In [1]:
```
# Covid-19 project
# Investigate whether deaths caused by COVID-19 by country can be predicted by
examining, analizing and using
# relevant common, well-established data

# ML algorithm used:
    # XGBoost regression model.

# Relevant common data by country
    # Continent -->
        # 2020 data from https://simple.wikipedia.org/wiki/List_of_countries_b
y_continents
    # Population density (Population per square km) -->
        # 2018 data from https://data.worldbank.org/indicator/EN.POP.DNST
    # Percentage of population in urban agglomerations of more than 1 million
 (Agglomerates (%)) -->
        # 2019 data from https://data.worldbank.org/indicator/EN.URB.MCTY.TL.Z
S
    # Population age distribution: percentage of population in the following a
ge groups - 0-14, 15-64, 65- -->
        # 2020 data from http://wdi.worldbank.org/table/2.1
    # GDP per cpita -->
        # 2019 data from https://data.worldbank.org/indicator/NY.GDP.PCAP.CD
    # Healthcare Access and Quality (HAQ) Index -->
        # 2016 data from https://www.thelancet.com/journals/lancet/article/PII
S0140-6736(18)30994-2/fulltext

# COVID-19 data
    # Data up to 2020-07-22 from https://coronavirus.jhu.edu/data/mortality wh
ich includes:
        # Confirmed positive cases
        # Deaths
        # Case fatality (percentage of deaths among positive cases)
        # Deaths per 100K of the county population

# All data was wrangled and compiled in one source file, ms_covid19_2020_07_2
2.csv, available on
# https://github.com/marin-stoytchev/data-science-projects/tree/master/covid_1
9_project
```

In [2]:
```
# Import libraries

import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
sns.set(style = "whitegrid", font_scale = 1.5)
```

In [3]:
```
# Ignore warnings

import warnings
warnings.filterwarnings('ignore')
```

In [4]:
```
# Read data

data = pd.read_csv('covid19_2020_07_22.csv')
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 159 entries, 0 to 158
Data columns (total 13 columns):
 #   Column                 Non-Null Count  Dtype  
---  ------                 --------------  -----  
 0   Country                159 non-null    object 
 1   Continent              159 non-null    object 
 2   Population per sqr km  159 non-null    float64
 3   Agglomerates (%)       159 non-null    float64
 4   Age 0-14 (%)           159 non-null    int64  
 5   Age 15-64 (%)          159 non-null    int64  
 6   Age 65- (%)            159 non-null    int64  
 7   GDP per capita ($)     159 non-null    float64
 8   HAQ Index              159 non-null    int64  
 9   Confirmed              159 non-null    int64  
 10  Deaths                 159 non-null    int64  
 11  Case fatality          159 non-null    float64
 12  Deaths per 100K        159 non-null    float64
dtypes: float64(5), int64(6), object(2)
memory usage: 16.3+ KB
```

In [5]:
```
# Preview data

data.head(10)
```

Out[5]:

	Country	Continent	Population per sqr km	Agglomerates (%)	Age 0-14 (%)	Age 15-64 (%)	Age 65- (%)	GDP per capita ($)	HAQ Index	Confirmed
0	Afghanistan	Asia	56.94	10.81	42	55	3	502.11	26	35727
1	Albania	Europe	104.61	0.00	17	68	14	5352.85	75	4358
2	Algeria	Africa	17.73	6.33	31	63	7	3948.30	63	24872
3	Andorra	Europe	163.84	0.00	14	70	16	40886.40	95	889
4	Angola	Africa	24.71	25.27	47	51	2	2973.59	33	812
5	Antigua and Barbuda	N. America	218.83	0.00	22	69	9	17790.30	70	76
6	Argentina	S. America	16.26	42.90	25	64	11	10006.14	68	141900
7	Armenia	Asia	103.68	36.62	21	68	11	4622.73	71	35693
8	Australia	Australia	3.25	60.89	19	65	16	54907.10	96	13302
9	Austria	Europe	107.13	21.57	14	67	19	50277.27	94	19929

In [6]:
```
# Note: the zero values in 'Agglomerates (%)' are true 0s since the correspond
ing coutries have no cities over 1 million
```

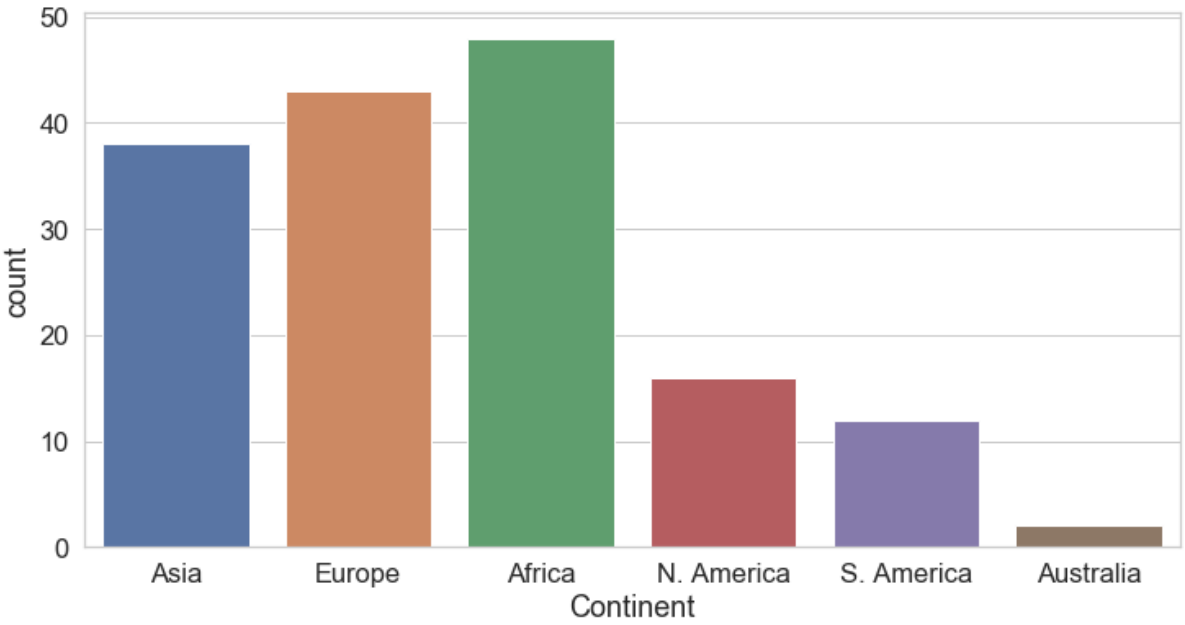
In [7]:
```
# 1) EDA
```

In [8]:
```
# For consistency convert 'Case fatality' from rational numbers (ratios) to pe
rcentages

data['Case fatality'] = 100 * data['Case fatality']
```

In [9]:
```
# Get data column names
data.columns
```

Out[9]:
```
Index(['Country', 'Continent', 'Population per sqr km', 'Agglomerates (%)',
       'Age 0-14 (%)', 'Age 15-64 (%)', 'Age 65- (%)', 'GDP per capita ($)',
       'HAQ Index', 'Confirmed', 'Deaths', 'Case fatality', 'Deaths per 100
K'],
      dtype='object')
```

In [10]:
```
# Countplot of number of coutries by continent

plt.figure(figsize = (12, 6))
sns.countplot(data['Continent'])
plt.show()
```



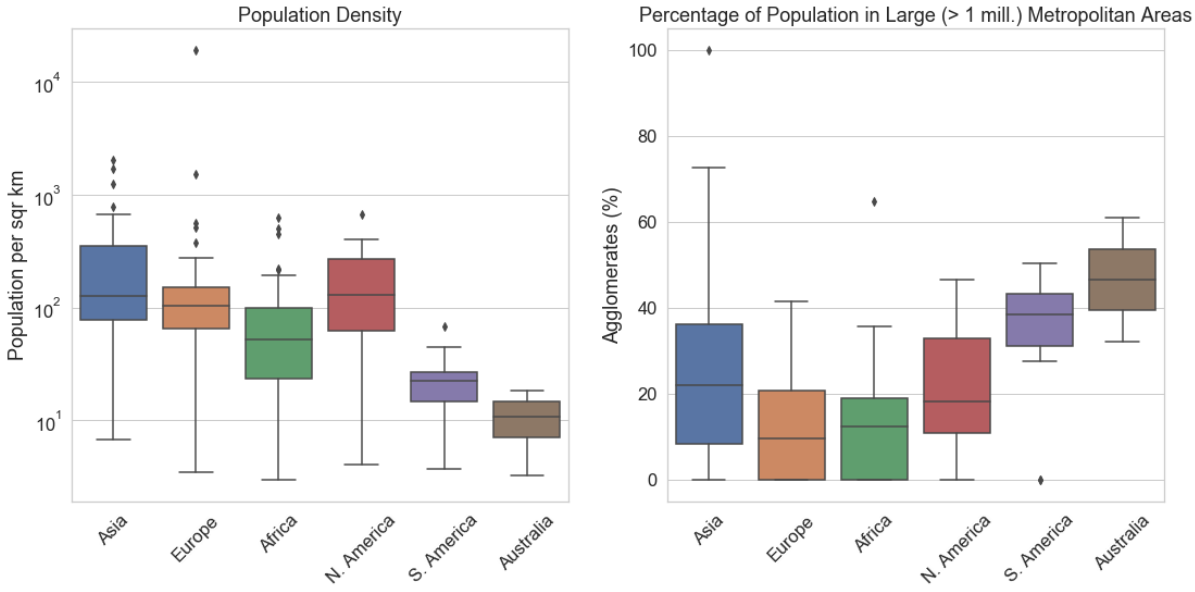
In [11]:
```
# Get precise count of countries by continent

data['Continent'].value_counts()
```

Out[11]:
```
Africa        48
Europe        43
Asia          38
N. America    16
S. America    12
Australia      2
Name: Continent, dtype: int64
```

In [12]:
```
# Africa, Europe and Asia have the largest representation, followed by North a
nd South America;
# Australian continent is represented by two countries only --> Australia and
 New Zeeland
```

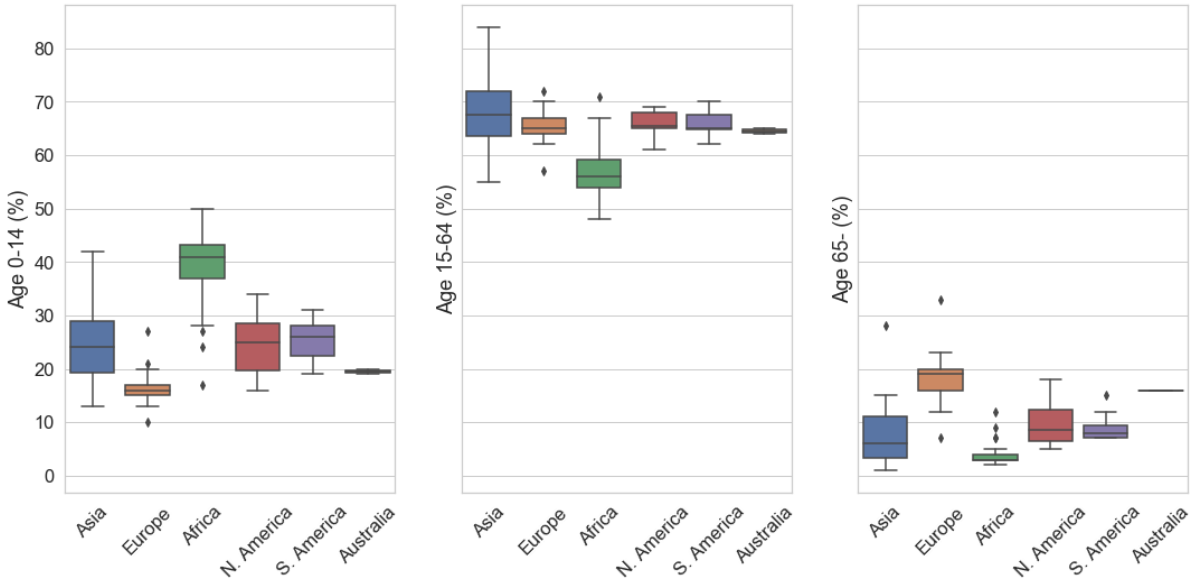
In [13]:
```
# Examine distributions of feature values by continent via boxplots
```

In [14]:
```
# Boxplots of Population Density and Percentage of people living in large metr
o areas (> 1 mill.) vs. Continent

fig, axes = plt.subplots(1, 2, figsize=(18, 8), sharey = False)

sns.boxplot(x = 'Continent', y = 'Population per sqr km', data = data, ax = ax
es[0])
axes[0].set(xlabel = None)
axes[0].tick_params(axis = 'x', rotation = 45)
axes[0].set(yscale = 'log')
axes[0].set(title = 'Population Density')

sns.boxplot(x = 'Continent', y = 'Agglomerates (%)', data = data, ax = axes[1
])
axes[1].set(xlabel = None)
axes[1].tick_params(axis = 'x', rotation = 45)
axes[1].set(title = 'Percentage of Population in Large (> 1 mill.) Metropolita
n Areas')

plt.show()
```



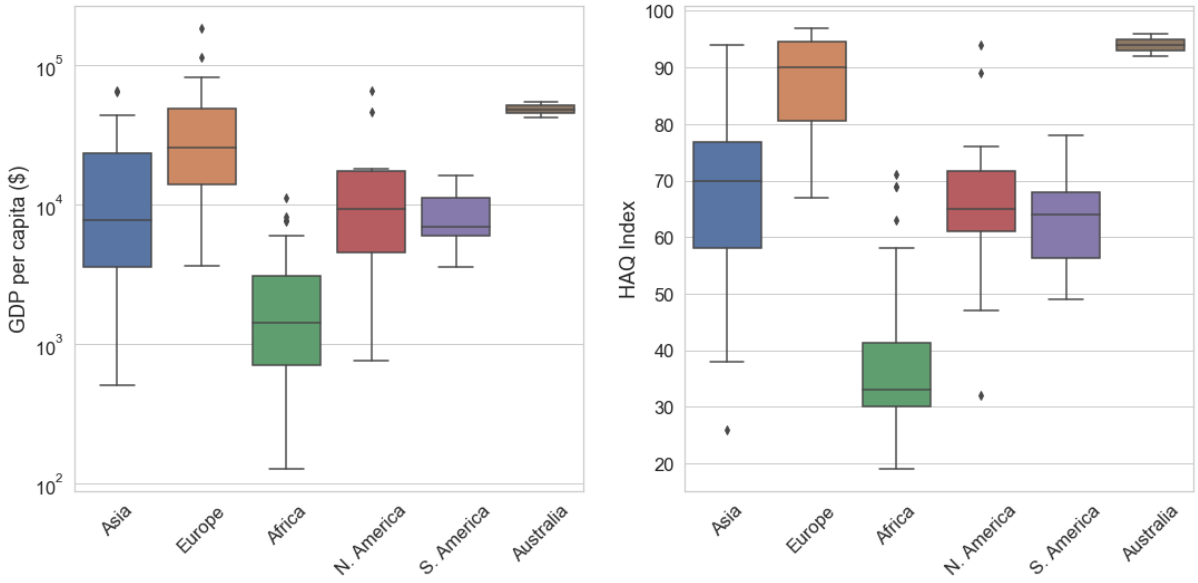
In [15]:
```
# Two trends are observed
#1) High population density with low(er) percentege of people in large (> 1 mi
ll.) metro areas -->
    # Asia, Europe, Africa, N. America
#2) Low population density with high(er) percentege of people in large (> 1 mi
ll.) metro areas -->
    # S. America, Australia
```

In [16]:
```
# Boxplots of Age Demographics vs. Continent

fig, axes = plt.subplots(1, 3, figsize=(18, 8), sharey = True)

sns.boxplot(x = 'Continent', y = 'Age 0-14 (%)', data = data, ax = axes[0])
axes[0].set(xlabel = None)
axes[0].tick_params(axis = 'x', rotation = 45)
axes[0].set_yticks(np.arange(0, 100, 10))

sns.boxplot(x = 'Continent', y = 'Age 15-64 (%)', data = data, ax = axes[1])
axes[1].set(xlabel = None)
axes[1].tick_params(axis = 'x', rotation = 45)

sns.boxplot(x = 'Continent', y = 'Age 65- (%)', data = data, ax = axes[2])
axes[2].set(xlabel = None)
axes[2].tick_params(axis = 'x', rotation = 45)

plt.tight_layout
plt.show()
```



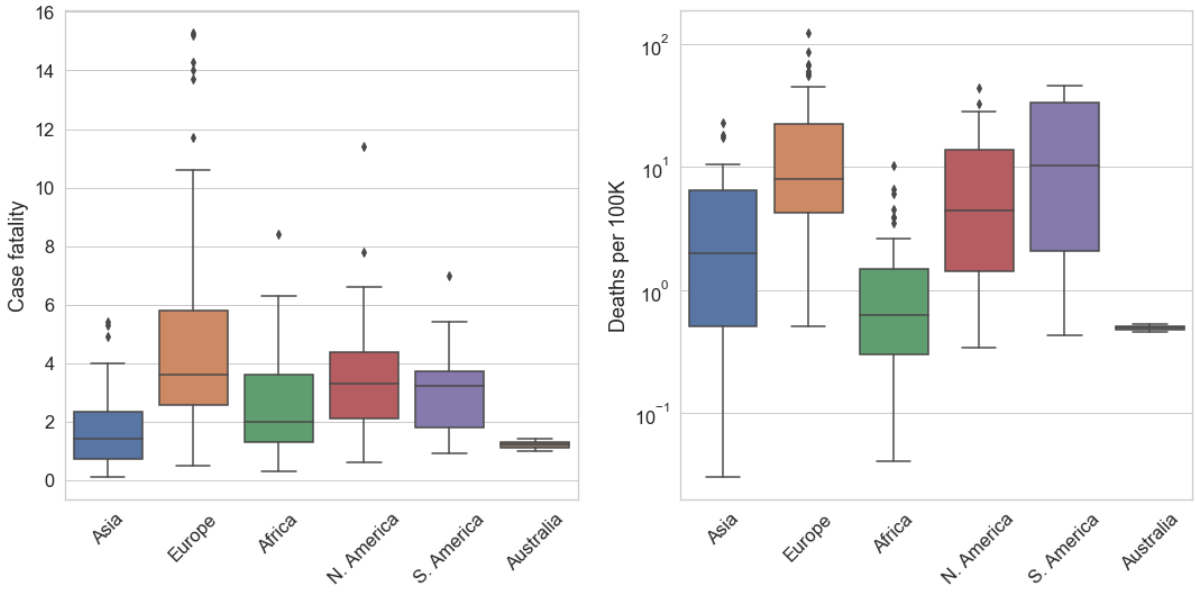
In [17]:
```
# Main observations:
    # 1) Africa: 'youngest' continent with average of ~ 40 % of population bel
ow 15 years old and only ~ 3 % older than 64
    # 2) Europe: 'oldest' continent with average of ~ 15 % of population below
15 years old and ~ 20 % older than 64
    # 3) Rest of continets: 'middle-aged' with similar age demographics with s
ome deviations (more pronounced for Age 65-)
```

In [18]:
```
# Boxplots of GDP per capita and HAQ Index vs. Continent

fig, axes = plt.subplots(1, 2, figsize=(18, 8), sharey = False)

sns.boxplot(x = 'Continent', y = 'GDP per capita ($)', data = data, ax = axes[
0])
axes[0].tick_params(axis = 'x', rotation = 45)
axes[0].set(yscale = 'log')
axes[0].set(xlabel = None)

sns.boxplot(x = 'Continent', y = 'HAQ Index', data = data, ax = axes[1])
axes[1].tick_params(axis = 'x', rotation = 45)
axes[1].set(xlabel = None)

plt.show()
```



In [19]:
```
# Clear visual corellation between these two features (natural to expect)
# Lowest score in both charts: Africa
# Max scores in both charts: Australia + New Zeeland, Europe
# Middle socres:Asia, N. America, S. America
```

In [20]:
```
# Boxplots of the two possible targets, Case fatality and Deaths per 100K, vs. Continent

fig, axes = plt.subplots(1, 2, figsize=(18, 8), sharey = False)

sns.boxplot(x = 'Continent', y = 'Case fatality', data = data, ax = axes[0])
axes[0].tick_params(axis = 'x', rotation = 45)
axes[0].set(xlabel = None)

sns.boxplot(x = 'Continent', y = 'Deaths per 100K', data = data, ax = axes[1])
axes[1].tick_params(axis = 'x', rotation = 45)
axes[1].set(xlabel = None)
axes[1].set(yscale = 'log')

plt.show()
```



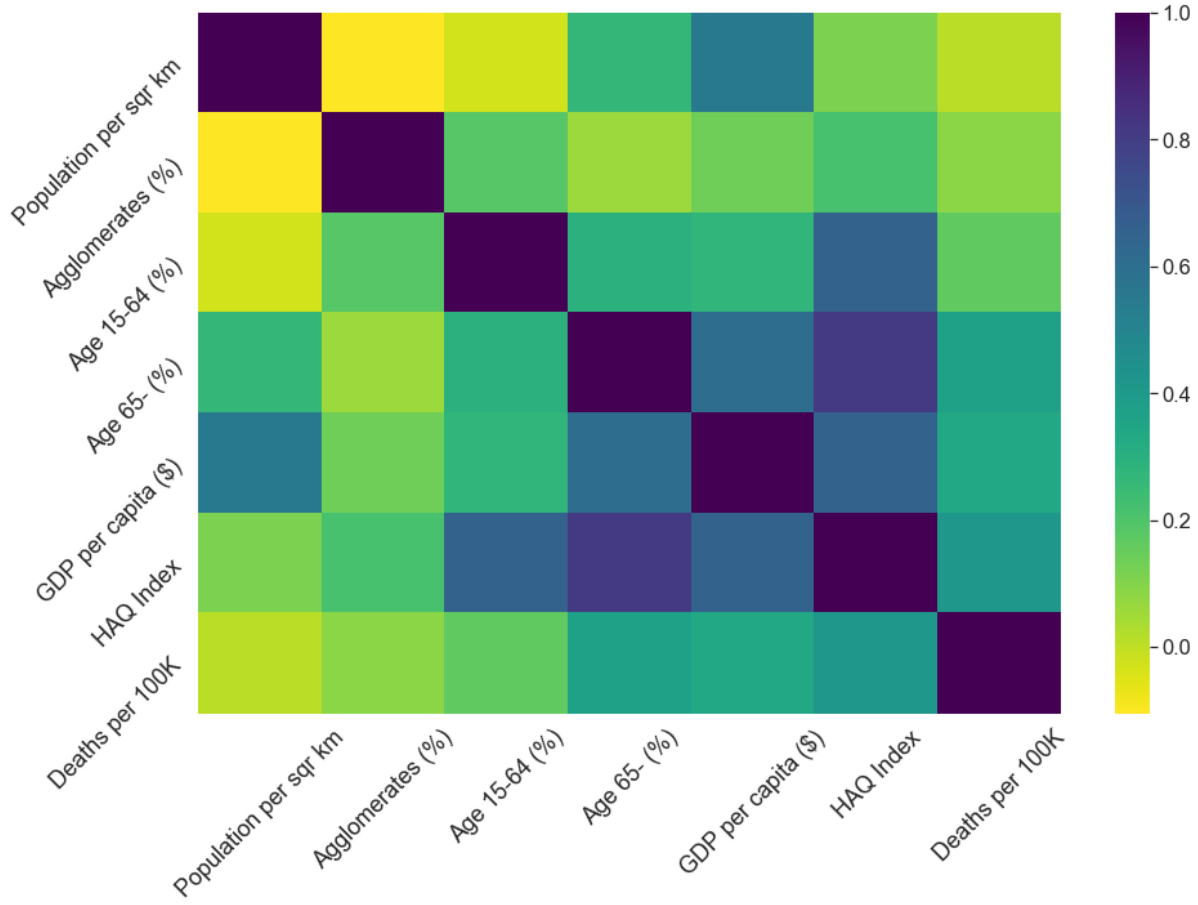
In [21]:
```
# Both 'Case fatality' and 'Deaths per 100K' show large variations
# However, for many reasons 'Case fatality' is not considered a reliable measure -->
    # select 'Deaths per 100K' as target
```

In [22]:
```
# For better correlation and pairplot visualization create new dataset, data_
1, consisting of most relevant features

data_1 = data[['Population per sqr km', 'Agglomerates (%)', 'Age 15-64 (%)',
'Age 65- (%)', 'GDP per capita ($)',
               'HAQ Index','Deaths per 100K']]
# 'Age 0-14 (%)' is being dropped because of explicit relationship with 'Age 1
5-64 (%)' and 'Age 65- (%)' -->
    # 'Age 0-14 (%)' = 100 - ('Age 15-64 (%)' + 'Age 65- (%)')

data_1.head(10)
```

Out[22]:

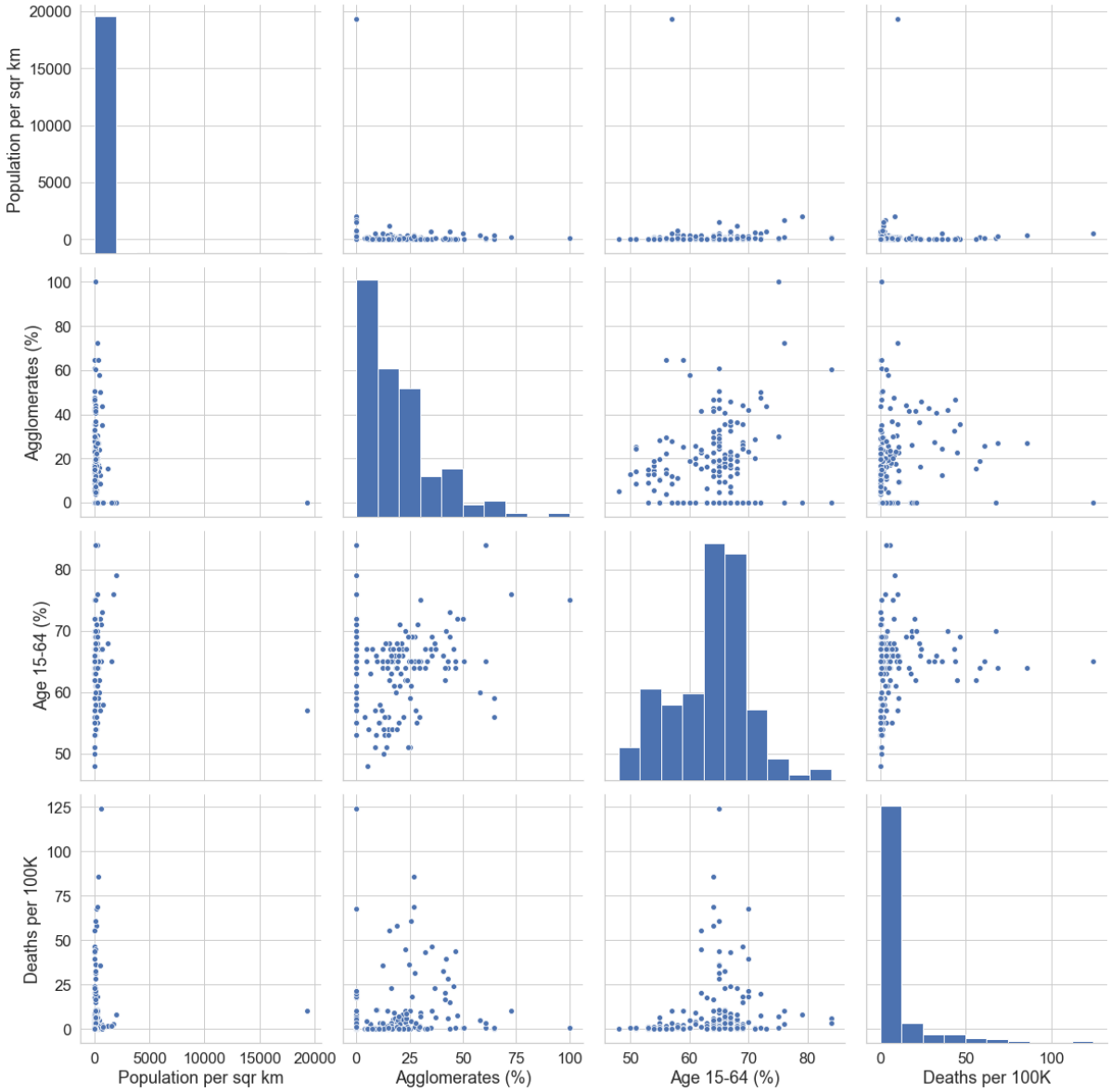
	Population per sqr km	Agglomerates (%)	Age 15-64 (%)	Age 65- (%)	GDP per capita ($)	HAQ Index	Deaths per 100K
0	56.94	10.81	55	3	502.11	26	3.20
1	104.61	0.00	68	14	5352.85	75	4.19
2	17.73	6.33	63	7	3948.30	63	2.63
3	163.84	0.00	70	16	40886.40	95	67.53
4	24.71	25.27	51	2	2973.59	33	0.11
5	218.83	0.00	69	9	17790.30	70	3.12
6	16.26	42.90	64	11	10006.14	68	5.82
7	103.68	36.62	68	11	4622.73	71	22.97
8	3.25	60.89	65	16	54907.10	96	0.53
9	107.13	21.57	67	19	50277.27	94	8.04

In [23]:
```
# Plot heatmap of the correlation matrix for data_1 to examine for highly-corr
elated features

plt.figure(figsize = (15, 10))
sns.heatmap(data_1.corr(), cmap = 'viridis_r')
plt.tick_params(labelsize = 18, rotation = 45)
plt.show()
```



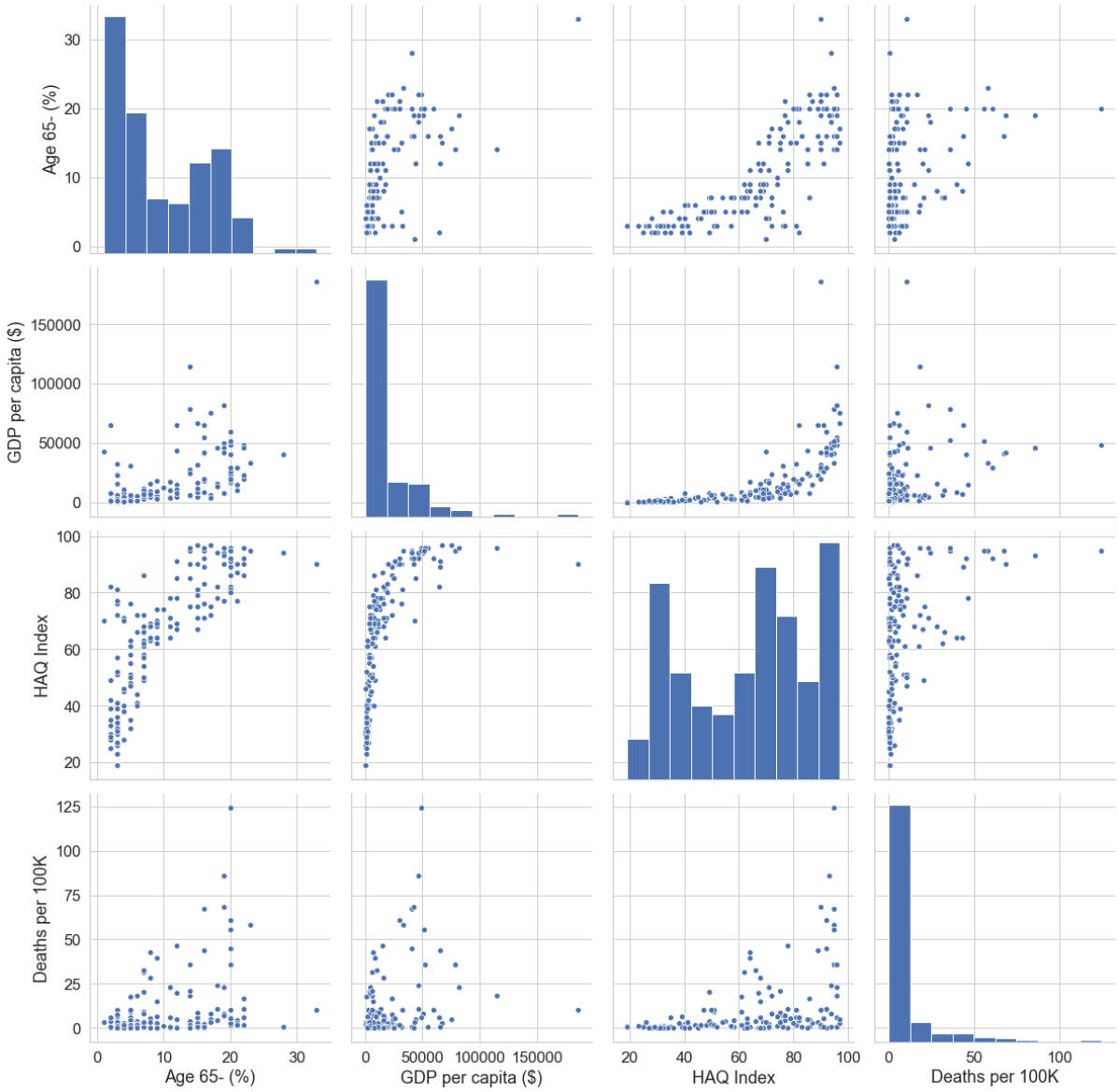
In [24]:
```
# No strong correlation between most of the features
# Higher degree of correlation is observed between
    # 'HAQ Index' and 'Age 65- (%)'
    # 'HAQ Index' and 'Age 15-64 (%)'
    # 'HAQ Index' and 'GDP per capita ($)'
    # all of these are natural to expect
# Surprisingly, very low correlation is observed between 'Deaths per 100K' and
the two population density features
```

In [25]:
```
# For better readability, create pairplot with first half of data only + target

sns.pairplot(data_1.iloc[:, [0, 1, 2, 6]], height = 4, aspect = 1)
plt.tight_layout
plt.show()
```



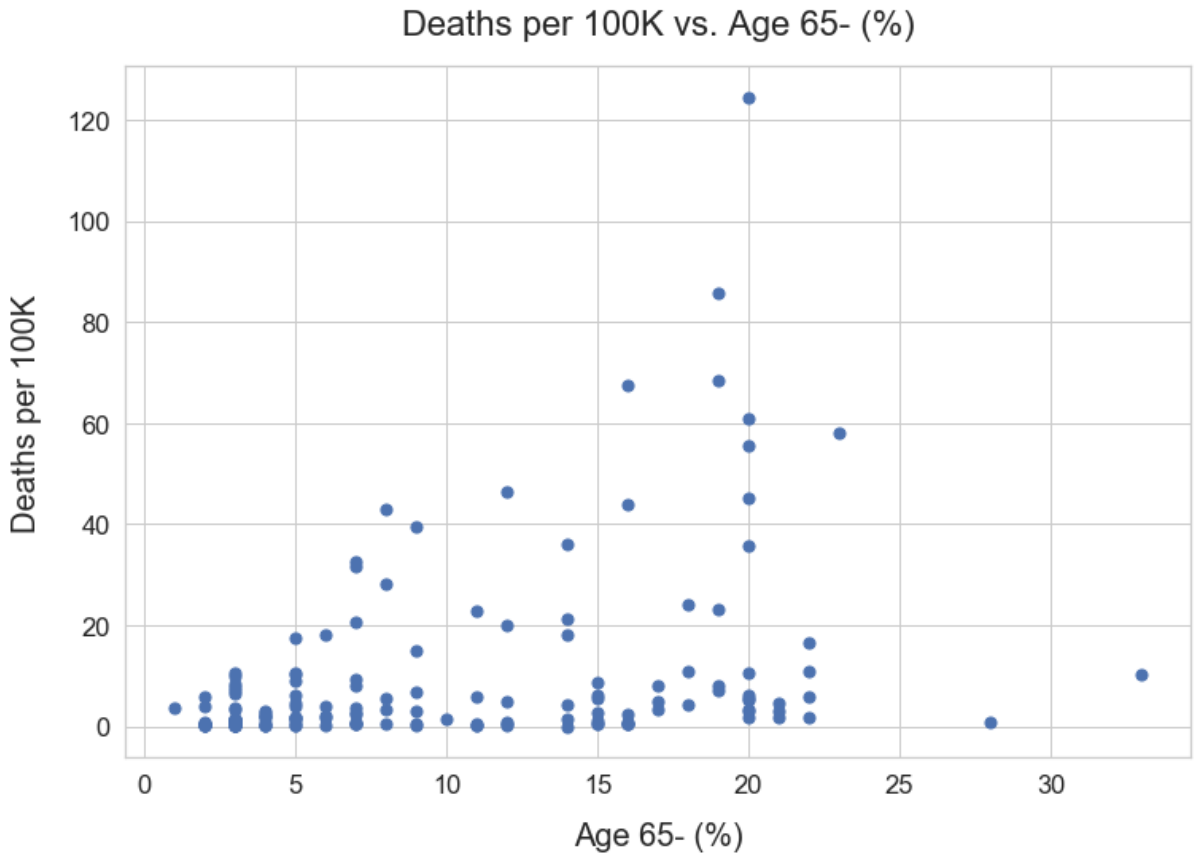
In [26]:
```
# There appear to be no clear dependence of the target on the features plotted here and dependence between features as well
# Note: Population Density distribution plotted here is strongly skewed because of a single extremely large value (Monaco)
```

In [27]:
```
# Create pairplot with second half of data + target

sns.pairplot(data_1.iloc[:, [3, 4, 5, 6]], height = 4, aspect = 1)
plt.tight_layout
plt.show()
```



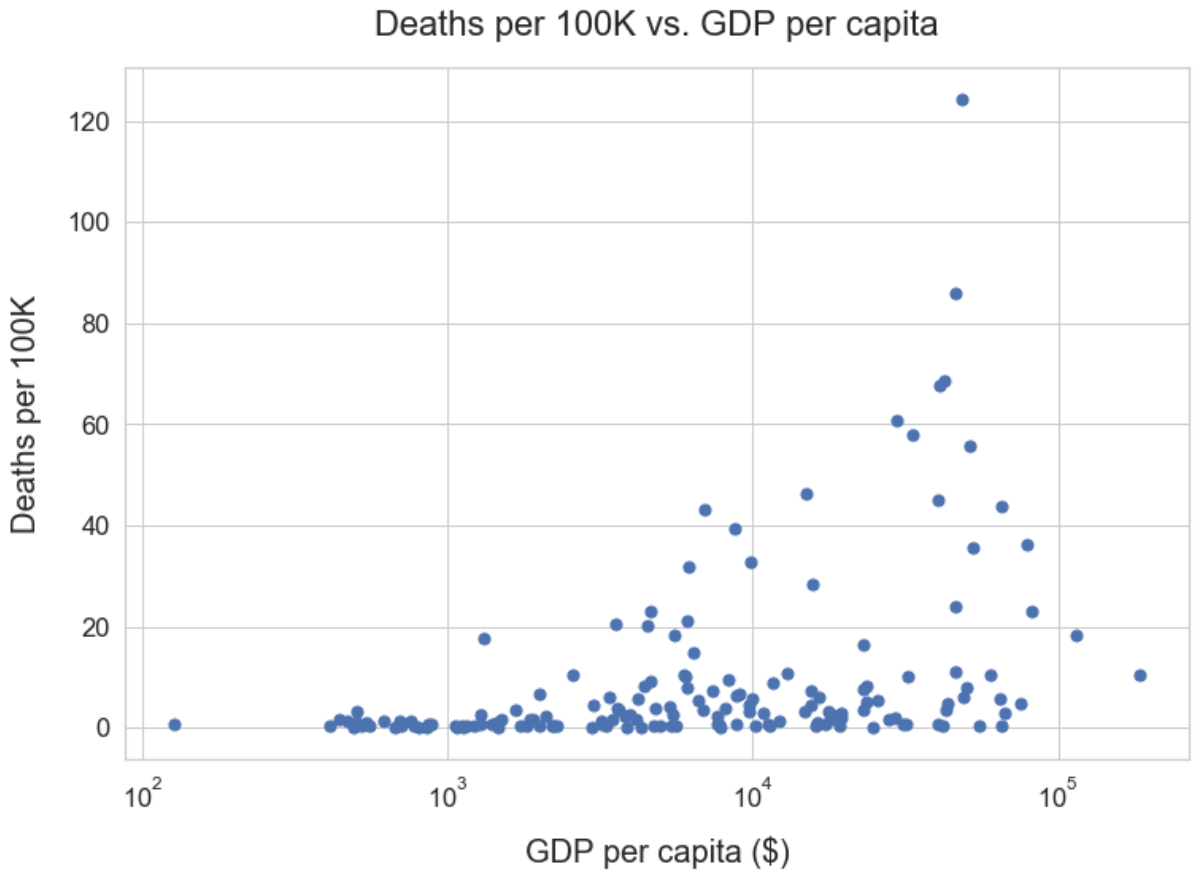
In [28]:
```
# A more defined relationship is observed between 'HAQ Index' and 'Age 65-
 (%)' as already indicated by the correlation matrix
# To lesser degree relationship is observed between 'HAQ Index' and 'GDP per c
apita ($)', as well
# However, the relationships between Deths per 100K and these three features i
s not clear --> investigate these in more detail
```

In [29]:
```
# Create scatterplot between 'Deaths per 100K' and 'Age 65-'

plt.figure(figsize = (12, 8))
plt.scatter(data['Age 65- (%)'], data['Deaths per 100K'], s = 50, c = 'b')
plt.xlabel('Age 65- (%)', fontsize = 20, labelpad = 15)
plt.ylabel('Deaths per 100K', fontsize = 20, labelpad = 15)
plt.title('Deaths per 100K vs. Age 65- (%)', fontsize = 22, pad = 20)

plt.show()
```



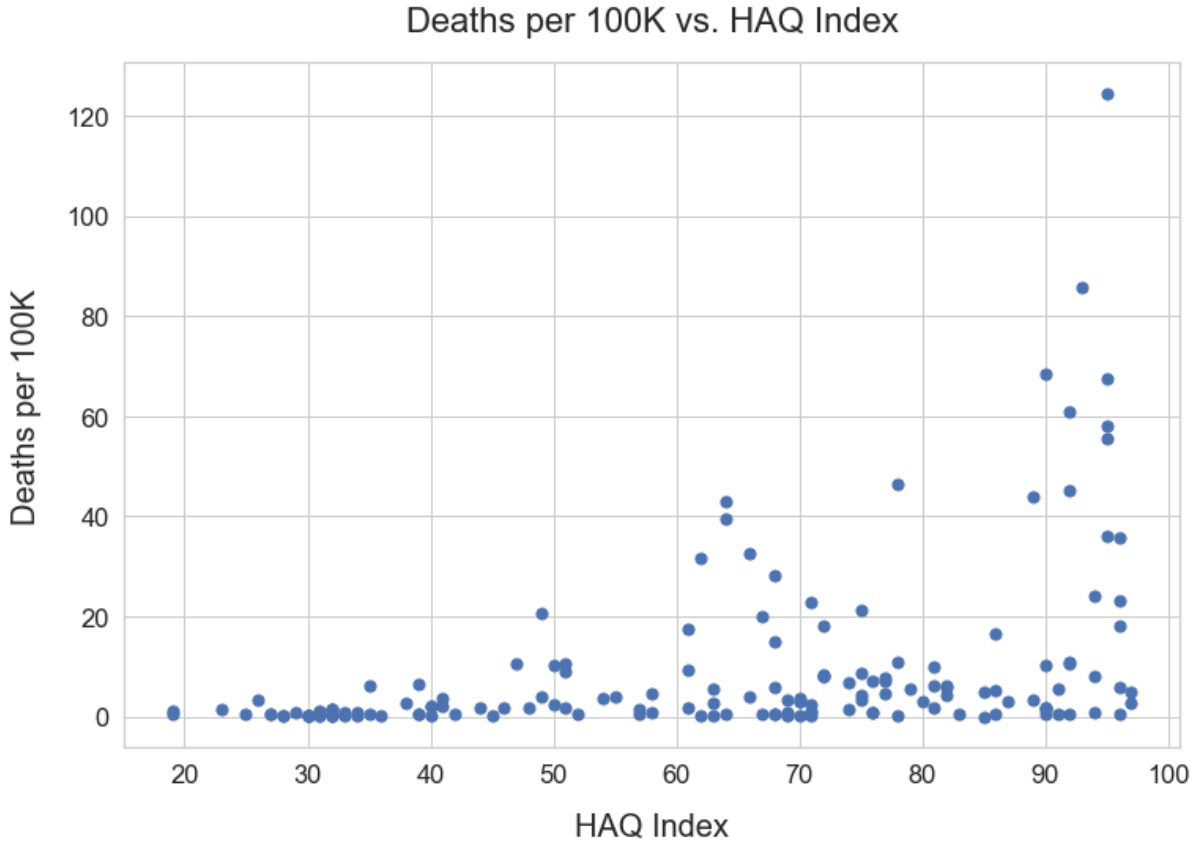
In [30]:
```
# Main observations from plot
# 1) Some of the highest death rate values are observed for the percentage of
 population older than 65 being within 15-25 %
    # However, there is no consitent relationship in this range since the majo
rity of death rate values are still very low
    # and the two data points with highest percentage of people older than 65
 show low death rate
# 2) Consistently low death rate values are observed for the percentage of peo
ple above 65 being within 0-5 %

# These observations are consistent with studies showng that COVID-19 has high
est mortality rate for people older than 65
```

In [31]:
```
# Create scatterplot between 'Deaths per 100K' and 'GDP per capita ($)'

plt.figure(figsize = (12, 8))
plt.scatter(data['GDP per capita ($)'], data['Deaths per 100K'], s = 50, c =
'b')
plt.xscale('log')
plt.xlabel('GDP per capita ($)', fontsize = 20, labelpad = 15)
plt.ylabel('Deaths per 100K', fontsize = 20, labelpad = 15)
plt.title('Deaths per 100K vs. GDP per capita', fontsize = 22, pad = 20)

plt.show()
```



In [32]:
```
# This result is surprising because it defies conventional logic
    # 1) Counrties with lowest GDP per capita consistently show lowest number
 of deaths per 100k
    # 2) As GDP per capita increases, so is the death rate --> highest death r
ates are observed for very high GDP values
```

In [33]:
```
# Create scatterplot between 'Deaths per 100K' and 'HAQ Index'

plt.figure(figsize = (12, 8))
plt.scatter(data['HAQ Index'], data['Deaths per 100K'], s = 50, c = 'b')
plt.xlabel('HAQ Index', fontsize = 20, labelpad = 15)
plt.ylabel('Deaths per 100K', fontsize = 20, labelpad = 15)
plt.title('Deaths per 100K vs. HAQ Index', fontsize = 22, pad = 20)

plt.show()
```



In [34]:
```
# This plot resembles the previous plot and again shows a counterintuitive relationship
    # 1) Counrties with the lowest HAQ Index consistently show lowest deaths per 100k
    # 2) Counrties with the highest HAQ Index (best healthcare) show the highest deaths per 100k observed

# The two relationships revealed here between mortality rate and GDP and Healthcare quality is suprising and
# raises questions about the reliability of COVID-19 data
# To some extent one can contribute the low death rates at the low ranges of these features with the low score of people above 65
# However, this argument cannot be applied to explain the wide variations in death rate for the high end ranges
```

In [35]:
```
# 2) Predicting HAQ Index based on conventional factors using XGBoost

# This is done to establish that the factors considerd here can be used to pre
dict accurately strictly medicaly-derived feature
    # see https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(18)3
0994-2/fulltext on how HAQ Index is derived
```

In [36]:
```
# Create new dataset which include all features relevant to this problem

data.columns
```

Out[36]:
```
Index(['Country', 'Continent', 'Population per sqr km', 'Agglomerates (%)',
       'Age 0-14 (%)', 'Age 15-64 (%)', 'Age 65- (%)', 'GDP per capita ($)',
       'HAQ Index', 'Confirmed', 'Deaths', 'Case fatality', 'Deaths per 100
K'],
      dtype='object')
```

In [37]:
```
# New data subset to be used with model

data_2 = data[['Continent', 'Population per sqr km', 'Agglomerates (%)','Age 1
5-64 (%)', 'Age 65- (%)',
               'GDP per capita ($)', 'HAQ Index', 'Deaths per 100K']]
data_2.head(10)
```

Out[37]:

	Continent	Population per sqr km	Agglomerates (%)	Age 15-64 (%)	Age 65- (%)	GDP per capita ($)	HAQ Index	Deaths per 100K
0	Asia	56.94	10.81	55	3	502.11	26	3.20
1	Europe	104.61	0.00	68	14	5352.85	75	4.19
2	Africa	17.73	6.33	63	7	3948.30	63	2.63
3	Europe	163.84	0.00	70	16	40886.40	95	67.53
4	Africa	24.71	25.27	51	2	2973.59	33	0.11
5	N. America	218.83	0.00	69	9	17790.30	70	3.12
6	S. America	16.26	42.90	64	11	10006.14	68	5.82
7	Asia	103.68	36.62	68	11	4622.73	71	22.97
8	Australia	3.25	60.89	65	16	54907.10	96	0.53
9	Europe	107.13	21.57	67	19	50277.27	94	8.04

In [38]:
```
# In order to be able to use XGBoost transform 'Continent' values into numeric categorical values

data_2['Continent'].replace({'Africa': 1, 'Asia': 2, 'Europe': 3, 'N. America': 4,
                             'S. America': 5, 'Australia': 6}, inplace=True)

data_2.head(10)
```

Out[38]:

	Continent	Population per sqr km	Agglomerates (%)	Age 15-64 (%)	Age 65- (%)	GDP per capita ($)	HAQ Index	Deaths per 100K
0	2	56.94	10.81	55	3	502.11	26	3.20
1	3	104.61	0.00	68	14	5352.85	75	4.19
2	1	17.73	6.33	63	7	3948.30	63	2.63
3	3	163.84	0.00	70	16	40886.40	95	67.53
4	1	24.71	25.27	51	2	2973.59	33	0.11
5	4	218.83	0.00	69	9	17790.30	70	3.12
6	5	16.26	42.90	64	11	10006.14	68	5.82
7	2	103.68	36.62	68	11	4622.73	71	22.97
8	6	3.25	60.89	65	16	54907.10	96	0.53
9	3	107.13	21.57	67	19	50277.27	94	8.04

In [39]:
```
# Create features and target from data_2 which we will use with XGBRegressor model

X = data_2.iloc[:, :-2].values # all columns, but last two - HAQ Index and Deaths per 100K
y = data_2.iloc[:, -2].values # HAQ Index column
```

In [40]:
```
# Train/test split

from sklearn.model_selection import train_test_split

X_train_1, X_test_1, y_train_1, y_test_1 = train_test_split(X, y, test_size = 0.2, random_state = 0)
```

In [41]:
```
# For best predictions, apply model optimization by using hyperopt

from xgboost import XGBRegressor
from hyperopt import fmin, tpe, hp, STATUS_OK, Trials, space_eval
from sklearn import metrics

# Create hyperparameter space to search over
space = {'max_depth': hp.choice('max_depth', np.arange(3, 15, 1, dtype = int
)),
        'n_estimators': hp.choice('n_estimators', np.arange(50, 300, 10, dtype
= int)),
        'colsample_bytree': hp.quniform('colsample_bytree', 0.5, 1.0, 0.1),
        'min_child_weight': hp.choice('min_child_weight', np.arange(0, 10, 1,
dtype = int)),
        'subsample': hp.quniform('subsample', 0.5, 1.0, 0.1),
        'learning_rate': hp.quniform('learning_rate', 0.1, 0.3, 0.1),
         'gamma': hp.choice('gamma', np.arange(0, 100, 0.5, dtype = float)),
         'reg_alpha': hp.choice('reg_alpha', np.arange(0, 100, 0.5, dtype = fl
oat)),
         'reg_lambda': hp.choice('reg_lambda', np.arange(0, 100, 0.5, dtype =
float)),

        'objective':'reg:squarederror',

        'eval_metric': 'rmse'}


def score(params):
    model = XGBRegressor(**params)

    model.fit(X_train_1, y_train_1, eval_set=[(X_train_1, y_train_1), (X_test_
1, y_test_1)],
              verbose=False, early_stopping_rounds=10)
    y_pred = model.predict(X_test_1)
    score = np.sqrt(metrics.mean_squared_error(y_test_1, y_pred))
    print(score)
    return {'loss': score, 'status': STATUS_OK}

def optimize(trials, space):

    best = fmin(score, space, algo = tpe.suggest, max_evals = 500)
    return best

trials = Trials()
best_params = optimize(trials, space)
```

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7.294142928256345
100%|████████████████████████████████████████████████| 500/500 [01:10<00:00,
7.04trial/s, best loss: 6.06907235247408]
```

In [42]:
```
# Return best parameters

space_eval(space, best_params)
```

Out[42]:
```
{'colsample_bytree': 0.7000000000000001,
 'eval_metric': 'rmse',
 'gamma': 11.5,
 'learning_rate': 0.30000000000000004,
 'max_depth': 13,
 'min_child_weight': 8,
 'n_estimators': 280,
 'objective': 'reg:squarederror',
 'reg_alpha': 2.0,
 'reg_lambda': 47.5,
 'subsample': 0.5}
```

In [43]:
```
# Create optimized model

model_1 = XGBRegressor(colsample_bytree = 0.7,
                       gamma = 11.5,
                       learning_rate = 0.3,
                       max_depth = 13,
                       min_child_weight = 8,
                       n_estimators = 280,
                       reg_alpha = 2.0,
                       reg_lambda = 47.5,
                       subsample = 0.5,
                       objective = 'reg:squarederror')
```

In [44]:
```
# Fit

model_1.fit(X_train_1, y_train_1,
              eval_set = [(X_train_1, y_train_1), (X_test_1, y_test_1)],
              eval_metric = 'rmse',
              verbose = True,
              early_stopping_rounds = 10)
```

```
[0]     validation_0-rmse:57.189        validation_1-rmse:55.6922
Multiple eval metrics have been passed: 'validation_1-rmse' will be used for
early stopping.

Will train until validation_1-rmse hasn't improved in 10 rounds.
[1]     validation_0-rmse:49.1779       validation_1-rmse:47.8821
[2]     validation_0-rmse:42.1031       validation_1-rmse:40.9627
[3]     validation_0-rmse:36.8084       validation_1-rmse:35.7901
[4]     validation_0-rmse:32.1514       validation_1-rmse:31.2491
[5]     validation_0-rmse:28.7791       validation_1-rmse:28.1268
[6]     validation_0-rmse:25.2245       validation_1-rmse:24.5759
[7]     validation_0-rmse:22.9984       validation_1-rmse:22.3284
[8]     validation_0-rmse:20.5078       validation_1-rmse:19.7732
[9]     validation_0-rmse:18.7698       validation_1-rmse:18.1812
[10]    validation_0-rmse:17.3946       validation_1-rmse:16.8539
[11]    validation_0-rmse:15.9217       validation_1-rmse:15.2939
[12]    validation_0-rmse:14.7118       validation_1-rmse:14.009
[13]    validation_0-rmse:13.8247       validation_1-rmse:13.0809
[14]    validation_0-rmse:13.0072       validation_1-rmse:12.3089
[15]    validation_0-rmse:12.3189       validation_1-rmse:11.6028
[16]    validation_0-rmse:11.6628       validation_1-rmse:10.9877
[17]    validation_0-rmse:11.1392       validation_1-rmse:10.4575
[18]    validation_0-rmse:10.511        validation_1-rmse:9.87743
[19]    validation_0-rmse:10.0419       validation_1-rmse:9.43994
[20]    validation_0-rmse:9.63143       validation_1-rmse:9.11682
[21]    validation_0-rmse:9.22318       validation_1-rmse:8.76815
[22]    validation_0-rmse:8.95558       validation_1-rmse:8.67343
[23]    validation_0-rmse:8.62912       validation_1-rmse:8.4731
[24]    validation_0-rmse:8.33733       validation_1-rmse:8.3083
[25]    validation_0-rmse:8.11496       validation_1-rmse:8.04827
[26]    validation_0-rmse:7.87107       validation_1-rmse:7.82756
[27]    validation_0-rmse:7.69083       validation_1-rmse:7.66151
[28]    validation_0-rmse:7.50681       validation_1-rmse:7.56733
[29]    validation_0-rmse:7.3062        validation_1-rmse:7.39902
[30]    validation_0-rmse:7.10135       validation_1-rmse:7.27391
[31]    validation_0-rmse:7.00115       validation_1-rmse:7.20213
[32]    validation_0-rmse:6.85609       validation_1-rmse:7.05332
[33]    validation_0-rmse:6.73473       validation_1-rmse:6.95566
[34]    validation_0-rmse:6.65111       validation_1-rmse:6.8711
[35]    validation_0-rmse:6.54654       validation_1-rmse:6.75178
[36]    validation_0-rmse:6.38576       validation_1-rmse:6.73305
[37]    validation_0-rmse:6.32618       validation_1-rmse:6.69609
[38]    validation_0-rmse:6.24108       validation_1-rmse:6.59191
[39]    validation_0-rmse:6.20857       validation_1-rmse:6.54519
[40]    validation_0-rmse:6.11862       validation_1-rmse:6.46052
[41]    validation_0-rmse:6.01036       validation_1-rmse:6.46701
[42]    validation_0-rmse:5.9825        validation_1-rmse:6.43698
[43]    validation_0-rmse:5.94397       validation_1-rmse:6.40769
[44]    validation_0-rmse:5.89973       validation_1-rmse:6.35237
[45]    validation_0-rmse:5.84903       validation_1-rmse:6.32668
[46]    validation_0-rmse:5.81287       validation_1-rmse:6.32105
[47]    validation_0-rmse:5.76635       validation_1-rmse:6.31389
[48]    validation_0-rmse:5.71895       validation_1-rmse:6.29487
[49]    validation_0-rmse:5.69976       validation_1-rmse:6.29562
[50]    validation_0-rmse:5.65535       validation_1-rmse:6.20943
[51]    validation_0-rmse:5.63568       validation_1-rmse:6.20051
[52]    validation_0-rmse:5.61182       validation_1-rmse:6.20098
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[53]    validation_0-rmse:5.57822       validation_1-rmse:6.14155
[54]    validation_0-rmse:5.54504       validation_1-rmse:6.13651
[55]    validation_0-rmse:5.52302       validation_1-rmse:6.10436
[56]    validation_0-rmse:5.51194       validation_1-rmse:6.06917
[57]    validation_0-rmse:5.49035       validation_1-rmse:6.06907
[58]    validation_0-rmse:5.44343       validation_1-rmse:6.10545
[59]    validation_0-rmse:5.40344       validation_1-rmse:6.12718
[60]    validation_0-rmse:5.39536       validation_1-rmse:6.14155
[61]    validation_0-rmse:5.3531        validation_1-rmse:6.17362
[62]    validation_0-rmse:5.30952       validation_1-rmse:6.1717
[63]    validation_0-rmse:5.29359       validation_1-rmse:6.17287
[64]    validation_0-rmse:5.28788       validation_1-rmse:6.2065
[65]    validation_0-rmse:5.27778       validation_1-rmse:6.18599
[66]    validation_0-rmse:5.2757        validation_1-rmse:6.2131
[67]    validation_0-rmse:5.26165       validation_1-rmse:6.19659
Stopping. Best iteration:
[57]    validation_0-rmse:5.49035       validation_1-rmse:6.06907
```

Out[44]:
```
XGBRegressor(base_score=0.5, booster='gbtree', colsample_bylevel=1,
             colsample_bynode=1, colsample_bytree=0.7, gamma=11.5,
             importance_type='gain', learning_rate=0.3, max_delta_step=0,
             max_depth=13, min_child_weight=8, missing=None, n_estimators=28
0,
             n_jobs=1, nthread=None, objective='reg:squarederror',
             random_state=0, reg_alpha=2.0, reg_lambda=47.5, scale_pos_weight
=1,
             seed=None, silent=None, subsample=0.5, verbosity=1)
```

In [45]:
```
# Predict

y_pred_1 = model_1.predict(X_test_1)
```

In [46]:
```
# Compare predictions, y_pred_1, to test values, y_test_1, using scatterplot

# create line to represent perfect fit to y_test

y_line_1 = np.arange(int(y_test_1.min()) - 10, int(y_test_1.max()) + 10)

# set axes limits - adjust if necessary
x_min_1 = 0
x_max_1 = y_test_1.max() + 10
d_x_1 = 10

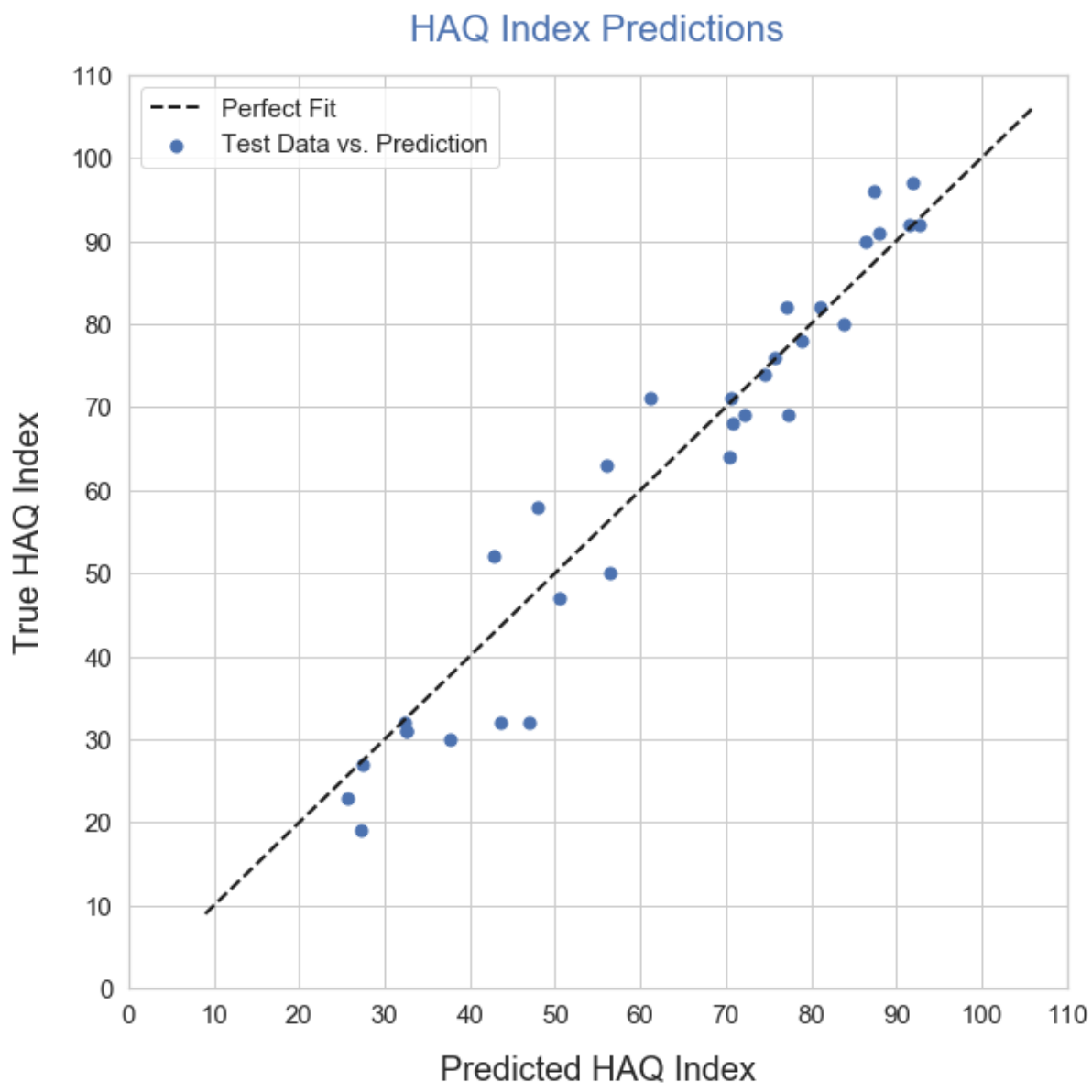
y_min_1 = 0
y_max_1 = y_test_1.max() + 10
d_y_1 = 10

plt.figure(figsize = (10, 10))
ax = plt.axes()

ax.set_xlim(x_min_1, x_max_1)
ax.set_xticks(np.arange(x_min_1, x_max_1 + d_x_1, d_x_1))

ax.set_ylim(y_min_1, y_max_1)
ax.set_yticks(np.arange(y_min_1, y_max_1 + d_y_1, d_y_1))

plt.scatter(y_pred_1, y_test_1, s = 50, c = 'b', label = 'Test Data vs. Predic
tion')
plt.plot(y_line_1, y_line_1, 'k--', lw = 2, label = 'Perfect Fit')
plt.xlabel('Predicted HAQ Index', fontsize = 20, labelpad = 15)
plt.ylabel('True HAQ Index', fontsize = 20, labelpad = 15)
plt.title('HAQ Index Predictions', fontsize = 22, c = 'b', pad = 20)
plt.legend(fontsize = 15)
plt.tick_params(labelsize = 15)
plt.show()
```



In [47]:
```
# The predicted HAQ Index values are close to the true test values
```

In [48]:
```
# Get RMSE as a measure of predictions accuracy

# Absolute RMSE
rmse_1 = np.sqrt(metrics.mean_squared_error(y_test_1, y_pred_1))

# Normalized RMSE --> more adequate measure for comparison with other models - 
ptovides the error in terms of data avg.
rmse_1_norm = rmse_1/y_test_1.mean()

print('Absolute RMSE_1:', round(rmse_1, 4))
print('Normalized RMSE_1:', round(rmse_1_norm, 4))
```

```
Absolute RMSE_1: 6.0691
Normalized RMSE_1: 0.0986
```

In [49]:
```
# The results indicate good model accuracy --> predictions error is only 10 % 
 of the test values average
```

In [50]:
```
# Get feature importances

feature_imp = pd.Series(model_1.feature_importances_,index = data_2.iloc[:, :-
2].columns).sort_values(ascending = False)
feature_imp
```

Out[50]:
```
GDP per capita ($)       0.328757
Age 15-64 (%)            0.237040
Age 65- (%)              0.214159
Continent                0.135992
Agglomerates (%)         0.046097
Population per sqr km    0.037955
dtype: float32
```

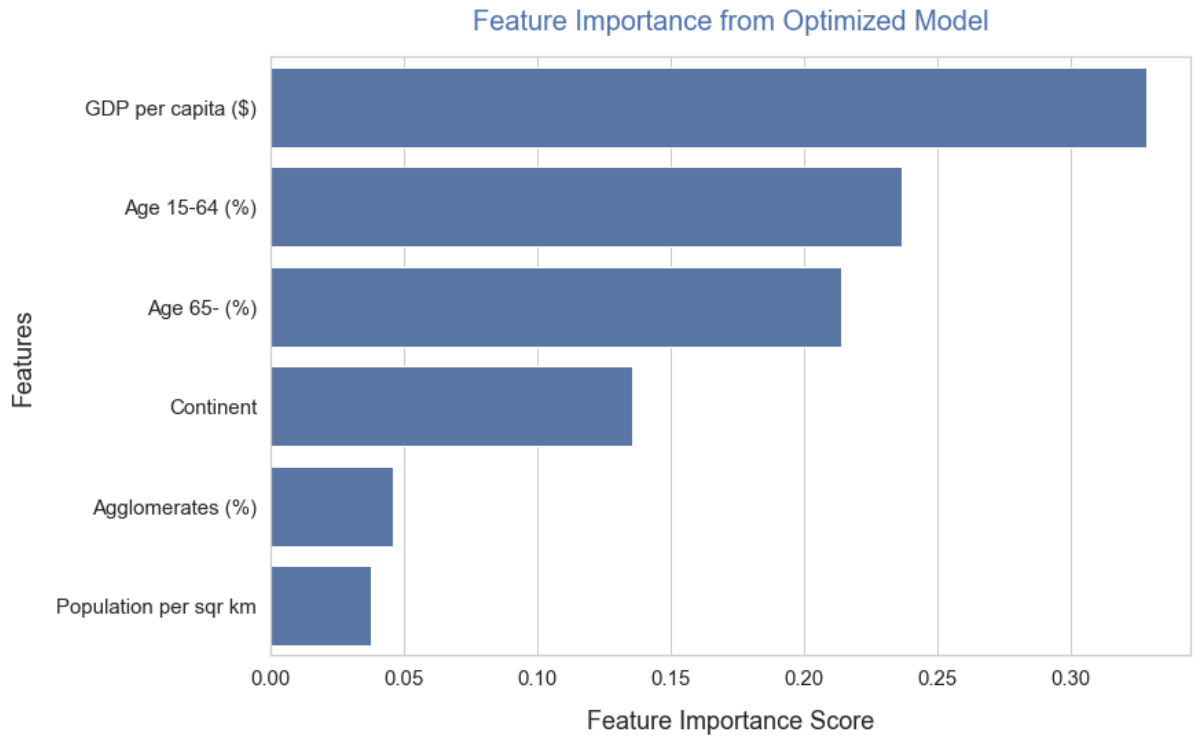
In [51]:
```
# Visualize feature importances

plt.figure(figsize=(12,8))

sns.barplot(x=feature_imp, y=feature_imp.index, color = 'b')

plt.xlabel('Feature Importance Score', fontsize = 18, labelpad = 15)
plt.ylabel('Features', fontsize = 18, labelpad = 15)
plt.title('Feature Importance from Optimized Model', fontsize = 20, pad = 20,
c = 'b')
plt.tick_params(labelsize = 15)

plt.show()
```



In [52]:
```
# Main observations:
    # 1) Top features by impotance are GDP per capita and the two age groups a
s already indicated by the correlation matrix
    # 2) The two population density features are the least important in determ
ining HAQ Index values
```

In [53]:
```
# This concludes Section 2
# It has been demonstrated that an ML model using the features selected here c
an accurately predict
# the strictly medical countries ratings, HAQ Index
```

In [54]:
```
# 3) Predicting Deaths per 100K based on conventional factors using XGBoost
```

In [55]:
```
# Create features and target from data_2 which we will use with XGBRegressor m
odel

X = data_2.iloc[:, :-1].values # all columns, but last - include HAQ Index in
 predicting Deaths per 100K
y = data_2.iloc[:, -1].values # Deaths per 100K column
```

In [56]:
```
# Train/test split

X_train_2, X_test_2, y_train_2, y_test_2 = train_test_split(X, y, test_size =
0.2, random_state = 0)
```

In [57]:
```
# For best predictions, apply model optimization by using hyperopt

# Create hyperparameter space to search over
space = {'max_depth': hp.choice('max_depth', np.arange(3, 15, 1, dtype = int
)),
        'n_estimators': hp.choice('n_estimators', np.arange(50, 300, 10, dtype
= int)),
        'colsample_bytree': hp.quniform('colsample_bytree', 0.5, 1.0, 0.1),
        'min_child_weight': hp.choice('min_child_weight', np.arange(0, 10, 1,
dtype = int)),
        'subsample': hp.quniform('subsample', 0.5, 1.0, 0.1),
        'learning_rate': hp.quniform('learning_rate', 0.1, 0.3, 0.1),
         'gamma': hp.choice('gamma', np.arange(0, 100, 0.5, dtype = float)),
         'reg_alpha': hp.choice('reg_alpha', np.arange(0, 100, 0.5, dtype = fl
oat)),
         'reg_lambda': hp.choice('reg_lambda', np.arange(0, 100, 0.5, dtype =
float)),

        'objective':'reg:squarederror',

        'eval_metric': 'rmse'}


def score(params):
    model = XGBRegressor(**params)

    model.fit(X_train_2, y_train_2, eval_set=[(X_train_2, y_train_2), (X_test_
2, y_test_2)],
              verbose=False, early_stopping_rounds=10)
    y_pred = model.predict(X_test_2)
    score = np.sqrt(metrics.mean_squared_error(y_test_2, y_pred))
    print(score)
    return {'loss': score, 'status': STATUS_OK}

def optimize(trials, space):

    best = fmin(score, space, algo = tpe.suggest, max_evals = 500)
    return best

trials = Trials()
best_params = optimize(trials, space)
```

```
7.080724824919022
7.153799810487325
7.220746556792694
7.0778522589409825
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7.060534996527395
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```

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7.048233747110725
7.134655135093744
100%|██████████████████████████████████████████████| 500/500 [00:43<00:00, 1
1.49trial/s, best loss: 6.9197203512938215]
```

In [58]:
```
# Return best parameters

space_eval(space, best_params)
```

Out[58]:
```
{'colsample_bytree': 0.5,
 'eval_metric': 'rmse',
 'gamma': 12.0,
 'learning_rate': 0.2,
 'max_depth': 12,
 'min_child_weight': 2,
 'n_estimators': 100,
 'objective': 'reg:squarederror',
 'reg_alpha': 12.0,
 'reg_lambda': 79.5,
 'subsample': 0.9}
```

In [59]:
```
# Create optimized model

model_2 = XGBRegressor(colsample_bytree = 0.5,
                       gamma = 12.0,
                       learning_rate = 0.2,
                       max_depth = 12,
                       min_child_weight = 2,
                       n_estimators = 100,
                       reg_alpha = 12.0,
                       reg_lambda = 79.5,
                       subsample = 0.9,
                       objective = 'reg:squarederror')
```

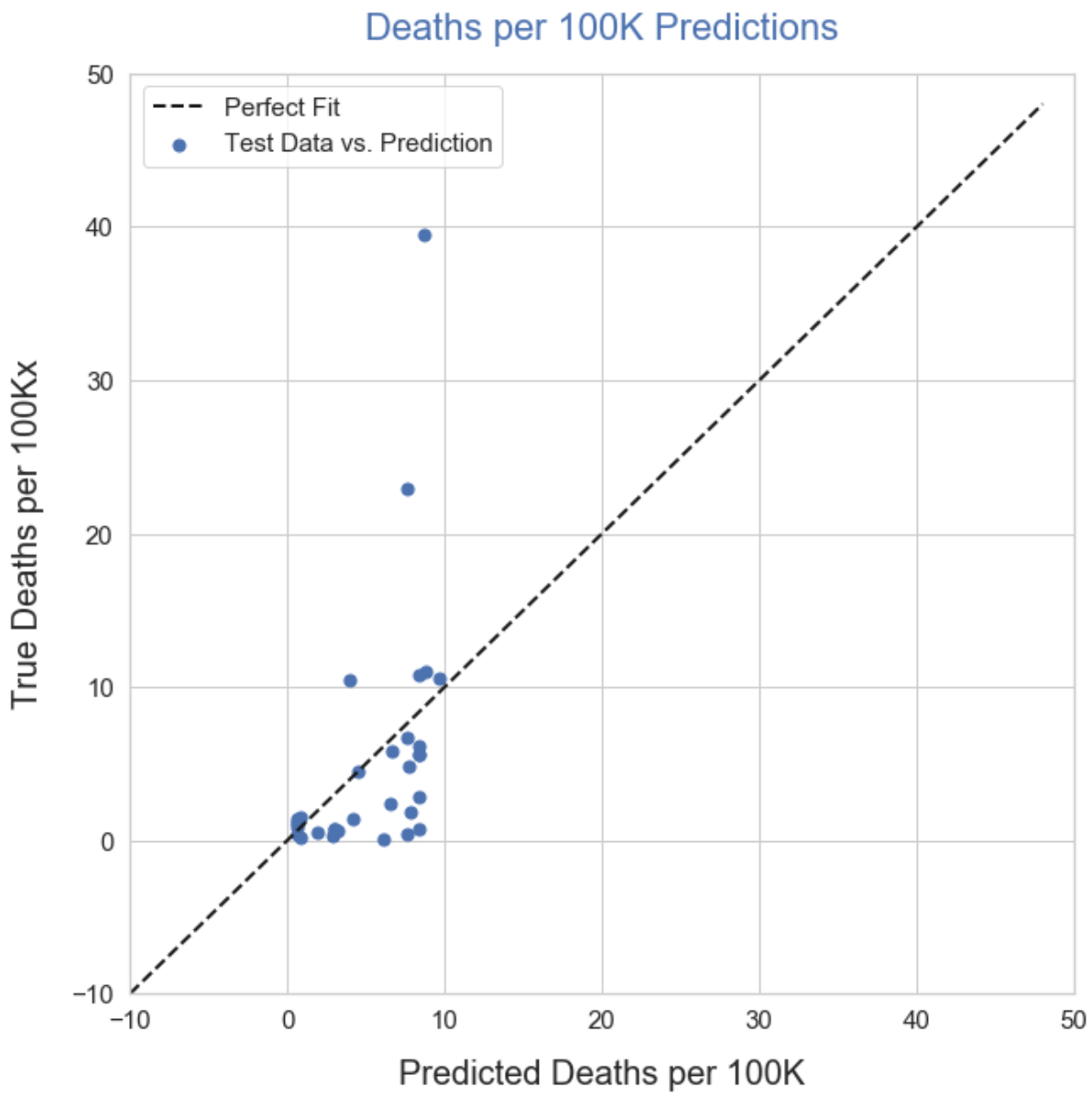
In [60]:
```
# Fit

model_2.fit(X_train_2, y_train_2,
             eval_set = [(X_train_2, y_train_2), (X_test_2, y_test_2)],
             eval_metric = 'rmse',
             verbose = True,
             early_stopping_rounds = 10)
```

```
[0]     validation_0-rmse:21.0956       validation_1-rmse:8.49323
Multiple eval metrics have been passed: 'validation_1-rmse' will be used for
early stopping.

Will train until validation_1-rmse hasn't improved in 10 rounds.
[1]     validation_0-rmse:20.6016       validation_1-rmse:8.00299
[2]     validation_0-rmse:20.1741       validation_1-rmse:7.66919
[3]     validation_0-rmse:19.8005       validation_1-rmse:7.39805
[4]     validation_0-rmse:19.4435       validation_1-rmse:7.16879
[5]     validation_0-rmse:19.0954       validation_1-rmse:7.0543
[6]     validation_0-rmse:18.7616       validation_1-rmse:6.99261
[7]     validation_0-rmse:18.5428       validation_1-rmse:6.91972
[8]     validation_0-rmse:18.2525       validation_1-rmse:7.03263
[9]     validation_0-rmse:17.9517       validation_1-rmse:7.05119
[10]    validation_0-rmse:17.7099       validation_1-rmse:7.10291
[11]    validation_0-rmse:17.4309       validation_1-rmse:7.13194
[12]    validation_0-rmse:17.1909       validation_1-rmse:7.12756
[13]    validation_0-rmse:16.9223       validation_1-rmse:7.14373
[14]    validation_0-rmse:16.7003       validation_1-rmse:7.22595
[15]    validation_0-rmse:16.5203       validation_1-rmse:7.25176
[16]    validation_0-rmse:16.3861       validation_1-rmse:7.31156
[17]    validation_0-rmse:16.2539       validation_1-rmse:7.41089
Stopping. Best iteration:
[7]     validation_0-rmse:18.5428       validation_1-rmse:6.91972
```

Out[60]:
```
XGBRegressor(base_score=0.5, booster='gbtree', colsample_bylevel=1,
             colsample_bynode=1, colsample_bytree=0.5, gamma=12.0,
             importance_type='gain', learning_rate=0.2, max_delta_step=0,
             max_depth=12, min_child_weight=2, missing=None, n_estimators=10
0,
             n_jobs=1, nthread=None, objective='reg:squarederror',
             random_state=0, reg_alpha=12.0, reg_lambda=79.5,
             scale_pos_weight=1, seed=None, silent=None, subsample=0.9,
             verbosity=1)
```

In [61]:
```
# Predict

y_pred_2 = model_2.predict(X_test_2)
```

In [62]:
```
# Compare predictions, y_pred_2, to test values, y_test_2, using scatterplot

# create line to represent perfect fit to y_test

y_line_2 = np.arange(int(y_test_2.min()) - 10, int(y_test_2.max()) + 10)

# set axes limits - adjust if necessary
x_min_2 = -10
x_max_2 = y_test_2.max() + 10
d_x_2 = 10

y_min_2 = -10
y_max_2 = y_test_2.max() + 10
d_y_2 = 10

plt.figure(figsize = (10, 10))
ax = plt.axes()

ax.set_xlim(x_min_2, x_max_2)
ax.set_xticks(np.arange(x_min_2, x_max_2 + d_x_2, d_x_2))

ax.set_ylim(y_min_2, y_max_2)
ax.set_yticks(np.arange(y_min_2, y_max_2 + d_y_2, d_y_2))

plt.scatter(y_pred_2, y_test_2, s = 50, c = 'b', label = 'Test Data vs. Predic
tion')
plt.plot(y_line_2, y_line_2, 'k--', lw = 2, label = 'Perfect Fit')
plt.xlabel('Predicted Deaths per 100K', fontsize = 20, labelpad = 15)
plt.ylabel('True Deaths per 100Kx', fontsize = 20, labelpad = 15)
plt.title('Deaths per 100K Predictions', fontsize = 22, c = 'b', pad = 20)
plt.legend(fontsize = 15)
plt.tick_params(labelsize = 15)
plt.show()
```



In [63]:
```
# Clearly, there is significant portion of predictions which deviate dramatica
ly from the true test values
```

In [64]:
```
# Get RMSE as a measure of predictions accuracy

# Absolute RMSE
rmse_2 = np.sqrt(metrics.mean_squared_error(y_test_2, y_pred_2))

# Normalized RMSE --> more adequate measure for comperison with other models;
 ptovides the error in terms of data avg.
rmse_2_norm = rmse_2/y_test_2.mean()

print('Absolute RMSE_2:', round(rmse_2, 4))
print('Normalized RMSE_2:', round(rmse_2_norm, 4))
```

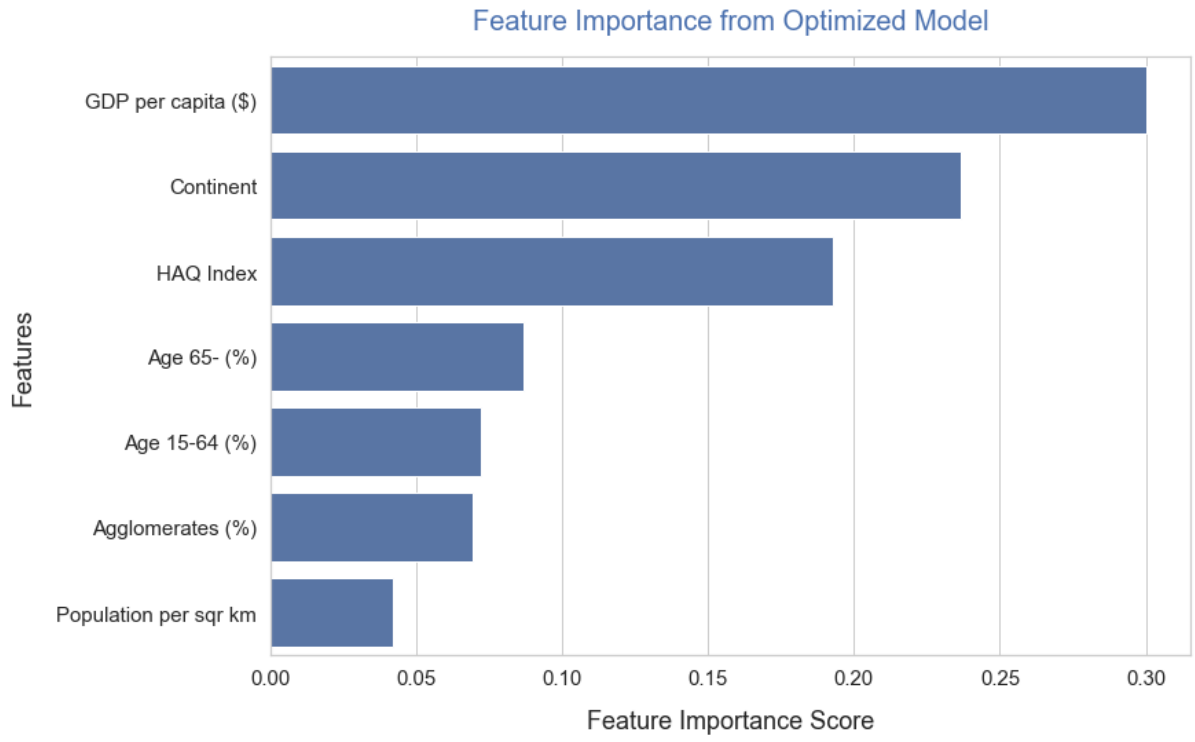
```
Absolute RMSE_2: 6.9197
Normalized RMSE_2: 1.3497
```

In [65]:
```
# As indicated by the scatter plot, the predictions have poor accuracy --> predictions error is 135 % of the test values average
```

In [66]:
```
# Get feature importances

feature_imp = pd.Series(model_2.feature_importances_,index = data_2.iloc[:, :-1].columns).sort_values(ascending = False)
feature_imp
```

Out[66]:
```
GDP per capita ($)       0.300316
Continent                0.236722
HAQ Index                0.192750
Age 65- (%)              0.086701
Age 15-64 (%)            0.072036
Agglomerates (%)         0.069342
Population per sqr km    0.042133
dtype: float32
```

In [67]:
```
# Visualize feature importances

plt.figure(figsize=(12,8))

sns.barplot(x = feature_imp, y = feature_imp.index, color = 'b')

plt.xlabel('Feature Importance Score', fontsize = 18, labelpad = 15)
plt.ylabel('Features', fontsize = 18, labelpad = 15)
plt.title('Feature Importance from Optimized Model', fontsize = 20, pad = 20, c = 'b')
plt.tick_params(labelsize = 15)

plt.show()
```

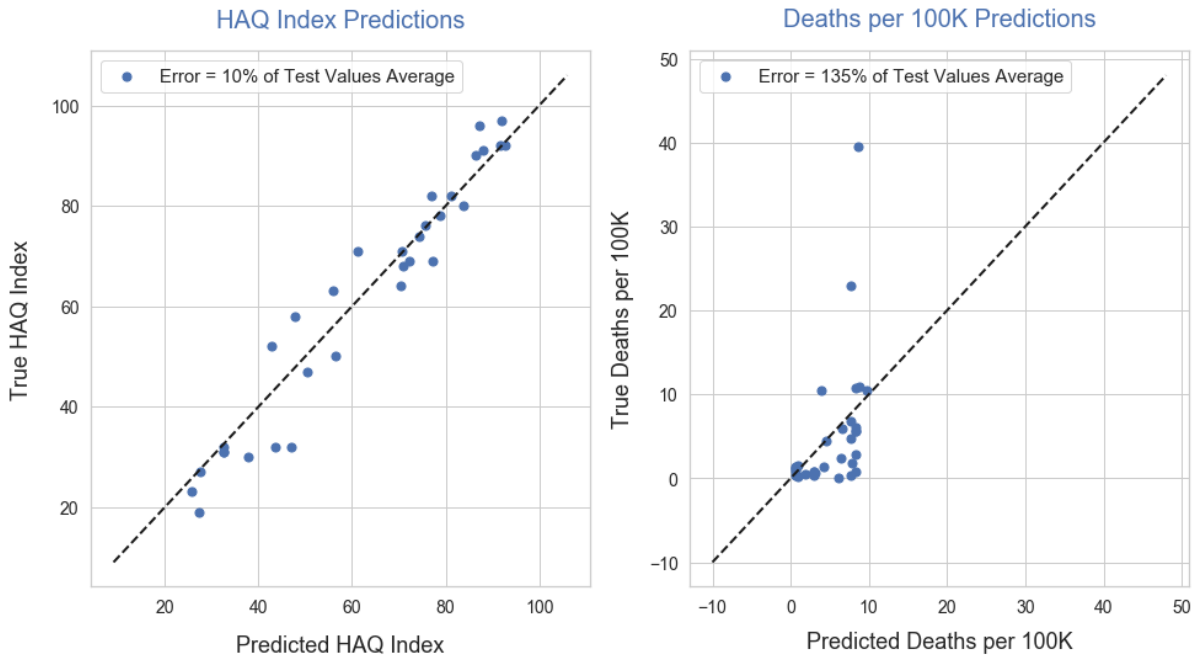


In [ ]:
```
# Main observations:
    # 1) Top feature by impotance are GDP per capita, Continent and HAQ Index
    # 2) Distant seconds are the two age groups-
    # 2) Population density features are again least important
```

In [68]:
```
# Conclusions from Section 3
    # 1) Deaths per 100K cannot be accurately predicted using the factors cons
idered here
    # 2) According to model Age Demografics and Population Density do not play
important role
```

In [69]:
```
# 4) Comparison between HAQ Index and Deaths per 100K predictions
```

In [70]:
```
# Demonstrate the contrast in predictions

fig, axes = plt.subplots(1, 2, sharey = False, figsize=(16,8))

# HAQ Index predictions
axes[0].scatter(y_pred_1, y_test_1, s = 50, c = 'b', label = 'Error = 10% of T
est Values Average')
axes[0].plot(y_line_1, y_line_1, 'k--', lw = 2)
axes[0].set_title('HAQ Index Predictions', fontsize = 20, c = 'b', pad = 20)
axes[0].set_xlabel('Predicted HAQ Index', fontsize = 18, labelpad = 15)
axes[0].set_ylabel('True HAQ Index', fontsize = 18, labelpad = 15)
axes[0].legend(fontsize = 15)
axes[0].tick_params(labelsize = 14)

# Optimized model predictions
axes[1].scatter(y_pred_2, y_test_2, s = 50, c = 'b', label = 'Error = 135% of
 Test Values Average')
axes[1].plot(y_line_2, y_line_2, 'k--', lw = 2)
axes[1].set_title('Deaths per 100K Predictions', fontsize = 20, c = 'b', pad =
20)
axes[1].set_xlabel('Predicted Deaths per 100K', fontsize = 18, labelpad = 12)
axes[1].set_ylabel('True Deaths per 100K', fontsize = 18, labelpad = 12)
axes[1].legend(fontsize = 15)
axes[1].tick_params(labelsize = 14)

plt.show()
```



In [71]:
```
# The two plots show dramatic difference between predicting HAQ Index and Deat
hs per 100K
```

In [72]:
```
# Conclusions from study

# Using common, well-established data and currenly the most powerfull ML algor
ithm for tabulated data:
    # a) it is possible to predict accurately the values of purely medical ran
king feature, HAQ Index
    # b) it is not possible to predict accurately the supposedly most reliable
COVID-19 data, Deaths per 100K

# EDA performed also shows that GDP and HAQ Index have logicaly inverted relat
ionships with Deaths per 100K -->
    # the higher the values of these two features, the higher the likelihood o
f high Deaths per 100K
    # the lower the values of these two features, the higher the likelihood of
low Deaths per 100K

# Based on the study results, the most logical conclusion is that the reported
COVID-19 data by country is not accurate -->
# cannot be reliably used to understand the reasons of how and why COVID-19 ha
s affected different countries in different way
```