Assignment 2 - `dplyr` exploration

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Overview

Before playing around with the various `dplyr` commands, we must define a dataset. In this case, we will be looking at the `gapminder` dataset. To access the `gapminder` dataset, we need to load the `gapminder` package. To be able to call and use `dplyr` commands, we must load the `tidyverse` package as well.

```
library(gapminder)
library(tidyverse)
```

Question 1 - Basic `dplyr`

1.1 - Filtering

Filter `gapminder` data to contain only observations from Canada, the United States, and Mexico in the 1970s.

```
gapminder %>%
  filter(country == "Canada" | country == "United States" | country == "Mexico",
         year >= 1970 & year < 1980) %>%
  knitr::kable()
```

country	continent	year	lifeExp	pop	gdpPercap
Canada	Americas	1972	72.880	22284500	18970.571
Canada	Americas	1977	74.210	23796400	22090.883
Mexico	Americas	1972	62.361	55984294	6809.407
Mexico	Americas	1977	65.032	63759976	7674.929
United States	Americas	1972	71.340	209896000	21806.036
United States	Americas	1977	73.380	220239000	24072.632

1.2 - Selecting

Let's select only `country` and `gdpPercap` variables from our filtered subset of the `gapminder` dataset.

```
gapminder %>%
  filter(country == 'Canada' | country == 'United States' | country == 'Mexico',
         year >= 1970 & year < 1980) %>%
  select(country, gdpPercap) %>%
  knitr::kable()
```

country	gdpPercap
Canada	18970.571
Canada	22090.883
Mexico	6809.407
Mexico	7674.929
United States	21806.036
United States	24072.632

1.3 - Mutating

Suppose we want to look at all the countries that have ever experienced a drop in life expectancy between 1952 and 2007. Let's define a new variable `lifeExp_change`, equaling the difference between life expectancy at one time point and life expectancy at the time point before (5 years earlier).

```
gapminder %>%
  group_by(country) %>%
  arrange(year) %>%
  mutate(lifeExp_change = lifeExp - lag(lifeExp)) %>%
  filter(lifeExp_change < 0)
```

```
# A tibble: 102 x 7
# Groups:   country [52]
   country        continent  year lifeExp      pop gdpPercap lifeExp_change
   <fct>          <fct>     <int>   <dbl>    <int>     <dbl>          <dbl>
 1 China          Asia       1962    44.5   6.66e8      488.         -6.05
 2 Cambodia       Asia       1972    40.3   7.45e6      422.         -5.10
 3 Czech Republic Europe     1972    70.3   9.86e6    13108.         -0.0900
 4 Netherlands    Europe     1972    73.8   1.33e7    18795.         -0.0700
 5 Slovak Republ~ Europe     1972    70.4   4.59e6     9674.         -0.63
 6 Bulgaria       Europe     1977    70.8   8.80e6     7612.         -0.09
 7 Cambodia       Asia       1977    31.2   6.98e6      525.         -9.10
 8 El Salvador    Americas   1977    56.7   4.28e6     5139.         -1.51
 9 Poland         Europe     1977    70.7   3.46e7     9508.         -0.180
10 Uganda         Africa     1977    50.4   1.15e7      844.         -0.666
# ... with 92 more rows
```

We can see that many countries have experienced a drop in life expectancy at some point between 1952 and 2007; however, what if we are only interested in countries that have experienced an overall life expectancy drop between the most recent year (2007) and the earliest year (1952).

```
gapminder %>%
  filter(year == 1952 | year == 2007) %>%
  group_by(country) %>%
  arrange(year) %>%
  mutate(lifeExp_change = lifeExp - lag(lifeExp)) %>%
  filter(lifeExp_change < 0) %>%
  knitr::kable()
```

country	continent	year	lifeExp	pop	gdpPercap	lifeExp_change
Swaziland	Africa	2007	39.613	1133066	4513.4806	-1.794
Zimbabwe	Africa	2007	43.487	12311143	469.7093	-4.964

From this output, we can see that the only countries that experienced an overall decline in life expectancy between 1952 and 2007 were Swaziland and Zimbabwe, with a decline of 1.794 and 4.964 years, respectively.

1.4 - Slicing

Now, let's filter the `gapminder` dataset to show the maximum GDP per capita experienced by each country.

```
gapminder %>%
  select(country, year, gdpPercap) %>%
  group_by(country) %>%
  mutate(max_gdpPercap = max(gdpPercap)) %>%
  filter(max_gdpPercap == gdpPercap) %>%
  select(country, year, max_gdpPercap)
```

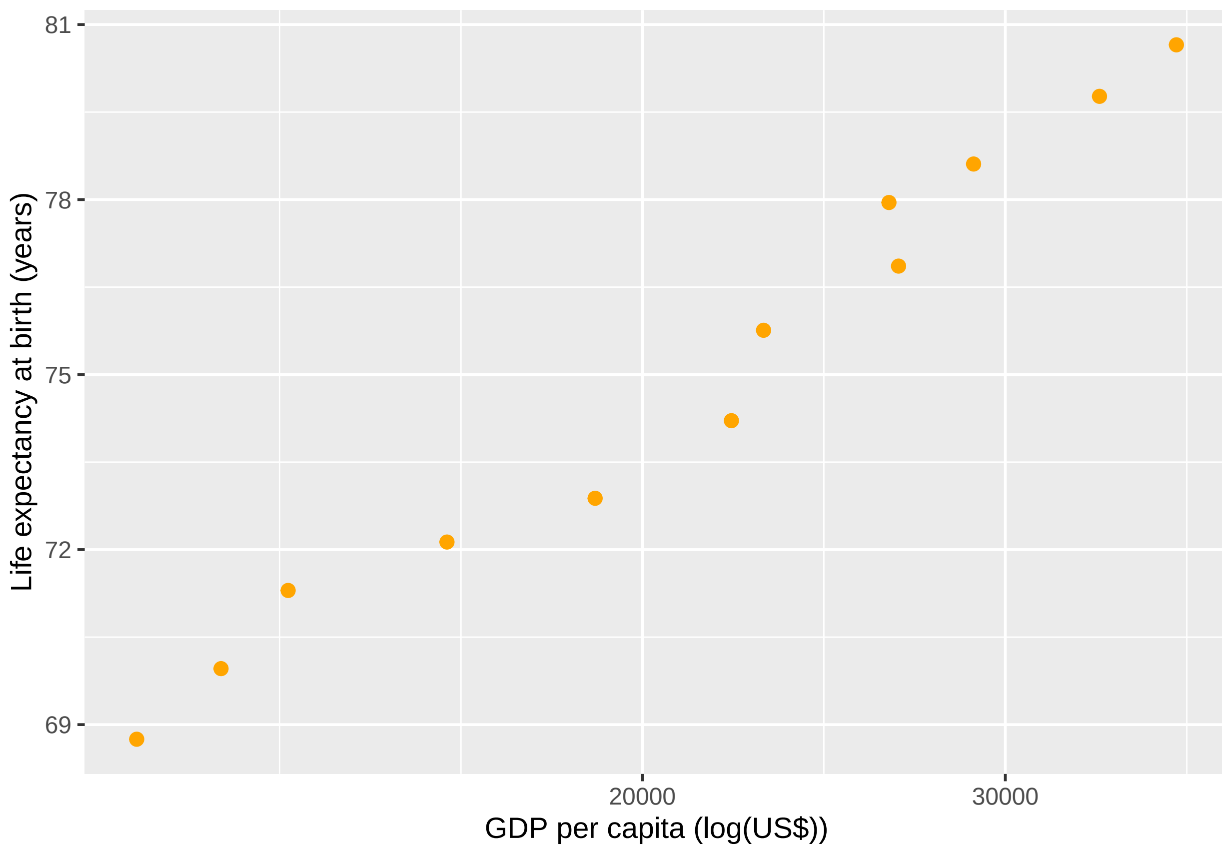
```
# A tibble: 142 x 3
# Groups:   country [142]
   country      year max_gdpPercap
   <fct>       <int>         <dbl>
 1 Afghanistan  1982          978.
 2 Albania      2007         5937.
 3 Algeria      2007         6223.
 4 Angola       1967         5523.
 5 Argentina    2007        12779.
 6 Australia    2007        34435.
 7 Austria      2007        36126.
 8 Bahrain      2007        29796.
 9 Bangladesh   2007         1391.
10 Belgium      2007        33693.
# ... with 132 more rows
```

This output allows us to determine the maximum GDP per capita experienced by each country between 1952 and 2007, and also in which year it was experienced.

1.5 - Plotting

Let's investigate the relationship between life expectancy and GDP per capita in Canada. To do this, we will create a scatterplot using `ggplot2`.

```
gapminder %>%
  filter(country == "Canada") %>%
  ggplot(aes(gdpPercap, lifeExp)) +
  geom_point(colour = "orange", size = 2) +
  scale_x_log10() +
  xlab("GDP per capita (log(US$))") +
  ylab("Life expectancy at birth (years)")
```



From this plot, we can see that in Canada, life expectancy has been increasing relatively linearly with the log transform of GDP per capita between the years of 1952 and 2007.

Question 2 - Variable Exploration

To perform individual variable exploration using `dplyr` we will choose one categorical variable and one quantitative variable to explore. Let's say we want to analyze `continent` as the categorical variable and `population` as the quantitative variable.

2.1 - Categorical

The categorical variable we are interested in exploring is `continent`. To start off, let's first investigate which continents are represented in our `gapminder` dataset.

```
levels(gapminder$continent)
```

```
[1] "Africa"   "Americas" "Asia"     "Europe"   "Oceania"
```

Categorical variable exploration is usually performed through the generation of frequency tables - let's generate one for the `continent` variable.

```r
gapminder %>%
  count(continent) %>%
  rename(count = n) %>%
  knitr::kable()
```

continent	count
Africa	624
Americas	300
Asia	396
Europe	360
Oceania	24

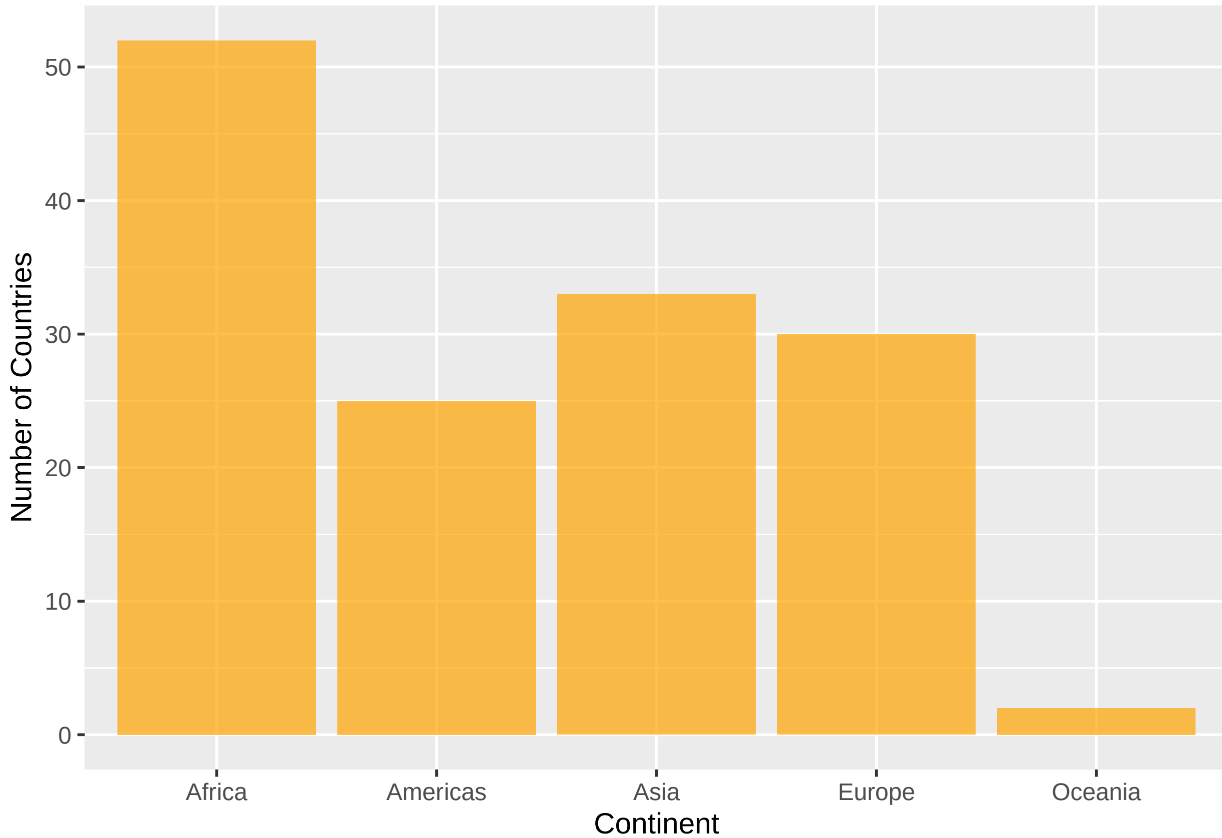
This command prints out the number of observations for each continent in our dataset. However, by looking at the `gapminder` dataset, we see that each country contributes 12 observations (represeting 12 time points) to the dataset. Suppose we want to know how many countries are in each continent for the `gapminder` dataset. To determine this, we need to remove replicates of the same country. The simpliest way to achieve this is to consider continent counts at each individual time point.

```r
gapminder %>%
  group_by(year) %>%
  count(continent) %>%
  rename(country_count = n)
```

```
# A tibble: 60 x 3
# Groups:   year [12]
    year continent country_count
   <int> <fct>             <int>
 1  1952 Africa               52
 2  1952 Americas             25
 3  1952 Asia                 33
 4  1952 Europe               30
 5  1952 Oceania               2
 6  1957 Africa               52
 7  1957 Americas             25
 8  1957 Asia                 33
 9  1957 Europe               30
10  1957 Oceania               2
# ... with 50 more rows
```

We see that country distirbution does not change from year to year - there are the same number of countries in each of the 5 continents: Africa, the Americas, Asia, Europe, and Oceania. In our dataset, 52 countries are represented from Africa, 25 countries from the Americas, 33 countries from Asia, 30 countries from Europe, and 2 countries from Oceania. Let's view this data graphically using a bar graph - because continent counts do not change between years, it is sufficient to plot data from a single time point.

```r
gapminder %>%
  filter(year == 2007) %>%
  ggplot(aes(continent)) +
  geom_bar(fill = "orange", alpha = 0.7) +
  ylab("Number of Countries") +
  xlab("Continent")
```



2.2 - Quantitative

Quantitative variable exploration is usually performed through the generation of 5-number summaries: min, 1st quartile, median, 3rd quartile, max. Let's generate a variation of the 5-number summary for the `pop` variable, including a measure of spread.

```
gapminder %>%
  summarise("min_pop (million)" = min(pop)/(10^6), "mean_pop (million)" = mean(pop)/(10^6),
            "median_pop (million)" = median(pop)/(10^6), "max_pop (million)" = max(pop)/(10^6),
            "sd_pop (million)" = sd(pop)/(10^6)) %>%
  knitr::kable()
```

min_pop (million)	mean_pop (million)	median_pop (million)	max_pop (million)	sd_pop (million)
0.060011	29.60121	7.023595	1318.683	106.1579

From the output, we can observe the minimum and maximum values for population as well as the median and mean values and the standard deviation. We observe a deviation between population mean and population median, suggesting that the distribution is skewed with greater density towards lower values (`mean_pop` > `median_pop`).

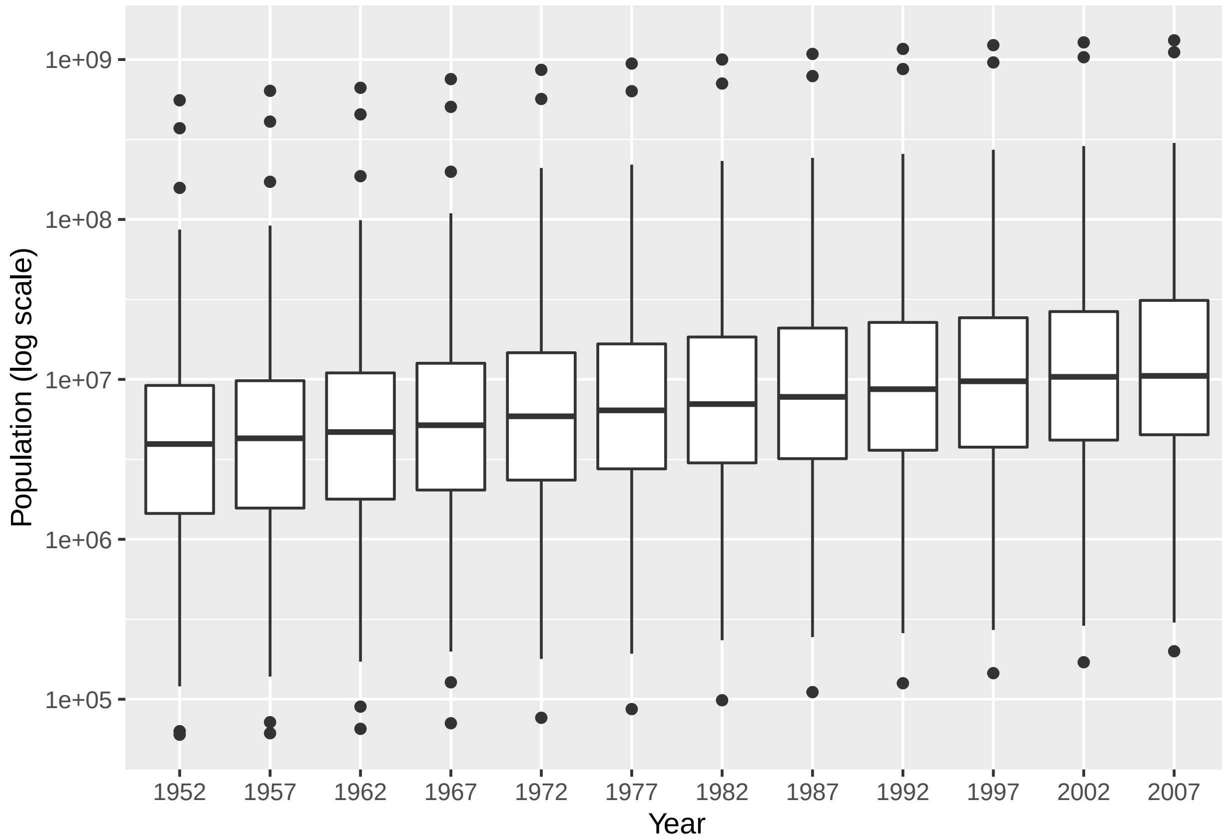
However, these values are difficult to interpret because they refer to the population distribution across all countries between 1952 and 2007. It may be more informative if we investigated the change in population distribution from year to year, for example.

```
gapminder %>%
  select(year, pop) %>%
  group_by(year) %>%
  summarise("min_pop (million)" = min(pop)/(10^6), "mean_pop (million)" = mean(pop)/(10^6),
            "median_pop (million)" = median(pop)/(10^6), "max_pop (million)" = max(pop)/(10^6),
            "sd_pop (million)" = sd(pop)/(10^6)) %>%
  knitr::kable()
```

year	min_pop (million)	mean_pop (million)	median_pop (million)	max_pop (million)	sd_pop (million)
1952	0.060011	16.95040	3.943953	556.2635	58.10086
1957	0.061325	18.76341	4.282942	637.4080	65.50429
1962	0.065345	20.42101	4.686039	665.7700	69.78865
1967	0.070787	22.65830	5.170176	754.5500	78.37548
1972	0.076595	25.18998	5.877997	862.0300	88.64682
1977	0.086796	27.67638	6.404037	943.4550	97.48109
1982	0.098593	30.20730	7.007320	1000.2810	105.09865
1987	0.110812	33.03857	7.774862	1084.0350	114.75618
1992	0.125911	35.99092	8.688686	1164.9700	124.50259
1997	0.145608	38.83947	9.735064	1230.0750	133.41739
2002	0.170372	41.45759	10.372919	1280.4000	140.84828
2007	0.199579	44.02122	10.517531	1318.6831	147.62140

From these summary statistics, we can see that there is a lot of variation in the `pop` variable - large standard deviation values with values progressively increasing over time, suggesting greater diversity in population size in more recent years. We also observe that the overall distribution of population has shifted to greater values, with all statistics increasing over time. To visualize this graphically, we can plot side-by-side boxplots representing global population data at each time point.

```
gapminder %>%
  mutate(year = factor(year)) %>%
  ggplot(aes(year, pop)) +
  geom_boxplot() +
  scale_y_log10("Population (log scale)") +
  xlab("Year")
```



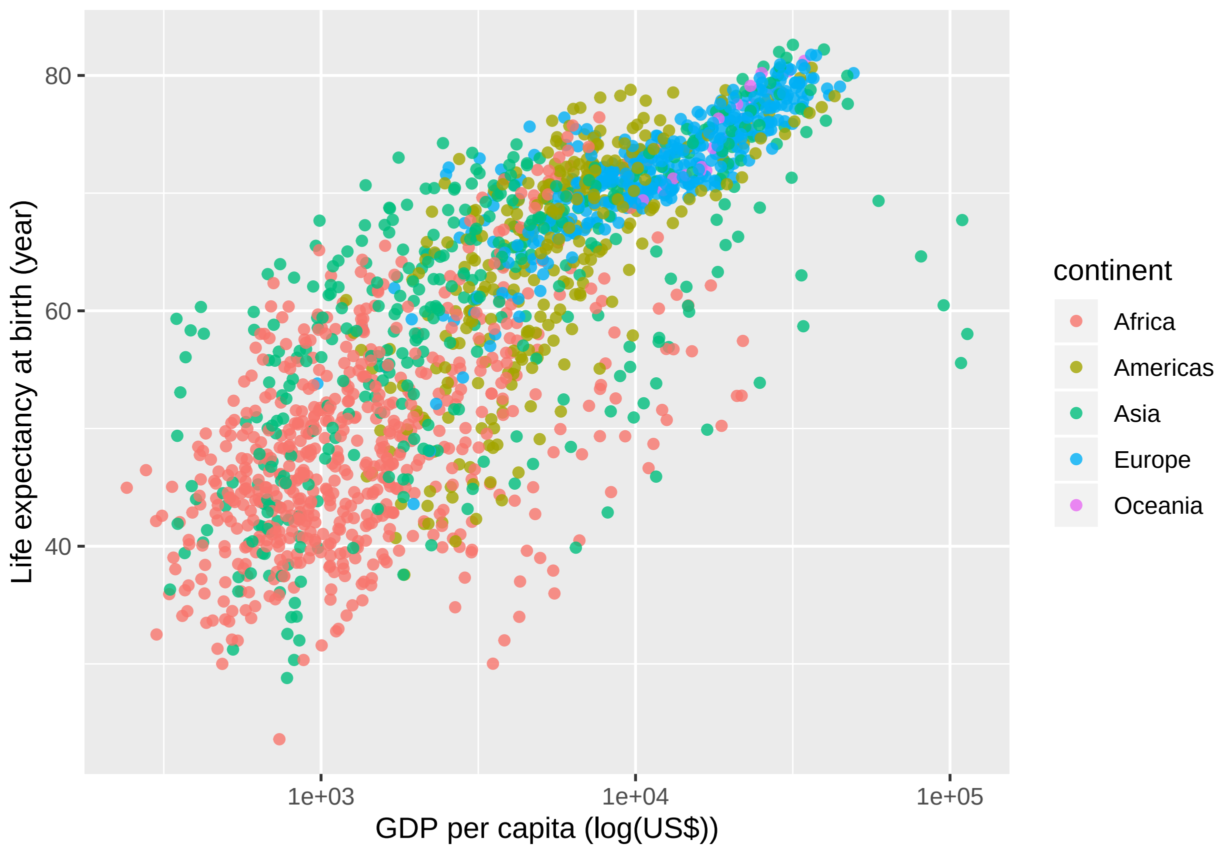
From this graph, we can observe a relatively consistent slow linear increase in log-transformed population over time, suggesting that between 1952 and 2007, global population has been steadily increasing. We also observe wide error bars and evident outliers, highlighting the population size diversity between countries globally.

Question 3 - Plot Exploration

3.1 - Scatterplot

The first plot type that we are going to explore is the scatterplot. Suppose we want to group the `gapminder` dataset by continent, and then plot the relationship between life expectancy at birth and GDP per capita, to investigate whether this relationship varies with continent.

```
gapminder %>%
  group_by(continent) %>%
  ggplot(aes(x = gdpPercap, y = lifeExp, colour = continent)) +
  geom_point(alpha = 0.8) +
  scale_x_log10() +
  ylab("Life expectancy at birth (year)") +
  xlab("GDP per capita (log(US$))")
```

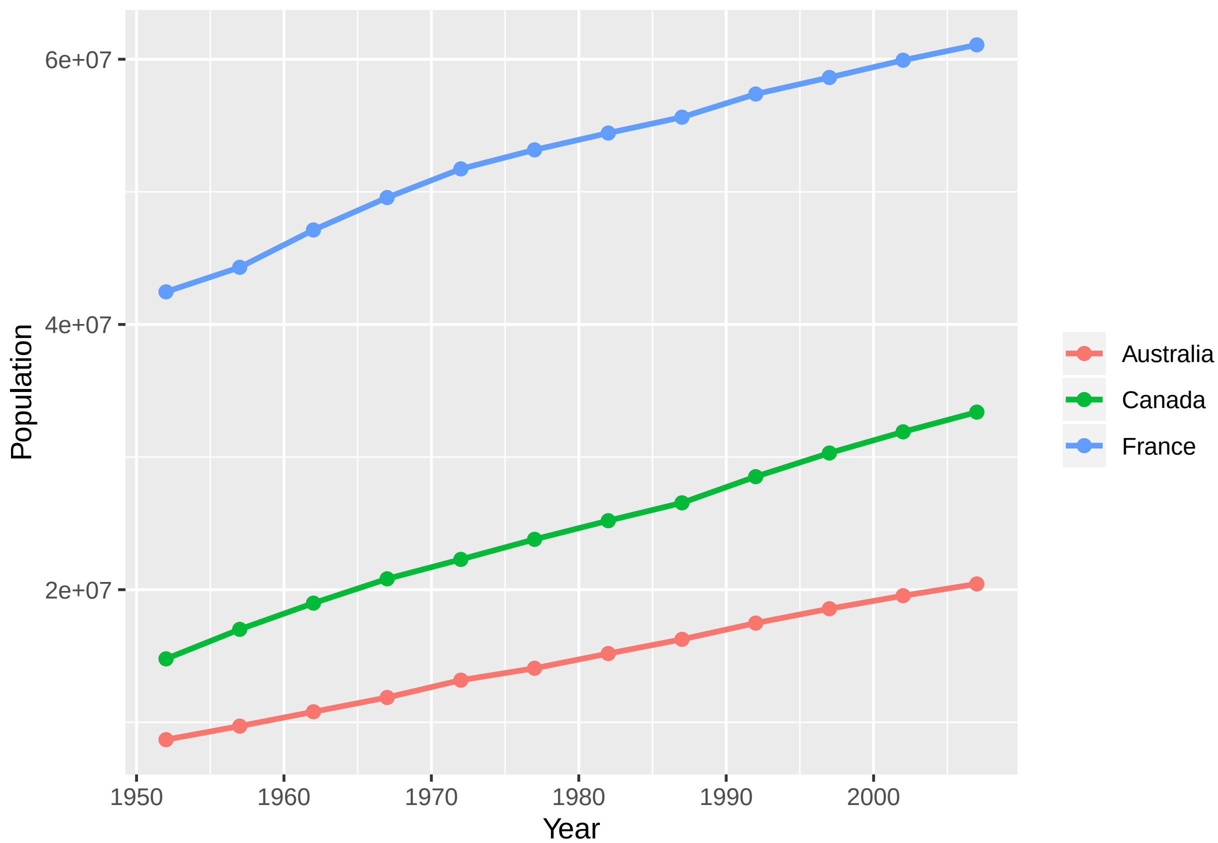


From the scatterplot, we can see that life expectancy and GDP per capita are roughly positively correlated, following a linear relationship. Not only does life expectancy tend to increase with GDP per capita, we can also observe that countries in Europe and Oceania tend to have higher life expectancy and GDP whereas countries in Africa tend to have lower life expectancy and GDP. Countries in the Americas and Asia seem to have more varied distributions of life expectancy and GDP with more discrepancy between countries. We also note that some countries in Africa and Asia deviate from the general trend of increasing life expectancy with higher GDP per capita.

3.2 - Time Series

The second plot type we are going to explore is a time series. Suppose we want to investigate how population has changed over time between 1952 and 2007 in Canada, France, and Australia. We can visualize this through making a time series plot and fitting individual trendlines for population data from each country.

```
gapminder %>%
  filter(country == "Canada" | country == "France" | country == "Australia") %>%
  ggplot(aes(x = year, y = pop, col = country)) +
  geom_point(size = 2) +
  geom_line(size = 1) +
  xlab("Year") +
  ylab("Population") +
  theme(legend.title=element_blank())
```



From observing the trendlines, we can see that all countries have experienced roughly linear increases in population over time. Canada and France seem to have similar rates of population increase, while the rate of increase in population is slower in Australia. We can infer that between 1952 and 2007, Canada and France have experienced an increase in population of approximately 20 million people, while Australia's population has increased by approximately 10 million people.

Bonus - Recycling

Evaluation of the following command:

```
filter(gapminder, country == c("Rwanda", "Afghanistan"))
```

```
# A tibble: 12 x 6
   country     continent  year lifeExp      pop gdpPercap
   <fct>       <fct>     <int>   <dbl>    <int>     <dbl>
 1 Afghanistan Asia       1957    30.3  9240934      821.
 2 Afghanistan Asia       1967    34.0 11537966      836.
 3 Afghanistan Asia       1977    38.4 14880372      786.
 4 Afghanistan Asia       1987    40.8 13867957      852.
 5 Afghanistan Asia       1997    41.8 22227415      635.
 6 Afghanistan Asia       2007    43.8 31889923      975.
 7 Rwanda      Africa     1952    40    2534927      493.
 8 Rwanda      Africa     1962    43    3051242      597.
```

```
 9 Rwanda      Africa     1972    44.6  3992121      591.
10 Rwanda      Africa     1982    46.2  5507565      882.
11 Rwanda      Africa     1992    23.6  7290203      737.
12 Rwanda      Africa     2002    43.4  7852401      786.
```

The analyst's goal was to obtain a subset of the `gapminder` dataset, containing data from Rwanda and Afghanistan. However, the output of the above command only returns 12 observations when there should have been 24 (12 observations for each country representing the 12 time points between 1952 and 2007). Each year should have both a Rwanda observation and an Afghanistan observation; however, in our subset, each year is only represented by one country. This suggests that the subsetted data is incomplete, and the analyst did not succeed in their initial goal.

To correctly obtain all data from Rwanda and Afghanistan, we can use the logical "or" operator (denoted as "|" in `dplyr`). The code below will return a dataframe that contains all observations from both Rwanda and Afghanistan.

```r
filter(gapminder, country == "Rwanda" | country == "Afghanistan")
```

```
# A tibble: 24 x 6
   country     continent  year lifeExp      pop gdpPercap
   <fct>       <fct>     <int>   <dbl>    <int>     <dbl>
 1 Afghanistan Asia       1952    28.8  8425333      779.
 2 Afghanistan Asia       1957    30.3  9240934      821.
 3 Afghanistan Asia       1962    32.0 10267083      853.
 4 Afghanistan Asia       1967    34.0 11537966      836.
 5 Afghanistan Asia       1972    36.1 13079460      740.
 6 Afghanistan Asia       1977    38.4 14880372      786.
 7 Afghanistan Asia       1982    39.9 12881816      978.
 8 Afghanistan Asia       1987    40.8 13867957      852.
 9 Afghanistan Asia       1992    41.7 16317921      649.
10 Afghanistan Asia       1997    41.8 22227415      635.
# ... with 14 more rows
```

From this output, we see that we are left with a dataframe of the correct dimensions (24 observations) with all data from Rwanda and Afghanistan between 1952 and 2007.