

Title: Use food diet to predict deaths

Introduction: How can food and healthy diet help to improve healthy life and reduce the death rate? The current study indicated that a healthy diet is very important to prevent various infections. Keeping a healthy immune system is so important. However, little knowledge has been developed about which countries' deaths rate are associated with the different kinds of food intaking, neither do we know what is the importance of food with rich nutrition and improve eating habits to combat spreading diseases. This project uses three different machine learning algorithms to analyze the data of Food\_Supply\_kcal(percentage of energy intake). The model results should indicate how accurately the food diet can predict the countries' death rate. In addition, the ranking of feature importance should summarize the food and diet from high to low importance to predict deaths.

```
In [5]: import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
import statsmodels.api as sm
from sklearn import metrics

from sklearn.linear_model import LinearRegression
from sklearn.linear_model import Ridge, Lasso, ElasticNet, LinearRegression
from sklearn.model_selection import train_test_split
from sklearn.model_selection import cross_val_score
from sklearn.metrics import mean_squared_error as MSE
from sklearn.svm import SVR
from sklearn.ensemble import RandomForestRegressor
from xgboost.sklearn import XGBRegressor
from sklearn.preprocessing import MinMaxScaler ## feature scaling

import matplotlib.pyplot as plt # visualization
import seaborn as sns
from termcolor import colored as cl # text customization
import itertools # advanced tools
import plotly.graph_objs as go
import plotly.offline as py
import plotly.express as px

plt.rcParams['figure.figsize'] = (6, 4)
plt.rcParams['font.size'] = 14

import seaborn as sns
import matplotlib.pyplot as plt
%matplotlib inline
```

## Loading data

```
In [6]: data_path = '/Users/Zhang/notebooks/LearningFuze/'
image_path = '/Users/Zhang/notebooks/LearningFuze/output/'
```

```
In [7]: death = pd.read_csv(data_path + 'data/Food_Supply_Quantity_kg_Data.csv')
```

```
In [8]: death.head()
```

```
Out[8]:
```

	Country	Alcoholic Beverages	Animal fats	Animal Products	Aquatic Products, Other	Cereals - Excluding Beer	Eggs	Fish, Seafood	Fruits - Excluding Wine	M
0	Afghanistan	0.0014	0.1973	9.4341	0.0	24.8097	0.2099	0.0350	5.3495	1.2
1	Albania	1.6719	0.1357	18.7684	0.0	5.7817	0.5815	0.2126	6.7861	1.8
2	Algeria	0.2711	0.0282	9.6334	0.0	13.6816	0.5277	0.2416	6.3801	1.1
3	Angola	5.8087	0.0560	4.9278	0.0	9.1085	0.0587	1.7707	6.0005	2.0
4	Antigua and Barbuda	3.5764	0.0087	16.6613	0.0	5.9960	0.2274	4.1489	10.7451	5.6

5 rows × 32 columns

```
In [9]: death.dtypes
```

```
Out[9]: Country                object
Alcoholic Beverages          float64
Animal fats                  float64
Animal Products              float64
Aquatic Products, Other      float64
Cereals - Excluding Beer     float64
Eggs                        float64
Fish, Seafood                float64
Fruits - Excluding Wine      float64
Meat                        float64
Milk - Excluding Butter      float64
Miscellaneous                float64
Offals                      float64
Oilcrops                    float64
Pulses                      float64
Spices                      float64
Starchy Roots                float64
Stimulants                   float64
Sugar & Sweeteners           float64
Sugar Crops                  float64
Treenuts                    float64
Vegetable Oils               float64
Vegetables                   float64
Vegetal Products             float64
Obesity                      float64
Undernourished                object
Confirmed                    float64
Deaths                      float64
Recovered                    float64
Active                      float64
Population                   float64
Unit (all except Population)  object
dtype: object
```

```
In [10]: death.columns = ['Country', 'Alcoholic_beverages', 'Animal_fats', 'Animal_P\n        'Aquatic_Products, Other', 'Cereals_Excluding_Beer', 'Eggs',\n        'Fish_Seafood', 'Fruits_Excluding Wine', 'Meat',\n        'Milk_Excluding Butter', 'Miscellaneous', 'Offals', 'Oilcrops',\n        'Pulses', 'Spices', 'Starchy_Roots', 'Stimulants', 'Sugar_Sweeteners\n        'Sugar_Crops', 'Treenuts', 'Vegetable Oils', 'Vegetables',\n        'Vegetal_Products', 'Obesity', 'Undernourished', 'Confirmed', 'Death\n        'Recovered', 'Active', 'Population', 'Unit']
```

```
In [11]: death.shape
```

```
Out[11]: (170, 32)
```

```
In [12]: death.columns
```

```
Out[12]: Index(['Country', 'Alcoholic_beverages', 'Animal_fats', 'Animal_Product\ns',\n               'Aquatic_Products, Other', 'Cereals_Excluding_Beer', 'Eggs',\n               'Fish_Seafood', 'Fruits_Excluding Wine', 'Meat',\n               'Milk_Excluding Butter', 'Miscellaneous', 'Offals', 'Oilcrops',\n               'Pulses', 'Spices', 'Starchy_Roots', 'Stimulants', 'Sugar_Sweetene\nrs',\n               'Sugar_Crops', 'Treenuts', 'Vegetable Oils', 'Vegetables',\n               'Vegetal_Products', 'Obesity', 'Undernourished', 'Confirmed', 'Dea\nths',\n               'Recovered', 'Active', 'Population', 'Unit'],\n              dtype='object')
```

## data cleaning and preprocessing

```
In [13]: death.isnull().sum()
```

```
Out[13]: Country                                0
Alcoholic_beverages                           0
Animal_fats                                    0
Animal_Products                               0
Aquatic_Products, Other                       0
Cereals_Excluding_Beer                       0
Eggs                                           0
Fish_Seafood                                  0
Fruits_Excluding_Wine                        0
Meat                                           0
Milk_Excluding_Butter                        0
Miscellaneous                                0
Offals                                         0
Oilcrops                                      0
Pulses                                        0
Spices                                        0
Starchy_Roots                                0
Stimulants                                   0
Sugar_Sweeteners                             0
Sugar_Crops                                  0
Treenuts                                      0
Vegetable_Oils                               0
Vegetables                                   0
Vegetal_Products                             0
Obesity                                       3
Undernourished                               7
Confirmed                                    6
Deaths                                       6
Recovered                                    6
Active                                       8
Population                                  0
Unit                                         0
dtype: int64
```

```
In [14]: ## plot the death to see any imbalanced data
## the provided death is continous variables, so the problems is to be appr
## the output are numerical variables, it CANNOT be the categorical variabl
## Classification of "0,1" cannot be meaningful in this case
## Use MSE, MAE, RMSE for metrics
```

```
In [15]: ### replace null value the mean value
death['Obesity'].fillna((death['Obesity'].mean()), inplace=True)
death['Confirmed'].fillna((death['Confirmed'].mean()), inplace=True)
death['Recovered'].fillna((death['Recovered'].mean()), inplace=True)
death['Deaths'].fillna((death['Deaths'].mean()), inplace=True)
```

```
In [16]: death.head()
```

```
Out[16]:
```

	Country	Alcoholic_beverages	Animal_fats	Animal_Products	Aquatic_Products, Other	Cereals_Exclud
0	Afghanistan	0.0014	0.1973	9.4341	0.0	
1	Albania	1.6719	0.1357	18.7684	0.0	
2	Algeria	0.2711	0.0282	9.6334	0.0	
3	Angola	5.8087	0.0560	4.9278	0.0	
4	Antigua and Barbuda	3.5764	0.0087	16.6613	0.0	

5 rows × 32 columns

```
In [17]: death.shape
```

```
Out[17]: (170, 32)
```

```
In [18]: ## find the categorical variables
s = (death.dtypes == 'object')
object_cols = list(s[s].index)

print("Categorical variables:")
print(object_cols)
```

```
Categorical variables:
['Country', 'Undernourished', 'Unit']
```

```
In [19]: ## drop unit
## process the categorical variable "Country", "unit" and "Undernourished" u
```

```
In [20]: ## observe the value of undernourished
death['Undernourished'].value_counts()
```

```
Out[20]: <2.5    44
        6.2     3
        16.5    3
        2.7     3
        7.1     3
        ..
        37.2    1
        7.5     1
        6.5     1
        9.5     1
        17      1
        Name: Undernourished, Length: 98, dtype: int64
```

```
In [21]: ## replace the min to "2.5"
death['Undernourished_new'] = death['Undernourished'].str.replace('<2.5','2.5')
```

```
In [22]: death['Undernourished_new'] = pd.to_numeric(death['Undernourished'], errors='coerce')
```

```
In [23]: ### use for loop to categorize
## def f(x):
##     if x == 1:
##         return 1
##     if (x >= 2.5) & (x < 10):
##         return 2
##     if (x >= 10) & (x < 20):
##         return 3
##     if x >= 20:
##         return 4
##     else:
##         return 'null'
## death['Undernourished_new'] = death.Undernourished_new.apply(f)
```

```
In [24]: death['Undernourished_new'].fillna(death['Undernourished_new'].mean(), inplace=True)
```

```
In [25]: death.Undernourished_new.describe()
```

```
Out[25]: count    170.000000
mean         14.457143
std          10.414519
min           2.500000
25%           7.275000
50%          14.457143
75%          14.457143
max          59.600000
Name: Undernourished_new, dtype: float64
```

```
In [26]: death_new = death.drop(['Undernourished', 'Country', 'Unit'], axis = 1)
```

```
In [27]: ## use other ways to futher clean the data
```

```
In [28]: death_new.drop_duplicates(inplace=True)
```

```
In [29]: len(death_new.dropna())
```

```
Out[29]: 162
```

```
In [30]: death_new.dropna(inplace=True)
```

```
In [31]: death_new.isnull().sum()
```

```
Out[31]: Alcoholic_beverages      0
         Animal_fats               0
         Animal_Products           0
         Aquatic_Products, Other    0
         Cereals_Excluding_Beer     0
         Eggs                      0
         Fish_Seafood              0
         Fruits_Excluding_Wine      0
         Meat                      0
         Milk_Excluding_Butter      0
         Miscellaneous             0
         Offals                    0
         Oilcrops                  0
         Pulses                    0
         Spices                    0
         Starchy_Roots             0
         Stimulants                 0
         Sugar_Sweeteners           0
         Sugar_Crops               0
         Treenuts                  0
         Vegetable_Oils             0
         Vegetables                 0
         Vegetal_Products           0
         Obesity                    0
         Confirmed                  0
         Deaths                    0
         Recovered                  0
         Active                     0
         Population                 0
         Undernourished_new         0
         dtype: int64
```

```
In [32]: death_new.shape ## data ready to use
```

```
Out[32]: (162, 30)
```

```
In [33]: death_new.describe
```

```
Out[33]: <bound method NDFrame.describe of      Alcoholic_beverages  Animal_fats
Animal_Products  \
0      0.0014      0.1973      9.4341
1      1.6719      0.1357     18.7684
2      0.2711      0.0282      9.6334
3      5.8087      0.0560      4.9278
4      3.5764      0.0087     16.6613
..      ...      ...      ...
165     2.5952      0.0403     14.7565
166     1.4591      0.1640      8.5765
167     0.0364      0.0446      5.7874
168     5.7360      0.0829      6.0197
169     4.0552      0.0755      8.1489

      Aquatic_Products, Other  Cereals_Excluding_Beer  Eggs  Fish_Seafoo
d  \
0      0.0000      24.8097  0.2099      0.035
0
1      0.0000      5.7817  0.5815      0.212
6
2      0.0000     13.6816  0.5277      0.241
6
3      0.0000      9.1085  0.0587      1.770
7
4      0.0000      5.9960  0.2274      4.148
9
..      ...      ...      ...
...
165     0.0000     12.9253  0.3389      0.945
6
166     0.0042     16.8740  0.3077      2.639
2
167     0.0000     27.2077  0.2579      0.524
0
168     0.0000     21.1938  0.3399      1.692
4
169     0.0000     22.6240  0.2678      0.551
8

      Fruits_Excluding Wine  Meat  Milk_Excluding Butter  ...  \
0      5.3495  1.2020      7.5828  ...
1      6.7861  1.8845     15.7213  ...
2      6.3801  1.1305      7.6189  ...
3      6.0005  2.0571      0.8311  ...
4     10.7451  5.6888      6.3663  ...
..      ...      ...      ...
165     7.6460  3.8328      9.3920  ...
166     5.9029  4.4382      0.6069  ...
167     5.1344  2.7871      1.8911  ...
168     1.0183  1.8427      1.7570  ...
169     2.2000  2.6142      4.4310  ...

      Vegetable Oils  Vegetables  Vegetal_Products  Obesity  Confirmed  \
0      0.5345      6.7642      40.5645      4.5      0.142134
1      0.3261     11.7753      31.2304     22.3      2.967301
```



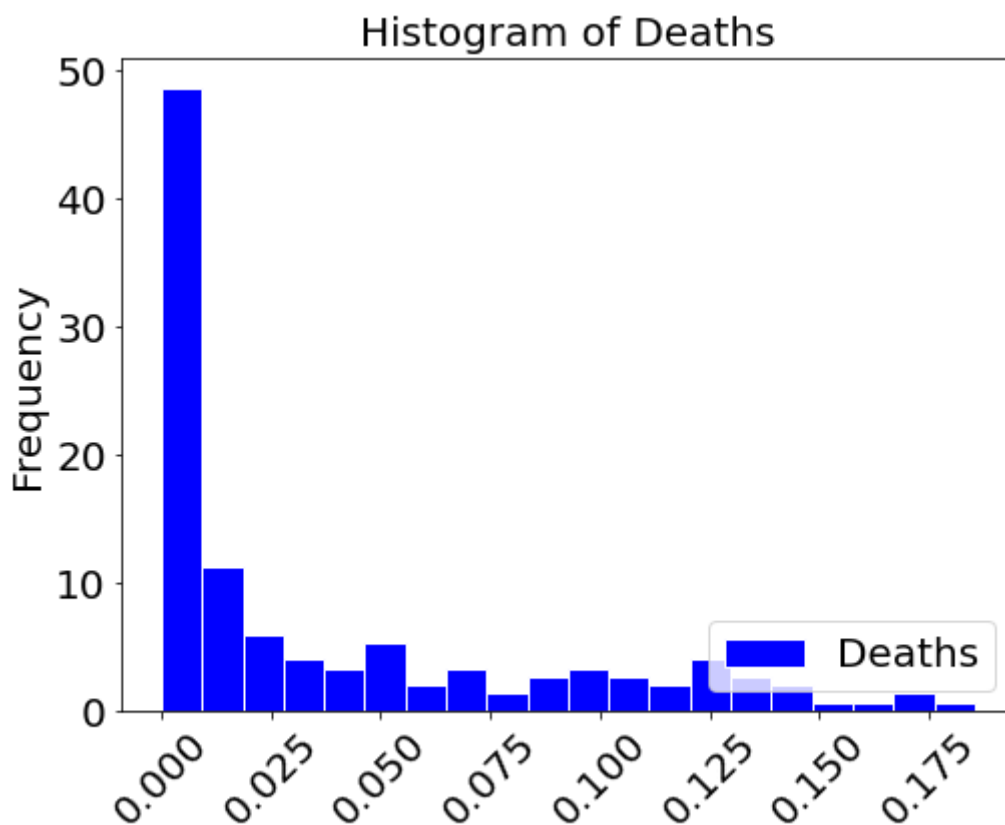
2	1.0310	11.6484	40.3651	26.6	0.244897
3	0.6463	2.3041	45.0722	6.8	0.061687
4	0.8102	5.4495	33.3233	19.1	0.293878
..	...	...	...	...	...
165	1.3734	4.1474	35.2416	25.2	0.452585
166	0.2201	11.9508	41.4232	2.1	0.002063
167	1.0811	3.2135	44.2126	14.1	0.007131
168	0.6657	3.4649	43.9789	6.5	0.334133
169	1.7103	2.3213	41.8526	12.3	0.232033

	Deaths	Recovered	Active	Population	Undernourished_new
0	0.006186	0.123374	0.012574	38928000.0	29.800000
1	0.050951	1.792636	1.123714	2838000.0	6.200000
2	0.006558	0.167572	0.070767	44357000.0	3.900000
3	0.001461	0.056808	0.003419	32522000.0	25.000000
4	0.007143	0.190816	0.095918	98000.0	14.457143
..	...	...	...	...	...
165	0.004287	0.424399	0.023899	28645000.0	21.200000
166	0.000036	0.001526	0.000501	96209000.0	9.300000
167	0.002062	0.004788	0.000282	29826000.0	38.900000
168	0.004564	0.290524	0.039045	18384000.0	46.700000
169	0.008854	0.190964	0.032214	14863000.0	51.300000

[162 rows x 30 columns]>

In [34]: *## feature scaling varies.. need further feature scaling*

```
In [35]: ## plot the death rate
death_new.Deaths.plot(kind = 'hist', bins=20,density=True, figsize=(8,6),co
plt.title('Histogram of Death',size = 20);
plt.xlabel('',size = 20);
plt.ylabel('Frequency',size = 20);
plt.title('Histogram of Deaths',size = 20);
plt.xticks(size = 20,rotation=45)
plt.yticks(size = 20)
plt.legend(loc=4, prop={'size': 20})
plt.savefig(r'output/age_hist.png', dpi=300, bbox_inches='tight')
plt.show()
```



```
In [36]: ## the distribution are extremely right skewed, majority of the data are cl
## transform the data to range of '0,1' use minmax.scale
```

## Feature engineering

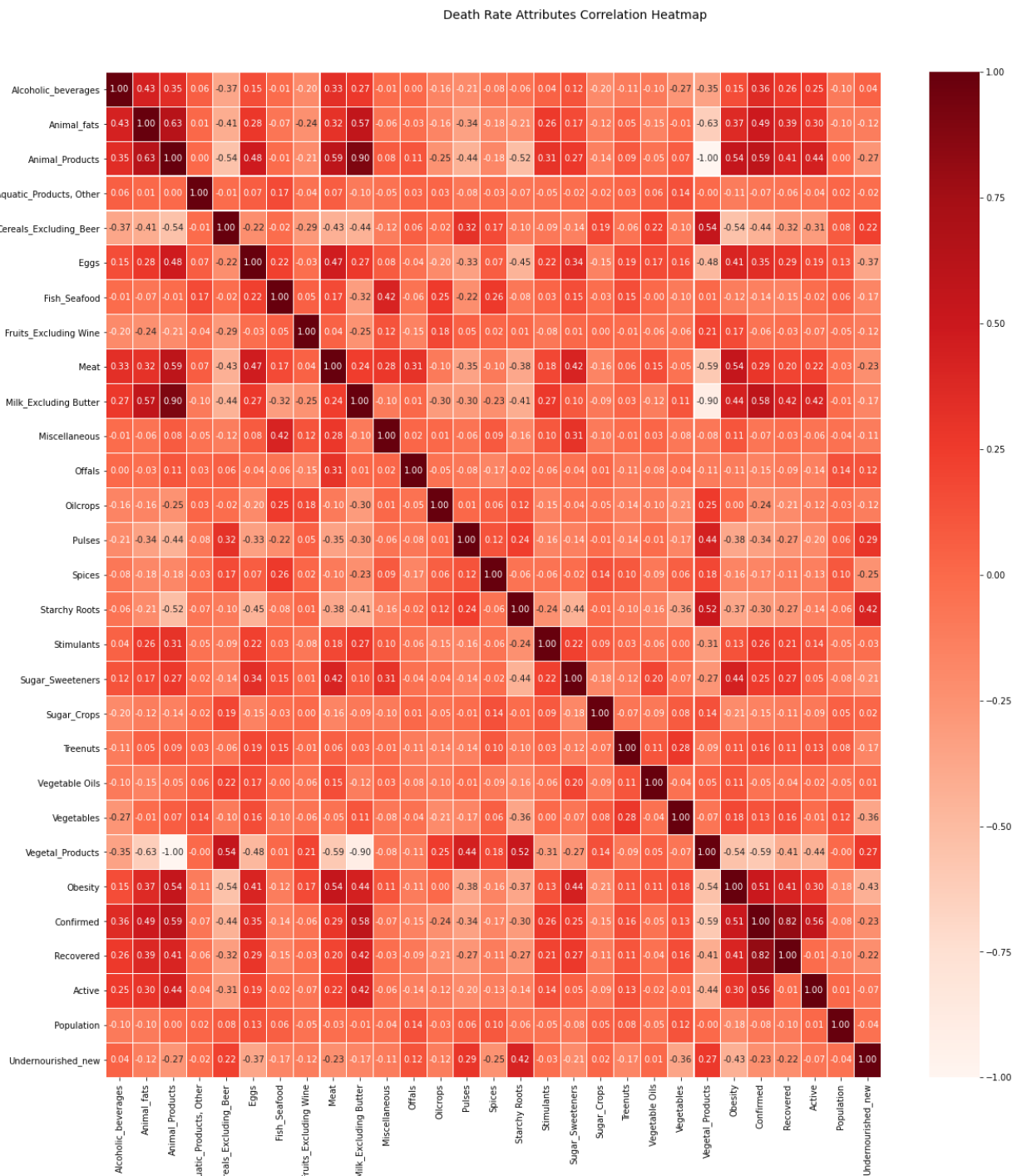
```
In [37]: ## correklation matrix
death_new.corr()
```

Out[37]:

	Alcoholic_beverages	Animal_fats	Animal_Products	Aquatic_Products, Other	Cere:
<b>Alcoholic_beverages</b>	1.000000	0.433924	0.351646	0.060102	
<b>Animal_fats</b>	0.433924	1.000000	0.633236	0.005328	
<b>Animal_Products</b>	0.351646	0.633236	1.000000	0.000321	
<b>Aquatic_Products, Other</b>	0.060102	0.005328	0.000321	1.000000	
<b>Cereals_Excluding_Beer</b>	-0.366784	-0.410585	-0.537847	-0.009767	
<b>Eggs</b>	0.147727	0.275366	0.483142	0.073471	
<b>Fish_Seafood</b>	-0.008807	-0.067951	-0.006359	0.168633	
<b>Fruits_Excluding_Wine</b>	-0.196503	-0.241647	-0.205165	-0.042335	
<b>Meat</b>	0.328021	0.324346	0.585222	0.071402	
<b>Milk_Excluding_Butter</b>	0.265818	0.573629	0.900917	-0.096266	
<b>Miscellaneous</b>	-0.006880	-0.062259	0.079161	-0.047654	
<b>Offals</b>	0.000236	-0.032298	0.114030	0.025688	
<b>Oilcrops</b>	-0.158279	-0.158425	-0.253903	0.025703	
<b>Pulses</b>	-0.207427	-0.342981	-0.442456	-0.076116	
<b>Spices</b>	-0.083472	-0.178545	-0.184567	-0.030962	
<b>Starchy_Roots</b>	-0.064524	-0.214324	-0.518404	-0.067925	
<b>Stimulants</b>	0.043901	0.259924	0.309943	-0.045133	
<b>Sugar_Sweeteners</b>	0.120665	0.168768	0.268206	-0.016951	
<b>Sugar_Crops</b>	-0.197143	-0.123708	-0.139790	-0.021012	
<b>Treenuts</b>	-0.105772	0.047142	0.087807	0.025005	
<b>Vegetable_Oils</b>	-0.097642	-0.145675	-0.053824	0.058724	
<b>Vegetables</b>	-0.270554	-0.013748	0.073080	0.135112	
<b>Vegetal_Products</b>	-0.351720	-0.633128	-1.000000	-0.000294	
<b>Obesity</b>	0.154923	0.374338	0.543293	-0.107291	
<b>Confirmed</b>	0.362384	0.494776	0.593105	-0.074362	
<b>Deaths</b>	0.404866	0.497139	0.537762	-0.067495	
<b>Recovered</b>	0.262248	0.388815	0.414246	-0.064659	
<b>Active</b>	0.250366	0.299180	0.436103	-0.036188	
<b>Population</b>	-0.099160	-0.097362	0.002157	0.024388	
<b>Undernourished_new</b>	0.036051	-0.115072	-0.266866	-0.016677	

30 rows × 30 columns

```
In [38]: # for visualizing correlations
f, ax = plt.subplots(figsize=(20, 20))
corr = death_new.drop(['Deaths'], axis = 1).corr()
sns.heatmap(round(corr, 2), annot=True, ax=ax, cmap="Reds", fmt='.2f', linewidth
f.subplots_adjust(top=0.93)
title = f.suptitle('Death Rate Attributes Correlation Heatmap', fontsize=14
```



```
In [39]: ## there are no variables that have a strong correlation to all other varia
## the results show strong correlations such as confirmed, active and veget
## other strong correlations such as cereals beers to Alcoholic, Miscellane
## the results show the poor correlations such as animal products and Misce
```

## Train the data

```
In [40]: # visualize a minmax scaler transform of the sonar dataset
from pandas import read_csv
from pandas import DataFrame
from pandas.plotting import scatter_matrix
from sklearn.preprocessing import MinMaxScaler
from matplotlib import pyplot
```

```
In [41]: # split into inputs and outputs
feature_cols = death_new.columns.drop(['Deaths'])
X = death_new[feature_cols]

# Create response vector (y)
y = death_new.Deaths
```

```
In [42]: ## transform the features
from sklearn.preprocessing import StandardScaler
X = StandardScaler().fit_transform(X)
```

```
In [43]: ## use logarithmic to transform the y which is extremely skewed.
y_trans = np.sqrt(y)
```

```
In [ ]: ## from sklearn.preprocessing import MinMaxScaler
## y = MinMaxScaler().fit_transform(y.values.reshape(-1, 1))
```

```
In [ ]: ## transform log square root
## to estimate, exp()
```

```
In [44]: print(X.shape, y_trans.shape)

(162, 29) (162,)
```

```
In [45]: ## Create the train/test split.
X_train, X_test, y_train, y_test = train_test_split(X, y_trans, train_size=
```

```
In [46]: X_train.shape
```

```
Out[46]: (129, 29)
```

```
In [47]: X_test.shape
```

```
Out[47]: (33, 29)
```

```
In [48]: y_train.shape
```

```
Out[48]: (129,)
```

```
In [49]: y_test.shape
```

```
Out[49]: (33,)
```

## Machine Learning

```
In [50]: ## Ridge regression  
## optimal value of alpha for ridge regression when All coefficients zero,
```

```
In [51]: ridge_alphas = np.logspace(0, 5, 200)  
  
optimal_ridge = RidgeCV(alphas=ridge_alphas, cv=10)  
optimal_ridge.fit(X_train, y_train)  
  
print(optimal_ridge.alpha_)  
  
30.36771118035459
```

```
In [52]: ## calculate R2 of ridge regression  
## R2 is high model looks good  
  
train_preds = optimal_ridge.predict(X_train)  
optimal_ridge.score(X_train, y_train)
```

```
Out[52]: 0.7965181812120233
```

## cross-validate score

```
In [53]: ## calculate 10 folds Cross validation score and mean  
ridge_scores = cross_val_score(optimal_ridge, X_train, y_train, cv=10)  
  
print(ridge_scores)  
print(np.mean(ridge_scores))
```

```
[0.69550047 0.47157677 0.68375667 0.55410032 0.78349861 0.73532483  
 0.97805967 0.51176456 0.49372232 0.74108159]  
0.6648385819318452
```

## Model Evaluation

```
In [54]: from sklearn.metrics import mean_squared_error, mean_absolute_error, r2_score

# use mean squared error, mean absolute error and R2 to evaluate the model.
def show_scores(model, X_train, X_test, y_train, y_test):
    train_preds = model.predict(X_train)
    test_preds = model.predict(X_test)
    scores = {'Training MAE': mean_absolute_error(y_train, train_preds),
              'Test MAE': mean_absolute_error(y_test, test_preds),
              'Training MSE': mean_squared_error(y_train, train_preds),
              'Test MSE': mean_squared_error(y_test, test_preds),
              'Training R^2': r2_score(y_train, train_preds),
              'Test R^2': r2_score(y_test, test_preds)}
    return scores
```

```
In [55]: show_scores(optimal_ridge, X_train, X_test , y_train, y_test)
```

```
Out[55]: {'Training MAE': 0.040523980899040454,
          'Test MAE': 0.04712884384545657,
          'Training MSE': 0.002915215754985201,
          'Test MSE': 0.0035512516031912336,
          'Training R^2': 0.7965181812120233,
          'Test R^2': 0.8019102492715857}
```

```
In [56]: ## use other models
## create pipeline
from sklearn.pipeline import Pipeline

regressor = Pipeline([
    ('scaler', StandardScaler()),
    ('estimator', Ridge(random_state=28))
])
```

## Machine learning

```

In [57]: ## introduced other models of Support vector regressor and random forest
## remove SRV replace KNN or Decision tree

from sklearn.tree import DecisionTreeRegressor
from sklearn.ensemble import RandomForestRegressor
from xgboost.sklearn import XGBRegressor

# First, we create a dict with our desired models
models = {'Ridge':Ridge(random_state=28),
          'Tree_model':DecisionTreeRegressor(max_depth=3, random_state=1),
          'RandomForest':RandomForestRegressor(),
          'XGBoost':XGBRegressor(n_estimators = 1000, learning_rate = 0.05)}

# Now to build the function that tests each model
def model_build(model, X_train, y_train, X_test, y_test, scale=True):

    if scale:
        regressor = Pipeline([
            ('scaler', StandardScaler()),
            ('estimator', model)
        ])

    else:
        regressor = Pipeline([
            ('estimator', model)
        ])

    # Training
    regressor.fit(X_train, y_train)

    # Scoring the training set

    train_preds = regressor.predict(X_train)
    print(f"R2 on single split: {regressor.score(X_train, y_train)}")

    # Cross validate
    cv_score = cross_val_score(regressor, X_train, y_train, cv = 10)

    print(f"Cross validate R2 score: {cv_score.mean()}")

    # Scoring the test set
    for k, v in show_scores(regressor, X_train, X_test, y_train, y_test).items():
        print(" ", k, v)

```



```
In [58]: for name, model in models.items():
          print(f"==== Scoring {name} model====")

          if name == 'RandomForest' or name == 'XGBoost' or name == 'Tree_model':
              model_build(model, X_train, y_train, X_test, y_test, scale=False)
          else:
              model_build(model, X_train, y_train, X_test, y_test,)
          print()
          print(40*"=")
```

```
==== Scoring Ridge model====
R2 on single split: 0.8124245223869887
Cross validate R2 score: 0.3919834789170463
    Training MAE 0.03857228641175126
    Test MAE 0.054205418755947664
    Training MSE 0.002687330941129937
    Test MSE 0.004710726811744006
    Training R^2 0.8124245223869887
    Test R^2 0.7372344164380014
```

```
=====
==== Scoring Tree_model model====
R2 on single split: 0.9131929989271381
Cross validate R2 score: 0.7035976265534025
    Training MAE 0.026019425475613783
    Test MAE 0.04481547960948823
    Training MSE 0.0012436547829086787
    Test MSE 0.004073215006498119
    Training R^2 0.9131929989271381
    Test R^2 0.7727949930172833
```

```
=====
==== Scoring RandomForest model====
R2 on single split: 0.9762874291078611
Cross validate R2 score: 0.7740692735313153
    Training MAE 0.012782556785800333
    Test MAE 0.036550666777351505
    Training MSE 0.00033972204822876976
    Test MSE 0.0026455966958288035
    Training R^2 0.9762874291078611
    Test R^2 0.8524279187839839
```

```
=====
==== Scoring XGBoost model====
R2 on single split: 0.999977856129166
Cross validate R2 score: 0.7442703358353759
    Training MAE 0.0004306367784147577
    Test MAE 0.03862432091701861
    Training MSE 3.172478087537164e-07
    Test MSE 0.003034460330831356
    Training R^2 0.999977856129166
    Test R^2 0.8307370026980102
```

```
=====
```

```
In [77]: ## calculate the RMSE of all models
Ridge_RMSE = np.sqrt(0.004710726811744006)
Tree_RMSE = np.sqrt(0.004073215006498119)
RF_RMSE = np.sqrt(0.0026455966958288035)
XGBoost_RMSE = np.sqrt(0.003034460330831356)
```

```
In [78]: print(Ridge_RMSE)
print(Tree_RMSE)
print(RF_RMSE)
print(XGBoost_RMSE)

0.06863473473208741
0.0638217439944892
0.05143536425290292
0.05508593587143052
```

```
In [61]: ## the results indicate the XGboosting has the lowest test MSE and test MAE
## the next is to hyperparameters tuning for XGBoosting
```

## Hyperparameters Tunning

```
In [79]: ## set up the parameters for regression

xgb = XGBRegressor()

parameters = {'nthread':[4],
               'objective':['reg:squarederror'],
               'learning_rate': [.03, 0.05, .07], #so called `eta` value
               'max_depth': [5, 6, 7],
               'min_child_weight': [4],
               'subsample': [0.7],
               'colsample_bytree': [0.7],
               'n_estimators': [500, 1000]}
```

```
In [80]: ## use grid search to find the best grid

from sklearn.model_selection import GridSearchCV

xgb_grid = GridSearchCV(xgb, parameters, cv = 5, n_jobs = 4, verbose = True)

xgb_grid.fit(X_train, y_train)

print(xgb_grid.best_score_)
print(xgb_grid.best_params_)
```

```
Fitting 5 folds for each of 18 candidates, totalling 90 fits
0.8160060853703651
{'colsample_bytree': 0.7, 'learning_rate': 0.07, 'max_depth': 5, 'min_child_weight': 4, 'n_estimators': 1000, 'nthread': 4, 'objective': 'reg:squarederror', 'subsample': 0.7}
```

```
In [64]: xgb_best = XGBRegressor(colsample_bytree = 0.7,  
                                learning_rate = 0.05,  
                                max_depth = 5,  
                                min_child_weight = 4,  
                                n_estimators = 1000,  
                                nthread = 4,  
                                objective = 'reg:squarederror',  
                                subsample = 0.7)
```

```
In [81]: model_build(xgb_best, X_train, y_train, X_test, y_test, scale=False)
```

```
R2 on single split: 0.9999892957100863  
Cross validate R2 score: 0.7652098308783224  
Training MAE 0.00028740662751354745  
Test MAE 0.03553743053660788  
Training MSE 1.5335677058625871e-07  
Test MSE 0.0026104127632680177  
Training R^2 0.9999892957100863  
Test R^2 0.8543904878186163
```

```
In [82]: ## calculate RMSE  
Test_RMSE = np.sqrt(0.0026104127632680177)  
print(Test_RMSE)
```

```
0.051092198653688976
```

```
In [83]: ## plot feature importance graph
```

```
In [84]: ## re-define the tree model  
Tree_model = DecisionTreeRegressor(max_depth=3, random_state=1)  
Tree_model.fit(X_train, y_train)
```

```
Out[84]: DecisionTreeRegressor(max_depth=3, random_state=1)
```

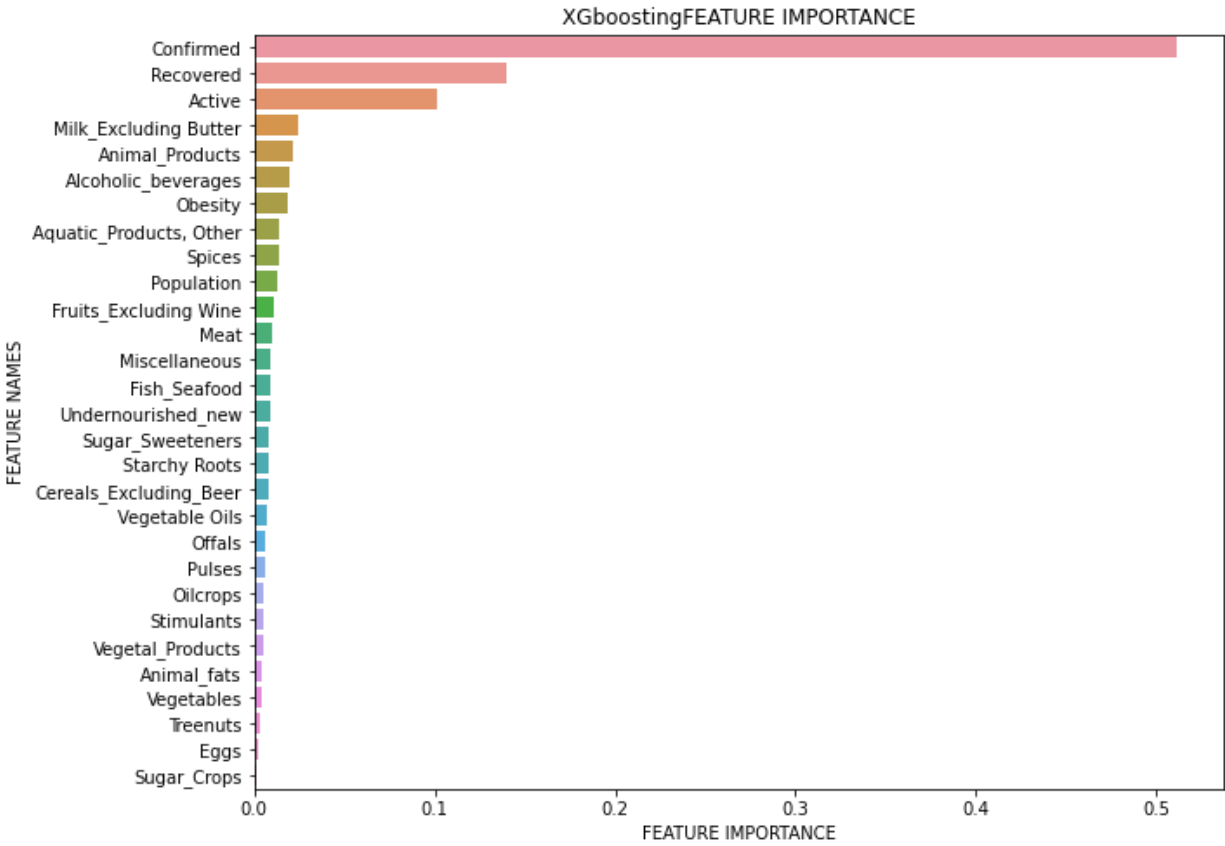
```
In [85]: def plot_feature_importance(importance, names, model_type):  
  
    feature_importance = np.array(importance)  
    feature_names = np.array(names)  
  
    data = {'feature_names': feature_names, 'feature_importance': feature_importance}  
    df = pd.DataFrame(data)  
  
    df.sort_values(by=['feature_importance'], ascending=False, inplace=True)  
  
    #Define size of bar plot  
    plt.figure(figsize=(10,8))  
    #Plot Searborn bar chart  
    sns.barplot(x=df['feature_importance'], y=df['feature_names'])  
    #Add chart labels  
    plt.title(model_type + 'FEATURE IMPORTANCE')  
    plt.xlabel('FEATURE IMPORTANCE')  
    plt.ylabel('FEATURE NAMES')
```

```
In [86]: ## feature importance of XGboosting
pd.DataFrame({'feature':feature_cols, 'importance':xgb_best.feature_importa
```

Out[86]:

	feature	importance
24	Confirmed	0.511461
25	Recovered	0.140178
26	Active	0.100948
9	Milk_Excluding Butter	0.024808
2	Animal_Products	0.021917
0	Alcoholic_beverages	0.019346
23	Obesity	0.018556
3	Aquatic_Products, Other	0.013735
14	Spices	0.013439
27	Population	0.012495
7	Fruits_Excluding Wine	0.011196
8	Meat	0.010230
10	Miscellaneous	0.009274
6	Fish_Seafood	0.009211
28	Undernourished_new	0.008523
17	Sugar_Sweeteners	0.008042
15	Starchy Roots	0.007918
4	Cereals_Excluding_Beer	0.007822
20	Vegetable Oils	0.007349
11	Offals	0.006425
13	Pulses	0.006043
12	Oilcrops	0.005265
16	Stimulants	0.005263
22	Vegetal_Products	0.004999
1	Animal_fats	0.004296
21	Vegetables	0.004254
19	Treenuts	0.003486
5	Eggs	0.002472
18	Sugar_Crops	0.001051

```
In [87]: plot_feature_importance(xgb_best.feature_importances_,feature_cols,'XGboost'
```

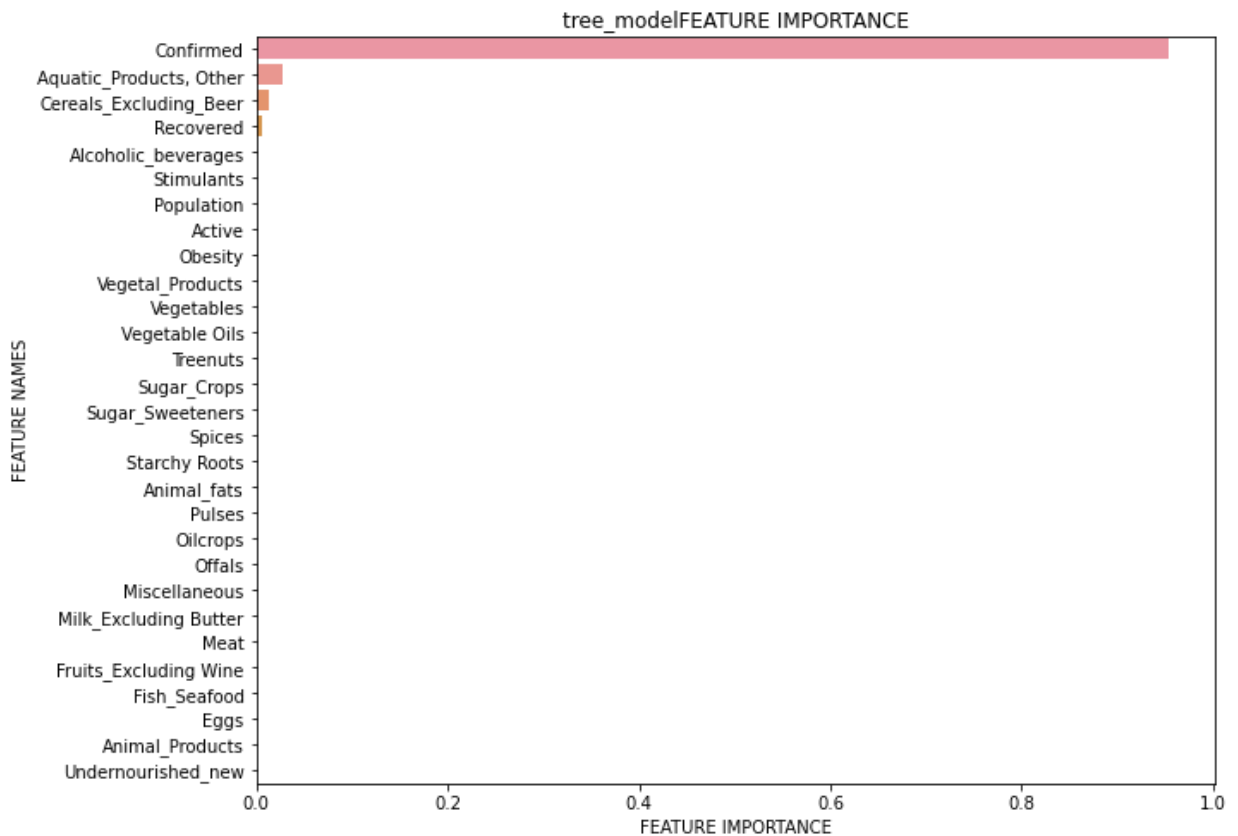


```
In [88]: ## feature importance of tree
pd.DataFrame({'feature':feature_cols, 'importance':Tree_model.feature_importance_})
```

```
Out[88]:
```

	feature	importance
24	Confirmed	0.953770
3	Aquatic_Products, Other	0.026582
4	Cereals_Excluding_Beer	0.012880
25	Recovered	0.006769
0	Alcoholic_beverages	0.000000
16	Stimulants	0.000000
27	Population	0.000000
26	Active	0.000000
23	Obesity	0.000000
22	Vegetal_Products	0.000000
21	Vegetables	0.000000
20	Vegetable Oils	0.000000
19	Treenuts	0.000000
18	Sugar_Crops	0.000000
17	Sugar_Sweeteners	0.000000
14	Spices	0.000000
15	Starchy Roots	0.000000
1	Animal_fats	0.000000
13	Pulses	0.000000
12	Oilcrops	0.000000
11	Offals	0.000000
10	Miscellaneous	0.000000
9	Milk_Excluding Butter	0.000000
8	Meat	0.000000
7	Fruits_Excluding Wine	0.000000
6	Fish_Seafood	0.000000
5	Eggs	0.000000
2	Animal_Products	0.000000
28	Undernourished_new	0.000000

```
In [89]: plot_feature_importance(Tree_model.feature_importances_,feature_cols,'tree_
```



```
In [90]: ## create tree graph
```

```
In [91]: from sklearn.tree import export_graphviz
from sklearn import tree

export_graphviz(Tree_model, out_file='tree.dot', feature_names=feature_cols
```

```
In [92]: import pydotplus

tree = tree.export_graphviz(Tree_model, out_file=None)
graph = pydotplus.graph_from_dot_data(tree)
graph.write_jpg("output/food_deaths_tree.jpg")
```

```
Out[92]: True
```

## Conclusion and Next step

The purpose of the study is to use the food diet and nutrition of countries to predict the death rate. The current study used four machine learning algorithms to predict the results. The ridge regression results show the 10 folds cross-validation score is relatively high in the range of .48 ~.98. the average cross-validation score is .66. Test data MAE .047, and test MSE is 0.004. In comparing

other three different models including decision tree, random forest, ensembled random forest, and XGboosting, the results of XGboosting seems the best with the lowest RMAE(the root of mean absolute error) and RMSE (root fo mean squared error). Further hyperparameter tuning is applied. The grid search is used to find the best parameter. The results of XGboosting indicated the test RMSE =0.05. The feature importance was the plot for the decision tree and XGboosting. The XGBoosting model shows the ranking of the important features are confirmed, recovered, Active, Fruit\_excluding wines and Milk\_excluding butter, etc. The decision tree shows the ranking of the important features are confirmed, Acquatic\_product, undernourished and recovered, etc. The decision tree shows at the confirmed rate  $<-.238$ , the predicted deaths are likely to be true. on the nodes of recovered of value  $-.09$ , 79 samples are assigned to two tree leaves, among them 68 cases predicted deaths are more likely to die if the confirmed  $<-.753$ , on the other hand, the leftover 11 cases who are predicted deaths are likely to be dead at the point of fruit\_excluding wine is  $<.023$

## Next step

From the results of the decision tree and XGboosting results, only a few features are important such as confirmed, Aquatic\_products, undernourished, and recovery. Next step I will continue to adjust the model with only useful features and rerun the model for improved model fit.