Child_Mortality_Rate_NCao

October 27, 2018

1 Project: Child Mortality Rate

1.1 Table of Contents

Introduction

In this project, we are interested in finding out the trend in child mortality in the world for the year 2010. More specifically, we would like to answer the following questions:

1) Is there a stark difference regarding child mortality across different regions in the world?
2) Is improved sanitation associated with a reduction in child mortality?
3) Does government spending on health negatively correlate with child mortality?
4) Is there a negative correlation between life expectancy and child mortality?

With these questions, one dependent variable (child mortality) and three independent variables (improved sanitation, government spending on health, and life expectancy) are identified.

In [505]:
```
# First, import necessary packages for data wrangling and data visualization
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import scipy.stats as stats
from sklearn import linear_model
import statsmodels.api as sm
%matplotlib inline
```

Data Wrangling

To prepare for the data analysis process, five sets of data from the Gapminder website have been downloaded. They are: + Child mortality rate + Improved sanitation proportion + Health spending (Government spending on health) + Life expectancy + Geography

In the data cleaning process, these data sets will be merged and the final dataset will comprise the desired year (2010), all the world's main regions, and the interested variables (1 dependent and 3 independent variables previously stated) to answer the aforementioned four questions.

1.1.1 Data exploration

First, we will load all the necessary datasets, inspect data types, and look for instances of missing data. We will perform this one dataset at a time. Since we are only interested in the year 2010, we will filter all the datasets to reflect variables for this particular year.

1) Child mortality Child mortality dataset comprises data that indicates the number of deaths per 1000 live births per year for countries in different regions on Earth.

```
In [506]: # Load data and take a look at the first few lines
          child_mortality = pd.read_csv('child_mortality.csv')
          child_mortality.head(3) # See the first three lines
```

```
Out[506]:            geo   1800   1801   1802   1803   1804   1805   1806   1807   1808  \
          0  Afghanistan  469.0  469.0  469.0  469.0  469.0  469.0  470.0  470.0  470.0
          1      Albania  375.0  375.0  375.0  375.0  375.0  375.0  375.0  375.0  375.0
          2      Algeria  460.0  460.0  460.0  460.0  460.0  460.0  460.0  460.0  460.0

             ...   2009  2010  2011  2012  2013  2014  2015  2016  2017  2018
          0  ...   94.1  90.2  86.4  82.8  79.3  76.1  73.2  70.4  68.2  65.9
          1  ...   17.2  16.6  16.0  15.4  14.9  14.4  14.0  13.5  13.3  12.9
          2  ...   28.3  27.3  26.6  26.1  25.8  25.6  25.5  25.2  23.9  23.1

          [3 rows x 220 columns]
```

```
In [507]: # See the summary of our data. We can see that there are 193 countries
              # and the period involved is 1800 to 2018.
              # The data types (1 object for countries and 219 for child mortality rate) are a
          child_mortality.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 193 entries, 0 to 192
Columns: 220 entries, geo to 2018
dtypes: float64(219), object(1)
memory usage: 331.8+ KB
```

Filter the dataset to the year '2010' and check for missing value. There is none.

```
In [508]: # Get the two columns needed for our new dataset:
              # 'geo' for countries and '2010' for our year of interest
          year_cm = ['geo','2010']

          child_mortality = child_mortality[year_cm]

          # Check for missing values. This returns the total number of missing values.
              # There is none in this case.
          child_mortality.isnull().sum()
```

```
Out[508]: geo     0
          2010    0
          dtype: int64
```

```
In [509]: # Double check to see the dimension of our new dataset. There are 193 rows (countrie
              # two columns (country name and child mortality rate in 2010)
          child_mortality.shape
```

```
Out[509]: (193, 2)
```

```
In [510]: # Take a look at the first few rows for the new dataset to make sure everything look
          child_mortality.head(3)
```

```
Out[510]:            geo  2010
          0  Afghanistan  90.2
          1      Albania  16.6
          2      Algeria  27.3
```

Now, we have the filtered data with countries and the child mortality rate for the year 2010, as we wished.

2) Geography The first question is about child mortality difference in various regions of the world; therefore, the regions that countries are part of are to be incorporated into the final clean dataset. We will use the dataset 'geography.csv' which includes names and regions of world's countries.

```
In [511]: # Read in geography
          geography = pd.read_csv('geography.csv')

          # Take a look at the first three lines to familiarize ourselves with this dataset
          geography.head(3)
```

```
Out[511]:    geo         name four_regions eight_regions                six_regions  \
          0  afg  Afghanistan         asia     asia_west                 south_asia
          1  alb      Albania       europe   europe_east        europe_central_asia
          2  dza      Algeria       africa  africa_north  middle_east_north_africa

            members_oecd_g77  Latitude  Longitude UN member since  \
          0              g77      33.0       66.0      19/11/1946
          1           others      41.0       20.0      14/12/1955
          2              g77      28.0        3.0       8/10/1962

                    World bank region World bank income group 2017
          0                South Asia                   Low income
          1        Europe & Central Asia          Upper middle income
          2  Middle East & North Africa          Upper middle income
```

There are a few types of region classification involved. Let's explore the unique values for a few interested regions.

In [512]:
```
# df['column'].unique() will return all the unique values for the filtered column
# Let's apply '.unique()' to get the unique values for each region type.

# Get the unique regions in 'eight_regions' column
geography['eight_regions'].unique()
```

Out[512]:
```
array(['asia_west', 'europe_east', 'africa_north', 'europe_west',
       'africa_sub_saharan', 'america_north', 'america_south',
       'east_asia_pacific'], dtype=object)
```

In [513]:
```
# Get the unique regions in 'six_regions' column
geography['six_regions'].unique()
```

Out[513]:
```
array(['south_asia', 'europe_central_asia', 'middle_east_north_africa',
       'sub_saharan_africa', 'america', 'east_asia_pacific'], dtype=object)
```

In [514]:
```
# Get the unique regions in 'World bank income group 2017' column
geography['World bank income group 2017'].unique()
```

Out[514]:
```
array(['Low income', 'Upper middle income', 'High income',
       'Lower middle income', nan], dtype=object)
```

In [515]:
```
# # Get the unique regions in 'World bank region' column
geography['World bank region'].unique()
```

Out[515]:
```
array(['South Asia', 'Europe & Central Asia', 'Middle East & North Africa',
       'Sub-Saharan Africa', 'Latin America & Caribbean',
       'East Asia & Pacific', 'North America', nan], dtype=object)
```

From the above result, let's filter the dataset to zoom in onto specific regions of interest and check for missing values.

In [516]:
```
# Filter out our regions of interest from 'geography.'
    # We are interested in all regions except for 'World bank region'
regions = geography[['name', 'four_regions', 'eight_regions',
                     'six_regions', 'World bank income group 2017']]

# Check for missing value. This should give us the count of missing values in each c
regions.isnull().sum()
```

Out[516]:
```
name                            0
four_regions                    0
eight_regions                   0
six_regions                     0
World bank income group 2017    1
dtype: int64
```

We have one missing value. Let's see which country has missing value for 'World bank income group 2017'

```
In [517]: # Utilize 'np.where()' and chain with 'is.na()' to return the index of missing value
              # in the 'World bank income group 2017' column
          # Note: We follow one of the suggestions from this link
          # https://stackoverflow.com/questions/14016247/
              # find-integer-index-of-rows-with-nan-in-pandas-dataframe
          np.where(regions['World bank income group 2017'].isna())

Out[517]: (array([72]),)

In [518]: # Explore the missing data
          regions.iloc[72]

Out[518]: name                                                 Holy See
          four_regions                                           europe
          eight_regions                                     europe_west
          six_regions                                europe_central_asia
          World bank income group 2017                              NaN
          Name: 72, dtype: object
```

Holy See is not a country (https://www.worldatlas.com/articles/what-is-the-difference-between-vatican-city-and-the-holy-see.html). So eventually, when we merge the dataframe 'regions' to our dataset, it will get dropped. We do not have to do anything about it now.

3) Health Spending This dataset shows the goverment expenditure on health per capita in USD. Let's read in the data.

```
In [519]: # Read in the data
          health_spending = pd.read_csv('health_spending.csv')

          # Explore the first few lines
          health_spending.head(3)

Out[519]:   Per capita government expenditure on health at average exchange rate (US$)  \
          0                                           Abkhazia
          1                                        Afghanistan
          2                              Akrotiri and Dhekelia

             1995  1996  1997  1998  1999  2000  2001      2002      2003     2004  \
          0   NaN   NaN   NaN   NaN   NaN   NaN   NaN       NaN       NaN      NaN
          1   NaN   NaN   NaN   NaN   NaN   NaN   NaN  0.832643  1.250118  1.61416
          2   NaN   NaN   NaN   NaN   NaN   NaN   NaN       NaN       NaN      NaN

                 2005      2006      2007      2008      2009      2010
          0       NaN       NaN       NaN       NaN       NaN       NaN
          1  2.525066  2.813779  3.503426  3.744613  3.908887  4.390408
          2       NaN       NaN       NaN       NaN       NaN       NaN
```

Filter the data to the year 2010 and check for missing values. Prior to filtering, we should change the first column name for readability.

```
In [520]: # Change first column name to 'Expenditure (USD)' for readability
          health_spending.rename(
          columns = {'Per capita government expenditure on health at average exchange rate (US$
                     'Expenditure (USD)'},
          inplace = True)

          # Filter data for year 2010. Subset only two columns 'Expenditure (USD)' for country
              # and '2010' for health spending values
          cols_hs = ['Expenditure (USD)','2010']
          health_spending = health_spending[cols_hs]

In [521]: # Count how many missing values in the new dataset
          health_spending.isnull().sum()

Out[521]: Expenditure (USD)     0
          2010                 78
          dtype: int64
```

There are 78 missing values out of the 265 countries, which is odd since there are only 193 countries. We will explore this at further depth in the data cleaning process.

```
In [522]: # Get the dimension of the new dataset. There are 265 rows (countries) and two colum
              # (health spending values and country name)
          health_spending.shape

Out[522]: (265, 2)
```

4) Improved Sanitation This dataset shows the proportion of the population in each country using improved sanitation facilities over the years.

```
In [523]: # Read in the data
          improved_sanitation = pd.read_csv('improved_sanitation.csv', sep=',', engine='python

          # Note: we choose to include 'sep' and 'engine' because reading in the file the regu
              # gave errors due to encoding. To be able to read in the file,
              #we decided to follow the advice from this page
              # https://stackoverflow.com/questions/12468179/
                  # unicodedecodeerror-utf8-codec-cant-decode-byte-0x9c

          # Check first three lines
          improved_sanitation.head(3)

Out[523]:   Proportion of the population using improved sanitation facilities, total  \
          0                                            Abkhazia
          1                                         Afghanistan
          2                               Akrotiri and Dhekelia

             1990  1991  1992  1993  1994  1995  1996  1997  1998  ...   2001  2002  \
          0   NaN   NaN   NaN   NaN   NaN   NaN   NaN   NaN   NaN  ...    NaN   NaN
```

```
1    NaN  29.0  29.0  29.0  29.0  29.0  29.0  30.0  30.0  ...   32.0  33.0
2    NaN   NaN   NaN   NaN   NaN   NaN   NaN   NaN   NaN  ...    NaN   NaN

   2003  2004  2005  2006  2007  2008  2009  2010
0   NaN   NaN   NaN   NaN   NaN   NaN   NaN   NaN
1  34.0  34.0  35.0  35.0  37.0  37.0  37.0  37.0
2   NaN   NaN   NaN   NaN   NaN   NaN   NaN   NaN

[3 rows x 22 columns]
```

Filter the data to the year 2010 and check for missing values. Just like before, we will change the first column name to 'Country' for better readability.

In [524]:
```python
# Change one column name for readability
improved_sanitation.rename(
columns = {'Proportion of the population using improved sanitation facilities, total
inplace = True)

# Filter our data to include country name and values for improved sanitation
cols_is = ['Country', '2010']
improved_sanitation = improved_sanitation[cols_is]
```

In [525]:
```python
# Check for missing values
improved_sanitation.isnull().sum()
```

Out[525]:
```
Country      0
2010       104
dtype: int64
```

There are 104 missing values out of the 275 countries, which is also odd since there are only 193 countries. We will take the same approach and look at this in more detail in the data cleaning process.

In [526]:
```python
# Get the dimension of the newly filtered dataset. There are 275 rows (countries)
    # and two columns (Country and improved sanitation proportion for 2010)
improved_sanitation.shape
```

Out[526]:
```
(275, 2)
```

5) Life expectancy Life expectancy indicates the average time (in number of years) a population is expected to live.

In [527]:
```python
# Read in the data
life_expectancy = pd.read_csv('life_expectancy.csv', sep = ',', engine = 'python')

# Note: we choose to include 'sep' and 'engine' because reading in the file the regu
    # gave errors due to encoding. To be able to read in the file,
    #we decided to follow the advice from this page
    # https://stackoverflow.com/questions/12468179/
```

```
    # unicodedecodeerror-utf8-codec-cant-decode-byte-0x9c

# Check the first three lines
life_expectancy.head(3)
```

```
Out[527]:         Life expectancy   1800  1801   1802   1803   1804   1805   1806  \
          0              Abkhazia    NaN   NaN    NaN    NaN    NaN    NaN    NaN
          1           Afghanistan  28.21  28.2  28.19  28.18  28.17  28.16  28.15
          2  Akrotiri and Dhekelia    NaN   NaN    NaN    NaN    NaN    NaN    NaN

              1807   1808  ...   2007  2008  2009  2010  2011  2012  2013  2014  2015  \
          0    NaN    NaN  ...    NaN   NaN   NaN   NaN   NaN   NaN   NaN   NaN   NaN
          1  28.14  28.13  ...   52.4  52.8  53.3  53.6  54.0  54.4  54.8  54.9  53.8
          2    NaN    NaN  ...    NaN   NaN   NaN   NaN   NaN   NaN   NaN   NaN   NaN

              2016
          0    NaN
          1  52.72
          2    NaN

          [3 rows x 218 columns]
```

Filter the data to the year 2010 and check for missing values.

```
In [528]: # Filter the data, choosing to keep only two columns that show country names
              # and life expectancy for 2010
          cols_le = ['Life expectancy', '2010']
          life_expectancy = life_expectancy[cols_le]
```

```
In [529]: # Count the total missing values
          life_expectancy.isnull().sum()
```

```
Out[529]: Life expectancy    739
          2010               791
          dtype: int64
```

There are 739 missing values out of the 999 countries, which poses doubts since there are only 193 countries. Also, there are 791 missing values in the column ’2010’. Like before, let’s take the same approach and look at this in more detail in the data cleaning process.

```
In [530]: # Get the dimension for the newly filtered data shape. There are 999 values for coun
              # and two columns (country namd and life expectancy for 2010)
          life_expectancy.shape
```

```
Out[530]: (999, 2)
```

Data Cleaning
It’s quite clear that the data is nowhere near the quality we need to perform Exploratory Data Analysis. Therefore, we have to make sure it is clean first. There are three steps we will take in data cleaning. + First, we will rename the columns in a systematic approach. We want to make sure the column names are short and indicative of the content they convey. + Second, we will merge our five data sets. + Third, we will impute missing values for each variable in the final dataset. We will approach each case individually.

Step 1: Renaming Columns First of all, let's rename the first column in each data set to 'Country' and the second column to the corresponding variable.

In [531]:
```
# Improved Sanitation

# Check the column names
improved_sanitation.columns
```

Out[531]:
```
Index(['Country', '2010'], dtype='object')
```

In [532]:
```
# Rename the two columns to 'Country' and 'Improved Sanitation Proportion'
improved_sanitation.columns = ['Country', 'Improved Sanitation Proportion']

# Check the first few lines of the new dataframe
improved_sanitation.head(3) # good to go
```

Out[532]:

	Country	Improved Sanitation Proportion
0	Abkhazia	NaN
1	Afghanistan	37.0
2	Akrotiri and Dhekelia	NaN

In [533]:
```
# Health Spending

# Check the column names
health_spending.columns
```

Out[533]:
```
Index(['Expenditure (USD)', '2010'], dtype='object')
```

In [534]:
```
# Rename the two columns to 'Country' and 'Government Expenditure on Health (USD)'
health_spending.columns = ['Country', 'Government Expenditure on Health (USD)']

# Check the first few lines of the new dataframe
health_spending.head(3) # good to go
```

Out[534]:

	Country	Government Expenditure on Health (USD)
0	Abkhazia	NaN
1	Afghanistan	4.390408
2	Akrotiri and Dhekelia	NaN

In [535]:
```
# Child mortality

# Check the column names
child_mortality.columns
```

Out[535]:
```
Index(['geo', '2010'], dtype='object')
```

In [536]:
```
# Rename the two columns to 'Country' and 'Child Mortality Rate'
child_mortality.columns = ['Country', 'Child Mortality Rate']

# Check the first few lines of the new dataframe
child_mortality.head(3) # good to go
```

```
Out[536]:        Country  Child Mortality Rate
          0  Afghanistan                  90.2
          1      Albania                  16.6
          2      Algeria                  27.3
```

```
In [537]: # Life expectancy

          # Check the column names
          life_expectancy.columns
```

```
Out[537]: Index(['Life expectancy', '2010'], dtype='object')
```

```
In [538]: # Rename the two columns to 'Country' and 'Life Expectancy'
          life_expectancy.columns = ['Country', 'Life Expectancy']

          # Check the first few lines of the new dataframe
          life_expectancy.head(3) # good to go
```

```
Out[538]:                   Country  Life Expectancy
          0                Abkhazia              NaN
          1             Afghanistan             53.6
          2  Akrotiri and Dhekelia              NaN
```

```
In [539]: # Regions

          # Check the column names
          regions.columns
```

```
Out[539]: Index(['name', 'four_regions', 'eight_regions', 'six_regions',
                 'World bank income group 2017'],
                dtype='object')
```

According to this link (https://datahelpdesk.worldbank.org/knowledgebase/articles/906519-world-bank-country-and-lending-groups), the World Bank classifies the world into 7 regions; therefore, we will drop the 'six_regions' column and keep the rest: four regions for overall analysis, eight regions for more granular analysis, and world bank income group in case we want to have further analysis.

```
In [540]: # Use 'del' to delete the 'six_regions' column
          del regions['six_regions']
```

```
In [541]: # Check the column names again, we should have no 'six_regions' column
          regions.columns
```

```
Out[541]: Index(['name', 'four_regions', 'eight_regions',
                 'World bank income group 2017'],
                dtype='object')
```

```
In [542]: # Rename the four columns in 'regions' to
              # 'Country', 'Four Regions','Eight Regions', 'World Bank Income Group'
          regions.columns = ['Country', 'Four Regions','Eight Regions', 'World Bank Income Grou

          # Check the first few lines of the new dataframe
          regions.head(3) # good to go
```

```
Out[542]:        Country Four Regions Eight Regions World Bank Income Group
          0  Afghanistan         asia     asia_west              Low income
          1      Albania       europe   europe_east     Upper middle income
          2      Algeria       africa  africa_north     Upper middle income
```

Step 2: Data merging Before merging the datasets, let's look at the missing value pattern and gather all the necessary information to prepare for the missing data imputation process.

As noted above, the three datasets: "health_spending" ,"improved_sanitation", and "life_expectancy" have missing values. Our initial guess is it has something to do with the countries as it seems there are many more countries than the actual number of countries in the world. To look further into this, we will utilize the '.nunique()' method to explore these datasets.

```
In [543]: # Get the total count of unique values, in this case unique countries
          improved_sanitation['Country'].nunique()
```

```
Out[543]: 275
```

```
In [544]: # Check the first few lines
          improved_sanitation.head(3)
```

```
Out[544]:                  Country  Improved Sanitation Proportion
          0               Abkhazia                             NaN
          1            Afghanistan                            37.0
          2  Akrotiri and Dhekelia                             NaN
```

```
In [545]: # Check the last few lines
          improved_sanitation.tail(3)
```

```
Out[545]:              Country  Improved Sanitation Proportion
          272   Chinese Taipei                             NaN
          273  Saint Eustatius                             NaN
          274             Saba                             NaN
```

Let's compare what was just being found (the unique number of countries) with the unique number of countries in 'regions'

```
In [546]: # Get the total number of unique countries in 'regions'
          regions['Country'].nunique()
```

```
Out[546]: 197
```

```
In [547]: # Check the first few lines
          regions.head(3)
```

Out[547]:
```
       Country Four Regions Eight Regions World Bank Income Group
0  Afghanistan         asia     asia_west            Low income
1      Albania       europe   europe_east   Upper middle income
2      Algeria       africa  africa_north   Upper middle income
```

In [548]:
```
# Check the last few lines
regions.tail(3)
```

Out[548]:
```
         Country Four Regions       Eight Regions World Bank Income Group
194       Zambia       africa  africa_sub_saharan     Lower middle income
195     Zimbabwe       africa  africa_sub_saharan              Low income
196  South Sudan       africa  africa_sub_saharan              Low income
```

It is interesting that there are 197 countries; eventually, we want to look at data for only 193 countries that are member states of the United Nations. But this does not seem to be a big issue; we can revisit this later. The important point is there are obviously regions included in the 'improved_sanitation' dataset that are not actual countries. For example, 'Bonaire' is a municipality belonging to the Netherlands (https://en.wikipedia.org/wiki/Bonaire) while Sark belongs to the UK (https://en.wikipedia.org/wiki/Sark). This is very likely the reason why "health_spending" ,"improved_sanitation", and "life_expectancy" have many more observations in the 'Country' column. Before proceeding further, it's important to keep in mind that 'life_expectancy' has 999 values in the column 'Country', so there might be something else going on. Let's take a look.

In [549]:
```
# Get the total number of unique values in the column 'Country'
    # in the 'life_expectancy' dataframe
life_expectancy['Country'].nunique()
```

Out[549]: 260

Interesting, there are only 260 unique values. So there must be repeated values in the 999 values of the column 'Country,' the issue might not be too hard to solve, after all. Let's explore 'life_expectancy' a bit further.

In [550]:
```
# Life expectancy

# Check the first few lines
life_expectancy.head(3)
```

Out[550]:
```
                 Country  Life Expectancy
0               Abkhazia              NaN
1            Afghanistan             53.6
2  Akrotiri and Dhekelia              NaN
```

In [551]:
```
# Check the last few lines
life_expectancy.tail(3)
```

Out[551]:
```
    Country  Life Expectancy
996     NaN              NaN
997     NaN              NaN
998     NaN              NaN
```

In [552]:
```
# Count the total number of missing values
life_expectancy['Country'].isnull().sum()
```

Out[552]: 739

There are 739 missing values in the column 'Country' alone. Since the country names cannot be imputed, let's drop them and look at the remaining values.

In [553]:
```
# Drop missing values in the column 'Country' in 'life_expectancy.'
  # Use 'inplace = True' to make the changes permanent
life_expectancy['Country'].dropna(inplace = True)
```

In [554]:
```
# Now, let's remind ourselves how many unique countries there are in the 'Country' c
life_expectancy['Country'].nunique()
```

Out[554]: 260

In [555]:
```
# Similarly, double check to see how many unique countries in the 'Life Expectancy'
life_expectancy['Life Expectancy'].nunique()
```

Out[555]: 159

In [556]:
```
# Take a look at the first few lines
life_expectancy.head(3)
```

Out[556]:

	Country	Life Expectancy
0	Abkhazia	NaN
1	Afghanistan	53.6
2	Akrotiri and Dhekelia	NaN

Now, we have similar missing issue across all the three datasets. Upon further investigation, we will go with 193 countries (https://onestep4ward.com/how-many-countries-in-the-world/). The reasonable way to drop the regions-mistakenly-considered-countries in 'life_expectancy', 'improved_sanitation', 'regions', and 'health_spending' are to left join these to 'child_mortality' (child_mortality being the left dataframe/ table). But first, let's make sure 'child_mortality' has all the 193 unique values for 'Country.'

In [557]:
```
# Count the unique values in 'Country' column for 'child_mortality'
child_mortality['Country'].nunique()
```

Out[557]: 193

In [558]:
```
# Take a look at the first few lines
child_mortality.head(3)
```

Out[558]:

	Country	Child Mortality Rate
0	Afghanistan	90.2
1	Albania	16.6
2	Algeria	27.3

```
In [559]: # Take a look at the last few lines
          child_mortality.tail(3)

Out[559]:       Country  Child Mortality Rate
          190     Yemen                  56.3
          191    Zambia                  83.1
          192  Zimbabwe                  89.9
```

Yes! It has 193 countries, just as expected. Now, let's join all the five datasets together using pd.merge(). This will drop the non-countries, assuming all other countries are spelled exactly like the countries in 'child_mortality'. We can investigate further if we run into issues. We are naming the joined datasets 'test + a number' first and will convert it into a more meaningful name once we take care of all the arisen issues.

First, let's left join health_spending to child_mortality

```
In [560]: # Left join 'health_spending' to 'child_mortality' on the key 'Country' in both data
          test1 = pd.merge(child_mortality, health_spending, left_on = 'Country',
                                          right_on = 'Country', how = 'left')

In [561]: # Test to make sure the resulting 'test1' dataframe has 193 unique countries
          test1['Country'].nunique()

Out[561]: 193

In [562]: # Check the first three rows
          test1.head(3) # It looks fine

Out[562]:        Country  Child Mortality Rate  Government Expenditure on Health (USD)
          0  Afghanistan                  90.2                                4.390408
          1      Albania                  16.6                               94.023613
          2      Algeria                  27.3                              138.840923
```

So far so good. Let's continue to merge the resulting dataset with improved_sanitation.

```
In [563]: # Left join 'improved_sanitation' to 'test1' on the key 'Country' in both dataframes
          test2 = pd.merge(test1, improved_sanitation, left_on = 'Country',
                                          right_on = 'Country', how ='left')

In [564]: # Test to make sure the resulting 'test2' dataframe has 193 unique countries
          test2['Country'].nunique() # It looks fine

Out[564]: 193

In [565]: # Check the first few lines
          test2.head(3)

Out[565]:        Country  Child Mortality Rate  Government Expenditure on Health (USD)  \
          0  Afghanistan                  90.2                                4.390408
          1      Albania                  16.6                               94.023613
          2      Algeria                  27.3                              138.840923
```

```
   Improved Sanitation Proportion
0                            37.0
1                            94.0
2                            95.0
```

Proceed to left join life_expectancy to test2.

```
In [566]: # Left join 'life_expectancy' to 'test2' on the key 'Country' in both dataframes
          test3 = pd.merge(test2, life_expectancy, left_on = 'Country',
                                          right_on = 'Country', how = 'left')

In [567]: # Test to make sure the resulting 'test3' dataframe has 193 unique countries
          test3['Country'].nunique()

Out[567]: 193

In [568]: # Check the first few lines
          test3.head(3)

Out[568]:        Country  Child Mortality Rate  Government Expenditure on Health (USD)  \
          0  Afghanistan                  90.2                                4.390408
          1      Albania                  16.6                               94.023613
          2      Algeria                  27.3                              138.840923

             Improved Sanitation Proportion  Life Expectancy
          0                            37.0             53.6
          1                            94.0             77.2
          2                            95.0             76.0
```

Last but not least, merge the resulting dataset with regions.

```
In [569]: # Left join 'regions' to 'test3' on the key 'Country' in both dataframes
          test4 = pd.merge(test3, regions, left_on = 'Country',
                                          right_on = 'Country', how = 'left')

In [570]: # Test to make sure the resulting 'test4' dataframe has 193 unique countries
          test4['Country'].nunique()

Out[570]: 193

In [571]: # Check the first few lines
          test4.head(3)

Out[571]:        Country  Child Mortality Rate  Government Expenditure on Health (USD)  \
          0  Afghanistan                  90.2                                4.390408
          1      Albania                  16.6                               94.023613
          2      Algeria                  27.3                              138.840923

             Improved Sanitation Proportion  Life Expectancy Four Regions Eight Regions  \
```

```
0                             37.0             53.6         asia     asia_west
1                             94.0             77.2       europe   europe_east
2                             95.0             76.0       africa  africa_north

  World Bank Income Group
0              Low income
1     Upper middle income
2     Upper middle income
```

So far, we are yet to encounter an issue. We will give 'test4' a more meaningful name and look into imputing missing value for each column (Step 3).

```
In [572]: project = test4
```

1.1.2 Step 3: Missing Data Imputation

Let's take a look at our merged dataset to count how many missing values we have to deal with.

```
In [573]: # Summary of 'project' dataframe
          project.info()

<class 'pandas.core.frame.DataFrame'>
Int64Index: 193 entries, 0 to 192
Data columns (total 8 columns):
Country                                  193 non-null object
Child Mortality Rate                     193 non-null float64
Government Expenditure on Health (USD)   185 non-null float64
Improved Sanitation Proportion           166 non-null float64
Life Expectancy                          186 non-null float64
Four Regions                             193 non-null object
Eight Regions                            193 non-null object
World Bank Income Group                  193 non-null object
dtypes: float64(4), object(4)
memory usage: 13.6+ KB
```

It's worth noting that the data types look good. Now, et's count the number of missing values.

```
In [574]: # Number of missing values in column 'Government Expenditure on Health (USD)'
          project['Government Expenditure on Health (USD)'].isnull().sum()

Out[574]: 8

In [575]: # Number of missing values in column 'Improved Sanitation Proportion'
          project['Improved Sanitation Proportion'].isnull().sum()

Out[575]: 27

In [576]: # Number of missing values in column 'Life Expectancy'
          project['Life Expectancy'].isnull().sum()
```

Out[576]: 7

There are: > + 8 missing values in 'Government Expenditure on Health (USD)' > + 27 in 'Improved Sanitation Proportion' > + 7 in 'Life Expectancy'

Since each row represents a country, and we have data for many years (from the original dataset), we can impute missing values by taking the average of the 2 years prior (2008 - 2009) or the average of one year prior (2009) and one year after (2011), depending on the availability of the data. Let's look at each case carefully.

i. Government Expenditure on Health (USD)

```
In [577]: # Get the index of missing values
          # Note: We follow one of the suggestions from this link
          # https://stackoverflow.com/questions/14016247/
              # find-integer-index-of-rows-with-nan-in-pandas-dataframe
          index_expenditure = np.where(project['Government Expenditure on Health (USD)'].isna(

          index_expenditure
```

```
Out[577]: (array([ 72, 108, 122, 125, 130, 154, 157, 192]),)
```

Since the index of the original dataset is different from the index of the new data ('project)', let's extract the corresponding country names that have misisng values before proceeding further.

```
In [578]: # Return the country with missing value for index 72
          project.iloc[72,]['Country']
```

```
Out[578]: 'Honduras'
```

```
In [579]: # Return the country with missing value for index 108
          project.iloc[108,]['Country']
```

```
Out[579]: 'Mexico'
```

```
In [580]: # Return the country with missing value for index 122
          project.iloc[122,]['Country']
```

```
Out[580]: 'Nicaragua'
```

```
In [581]: # Return the country with missing value for index 125
          project.iloc[125,]['Country']
```

```
Out[581]: 'North Korea'
```

```
In [582]: # Return the country with missing value for index 130
          project.iloc[130,]['Country']
```

```
Out[582]: 'Palestine'
```

```
In [583]: # Return the country with missing value for index 154
          project.iloc[154,]['Country']
```

```
Out[583]: 'Somalia'
```

```
In [584]: # Return the country with missing value for index 157
          project.iloc[157,]['Country']
```

```
Out[584]: 'South Sudan'
```

```
In [585]: # Return the country with missing value for index 192
          project.iloc[192,]['Country']
```

```
Out[585]: 'Zimbabwe'
```

Now, let's read in the orignginal government expenditure dataset for missing data imputation.

```
In [586]: # Read in original government expenditure
          health_spending_original = pd.read_csv('health_spending.csv')

          # Check the first few rows
          health_spending_original.head(3)
```

```
Out[586]:   Per capita government expenditure on health at average exchange rate (US$)  \
          0                                             Abkhazia
          1                                          Afghanistan
          2                                 Akrotiri and Dhekelia

             1995  1996  1997  1998  1999  2000  2001      2002      2003     2004  \
          0   NaN   NaN   NaN   NaN   NaN   NaN   NaN       NaN       NaN      NaN
          1   NaN   NaN   NaN   NaN   NaN   NaN   NaN  0.832643  1.250118  1.61416
          2   NaN   NaN   NaN   NaN   NaN   NaN   NaN       NaN       NaN      NaN

                 2005      2006      2007      2008      2009      2010
          0       NaN       NaN       NaN       NaN       NaN       NaN
          1  2.525066  2.813779  3.503426  3.744613  3.908887  4.390408
          2       NaN       NaN       NaN       NaN       NaN       NaN
```

```
In [587]: # Look at the columns of the dataset to see the range of values
          health_spending_original.columns
```

```
Out[587]: Index(['Per capita government expenditure on health at average exchange rate (US$)',
                 '1995', '1996', '1997', '1998', '1999', '2000', '2001', '2002', '2003',
                 '2004', '2005', '2006', '2007', '2008', '2009', '2010'],
                dtype='object')
```

Since 2010 is the last year in the dataset, we will impute missing data by taking the average of the 2 years prior to 2010 (2008 - 2009). The first column name will be changed for better readability.

```
In [588]: # Change the first column name to 'Country'
          health_spending_original.rename(
          columns = {'Per capita government expenditure on health at average exchange rate (US$
          inplace = True)
```

```
In [589]: # Filter the original data to get necessary columns: 'Country' and three years: 2008
          cols = ['Country','2008', '2009', '2010']

          health_spending_NA_imputation = health_spending_original[cols]

In [590]: # Check the filtered dataframe
          health_spending_NA_imputation.head(3)

Out[590]:                   Country      2008      2009      2010
          0                Abkhazia       NaN       NaN       NaN
          1             Afghanistan  3.744613  3.908887  4.390408
          2  Akrotiri and Dhekelia       NaN       NaN       NaN
```

Now, we will impute missing data. First, filter the rows corresponding with the eight countries extracted above, then begin imputation.

```
In [591]: # https://stackoverflow.com/questions/12096252/
              # use-a-list-of-values-to-select-rows-from-a-pandas-dataframe

          # Get a list of these countries and use it to filter the corresponding rows
          country_expenditure_NA = ['Honduras', 'Mexico', 'Nicaragua', 'North Korea',
                                    'Palestine', 'Somalia','South Sudan', 'Zimbabwe']
          health_spending_NA_imputation[health_spending_NA_imputation['Country'].isin(country_e

Out[591]:          Country        2008        2009  2010
          97      Honduras   70.818311   89.174442   NaN
          116  North Korea         NaN         NaN   NaN
          144       Mexico  280.800163  253.196458   NaN
          162    Nicaragua   57.708726   56.963809   NaN
          208      Somalia         NaN         NaN   NaN
          257     Zimbabwe         NaN         NaN   NaN
          259  South Sudan         NaN         NaN   NaN
```

From the above result, we can see that we can impute missing values for Honduras, Mexico, and Nicaragua. We will drop 4 countries: North Korea, Somalia, Zimbabwe, and South Sudan due to the fact that these countries do not have spending data for previous years. Also, as there is no data for Palestine, we will drop this country.

- Honduras

```
In [592]: # Get the row corresponding to Honduras from the filtered dataframe
          honduras_row = health_spending_NA_imputation.loc[health_spending_NA_imputation['Coun

In [593]: # Double check to make sure the result is what we want
          honduras_row

Out[593]:      Country       2008       2009  2010
          97  Honduras  70.818311  89.174442   NaN
```

```
In [594]: # Replace the missing value for 2010 by taking the average of health spending in 200
               # We use '.fillna()' chained with '.mean()' for this task
               # 'inplace = True' makes the change permanent
          honduras_row['2010'].fillna(honduras_row.mean(axis = 1), inplace = True)

          # Double check to see if the missing value is filled
          honduras_row # It looks reasonable and good
```

```
/Users/Pain_de_mie/anaconda3/lib/python3.6/site-packages/pandas/core/generic.py:5430: SettingWi
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/stable/indexing.html
  self._update_inplace(new_data)
```

```
Out[594]:      Country       2008       2009       2010
          97  Honduras  70.818311  89.174442  79.996376
```

- Mexico

```
In [595]: # Get the row corresponding to Mexico from the filtered dataframe
          mexico_row = health_spending_NA_imputation.loc[health_spending_NA_imputation['Country

          # Double check to make sure the result is what we want
          mexico_row
```

```
Out[595]:     Country        2008        2009  2010
          144  Mexico  280.800163  253.196458   NaN
```

```
In [596]: # Replace the missing value for 2010 by taking the average of health spending in 200
               # We use '.fillna()' chained with '.mean()' for this task
               # 'inplace = True' makes the change permanent
          mexico_row['2010'].fillna(mexico_row.mean(axis = 1), inplace = True)

          # Double check to see if the missing value is filled
          mexico_row # It looks reasonable and good
```

```
/Users/Pain_de_mie/anaconda3/lib/python3.6/site-packages/pandas/core/generic.py:5430: SettingWi
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/stable/indexing.html
  self._update_inplace(new_data)
```

```
Out[596]:     Country        2008        2009       2010
          144  Mexico  280.800163  253.196458  266.99831
```

- Nicaragua

In [597]:
```
# Get the row corresponding to Nicaragua from the filtered dataframe
nicaragua_row = health_spending_NA_imputation.loc[health_spending_NA_imputation['Cou

# Double check to make sure the result is what we want
nicaragua_row
```

Out[597]:
```
       Country       2008       2009  2010
162  Nicaragua  57.708726  56.963809   NaN
```

In [598]:
```
# Replace the missing value for 2010 by taking the average of health spending in 200
     # We use '.fillna()' chained with '.mean()' for this task
     # 'inplace = True' makes the change permanent
nicaragua_row['2010'].fillna(nicaragua_row.mean(axis = 1), inplace = True)

# Double check to see if the missing value is filled
nicaragua_row # It looks reasonable and good
```

```
/Users/Pain_de_mie/anaconda3/lib/python3.6/site-packages/pandas/core/generic.py:5430: SettingW
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/stable/indexing.htm
  self._update_inplace(new_data)
```

Out[598]:
```
       Country       2008       2009       2010
162  Nicaragua  57.708726  56.963809  57.336267
```

So, before we take care of missing data for other variables, we will: + drop these 5 countries in our 'project' dataset : North Korea, Palestine, Somalia, South Sudan, and Zimbabwe + replace the missing values for 3 countries: 'Honduras', 'Mexico', and 'Nicaragua'

In [599]:
```
# Let's backup the project first
project_backup  = project

# Write it to a csv file
project.to_csv('project_backup.csv')
```

Drop the five aforementioned countries. Even though the index is known, let's double check each case.

In [600]:
```
# Check the first few lines
project.head(2)
```

Out[600]:
```
       Country  Child Mortality Rate  Government Expenditure on Health (USD)  \
0  Afghanistan                  90.2                                4.390408
1      Albania                  16.6                               94.023613

   Improved Sanitation Proportion  Life Expectancy Four Regions Eight Regions  \
0                            37.0             53.6         asia     asia_west
```

```
1                          94.0            77.2       europe   europe_east

  World Bank Income Group
0             Low income
1     Upper middle income
```

In [601]:
```
# Make sure we drop the right country (index 125)
project.loc[project['Country'] == 'North Korea',:]
```

Out[601]:
```
         Country  Child Mortality Rate  \
125  North Korea                  29.5

     Government Expenditure on Health (USD)  Improved Sanitation Proportion  \
125                                     NaN                             80.0

     Life Expectancy Four Regions      Eight Regions World Bank Income Group
125             71.2         asia  east_asia_pacific              Low income
```

In [602]:
```
# Make sure we drop the right country (index 130)
project.loc[project['Country'] == 'Palestine',:]
```

Out[602]:
```
       Country  Child Mortality Rate  Government Expenditure on Health (USD)  \
130  Palestine                  23.0                                     NaN

     Improved Sanitation Proportion  Life Expectancy Four Regions  \
130                             NaN              NaN         asia

    Eight Regions World Bank Income Group
130     asia_west     Lower middle income
```

In [603]:
```
# Make sure we drop the right country (index 154)
project.loc[project['Country'] == 'Somalia',:]
```

Out[603]:
```
     Country  Child Mortality Rate  Government Expenditure on Health (USD)  \
154  Somalia                 159.0                                     NaN

     Improved Sanitation Proportion  Life Expectancy Four Regions  \
154                            23.0             51.6       africa

          Eight Regions World Bank Income Group
154  africa_sub_saharan              Low income
```

In [604]:
```
# Make sure we drop the right country (index 157)
project.loc[project['Country'] == 'South Sudan',:]
```

Out[604]:
```
         Country  Child Mortality Rate  \
157  South Sudan                 113.0

     Government Expenditure on Health (USD)  Improved Sanitation Proportion  \
```

```
157                                   NaN                              NaN

     Life Expectancy Four Regions       Eight Regions World Bank Income Group
157             56.0       africa  africa_sub_saharan              Low income
```

```
In [605]: # Make sure we drop the right country (index 192)
          project.loc[project['Country'] == 'Zimbabwe',:]
```

```
Out[605]:       Country  Child Mortality Rate  Government Expenditure on Health (USD)  \
          192  Zimbabwe                  89.9                                     NaN

               Improved Sanitation Proportion  Life Expectancy Four Regions  \
          192                            40.0             49.1       africa

                    Eight Regions World Bank Income Group
          192  africa_sub_saharan              Low income
```

```
In [606]: # All the indices confirm the countries we need to drop. Let's go ahead and drop them
          project.drop([125,130,154,157,192], inplace = True)
```

```
In [607]: # Check the resulting dataset
          project.shape
```

```
Out[607]: (188, 8)
```

Since five countries were dropped (for Palestine there was no data present), we are now left with 188 countries. Now we will replace the missing values for three countries: 'Honduras', 'Mexico', 'Nicaragua'. We will use the '.at' method to access a single value in a dataframe (https://pandas.pydata.org/pandas-docs/stable/generated/pandas.DataFrame.at.html)

- Honduras

```
In [608]: # Replace missing value corresponding with index 72 for Honduras
              # with the imputed missing data from 'honduras_row', column '2010'
          project.at[72,'Government Expenditure on Health (USD)']= honduras_row['2010']
```

```
In [609]: # Double check to make sure the missing value was replaced correctly
          project.loc[project['Country'] == 'Honduras','Government Expenditure on Health (USD)
```

```
Out[609]: 72    79.996376
          Name: Government Expenditure on Health (USD), dtype: float64
```

- Mexico

```
In [610]: # Replace missing value corresponding with index 108 for Mexico
              # with the imputed missing data from 'mexico_row', column '2010'
          project.at[108,'Government Expenditure on Health (USD)']= mexico_row['2010']
```

```
In [611]: # Double check to make sure the missing value was replaced correctly
          project.loc[project['Country'] == 'Mexico','Government Expenditure on Health (USD)']
```

```
Out[611]: 108    266.99831
          Name: Government Expenditure on Health (USD), dtype: float64
```

- Nicaragua

```
In [612]: # Replace missing value corresponding with index 108 for Mexico
              # with the imputed missing data from 'nicaragua_row', column '2010'
          project.at[122,'Government Expenditure on Health (USD)']= nicaragua_row['2010']
```

```
In [613]: # Double check to make sure the missing value was replaced correctly
          project.loc[project['Country'] == 'Nicaragua','Government Expenditure on Health (USD
```

```
Out[613]: 122    57.336267
          Name: Government Expenditure on Health (USD), dtype: float64
```

Let's utilize the same techniques to fill in missing values for the remaining two columns ('Improved Sanitation Proportion' and 'Life Expectancy'). Before proceeding further, let's take a look at our dataset, we should have no missing values in the 'Government Expenditure on Health (USD)' column.

```
In [614]: # Count total missing values in each column of the 'project' dataset
          project.isnull().sum()
```

```
Out[614]: Country                                    0
          Child Mortality Rate                       0
          Government Expenditure on Health (USD)     0
          Improved Sanitation Proportion            25
          Life Expectancy                            6
          Four Regions                               0
          Eight Regions                              0
          World Bank Income Group                    0
          dtype: int64
```

As expected, there is no missing value in 'Government Expenditure on Health.' Time to impute missing values for the remaining two columns.

ii. Life Expectancy

```
In [615]: # Get the index of missing values
          # Note: We follow one of the suggestions from this link
          # https://stackoverflow.com/questions/14016247/
              # find-integer-index-of-rows-with-nan-in-pandas-dataframe

          index_life_expectancy = np.where(project['Life Expectancy'].isna())
          index_life_expectancy
```

```
Out[615]: (array([111, 118, 128, 141, 156, 175]),)
```

Let's get the names of the countries corresponding to the index values.

```
In [616]: # Take a look at the first few rows to remind us what 'project' looks like first
          project.head(3)
```

```
Out[616]:        Country  Child Mortality Rate  Government Expenditure on Health (USD)  \
          0  Afghanistan                  90.2                                4.390408
          1      Albania                  16.6                               94.023613
          2      Algeria                  27.3                              138.840923

             Improved Sanitation Proportion  Life Expectancy Four Regions Eight Regions  \
          0                            37.0             53.6         asia     asia_west
          1                            94.0             77.2       europe   europe_east
          2                            95.0             76.0       africa  africa_north

            World Bank Income Group
          0              Low income
          1     Upper middle income
          2     Upper middle income
```

```
In [617]: # Return the country with missing value for index 111
          project.iloc[111]['Country']
```

```
Out[617]: 'Monaco'
```

```
In [618]: # Return the country with missing value for index 118
          project.iloc[118]['Country']
```

```
Out[618]: 'Nauru'
```

```
In [619]: # Return the country with missing value for index 128
          project.iloc[128]['Country']
```

```
Out[619]: 'Palau'
```

```
In [620]: # Return the country with missing value for index 141
          project.iloc[141]['Country']
```

```
Out[620]: 'San Marino'
```

```
In [621]: # Return the country with missing value for index 156
          project.iloc[156]['Country']
```

```
Out[621]: 'St. Kitts and Nevis'
```

```
In [622]: # Return the country with missing value for index 175
          project.iloc[175]['Country']
```

```
Out[622]: 'Tuvalu'
```

Now, let's read in the original life expectancy dataset for missing data imputation.

```
In [623]: # Read in the original 'life_expectancy' file
          life_expectancy_original = pd.read_csv('life_expectancy.csv',
                                                  sep = ',', engine = 'python')
          # Check the first few rows
          life_expectancy_original.head(3)
```

```
Out[623]:        Life expectancy   1800  1801   1802   1803   1804   1805   1806  \
          0             Abkhazia    NaN   NaN    NaN    NaN    NaN    NaN    NaN
          1          Afghanistan  28.21  28.2  28.19  28.18  28.17  28.16  28.15
          2  Akrotiri and Dhekelia    NaN   NaN    NaN    NaN    NaN    NaN    NaN

              1807   1808  ...   2007  2008  2009  2010  2011  2012  2013  2014  2015  \
          0    NaN    NaN  ...    NaN   NaN   NaN   NaN   NaN   NaN   NaN   NaN   NaN
          1  28.14  28.13  ...   52.4  52.8  53.3  53.6  54.0  54.4  54.8  54.9  53.8
          2    NaN    NaN  ...    NaN   NaN   NaN   NaN   NaN   NaN   NaN   NaN   NaN

              2016
          0    NaN
          1  52.72
          2    NaN

          [3 rows x 218 columns]
```

```
In [624]: # See what columns are in the data and check the range
          life_expectancy_original.columns
```

```
Out[624]: Index(['Life expectancy', '1800', '1801', '1802', '1803', '1804', '1805',
                 '1806', '1807', '1808',
                 ...
                 '2007', '2008', '2009', '2010', '2011', '2012', '2013', '2014', '2015',
                 '2016'],
                dtype='object', length=218)
```

```
In [625]: # Change first column name for better readability
          life_expectancy_original.rename(columns = {'Life expectancy':'Country'}, inplace = T
```

Replace the missing value with the average value from the year prior and after (2009 and 2011)

```
In [626]: # Filter the dataframe to get only necessary values: 'Country' and the three years 2
          life_expectancy_NA_imputation = life_expectancy_original[['Country', '2009', '2010',

          # Checked the first few rows of the filtered dataframe
          life_expectancy_NA_imputation.head(3)
```

```
Out[626]:                Country  2009  2010  2011
          0             Abkhazia   NaN   NaN   NaN
          1          Afghanistan  53.3  53.6  54.0
          2  Akrotiri and Dhekelia   NaN   NaN   NaN
```

Now, we will impute missing data. First, filter the rows corresponding with the countries extracted above, then begin imputation.

```
In [627]: # Filtered the rows corresponding with six countries with missing values we derived 
          country_life_exp_NA = ['Monaco', 'Nauru', 'Palau',
                                 'San Marino','St. Kitts and Nevis', 'Tuvalu']

          # Get the rows corresponding with such countries
          life_expectancy_NA_imputation[life_expectancy_NA_imputation['Country'].isin(country_l
```

```
Out[627]:                 Country  2009  2010  2011
          147              Monaco   NaN   NaN   NaN
          155               Nauru   NaN   NaN   NaN
          172               Palau   NaN   NaN   NaN
          189 St. Kitts and Nevis   NaN   NaN   NaN
          195          San Marino   NaN   NaN   NaN
          235              Tuvalu   NaN   NaN   NaN
```

Since we don't have values for the year prior and the year after for all the countries with missing values, we will drop all these countries.

```
In [628]: # Drop the rows corresponding with such countries and make the changes permanent
          project.drop([111, 118, 128, 141, 156, 175], inplace = True)
```

Test to see how many missing values we have left. We should see no missing value for column 'Life Expectancy'

```
In [629]: # Count the total of missing values in each column in the 'project' dataset
          project.isnull().sum()
```

```
Out[629]: Country                                  0
          Child Mortality Rate                     0
          Government Expenditure on Health (USD)   0
          Improved Sanitation Proportion          24
          Life Expectancy                          4
          Four Regions                             0
          Eight Regions                            0
          World Bank Income Group                  0
          dtype: int64
```

That's surprisingly not the case. We still have four missing values for 'Life Expectancy'. Let's investigate this further. But first, let's reset index.

```
In [630]: # Reset index
          project.reset_index(drop = True,inplace = True)

          # Check the first few rows
          project.head(3)
```

```
Out[630]:        Country  Child Mortality Rate  Government Expenditure on Health (USD)  \
          0  Afghanistan                  90.2                                4.390408
          1      Albania                  16.6                               94.023613
          2      Algeria                  27.3                              138.840923

             Improved Sanitation Proportion  Life Expectancy Four Regions Eight Regions  \
          0                            37.0             53.6         asia     asia_west
          1                            94.0             77.2       europe   europe_east
          2                            95.0             76.0       africa  africa_north

            World Bank Income Group
          0              Low income
          1     Upper middle income
          2     Upper middle income
```

Return the indices of missing values and use them to return the countries with missing values, just as we did before.

```
In [631]: # Return the indices of missing values
          np.where(project['Life Expectancy'].isna())

Out[631]: (array([125, 137, 151, 169]),)

In [632]: # Return the country with missing value for index 125
          project.iloc[125]['Country']

Out[632]: 'Palau'

In [633]: # Return the country with missing value for index 137
          project.iloc[137]['Country']

Out[633]: 'San Marino'

In [634]: # Return the country with missing value for index 151
          project.iloc[151]['Country']

Out[634]: 'St. Kitts and Nevis'

In [635]: # Return the country with missing value for index 169
          project.iloc[169]['Country']

Out[635]: 'Tuvalu'
```

These four countries were the same countries we saw before, which is why 'np.where' did not pick up the first time (overlapping values). We will drop these, but first, let's make sure we cannot impute missing values for these four countries by following a similar approach.

```
In [636]: # Filter the rows corresponding to these four countries
          country_life_exp_NA_2 = ['Palau', 'San Marino','St. Kitts and Nevis', 'Tuvalu']
          life_expectancy_NA_imputation[life_expectancy_NA_imputation['Country'].isin(country_
```

```
Out[636]:                  Country  2009  2010  2011
        147                Monaco   NaN   NaN   NaN
        155                 Nauru   NaN   NaN   NaN
        172                 Palau   NaN   NaN   NaN
        189  St. Kitts and Nevis   NaN   NaN   NaN
        195            San Marino   NaN   NaN   NaN
        235                Tuvalu   NaN   NaN   NaN
```

Missing values throughout just like before. Let's drop these the four rows corresponding to the four countries and proceed further, imputing missing values for the last variable.

```
In [637]: # Drop the rows corresponding to these missing values and make the changes permanent
          project.drop([125,137, 151, 169], inplace = True)
```

```
In [638]: # Now let's count how many missing values we have.
              # We should only have one column with missing values left
          project.isnull().sum()
```

```
Out[638]: Country                                    0
          Child Mortality Rate                       0
          Government Expenditure on Health (USD)     0
          Improved Sanitation Proportion            23
          Life Expectancy                            0
          Four Regions                               0
          Eight Regions                              0
          World Bank Income Group                    0
          dtype: int64
```

```
In [639]: # Check to see how many countries we have now
          project.shape
```

```
Out[639]: (178, 8)
```

Now, we are left with 178 countries. Last but not least, we will impute missing data for 'Improved Sanitation Proportion', utilizing the same approach.

iii. Improved Sanitation Proportion

```
In [640]: # Return the indices of missing values
          np.where(project['Improved Sanitation Proportion'].isna())
```

```
Out[640]: (array([  5,   6,  12,  24,  48,  53,  54,  81,  87,  91,  92,  96, 109,
                  119, 125, 130, 133, 137, 140, 145, 150, 163, 174]),)
```

```
In [641]: # Get the list of countries with missing values corresponding to every single index 
          print(project.iloc[5]['Country'])
          print(project.iloc[6]['Country'])
          print(project.iloc[12]['Country'])
          print(project.iloc[24]['Country'])
```

```
print(project.iloc[48]['Country'])
print(project.iloc[53]['Country'])
print(project.iloc[54]['Country'])
print(project.iloc[81]['Country'])
print(project.iloc[87]['Country'])
print(project.iloc[91]['Country'])
print(project.iloc[92]['Country'])
print(project.iloc[96]['Country'])
print(project.iloc[109]['Country'])
print(project.iloc[119]['Country'])
print(project.iloc[125]['Country'])
print(project.iloc[130]['Country'])
print(project.iloc[133]['Country'])
print(project.iloc[137]['Country'])
print(project.iloc[140]['Country'])
print(project.iloc[145]['Country'])
print(project.iloc[150]['Country'])
print(project.iloc[163]['Country'])
print(project.iloc[174]['Country'])
```

```
Antigua and Barbuda
Argentina
Bahrain
Brunei
Dominica
Equatorial Guinea
Eritrea
Italy
Kiribati
Latvia
Lebanon
Lithuania
Micronesia, Fed. Sts.
New Zealand
Panama
Poland
Romania
Saudi Arabia
Seychelles
Solomon Islands
St. Vincent and the Grenadines
Tunisia
Venezuela
```

In [642]:
```
# Now, let's read in the original file
improved_sanitation_original = pd.read_csv('improved_sanitation.csv',
                                           sep = ',', engine = 'python')
```

```
# Check the first few rows
improved_sanitation_original.head(3)
```

Out[642]:

```
  Proportion of the population using improved sanitation facilities, total  \
0                                           Abkhazia
1                                        Afghanistan
2                              Akrotiri and Dhekelia

   1990  1991  1992  1993  1994  1995  1996  1997  1998  ...   2001  2002  \
0   NaN   NaN   NaN   NaN   NaN   NaN   NaN   NaN   NaN  ...    NaN   NaN
1   NaN  29.0  29.0  29.0  29.0  29.0  29.0  30.0  30.0  ...   32.0  33.0
2   NaN   NaN   NaN   NaN   NaN   NaN   NaN   NaN   NaN  ...    NaN   NaN

   2003  2004  2005  2006  2007  2008  2009  2010
0   NaN   NaN   NaN   NaN   NaN   NaN   NaN   NaN
1  34.0  34.0  35.0  35.0  37.0  37.0  37.0  37.0
2   NaN   NaN   NaN   NaN   NaN   NaN   NaN   NaN

[3 rows x 22 columns]
```

In [643]:

```
# Change the first column's name for better readability
improved_sanitation_original.rename(
    columns = {'Proportion of the population using improved sanitation facilities, to
               'Country'}, inplace = True)
```

In [644]:

```
# Filter the original dataset to get only the columns we need: '
    # Country' and the three years: 2008 to 2010
improved_sanitation_NA_imputation = improved_sanitation_original[
    ['Country', '2008', '2009', '2010']]

# Check the first few rows of the resulting filtered dataframe
improved_sanitation_NA_imputation.head(3)
```

Out[644]:

```
                 Country  2008  2009  2010
0               Abkhazia   NaN   NaN   NaN
1            Afghanistan  37.0  37.0  37.0
2  Akrotiri and Dhekelia   NaN   NaN   NaN
```

In [645]:

```
# Filter out the rows corresponding with the countries with missing values.
    # List of countries with missing values was derived earlier.
country_sanitation_NA = ['Antigua and Barbuda', 'Argentina','Bahrain',
                          'Brunei','Dominica','Equatorial Guinea',
                          'Eritrea','Italy','Kiribati','Latvia','Lebanon',
                          'Lithuania', 'Micronesia, Fed. Sts.', 'New Zealand',
                          'Panama','Poland', 'Romania', 'Saudi Arabia',
                          'Seychelles', 'Solomon Islands',
                          'St. Vincent and the Grenadines','Tunisia','Venezuela']
```

```
improved_sanitation_NA_imputation[
    improved_sanitation_NA_imputation['Country'].isin(country_sanitation_NA)]
```

Out[645]:

```
                         Country  2008  2009  2010
9            Antigua and Barbuda   NaN   NaN   NaN
10                     Argentina   NaN   NaN   NaN
17                       Bahrain   NaN   NaN   NaN
31                        Brunei   NaN   NaN   NaN
61                      Dominica   NaN   NaN   NaN
67             Equatorial Guinea   NaN   NaN   NaN
68                       Eritrea  14.0   NaN   NaN
108                        Italy   NaN   NaN   NaN
115                     Kiribati   NaN   NaN   NaN
123                       Latvia  78.0  78.0   NaN
124                      Lebanon   NaN   NaN   NaN
129                    Lithuania  86.0  86.0   NaN
145        Micronesia, Fed. Sts.   NaN   NaN   NaN
160                  New Zealand   NaN   NaN   NaN
173                       Panama  69.0  69.0   NaN
179                       Poland  90.0   NaN   NaN
184                      Romania  73.0   NaN   NaN
192  St. Vincent and the Grenadines   NaN   NaN   NaN
197                 Saudi Arabia   NaN   NaN   NaN
202                   Seychelles   NaN   NaN   NaN
207              Solomon Islands   NaN   NaN   NaN
231                      Tunisia  85.0  85.0   NaN
246                    Venezuela   NaN   NaN   NaN
```

Out of these, it only makes sense to impute the missing values for Latvia, Lithuania, Panama, and Tunisia.

In [646]:

```
# Get the row corresponding to Latvia from the filtered dataframe
latvia_row = improved_sanitation_NA_imputation.loc[
    improved_sanitation_NA_imputation['Country'] == 'Latvia']

# Double check to make sure the result is what we want
latvia_row
```

Out[646]:

```
    Country  2008  2009  2010
123  Latvia  78.0  78.0   NaN
```

In [647]:

```
# Replace the missing value for 2010 by
    # taking the average of improved sanitation proportion in 2008 and 2009
    # We use '.fillna()' chained with '.mean()' for this task
    # 'inplace = True' makes the change permanent
latvia_row['2010'].fillna(latvia_row.mean(axis = 1), inplace = True)
```

```
/Users/Pain_de_mie/anaconda3/lib/python3.6/site-packages/pandas/core/generic.py:5430: SettingW
A value is trying to be set on a copy of a slice from a DataFrame
```

```
See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/stable/indexing.html
  self._update_inplace(new_data)
```

In [648]:
```python
# Double check to see if the missing value is filled
latvia_row
```

Out[648]:

	Country	2008	2009	2010
123	Latvia	78.0	78.0	78.0

In [649]:
```python
# Get the row corresponding to Lithuania from the filtered dataframe
lithuania_row = improved_sanitation_NA_imputation.loc[
    improved_sanitation_NA_imputation['Country'] == 'Lithuania']

# Double check to make sure the result is what we want
lithuania_row
```

Out[649]:

	Country	2008	2009	2010
129	Lithuania	86.0	86.0	NaN

In [650]:
```python
# Replace the missing value for 2010 by
    # taking the average of improved sanitation proportion in 2008 and 2009
    # We use '.fillna()' chained with '.mean()' for this task
    # 'inplace = True' makes the change permanent
lithuania_row['2010'].fillna(lithuania_row.mean(axis = 1), inplace = True)
```

```
/Users/Pain_de_mie/anaconda3/lib/python3.6/site-packages/pandas/core/generic.py:5430: SettingWi
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/stable/indexing.html
  self._update_inplace(new_data)
```

In [651]:
```python
# Double check to see if the missing value is filled
lithuania_row
```

Out[651]:

	Country	2008	2009	2010
129	Lithuania	86.0	86.0	86.0

In [652]:
```python
# Get the row corresponding to Panama from the filtered dataframe
panama_row = improved_sanitation_NA_imputation.loc[
    improved_sanitation_NA_imputation['Country'] == 'Panama']

# Double check to make sure the result is what we want
panama_row
```

Out[652]:

	Country	2008	2009	2010
173	Panama	69.0	69.0	NaN

```
In [653]: # Replace the missing value for 2010 by
              # taking the average of improved sanitation proportion in 2008 and 2009
              # We use '.fillna()' chained with '.mean()' for this task
              # 'inplace = True' makes the change permanent
          panama_row['2010'].fillna(panama_row.mean(axis = 1), inplace = True)

/Users/Pain_de_mie/anaconda3/lib/python3.6/site-packages/pandas/core/generic.py:5430: SettingWi
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/stable/indexing.html
  self._update_inplace(new_data)
```

```
In [654]: # Double check to see if the missing value is filled
          panama_row

Out[654]:     Country  2008  2009  2010
          173  Panama  69.0  69.0  69.0
```

```
In [655]: # Get the row corresponding to Tunisia from the filtered dataframe
          tunisia_row = improved_sanitation_NA_imputation.loc[
              improved_sanitation_NA_imputation['Country'] == 'Tunisia']

          # Double check to make sure the result is what we want
          tunisia_row

Out[655]:      Country  2008  2009  2010
          231  Tunisia  85.0  85.0   NaN
```

```
In [656]: # Replace the missing value for 2010 by
              # taking the average of improved sanitation proportion in 2008 and 2009
              # We use '.fillna()' chained with '.mean()' for this task
              # 'inplace = True' makes the change permanent
          tunisia_row['2010'].fillna(tunisia_row.mean(axis = 1), inplace = True)

/Users/Pain_de_mie/anaconda3/lib/python3.6/site-packages/pandas/core/generic.py:5430: SettingWi
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/stable/indexing.html
  self._update_inplace(new_data)
```

```
In [657]: # Double check to see if the missing value is filled
          tunisia_row

Out[657]:      Country  2008  2009  2010
          231  Tunisia  85.0  85.0  85.0
```

Now let's drop the countries whose missing values we cannot impute and replace missing values with the corresponding values we just found for the four countries: Latvia, Lithuania, Tunisia, and Panama.

```
In [658]: # https://stackoverflow.com/questions/28679930/
              # how-to-drop-rows-from-pandas-data-frame-that-contains-a-particular-string-in-a

          # Get the list of countries that we cannot impute missing values to drop them
          countries_to_drop = ['Antigua and Barbuda', 'Argentina','Bahrain',
                               'Brunei','Dominica','Equatorial Guinea','Eritrea',
                               'Italy','Kiribati','Lebanon','Micronesia, Fed. Sts.',
                               'New Zealand','Poland', 'Romania', 'Saudi Arabia',
                               'Seychelles', 'Solomon Islands',
                              'St. Vincent and the Grenadines','Venezuela']

          # Drop the rows corresponding to these countries from the 'project' dataset
          project = project[~project['Country'].isin(countries_to_drop)]

In [659]: # Replace missing value corresponding with Latvia with the imputed missing data
              # from'latvia_row', column '2010'
          project.at[project['Country']=='Latvia','Improved Sanitation Proportion'] = latvia_ro

/Users/Pain_de_mie/anaconda3/lib/python3.6/site-packages/pandas/core/indexing.py:543: SettingWi
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/stable/indexing.html
  self.obj[item] = s


In [660]: # Replace missing value corresponding with Lithuania with the imputed missing data
              # from 'lithuania_row', column '2010'
          project.at[project['Country']=='Lithuania','Improved Sanitation Proportion']= lithuan

/Users/Pain_de_mie/anaconda3/lib/python3.6/site-packages/pandas/core/indexing.py:543: SettingWi
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/stable/indexing.html
  self.obj[item] = s


In [661]: # Replace missing value corresponding with Tunisia with the imputed missing data
              # from 'tunisia_row', column '2010'
          project.at[project['Country']=='Tunisia','Improved Sanitation Proportion']= tunisia_r

/Users/Pain_de_mie/anaconda3/lib/python3.6/site-packages/pandas/core/indexing.py:543: SettingWi
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/stable/indexing.html
  self.obj[item] = s
```

In [662]: # Replace missing value corresponding with Panama with the imputed missing data
```
          # from 'panama_row', column '2010'
project.at[project['Country']=='Panama','Improved Sanitation Proportion']= panama_row
```

```
/Users/Pain_de_mie/anaconda3/lib/python3.6/site-packages/pandas/core/indexing.py:543: SettingWi
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/stable/indexing.html
  self.obj[item] = s
```

In [663]:
```
# Now, let's count the total missing values in 'project.' We expect to have none.
project.isnull().sum()
```

Out[663]:
```
Country                                    0
Child Mortality Rate                       0
Government Expenditure on Health (USD)     0
Improved Sanitation Proportion             4
Life Expectancy                            0
Four Regions                               0
Eight Regions                              0
World Bank Income Group                    0
dtype: int64
```

That's not the case, yet. We stil have four missing values in 'Improved Sanitation Proportion.' Let's investigate this further.

In [664]:
```
# Get the indeces of missing values in 'Improved Sanitation Proportion'
np.where(project['Improved Sanitation Proportion'].isna())
```

Out[664]:
```
(array([ 82,  86, 113, 145]),)
```

In [665]:
```
# Get the contries with missing values corresponding to these above indices
print(project.iloc[82]['Country'])
print(project.iloc[86]['Country'])
print(project.iloc[113]['Country'])
print(project.iloc[145]['Country'])
```

```
Latvia
Lithuania
Panama
Tunisia
```

In [666]:
```
# These are the same countries we saw before; it's probably why 'np.where()'
    # was not able to pick them up. Let's get the rows corresponding to these countr
country_sanitation_NA_1 = ['Latvia','Lithuania', 'Panama','Tunisia']

improved_sanitation_NA_imputation[
    improved_sanitation_NA_imputation['Country'].isin(country_sanitation_NA_1)]
```

```
Out[666]:        Country  2008  2009  2010
          123     Latvia  78.0  78.0   NaN
          129  Lithuania  86.0  86.0   NaN
          173     Panama  69.0  69.0   NaN
          231    Tunisia  85.0  85.0   NaN
```

We already imputed missing data for these countries. So let's go ahead and drop them and check if we have our final clean data set.

```
In [667]: # Drop these last four missing values and make the changes permanent
          project.dropna(inplace = True)

/Users/Pain_de_mie/anaconda3/lib/python3.6/site-packages/ipykernel_launcher.py:2: SettingWithC
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/stable/indexing.html
```

```
In [668]: # Now, let's count how many missing values we have left. This time, we should see no
          project.isnull().sum()

Out[668]: Country                                   0
          Child Mortality Rate                      0
          Government Expenditure on Health (USD)    0
          Improved Sanitation Proportion            0
          Life Expectancy                           0
          Four Regions                              0
          Eight Regions                             0
          World Bank Income Group                   0
          dtype: int64
```

And, there is none! Let's quickly take a look at the summary of our final dataset to make sure everything looks good before we proceed further.

```
In [669]: # Get the summary of 'project'
          project.info()

<class 'pandas.core.frame.DataFrame'>
Int64Index: 155 entries, 0 to 181
Data columns (total 8 columns):
Country                                   155 non-null object
Child Mortality Rate                      155 non-null float64
Government Expenditure on Health (USD)    155 non-null float64
Improved Sanitation Proportion            155 non-null float64
Life Expectancy                           155 non-null float64
Four Regions                              155 non-null object
Eight Regions                             155 non-null object
World Bank Income Group                   155 non-null object
```

```
dtypes: float64(4), object(4)
memory usage: 10.9+ KB
```

```
In [670]: # Get the dimension of 'project'
          project.shape

Out[670]: (155, 8)
```

Everything looks good. We are left with 155 countries, which is a decent number. Let's quickly explore how many countries we have for each region, make a backup, and move on to Exploratory Data Analysis.

```
In [671]: # Count number of countries we have for each of the four regions
          project['Four Regions'].value_counts()

Out[671]: africa      46
          asia        42
          europe      40
          americas    27
          Name: Four Regions, dtype: int64
```

Aside from americas, we have quite an even number of distribution per region. This gives us confidence to move to the next step.

```
In [672]: # Export our clean 'project' dataframe to a csv file
          project.to_csv('clean_df.csv')
```

Exploratory Data Analysis A few things we would like to accomplish for this part of the project.

1) Compute the summary statistics of the final data set.

2) Create visualization to answer each question being asked. Test to see if the ANOVA test can be carried out for the mean child mortality rate across regions (for question 1). If not, we will not perform the ANOVA test; instead, we will perform a Kruskal-Wallis H-test

- (Ref:
  - https://cyfar.org/types-statistical-tests
  - https://docs.scipy.org/doc/scipy/reference/generated/scipy.stats.f_oneway.html

Also, since there are three questions about association, compute the Pearson correlation test for each pair for question 2, 3, and 4.

3) Compute Multiple Regression Test combining all three independent and one dependent variables.

1.1.3 1) Summary statistics

Let's do a quick summary statistics of the final dataset.

```
In [673]: # Return the summary statistics for all columns in 'project' dataframe
          project.describe()
```

```
Out[673]:        Child Mortality Rate  Government Expenditure on Health (USD)  \
          count            155.000000                              155.000000
          mean              40.287097                              709.606979
          std               40.907775                             1343.475158
          min                2.600000                                2.087651
          25%                8.650000                               31.332824
          50%               23.300000                              134.433405
          75%               63.150000                              553.933134
          max              208.000000                             6905.530344

                 Improved Sanitation Proportion  Life Expectancy
          count                      155.000000       155.000000
          mean                        71.341935        70.210968
          std                         30.474481         9.189870
          min                          9.000000        32.200000
          25%                         47.500000        64.150000
          50%                         84.000000        71.800000
          75%                         98.000000        77.200000
          max                        100.000000        84.700000
```

- **Child Mortality Rate** > There is a substantial difference between the minimum child mortality rate (2.6 deaths / 1000 live births per year) and the maximum child mortality rate (208 deaths / 1000 live births per year). Since the 75th percentile (third quartile) is at 63, indicating that 75% of observations has child mortality rate of less than 63, max value 208 is suspected to be an outlier. We can test that later.

- **Government Expenditure on Health (USD)** > Similar to child mortality rate, there is a stark difference between the minimum health spending (2.09 USD / capita / year) and the maximum health spending (6906 USD / capita / year). Since the 75th percentile is at ~554 USD, indicating that 75% of countries spend less than or equal to 554 USD, the maximum value of 6906 USD is suspected to also be an outlier. An outlier in this case suggests there might potentially be a staggering difference in managing the budget on health among some countries. This can potentially be very interesting for future projects if we want to look at wealth distribution across the world.

- **Improved Sanitation Proportion** > The proportion of the population using improved sanitation facilities is also very different across countries with the min being 9% and the maximum being 100%. Since the 75th percentile is 98, we do not think 100% is an outlier. It's worth noting that the mean is 71% and the median is 84%, a very high number, which means in general the proportion of the population using improved sanitation facilities is high across the world.

- **Life Expectancy** > There is also a noticeable difference between the min (32.2 years) and the max value (84.7 years). It's interesting to note that the median is 71.8 years and the 75th percentile is 77.2 years, suggesting a very positive trend: the life expectancy is high across the world. With the 25th percentile being 64.15 years, this trend is further validated. Only 25% of the countries in the dataset have life expectancy lower than 64 years of age.

1.1.4 2) Answer research questions via visualization and simple linear regression

Question 1: Is there a stark difference regarding child mortality across different regions in the world? To answer this question, let's focus on a subset of the dataset.

In [674]:
```
# Filter our data for readability. We will keep the country names, all regions,
    # and child mortality rate
cols_subset = ['Country', 'Child Mortality Rate', 'Four Regions',
              'Eight Regions', 'World Bank Income Group']

child_mortality = project[cols_subset]
```

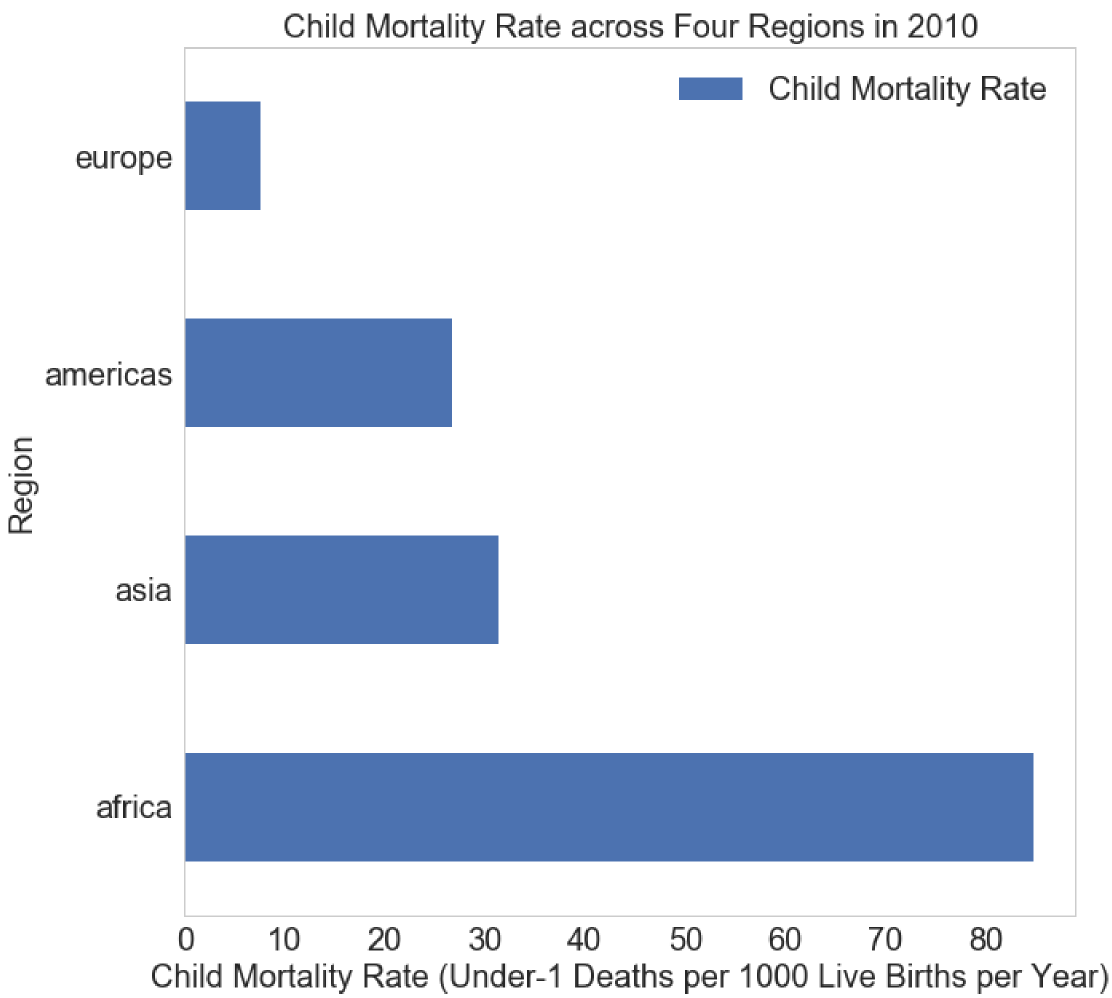
In [675]:
```
# Take a look at the first few rows of our filtered dataframe
child_mortality.head()
```

Out[675]:
```
       Country  Child Mortality Rate Four Regions       Eight Regions  \
0  Afghanistan                  90.2         asia           asia_west
1      Albania                  16.6       europe         europe_east
2      Algeria                  27.3       africa        africa_north
3      Andorra                   3.3       europe         europe_west
4       Angola                 119.0       africa  africa_sub_saharan

  World Bank Income Group
0              Low income
1     Upper middle income
2     Upper middle income
3             High income
4     Lower middle income
```

Let's plot a horizontal bar chart to see if there is a contrast in child mortality among different regions in the world. To do that, we first group the 'child_mortality' dataframe by four regions, then we will take the average value of child mortality rate by region, and then we will plot the chart.

In [676]:
```
# Sorting and editing chart inspired by this link
# https://stackoverflow.com/questions/27018622/pandas-groupby-sort-descending-order
# https://stackoverflow.com/questions/6390393/matplotlib-make-tick-labels-font-size-
# https://matplotlib.org/api/_as_gen/matplotlib.axes.Axes.locator_params.html

# Group child mortality rate values descendingly into four regions
four_reg = child_mortality.groupby('Four Regions').mean().sort_values(
    'Child Mortality Rate', ascending = False)
```

```
# Plot the horizontal bar chart. This should show the child mortality rate in ascend
    # broken down by four regions
four_reg.plot(kind = 'barh', figsize = (10,10))
plt.title('Child Mortality Rate across Four Regions in 2010', size = 20) # add the t
plt.xlabel('Child Mortality Rate (Under-1 Deaths per 1000 Live Births per Year)',
           size = 20) # add label for x-axis and increase the size
plt.ylabel('Region', size = 20) # add label for y-axis and increase the size
plt.locator_params(nbins = 10) # add more ticks to the x-axis for easy reading of va
```

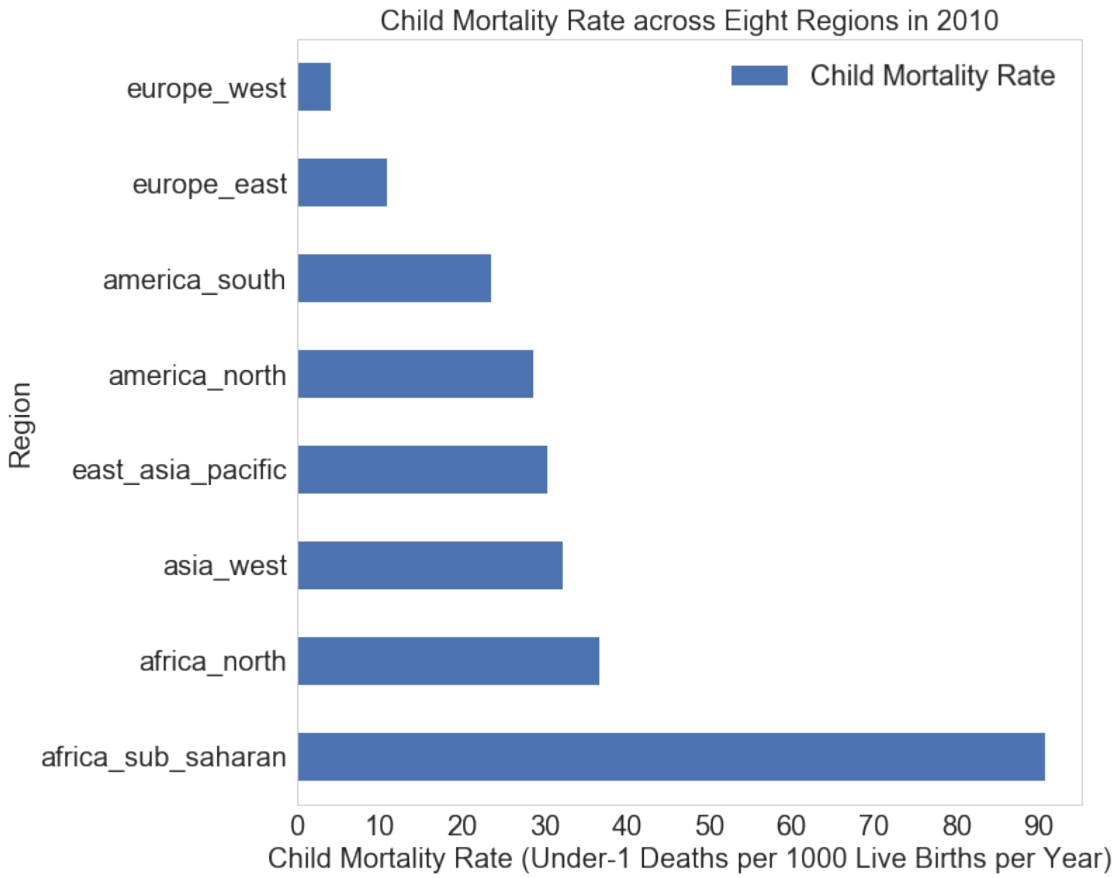


We can see very clearly that there is an undeniable difference among regions when it comes to child mortality rate. The average number of deaths of children under 1 year of age per 1000 live births is almost 10% (>80 out of 1000 per year) in Africa while the corresponding number for Europe, the continent with the lowest rate of mortality rate is fewer than 1% (fewer than 10 out of 1000). Americas and Asia, the two regions in the middle, exhibit a relatively low child mortality rate (23-30 per 1000 per year). It will be interesting to look at the sub-regions, especially in Africa to find out if this is the trend of the whole continent or if there is one sub-region driving the average number up. Let's do that.

In [677]:
```
# Remind ourselves what columns we have in 'child_mortality'
child_mortality.columns
```

Out[677]:
```
Index(['Country', 'Child Mortality Rate', 'Four Regions', 'Eight Regions',
       'World Bank Income Group'],
      dtype='object')
```

In [678]:
```
# Plot a similar horizontal bar chart but this time it should show
    # the child mortality rate broken down to eight regions

# Group child mortality rate values descendingly into eight regions
eight_reg = child_mortality.groupby('Eight Regions').mean().sort_values(
    'Child Mortality Rate', ascending = False)

# Plot the horizontal bar chart
eight_reg.plot(kind = 'barh', figsize = (10,10))
plt.title('Child Mortality Rate across Eight Regions in 2010', size = 20) # add titl
plt.xlabel('Child Mortality Rate (Under-1 Deaths per 1000 Live Births per Year)',
           size = 20) # add x-axis label and increase the size
plt.ylabel('Region', size = 20) # add y-axis label and increase the siz
plt.locator_params(nbins=10) # add more ticks to the x-axis for easy reading of valu
```



- Very interesting result! It's obvious that the Sub Saharan Africa exhibits a high number of child mortality rate (>90 child mortality cases per 1000 live birth) while the number of the other African region Africa North is very on par with the trend of most of the rest of the world (about 35 cases).
- Fascinatingly enough, the book I have been reading "Factfulness" by Hans Rosling discussed that child mortality rate has been improving over the years except for a very few regions and he mentioned Sub Saharan Africa. We can clearly see why!
- To look further into the range of mortality rate, let's plot a box plot for each region and layer it with a swarm plot to see the value points more clearly.

In [679]:
```
# Remind ourselves what columns there are in 'child_mortality'
child_mortality.columns
```

Out[679]:
```
Index(['Country', 'Child Mortality Rate', 'Four Regions', 'Eight Regions',
       'World Bank Income Group'],
      dtype='object')
```

In [680]:
```
# Get the descending order values of child mortality rate in each region to add to th
four_reg
```

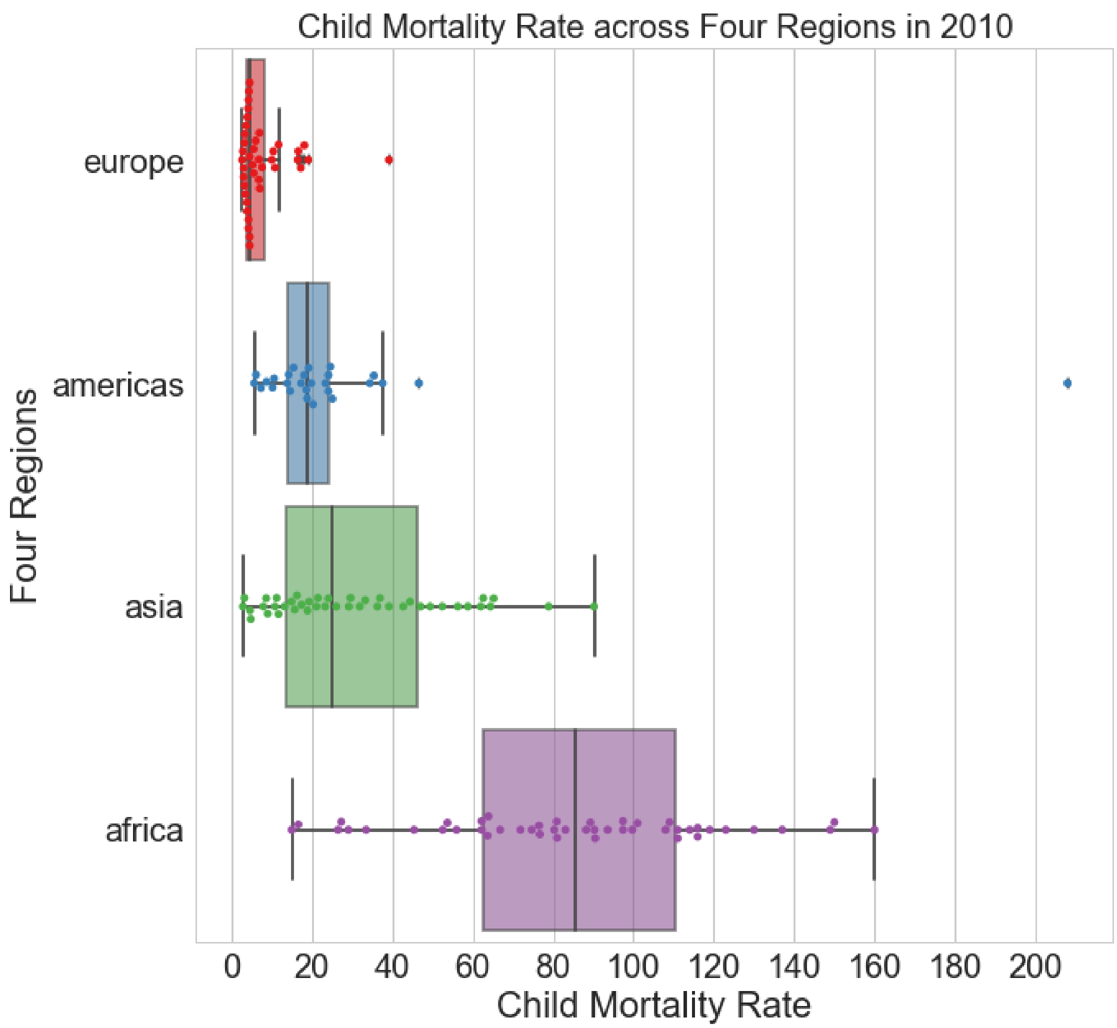
Out[680]:

Four Regions	Child Mortality Rate
africa	84.780435
asia	31.359524
americas	26.737037
europe	7.640000

In [681]:
```
# Seaborn boxplot
    # https://seaborn.pydata.org/generated/seaborn.boxplot.html
# To set figure size in seaborn
    # https://stackoverflow.com/questions/31594549/how-do-i-change-the-figure-size-fo
# To set title in seaborn
    # https://stackoverflow.com/questions/42406233/how-to-add-title-to-seaborn-boxplo
# Seaborn transparency
    # https://github.com/mwaskom/seaborn/issues/979
# Set axis size
    # https://seaborn.pydata.org/generated/seaborn.set_context.html

sns.set(rc={'figure.figsize':(10,10)}) # figure size
sns.set_style('whitegrid') # white grid
sns.set_context("notebook", font_scale = 2.0) # increase size of the titles of the ax

# plot horizontal boxplots
sns.boxplot(y = 'Four Regions', # Categories on y-axis
               x = 'Child Mortality Rate', # Categories on y-axis
               data = child_mortality, # dataframe
               order = ['europe', 'americas', 'asia', 'africa'], # order from 'four_r
               orient = 'h', boxprops = dict(alpha = 0.6), # horizontal orientation #
           width = 0.9, palette = 'Set1', # transparency level # width # color palet
```

```
                    ).set_title('Child Mortality Rate across Four Regions in 2010', size = 20)

plt.locator_params(nbins=20) # add more ticks to the x-axis for easy reading of valu

# plot swarmplots
sns.swarmplot(y = 'Four Regions', # Categories on y-axis
               x = 'Child Mortality Rate', # Categories on y-axis
               data = child_mortality, # dataframe
              order = ['europe', 'americas', 'asia', 'africa'], # order from 'four_r
              palette = 'Set1', orient = 'h').set_title( # horizontal orientation # 
                    'Child Mortality Rate across Four Regions in 2010', # set title
                size = 20) # increase the size of the title
```

Out[681]: Text(0.5,1,'Child Mortality Rate across Four Regions in 2010')



This plot gives a similar picture compared to the bar plot; however, we can see very clearly the distribution of mortality rates, the interquartile range(s) (IQR), the medians, and outliers for all regions. + **Europe** > This region has a very small IQR (showned by the width of the box). It not only indicates the smallest child mortality rate but also exhibits a consistent trend. The outlier of Europe stays well within the smaller size of child mortality rate, so there's no need to discuss further. It's worth noting that aside from one outlier, all child mortality rate values are smaller than 20, which is extremely impressive and potentially suggests the advanced development of this region compared to the rest of the world. Furthermore, the swarm plot shows that the majority of points are on the lower end of the box, which proves more convincingly the point made above. Also, since the width of the box plot is very small, it indicates an approximately even rate when it comes to child mortality (most countries have values very close to one another). + **Americas** > Besides two outliers, all child mortality rate values are smaller than 30, which is also a very positive trend. It's worth noting that even for the countries with the smallest child mortality rate, americas region falls behind europes region as europes region has more countries with even smaller child mortality rate. The boxplot is wider than Europe but not as wide as Asia and Africa, indicating a fairly even rate when it comes to child mortality (the vast majortiy of countries have values close to one another). + **Asia** > Wider boxplot shows a wider distribution of values with 75% of values are fewer than 50. The maximum child mortality rate is only a bit higher than the median value of Africa. Wider boxplot indicates an uneven distribution of rate (some countries have very small child mortality rates while some countries have much larger values). Interestingly enough, the lowest mortality rate is very comparable to that of Europes and smaller than that of Americas, potentially suggesting a comparable development in some countries in Asia. This can be a topic of interest for future research. + **Africa** > The boxplot for this region gives a much more granular approach and confirms the finding from the two bar charts above. Such wide width indicates a stagerringly different pictures within the same region. Sub Saharan countries have extremely high child mortality rates, some as high as 160 while countries in North Africa have much lower child mortality rates, some as comparable as those in the lower end of Asia and Americas. 50% of values are above 80, painting a potentially grim picture of the current state of development of such countries.

Just like earlier, let's plot boxplots showing child mortality rates for all eight regions. But before doing so, let's find out which country in Americas has the child mortality rate greater than 200 (the blue outlier in the blue boxplot)

```
In [682]: # Filter all rows corresponding to 'americas' from 'child_mortality'
          americas = child_mortality[child_mortality['Four Regions'] == 'americas']

          # Filter the row corresponding to the child mortality rate value of greater than 200
          americas.loc[americas['Child Mortality Rate'] > 200]
```

```
Out[682]:    Country  Child Mortality Rate Four Regions  Eight Regions  \
          71   Haiti                 208.0     americas  america_north

             World Bank Income Group
          71              Low income
```

It makes so much sense for this country to be Haiti as Haiti suffered a serious earth quake and extremly low GDP growth in 2010. (https://www.worldvision.org/disaster-relief-news-stories/2010-haiti-earthquake-facts and http://www.worldbank.org/en/country/haiti). It will be interesting to look at the trend in child mortality rate in Haiti to see if the child mortality rate in 2010 is indeed an outlier or is it part of the regular trend. We will address this later.

Now, proceed with plotting child mortality rate for eight regions.

In [683]:
```python
# What columns we have in child_mortality?
child_mortality.columns
```

Out[683]:
```
Index(['Country', 'Child Mortality Rate', 'Four Regions', 'Eight Regions',
       'World Bank Income Group'],
      dtype='object')
```

In [684]:
```python
# Get the order of child mortality rate in each of eight regions to add to the plot
eight_reg
```

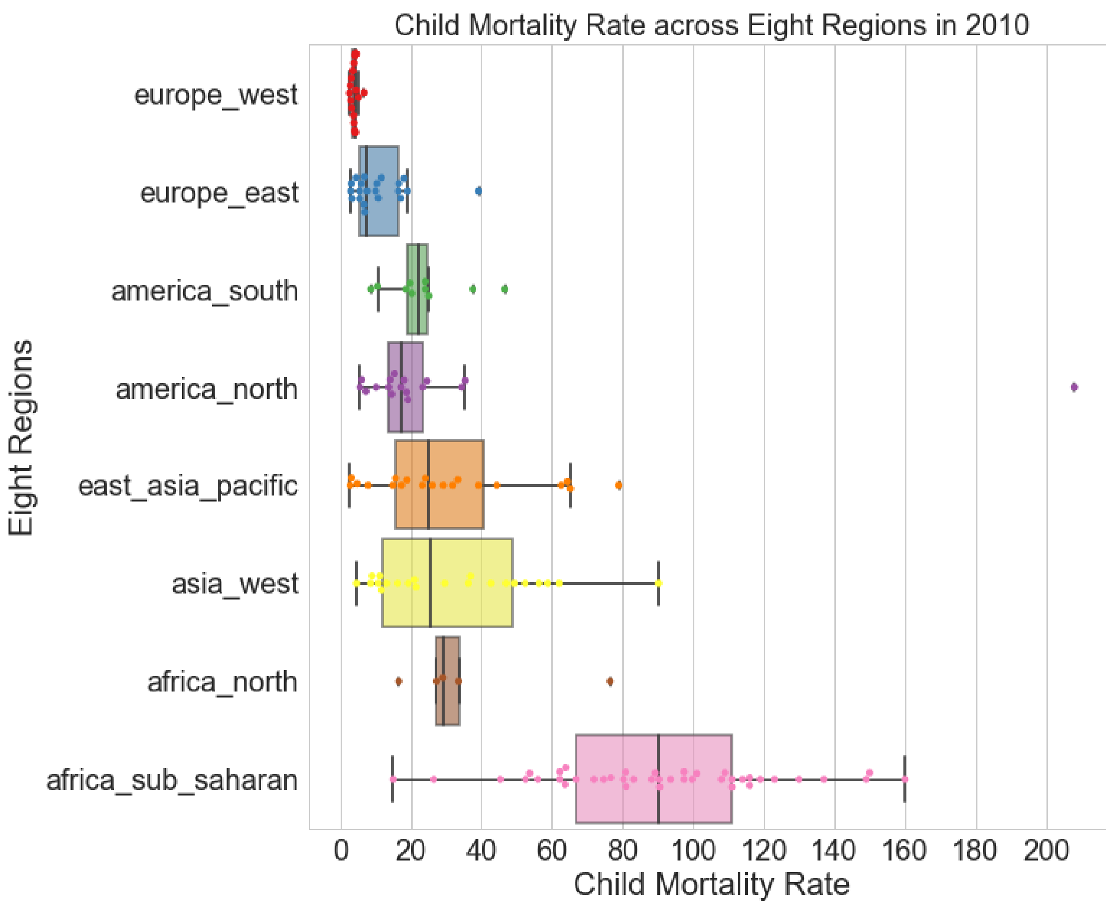
Out[684]:

Eight Regions	Child Mortality Rate
africa_sub_saharan	90.656098
africa_north	36.600000
asia_west	32.222727
east_asia_pacific	30.410000
america_north	28.611765
america_south	23.550000
europe_east	10.904762
europe_west	4.031579

In [685]:
```python
sns.set(rc={'figure.figsize':(10,10)}) # figure size
sns.set_style('whitegrid') # set the grid to be white
sns.set_context("notebook", font_scale=2.0) # increase size of axis title

# plot box plots
sns.boxplot(y = 'Eight Regions', # categories of regions on y-axis
               x = 'Child Mortality Rate', # child mortality rate on x-axis
               data = child_mortality, # dataframe
               order = ['europe_west', 'europe_east', # order from 'eight_reg' above
                        'america_south', 'america_north',
                       'east_asia_pacific', 'asia_west',
                        'africa_north', 'africa_sub_saharan'],
    orient = 'h', boxprops = dict(alpha = 0.6), # horizontal boxplot # transparency
           width = 0.9, palette = 'Set1', # boxplot width and color palette
           ).set_title('Child Mortality Rate across Eight Regions in 2010', # add a
                       size = 20) # increase the size of the title

plt.locator_params(nbins=20) # add more ticks to the x-axis for easy reading of valu

# plot swarmplots
sns.swarmplot(y = 'Eight Regions', # categories of regions on y-axis
               x = 'Child Mortality Rate', # child mortality rate on x-axis
              data = child_mortality, # dataframe
              order = ['europe_west', 'europe_east', # order from 'eight_reg' above
                       'america_south', 'america_north',
                       'east_asia_pacific', 'asia_west',
                       'africa_north', 'africa_sub_saharan'],
              palette = 'Set1', # color palette
```

```
                orient = 'h').set_title('Child Mortality Rate across Eight Regions in 2
                  size = 20)  # horizontal swarm plots, add a tile,
                              # and increase the size of the title
```

Out[685]: Text(0.5,1,'Child Mortality Rate across Eight Regions in 2010')



Two more interesting observations can be drawn from this plot. + The Western European countries have close to zero child mortality rate and much lower compared to the Eastern European countries. + The region with the highest child mortality rate is Sub Saharan Africa with more than 50% of countries having the child mortality rate of more than 90.

Next, let's test to see if we can perform the ANOVA test for the mean child mortality rate across regions. Let's check to see if the distribution of child mortality rate in each region is normally distributed. This is an important assumption of ANOVA (https://statistics.laerd.com/statistical-guides/one-way-anova-statistical-guide-3.php). If this assumption is not met, we will go ahead and carry out the Kruskal-Wallis H Test which does not require normality as an assumption.

In [686]:
```
# Take a look at the first few rows of 'child_mortality'
child_mortality.head(2)
```

Out[686]:
```
       Country  Child Mortality Rate Four Regions Eight Regions  \
0  Afghanistan                  90.2         asia     asia_west
```

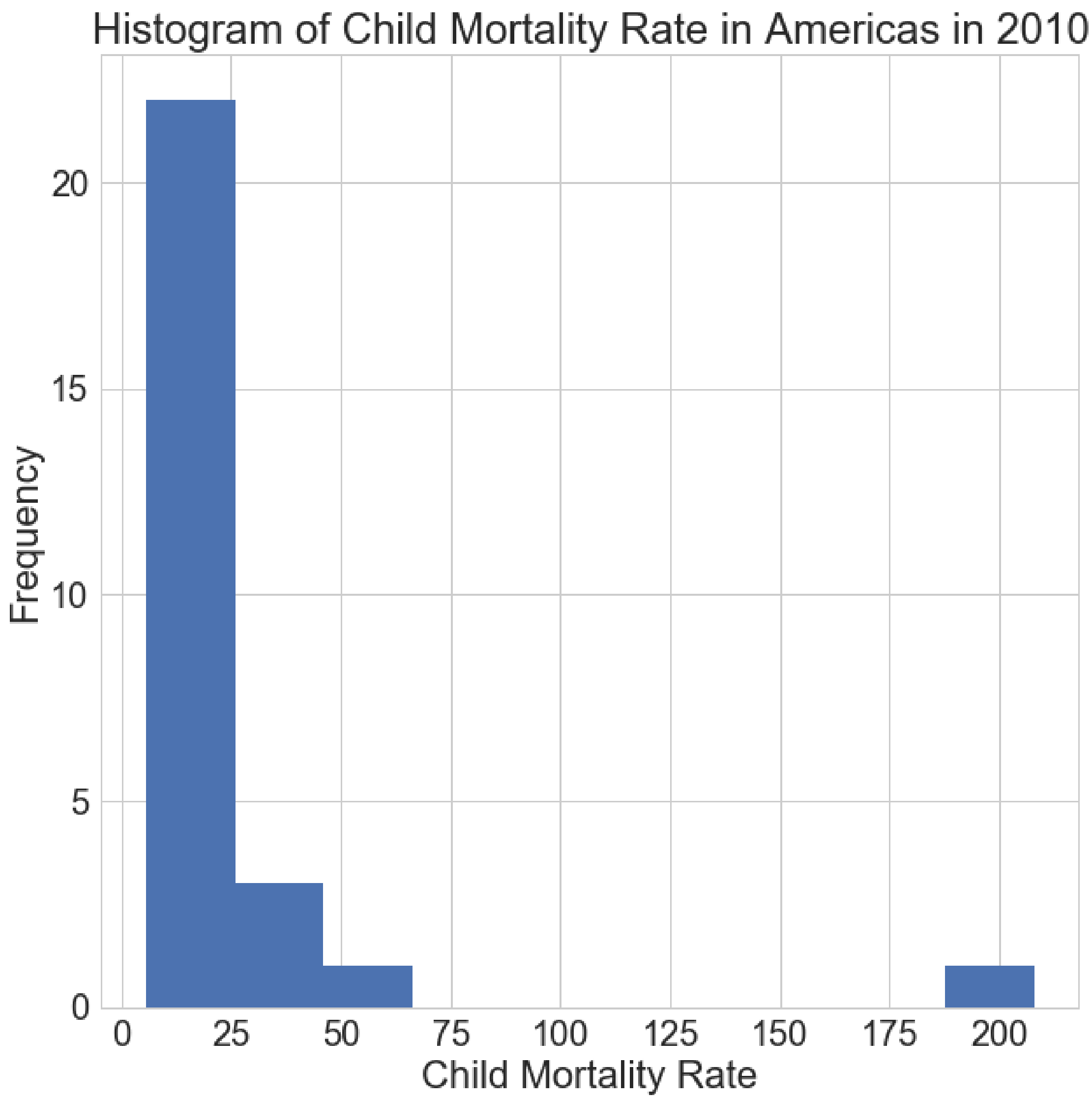
```
1      Albania                  16.6       europe   europe_east

  World Bank Income Group
0              Low income
1     Upper middle income
```

Subset data for each of the four regions so that we can plot the histogram for each region.

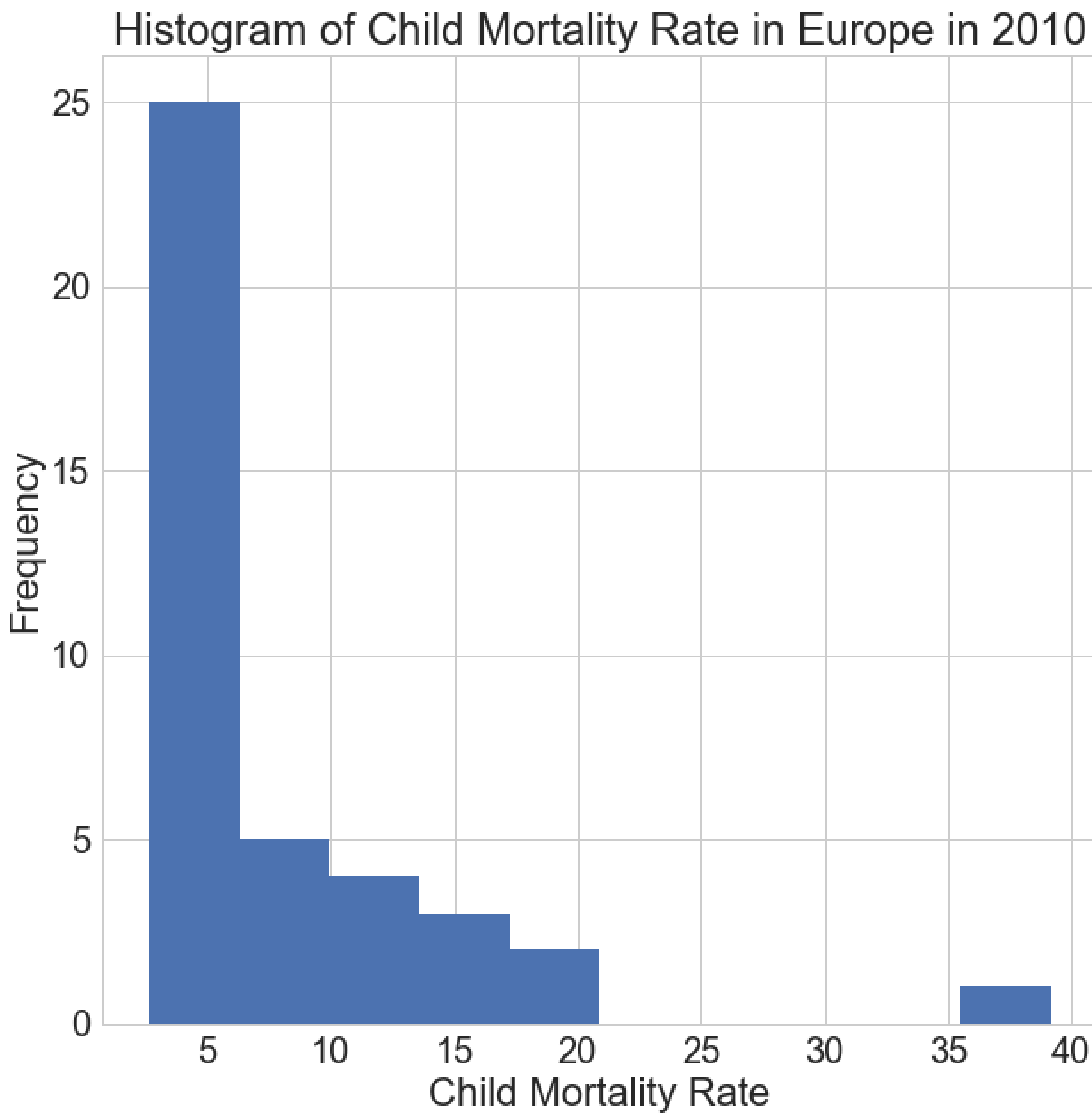
```
In [687]: # Americas
          americas = child_mortality[child_mortality['Four Regions'] == 'americas'].reset_inde

          # Eurpe
          europe = child_mortality[child_mortality['Four Regions'] == 'europe'].reset_index(dro

          # Asia
          asia = child_mortality[child_mortality['Four Regions'] == 'asia'].reset_index(drop =

          # Africa
          africa = child_mortality[child_mortality['Four Regions'] == 'africa'].reset_index(dro
```

Plot a histogram of child mortality rate for each region.

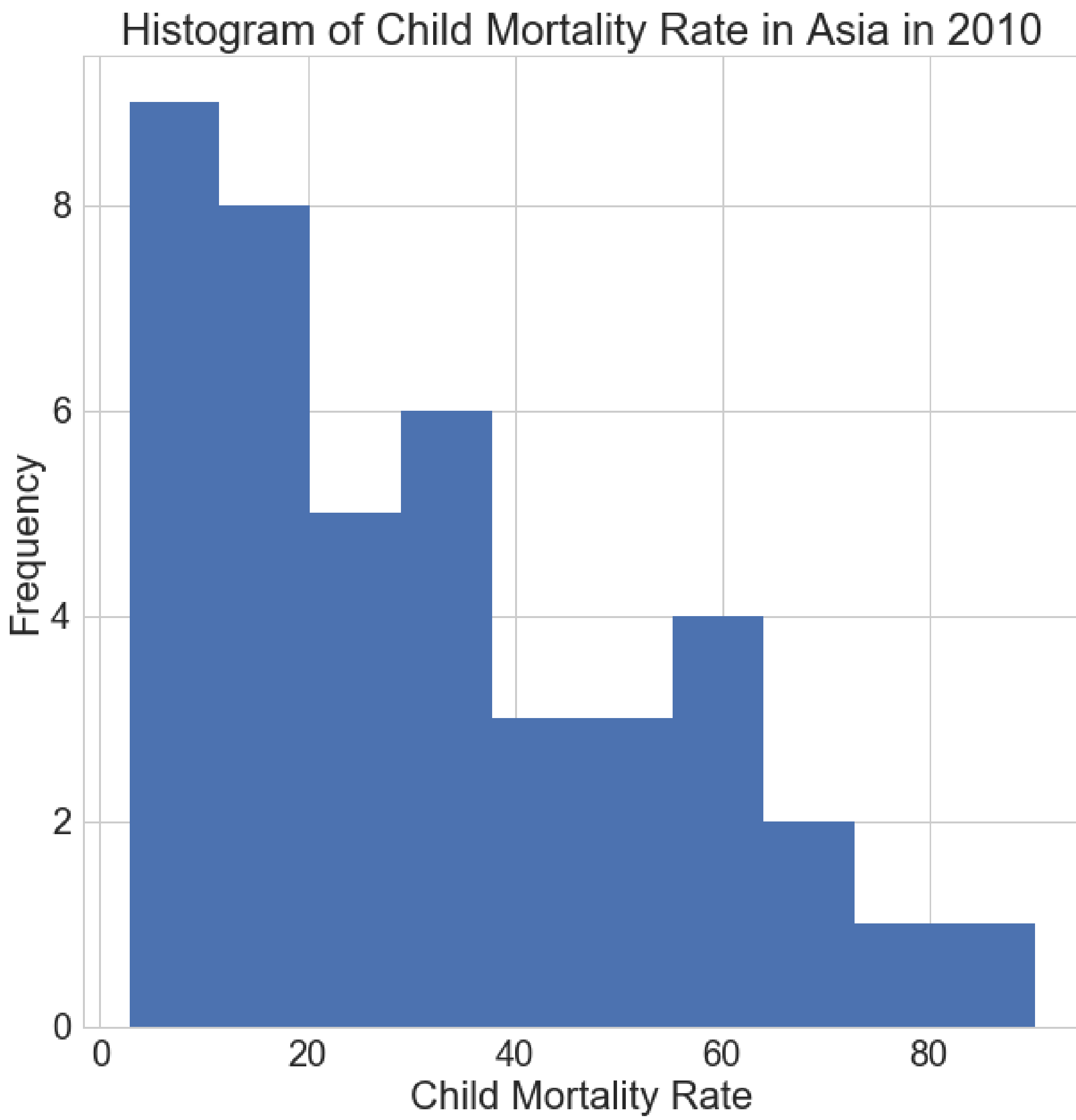
```
In [688]: # Histogram of child mortality rate in Americas
          americas.hist('Child Mortality Rate')

          plt.xlabel('Child Mortality Rate')
          plt.ylabel('Frequency')
          plt.title('Histogram of Child Mortality Rate in Americas in 2010')

Out[688]: Text(0.5,1,'Histogram of Child Mortality Rate in Americas in 2010')
```



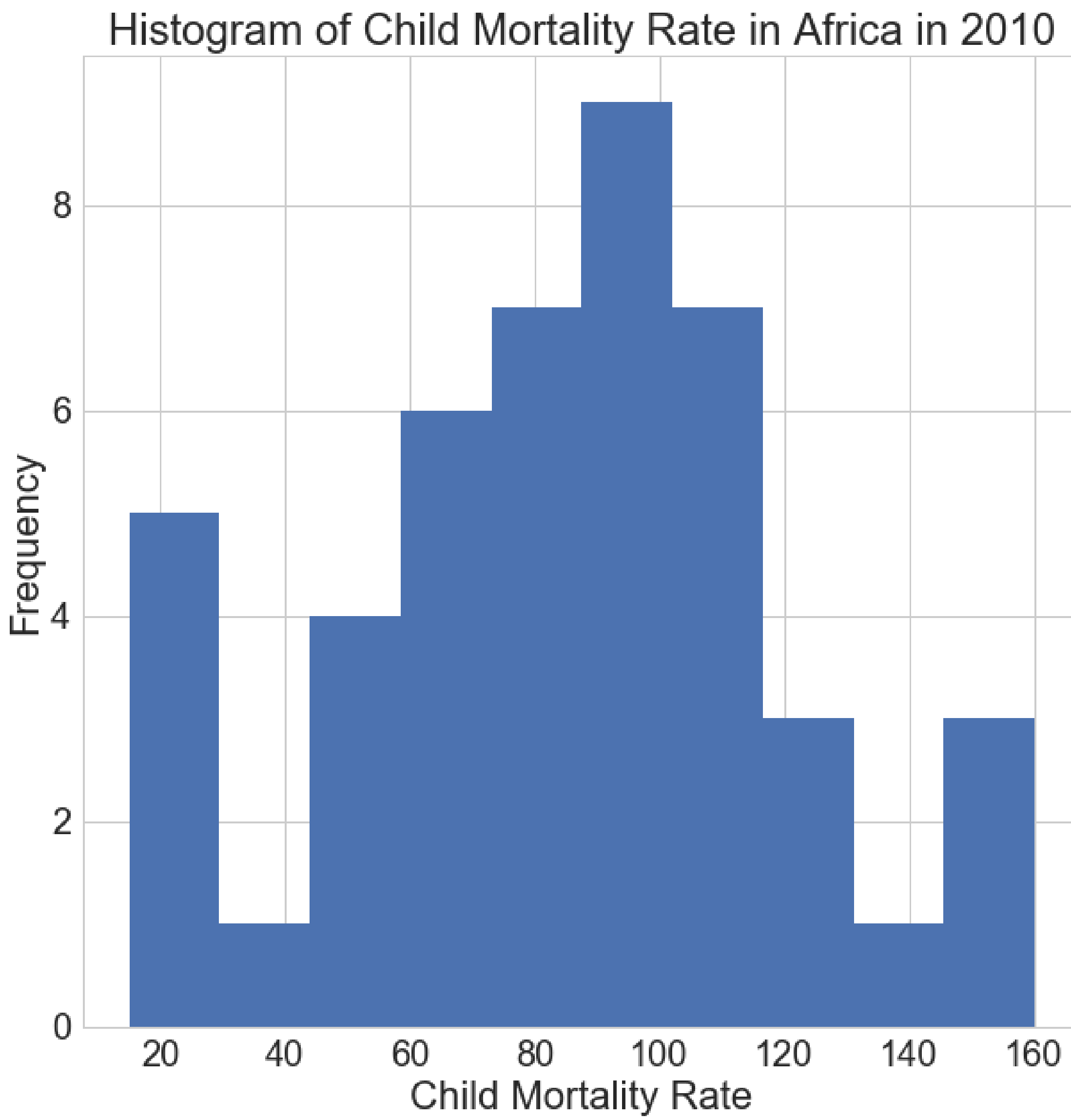

```
In [689]: # Histogram of child mortality rate in Europe
          europe.hist('Child Mortality Rate')
          plt.xlabel('Child Mortality Rate')
          plt.ylabel('Frequency')
          plt.title('Histogram of Child Mortality Rate in Europe in 2010')

Out[689]: Text(0.5,1,'Histogram of Child Mortality Rate in Europe in 2010')
```




```
In [690]: # Histogram of child mortality rate in Asia
          asia.hist('Child Mortality Rate')
          plt.xlabel('Child Mortality Rate')
          plt.ylabel('Frequency')
          plt.title('Histogram of Child Mortality Rate in Asia in 2010')

Out[690]: Text(0.5,1,'Histogram of Child Mortality Rate in Asia in 2010')
```




```
In [691]: # Histogram of child mortality rate in Africa
          africa.hist('Child Mortality Rate')
          plt.xlabel('Child Mortality Rate')
          plt.ylabel('Frequency')
          plt.title('Histogram of Child Mortality Rate in Africa in 2010')

Out[691]: Text(0.5,1,'Histogram of Child Mortality Rate in Africa in 2010')
```



Only Africa has a normal distribution. Let's go ahead and carry out the Kruskal-Wallis H Test. (https://docs.scipy.org/doc/scipy/reference/generated/scipy.stats.kruskal.html#scipy.stats.kruskal). According to the Scipy documentation, this test tests "the null hypothesis that the population median of all of the groups are equal" and it is the nonparametric version of ANOVA. There are also assumptions for the Kruskal-Wallis H Test, let's check if our data meet the assumptions. (https://statistics.laerd.com/spss-tutorials/kruskal-wallis-h-test-using-spss-statistics.php) (http://www.biostathandbook.com/kruskalwallis.html)

- Dependent variable is measured at ordinal or continuous level (child mortality is at continuous level => checked)
- Independent variables: two or more categorical and indendent groups (our four regions => checked)
- Independece of observations: checked

- Different groups have the similar distribution and groups with different standard deviations have different distributions. Let's look at the summary statistics and compare those with the histograms for each region to check this.

```
In [692]: # Summary statistics regarding child mortality rate of each of the four regions
          child_mortality.groupby('Four Regions').describe()
```

```
Out[692]:             Child Mortality Rate                                              \
                                     count       mean        std   min     25%    50%
          Four Regions
          africa                      46.0  84.780435  35.506761  15.0  62.575  85.65
          americas                    27.0  26.737037  37.562329   5.6  14.000  18.80
          asia                        42.0  31.359524  22.316351   2.8  13.625  25.10
          europe                      40.0   7.640000   6.929269   2.6   3.875   4.50


                           75%    max
          Four Regions
          africa        110.50  160.0
          americas       24.35  208.0
          asia           46.35   90.2
          europe          8.20   39.2
```

Since americas has a clear outlier (Haiti) which can greatly affect the standard deviation, let's drop Haiti and compute the summary statistics again.

```
In [693]: # Return the row corresponding to 'Haiti'
          americas[americas['Country'] == 'Haiti']
```

```
Out[693]:    Country  Child Mortality Rate Four Regions  Eight Regions  \
          16   Haiti                 208.0     americas  america_north

             World Bank Income Group
          16              Low income
```

```
In [694]: # Drop Haiti row
          americas.drop(16, inplace = True)
```

```
In [695]: # Now, check the summary statistics for americas with Haiti not being in the picture
          americas.describe()
```

```
Out[695]:        Child Mortality Rate
          count             26.000000
          mean              19.765385
          std               10.127544
          min                5.600000
          25%               13.900000
          50%               18.700000
          75%               24.100000
          max               46.600000
```

The standard deviation goes from 37 to 10. What a change. Now we can safely say that the distribution of different groups (Asia, Europe, Americas) have similar shape (from the histograms: right-skewed distribution) and the distribution of the group with different standard deviation (Africa) is different (normal distribution). The fourth assumption is met. Let's go ahead and carry out the Kruskal-Wallis H Test.

In [696]:
```
# Kruskal test from the 'scipy'
# https://docs.scipy.org/doc/scipy/reference/generated/scipy.stats.kruskal.html

stats.kruskal(americas['Child Mortality Rate'], europe['Child Mortality Rate'],
              asia['Child Mortality Rate'], africa['Child Mortality Rate'])
```

Out[696]:
```
KruskalResult(statistic=102.99235987111058, pvalue=3.5317730005966083e-22)
```

With such an extremely small p-value, we reject the null hypothesis. There is a statistically significant difference of the population median of all the groups (regions) involved for child mortality rate. This confirms our finding earlier and makes our conclusion substantially stronger.

To conclude, there is a striking difference on child mortality rate among different regions in the world in 2010. Europe has the lowest child mortality rate and Africa has the highest. Haiti is the outlier with more than 200 deaths per 1000 live births in 2010, most likely due to the devastating 2010 earthquake. Now, we will move on to the next quesion.

1.1.5 Question 2: Is improved sanitation associated with a reduction in child mortality?

To answer this question, let's look at the correlation of improved sanitation and child mortality rate, then compute the Pearson correlation and plot a scatter plot to show the relationship between the two.

In [697]:
```
# Return the correlation pairs for all variables in 'project' dataset
project.corr()
```

Out[697]:
```
                                        Child Mortality Rate  \
Child Mortality Rate                                1.000000
Government Expenditure on Health (USD)             -0.428113
Improved Sanitation Proportion                     -0.846058
Life Expectancy                                    -0.891286

                                        Government Expenditure on Health (USD)  \
Child Mortality Rate                                                  -0.428113
Government Expenditure on Health (USD)                                 1.000000
Improved Sanitation Proportion                                         0.453286
Life Expectancy                                                        0.530483

                                        Improved Sanitation Proportion  \
Child Mortality Rate                                         -0.846058
Government Expenditure on Health (USD)                        0.453286
Improved Sanitation Proportion                                1.000000
Life Expectancy                                               0.791415
```

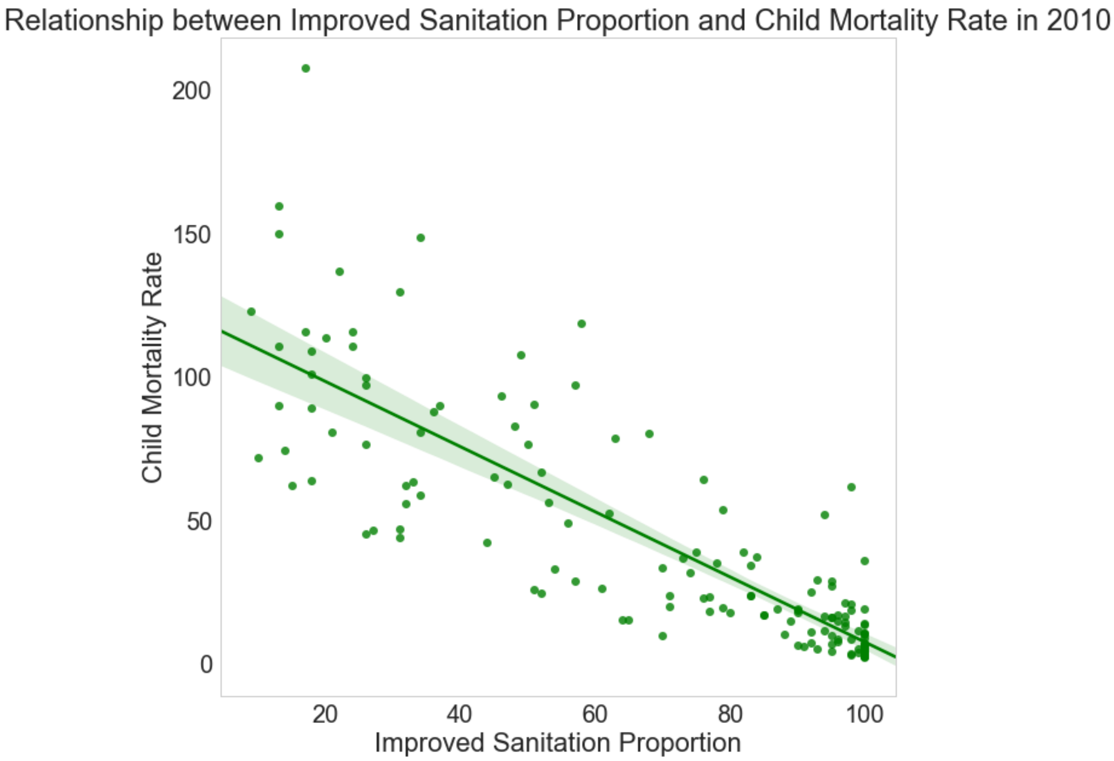
```
                                                  Life Expectancy
Child Mortality Rate                                    -0.891286
Government Expenditure on Health (USD)                  0.530483
Improved Sanitation Proportion                          0.791415
Life Expectancy                                         1.000000
```

We can see that 'Improved Sanitation Proportion' is strongly and negatively associated with 'Child Mortality Rate', suggesting that improved sanitation is definitely associated with a reduction in child mortality. Let's test the strength of the association and draw the linear fit line on a scatter plot.

```
In [698]: # Pearson correlation
          # https://docs.scipy.org/doc/scipy-0.14.0/reference/generated/scipy.stats.pearsonr.h

          stats.pearsonr(project['Improved Sanitation Proportion'],
                         project['Child Mortality Rate'])

Out[698]: (-0.84605755659259674, 1.2051906041551455e-43)
```

Result from the Pearson correlation test confirms that the association is strong, negative, and statistically significant (indicated by an extremely low p-value). Time for the scatterplot to visualize the relationship between these two variables.

```
In [699]: # http://seaborn.pydata.org/generated/seaborn.regplot.html?highlight=regplot#seaborn
          # https://seaborn.pydata.org/generated/seaborn.set_context.html

          sns.set(rc={'figure.figsize':(10,10)}) # figure size
          sns.set_style('whitegrid', {'axes.grid' : False}) # white background and remove grid
          sns.set_context("notebook", font_scale=2.0) # increase size of axis title
                                                      # and choose 'notebook' context

          # plot a regression plot (scatter plot + linear fit)
          sns.regplot(x = 'Improved Sanitation Proportion',
                       # independent variable:'Improved Sanitation Proportion'
                      y = 'Child Mortality Rate', color = 'g', # green color
                       # dependent variable: 'Child Mortality Rate'
                      data = project).set_title( # data # set title
              'Relationship between Improved Sanitation Proportion and Child Mortality Rate in

Out[699]: Text(0.5,1,'Relationship between Improved Sanitation Proportion and Child Mortality R
```

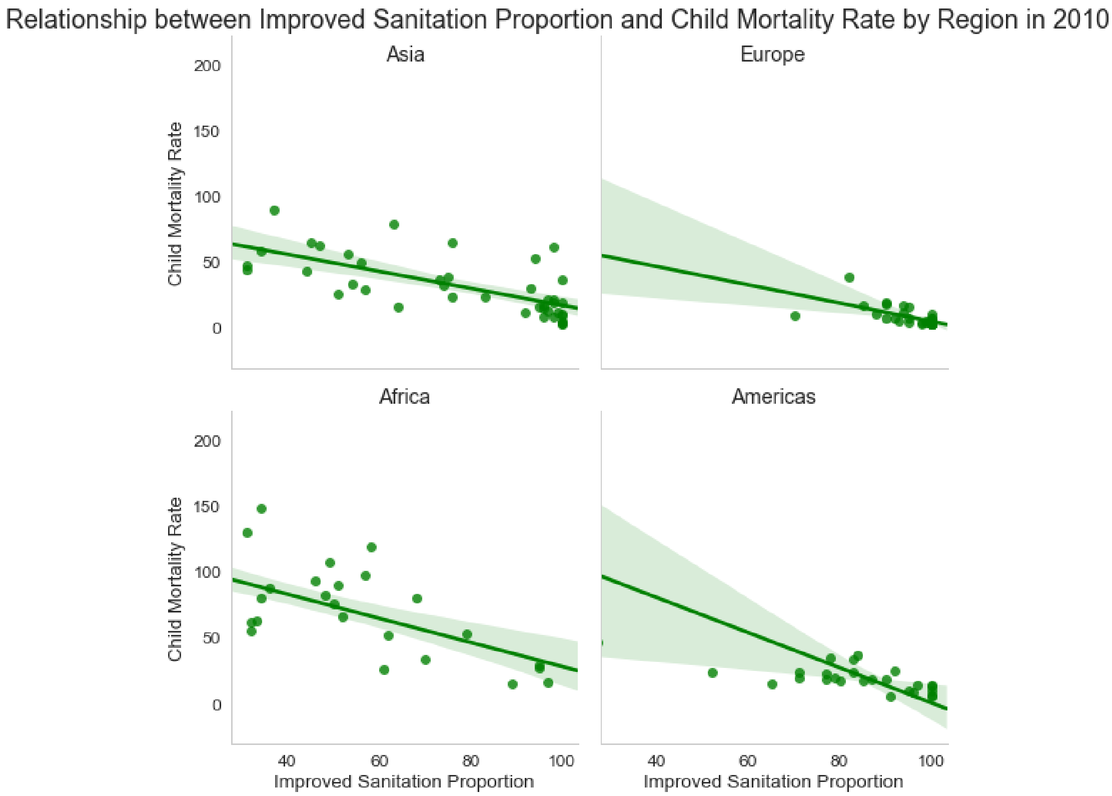


The negative association is clear and strong. We can conclude that the higher proportion of population having access to improved sanitation facilities is associated with the lower child mortality rate. Just like before, let's look at the association by region.

```
In [700]: # https://seaborn.pydata.org/generated/seaborn.FacetGrid.html
          # http://seaborn.pydata.org/generated/seaborn.regplot.html?highlight=regplot#seaborn
          # https://seaborn.pydata.org/generated/seaborn.set_context.html
          # https://stackoverflow.com/questions/29813694/how-to-add-a-title-to-seaborn-facet-p
          # https://stackoverflow.com/questions/43920341/python-seaborn-facetgrid-change-title
          # https://stackoverflow.com/questions/12750355/python-matplotlib-figure-title-overla
          sns.set(rc={'figure.figsize':(5,5)}) # figure size
          sns.set_style('whitegrid', {'axes.grid' : False}) # set white background and remove
          sns.set_context("notebook", font_scale = 1.2) # increase size of axis title
                                                         # choose 'notebook' context
          g = sns.FacetGrid(project, col = "Four Regions", # divide plots by regions
                            col_wrap = 2, size = 4) # two columns and size of faceted plots

          # scatter plot + linear fit
          g = g.map(sns.regplot, 'Improved Sanitation Proportion','Child Mortality Rate', colo

          g.fig.suptitle(
              'Relationship between Improved Sanitation Proportion and Child Mortality Rate by
              fontsize = 18) # Main title
```

```
# set titles for subplots, adjusting the titles of the first two plots on the first
    # so that they won't overlap with the title
axes = g.axes.flatten() #
axes[0].set_title("Asia", y = 0.9)
axes[1].set_title("Europe" , y = 0.9)
axes[2].set_title("Africa")
axes[3].set_title("Americas")
```

Out[700]: Text(0.5,1,'Americas')



It is very clear that the negative association is reflected in each region. According to the analyses we did earlier, it's not a surprise that the proportion of improved sanitation tends to be higher in Europe and Americas. There are only a few countries in Africa with proportion of improved sanitation greater than 80%. To see the contrast of Europe and Africa, we can employ one more plot, the pair plot broken down by four regions. But first, let's test the strength of the association in each region by using the Pearson test.

In [701]:
```
# Create four subsets for four regions, remove the outlier Haiti

# Americas
americas_sanitation = project[project['Four Regions'] == 'americas'].reset_index(dro

# Europe
```

```
europe_sanitation = project[project['Four Regions'] == 'europe'].reset_index(drop = T

# Asia
asia_sanitation = project[project['Four Regions'] == 'asia'].reset_index(drop = True)

# Africa
africa_sanitation = project[project['Four Regions'] == 'africa'].reset_index(drop = T
```

In [702]:
```
# Get the row corresponding with Haiti
americas_sanitation[americas_sanitation['Country'] == 'Haiti']
```

Out[702]:
```
   Country  Child Mortality Rate  Government Expenditure on Health (USD)  \
16   Haiti                 208.0                                9.953451

    Improved Sanitation Proportion  Life Expectancy Four Regions  \
16                            17.0             32.2     americas

    Eight Regions World Bank Income Group
16  america_north              Low income
```

In [703]:
```
# Drop Haiti and make the change permanent
americas_sanitation.drop(16, inplace = True)
```

In [704]:
```
# Pearson correlation
# https://docs.scipy.org/doc/scipy-0.14.0/reference/generated/scipy.stats.pearsonr.h
# Americas
stats.pearsonr(x = americas_sanitation['Improved Sanitation Proportion'],
               y = americas_sanitation['Child Mortality Rate'])
```

Out[704]:
```
(-0.68770345296026558, 0.00010356493075546005)
```

In [705]:
```
# Europe
stats.pearsonr(x = europe_sanitation['Improved Sanitation Proportion'],
               y = europe_sanitation['Child Mortality Rate'])
```

Out[705]:
```
(-0.63552330142848112, 1.0530407683225872e-05)
```

In [706]:
```
# Asia
stats.pearsonr(x = asia_sanitation['Improved Sanitation Proportion'],
               y = asia_sanitation['Child Mortality Rate'])
```

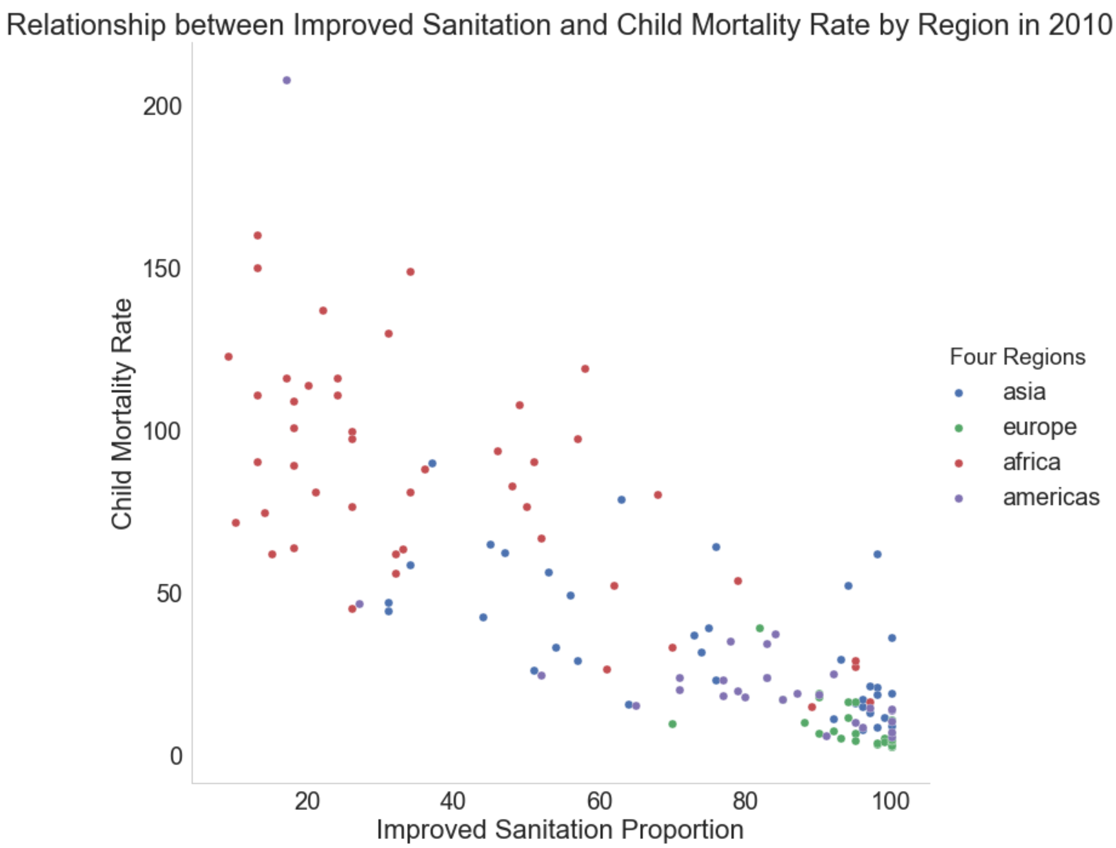
Out[706]:
```
(-0.68559909916605, 5.4436779105670047e-07)
```

In [707]:
```
# Africa
stats.pearsonr(x = africa_sanitation['Improved Sanitation Proportion'],
               y = africa_sanitation['Child Mortality Rate'])
```

Out[707]:
```
(-0.64282655050613313, 1.4570466853980898e-06)
```

The negative association is strong, consistent, and statistically significant in each case. Now, let's plot the pair plot broken down by region.

```
In [708]: # http://seaborn.pydata.org/generated/seaborn.regplot.html?highlight=regplot#seaborn
          # https://seaborn.pydata.org/generated/seaborn.set_context.html
          # https://seaborn.pydata.org/generated/seaborn.pairplot.html

          sns.set(rc={'figure.figsize':(10,10)}) # figure size
          sns.set_style('whitegrid', {'axes.grid' : False}) # set background white and remove
          sns.set_context("notebook", font_scale=2) # increase size of axis title
                                                    # & set context to 'notebook'

          # scatterplot, 'hue' indicates the regions broken down
          sns.pairplot(x_vars=['Improved Sanitation Proportion'], # independent variable
                       y_vars=['Child Mortality Rate'], data = project, # dependent variabl #
                       hue="Four Regions", # regions and size
                       size=10)

          plt.title( # add a title
              'Relationship between Improved Sanitation and Child Mortality Rate by Region in

Out[708]: Text(0.5,1,'Relationship between Improved Sanitation and Child Mortality Rate by Reg
```



Clearly , most of the red dots (Africa) are on the left side (lower proportion of population having access to improved sanitation) while all the green dots (Europe) stay on the right side (higher proportion of population having access to improved sanitation). There is only one country in Europe with improved sanitation less than 80%.

Question 3 : Does health spending negatively correlate with child mortality? Just like before, we will look at the correlation table first, then we will confirm with carrying out Pearson test and plotting the scatter plot, and eventually, we will look at the trend in different regions.

```
In [709]: # Correlation table indicating the strength and direction of association
              # between each pair of 'project'
          project.corr()
```

```
Out[709]:                                         Child Mortality Rate  \
          Child Mortality Rate                                1.000000
          Government Expenditure on Health (USD)             -0.428113
          Improved Sanitation Proportion                     -0.846058
          Life Expectancy                                    -0.891286

                                                  Government Expenditure on Health (USD)  \
          Child Mortality Rate                                                 -0.428113
          Government Expenditure on Health (USD)                                1.000000
          Improved Sanitation Proportion                                        0.453286
          Life Expectancy                                                       0.530483

                                                  Improved Sanitation Proportion  \
          Child Mortality Rate                                         -0.846058
          Government Expenditure on Health (USD)                        0.453286
          Improved Sanitation Proportion                                1.000000
          Life Expectancy                                               0.791415

                                                  Life Expectancy
          Child Mortality Rate                          -0.891286
          Government Expenditure on Health (USD)         0.530483
          Improved Sanitation Proportion                 0.791415
          Life Expectancy                                1.000000
```

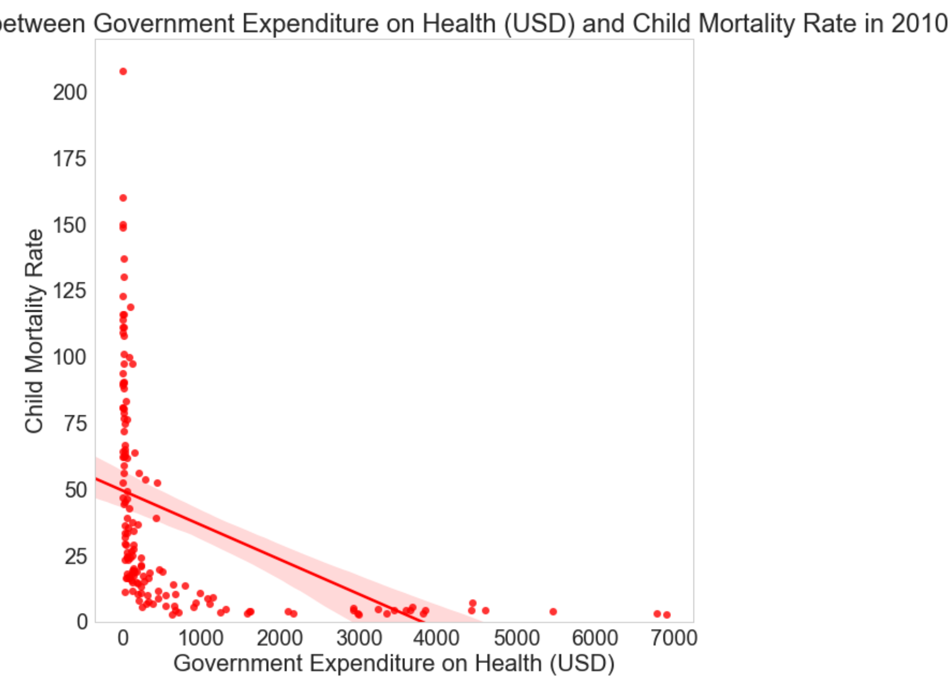
Health spending (Government expenditure per capita on health) is also negatively and weakly correlated with child mortality rate. It means a higher spending on health is associated with a lower child mortality rate. Let's confirm that by performing Pearson correlation test and plotting a scatter plot with a linear fit line.

```
In [710]: # Pearson correlation
          # https://docs.scipy.org/doc/scipy-0.14.0/reference/generated/scipy.stats.pearsonr.h
          stats.pearsonr(project['Government Expenditure on Health (USD)'],
                         project['Child Mortality Rate'])
```

```
Out[710]: (-0.42811287597410069, 2.7491302283195621e-08)
```

The result from the Pearson correlation test shows a weak yet statistically significant negative association. Let's look at the association by region then perform Pearson test for each region.

```
In [711]: # http://seaborn.pydata.org/generated/seaborn.regplot.html?highlight=regplot#seaborn
          # https://seaborn.pydata.org/generated/seaborn.set_context.html

          sns.set(rc={'figure.figsize':(10,10)}) # figure size
          sns.set_style('whitegrid', {'axes.grid' : False}) # set white background and remove g
          sns.set_context("notebook", font_scale=2.0) # increase size of axis title
                                                      # and choose 'notebook' content

          # plot a regression plot (scatter plot + linear fit)
          sns.regplot(x = 'Government Expenditure on Health (USD)',
                      # independent variable:'Government Expenditure on Health (USD)'
                     y = 'Child Mortality Rate', color = 'red', # choose red color
                      # dependent variable: 'Child Mortality Rate'
                  data = project).set_title( # data # add a title
          'Relationship between Government Expenditure on Health (USD) and Child Mortality Rate

          plt.ylim(0,220) # limit values of y-axis

Out[711]: (0, 220)
```

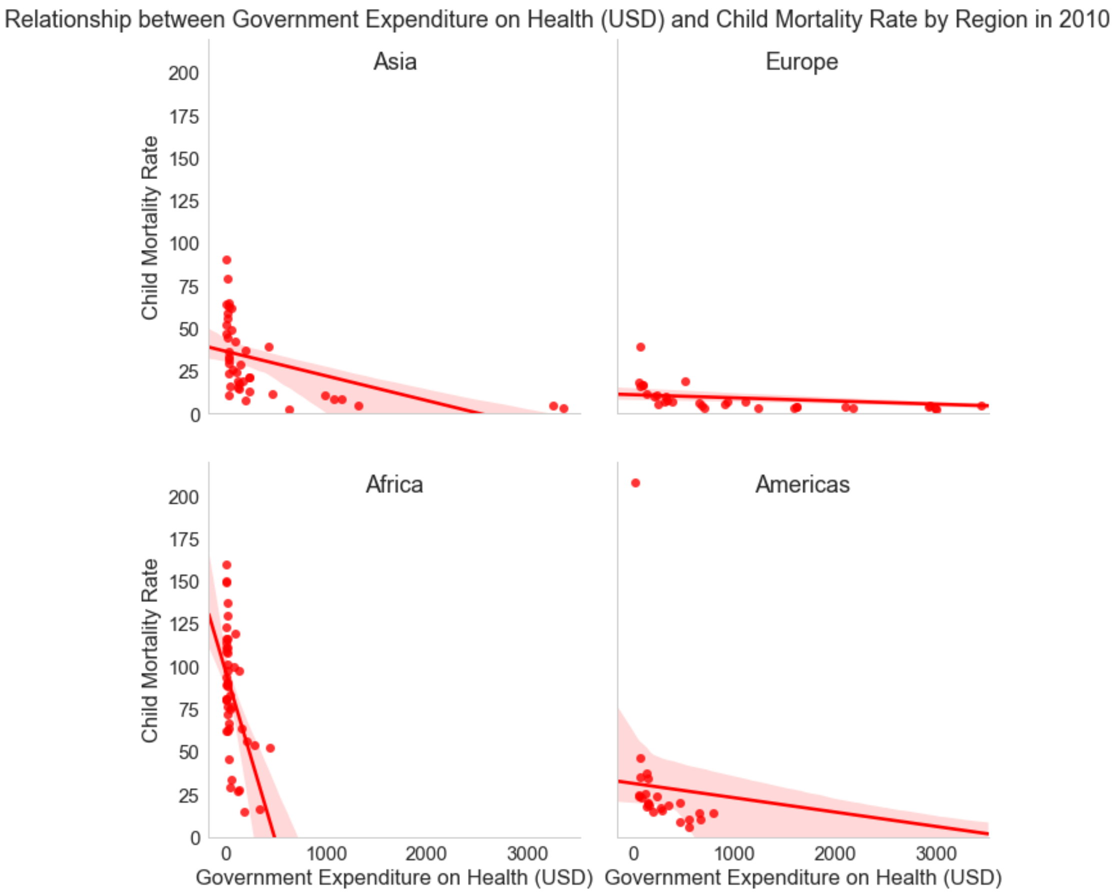


Even though the negative association is there, it is very weak (only -0.4), so the trend is not clear. On the left of the plot, there are many countries with little to no government expenditure on health with apparent difference in child mortality rate. The obvious trend is >1000 USD spent per capita per year is associated with a very low child mortality rate. We can look at the trend further by plotting the scatter plot by regions.

```
In [712]: # https://seaborn.pydata.org/generated/seaborn.FacetGrid.html
          # http://seaborn.pydata.org/generated/seaborn.regplot.html?highlight=regplot#seaborn
```

```python
# https://seaborn.pydata.org/generated/seaborn.set_context.html
# https://stackoverflow.com/questions/29813694/how-to-add-a-title-to-seaborn-facet-p
# https://stackoverflow.com/questions/43920341/python-seaborn-facetgrid-change-title
# https://stackoverflow.com/questions/12750355/python-matplotlib-figure-title-overla
sns.set(rc={'figure.figsize':(10,10)}) # figure size
sns.set_style('whitegrid', {'axes.grid' : False}) # set white background and remove
sns.set_context("notebook", font_scale=1.5) # increase size of axis title
                                            # choose the 'notebook' context
g = sns.FacetGrid(project, col = "Four Regions", # divide plots by regions
                  col_wrap = 2, size = 5) # two columns and size of faceted plots

# scatter plot + linear fit
g = g.map(sns.regplot, 'Government Expenditure on Health (USD)','Child Mortality Rat
          color = 'red') # red color

g.fig.suptitle(
    'Relationship between Government Expenditure on Health (USD) and Child Mortality
    fontsize = 18) # main title

plt.ylim(0,220) # y-axis limit

# set titles for subplots, adjusting the titles of all sub-plots
axes = g.axes.flatten()
axes[0].set_title("Asia", y = 0.9)
axes[1].set_title("Europe" , y = 0.9)
axes[2].set_title("Africa", y = 0.9)
axes[3].set_title("Americas", y = 0.9)
```

Out[712]: Text(0.5,0.9,'Americas')



These four plots show the negative yet weak association between health spending and child mortality rate. Let's confirm this and see how strong such association is by performing correlation test by region.

```
In [713]: # Create four subsets for four regions, remove the outlier Haiti

          # Americas
          americas_spending = project[project['Four Regions'] == 'americas'].reset_index(drop =

          # Europe
          europe_spending = project[project['Four Regions'] == 'europe'].reset_index(drop = Tr

          # Asia
          asia_spending = project[project['Four Regions'] == 'asia'].reset_index(drop = True)

          # Africa
          africa_spending = project[project['Four Regions'] == 'africa'].reset_index(drop = Tr

In [714]: # Get the row corresponding to Haiti
          americas_spending[americas_spending['Country'] == 'Haiti']
```

Out[714]:
```
   Country  Child Mortality Rate  Government Expenditure on Health (USD)  \
16   Haiti                 208.0                                9.953451

    Improved Sanitation Proportion  Life Expectancy Four Regions  \
16                            17.0             32.2     americas

    Eight Regions World Bank Income Group
16  america_north              Low income
```

In [715]:
```
# Drop Haiti and make the change permanent
americas_spending.drop(16, inplace = True)
```

In [716]:
```
# Pearson correlation
# https://docs.scipy.org/doc/scipy-0.14.0/reference/generated/scipy.stats.pearsonr.h

# Americas
stats.pearsonr(x = americas_spending['Government Expenditure on Health (USD)'],
               y = americas_spending['Child Mortality Rate'])
```

Out[716]:
```
(-0.50156992346077689, 0.00904013994165212)
```

In [717]:
```
# Europe
stats.pearsonr(x = europe_spending['Government Expenditure on Health (USD)'],
               y = europe_spending['Child Mortality Rate'])
```

Out[717]:
```
(-0.50739425901048729, 0.00083262269672421585)
```

In [718]:
```
# Asia
stats.pearsonr(x = asia_spending['Government Expenditure on Health (USD)'],
               y = asia_spending['Child Mortality Rate'])
```

Out[718]:
```
(-0.48123520014451154, 0.0012539307605853318)
```

In [719]:
```
# Africa
stats.pearsonr(x = africa_spending['Government Expenditure on Health (USD)'],
               y = africa_spending['Child Mortality Rate'])
```

Out[719]:
```
(-0.5333188143724461, 0.00013548134787950031)
```

Pearson correltion test for each region shows a weak yet statistically significant negative association between child moratlity rate and health spending. Since the association is weak, we find it unnecessary to look at the trend further by region. Let's move on to question 4.

Question 4 : Is there a negative correlation between life expectancy and child mortality? Since these are all numeric data, we will follow the same approach. + Investigate the correlation table first and carry out Pearson test + Confirm finding with plotting + Explore trend(s) in different regions.

In [720]:
```
# Get the correlation table to see the pairwise association of variables in 'project
project.corr()
```

```
Out[720]:                                          Child Mortality Rate  \
          Child Mortality Rate                                 1.000000
          Government Expenditure on Health (USD)              -0.428113
          Improved Sanitation Proportion                      -0.846058
          Life Expectancy                                     -0.891286

                                                   Government Expenditure on Health (USD)  \
          Child Mortality Rate                                                  -0.428113
          Government Expenditure on Health (USD)                                 1.000000
          Improved Sanitation Proportion                                         0.453286
          Life Expectancy                                                        0.530483

                                                   Improved Sanitation Proportion  \
          Child Mortality Rate                                          -0.846058
          Government Expenditure on Health (USD)                         0.453286
          Improved Sanitation Proportion                                 1.000000
          Life Expectancy                                                0.791415

                                                   Life Expectancy
          Child Mortality Rate                           -0.891286
          Government Expenditure on Health (USD)          0.530483
          Improved Sanitation Proportion                  0.791415
          Life Expectancy                                 1.000000
```

Looking at the correlation table, we can see there is a strong negative association between 'Life Expectancy' and 'Child Mortality Rate' (-0.89). It indicates that countries with higher life expectancy tends to have lower child mortality rate. Let's confirm this finding with performing Pearson test and plotting scatter plots with linear fit.

```
In [721]: # Pearson correlation
          # https://docs.scipy.org/doc/scipy-0.14.0/reference/generated/scipy.stats.pearsonr.h
          stats.pearsonr(project['Life Expectancy'],
                         project['Child Mortality Rate'])
```

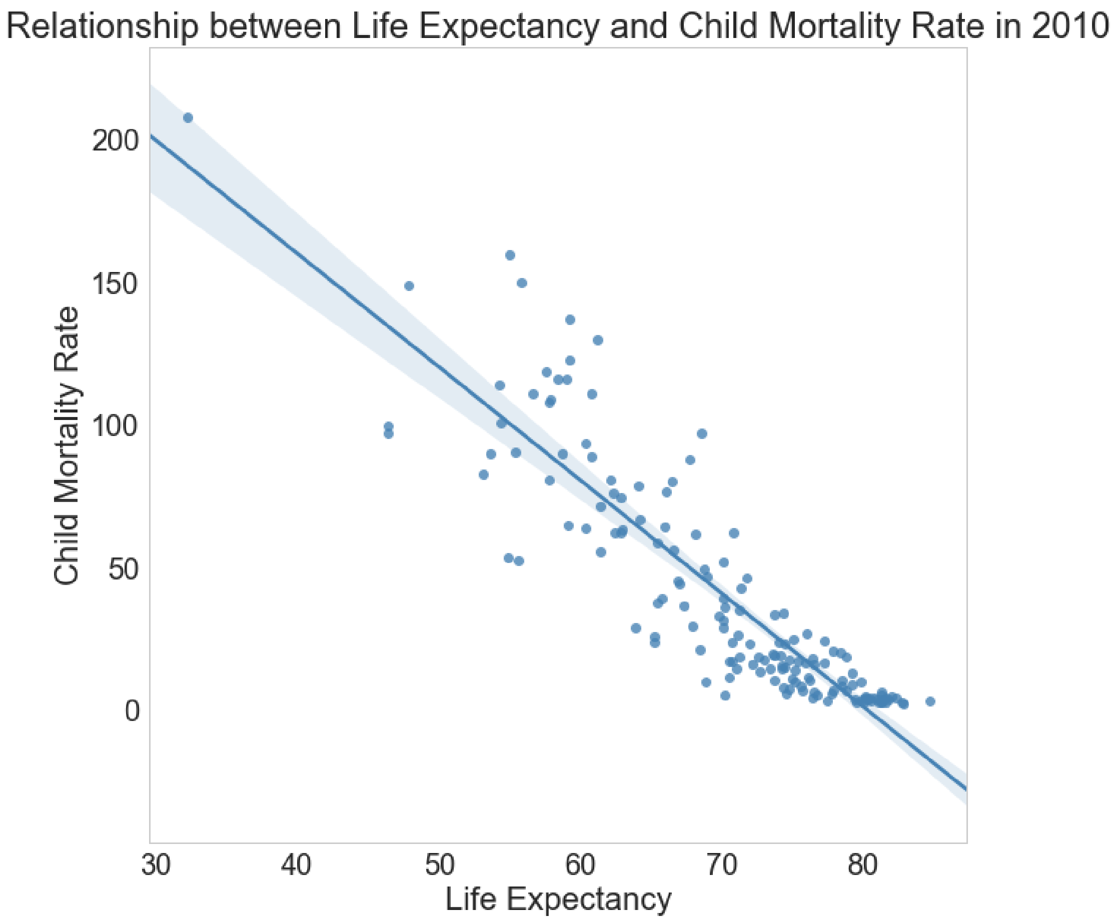
```
Out[721]: (-0.89128586778137775, 2.0227806671483004e-54)
```

Result from the Pearson correlation test confirms that the association is extremely strong, negative, and statistically significant (indicated by an extremely low p-value). Now, let's plot a scatterplot to visualize the relationship between these two variables.

```
In [722]: # http://seaborn.pydata.org/generated/seaborn.regplot.html?highlight=regplot#seaborn
          # https://seaborn.pydata.org/generated/seaborn.set_context.html
          sns.set(rc={'figure.figsize':(10,10)}) # figure size
          sns.set_style('whitegrid', {'axes.grid' : False}) # set white background and remove
          sns.set_context("notebook", font_scale=2.0) # increase size of axis title
                                                      # choose "notebook" context

          # plot a regression plot (scatter plot + linear fit)
          sns.regplot(x = 'Life Expectancy',
```

```
                  # independent variable:'Life Expectancy'
                 y = 'Child Mortality Rate',
                  # dependent variable: 'Child Mortality Rate'
                  color = 'steelblue', # choose color
                 data = project).set_title( # data # set title
          'Relationship between Life Expectancy and Child Mortality Rate in 2010')
```

Out[722]: Text(0.5,1,'Relationship between Life Expectancy and Child Mortality Rate in 2010')

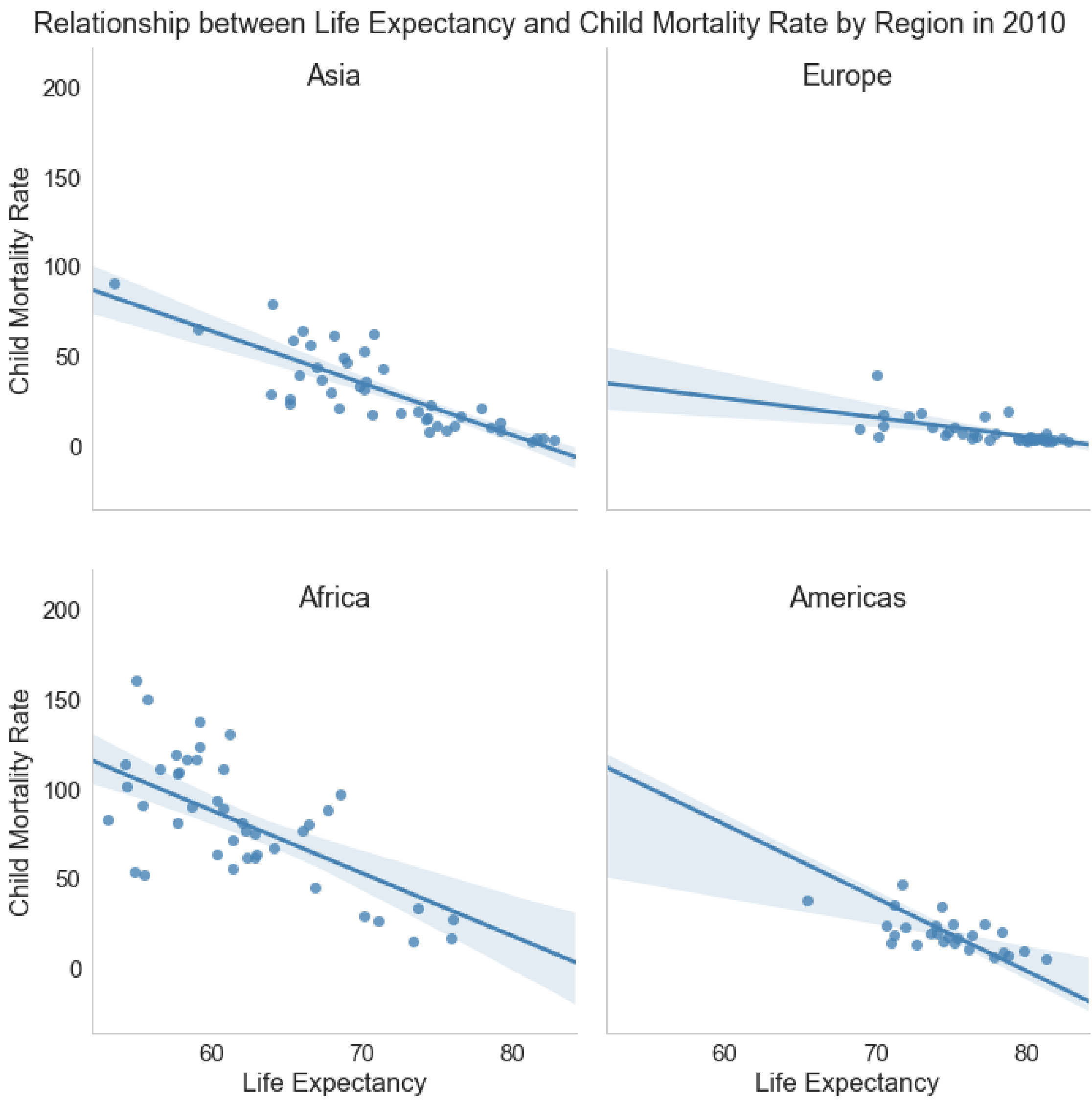


The extremely strong negative association between life expectancy and child mortality rate (strongest out of three independent variables versus the dependent variable) is undoubtedly observed here. Most points cluster around the linear fit line very closely. Also, we can see that the majority of points (countries) are having life expectancy greater than 60, as we noted earlier in the statistical summary. Now, let's look at the break down by region. We will want to plot two types of plots: the four scatter plots for each region and the pair plot with all regions in one plot.

In [723]:
```
# https://seaborn.pydata.org/generated/seaborn.FacetGrid.html
# http://seaborn.pydata.org/generated/seaborn.regplot.html?highlight=regplot#seaborn
# https://seaborn.pydata.org/generated/seaborn.set_context.html
# https://stackoverflow.com/questions/29813694/how-to-add-a-title-to-seaborn-facet-p
```

```
# https://stackoverflow.com/questions/43920341/python-seaborn-facetgrid-change-title
# https://stackoverflow.com/questions/12750355/python-matplotlib-figure-title-overla

sns.set(rc={'figure.figsize':(10,10)}) # figure size
sns.set_style('whitegrid', {'axes.grid' : False}) # set white background and remove
sns.set_context("notebook", font_scale=1.5) # increase size of axis title
                                            # choose 'notebook' context
g = sns.FacetGrid(project, col = "Four Regions", # divide plots by regions
                  col_wrap = 2, size = 5) # two columns and size of faceted plots

# scatter plot + linear fit
g = g.map(sns.regplot, 'Life Expectancy','Child Mortality Rate',
          color = 'steelblue')

g.fig.suptitle(
    'Relationship between Life Expectancy and Child Mortality Rate by Region in 2010
    fontsize = 18) # Main title

# set titles for subplots, adjusting the titles of the subplots
axes = g.axes.flatten()
axes[0].set_title("Asia", y = 0.9)
axes[1].set_title("Europe" , y = 0.9)
axes[2].set_title("Africa", y = 0.9)
axes[3].set_title("Americas", y = 0.9)
```

```
Out[723]: Text(0.5,0.9,'Americas')
```



Consistently across regions, we see a strong negative association between life expectancy and child mortality rate. Let's confirm it by performing Pearson tests for this pair of variables by region, then we will plot the scatter plot broken down by region just like we did before.

In [724]:
```
# Create four subsets for four regions, remove the outlier Haiti

# Americas
americas_life_exp = project[project['Four Regions'] == 'americas'].reset_index(drop =

# Europe
europe_life_exp = project[project['Four Regions'] == 'europe'].reset_index(drop = Tr

# Asia
asia_life_exp = project[project['Four Regions'] == 'asia'].reset_index(drop = True)
```

```
# Africa
africa_life_exp = project[project['Four Regions'] == 'africa'].reset_index(drop = Tru
```

```
In [725]: # Get the row correponding to Haiti
          americas_life_exp[americas_life_exp['Country'] == 'Haiti']
```

```
Out[725]:    Country  Child Mortality Rate  Government Expenditure on Health (USD)  \
          16   Haiti                 208.0                                9.953451

              Improved Sanitation Proportion  Life Expectancy Four Regions  \
          16                            17.0             32.2     americas

              Eight Regions World Bank Income Group
          16  america_north               Low income
```

```
In [726]: # Drop Haiti and make the change permanent
          americas_life_exp.drop(16, inplace = True)
```

```
In [727]: # Pearson correlation
          # https://docs.scipy.org/doc/scipy-0.14.0/reference/generated/scipy.stats.pearsonr.h

          # Americas
          stats.pearsonr(x = americas_life_exp['Life Expectancy'],
                         y = americas_life_exp['Child Mortality Rate'])
```

```
Out[727]: (-0.66173356796101257, 0.00023176837285867843)
```

```
In [728]: # Europe
          stats.pearsonr(x = europe_life_exp['Life Expectancy'],
                         y = europe_life_exp['Child Mortality Rate'])
```

```
Out[728]: (-0.62991244148935266, 1.3291895038250314e-05)
```

```
In [729]: # Asia
          stats.pearsonr(x = asia_life_exp['Life Expectancy'],
                         y = asia_life_exp['Child Mortality Rate'])
```

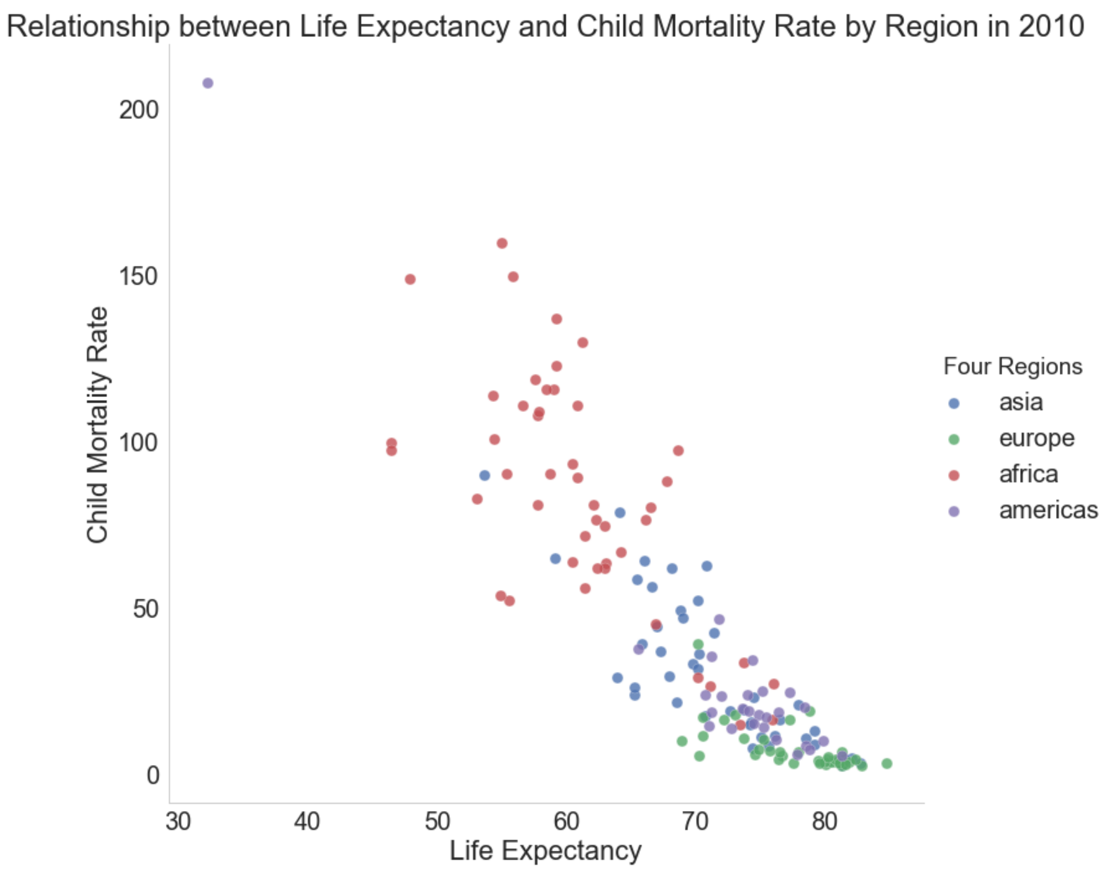
```
Out[729]: (-0.82141472244733282, 2.6537940929934148e-11)
```

```
In [730]: # Africa
          stats.pearsonr(x = africa_life_exp['Life Expectancy'],
                         y = africa_life_exp['Child Mortality Rate'])
```

```
Out[730]: (-0.68311207295951726, 1.6883030523098086e-07)
```

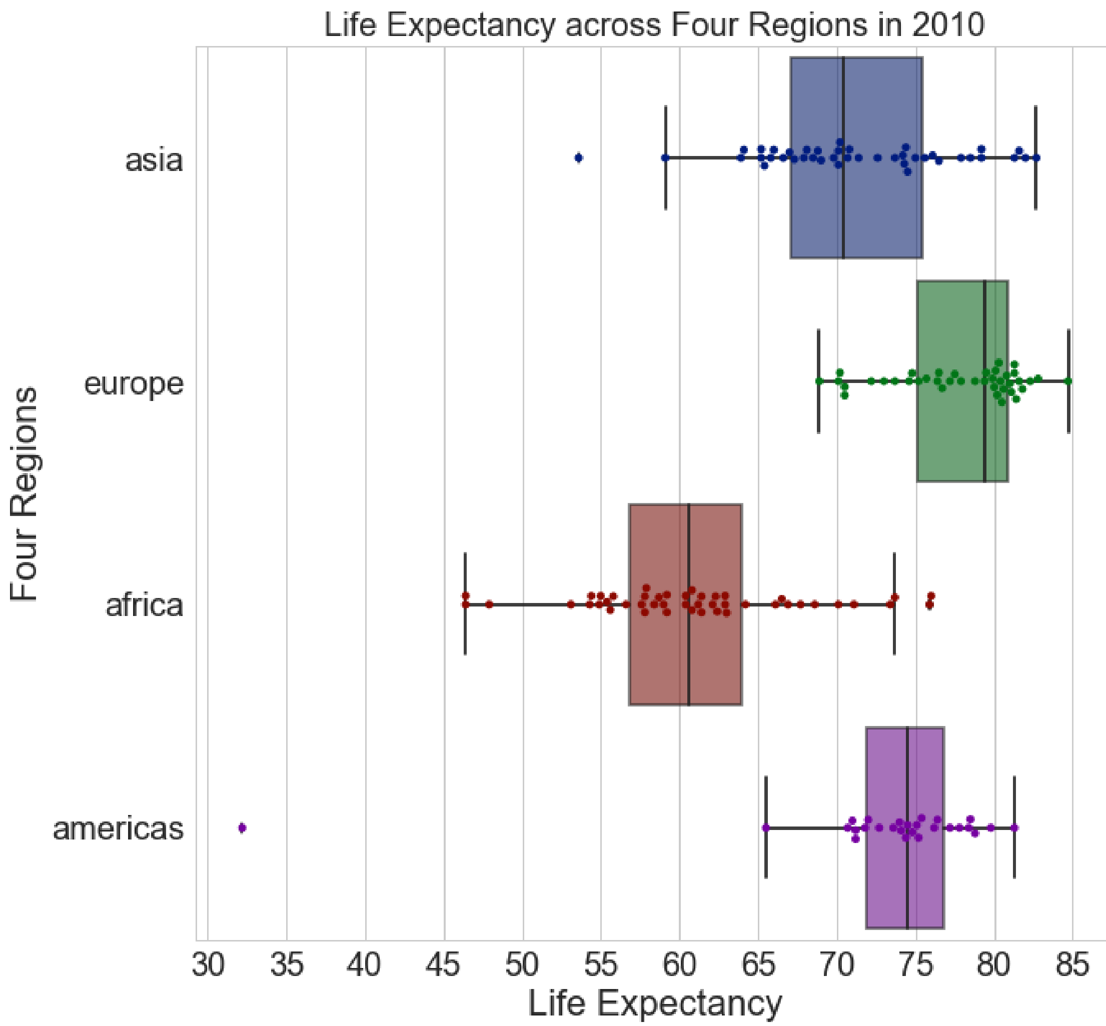
The negative association is strong, consistent, and statistically significant in each case. Now, let's plot the pair plot broken down by region.

```
In [731]: # http://seaborn.pydata.org/generated/seaborn.regplot.html?highlight=regplot#seaborn
          # https://seaborn.pydata.org/generated/seaborn.set_context.html
          # https://seaborn.pydata.org/generated/seaborn.pairplot.html
          # https://stackoverflow.com/questions/42181317/changing-the-size-of-seaborn-pairplot
          # (marker size)

          sns.set(rc={'figure.figsize':(10,10)}) # figure size
          sns.set_style('whitegrid', {'axes.grid' : False}) # set white background and remove
          sns.set_context("notebook", font_scale = 2) # increase size of axis title
                                                        # choose 'notebook' context

          # scatterplot, 'hue' indicates the regions broken down
          sns.pairplot(x_vars=['Life Expectancy'], # independent variable
                       y_vars=['Child Mortality Rate'], data = project, # dependent variabl # 
                       hue = "Four Regions", size = 10, # regions and size
                      plot_kws = {'s':80, 'alpha': 0.8}) # marker size and transparency level

          plt.title( # add a title
              'Relationship between Life Expectancy and Child Mortality Rate by Region in 2010

Out[731]: Text(0.5,1,'Relationship between Life Expectancy and Child Mortality Rate by Region i
```



It comes as no surprise that most African countries have generally lower life expectancy and higher child mortality rate. All countries in Europe have high life expectancy (all except one has life expectancy of more than 70 years of age). Countries in America have high life expectancy and low child mortality rate; the two trends are not as extreme as those of Europe. Asian countries have generally high life expectancy with the majority of the countries have life expectancy greater than 60. It will be interesting to see the life expectancy by region utilizing a box plot and a swarm plot and also see the relationship between life expectancy and child mortality rate by income group. Let's do that.

```
In [732]: # Seaborn boxplot
              # https://seaborn.pydata.org/generated/seaborn.boxplot.html
          # To set figure size in seaborn
              # https://stackoverflow.com/questions/31594549/how-do-i-change-the-figure-size-f
          # To set title in seaborn
              # https://stackoverflow.com/questions/42406233/how-to-add-title-to-seaborn-boxpl
          # Seaborn transparency
              # https://github.com/mwaskom/seaborn/issues/979
          # Set axis size
              # https://seaborn.pydata.org/generated/seaborn.set_context.html

          sns.set(rc={'figure.figsize':(10,10)}) # figure size
          sns.set_style('whitegrid') # white grid
          sns.set_context("notebook", font_scale=2.0) # increase size of axis title
                                                      # choose 'notebook' context
          # plot box plots
          sns.boxplot(y = 'Four Regions', # categories of regions
                         x = 'Life Expectancy',
                         data = project, orient = 'h', # horizontal boxplot
                      boxprops = dict(alpha = 0.6), # transparency level
                     width = 0.9, palette = 'dark', # boxplot width # color palette
              ).set_title('Life Expectancy across Four Regions in 2010', size = 20) # title an

          plt.locator_params(nbins=20) # add more ticks to x-axis for easier interpretation

          # plot swarmplots
          sns.swarmplot(y = 'Four Regions', # categories of regions
                         x = 'Life Expectancy',
                        data = project, palette = 'dark', # data and color palette
          orient = 'h').set_title('Life Expectancy across Four Regions in 2010', # horizontal
                          size = 20) #  size of titke

Out[732]: Text(0.5,1,'Life Expectancy across Four Regions in 2010')
```



Aside from the observations we made earlier, two more observations can be seen here.
+ The majority of countries has high life expectancy. Even for Africa with 25% of countries in the lower end (<57 years of age), 50% of countries in Africa have life expetancy higher than 61 years of age, a very positive trend. + There is one country in Americas with extremely low life expectancy, only 32-33 years of age. From what we observed earlier, since the data come from the year 2010, we suspect this country is Haiti, the country that experienced a devastating earth quake in 2010. Let's confirm our guess.

```
In [733]: # Return the row that has life expectancy less than 35 years of age
          project[project['Life Expectancy'] < 35]
```

```
Out[733]:    Country  Child Mortality Rate  Government Expenditure on Health (USD)  \
          71   Haiti                 208.0                                9.953451

              Improved Sanitation Proportion  Life Expectancy Four Regions  \
          71                            17.0             32.2     americas
```

```
    Eight Regions World Bank Income Group
71  america_north              Low income
```

It's indeed Haiti. Let's explore the life expectancy of Haiti in the years leading up to 2010 and after 2010 to see if it's indeed an outlier.

In [734]:
```
# Choose 5 years before and 5 years after 2010 and filter out the dataframe
cols_year = ['2005', '2006','2007', '2008','2009', '2010', '2011', '2012', '2013', '2
Haiti = life_expectancy_original[life_expectancy_original['Country'] == 'Haiti']
Haiti[cols_year]
```

Out[734]:

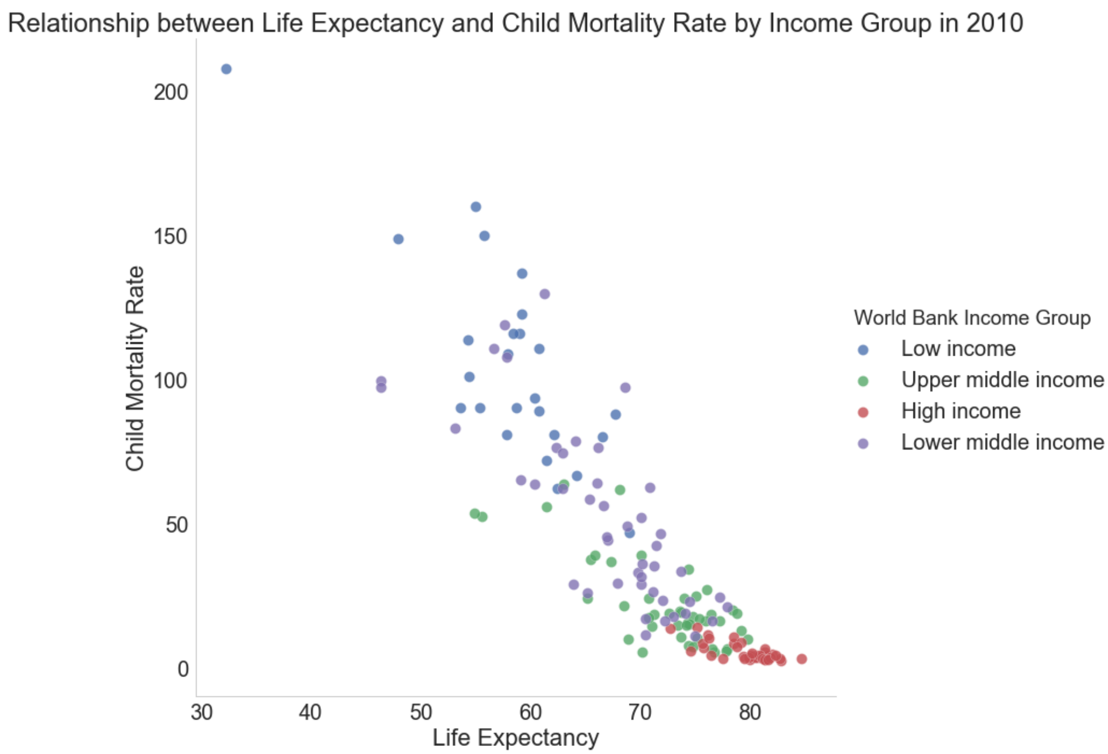
	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015
95	60.0	60.3	60.8	61.0	61.7	32.2	62.4	62.9	63.4	63.8	64.3

Clearly for Haiti, the year of 2010 is an odd year. Their life expectancy drops 50% from 61.7 years of age to 32.2 years of age. However, with the resilience of the country and the help from the international community, the country's life expectancy rose back to higher than the year of 2009 (62.4 years of age) and continued to rise during the years after.

Now, we would like to take a step further to explore the relationship between life expectancy and child mortality rate by income group by plotting a pair plot.

In [735]:
```
# http://seaborn.pydata.org/generated/seaborn.regplot.html?highlight=regplot#seaborn
# https://seaborn.pydata.org/generated/seaborn.set_context.html
# https://seaborn.pydata.org/generated/seaborn.pairplot.html
# https://stackoverflow.com/questions/42181317/changing-the-size-of-seaborn-pairplot-
# (marker size)

sns.set(rc={'figure.figsize':(10,10)}) # figure size
sns.set_style('whitegrid', {'axes.grid' : False}) # set white background and remove
sns.set_context("notebook", font_scale = 2) # increase size of axis title
                                            # choose 'notebook' context

# scatterplot, 'hue' indicates the income groups broken down
sns.pairplot(x_vars=['Life Expectancy'], # independent variable
             y_vars=['Child Mortality Rate'], data = project, # dependent variabl # 
             hue = "World Bank Income Group", size = 10,
            plot_kws = {'s':100, 'alpha': 0.8}) # marker size and transparency level

plt.title( # add a title
    'Relationship between Life Expectancy and Child Mortality Rate by Income Group i
```

Out[735]:
```
Text(0.5,1,'Relationship between Life Expectancy and Child Mortality Rate by Income 
```



Several observations can be made from this plot. + The outlier is Haiti + All high income countries have extremely high life expectancy (>70 years of age) and low child mortality rate (10-15 deaths out of 1000 live births per year) + Upper middle income countries have relatively high life expectancy (majority higher than 65 years of age) and relatively low child mortality rate (majority lower than 40 deaths per 1000 live births per year. + About a half of lower middle income countries have moderately high life expectancy (higher than 63 years of age) and about a half have moderately low child mortality rate (lower than 50 deaths per 1000 live births per year). + The other half of lower middle income countries exhibit the same trend of the low income countries: low life expectancy (less than 63 years of age) and high child mortality rate (more than 50 deahts per 1000 live births per year).

Overall, there is definitely a negative correlation between life expectancy and child mortality and the correlation is strong. Upon looking further into the relationship across regions, we see the similarly strong negative correlation. The breakdown of the association by income group was worthy of attention as clear trends were denoted.

1.1.6 3) Multiple Linear Regression Test

- Dedependent variable: child mortality rate
- Independent variables: improved sanitation, health spending, and life expectancy.

References: + https://datatofish.com/multiple-linear-regression-python/ + http://nbviewer.jupyter.org/github/justmarkham/DAT4/blob/master/notebooks/08_linear_regression.ipynb + http://scikit-learn.org/stable/tutorial/basic/tutorial.html + https://towardsdatascience.com/simple-and-multiple-linear-regression-in-python-c928425168f9 + http://blog.minitab.com/blog/adventures-in-statistics-2/how-to-interpret-regression-analysis-results-p-values-and-coefficients

Perform a multiple regression test will give us a better idea of how the three independent variables relate to the dependent variable and it is also part of the supervised learning mechanism which we can use for future project predicting the child mortality rate based on proportion of improved sanitation, government expenditure on health, and life expectancy. To perform multiple linear regression, we need to use scikit-learn (sklearn) and statsmodel (both were imported at the beginning).

In [736]:
```
# Review the columns of our dataset
project.columns
```

Out[736]:
```
Index(['Country', 'Child Mortality Rate',
       'Government Expenditure on Health (USD)',
       'Improved Sanitation Proportion', 'Life Expectancy', 'Four Regions',
       'Eight Regions', 'World Bank Income Group'],
      dtype='object')
```

Our independent variables are presented by variable X; our dependent variable is presented by the variable Y. We will fit the multiple linear regression model using scikit-learn.

In [737]:
```
# Independent variables
X = project[['Government Expenditure on Health (USD)','Improved Sanitation Proportio
                'Life Expectancy']]

# Dependent variable
Y = project['Child Mortality Rate']
```

In [738]:
```
# Multiple linear regression fit
lm = linear_model.LinearRegression()
lm.fit(X, Y)
```

Out[738]:
```
LinearRegression(copy_X=True, fit_intercept=True, n_jobs=None,
         normalize=False)
```

Now, let's look at the model summary before we interpret the result.

In [739]:
```
# Use statsmodels to print out the summary
X = sm.add_constant(X)

model = sm.OLS(Y, X).fit()

print_model = model.summary()
print(print_model)
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:     Child Mortality Rate   R-squared:                       0.852
Model:                              OLS   Adj. R-squared:                  0.849
Method:                   Least Squares   F-statistic:                     289.6
Date:                  Sat, 27 Oct 2018   Prob (F-statistic):           2.12e-62
```

```
Time:                        16:28:49   Log-Likelihood:                -646.65
No. Observations:                 155   AIC:                             1301.
Df Residuals:                     151   BIC:                             1313.
Df Model:                           3
Covariance Type:            nonrobust
==========================================================================================
                                          coef    std err          t      P>|t|      [0.025
------------------------------------------------------------------------------------------
const                                 272.2365     13.456     20.231      0.000     245.649
Government Expenditure on Health (USD)  0.0024      0.001      2.163      0.032       0.000
Improved Sanitation Proportion         -0.5150      0.069     -7.474      0.000      -0.651
Life Expectancy                        -2.8049      0.240    -11.674      0.000      -3.280
==============================================================================
Omnibus:                        9.092   Durbin-Watson:                   2.026
Prob(Omnibus):                  0.011   Jarque-Bera (JB):               10.011
Skew:                           0.446   Prob(JB):                      0.00670
Kurtosis:                       3.869   Cond. No.                     1.60e+04
==============================================================================

Warnings:
[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.
[2] The condition number is large, 1.6e+04. This might indicate that there are
strong multicollinearity or other numerical problems.
```

Interpretation + The R-squared and adjusted R-squared are high (0.852 and 0.849). R-squared is proportion of variance explained. It means roughly 85% of the variance can be explained by this model. + p-values are extremely small. All p-values are less than 0.05. The highest p-value is for 'Government Expenditure on Health (USD)' (0.03) which is also less than 0.05. This means we can reject the null hypothesis that the coefficient for each of the independent variable is equal to zero. All independent variables (or predictors) are meaningful addition to our model. + A unit increase in'Improved Sanitation Proportion' is associated with 0.515 unit decrease in child mortality rate + A unit increase in 'Life Expectancy' is associated with 2.80 unit decrease in child mortality rate + Notice the model warning that "The condition number is large, 1.6e+04. This might indicate that there are strong multicollinearity or other numerical problems." We suspect there is multicollinearity as the coefficient for 'Government Expenditure on Health (USD)' is positive, suggesting a positive association between health spending and child mortality rate, which is different from our finding earlier. Let's dive deeper into this by looking at the correlation table again.

In [740]:
```
# Correlation table shows pairwise association of variables in 'project'
project.corr()
```

Out[740]:
```
                                        Child Mortality Rate  \
Child Mortality Rate                                1.000000
Government Expenditure on Health (USD)             -0.428113
Improved Sanitation Proportion                     -0.846058
Life Expectancy                                    -0.891286
```

```
                                        Government Expenditure on Health (USD)  \
Child Mortality Rate                                                  -0.428113
Government Expenditure on Health (USD)                                 1.000000
Improved Sanitation Proportion                                         0.453286
Life Expectancy                                                        0.530483

                                        Improved Sanitation Proportion  \
Child Mortality Rate                                          -0.846058
Government Expenditure on Health (USD)                         0.453286
Improved Sanitation Proportion                                 1.000000
Life Expectancy                                                0.791415

                                        Life Expectancy
Child Mortality Rate                          -0.891286
Government Expenditure on Health (USD)         0.530483
Improved Sanitation Proportion                 0.791415
Life Expectancy                                1.000000
```

We can see that 'Improved Sanitation Proportion' is highly (and positively) correlated with 'Life Expectancy' (0.79). Also, 'Goverment Expenditure on Health (USD)' is positively correlated with 'Life Expectancy' (0.53). Furthermore, 'Improved Sanitation Proportion' is weakly (and positively) correlated with 'Goverment Expenditure on Health (USD)' (0.45). The multicollinearity is apparent.

Our multiple linear regression model only has three independent variables. For future research, we will include more variables and calculate the variance inflation factor to explore multicollinearity. We plan to build a more robust model in the future; as of now, we can see that each independent variable is negatively correlated with the dependent variable (from previous section), and the multiple linear regression reflects the same trend for the most part. We indeed need to incorporate more variables for better interpretation.

Limitations There are several noteworthy limitations of the project. > 1) Missing data + There were missing data instances that could not be imputed, making it impossible to look at the entire picture of the world (we ended up with 155 countries instead of 193 countries).

2) Multicollinearity

- The moderately strong to strong associations among independent variables prompted the need for more comprehensive future work to address such issue.

3) The complexity data wrangling methods

- A variety of methods was employed beyond the scope of the lectures. This challenge, however, was well worth the effort. Looking back, it might have slowed down the data analysis process and the methods employed might not have been the optimal ones. Further studies are definitely needed.

Despite such limitations, we believe the data was sufficient to prove our findings. This will be discussed in the conclusions section.

Conclusions In this project, we use data from Gapminder to answer four questions about child mortality rate in 2010. The data included in the project are: + Child mortality rate + Improved sanitation + Health spending (Government spending on health) + Life expectancy + Geography

The dependent variable is child mortality rate; the independent variables are improved sanitation, health spending, and life expectancy. Geography data were utilized to extract geographical regions needed for exploratory data analysis (EDA).

The EDA process yields the following findings and results.

- There is a substantial difference in child mortality rate acorss world regions with Sub Saharan Africa being the region with the highest child mortality rate and Western Europe being the region with the lowest child mortality rate.
- Improved sanitation is negatively correlated with child mortality rate. Countries with higher proportion of the population having access to improved sanitation facilities tend to have lower child mortality rate. This negative association is strong and steady across regions.
- Government spending on health weakly and negatively correlate with child mortality rate. Countries with higher spending on health tend to have lower child mortality rate. This negative correlation is weak and relatively consistent across regions.
- There is an extremely strong association between life expectancy and child mortality rate. Countries with higher life expectancy tend to experience lower child mortality rate. This negative correlation is strong (the strongest out of the three independent variables vs. dependent variable associations) and steady across regions.
- Multiple linear regression shows somewhat the same negative correlation. However, due to multicollinearity, the accuracy and robustness of the model is questionable. We need to incorporate more variables in future project to address this limitation.