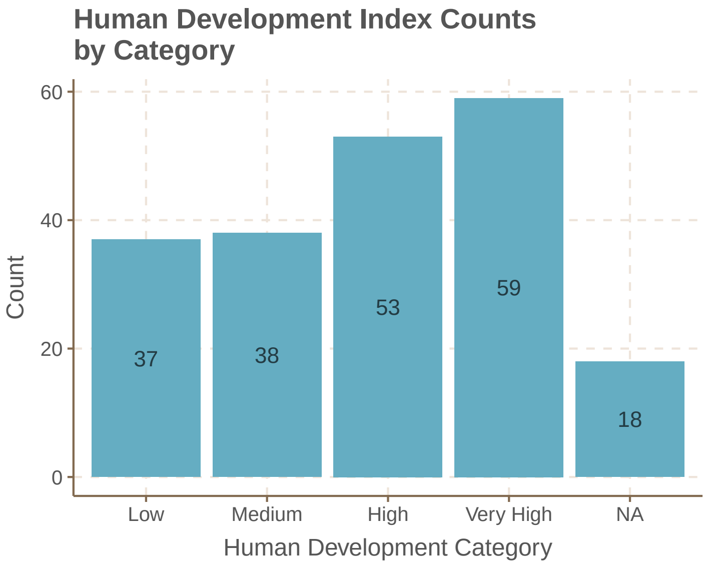
minimum	q1	median	mean	q3	maximum	na
36.5726	6734.07	27424.07	383069.6	190463	18624500	10

Taking the log transform and plotting:

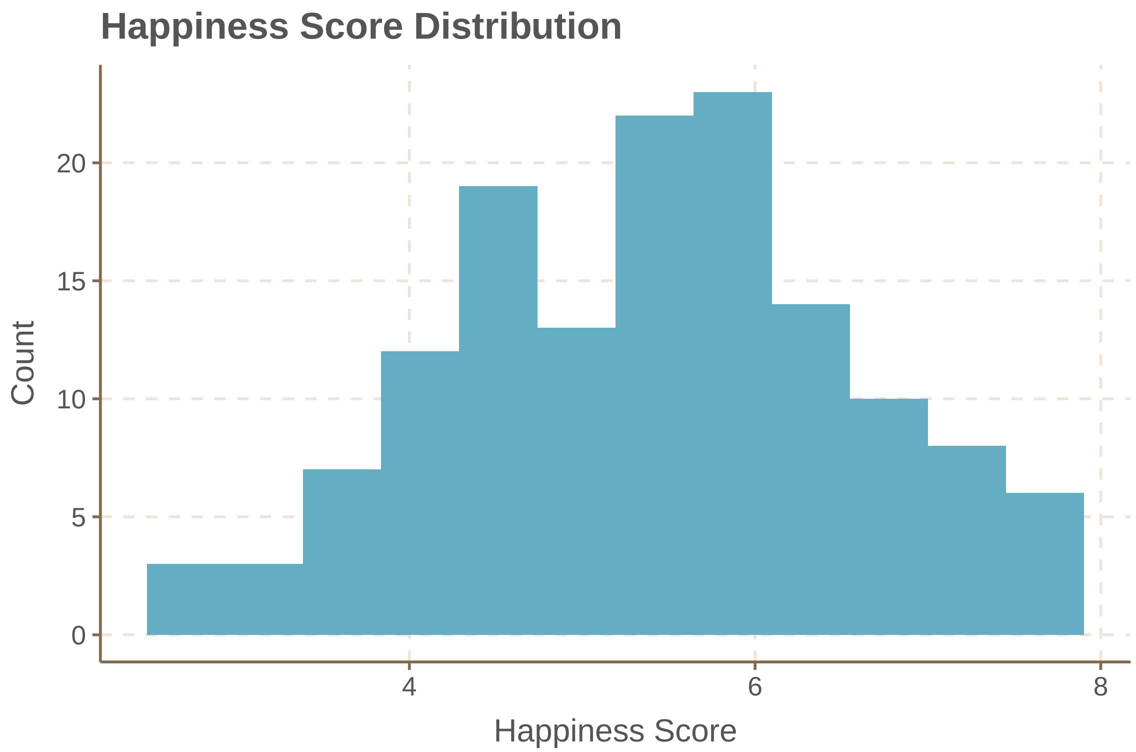


Exploring the Human Development Index variables:

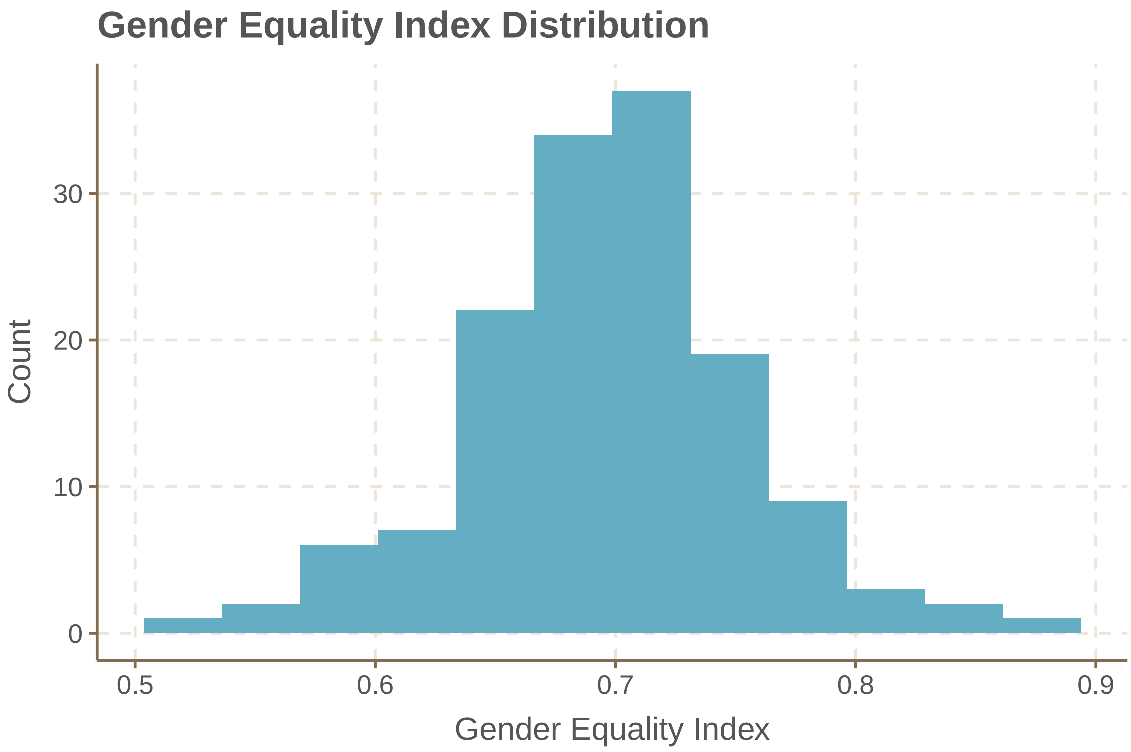




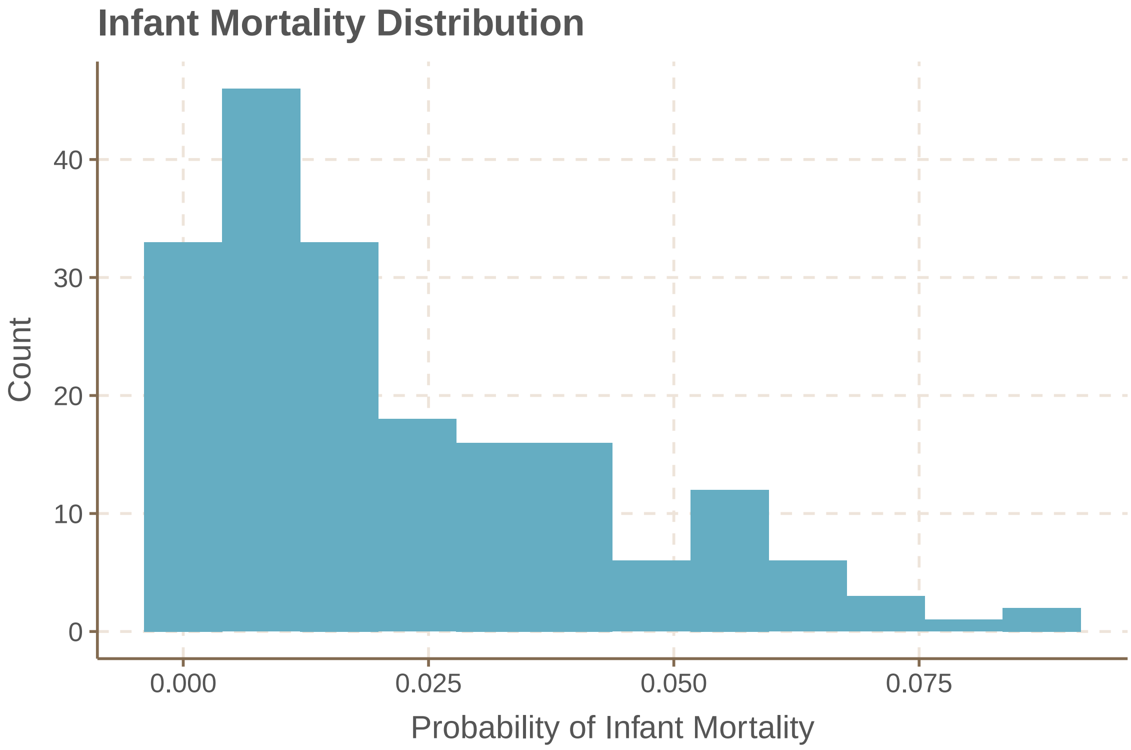
Exploring the World Happiness Report data:



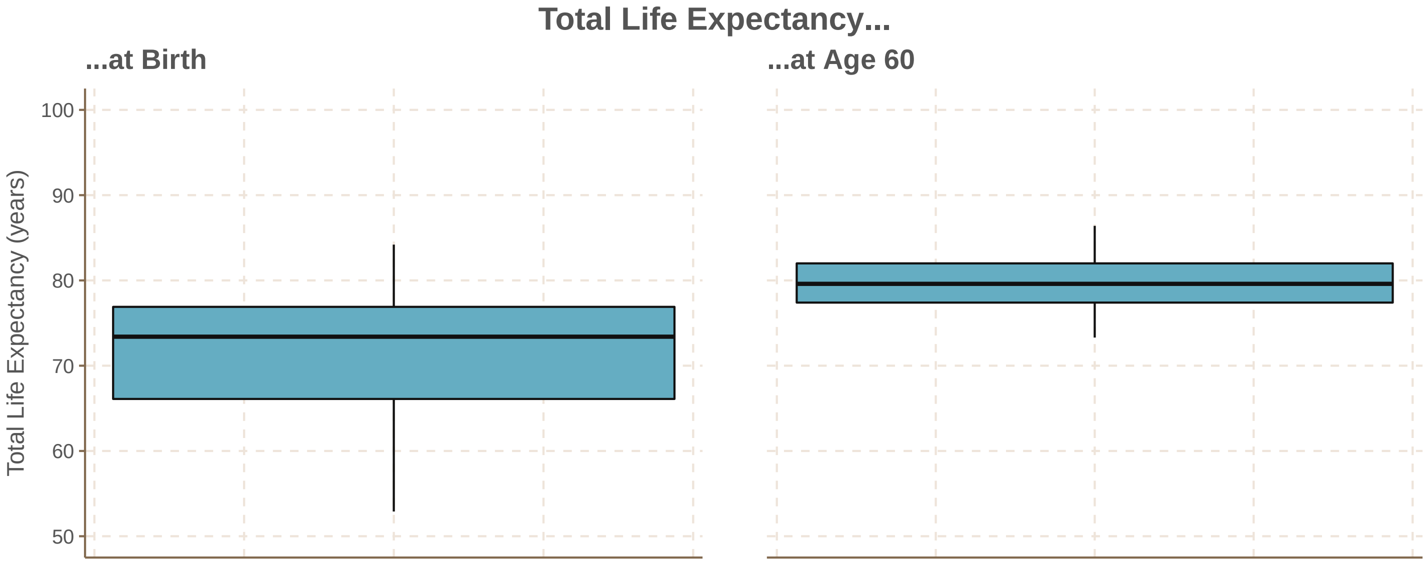
Exploring the gender equality index data:



Exploring the WHO infant mortality rate data:

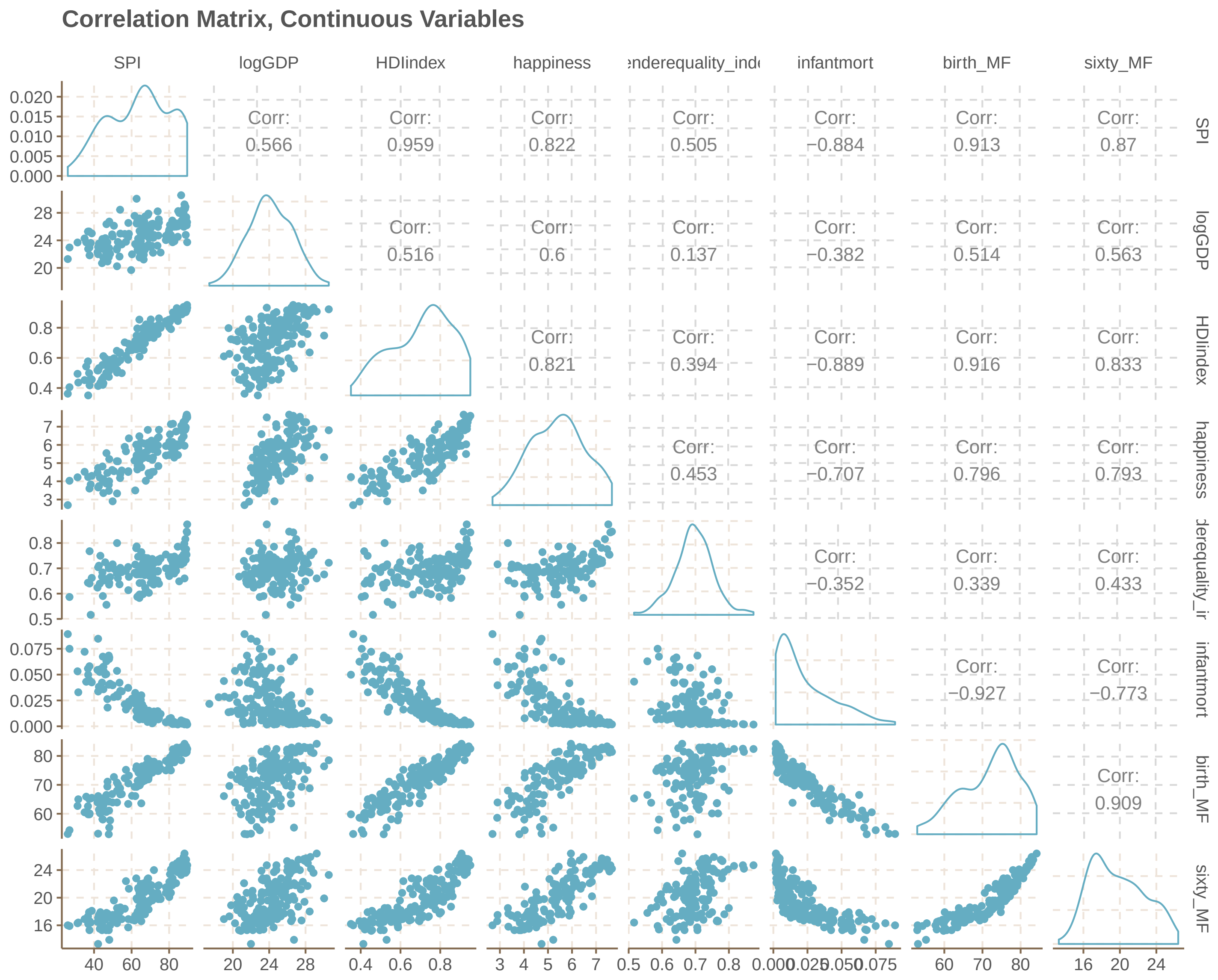


Exploring the WHO life expectancy data:



Investigating pairwise relationships between continuous variables:

```
alldata <- alldata %>% mutate(logGDP = log(GDP_USD_2018))

corrplot <- ggpairs(data = alldata, columns = c(5, 15, 8, 10:14),
                    title = "Correlation Matrix, Continuous Variables")
corrplot
```



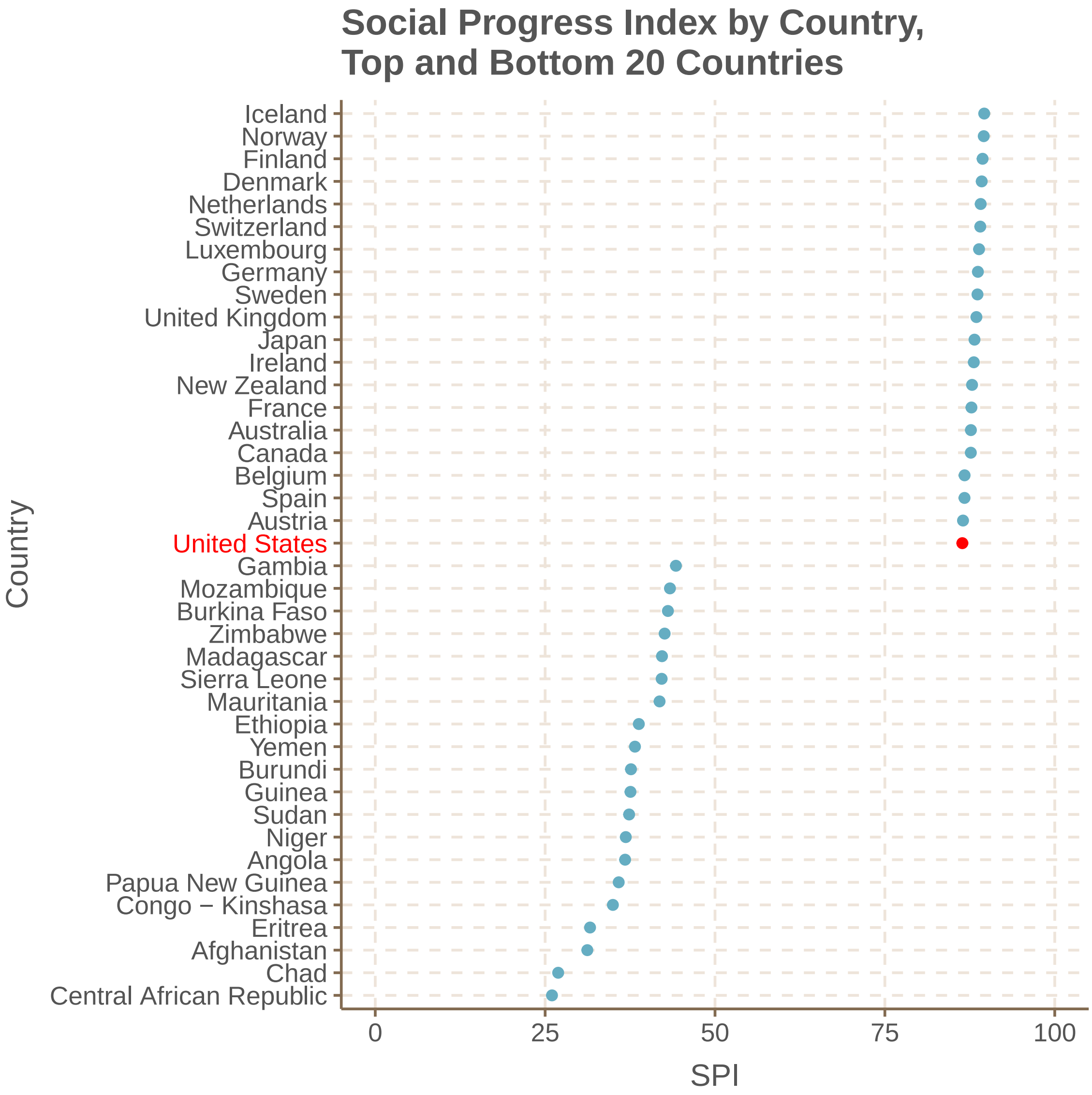
Strong positive linear relationships are seen between `HDIindex` and `SPI`, `happiness`, and `birth_MF`; between `SPI` and `happiness`, `birth_MF`, and `sixty_MF`; and between `happiness` and `sixty_MF`. Additionally, strong positive relationships that are possibly nonlinear are seen between `HDI_index` and `sixty_MF`, and between `birth_MF` and `sixty_MF`.

Strong negative relationships are seen between `infantmort` and `birth_MF`, between `HDIindex` and `infantmort`, and between `SPI` and `infantmort`, though the latter two of these may not necessarily be linear. A strong negative nonlinear relationship is seen between `infantmort` and `sixty_MF`.

Since the goal of this analysis is to compare countries with particular focus on the United States, factor-ordered bivariate plots were generated to explore how the countries compare across the variables of interest, with the United States denoted in red.

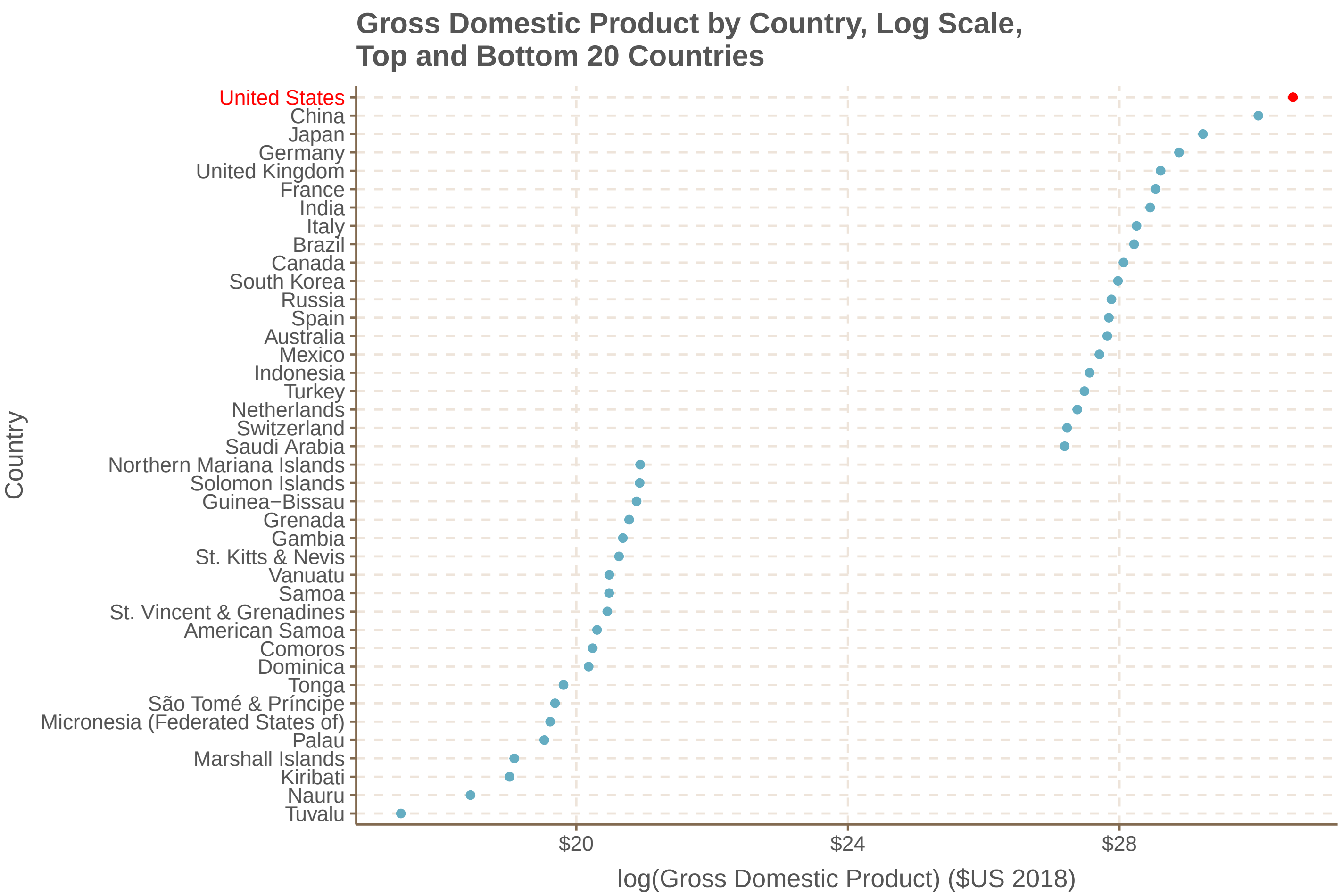
First, the top and bottom 20 countries were compared by Social Progress Index:

```
alldata_SPI <- alldata %>%
  filter(!is.na(SPI) == TRUE) %>%
  arrange(desc(SPI)) %>%
  select(SPI, country, US, color)

alldata_SPI_top20 <- alldata_SPI %>% head(20)
alldata_SPI_bot20 <- alldata_SPI %>% tail(20)
alldata_SPI40 <- bind_rows(alldata_SPI_top20, alldata_SPI_bot20)

colors <- alldata_SPI40$color[order(alldata_SPI40$SPI)]

SPI_country_point <- ggplot(data = alldata_SPI40, aes(x = SPI,
                                                    y = fct_reorder(country, SPI), color = US)) +
  geom_point() +
  scale_color_manual(values = c("US" = "red", "Non US" = "#65ADC2")) +
  theme(axis.text.y = element_text(color = colors)) +
  guides(color = FALSE) +
  xlim(0, 100) +
  xlab("SPI") +
  ylab("Country") +
  ggtitle("Social Progress Index by Country, \nTop and Bottom 20 Countries")
SPI_country_point
```



The United States ranks twentieth in social progress.

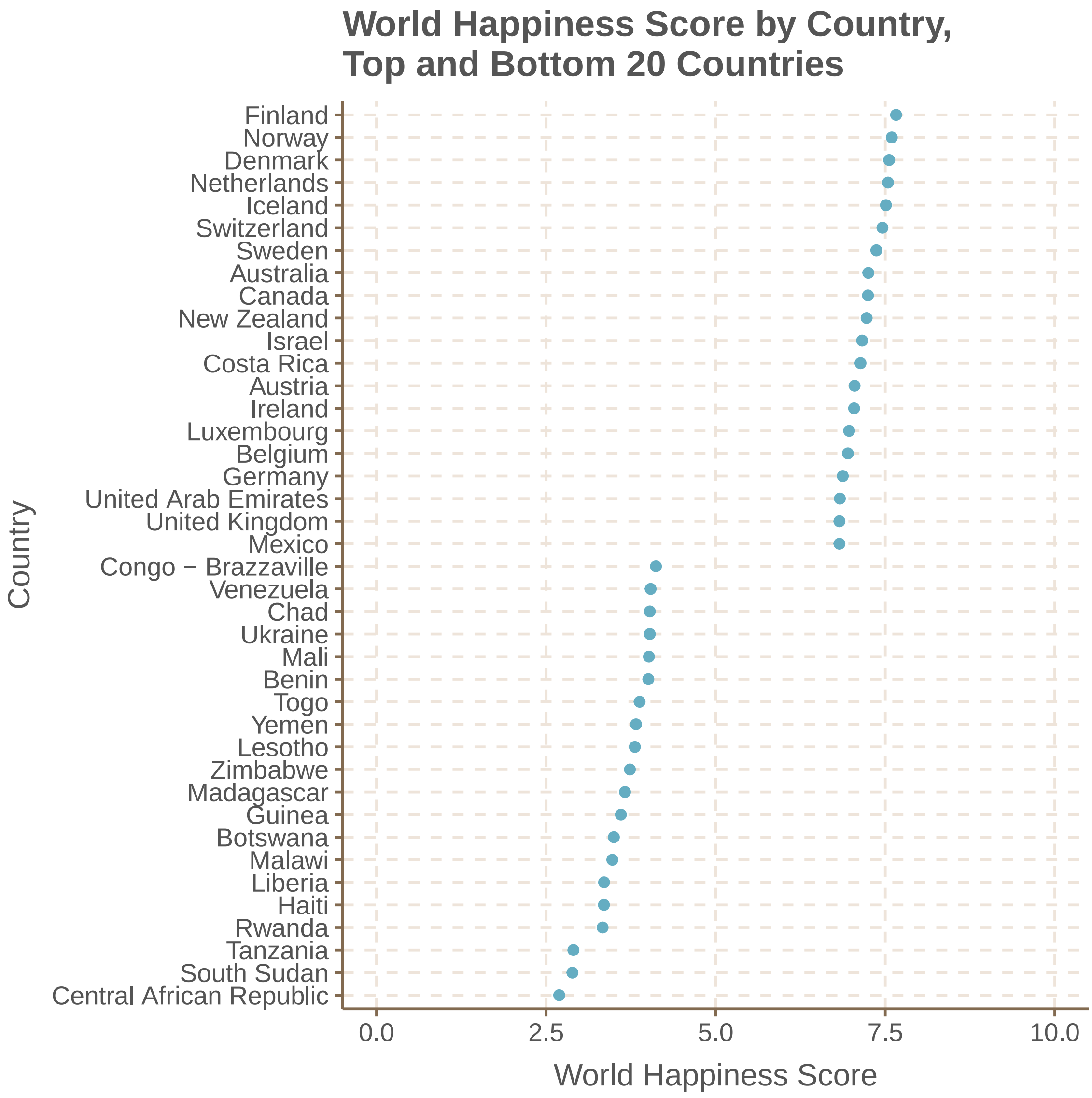
Next, exploring GDP by country (code for this and subsequent country-level plots not shown for brevity):



Gross Domestic Product by Country, Log Scale, Top and Bottom 20 Countries

The United States has the world's largest GDP.

Next, World Happiness Score:

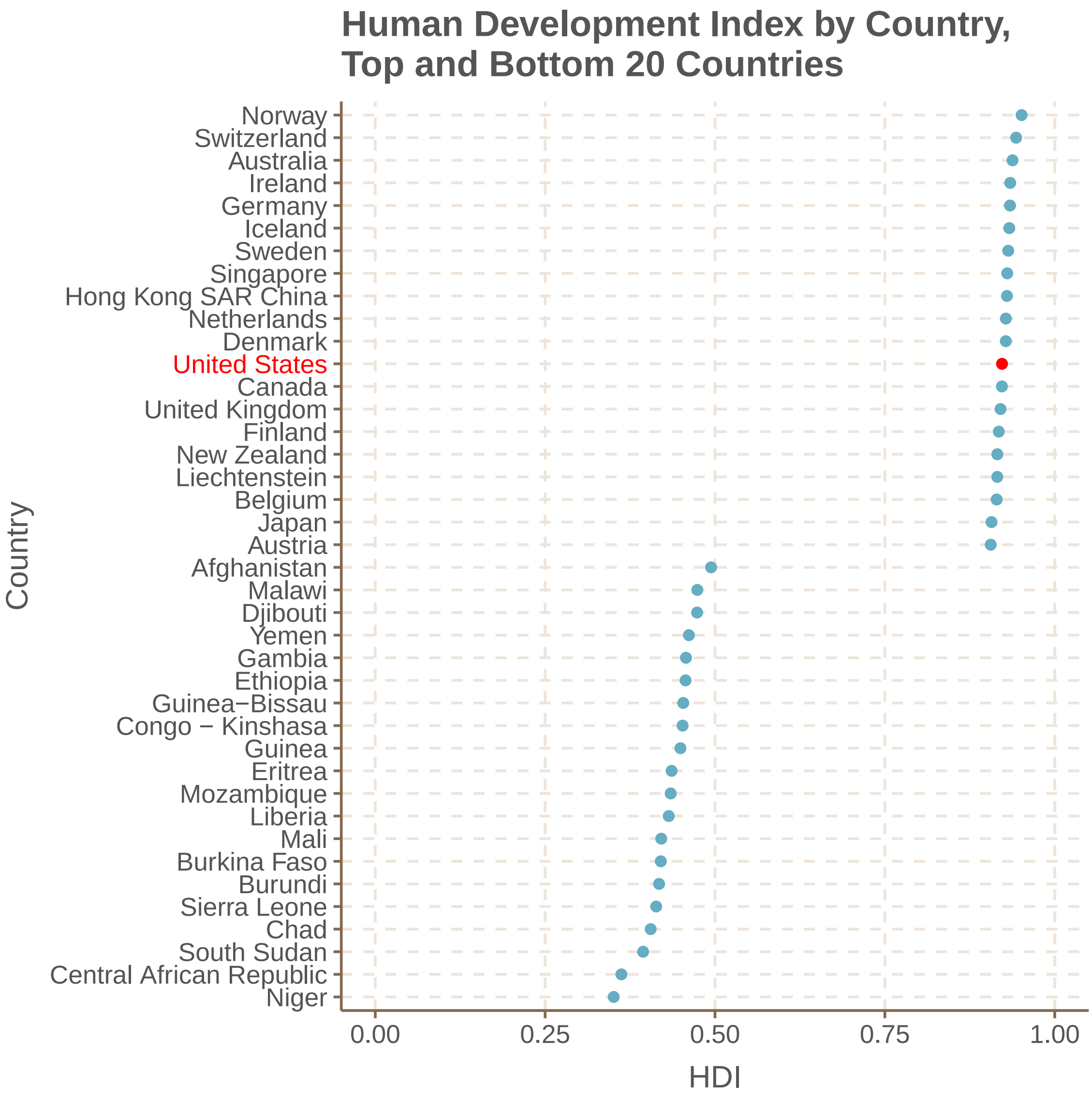


```r
which(alldata_WHR$country == "United States")
```

```
## [1] 21
```

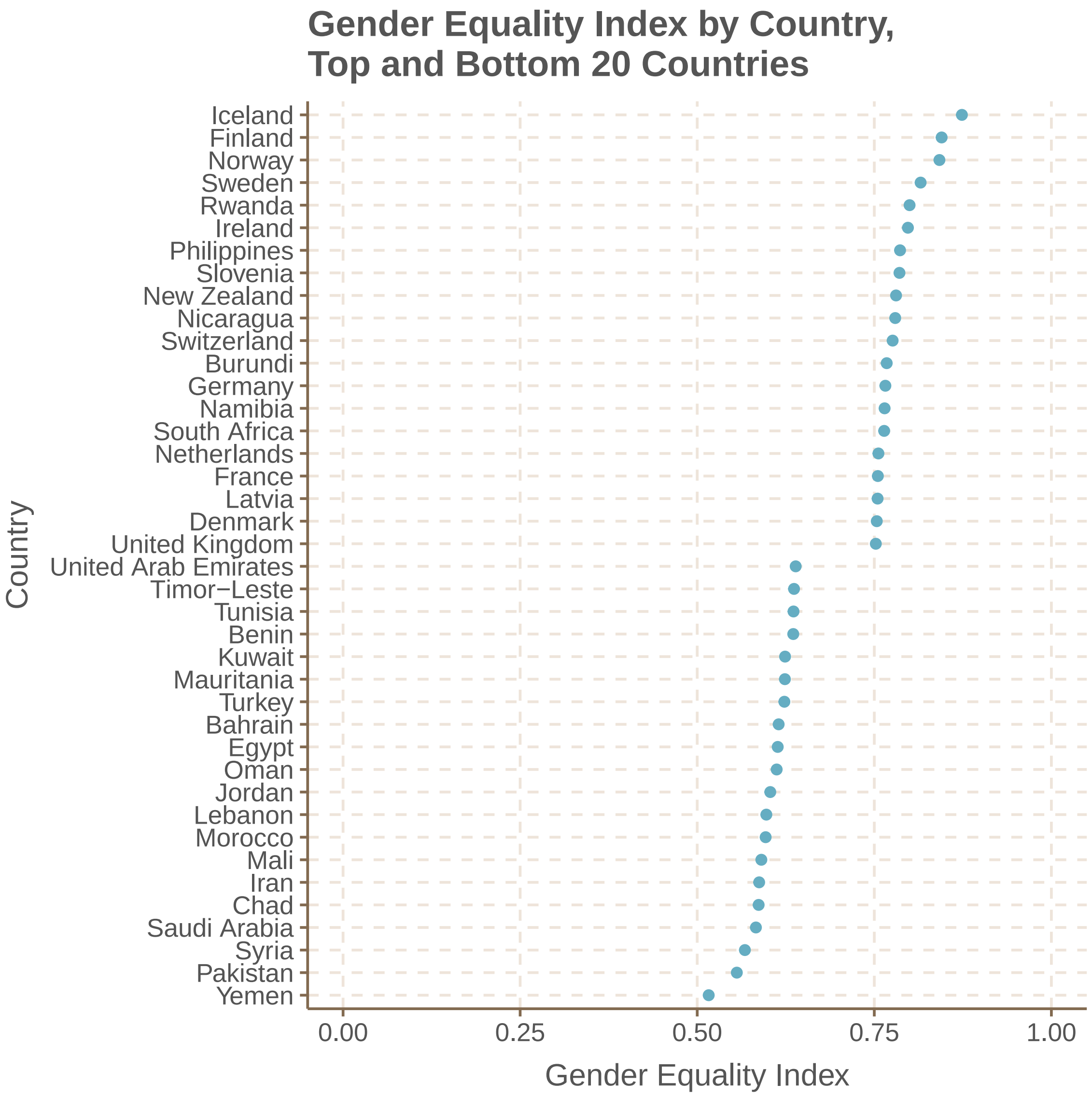
The United States is not among the top 20 countries in terms of happiness; it ranks 21st.

Next, the Human Development Index:



The United States ranks twelfth by HDI.

Exploring gender equality:

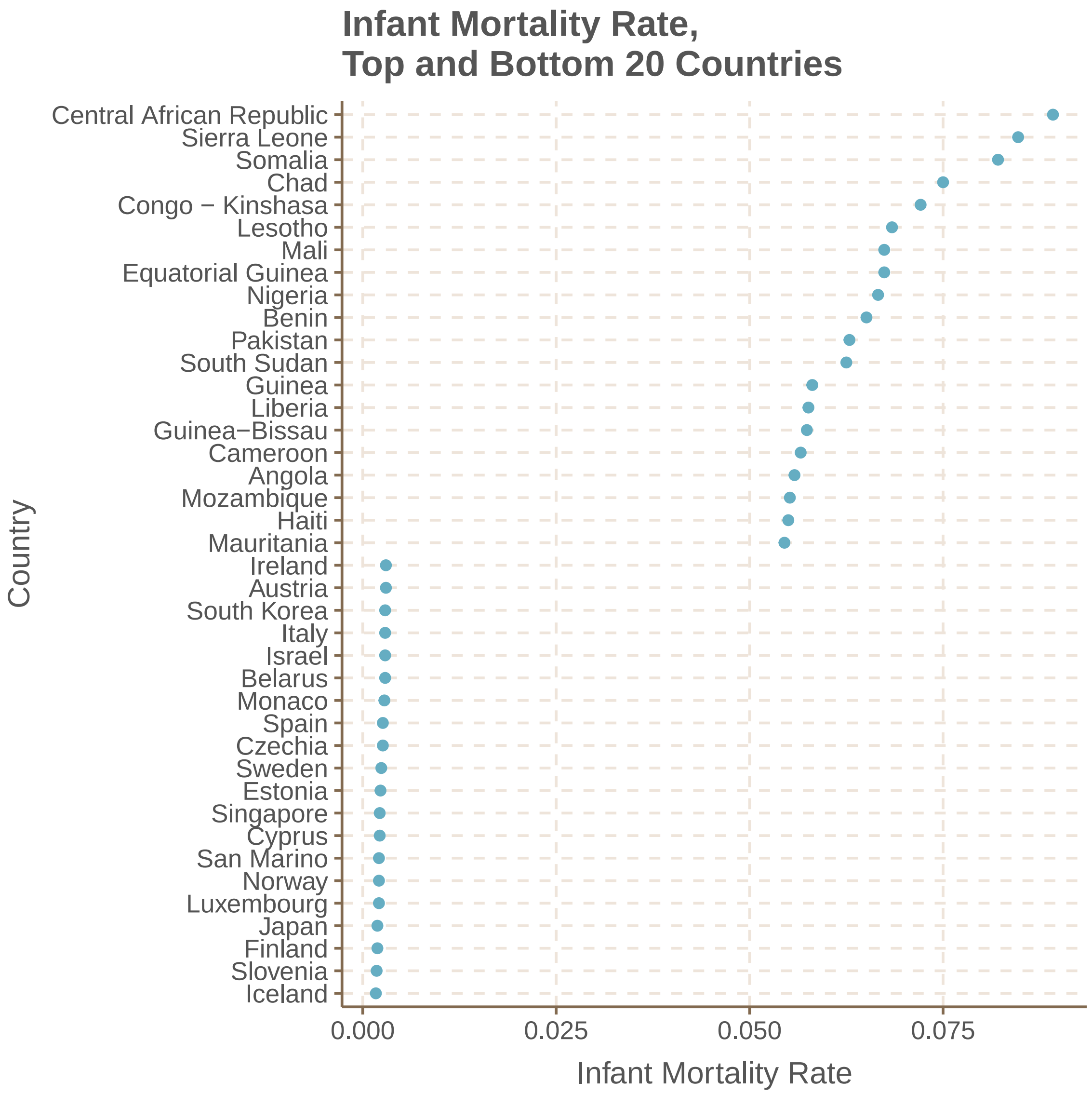


```
which(alldata_gender$country == "United States")
```

```
## [1] 45
```

The United States is not among the top 20 countries in terms of gender equality; it ranks 45th.

Examining infant mortality:

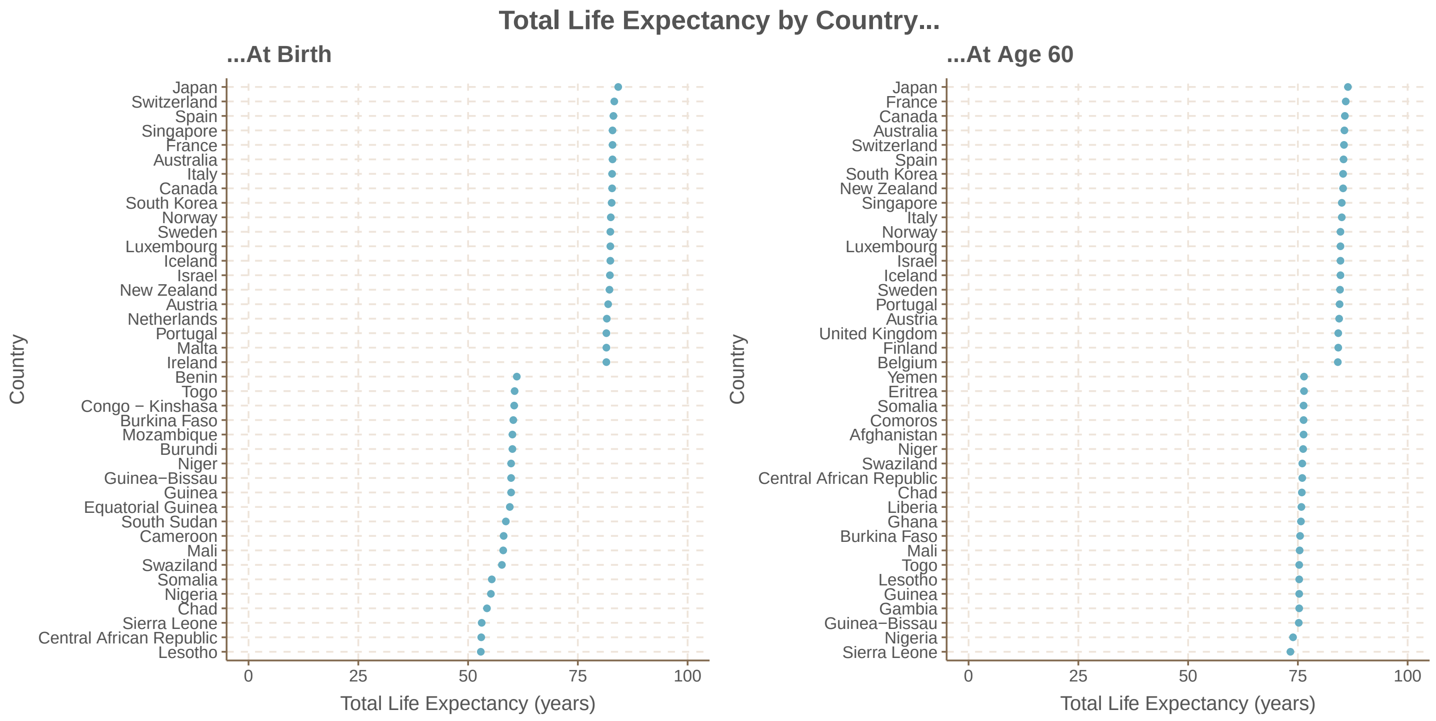


```
alldata_infantmort_asc <- alldata_infantmort %>% arrange(infantmort)
which(alldata_infantmort_asc$country == "United States")
```

```
## [1] 46
```

The United States has the world’s 46th lowest infant mortality rate.

Finally, exploring life expectancy:



```
which(alldata_lifeexp_birth$country == "United States")
```

```
## [1] 34
```

```
which(alldata_lifeexp_sixty$country == "United States")
```

```
## [1] 31
```

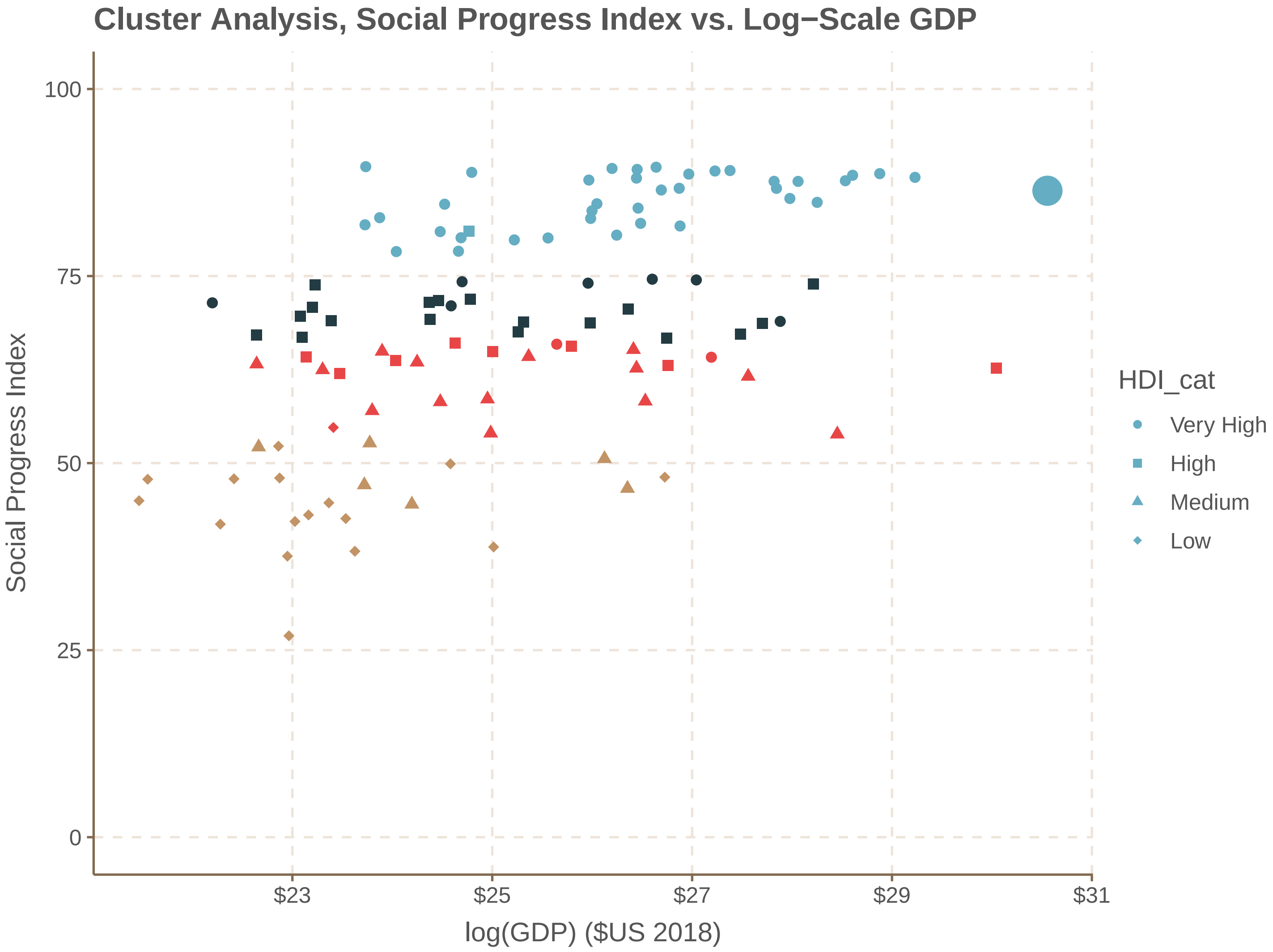
Once again, the United States is not among the top 20 countries for life expectancy, ranking 34th and 31st respectively for life expectancy at birth and at 60 years of age.

Clustering Analysis

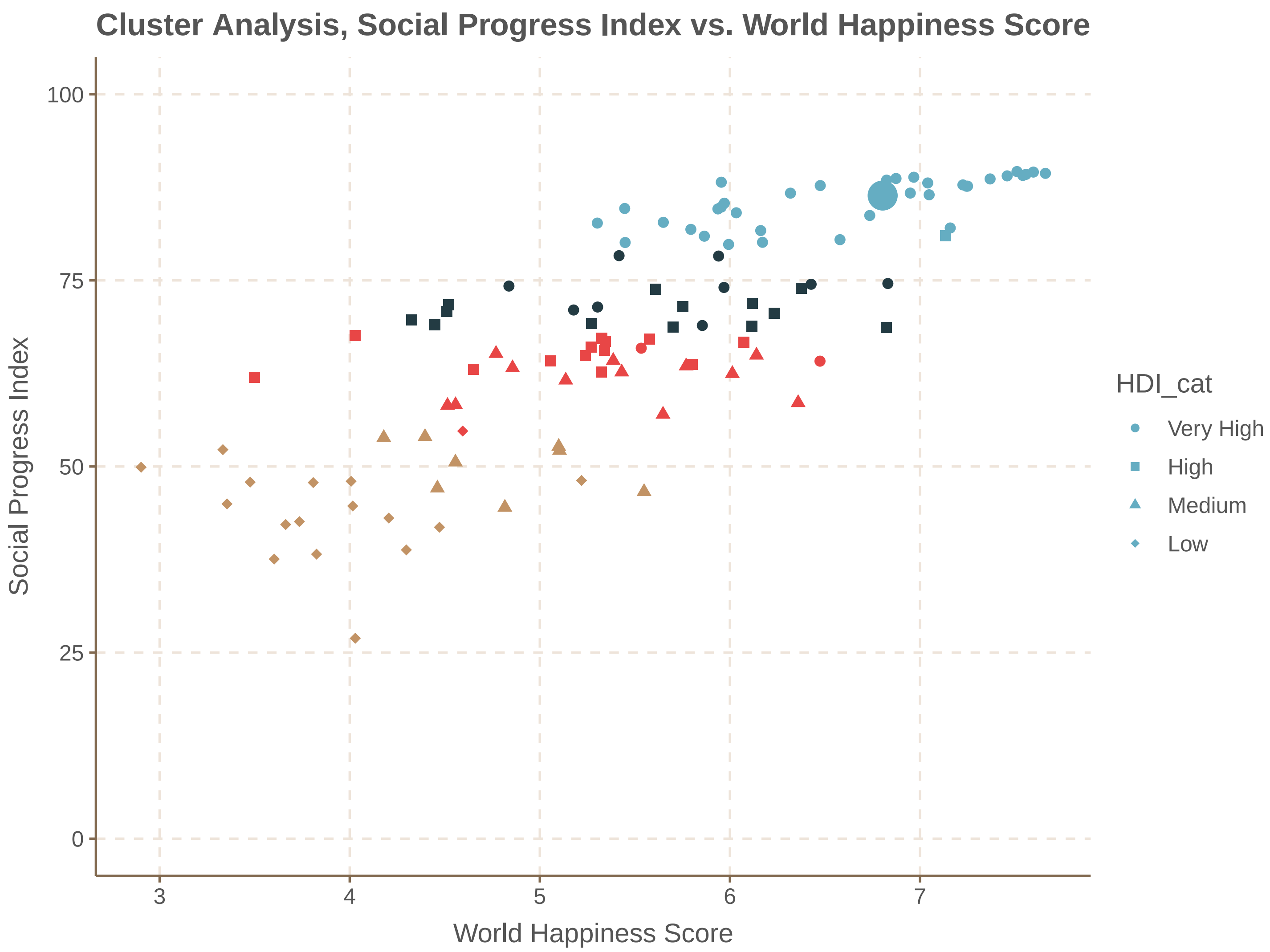
```
kmdf <- function(data, x, y, z){
  kmdata <- data %>%
    select(x, y, z)
  kmdata <- return(kmdata)
}
```

Clustering happiness versus log GDP:

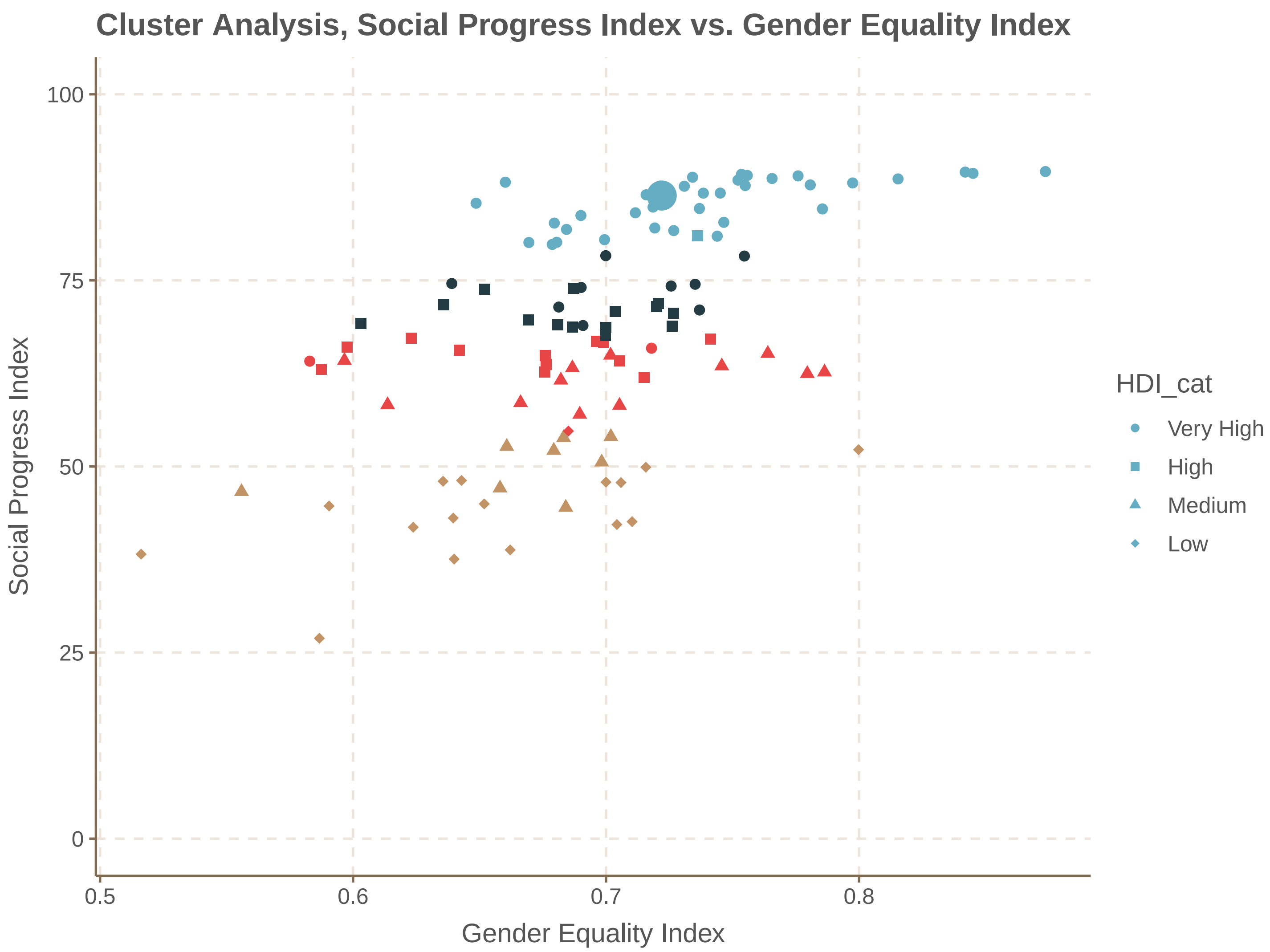
```
kmdata <- kmdf(clusterdata, "country", "SPI", "logGDP")

set.seed(19811221)
km_SPI_GDP <- kmeans(kmdata[, 2:3], 4)
km_SPI_GDP_cluster <- as.factor(km_SPI_GDP$cluster)

clusterdata1 <- cbind(clusterdata, km_SPI_GDP_cluster)

km_SPI_GDP_plot <- ggplot(data = clusterdata1,
                          aes(x = logGDP, y = SPI,
                              color = km_SPI_GDP_cluster,
                              size = US,
                              shape = HDI_cat)) +
  geom_point() +
  ylim(0, 100) +
  scale_shape_manual(values = c(18, 17, 15, 16)) +
  scale_x_continuous(labels = scales::dollar_format(prefix = "$")) +
  guides(color = FALSE, size = FALSE, shape = guide_legend(reverse = TRUE)) +
  xlab("log(GDP) ($US 2018)") +
  ylab("Social Progress Index") +
  ggtitle("Cluster Analysis, Social Progress Index vs. Log-Scale GDP")
km_SPI_GDP_plot
```



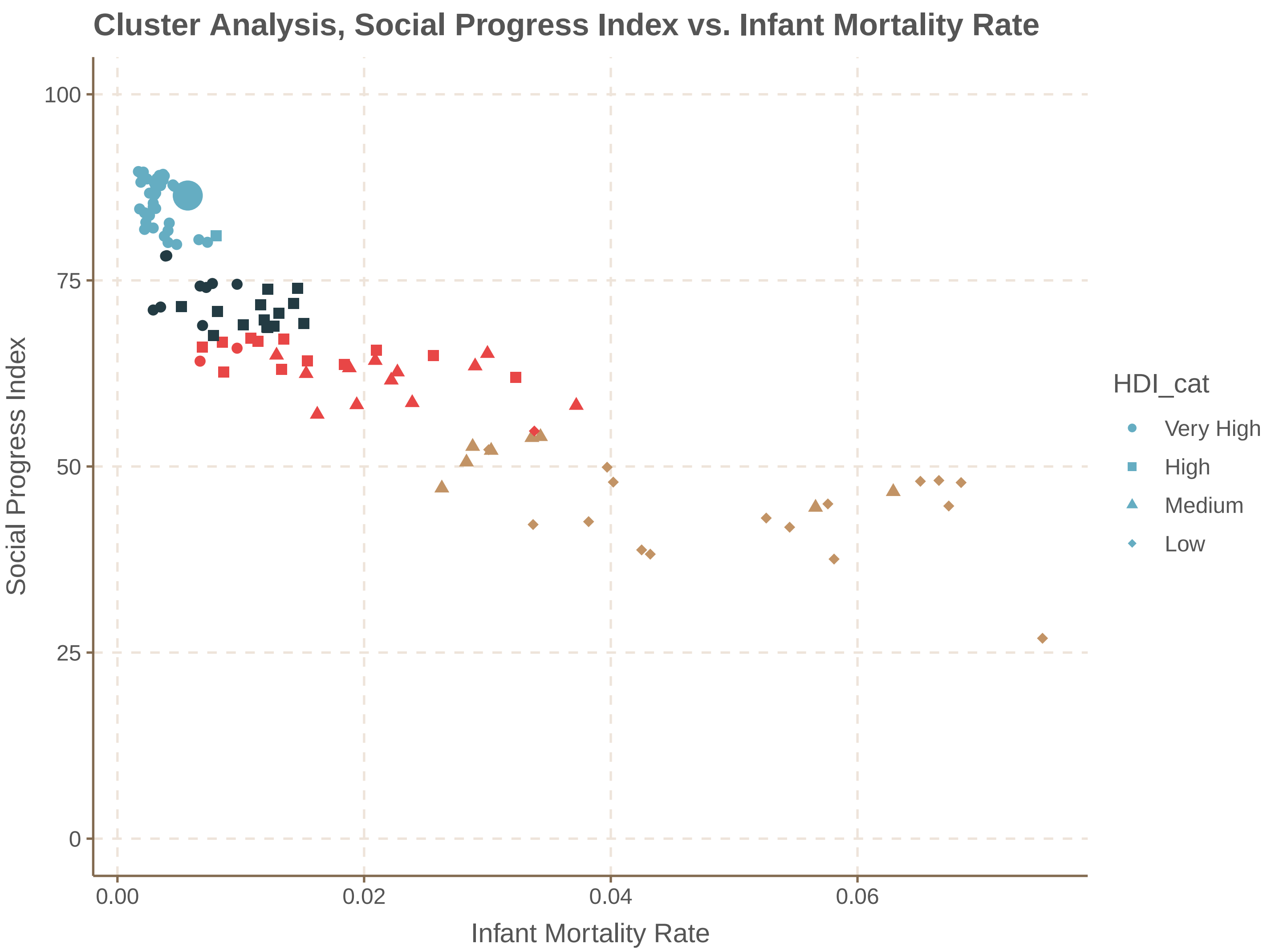
Clustering social progress versus happiness (code for this and subsequent clustering not shown for brevity):



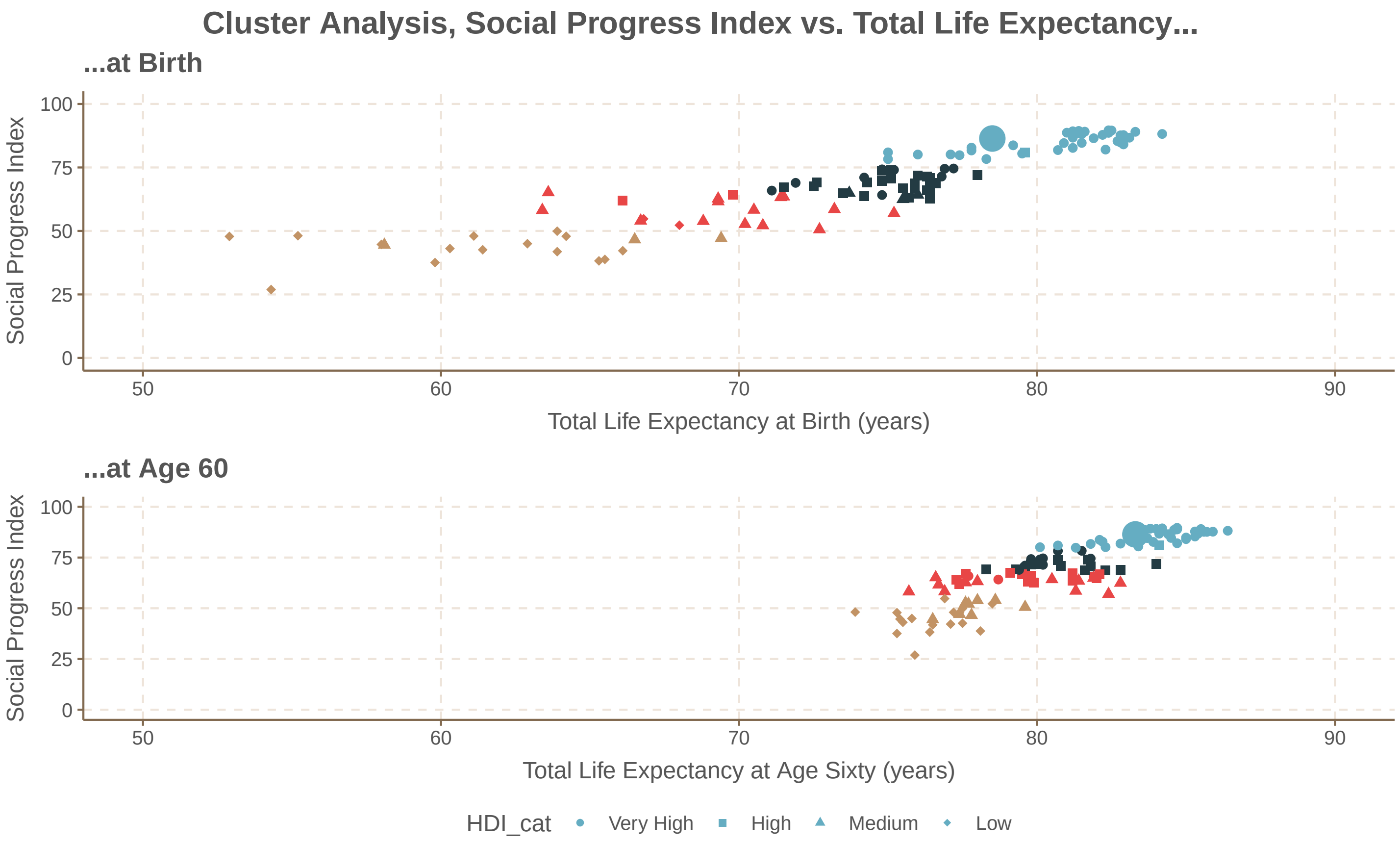
Clustering social progress versus gender equality:



Clustering social progress versus infant mortality:



Clustering social progress versus life expectancy:



Discussion

Limitations

Conclusion

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