Project3

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1 Project 3

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1.1 Part 1

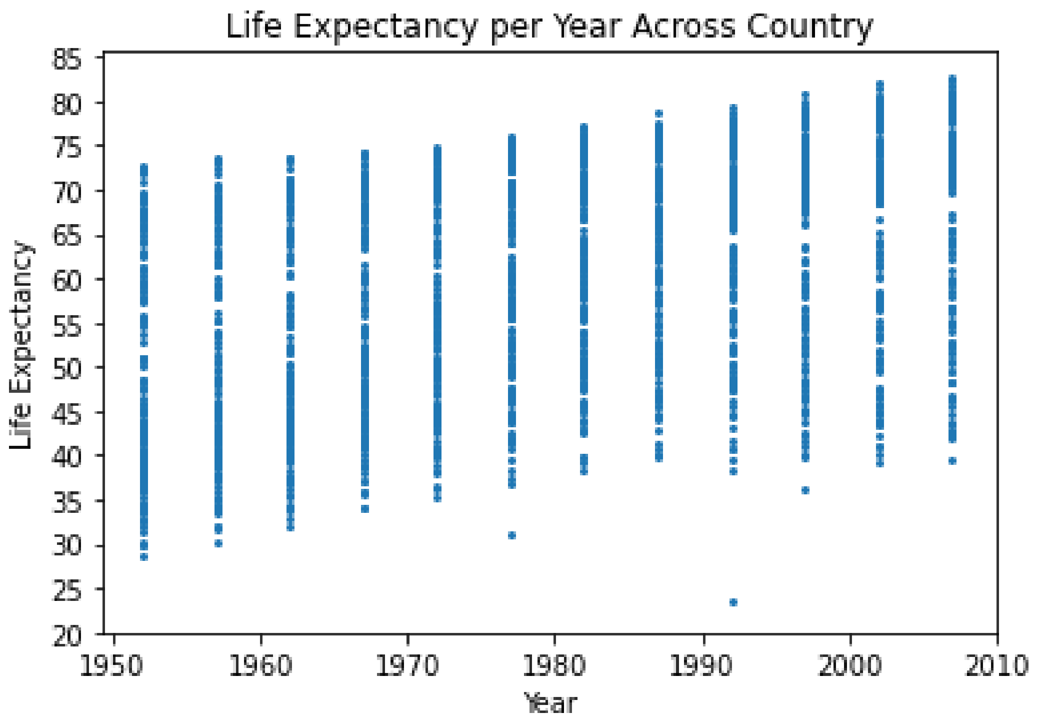
1.1.1 Importing Data

[202]:
```
import pandas as pd
import requests

url = 'https://raw.githubusercontent.com/jennybc/gapminder/main/data-raw/
  ↪08_gap-every-five-years.tsv'
res = requests.get(url, allow_redirects=True)
with open('08_gap-every-five-years.tsv','wb') as file:
    file.write(res.content)

data = pd.read_csv("08_gap-every-five-years.tsv", sep='\t')
data.head()
```

[202]:
```
       country continent  year  lifeExp       pop   gdpPercap
0  Afghanistan      Asia  1952   28.801   8425333  779.445314
1  Afghanistan      Asia  1957   30.332   9240934  820.853030
2  Afghanistan      Asia  1962   31.997  10267083  853.100710
3  Afghanistan      Asia  1967   34.020  11537966  836.197138
4  Afghanistan      Asia  1972   36.088  13079460  739.981106
```

1.1.2 Exercise 1

[203]:
```
import numpy as np
import matplotlib.pyplot as plt

plt.scatter(data.year, data.lifeExp, s = 4)
plt.title("Life Expectancy per Year Across Country")
plt.xlabel("Year")
plt.ylabel("Life Expectancy")
plt.xticks(np.arange(1950, 2011, 10))
plt.yticks(np.arange(20, 86, 5))

plt.show()
```



I imported the data from a get request, using the url for the raw .tsv file on github. I then used the matplotlib.pyplot function scatter in order to create a scatter plot create the scatter plot. I cleaned up the plot and adjusted the axes to make the plot look nice and better-readable.

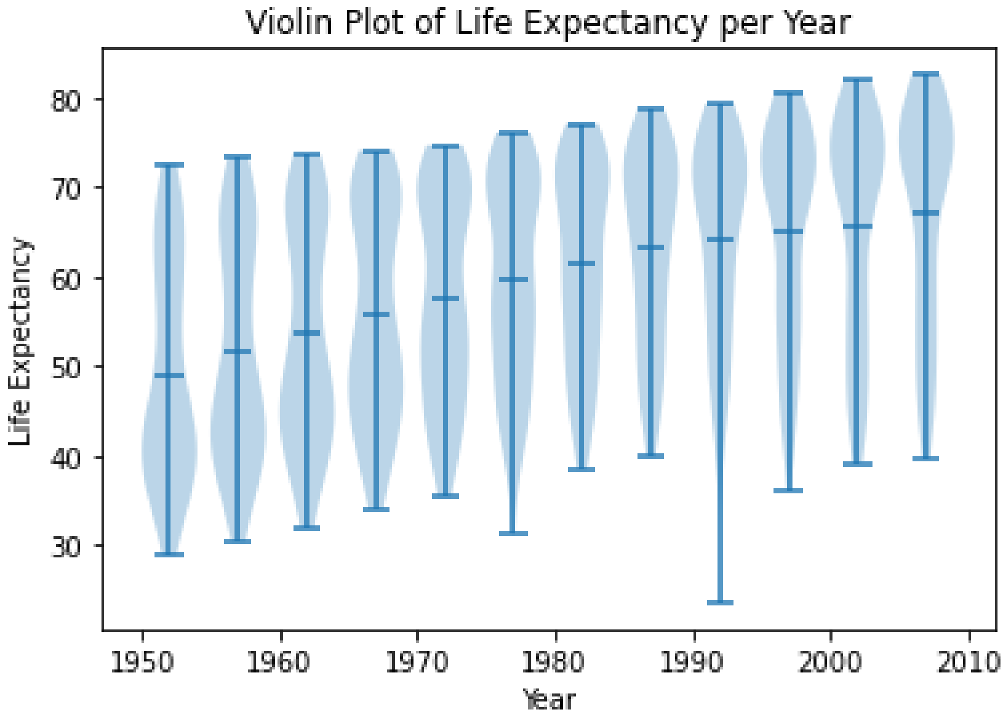
1.1.3 Question 1

There is an increasing trend for life expectancy across time that appears to be linear. The average life expectancy seems to grow from ~50 years old in 1952 to ~60 years old in 2007. Although not perfectly linear, the life expectancy generally increases by a steady amount per 5 years.

1.1.4 Violin Plot

[80]:
```
fig, ax = plt.subplots()

life_exp_per_year = []

for c, col in data.groupby("year"):
    life_exp_per_year.append(col['lifeExp'])
```

```
years = []
years = data['year'].unique()

ax.violinplot(life_exp_per_year,years,widths=4,showmeans=True)
ax.set_xlabel("Year")
ax.set_ylabel("Life Expectancy")
ax.set_title("Violin Plot of Life Expectancy per Year")
fig.savefig("violin.png")
```



1.1.5 Question 2

The distribution is skewed, and trends from bottom-heavy to top-heavy. Years like 1977 and 1992 stand out as especially skewed because of their long tails. In terms of modality, the data seems to be unimodal from 1952 to 1957 and 1982 to 2007. The earlier years have the mode in the bottom half, whereas it is in the top half for later years. The middle years (1962-1977) pretty clearly have a violin shape that shows the data is bimodal. It is not symmetric around the center because it is not a cnormal distribution.

1.1.6 Question 3

It is fairly visually evident from this data that there seems to be a strong, positive relationship between life expectancy and year across many countries, so I would reject the null hypothesis.

1.1.7 Question 4

The violin plot of residuals vs year should be still have a linear relationship and have the same numer of modes as the violin plot of life expectancy.

1.1.8 Question 5

The violin plot should be a normal distribution which is symmetric and centers around 0.

1.1.9 Exercise 2

[118]:
```
import statsmodels.formula.api as sm

result = sm.ols(formula="lifeExp ~ year", data=data[['year', 'lifeExp']].
 ↪sort_values(by=['year'], ascending=True).reset_index(drop=True)).fit()
print (result.summary())
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:                lifeExp   R-squared:                       0.190
Model:                            OLS   Adj. R-squared:                  0.189
Method:                 Least Squares   F-statistic:                     398.6
Date:                Tue, 26 Apr 2022   Prob (F-statistic):           7.55e-80
Time:                        22:04:01   Log-Likelihood:                -6597.9
No. Observations:                1704   AIC:                         1.320e+04
Df Residuals:                    1702   BIC:                         1.321e+04
Df Model:                           1
Covariance Type:            nonrobust
==============================================================================
                 coef    std err          t      P>|t|      [0.025      0.975]
------------------------------------------------------------------------------
Intercept   -585.6522     32.314    -18.124      0.000    -649.031    -522.273
year           0.3259      0.016     19.965      0.000       0.294       0.358
==============================================================================
Omnibus:                      386.124   Durbin-Watson:                   1.875
Prob(Omnibus):                  0.000   Jarque-Bera (JB):               90.750
Skew:                          -0.268   Prob(JB):                     1.97e-20
Kurtosis:                       2.004   Cond. No.                     2.27e+05
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly
specified.
[2] The condition number is large, 2.27e+05. This might indicate that there are
strong multicollinearity or other numerical problems.
```

1.1.10 Question 6

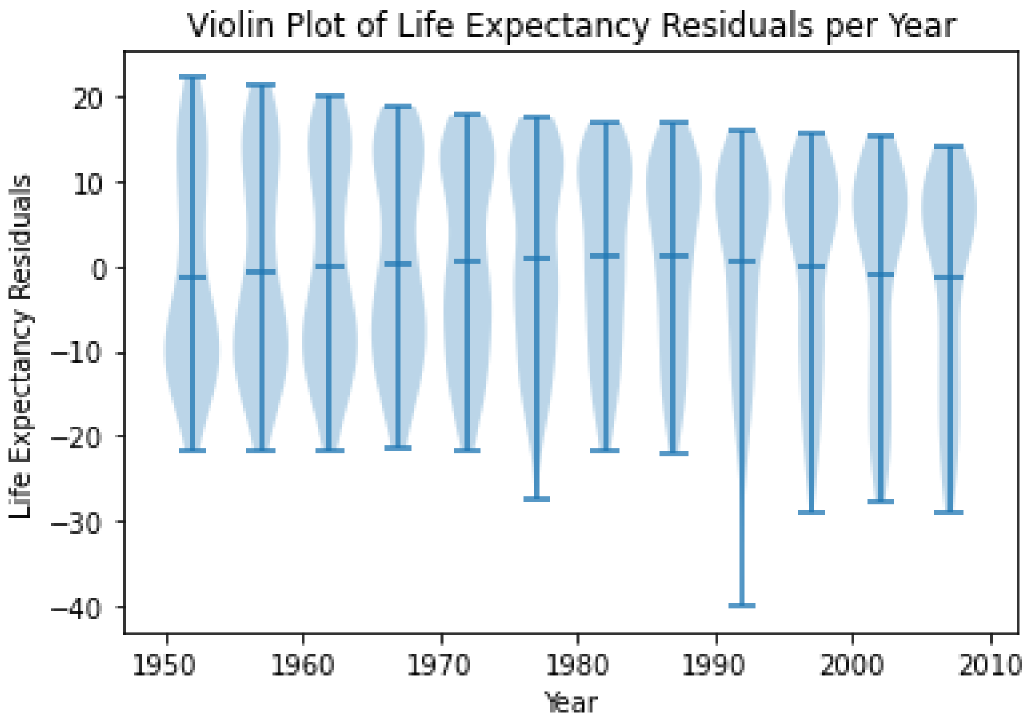
Life expectancy increases by 0.3259 yearly around the world according to this model.

1.1.11 Question 7

I do reject the null hypothesis of no relationship because the p-value is < 0.05 (7.55e-80), meaning the null hypothesis is not compatible with the data.

1.1.12 Exercise 3

[84]:
```
m = result.params.year
b = result.params.Intercept

data['expected'] = 0.0
for i, row in data.iterrows():
    y = (row['year']) * m + b
    data.at[i, 'expected'] =  y

residuals = []
for c, col in data.groupby("year"):
    residuals.append(col['lifeExp'] - col['expected'])

fig, ax = plt.subplots()

ax.violinplot(residuals,years,widths=4,showmeans=True)
ax.set_xlabel("Year")
ax.set_ylabel("Life Expectancy Residuals")
ax.set_title("Violin Plot of Life Expectancy Residuals per Year")
fig.savefig("violin.png")
```



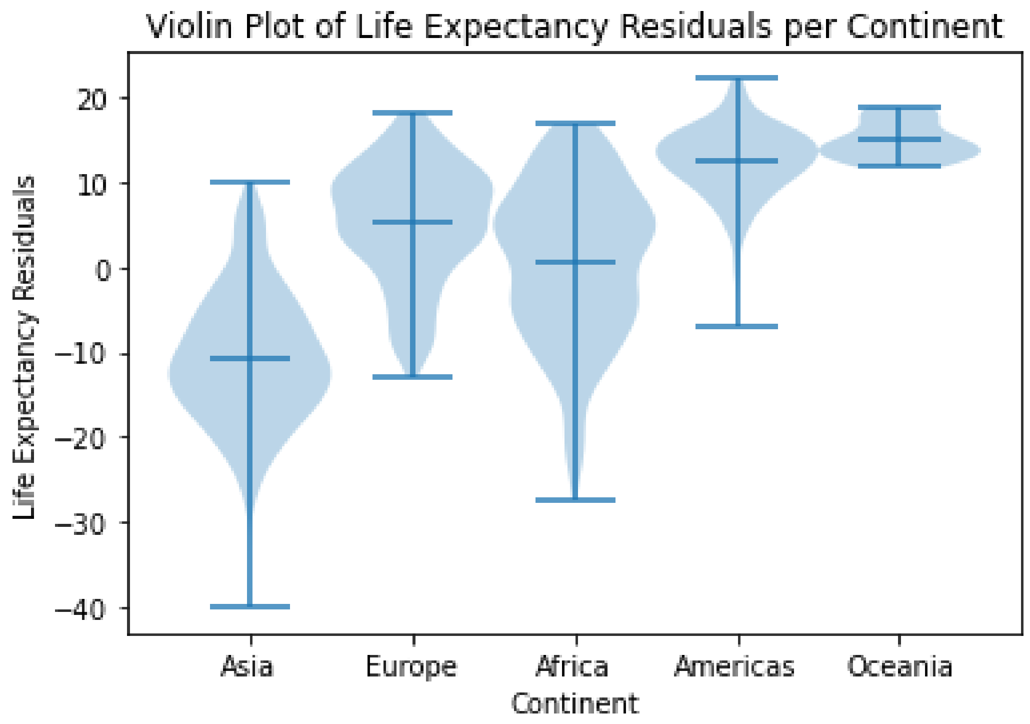
Using the regression model, I determined the expected value for each year. Then I created a list of residuals per year of every country by subtracting the life expectancy and expected value. Then I reused the code from the previous violin plot, this time using the residuals instead of the life expectancy.

1.1.13 Question 8

Yes because, as I expected, the violin plot of residuals is linear with similar modality to the life expectancy. It is also a normal distribution which is symmetric around 0, which I did not predict.

1.1.14 Exercise 4

[97]:
```
residuals2 = []
for c, col in data.groupby("continent"):
    residuals2.append(col['lifeExp'] - col['expected'])

fig, ax = plt.subplots()

continents = []
continents = data['continent'].unique()
conts_x = range(0, len(continents))

ax.violinplot(residuals2,conts_x,widths=1,showmeans=True)
ax.set_xlabel("Continent")
ax.set_xticks(ticks = conts_x, labels = continents)
ax.set_ylabel("Life Expectancy Residuals")
ax.set_title("Violin Plot of Life Expectancy Residuals per Continent")
fig.savefig("violin.png")
```



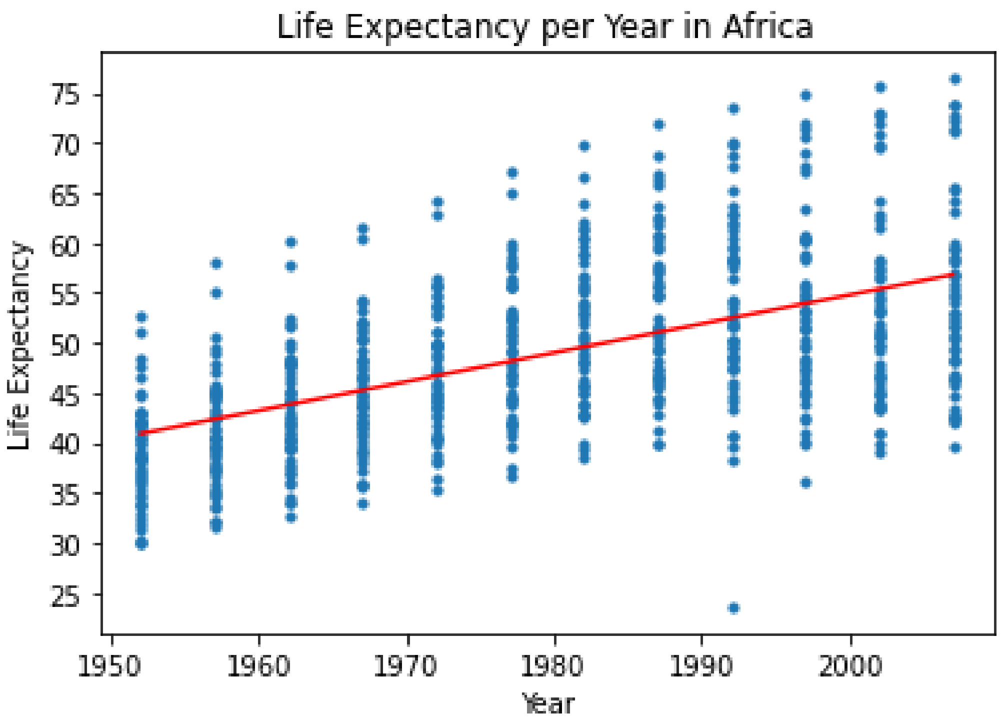
I used the same code as the third exercise, but instead of grouping by year when creating the list of residuals, I grouped by continent.

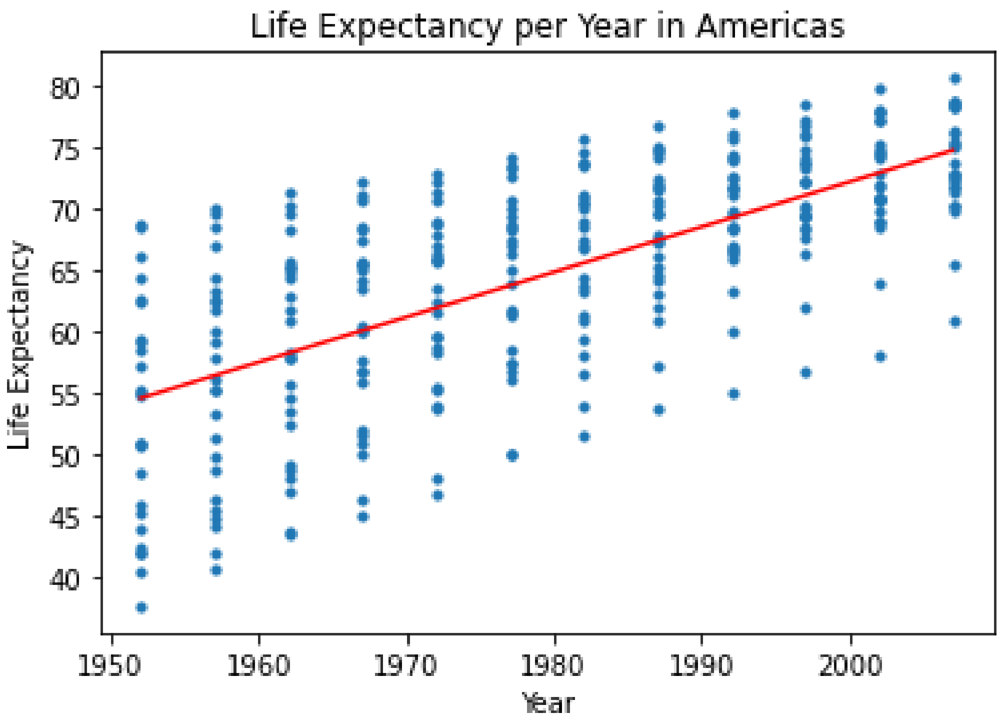
1.1.15 Question 9

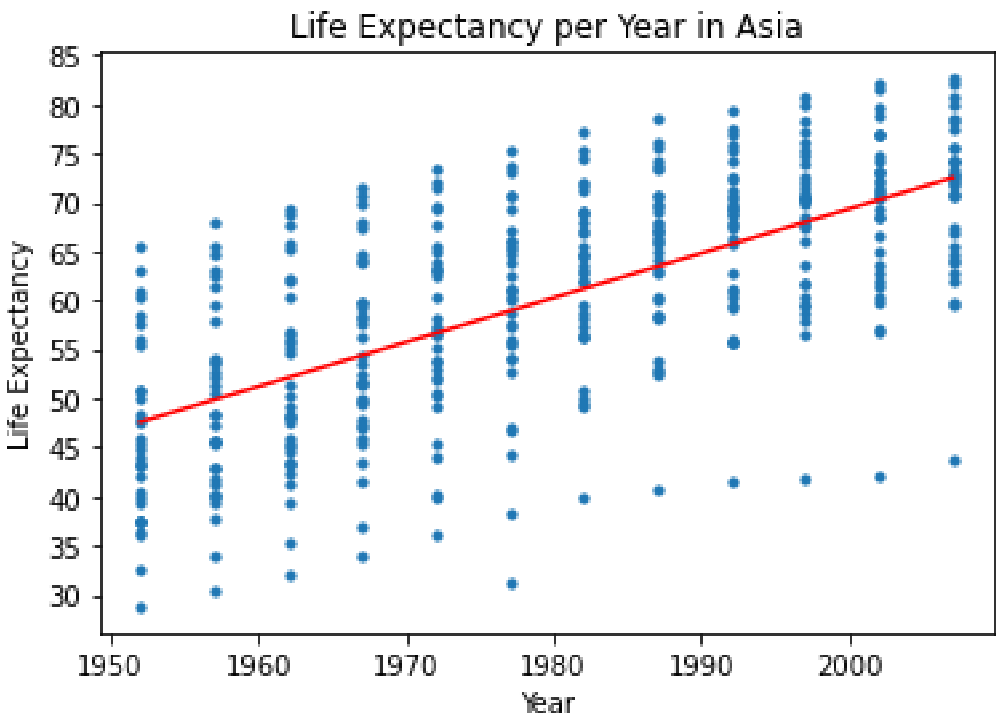
There is a dependence between model residual and continent because the means and distributions are different for each continent. When doing a regression analysis of life expectancy across time, I would suggest taking the continent into consideration.

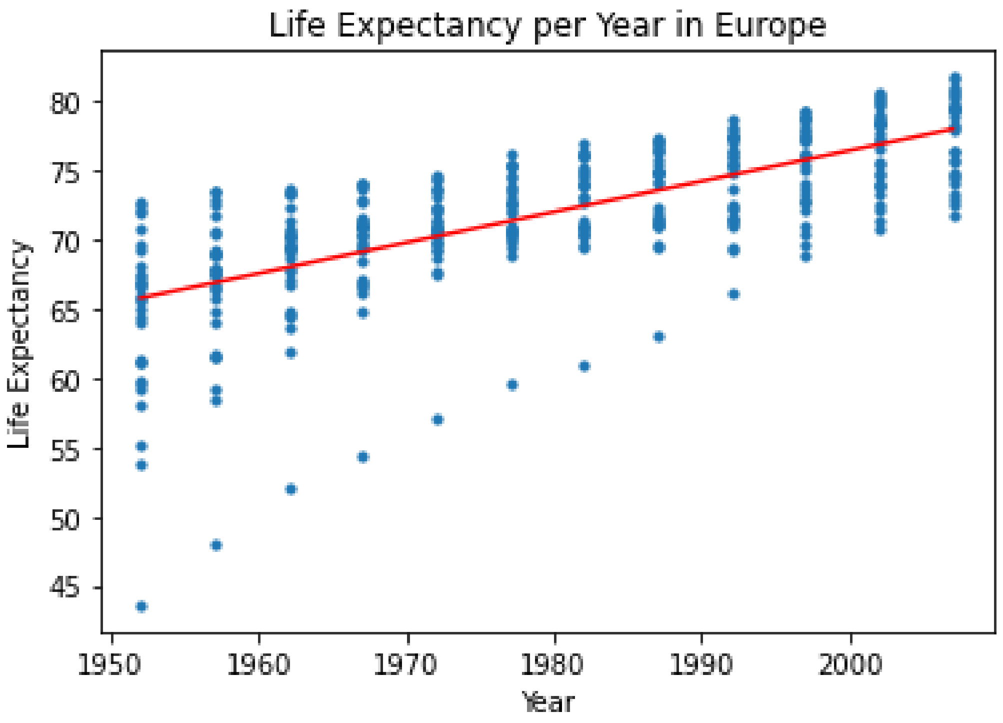
1.1.16 Exercise 5

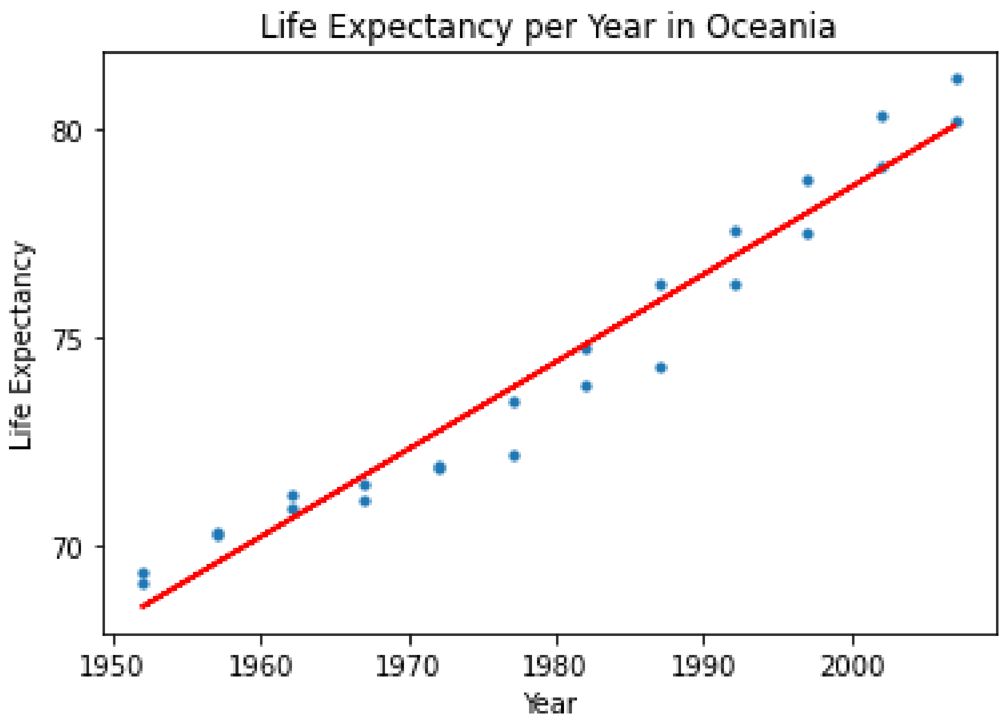
```
[204]: for c, col in data.groupby("continent"):
           plt.scatter(col.year, col.lifeExp, s = 10)
           plt.title("Life Expectancy per Year in " + c)
           plt.xlabel("Year")
           plt.ylabel("Life Expectancy")
           plt.xticks(np.arange(1950, 2011, 10))
           plt.yticks(np.arange(20, 86, 5))

           fit = np.polyfit(col.year, col.lifeExp, deg=1)
           plt.plot(col.year, fit[0] * col.year + fit[1], color='red')

           plt.show()
```


Life Expectancy per Year in Africa
Life Expectancy
Year
75
70
65
60
55
50
45
40
35
30
25
1950
1960
1970
1980
1990
2000


Life Expectancy per Year in Americas
Life Expectancy
Year
80
75
70
65
60
55
50
45
40
1950
1960
1970
1980
1990
2000


Life Expectancy per Year in Asia
Life Expectancy
Year
85
80
75
70
65
60
55
50
45
40
35
30
1950
1960
1970
1980
1990
2000


Life Expectancy per Year in Europe
Life Expectancy
Year
80
75
70
65
60
55
50
45
1950
1960
1970
1980
1990
2000



I used the same scatter plot code from the first exercise, but modified it such that it would only use the data for each respective continent. Then I used numpy polyfit to find the equation of the regression line and plotted it.

1.1.17 Question 10

Yes, the regression model should include an interaction term for continent and year because both are influential to life expectancy. The data and slope of the regression line varies greatly in each continent, showing the significance continent has on life expectancy.

1.1.18 Exercise 6

[120]:
```
regression = sm.ols(formula = 'lifeExp ~ year * continent', data = data).fit()
print(regression.summary())
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:                lifeExp   R-squared:                       0.693
Model:                            OLS   Adj. R-squared:                  0.691
Method:                 Least Squares   F-statistic:                     424.3
Date:                Tue, 26 Apr 2022   Prob (F-statistic):               0.00
Time:                        22:04:50   Log-Likelihood:                -5771.9
No. Observations:                1704   AIC:                         1.156e+04
Df Residuals:                    1694   BIC:                         1.162e+04
Df Model:                           9
```

```
Covariance Type:            nonrobust
================================================================================
==============
                                 coef    std err          t      P>|t|
[0.025      0.975]
--------------------------------------------------------------------------------
--------------
Intercept                   -524.2578     32.963    -15.904      0.000
-588.911    -459.605
continent[T.Americas]       -138.8484     57.851     -2.400      0.016
-252.315     -25.382
continent[T.Asia]           -312.6330     52.904     -5.909      0.000
-416.396    -208.870
continent[T.Europe]          156.8469     54.498      2.878      0.004
49.957     263.737
continent[T.Oceania]         182.3499    171.283      1.065      0.287
-153.599     518.298
year                           0.2895      0.017     17.387      0.000
0.257       0.322
year:continent[T.Americas]     0.0781      0.029      2.673      0.008
0.021       0.135
year:continent[T.Asia]         0.1636      0.027      6.121      0.000
0.111       0.216
year:continent[T.Europe]      -0.0676      0.028     -2.455      0.014
-0.122      -0.014
year:continent[T.Oceania]     -0.0793      0.087     -0.916      0.360
-0.249       0.090
==============================================================================
Omnibus:                       27.121   Durbin-Watson:                   0.242
Prob(Omnibus):                  0.000   Jarque-Bera (JB):               44.106
Skew:                          -0.121   Prob(JB):                     2.65e-10
Kurtosis:                       3.750   Cond. No.                     2.09e+06
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly
specified.
[2] The condition number is large, 2.09e+06. This might indicate that there are
strong multicollinearity or other numerical problems.
```

1.1.19 Question 11

Every parameter in the model is significantly different from 0 because they have p-values < 0.05. The only parameter which is not significantly different is Oceania because it's p-value, 0.36, is significantly > 0.05.

1.1.20 Question 12

[121]:
```
regression.params
```

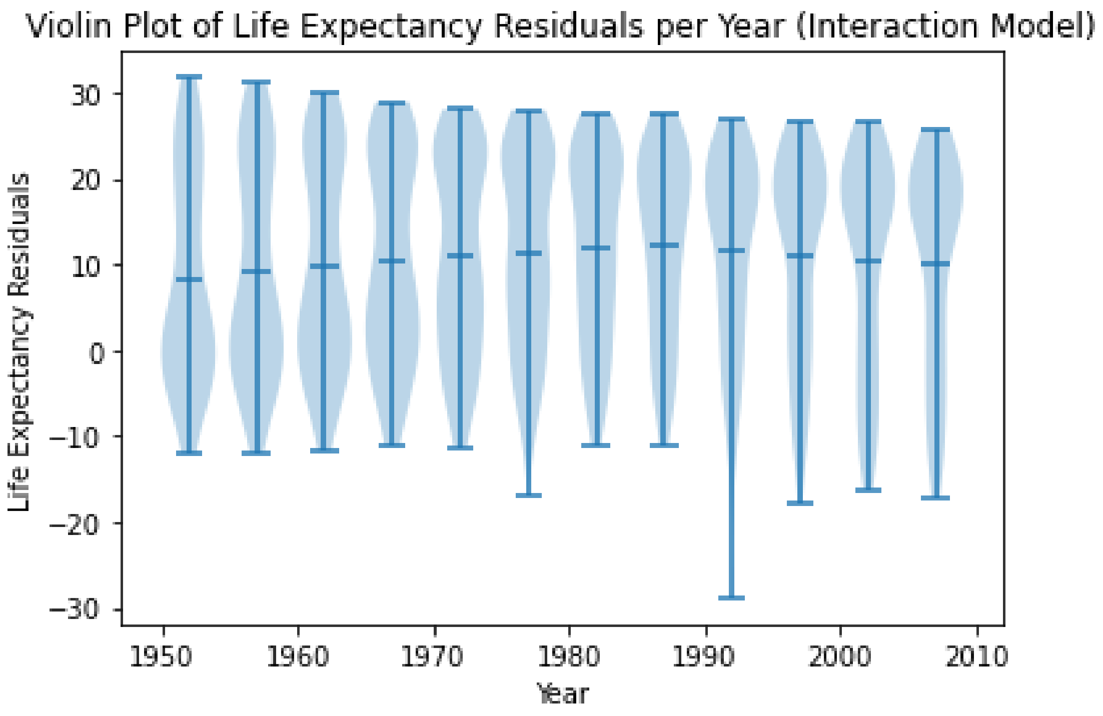
[121]:
```
Intercept                         -524.257846
continent[T.Americas]             -138.848447
continent[T.Asia]                 -312.633049
continent[T.Europe]                156.846852
continent[T.Oceania]               182.349883
year                                 0.289529
year:continent[T.Americas]           0.078122
year:continent[T.Asia]               0.163593
year:continent[T.Europe]            -0.067597
year:continent[T.Oceania]           -0.079257
dtype: float64
```

Since Africa is omitted, we see that Africa's life expectancy increases by 0.289529 per year. From there, we can calculate the increases based on Africa's increase.

Africa: 0.289529/year Americas: 0.289529 + 0.078122 = 0.367651/year Asia: 0.289529 + 0.163593 = 0.453122/year Europe: 0.289529 - 0.067597 = 0.221932/year Oceania: 0.289529 - 0.079257 = 0.210272/year

1.1.21 Exercise 7

[205]:
```
m = regression.params.year
b = regression.params.Intercept

data['expected'] = 0.0
for i, row in data.iterrows():
    y = (row['year']) * m + b
    data.at[i, 'expected'] =  y

residuals = []
for c, col in data.groupby("year"):
    residuals.append(col['lifeExp'] - col['expected'])

fig, ax = plt.subplots()

ax.violinplot(residuals,years,widths=4,showmeans=True)
ax.set_xlabel("Year")
ax.set_ylabel("Life Expectancy Residuals")
ax.set_title("Violin Plot of Life Expectancy Residuals per Year (Interaction␣
 ↪Model)")
fig.savefig("violin.png")
```



This plot does not match the assumptions of a linear regression model well. It is not symmetric or centered around 0.

1.2 Part 2

[167]:
```python
from sklearn import datasets
from sklearn.tree import DecisionTreeClassifier
import sklearn.model_selection as ms
import sklearn.metrics as met
from sklearn.model_selection import train_test_split
from sklearn.neighbors import KNeighborsClassifier

data = datasets.load_breast_cancer()
```

1.2.1 Decision Trees

[200]:
```python
ind = pd.DataFrame(data.data, columns=data.feature_names)

dep = pd.Categorical.from_codes(data.target, data.target_names)

ind_train, ind_test, dep_train, dep_test = ms.train_test_split(ind, dep,␣
 ↪random_state=42)

dt = DecisionTreeClassifier()
```

```
dt.fit(ind_train, dep_train)

predicted = dt.predict(ind_test)
predicted

actual = np.array(dep_test)
predictions = np.array(predicted)
m = met.confusion_matrix(actual, predictions)

accuracy = (m[0][0] + m[1][1]) / (m[0][0] + m[1][1] + m[0][1] + m[1][0])

print("Decision Tree Accuracy:", accuracy)
```

```
Decision Tree Accuracy: 0.951048951048951
```

1.2.2 k-NN Classification

[199]:
```
total_acc = 0

X_train, X_test, y_train, y_test = ms.train_test_split(data.data, data.target,␣
↪test_size=0.3)

knn = KNeighborsClassifier(n_neighbors=5)

knn.fit(X_train, y_train)

y_pred = knn.predict(X_test)

print("k-NN Accuracy", met.accuracy_score(y_test, y_pred))
```

```
k-NN Accuracy 0.935672514619883
```

I used the SKLearn breast cancer data to classify cancer scans as benign or malignant. For the decision tree classification I used cross-validation, and for the k-NN classification I used holdout classification with a 70/30 ratio. I am measuring performance based on accuracy. Based on this metric, both the decision tree and k-NN classification perform exceptionally well with accuracy above 90%. However, the decision tree classification just barely edges out k-NN classification, outperforming it by around 1.5%. I used SKLearn's test_train_split as my model selection procedure, which splits the data into subsets that minimize bias.