UNIVERSITY OF NAIROBI

SCHOOL OF COMPUTING & INFORMATICS

CCI 501 Machine Learning

Title: MultiVariare Linear Regression - Life Expectancy

Submitted by		
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Introduction

The business question: Life Expectancy forecasting helps in understanding what factors are most responsible for short and long lifespans in countries.

The goal: Forecast life expenctancy for a country.

How does this help UON ML 2022 Class?

- Gauge the technical skills required to prepare data and build a Linear regression ML model.
- Understand factors that influence life expectancy.

Assumptions

- The life expectancy can be described by the features in the dataset.

Using the data provided, Group F builds a life expectancy prediction model that is able to provide an approximate expected life span based on the features provided.
A linear regression model is built to model life expectancy based on the features provided.
Root Mean Squared Error is used as an evaluation metric.

Data Preprocessing and Visualization

This project leverages the Life Expectancy data provided by the lecturer. Below is a brief description of the data.

```
data.info()
✓ 0.1s

Output exceeds the size limit. Open the full output data in a text
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 2938 entries, 0 to 2937
Data columns (total 22 columns):
 #   Column                           Non-Null Count  Dtype
---  ------                           --------------  -----
 0   Country                          2938 non-null   object
 1   Year                             2938 non-null   int64
 2   Status                           2938 non-null   object
 3   Life expectancy                  2928 non-null   float64
 4   Adult Mortality                  2928 non-null   float64
 5   infant deaths                    2938 non-null   int64
 6   Alcohol                          2744 non-null   float64
 7   percentage expenditure           2938 non-null   float64
 8   Hepatitis B                      2385 non-null   float64
 9   Measles                          2938 non-null   int64
 10   BMI                             2904 non-null   float64
 11  under-five deaths                2938 non-null   int64
 12  Polio                            2919 non-null   float64
 13  Total expenditure                2712 non-null   float64
 14  Diphtheria                       2919 non-null   float64
 15   HIV/AIDS                        2938 non-null   float64
 16  GDP                              2490 non-null   float64
 17  Population                       2286 non-null   float64
 18   thinness  1-19 years            2904 non-null   float64
 19   thinness 5-9 years              2904 non-null   float64
...
 20  Income composition of resources  2771 non-null   float64
 21  Schooling                        2775 non-null   float64
dtypes: float64(16), int64(4), object(2)
memory usage: 505.1+ KB
```

There is a mixture of object and numeric data types. There are missing values in some of the columns. A further look at the percentage distribution of the data points across the columns reveal that quite a number of columns have missing values.

```
The dataset has 22 columns.
There are 14 columns that have missing values.

                                 Missing Values  % of Total Values
Population                                  652               22.2
Hepatitis B                                 553               18.8
GDP                                         448               15.2
Total expenditure                           226                7.7
Alcohol                                     194                6.6
Income composition of resources             167                5.7
Schooling                                   163                5.5
 BMI                                         34                1.2
 thinness  1-19 years                        34                1.2
 thinness 5-9 years                          34                1.2
Polio                                        19                0.6
Diphtheria                                   19                0.6
Life expectancy                              10                0.3
Adult Mortality                              10                0.3
```

A plot of life expectancy, which is the target variable, reveals the following:

1. This data is right tailed but seems to follow a normal distribution pattern.
2. The life expectancy steadily increases from late thirties to mid seventies.
3. Life expectancy between 70 and 75 seems the most frequent in the database.

Next step we check the correlation between life expectancy and all the other numeric variables.

```
Adult Mortality                   -0.696359
 HIV/AIDS                         -0.556556
 thinness  1-19 years             -0.477183
 thinness 5-9 years               -0.471584
under-five deaths                 -0.222529
infant deaths                     -0.196557
Measles                           -0.157586
Population                        -0.021538
Year                               0.170033
Total expenditure                  0.218086
Hepatitis B                        0.256762
percentage expenditure             0.381864
Alcohol                            0.404877
GDP                                0.461455
Polio                              0.465556
Diphtheria                         0.479495
 BMI                               0.567694
Income composition of resources    0.724776
Schooling                          0.751975
Life expectancy                    1.000000
Name: Life expectancy , dtype: float64
```

The following was observed:

1. While we find Adult Mortality to be strongly negatively correlated with life expectancy, it seems to be an obvious reason because more adult deaths mean a lower life expectancy.
2. HIV/AIDs has the second strongest negative correlation with life expectancy while Schooling has the strongest positive correlation with life expectancy.
3. Interestingly, higher intake of alcohol, diphtheria, and BMI results in a higher life expectancy.
4. Population has the highest percentage of missing values, yet its influence on the target variable is insignificant.

Missing values in a dataset can have a significant impact on the performance of a machine-learning model. Depending on the amount and distribution of missing values, they can cause various problems, such as:

- Reduced sample size: If a large number of observations are missing, the sample size will be reduced, which can limit the amount of data available for training and evaluating the model.

- Biased estimates: If the missing values are not missing at random, the estimates of the model's parameters can be biased, leading to inaccurate predictions.
- Reduced model performance: Missing values can lead to reduced model performance, as the model may not be able to learn from all the available data.
- Inconsistency: Depending on the algorithm used, missing values can cause inconsistencies in the optimization process and lead to unstable or suboptimal solutions.

Several techniques can be used to handle missing values in a dataset, such as:

1. Deleting observations: Deleting observations with missing values can be a simple solution, but it can lead to a loss of information if many observations are removed.
2. Imputing values: Imputing missing values with a statistical measure such as the mean, median, or mode can be a simple solution, but it can also introduce bias and lead to inaccurate predictions.
3. Using advanced imputation techniques: Techniques such as multiple imputation or matrix completion can be used to impute missing values more sophisticatedly.
4. Using models that are robust to missing values: Some machine learning models, such as random forests or gradient boosting, can be robust to missing values and do not require imputation.

Deleting observations with missing values, also known as listwise deletion, is considered the best way to handle missing values in certain situations because it can lead to unbiased estimates and improved model performance. This is because when missing values are not missing at random, imputing values can lead to biased estimates of the model's parameters and inaccurate predictions. By removing observations with missing values, the model is only trained on complete cases, which can reduce the potential for bias.

However, listwise deletion can also have downsides. It can lead to a loss of information if a large number of observations are removed, which can reduce the sample size and limit the amount of data available for training and evaluating the model. Additionally, if the missing values are not missing completely at random, deleting observations can lead to biased estimates in the sample that is used to train and evaluate the model.

In this case however, we choose to delete the missing values because according to Pearson’s correlation analysis, the variables with the highest missing values do not have a significant influence on the target variable.

```python
# Discard columns with missing values more than 20%

missing_df = missing_values_table(data);
missing_columns = list(missing_df[missing_df['% of Total Values'] > 20].index)
print('\n','We will remove %d column(s).' % len(missing_columns))

# Drop the columns
data = data.drop(columns = list(missing_columns))
```
✓ 0.8s

We use a statistical test to verify whether life expectancy has a normal distribution or not. A p-value smaller than 0.05 means the null hypothesis is rejected. As such, a p-value of 0.05 or greater means that the distribution is normal.

Life expectancy, therefore, does follow a normal distribution.

A Shapiro-Wilk test is also used to confirm whether the data has been drawn from a normal distribution. The results are similar to observations made using D'Agostino's K^2 Test.

```python
from scipy import stats

_, p = stats.normaltest(data['Life expectancy '])
print('Normal Test',format(p, '.3f'))
print(p <= 0.05)

# Check with Shapiro - Wilk test
from scipy.stats import shapiro

_, p = shapiro(data['Life expectancy '])
print('Shapiro Test', format( p, '.3f'))
print(p <= 0.05)
```
✓ 0.7s

```
Normal Test nan
False
Shapiro Test 1.000
False
```

We also look for countries with the highest and lowest life expectancy, respectively on average, across all years.

```python
data.groupby(['Country'])['Life expectancy '].mean().sort_values(ascending=False).head(20)
```

✓ 0.6s

```
Country
Japan                                                   82.53750
Sweden                                                  82.51875
Iceland                                                 82.44375
Switzerland                                             82.33125
France                                                  82.21875
Italy                                                   82.18750
Spain                                                   82.06875
Australia                                               81.81250
Norway                                                  81.79375
Canada                                                  81.68750
Austria                                                 81.48125
Singapore                                               81.47500
New Zealand                                             81.33750
Israel                                                  81.30000
Greece                                                  81.21875
Germany                                                 81.17500
Netherlands                                             81.13125
United Kingdom of Great Britain and Northern Ireland    80.79375
Luxembourg                                              80.78125
Finland                                                 80.71250
Name: Life expectancy , dtype: float64
```

```python
data.groupby(['Country'])['Life expectancy '].mean().dropna().sort_values(ascending=False).tail(20)
```

✓ 0.7s

```
Country
Burkina Faso                55.64375
Burundi                     55.53750
Guinea-Bissau               55.36875
Equatorial Guinea           55.31250
Mali                        54.93750
Cameroon                    54.01875
Zambia                      53.90625
South Sudan                 53.87500
Mozambique                  53.39375
Somalia                     53.31875
Nigeria                     51.35625
Swaziland                   51.32500
Zimbabwe                    50.48750
Cte d'Ivoire               50.38750
Chad                        50.38750
Malawi                      49.89375
Angola                      49.01875
Lesotho                     48.78125
Central African Republic    48.51250
Sierra Leone                46.11250
Name: Life expectancy , dtype: float64
```

Finally, we check the highest and lowest life expectancy grouped by year, respectively.

```
data.groupby(['Year', 'Country'])['Life expectancy '].mean().dropna().sc
✓ 0.9s

Year  Country
2004  Italy          89.0
2014  Portugal       89.0
      Finland        89.0
2007  Sweden         89.0
      France         89.0
2014  Germany        89.0
2007  Spain          89.0
2014  Belgium        89.0
2010  New Zealand    89.0
2008  France         89.0
2009  Norway         89.0
2011  Austria        88.0
2015  Slovenia       88.0
2006  Sweden         88.0
2012  Austria        88.0
2004  Iceland        88.0
2010  Netherlands    88.0
2005  Italy          88.0
2011  Luxembourg     88.0
2014  Greece         88.0
Name: Life expectancy , dtype: float64
```

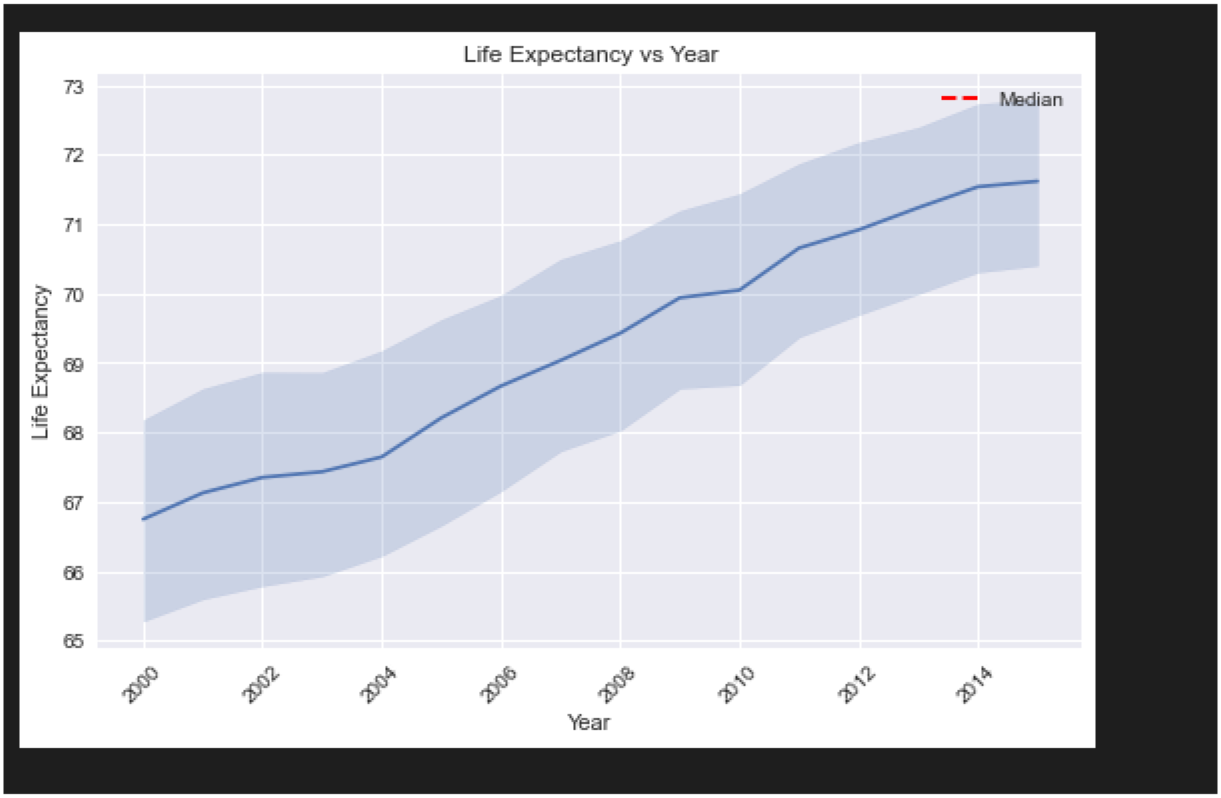
High life expectancy is consistent with high income countries across the years while low life expectancy is lowest in African countries.

```
data.groupby(['Year', 'Country'])['Life expectancy '].mean().dropna().sort_
```

```
✓ 0.9s
```

```
Year  Country
2004  Malawi          45.1
      Lesotho         44.8
2002  Zimbabwe        44.8
2001  Zambia          44.6
2003  Malawi          44.6
2005  Zimbabwe        44.6
      Lesotho         44.5
2003  Zimbabwe        44.5
2004  Zimbabwe        44.3
2006  Sierra Leone    44.3
2002  Malawi          44.0
2000  Zambia          43.8
2001  Malawi          43.5
2005  Sierra Leone    43.3
2000  Malawi          43.1
2004  Sierra Leone    42.3
2003  Sierra Leone    41.5
2001  Sierra Leone    41.0
2000  Sierra Leone    39.0
2010  Haiti           36.3
Name: Life expectancy , dtype: float64
```

Based on the Life Expectancy vs Year plot, there is a general increase in life expectancy across the years.



Multicollinearity

Collinearity, also known as multicollinearity, occurs when two or more predictor variables in a multiple regression model are highly correlated. This can cause problems in estimating and interpreting the model's parameters. When predictor variables are correlated, they explain some of the same variations in the response variable, and it becomes difficult to disentangle the individual effects of each predictor on the response.

When collinearity is present, the estimated regression coefficients can be imprecise, unstable, and difficult to interpret. The standard errors of the coefficients are typically inflated, which can lead to an increased risk of type I errors (false positives) in hypothesis testing.

The solution for multicollinearity can be dropping one or more correlated variables or using regularization methods like ridge or lasso regression, which can help reduce collinearity's impact by shrinking the coefficient estimates toward zero.

We drop values with a greater than or equal to 80% collinearity with the target variable.

```
# Remove the collinear features above a specified correlation coefficient
data = remove_collinear_features(data, 0.8);
```

0.1s

```
under-five deaths  | infant deaths | 1.0
GDP | percentage expenditure | 0.9
```

Machine Learning

Cost Function

We use Root Mean Squared Error as the evaluation metric. It is a commonly used metric for evaluating the performance of a model when making continuous predictions.

It is the square root of the average squared differences between the predicted and actual values. It is recommended because it helps to penalize large errors more heavily than small errors, which is often desirable in practical applications.

Additionally, because RMSE is in the same unit as the target variable, it is easy to interpret and understand. Finally, it is differentiable and can be used to optimize the model.

We create a baseline score based on the median life expectancy value. We use this to evaluate how better our model is compared to a median guess.

```
# Create a Baseline
#Metric: Root Mean Squared Error

# Function to calculate root mean squared error.
# This function calculates root mean squared errors between true values and predictions

def rmse(y_true, y_pred):
    mse = np.square(np.subtract(y_true,y_pred)).mean()
    rmse = math.sqrt(abs(mse))
    return rmse

baseline = np.median(encoded_y)


print('The baseline guess is a score of %0.2f' % baseline)
print("Baseline Performance on the test set: RMSE = %0.2f" % rmse(encoded_y_val, baseline))
```

0.8s

```
The baseline guess is a score of 72.00
Baseline Performance on the test set: RMSE = 9.71
```

Since we only dropped data with missing values more than 20%, for the remaining values, we imputed based on the median. Median imputation is often preferred over other imputation methods, such as mean imputation because it is less sensitive to outliers.

Imputation

Mean imputation is sensitive to outliers, meaning that if there are extreme values in the data, the mean will be heavily influenced by these values. The imputed value may not be representative of the majority of the data. In contrast, the median is a robust statistic, meaning that it is not affected by extreme values, and it is a better representation of the central tendency of the data.

Additionally, median imputation is preferred in situations where the distribution of the variable is skewed because the median is a better measure of central tendency for skewed distributions than the mean.

It's also important to note that median imputation does not change the distribution of the variable. It will not introduce bias in the model if the missing data are missing completely at random. However, median imputation can also have downsides. It can lead to a loss of information if the missing values are not entirely missing at random, and it does not account for the relationship between the variable with missing values and the other variables in the dataset. More advanced imputation techniques, such as multiple imputations or using predictive models for imputation, can be more appropriate.

```
#Imputer object
imputer = Imputer(strategy = 'median')

#Fitting on train da
imputer.fit(encoded_X)

#Transform train and test data
encoded_X = imputer.transform(encoded_X)
encoded_X_val = imputer.transform(encoded_X_val)
```

✓ 0.7s

```
print('\n', 'Checking all data is finite')
print('-' * 30)

#Making sure all values are finite
print (np.where(~np.isfinite(encoded_X)))
print (np.where(~np.isfinite(encoded_X_val)))
```

✓ 0.6s

Data Scaling

We used normalization for scaling.

```
#Training, testing and evaluating a model
def train_test_evaluate(ml_model):
    print(ml_model)
    start = time.time()

    #Train

    # # Normalizing the features so that different units do not affect the algorithms.
    # While this process is not necessary for tree-based models, nevertheless, it is a good practice
    model = TransformedTargetRegressor(regressor= ml_model,
                                        transformer = MinMaxScaler()
                                        ).fit(encoded_X,encoded_y)




    #Test
    # Inverse transformation happens at this step
    model_pred = model.predict(encoded_X_val)

    #Evaluate
    model_rmse = rmse(encoded_y_val, model_pred)


    end = time.time()
    time_taken = end - start

    print('Time taken: %0.2f' %time_taken, 's.')

    #Return performance metric
    return model_rmse
```
✓ 0.8s

Normalization is a technique that scales the data to a fixed range, usually between 0 and 1. It is typically used when the data has a Gaussian (or normal) distribution or when the data's scale is unknown. Normalizing the data can make it easier to compare data from different sources or to compare data that has been measured in different units.

Normalization is preferred over standardization when the data has a skewed distribution because standardization can amplify the effect of outliers in the data. In contrast, normalization can make the data more robust to outliers. Additionally, normalization makes it easy to interpret the data as the values will be between 0 and 1.

Modeling

We run the linear regression model using its default parameters. Our RMSE was significantly lower than the baseline RMSE, which means we can use ML for life expectancy forecasting.

```
...   LinearRegression()
      R Squared:  0.80947176781309
      Time taken: 0.01 s.
      Linear Regression Root Mean Squared Error: 4.1269
```

We also attempted to implement a linear regression model from scratch, including implementing the gradient descent function. The final RMSE was slightly higher than the RMSE with Scikit Learn.

Multivariate Linear Regression from Scratch

An attempt to implement the cost function and gradient descent from scratch.

```
ones = np.ones([encoded_X.shape[0], 1])
print(ones)
encoded_X = np.concatenate((ones, encoded_X), axis=1)
encoded_y = encoded_y.values
```

✓ 0.8s

```
[[1.]
 [1.]
 [1.]
 ...
 [1.]
 [1.]
 [1.]]
```

```
theta = np.zeros([1, encoded_X.shape[1]])
print(theta)

#Hyperparameters
alpha = 0.001 #Learning rate
iters = 10 #Number of iterations to perform gradient descent (epochs)
```

✓ 0.7s

```
[[0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0.]]
```

```
# Cost function
def compute_cost(X,y,theta):
    inner = np.power(((X @ theta.T)-y),2)
    return np.sum(inner)/(2 * len(X))
```

✓ 0.7s

```
# Gradient descent and cost function
gradient, cost = gradient_descent(encoded_X, encoded_y, theta, iter
print(gradient)

final_cost = compute_cost(encoded_X,encoded_y,gradient)
print(final_cost)
```

✓ 0.1s

```
1277228993317.8599
1.8791735078274533e+22
2.782399150751728 4e+32
4.1197971971377284e+42
6.100033904634616e+52
9.032098391684809e+62
1.3373499661222575e+73
1.9801654657944706e+83
2.9319590019465247e+93
4.341245081580223e+103
[[-1.61330922e+43 -2.97443739e+45 -5.12249072e+45 -5.83730838e+43
  -3.38959740e+45 -1.19860631e+45 -8.44677348e+47 -3.44630984e+44
  -1.11917889e+45 -7.61082700e+43 -1.08691527e+45 -4.14891812e+43
  -1.53143023e+44 -1.54800625e+44 -8.38148100e+42 -1.62932327e+44]]
4.341245081580223e+103
```

Our R2 squared score is 0.81.

Conclusion

We find that machine learning can be applied to the process of life expectancy prediction. Future steps would include tweaking the model parameters to see if its possible to improve the prediction capabilities.