Analysis of Covid-19 in Germany

This project was completed by Crispen Chisina, Zhanarbek Osmonaliev and Htet Naing Phyo.

In [ ]:

```
# importing the necessary libraries
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.metrics import accuracy_score, confusion_matrix
%matplotlib inline

covid_de = pd.read_csv('covid_germany/covid_de.csv')
demographics_de = pd.read_csv('covid_germany/demographics_de.csv')
google_covid_de = pd.read_csv("covid_germany/de_comp_covid.csv")
```

In [ ]:

```
covid_de.head()
```

Out[ ]:

	state	county	age_group	gender	date	cases	deaths	recovered
0	Baden-Wuerttemberg	LK Alb-Donau-Kreis	00-04	F	2020-03-27	1	0	1
1	Baden-Wuerttemberg	LK Alb-Donau-Kreis	00-04	F	2020-03-28	1	0	1
2	Baden-Wuerttemberg	LK Alb-Donau-Kreis	00-04	F	2020-04-03	1	0	1
3	Baden-Wuerttemberg	LK Alb-Donau-Kreis	00-04	F	2020-10-18	1	0	1
4	Baden-Wuerttemberg	LK Alb-Donau-Kreis	00-04	F	2020-10-22	1	0	1

In [ ]:

```
demographics_de.head()
```

Out[ ]:

	state	gender	age_group	population
0	Baden-Wuerttemberg	female	00-04	261674
1	Baden-Wuerttemberg	female	05-14	490822
2	Baden-Wuerttemberg	female	15-34	1293488
3	Baden-Wuerttemberg	female	35-59	1919649
4	Baden-Wuerttemberg	female	60-79	1182736

Data cleaning

In [ ]:

```
covid_de.date = pd.to_datetime(covid_de.date, infer_datetime_format = True)
```

```
google_covid_de.date = pd.to_datetime(google_covid_de.date, infer_datetime_format = Tru
#convert the date column in the covid dataset to date time format
```

In [ ]:

```
covid_de.dtypes
```

Out[ ]:

```
state                object
county               object
age_group            object
gender               object
date         datetime64[ns]
cases                 int64
deaths                int64
recovered             int64
dtype: object
```

Missing Values

In [ ]:

```
covid_de.isnull().sum()
# check for missing values
```

Out[ ]:

```
state            0
county           0
age_group     2244
gender       13916
date             0
cases            0
deaths           0
recovered        0
dtype: int64
```

In [ ]:

```
demographics_de.isnull().sum()
```

Out[ ]:

```
state         0
gender        0
age_group     0
population    0
dtype: int64
```

In [ ]:

```
covid_de[covid_de['gender'].isnull()].head(5)
```

Out[ ]:

	state	county	age_group	gender	date	cases	deaths	recovered
315	Baden-Wuerttemberg	LK Alb-Donau-Kreis	05-14	NaN	2020-10-30	1	0	1
316	Baden-Wuerttemberg	LK Alb-Donau-Kreis	05-14	NaN	2020-11-19	1	0	1
798	Baden-Wuerttemberg	LK Alb-Donau-Kreis	15-34	NaN	2020-10-28	1	0	1
799	Baden-Wuerttemberg	LK Alb-Donau-Kreis	15-34	NaN	2020-10-30	2	0	2
800	Baden-Wuerttemberg	LK Alb-Donau-Kreis	15-34	NaN	2020-11-01	1	0	1

In [ ]:

```
covid_de[covid_de['age_group'].isnull()].head(5)
```

Out[ ]:

	state	county	age_group	gender	date	cases	deaths	recovered
1919	Baden-Wuerttemberg	LK Alb-Donau-Kreis	NaN	F	2020-10-26	1	0	1
1920	Baden-Wuerttemberg	LK Alb-Donau-Kreis	NaN	F	2020-11-19	1	0	1
1921	Baden-Wuerttemberg	LK Alb-Donau-Kreis	NaN	F	2020-12-24	1	0	1
1922	Baden-Wuerttemberg	LK Alb-Donau-Kreis	NaN	M	2021-03-31	1	0	0
6114	Baden-Wuerttemberg	LK Boeblingen	NaN	M	2021-01-30	1	0	1

In [ ]:

```
covid_de['age_group'].isnull().sum()/len(covid_de) * 100

# only 0.3246% in the age group column are missing so we can just drop the rows since i
# percentages
```

Out[ ]:

```
0.32464056618240633
```

In [ ]:

```
covid_de['gender'].isnull().sum()/len(covid_de) * 100
# only 2.01% of the entries in the gender column are missing so we can just drop the ro
# percentages
```

Out[ ]:

```
2.0132344558798425
```

In [ ]:

```
# drop missing rows in age group rows
covid_de = covid_de[covid_de['age_group'].notna()]
```

In [ ]:

```
# drop missing rows in gender group rows
covid_df = covid_de[covid_de['gender'].notna()]
```

In [ ]:

```
covid_df.isnull().sum()
```

Out[ ]:

```
state        0
county       0
age_group    0
gender       0
date         0
cases        0
deaths       0
recovered    0
dtype: int64
```

In [ ]:

```
vital_attributes = ["date", "new_confirmed", "new_deceased", "new_persons_fully_vaccina
```

```
google_covid_de.drop(google_covid_de.columns.difference(vital_attributes), axis=1, inpl
```

Duplicates

In [ ]:

```
print('number of duplicated rows in "covid" :', covid_df.duplicated().sum())
print('')
print('number of duplicated rows in "demographics" :', demographics_de.duplicated().sum
```

```
number of duplicated rows in "covid" : 0

number of duplicated rows in "demographics" : 0
```

In [ ]:

```
covid_df[covid_df.duplicated(keep=False)].head()
```

Out[ ]:

state	county	age_group	gender	date	cases	deaths	recovered

In [ ]:

```
# drop duplicate entries
covid_df = covid_df.drop_duplicates()
print('number of duplicated rows in "covid" :', covid_df.duplicated().sum())
```

```
number of duplicated rows in "covid" : 0
```

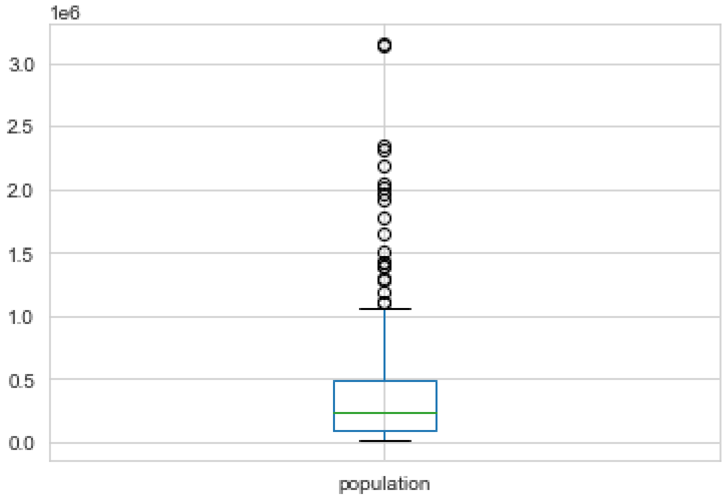
Outliers

In [ ]:

```
demographics_de.boxplot()
```

Out[ ]:

```
<AxesSubplot:>
```



In [ ]:

```
def outliers_loc(df, feature):
    q1 = df[feature].quantile(0.25)
    q3 = df[feature].quantile(0.75)
    iqr = q3 - q1
    upper_bound = q3 + 1.5*iqr
    lower_bound = q1 - 1.5*iqr
    ind = df.index[(df[feature] <= lower_bound) | (df[feature] >= upper_bound)]
    return ind
```

```
# function to detect location of outliers using Interquartile range
```

In [ ]:

```
def remove_out(df, indexes_ls):
    out_index_ls = sorted(set(indexes_ls))
    df = df.drop(out_index_ls)
    return df
# function to remove outliers given the location of the outliers
```

In [ ]:

```
outlrs_loc = outliers_loc(demographics_de, 'population')
print('number of outliers in "demographics_de" :', len(outlrs_loc))
```

```
number of outliers in "demographics_de" : 21
```

In [ ]:

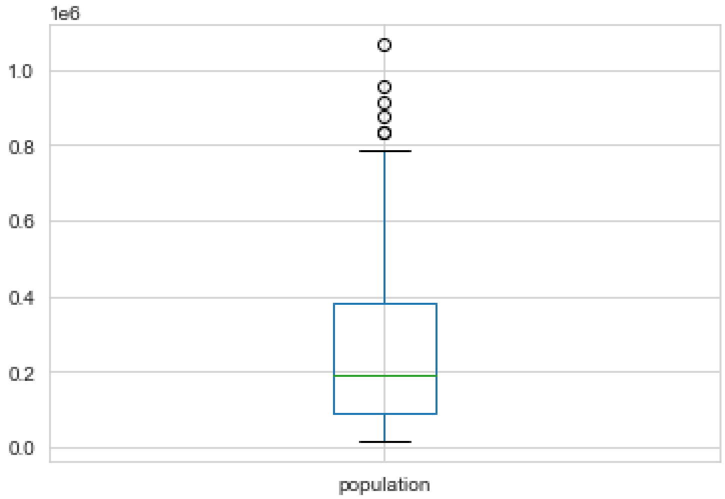
```
new_demographics_cleaned =  remove_out(demographics_de, outlrs_loc)
```

In [ ]:

```
new_demographics_cleaned.boxplot()
```

Out[ ]:

```
<AxesSubplot:>
```



In [ ]:

```
len(outliers_loc(new_demographics_cleaned, 'population'))
# most of the outliers have been removed since
# we can not completely remove all outliers the
# remaining 6 are negligable so we can leave them in the dataset
```

Out[ ]:

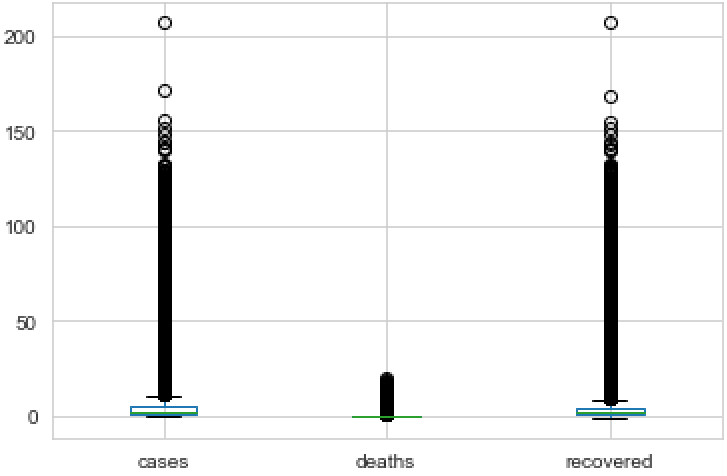
```
6
```

In [ ]:

```
covid_df.boxplot()
# the covid dataset has alot of outliers
```

Out[ ]:

```
<AxesSubplot:>
```



In [ ]:
```
outlrs_indexes = outliers_loc(covid_df, 'cases')
```

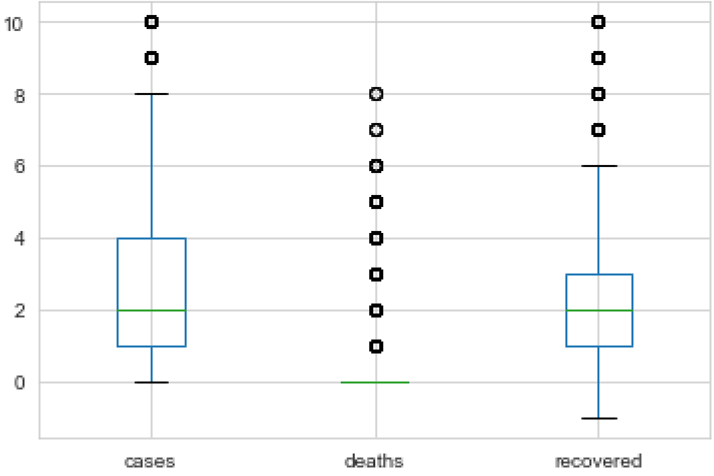
In [ ]:
```
len(outlrs_indexes)
```

Out[ ]:
```
59162
```

In [ ]:
```
new_covid_df_cleaned =  remove_out(covid_df, outlrs_indexes)
```

In [ ]:
```
new_covid_df_cleaned.boxplot()
# most of the outliers have been removed and since we can not remove all
# we can just leave the remaining
```

Out[ ]:
```
<AxesSubplot:>
```



In [ ]:
```
new_demographics_cleaned = new_demographics_cleaned.replace(['female', 'male'], ['F', '
```

In [ ]:
```
merged_data = new_covid_df_cleaned.merge(new_demographics_cleaned,
                                         how = 'inner', on = ['state', 'gender', 'age_g

# merge the cleaned demographics and covid dataset
```

```
In [ ]: merged_data.shape
```

```
Out[ ]: (385640, 9)
```

final data sets new_covid_df_cleaned, new_demographics_cleaned and merged_data

Cleaning and Filling Missing Values in the Additional Dataset

1) We will select the data starting from February 21th 2020 till May 2nd 2022, as it has almost no missing values.

2) Next, we fill in empty values in `new_persons_fully_vaccinated` and `cumulative_persons_fully_vaccinated` with 0s, since there were no vaccinated people recorded in the beginning of the pandemic.

3) Lastly, we drop incomplete columns, as the number of them is negligible in relation to the whole dataset.

```
In [ ]: google_covid_de.isnull().sum()
```

```
Out[ ]: date                               0
        new_confirmed                      5
        new_deceased                       5
        new_persons_fully_vaccinated     371
        mobility_retail_and_recreation    50
        mobility_grocery_and_pharmacy     50
        mobility_parks                    50
        mobility_transit_stations         50
        mobility_workplaces               50
        mobility_residential              50
        testing_policy                     6
        facial_coverings                   6
        vaccination_policy                 6
        average_temperature_celsius        9
        dtype: int64
```

```
In [ ]: google_covid_de['new_persons_fully_vaccinated'] = google_covid_de['new_persons_fully_va
        google_covid_de = google_covid_de[51:851]
        google_covid_de.isnull().sum()
```

```
Out[ ]: date                              0
        new_confirmed                     0
        new_deceased                      0
        new_persons_fully_vaccinated      0
        mobility_retail_and_recreation    0
        mobility_grocery_and_pharmacy     0
        mobility_parks                    0
        mobility_transit_stations         0
        mobility_workplaces               0
        mobility_residential              0
        testing_policy                    0
        facial_coverings                  0
        vaccination_policy                0
```

```
average_temperature_celsius       1
dtype: int64
```

In [ ]:

```
google_covid_de = google_covid_de[google_covid_de['average_temperature_celsius'].notna(
google_covid_de.isnull().sum()
```

Out[ ]:

```
date                              0
new_confirmed                     0
new_deceased                      0
new_persons_fully_vaccinated      0
mobility_retail_and_recreation    0
mobility_grocery_and_pharmacy     0
mobility_parks                    0
mobility_transit_stations         0
mobility_workplaces               0
mobility_residential              0
testing_policy                    0
facial_coverings                  0
vaccination_policy                0
average_temperature_celsius       0
dtype: int64
```

Data Analysis

Covid cases trend in Germany

In [ ]:

```
covidcases_bydate = new_covid_df_cleaned.groupby('date').sum()
# find the sum for cases, deaths and recovered by date in order to visualize trends
```

In [ ]:

```
covidcases_bydate.head()
```

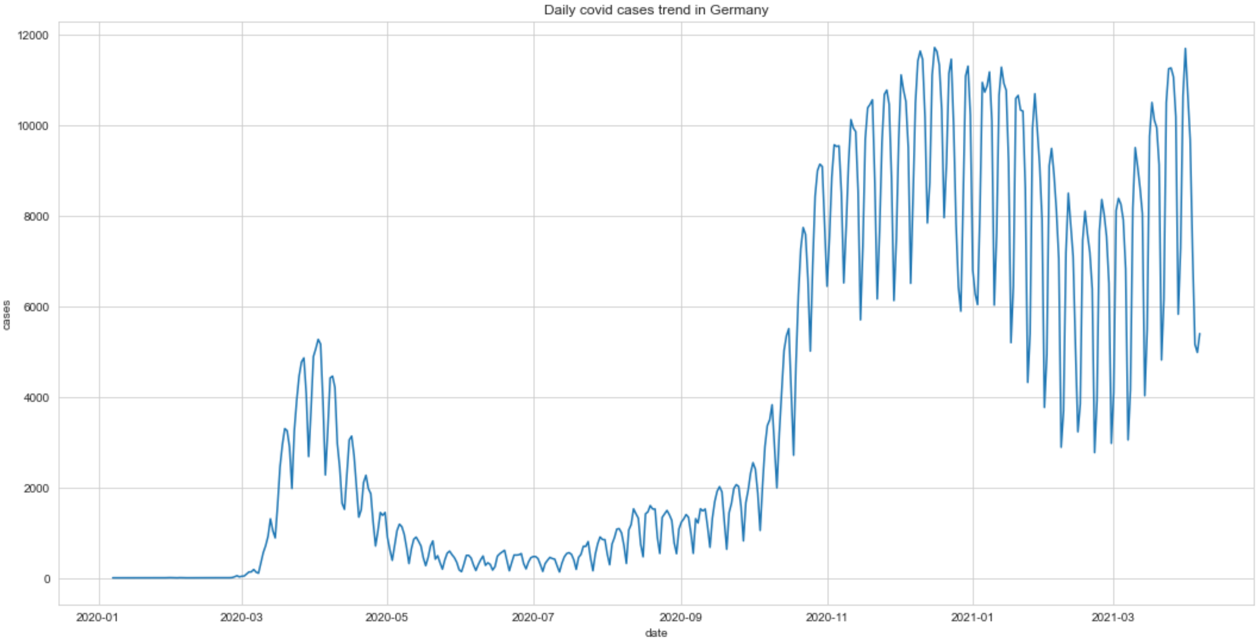
Out[ ]:

	cases	deaths	recovered
date			
2020-01-07	1	0	1
2020-01-19	1	0	1
2020-01-23	1	0	1
2020-01-25	1	0	1
2020-01-28	2	0	2

In [ ]:

```
from matplotlib.gridspec import GridSpec

sns.set_style("whitegrid")
plt.figure(figsize=(18,9))
plt.title('Daily covid cases trend in Germany')
p=sns.lineplot(data=covidcases_bydate.cases)
```



- From the graph above it looks like there was a slight peak betwen March 2020 and May 2020, which was the time corona spread but there was a decline in cases after maybe because of lockdown measures
- However, there was a second wave in the start of 2021 because of the new variant and the number of cases peaked near the start of 2021.
- Moreover it also looks like in april there was another wave of surge of number of cases in april 2021

Trend of cases by states

In [ ]:

```
covid_bystate = new_covid_df_cleaned.groupby(by=["state", "date"]).sum()
# find the sum for cases, deaths and recovered by date and state in order to visualize
```

In [ ]:

```
covid_bystate.reset_index(inplace=True)
```

In [ ]:

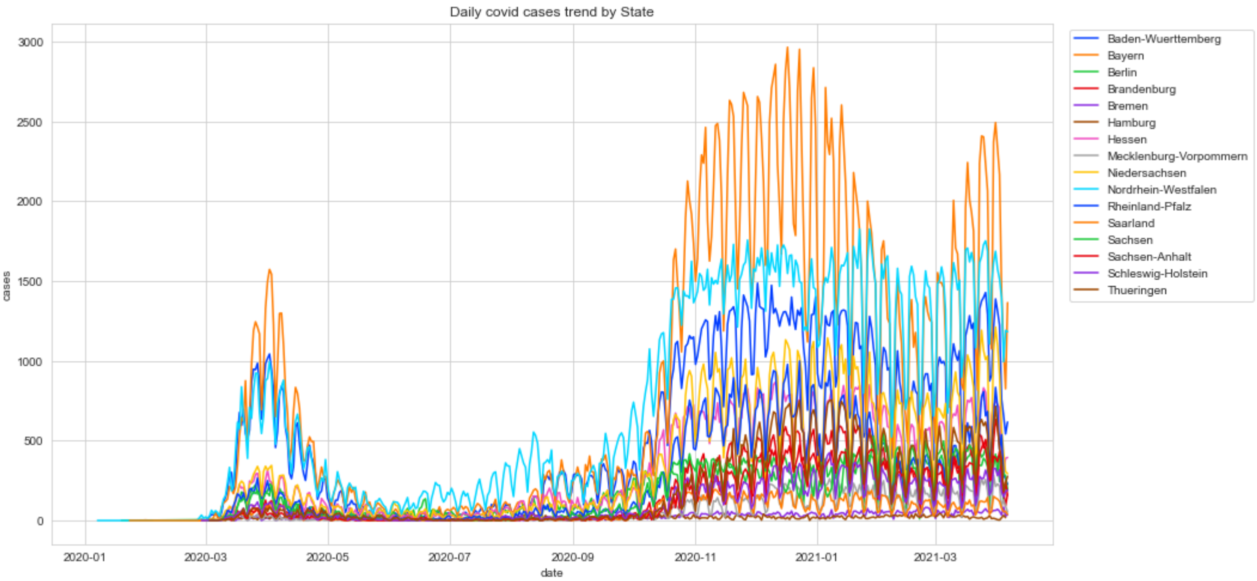
```
covid_bystate.head()
```

Out[ ]:

	state	date	cases	deaths	recovered
0	Baden-Wuerttemberg	2020-02-24	1	0	1
1	Baden-Wuerttemberg	2020-02-25	2	0	2
2	Baden-Wuerttemberg	2020-02-26	4	0	4
3	Baden-Wuerttemberg	2020-02-27	3	0	3
4	Baden-Wuerttemberg	2020-02-28	7	0	7

In [ ]:

```
plt.figure(figsize=(15,8))
ln = sns.lineplot(data=covid_bystate, x="date", y="cases", hue="state", palette = 'brig
ln.legend(bbox_to_anchor=(1.01, 1), loc='upper left')
plt.title("Daily covid cases trend by State")
plt.show()
```



- from the graph above one can see that in the peak monnths Bayern contributed more in the rise of cases in Germany
- however just comparing the numbers can be misleading because population sizes also plays a key part so it is bettter to compare the ratios population

In [ ]:

```
cov_demo_df = merged_data.copy()

cov_demo_df['Cases per population'] = merged_data.cases/merged_data.population

cov_demo_df['Deaths per population'] = merged_data.deaths/merged_data.population
```

In [ ]:

```
state_data = cov_demo_df.groupby('state').sum().sort_values('Cases per population', asc
state_data['Fatality'] = (state_data.deaths / state_data.cases) * 100
```

In [ ]:

```
state_data.head()
```

Out[ ]:

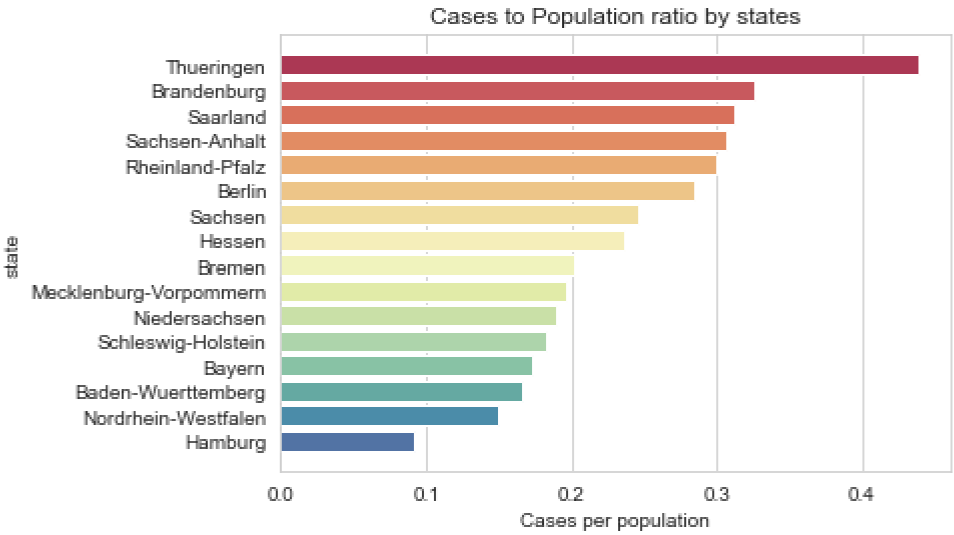
	cases	deaths	recovered	population	Cases per population	Deaths per population	Fatality
state							
Thueringen	75904	2922	67032	6242867987	0.438883	0.031175	3.849599
Brandenburg	65225	2678	57138	6002839509	0.326002	0.024993	4.105788
Saarland	24061	732	22147	936841656	0.312279	0.017114	3.042268
Sachsen-Anhalt	52541	2021	45324	4043605652	0.306906	0.020174	3.846520
Rheinland-Pfalz	104470	2958	93558	19854720609	0.299543	0.017746	2.831435

In [ ]:

```
sns.barplot(data = state_data, x='Cases per population', y=state_data.index, palette='S
plt.title("Cases to Population ratio by states")
plt.plot()
```

Out[ ]:

```
[]
```



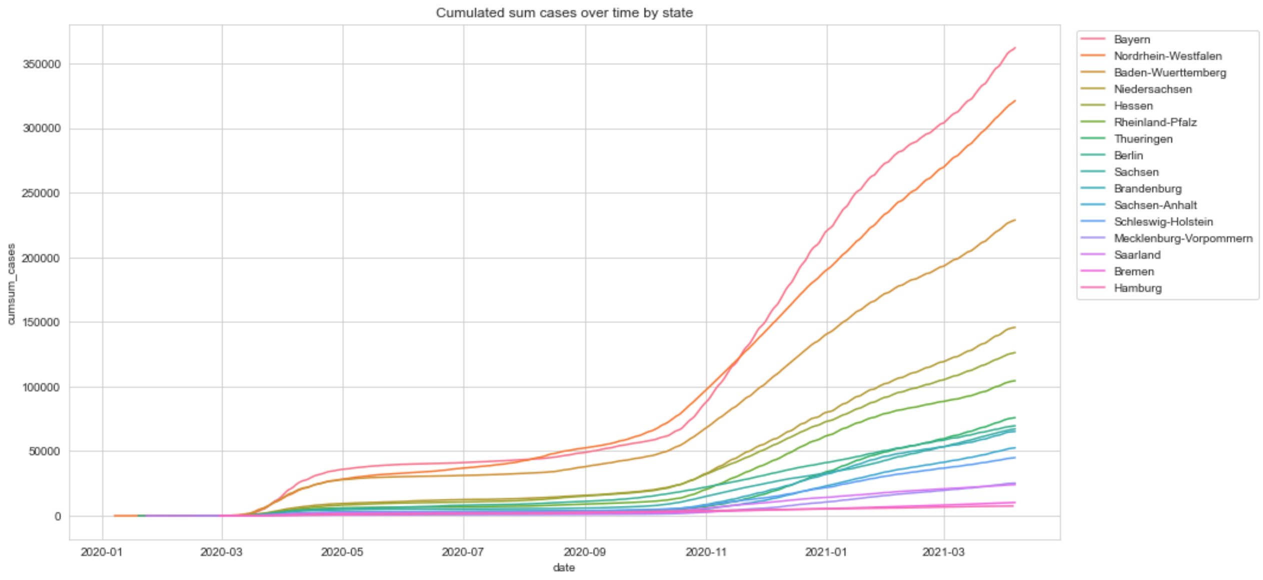
- From the graph above one can see the full story that although Bayern contributed more to the spike in covid cases because it has a larger population but when we compare cases to population ratio bayern is one of the bottom 4 but Thueringen had the highest.

Rates of Cases by State

In [ ]:

```
state_sum = new_covid_df_cleaned.groupby(by=["state", "date"]).sum()
state_sum = state_sum.replace([np.inf, -np.inf], 0)
state_sum["cumsum_cases"] = state_sum.groupby(level=-2)["cases"].cumsum()
state_sum = state_sum.reset_index()

plt.figure(figsize=(15,8))
ln = sns.lineplot(data=state_sum.sort_values("cumsum_cases", ascending=False), x="date"
ln.legend(bbox_to_anchor=(1.01, 1), loc='upper left')
plt.title("Cumulated sum cases over time by state")
plt.show()
```

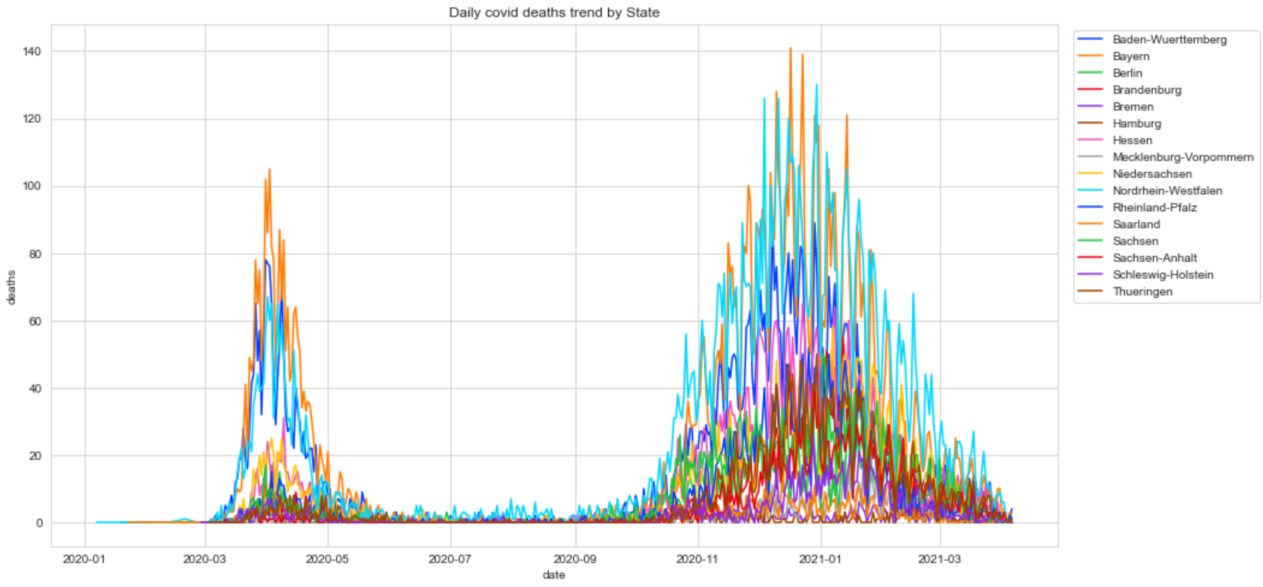


- from the graph above one can see that Bayern had the highest increasing rate and Hamburg had the lowest increasing rate

Trend of Death by State

In [ ]:

```
plt.figure(figsize=(15, 8))
ln = sns.lineplot(data=covid_bystate, x="date", y="deaths",
                  hue="state", palette='bright')
ln.legend(bbox_to_anchor=(1.01, 1), loc='upper left')
plt.title("Daily covid deaths trend by State")
plt.show()
```



- Highest deaths occured in Bayern and Nordhein-Westfalen states.
- Death cases in Nordhein-Westfalen seems to be relatively frequent even during the months when the cases died down.

In [ ]:

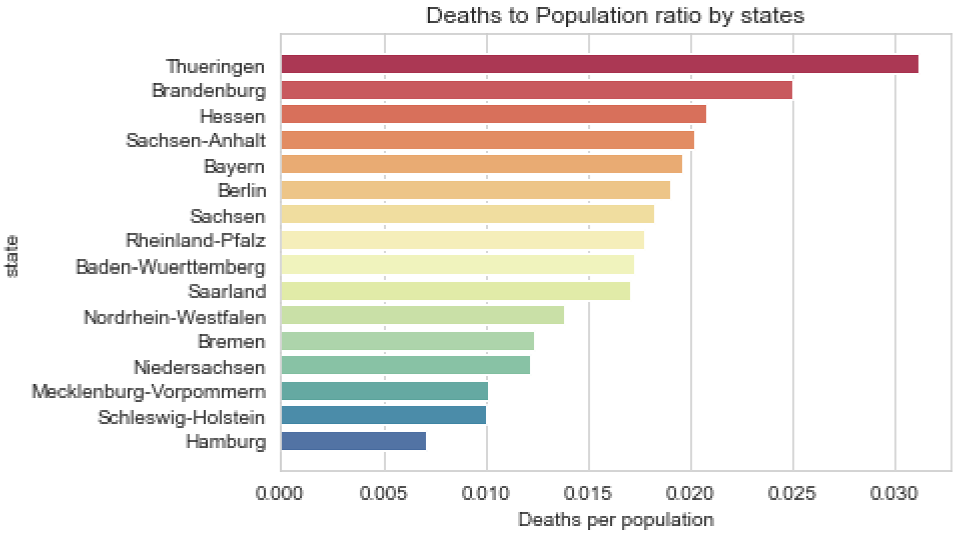
```
state_data = state_data.sort_values('Deaths per population', ascending=False)
```

In [ ]:

```
sns.barplot(data=state_data, x='Deaths per population',
            y=state_data.index, palette='Spectral')
plt.title("Deaths to Population ratio by states")
plt.plot()
```

Out[ ]:

```
[]
```



- Supporting results in previous cases to population ratio graphs, Theringen state had highest Deaths to Population ratio.

In [ ]:

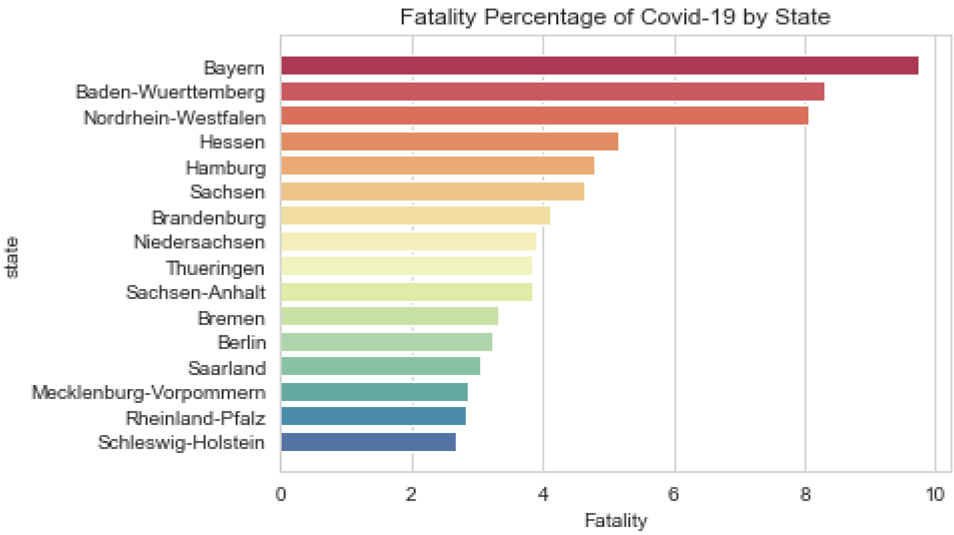
```
state_data = state_data.sort_values('Fatality', ascending=False)
```

In [ ]:

```
sns.barplot(data=state_data, x='Fatality',
            y=state_data.index, palette='Spectral')
plt.title("Fatality Percentage of Covid-19 by State")
plt.plot()
```

Out[ ]:

```
[]
```

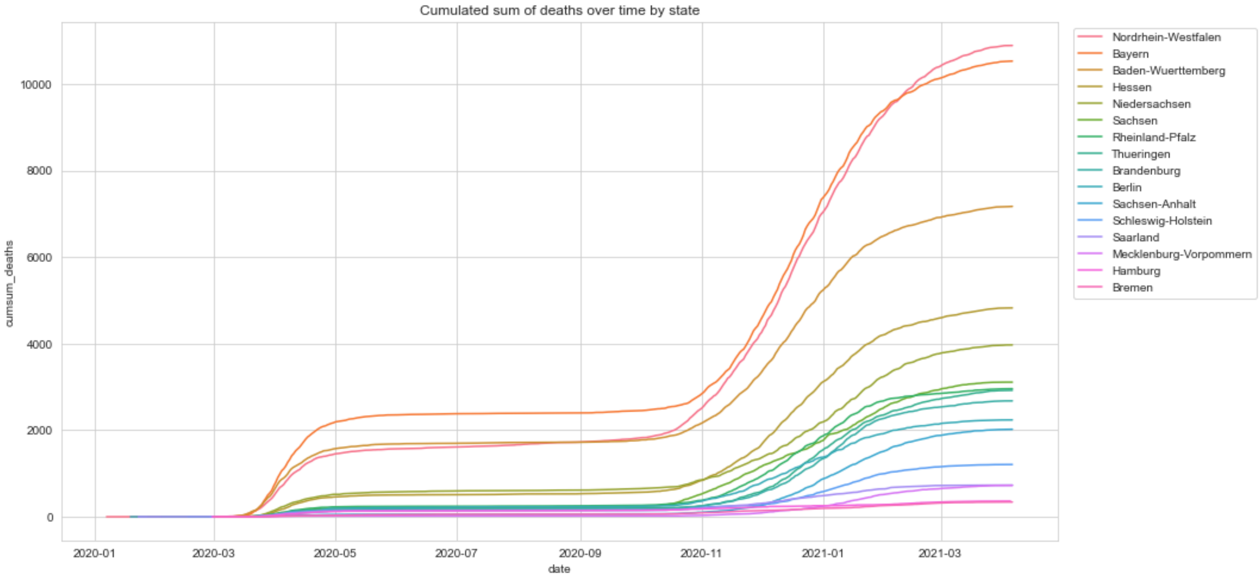


- Eventhough Death to Population ratio was smaller in state such as Bayern, in terms of Fatality, it is showing that states with bigger population and higher cases had more fatalities.
- For example, in Bayern, almost 10 percent of covid cases passed away where in Schleswig-Holstein, only 2 percent of death.

In [ ]:

```
state_sum = new_covid_df_cleaned.groupby(by=["state", "date"]).sum()
state_sum = state_sum.replace([np.inf, -np.inf], 0)
state_sum["cumsum_deaths"] = state_sum.groupby(level=-2)["deaths"].cumsum()
state_sum = state_sum.reset_index()

plt.figure(figsize=(15, 8))
ln = sns.lineplot(data=state_sum.sort_values(
    "cumsum_deaths", ascending=False), x="date", y="cumsum_deaths", hue="state")
ln.legend(bbox_to_anchor=(1.01, 1), loc='upper left')
plt.title("Cumulated sum of deaths over time by state")
plt.show()
```



- Nodhein-Westfalen has the highest rate of increasing death rate and lowest one is Bremen.

Age and Gender

In [ ]:

```
merged_data.head()
```

Out[ ]:

	state	county	age_group	gender	date	cases	deaths	recovered	population
0	Baden-Wuerttemberg	LK Alb-Donau-Kreis	00-04	F	2020-03-27	1	0	1	261674
1	Baden-Wuerttemberg	LK Alb-Donau-Kreis	00-04	F	2020-03-28	1	0	1	261674
2	Baden-Wuerttemberg	LK Alb-Donau-Kreis	00-04	F	2020-04-03	1	0	1	261674
3	Baden-Wuerttemberg	LK Alb-Donau-Kreis	00-04	F	2020-10-18	1	0	1	261674

	state	county	age_group	gender	date	cases	deaths	recovered	population
4	Baden-Wuerttemberg	LK Alb-Donau-Kreis	00-04	F	2020-10-22	1	0	1	261674

In [ ]:

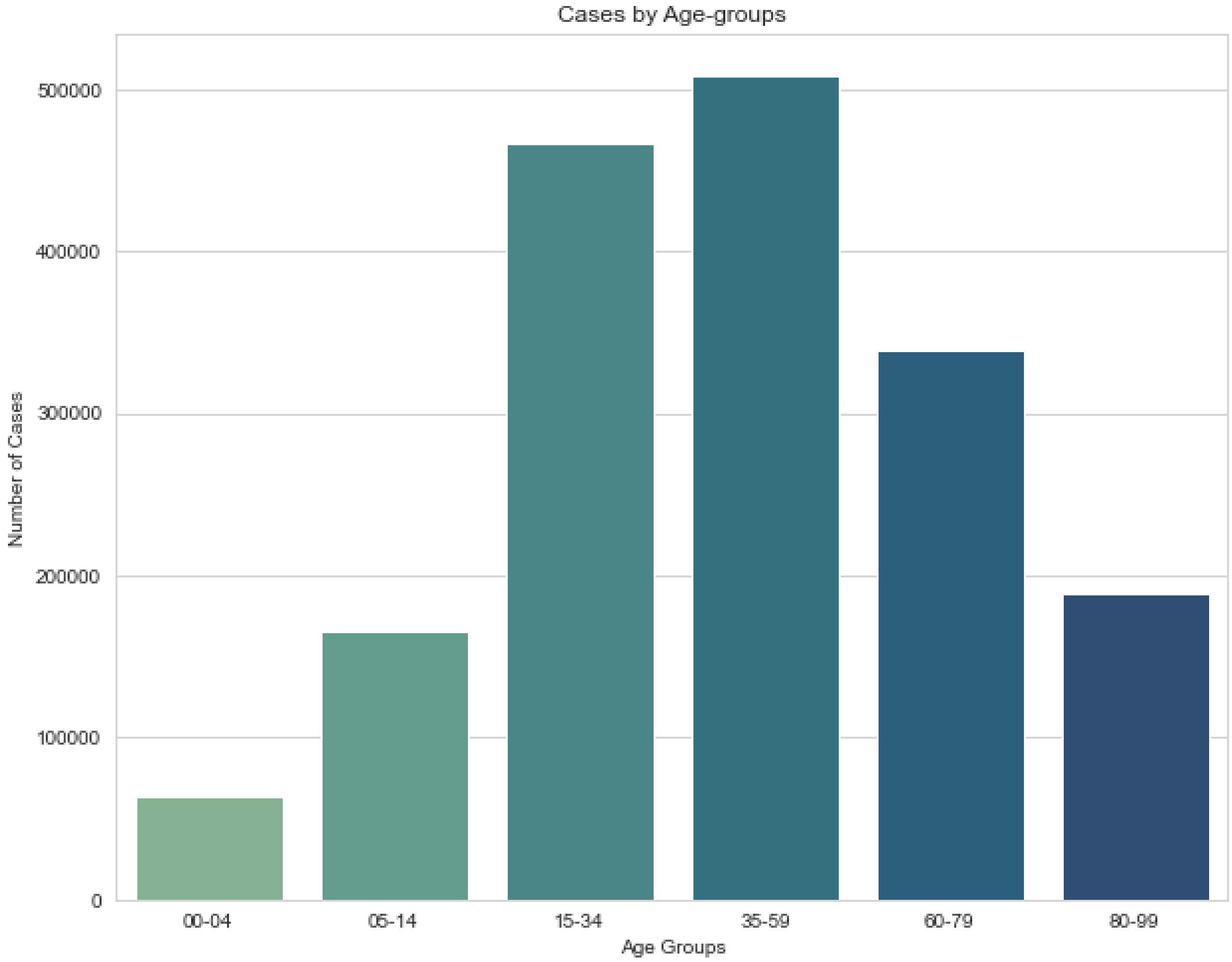
```
covidcases_by_age_group = new_covid_df_cleaned.groupby('age_group').sum()
covidcases_by_age_group= covidcases_by_age_group.reset_index()
covidcases_by_age_group.head(6)
```

Out[ ]:

	age_group	cases	deaths	recovered
0	00-04	63146	8	54523
1	05-14	165341	7	147330
2	15-34	466144	75	433436
3	35-59	508872	1383	474218
4	60-79	338541	16057	297036
5	80-99	189010	39142	141246

In [ ]:

```
plt.figure(figsize=(10, 8))
sns.barplot(data = covidcases_by_age_group,  x = "age_group", y = "cases", palette="cre
plt.title("Cases by Age-groups")
plt.xlabel('Age Groups')
plt.ylabel('Number of Cases')
plt.show()
```



- Age group of 35-59 has highest number of cases, followed by the group of 15-34, which are the age ranges that tend to commute to public places more.
- Age group of 0-4 has lowest number of cases.

In [ ]:

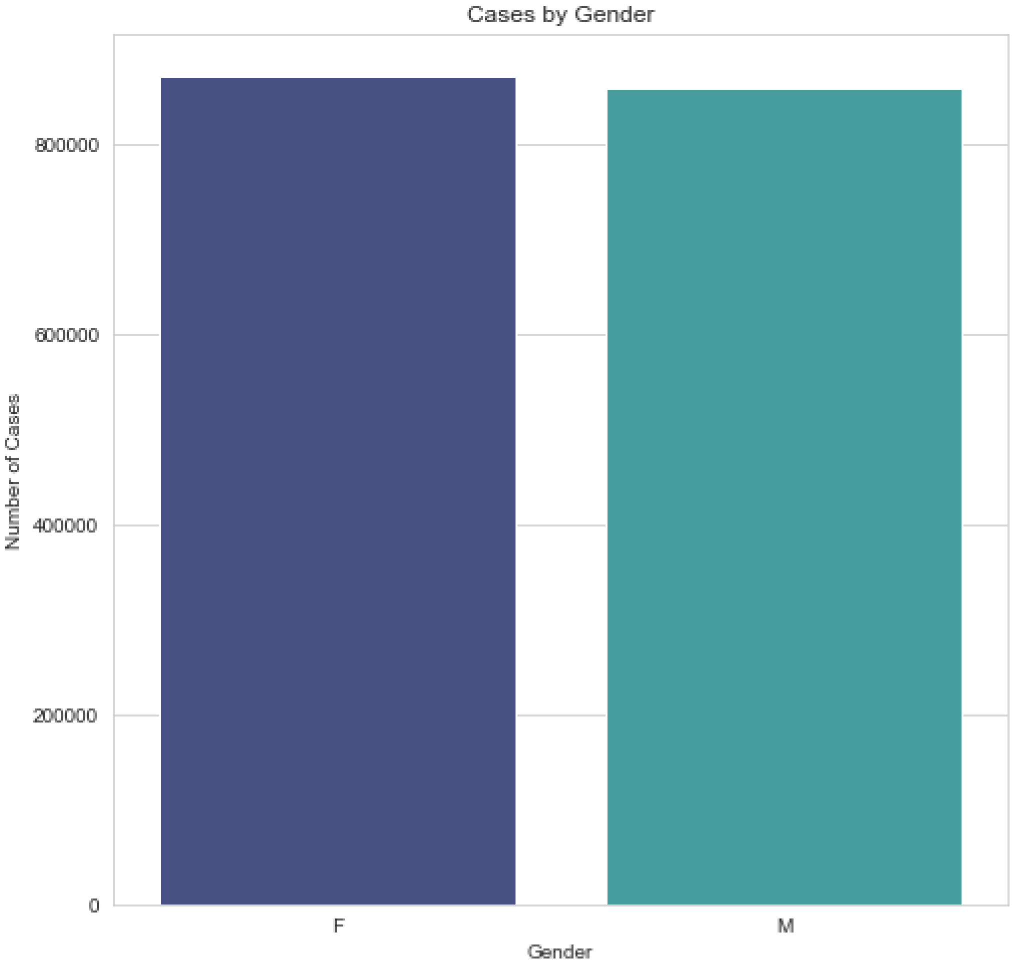
```
covidcases_by_gender = new_covid_df_cleaned.groupby('gender').sum()
covidcases_by_gender = covidcases_by_gender.reset_index()
covidcases_by_gender.head(6)
```

Out[ ]:

	gender	cases	deaths	recovered
0	F	872639	23825	785950
1	M	858415	32847	761839

In [ ]:

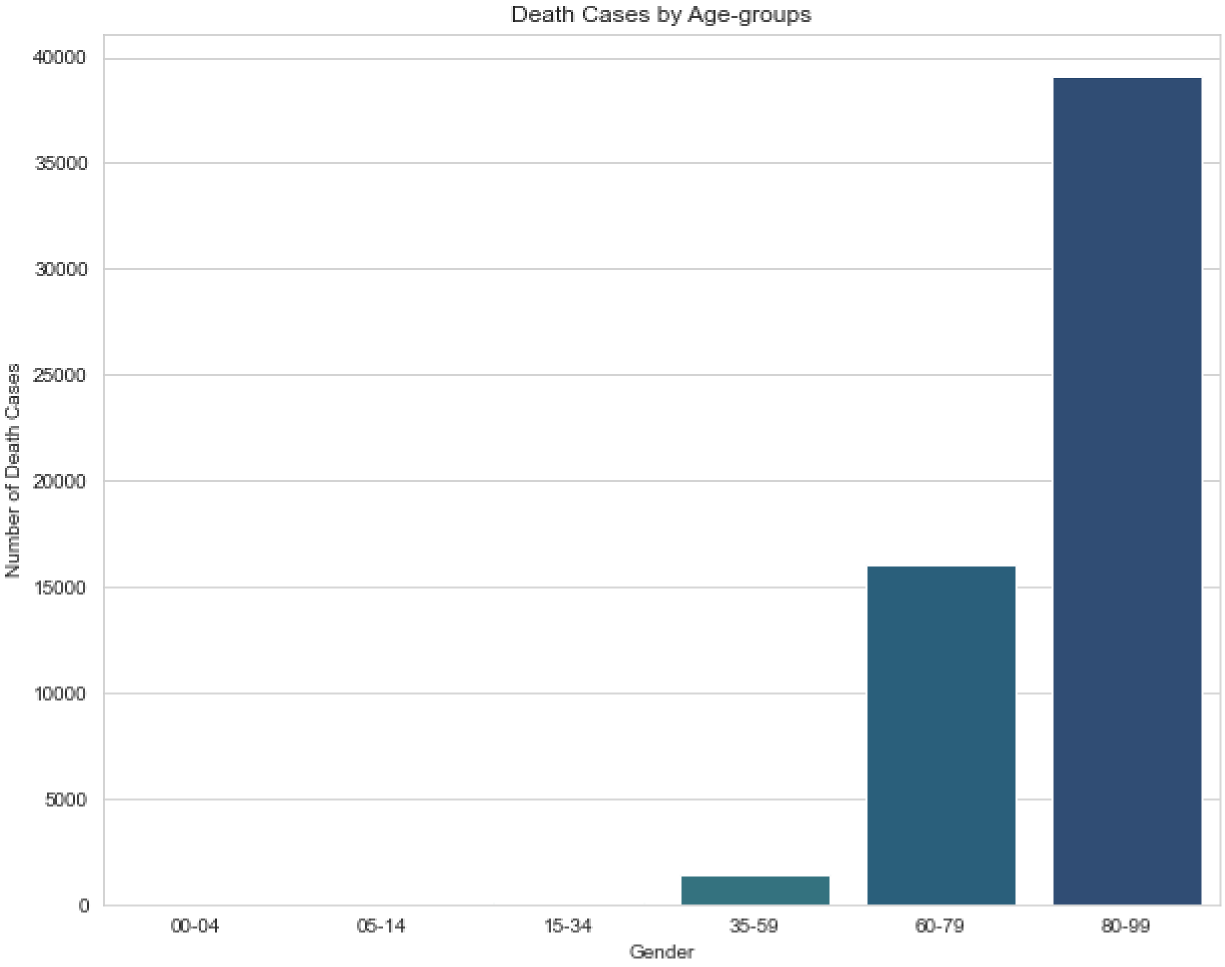
```
plt.figure(figsize=(8, 8))
sns.barplot(data = covidcases_by_gender, x="gender", y = "cases", palette="mako")
plt.title("Cases by Gender")
plt.xlabel('Gender')
plt.ylabel('Number of Cases')
plt.show()
```



- Female Covid 19 cases are higher than that of male only by a small margin. It can be concluded that Covid-19 cases occur equally in both genders.

In [ ]:

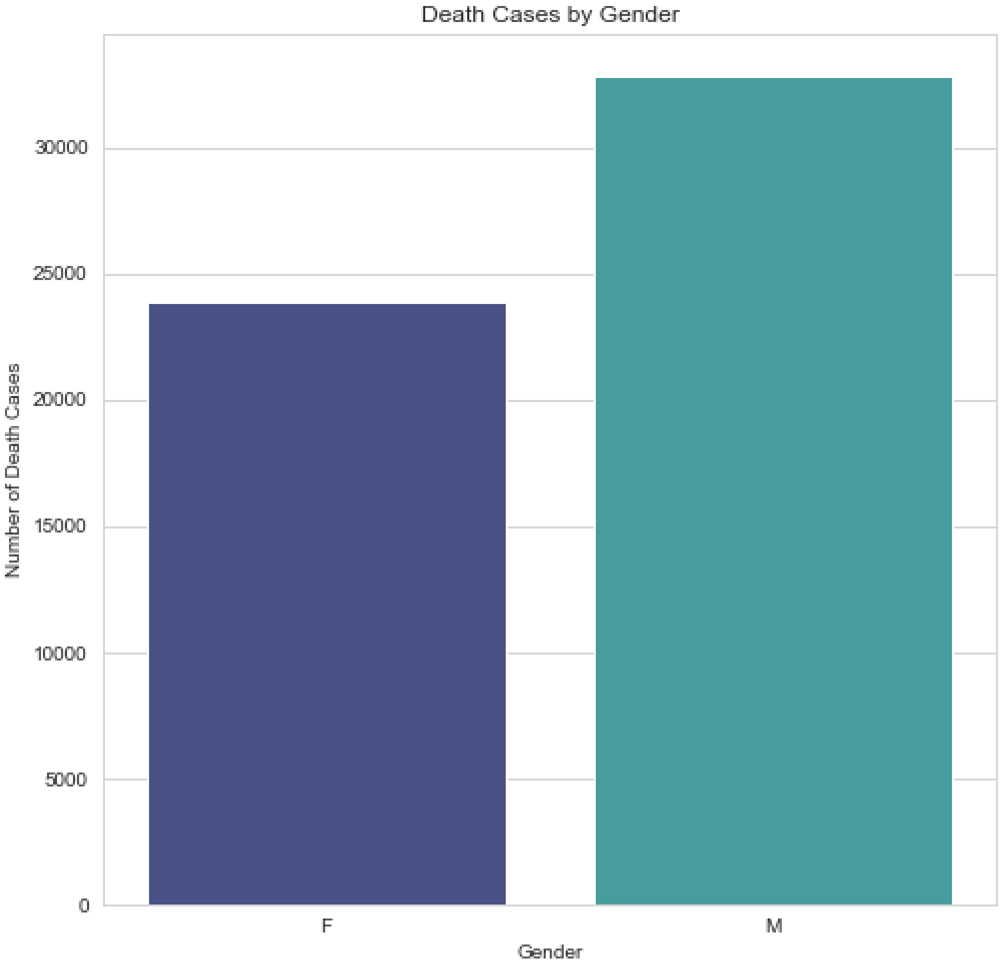
```
plt.figure(figsize=(10, 8))
sns.barplot(data=covidcases_by_age_group,
            x="age_group", y="deaths", palette="crest")
plt.title("Death Cases by Age-groups")
plt.xlabel('Gender')
plt.ylabel('Number of Death Cases')
plt.show()
```



- Even though age group of 80-99 has relatively lower cases by number, the death cases are around twice of other age-group combined.

In [ ]:

```
plt.figure(figsize=(8, 8))
sns.barplot(data=covidcases_by_gender, x="gender", y="deaths", palette="mako")
plt.title("Death Cases by Gender")
plt.xlabel('Gender')
plt.ylabel('Number of Death Cases')
plt.show()
```



- Covid-19 related deaths of males are relatively higher compared to females.

What contributes to the spread of COVID-19 in Germany?

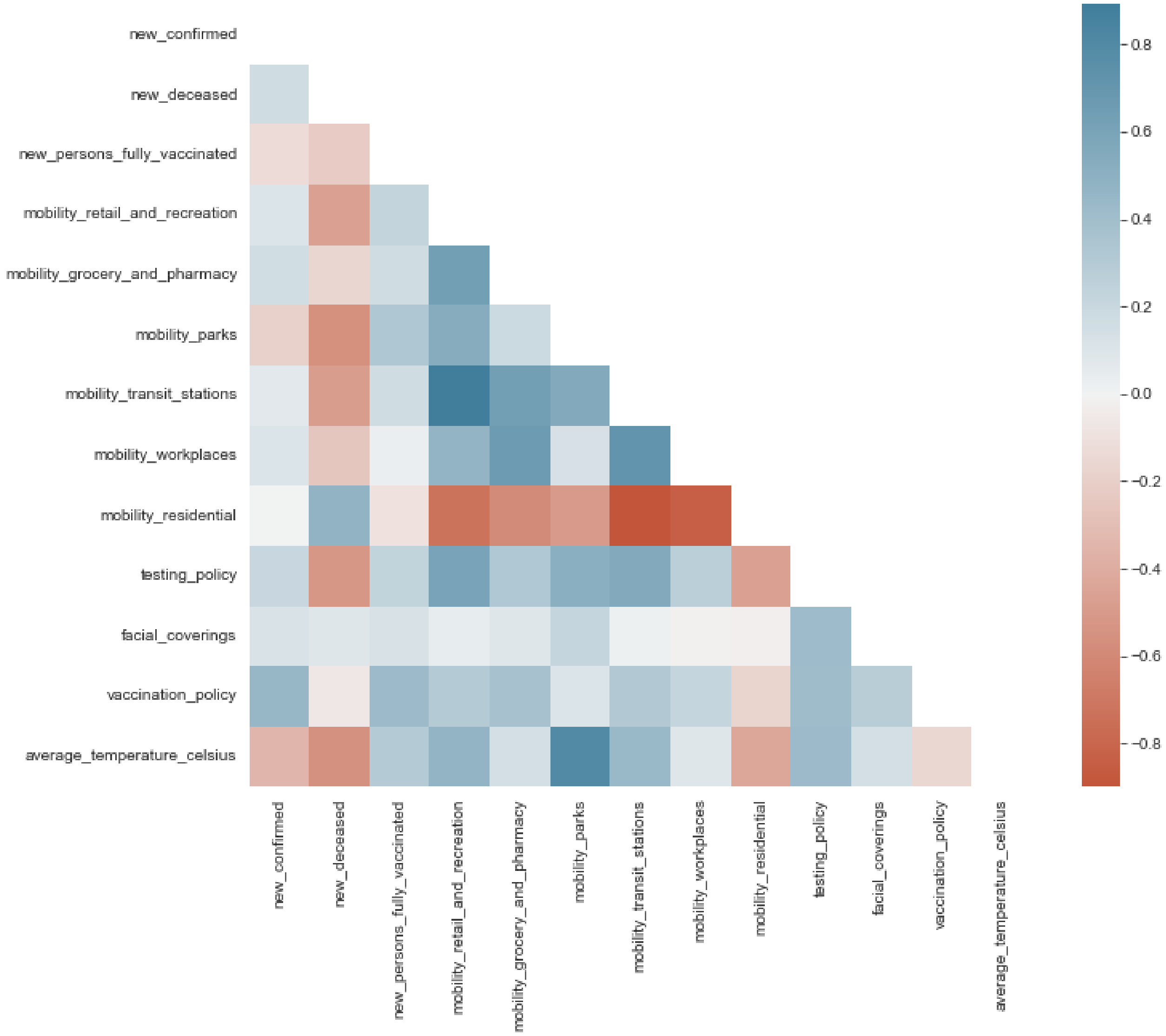
- When it comes to understanding what contributes to the spread of Covid-19 in Germany, we need to use an additonal dataset provided GoogleCloudPlatform. More info here open-covid-19.github.io

In [ ]:

```
corr = google_covid_de.corr()
f, ax = plt.subplots(figsize=(11,9))
mask = np.triu(np.ones_like(corr, dtype=bool))
cmap = sns.diverging_palette(20, 230, as_cmap=True)
sns.heatmap(corr, cmap=cmap, square=True, mask=mask)
```

Out[ ]:

```
<AxesSubplot:>
```



- By looking at the correlation table, we can see that `new confirmed cases` are negatively correlated with the average temperature. Meaning when the weather is colder, people tend to be sick more often.

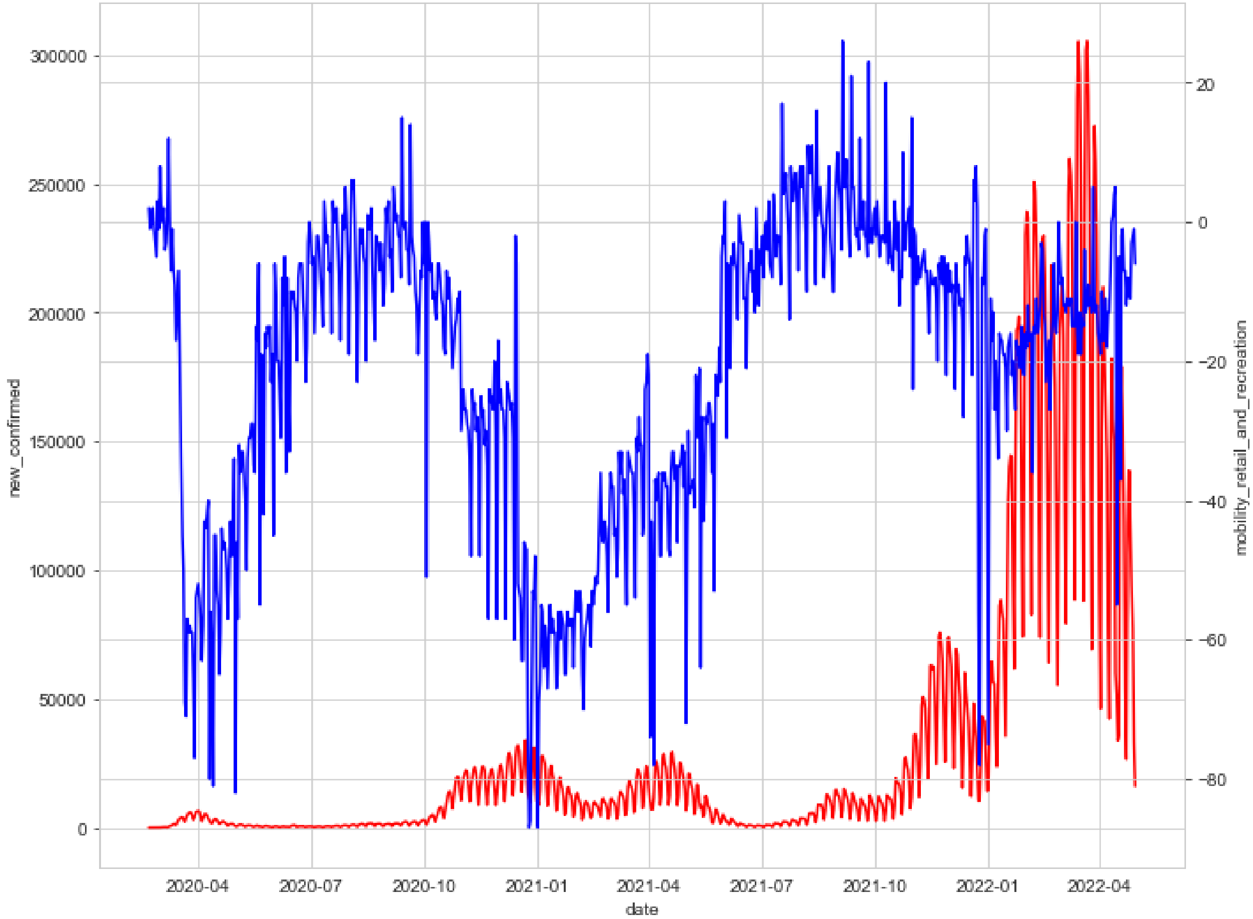
- In addition to that, let's analyze how people's movement affects the spread of COVID-19.

In [ ]:

```
plt.figure(figsize=(11,9))
sns.lineplot(x='date', y='new_confirmed', data=google_covid_de, color='r')
ax2 = plt.twinx()
sns.lineplot(x='date', y='mobility_retail_and_recreation', data=google_covid_de, color=
```

Out[ ]:

```
<AxesSubplot:xlabel='date', ylabel='mobility_retail_and_recreation'>
```



Modeling

In [ ]:

```
cov_model_df = new_covid_df_cleaned.groupby(by=["state", "county", 'age_group', 'gender
# calculate the sum of cases deaths and recovered and cases for each gender, age_group,
```

In [ ]:

```
cov_model_df.reset_index(inplace=True)
```

In [ ]:

```
new_merged = cov_model_df.merge(new_demographics_cleaned,
                                how = 'inner', on = ['state', 'gender', 'age_g
# merge the demographics data in order to obtain population
```

In [ ]:

```
new_merged.head()
```

Out[ ]:

	state	county	age_group	gender	cases	deaths	recovered	population
0	Baden-Wuerttemberg	LK Alb-Donau-Kreis	00-04	F	49	0	41	261674
1	Baden-Wuerttemberg	LK Biberach	00-04	F	49	0	44	261674
2	Baden-Wuerttemberg	LK Bodenseekreis	00-04	F	46	0	43	261674

	state	county	age_group	gender	cases	deaths	recovered	population
3	Baden-Wuerttemberg	LK Boeblingen	00-04	F	121	0	108	261674
4	Baden-Wuerttemberg	LK Breisgau-Hochschwarzwald	00-04	F	76	0	70	261674

In [ ]:

```
new_merged = new_merged.replace(['F', 'M'], [1, 0])
```

In [ ]:

```
new_merged['deaths'] = np.where(new_merged['deaths']> 0 , 1, 0)
```

In [ ]:

```
new_merged.isnull().sum()
```

Out[ ]:

```
state         0
county        0
age_group     0
gender        0
cases         0
deaths        0
recovered     0
population    0
dtype: int64
```

Training and Testing

In [ ]:

```
from sklearn.model_selection import train_test_split
from sklearn.model_selection import cross_val_score
```

In [ ]:

```
X=new_merged.drop(['state', 'county', 'age_group', 'deaths'], axis = 1)  # Features
y=new_merged['deaths']  # Labels

# Split dataset into training set and test set
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=4
```

Logistic Regression Modeling and Evaluation

In [ ]:

```
from sklearn.linear_model import LogisticRegression


logreg = LogisticRegression()
#fitting on logistic regression model
logreg.fit(X_train, y_train)

#predicting on decemeber month data
y_pred = logreg.predict(X_test)
```

In [ ]:

```
# Model Accuracy
print("Accuracy:",accuracy_score(y_test, y_pred) * 100)
```

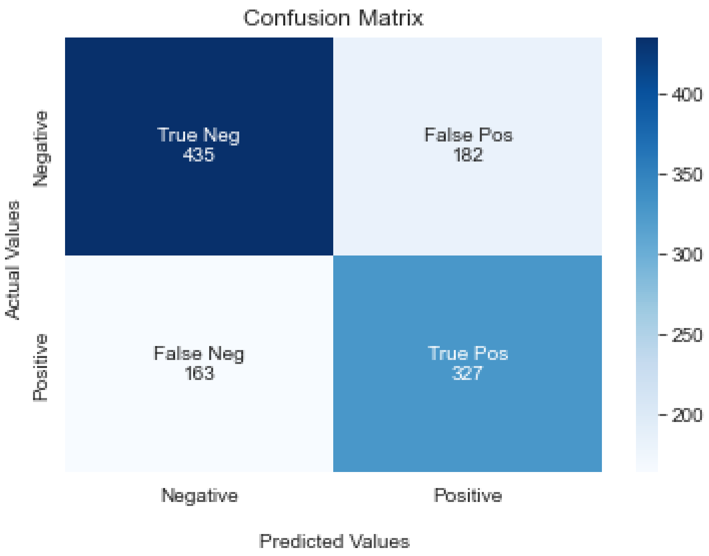
```
Accuracy: 68.83468834688347
```

In [ ]:

```
cf_matrix = confusion_matrix(y_test, y_pred)
```

In [ ]:

```
groups = ['True Neg', 'False Pos', 'False Neg', 'True Pos']
group_counts = ["{0:0.0f}".format(val) for val in
                cf_matrix.flatten()]
labels = [f"{g1}\n{g2}" for g1, g2 in
          zip(groups, group_counts)]
labels = np.asarray(labels).reshape(2, 2)
axes = sns.heatmap(cf_matrix, annot=labels, fmt='', cmap='Blues')
axes.set_title('Confusion Matrix')
axes.set_xlabel('\nPredicted Values')
axes.set_ylabel('Actual Values ')
axes.xaxis.set_ticklabels(['Negative', 'Positive'])
axes.yaxis.set_ticklabels(['Negative', 'Positive'])
plt.show()
```



In [ ]:

```
res_cfmatr = cf_matrix.flatten()
# precision = TP / (TP + FP)
precision = res_cfmatr[3] / (res_cfmatr[3] + res_cfmatr[1])
precision
```

Out[ ]:

```
0.6424361493123772
```

In [ ]:

```
# recall = TP / (TP + FN)
recall = res_cfmatr[3] / (res_cfmatr[3] + res_cfmatr[2])
recall
```

Out[ ]:

```
0.6673469387755102
```

In [ ]:

```
# f1 score = 2 * ((precision * recall)/ precision + recall)

f1score = 2 * ((precision * recall) / precision + recall)
f1score
```

Out[ ]:

```
2.669387755102041
```

In [ ]:

```python
cross_val_scores = cross_val_score(logreg, X, y,cv=10)
```

In [ ]:

```python
np.average(cross_val_scores)
```

Out[ ]:

```
0.7043794921644869
```

Random Forest Modelling and evaluation

In [ ]:

```python
from sklearn.ensemble import RandomForestClassifier

#Create a Gaussian Classifier
clf=RandomForestClassifier(n_estimators=100, random_state=42)

#Train the model using the training sets y_pred=clf.predict(X_test)
clf.fit(X_train,y_train)

y_pred=clf.predict(X_test)
```

In [ ]:

```python
# Model Accuracy
print("Accuracy:",accuracy_score(y_test, y_pred) * 100)
# the accuracy is high so the Random forest model performed well
```

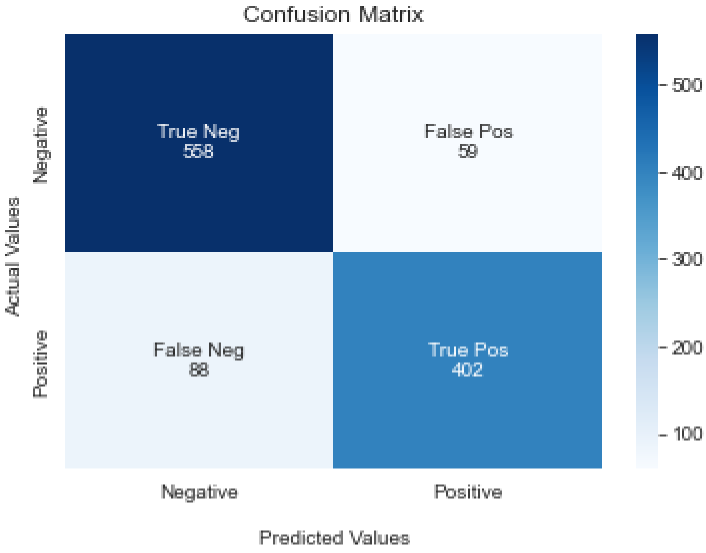
```
Accuracy: 86.72086720867209
```

In [ ]:

```python
cf_matrix = confusion_matrix(y_test, y_pred)
```

In [ ]:

```python
groups = ['True Neg','False Pos','False Neg','True Pos']
group_counts = ["{0:0.0f}".format(val) for val in
cf_matrix.flatten()]
labels = [f"{g1}\n{g2}" for g1, g2 in
zip(groups,group_counts)]
labels = np.asarray(labels).reshape(2,2)
axes = sns.heatmap(cf_matrix, annot=labels, fmt='', cmap='Blues')
axes.set_title('Confusion Matrix');
axes.set_xlabel('\nPredicted Values')
axes.set_ylabel('Actual Values ');
axes.xaxis.set_ticklabels(['Negative','Positive'])
axes.yaxis.set_ticklabels(['Negative','Positive'])
plt.show()
```



- from the above confusion matrix, the number of false negative and false positives are low which further shows the model performed well

In [ ]:

```
res_cfmatr = cf_matrix.flatten()
# precision = TP / (TP + FP)
precision = res_cfmatr[3]/ (res_cfmatr[3] + res_cfmatr[1])
precision
```

Out[ ]:

```
0.8720173535791758
```

In [ ]:

```
# recall = TP / (TP + FN)
recall = res_cfmatr[3]/ (res_cfmatr[3] + res_cfmatr[2])
recall
```

Out[ ]:

```
0.8204081632653061
```

In [ ]:

```
# f1 score = 2 * ((precision * recall)/ precision + recall)

f1score = 2 * ((precision * recall)/ precision + recall)
f1score
```

Out[ ]:

```
3.2816326530612243
```

Random Forest Cross Validation

In [ ]:

```
cross_val_scores = cross_val_score(RandomForestClassifier(n_estimators=100), X, y,cv=10
cross_val_scores
```

Out[ ]:

```
array([0.58536585, 0.88888889, 0.79403794, 0.61246612, 0.48780488,
       0.47696477, 0.4498645 , 0.47696477, 0.63858696, 0.75543478])
```

In [ ]:

```
np.average(cross_val_scores)
# the average score for cross validation is very low but if you look at cross_val_score
# you see that it performed well only a few times. One reason for this can be overfitti
```

Out[ ]:

```
0.616637946270767
```

K-NN Classifier Modeling and evaluation

In [ ]:

```
from sklearn.neighbors import KNeighborsClassifier
neigh = KNeighborsClassifier(n_neighbors=3)
neigh.fit(X_train, y_train)

y_pred = neigh.predict(X_test)
```

In [ ]:

```
# Model Accuracy
print("Accuracy:",accuracy_score(y_test, y_pred) * 100)
```

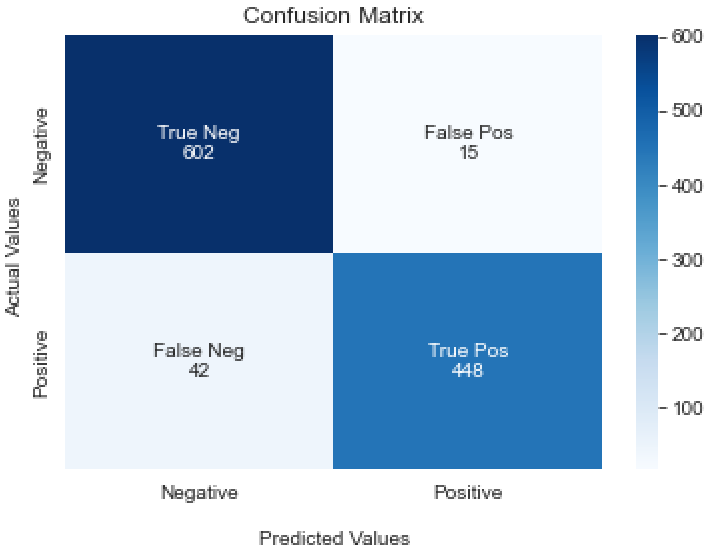
```
Accuracy: 94.85094850948511
```

In [ ]:

```
cf_matrix = confusion_matrix(y_test, y_pred)
```

In [ ]:

```
groups = ['True Neg','False Pos','False Neg','True Pos']
group_counts = ["{0:0.0f}".format(val) for val in
cf_matrix.flatten()]
labels = [f"{g1}\n{g2}" for g1, g2 in
zip(groups,group_counts)]
labels = np.asarray(labels).reshape(2,2)
axes = sns.heatmap(cf_matrix, annot=labels, fmt='', cmap='Blues')
axes.set_title('Confusion Matrix');
axes.set_xlabel('\nPredicted Values')
axes.set_ylabel('Actual Values ');
axes.xaxis.set_ticklabels(['Negative','Positive'])
axes.yaxis.set_ticklabels(['Negative','Positive'])
plt.show()
```



In [ ]:

```
res_cfmatr = cf_matrix.flatten()
# precision = TP / (TP + FP)
```

```
precision = res_cfmatr[3]/ (res_cfmatr[3] + res_cfmatr[1])
precision
```

Out[ ]:

```
0.9676025917926566
```

In [ ]:

```
# recall = TP / (TP + FN)
recall = res_cfmatr[3]/ (res_cfmatr[3] + res_cfmatr[2])
recall
```

Out[ ]:

```
0.9142857142857143
```

In [ ]:

```
# f1 score = 2 * ((precision * recall)/ precision + recall)

f1score = 2 * ((precision * recall)/ precision + recall)
f1score
```

Out[ ]:

```
3.657142857142857
```

KNN Cross Validation

In [ ]:

```
cross_val_scores = cross_val_score(KNeighborsClassifier(n_neighbors=3), X, y,cv=10)
cross_val_scores
```

Out[ ]:

```
array([0.3902439 , 0.7398374 , 0.42276423, 0.52574526, 0.49593496,
       0.61246612, 0.49864499, 0.42276423, 0.51902174, 0.72282609])
```

In [ ]:

```
np.average(cross_val_scores)
```

Out[ ]:

```
0.5350248910097796
```

Model	Accuracy	Precision	Recall	F1	Cross-valid
Logistic Regression	68.83	0.64	0.66	2.66	0.70
Random Forest	86.72	0.87	0.82	3.28	0.61
KNN	94.85	0.96	0.91	3.657	0.53

- Logistic Regression was not performing as expected as it is linear and our training data sets was not calibrated well enough.
- Random forest performed better but it has issues with overfitting.
- KNN performs the best as its neighboring method is expected to perform better in population data and our data was not high dimensional.
- Cross validation results were not promising for KNN and further analysis need to be done to know what are the underlying reasons.