World_Health

February 19, 2025

```
<h1><b>Identifying Key Factors Influencing Variant Severity</b></h1>
```

0.1 Problem Statement

Goal: Analyze Covid-19 public health dataset to determine which factors contribute to a variant being more severe.

Background : This dataset contains records related to different COVID-19 variants detected across various countries. It provides key epidemiological insights, including the number of cases, deaths, recoveries, and hospitalizations for each variant. Additionally, it includes transmission rates, mutation counts, and severity levels. The dataset can be useful for analyzing the spread and impact of different variants over time. This dataset is a consolidated version combining variant-related data reported globally. It helps in understanding the patterns of transmission, mutation trends, and severity levels associated with different COVID-19 strains. Click here for the data dictonary

0.1.1 World Health DataSet

[246]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import plotly.express as px
import plotly.io as pio
import xgboost as xgb

from sklearn.model_selection import train_test_split, RandomizedSearchCV,␣
 ↪train_test_split
from sklearn import metrics
from sklearn.preprocessing import OneHotEncoder, LabelEncoder, StandardScaler
from sklearn.metrics import mean_squared_error, r2_score,␣
 ↪classification_report, accuracy_score, ConfusionMatrixDisplay,␣
 ↪mean_absolute_error
from sklearn.ensemble import RandomForestClassifier, RandomForestRegressor
from sklearn.linear_model import LinearRegression

pio.renderers.default = 'notebook'
```

0.2 Exploratory Data Analysis (EDA)

[9]:
```
covid = pd.read_csv('data/covid_variants.csv')
covid.sort_values('Date_Detected').head()
```

[9]:
```
     Variant    Country Date_Detected  Cases  Deaths  Recovered  Hospitalized  \
169     Beta  Australia    2020-01-09  69724    1422      66456          1363
985    Delta        USA    2020-01-11  31231    3155      28671          9918
403  Omicron    Germany    2020-01-11  10158    4117      18866           281
599    Alpha     France    2020-01-14  76121    3670      25983          2691
375  Epsilon  Australia    2020-01-14   3860    2606      30316          7219

     Transmission_Rate  Mutation_Count Severity_Level
169               1.04               1           Mild
985               2.41              12       Critical
403               1.81               8         Severe
599               1.14              11         Severe
375               0.83              12           Mild
```

[10]:
```
covid.isnull().sum()
```

[10]:
```
Variant              0
Country              0
Date_Detected        0
Cases                0
Deaths               0
Recovered            0
Hospitalized         0
Transmission_Rate    0
Mutation_Count       0
Severity_Level       0
dtype: int64
```

[11]:
```
covid.describe()
```

[11]:
```
              Cases       Deaths     Recovered  Hospitalized  \
count   1000.000000  1000.000000   1000.000000   1000.000000
mean   49217.413000  2574.546000  47788.435000   4970.183000
std    28789.556442  1427.131865  27632.058466   2912.573549
min      238.000000     2.000000    337.000000     11.000000
25%    23554.250000  1346.250000  23541.000000   2423.750000
50%    50199.000000  2657.000000  47390.000000   4940.000000
75%    74759.250000  3727.250000  71649.250000   7400.750000
max    99921.000000  4997.000000  94963.000000   9984.000000

       Transmission_Rate  Mutation_Count
count        1000.000000     1000.000000
mean            1.715070       10.023000
```

```
std             0.733849        5.414221
min             0.500000        1.000000
25%             1.080000        6.000000
50%             1.690000       10.000000
75%             2.360000       15.000000
max             3.000000       19.000000
```

[12]:
```
covid.columns = covid.columns.str.lower()
covid
```

[12]:
```
     variant  country date_detected  cases  deaths  recovered  hospitalized  \
0         Mu      USA    2022-03-19  38091     232      15458          1476
1      Delta   Canada    2021-06-29  79157    1552      58030          3967
2    Epsilon       UK    2022-07-18   7071    3270      83006          1976
3    Omicron       UK    2020-08-30  29239    2409      16401           385
4         Mu  Germany    2023-09-29  85545    3512       4181           272
..       …      …           …     …     …        …           …
995    Theta   Brazil    2023-08-14  74807     903      83213          8017
996    Theta    Japan    2022-03-26  78357     861      71282          1651
997  Epsilon  Germany    2023-08-22  61315    1083      49044           481
998     Beta    India    2023-10-10  55935     649      79129          2950
999     Zeta   Brazil    2020-12-12  49529    4134      12665          8748

     transmission_rate  mutation_count severity_level
0                 1.27              10       Moderate
1                 1.16               7       Moderate
2                 2.24              14           Mild
3                 0.98              16       Moderate
4                 0.73              15         Severe
..                 …               …            …
995               1.80              11       Critical
996               2.17              18       Critical
997               2.54              18       Moderate
998               1.15              10       Moderate
999               1.24               2         Severe

[1000 rows x 10 columns]
```

[13]:
```
covid.dtypes
```

[13]:
```
variant              object
country              object
date_detected        object
cases                 int64
deaths                int64
recovered             int64
hospitalized          int64
```

```
transmission_rate    float64
mutation_count         int64
severity_level        object
dtype: object
```

[14]:
```
covid['date_datetime'] = pd.to_datetime(covid['date_detected'])
```

[15]:
```
covid['date_datetime'] = pd.to_datetime(covid['date_datetime'])
```

[16]:
```
covid['month_year'] = covid['date_datetime'].dt.strftime('%Y-%m')
```

[17]:
```
covid.drop(columns =['date_detected', 'date_datetime'], inplace = True)
```

[18]:
```
covid = covid.sort_values('month_year')
```

[19]:
```
'''Calculating case fatality rate
Higher values indicate more deadly variants.'''
covid['case_fatality_rate'] = covid['deaths']/covid['cases']*100
covid['case_fatality_rate']
```

[19]:
```
609     0.954198
659     6.458621
700     4.845299
908     2.312840
640    10.555977
         …
728     3.593718
131     1.389057
815     1.909659
513     3.671580
866     9.068207
Name: case_fatality_rate, Length: 1000, dtype: float64
```

[20]:
```
'''Hospitalization Rate
Hospitalization rates are calculated as the number of residents in a␣
 ↪surveillance
area who are hospitalized with laboratory-confirmed COVID-19,
divided by the total population estimate for that area, or in this case "cases".
 ↪'''

covid['hospitalized_rate']= covid['hospitalized']/covid['cases']*100
covid['hospitalized_rate']
```

[20]:
```
609     2.241257
659     4.137921
700     7.750951
908    10.724040
```

```
640    42.684513
         …
728     9.019344
131    67.834280
815     5.008827
513    16.990369
866    23.245409
Name: hospitalized_rate, Length: 1000, dtype: float64
```

[21]:
```
'''Recovery Rate
Indicates how mild/severe a variant is.'''
covid['recovery_rate']= covid['recovered']/covid['cases']*100
covid['recovery_rate']
```

[21]:
```
609     40.795313
659     56.915128
700    106.755673
908     97.231939
640     25.663813
          …
728     89.985846
131    252.590893
815     97.227282
513    148.603203
866    138.962593
Name: recovery_rate, Length: 1000, dtype: float64
```

[22]:
```
'''Variant Prevalence in Country, Percentage of total cases in each country for␣
 ↪each variant
Helps understand which variant dominated in each region.'''

# Calculate total cases per country
total_cases_per_country = covid.groupby('country')['cases'].transform('sum')
total_cases_per_country

# Calculate variant prevalence in each country (%)
covid["variant_prevalence"] = (covid["cases"] / total_cases_per_country) * 100
covid["variant_prevalence"]
```

[22]:
```
609    1.344836
659    1.345284
700    1.570374
908    1.236301
640    0.368834
         …
728    1.586452
131    0.201958
```

```
815    1.523957
513    0.373891
866    0.719140
Name: variant_prevalence, Length: 1000, dtype: float64
```

[23]:
```
'''Mutation-to-Transmission Ratio
Helps assess if more mutations lead to increased spread.'''

covid['mutation_transmission_ratio']= covid['mutation_count']/
 ↪covid['transmission_rate']
covid['mutation_transmission_ratio']
```

[23]:
```
609     2.521008
659     2.439024
700     5.617978
908    13.333333
640     0.757576
         …
728    12.048193
131     8.755760
815     2.766798
513    18.421053
866     0.374532
Name: mutation_transmission_ratio, Length: 1000, dtype: float64
```

[24]:
```
# Helps capture the combined effect of mutations and spreadability
covid["mutation_transmission_interaction"] = covid["mutation_count"] *␣
 ↪covid["transmission_rate"]
covid["mutation_transmission_interaction"]
```

[24]:
```
609    14.28
659    10.25
700    17.80
908     7.50
640     1.32
       …
728     8.30
131    41.23
815    17.71
513    10.64
866     2.67
Name: mutation_transmission_interaction, Length: 1000, dtype: float64
```

[25]:
```
covid = pd.get_dummies(covid, columns=["variant"], dtype=int, drop_first=True)
```

[26]:
```
covid
```

[26]:

	country	cases	deaths	recovered	hospitalized	transmission_rate	\
609	Australia	67596	645	27576	1515	2.38	
659	Brazil	68126	4400	38774	2819	2.05	
700	India	78571	3807	83879	6090	1.78	
908	Brazil	62607	1448	60874	6714	0.75	
640	India	18454	1948	4736	7877	1.32	
..	…	…	…	…	…	…	
728	South Africa	74185	2666	66756	6691	0.83	
131	UK	8279	115	20912	5616	2.17	
815	France	71374	1363	69395	3575	2.53	
513	Australia	18793	690	27927	3193	0.76	
866	Japan	38442	3486	53420	8936	2.67	

	mutation_count	severity_level	month_year	case_fatality_rate	…	\
609	6	Moderate	2020-01	0.954198	…	
659	5	Mild	2020-01	6.458621	…	
700	10	Mild	2020-01	4.845299	…	
908	10	Critical	2020-01	2.312840	…	
640	1	Severe	2020-01	10.555977	…	
..	…	…	…	…	…	
728	10	Severe	2023-12	3.593718	…	
131	19	Mild	2023-12	1.389057	…	
815	7	Mild	2023-12	1.909659	…	
513	14	Moderate	2023-12	3.671580	…	
866	1	Moderate	2023-12	9.068207	…	

	mutation_transmission_interaction	variant_Beta	variant_Delta	\
609	14.28	0	0	
659	10.25	0	0	
700	17.80	0	0	
908	7.50	0	0	
640	1.32	0	0	
..	…	…	…	
728	8.30	1	0	
131	41.23	0	0	
815	17.71	1	0	
513	10.64	0	1	
866	2.67	0	0	

	variant_Epsilon	variant_Gamma	variant_Lambda	variant_Mu	\
609	1	0	0	0	
659	0	0	0	0	
700	0	0	0	1	
908	0	1	0	0	
640	0	0	0	0	
..	…	…	…	…	
728	0	0	0	0	

```
131                0              0                0           1
815                0              0                0           0
513                0              0                0           0
866                0              0                0           0

     variant_Omicron  variant_Theta  variant_Zeta
609                0              0             0
659                1              0             0
700                0              0             0
908                0              0             0
640                0              0             0
..               …              …             …
728                0              0             0
131                0              0             0
815                0              0             0
513                0              0             0
866                0              1             0

[1000 rows x 24 columns]
```

[27]:
```
covid.describe()
```

[27]:
```
              cases       deaths     recovered  hospitalized  \
count   1000.000000  1000.000000   1000.000000   1000.000000
mean   49217.413000  2574.546000  47788.435000   4970.183000
std    28789.556442  1427.131865  27632.058466   2912.573549
min      238.000000     2.000000    337.000000     11.000000
25%    23554.250000  1346.250000  23541.000000   2423.750000
50%    50199.000000  2657.000000  47390.000000   4940.000000
75%    74759.250000  3727.250000  71649.250000   7400.750000
max    99921.000000  4997.000000  94963.000000   9984.000000

       transmission_rate  mutation_count  case_fatality_rate  \
count        1000.000000     1000.000000         1000.000000
mean            1.715070       10.023000           16.282587
std             0.733849        5.414221           49.390641
min             0.500000        1.000000            0.006051
25%             1.080000        6.000000            2.885558
50%             1.690000       10.000000            5.393726
75%             2.360000       15.000000           10.199654
max             3.000000       19.000000          909.170306

       hospitalized_rate  recovery_rate  variant_prevalence  …  \
count        1000.000000    1000.000000         1000.000000  …
mean           35.834658     335.450791            1.000000  …
std           153.253370    1181.630934            0.587469  …
min             0.020670       0.374723            0.005022  …
```

```
25%              4.917339      47.358851            0.484286  …
50%             10.045960      96.386610            1.020760  …
75%             19.927423     192.983189            1.508676  …
max           2808.494208   18377.074236            2.430422  …

       mutation_transmission_interaction  variant_Beta  variant_Delta  \
count                        1000.000000    1000.00000    1000.000000
mean                           17.193710       0.08300       0.094000
std                            12.602369       0.27602       0.291975
min                             0.530000       0.00000       0.000000
25%                             6.885000       0.00000       0.000000
50%                            14.410000       0.00000       0.000000
75%                            24.750000       0.00000       0.000000
max                            55.670000       1.00000       1.000000

       variant_Epsilon  variant_Gamma  variant_Lambda   variant_Mu  \
count       1000.00000    1000.000000     1000.000000  1000.000000
mean           0.10000       0.110000        0.096000     0.094000
std            0.30015       0.313046        0.294739     0.291975
min            0.00000       0.000000        0.000000     0.000000
25%            0.00000       0.000000        0.000000     0.000000
50%            0.00000       0.000000        0.000000     0.000000
75%            0.00000       0.000000        0.000000     0.000000
max            1.00000       1.000000        1.000000     1.000000

       variant_Omicron  variant_Theta  variant_Zeta
count     1000.000000    1000.000000   1000.000000
mean         0.107000       0.107000      0.091000
std          0.309268       0.309268      0.287753
min          0.000000       0.000000      0.000000
25%          0.000000       0.000000      0.000000
50%          0.000000       0.000000      0.000000
75%          0.000000       0.000000      0.000000
max          1.000000       1.000000      1.000000

[8 rows x 21 columns]
```

[28]:
```
covid.isnull().sum()
```

[28]:
```
country                    0
cases                      0
deaths                     0
recovered                  0
hospitalized               0
transmission_rate          0
mutation_count             0
severity_level             0
```

```
month_year                          0
case_fatality_rate                  0
hospitalized_rate                   0
recovery_rate                       0
variant_prevalence                  0
mutation_transmission_ratio         0
mutation_transmission_interaction   0
variant_Beta                        0
variant_Delta                       0
variant_Epsilon                     0
variant_Gamma                       0
variant_Lambda                      0
variant_Mu                          0
variant_Omicron                     0
variant_Theta                       0
variant_Zeta                        0
dtype: int64
```

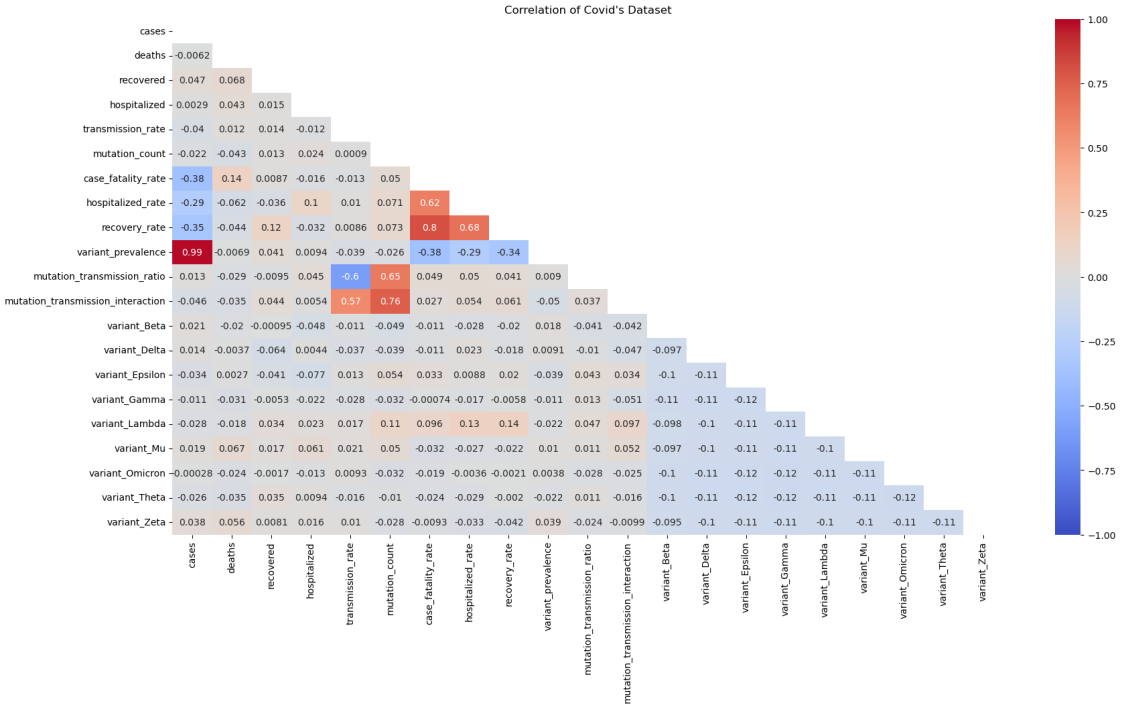
[29]:
```
covid.dtypes
```

[29]:
```
country                            object
cases                               int64
deaths                              int64
recovered                           int64
hospitalized                        int64
transmission_rate                 float64
mutation_count                      int64
severity_level                     object
month_year                         object
case_fatality_rate                float64
hospitalized_rate                 float64
recovery_rate                     float64
variant_prevalence                float64
mutation_transmission_ratio       float64
mutation_transmission_interaction float64
variant_Beta                        int64
variant_Delta                       int64
variant_Epsilon                     int64
variant_Gamma                       int64
variant_Lambda                      int64
variant_Mu                          int64
variant_Omicron                     int64
variant_Theta                       int64
variant_Zeta                        int64
dtype: object
```

0.3 EDA Visuals

[31]:
```
corr = covid.corr(numeric_only = True)
mask = np.zeros_like(corr)
mask[np.triu_indices_from(mask)] = True
```

[32]:
```
plt.figure(figsize = (20,10))
sns.heatmap(covid.corr(numeric_only = True),
            vmin = -1,
            vmax = 1,
            cmap = 'coolwarm',
            annot = True,
            mask = mask);

plt.title("Correlation of Covid's Dataset");
```



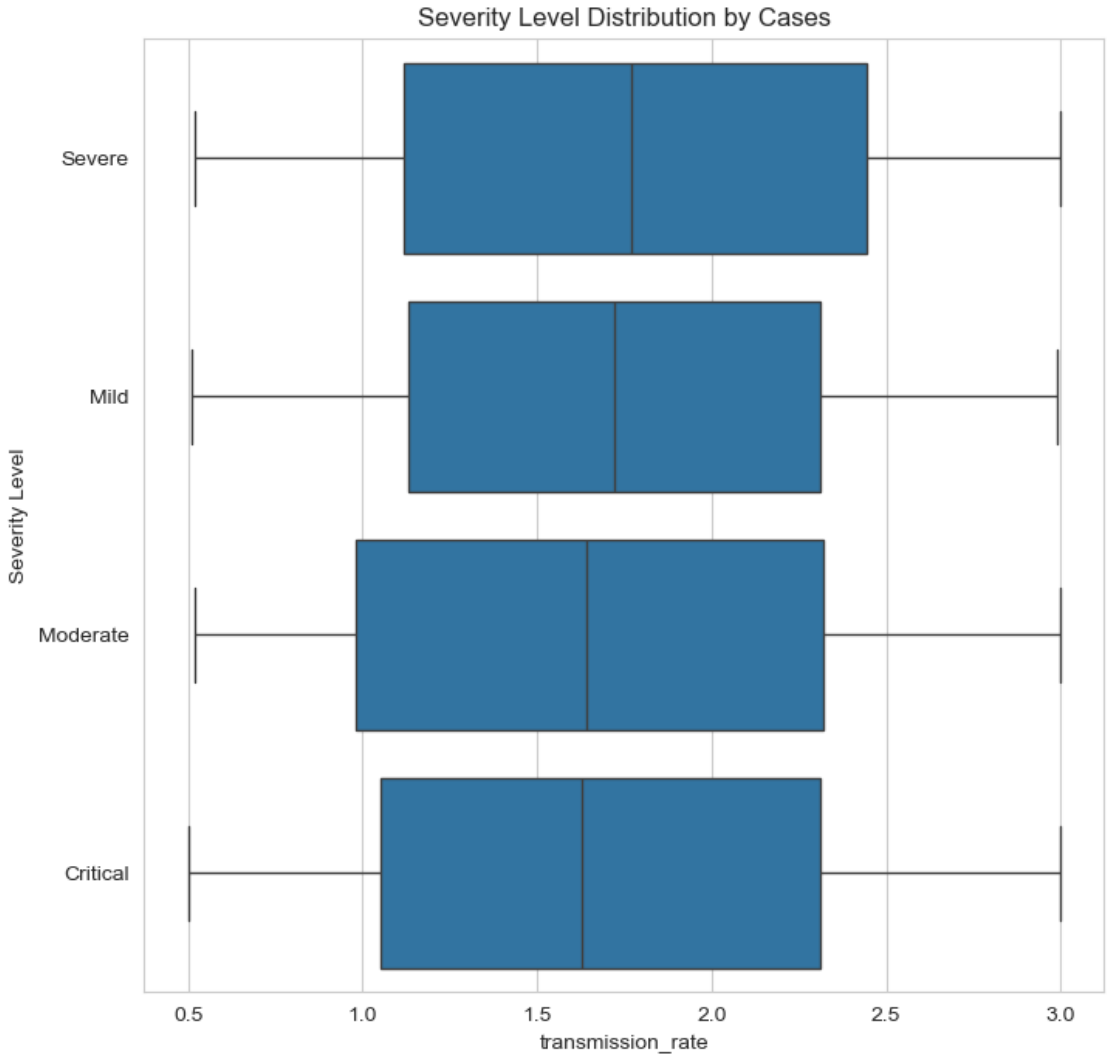
This heatmap helps us identify which factors contribute most to COVID-19 variant severity, guiding us in building a predictive model. It shows that higher fatality and hospitalization rates strongly correlate with severity, meaning variants with these traits are more dangerous. It also highlights strong positive correlations that should be used as key features in a machine learning model. By training a Random Forest Regressor with these features, we can predict how severe a new variant might be before it spreads widely. This helps health officials prepare hospitals, allocate resources, and issue early warnings based on predicted severity levels. Ultimately, the heatmap acts as a data driven decision making tool for both researchers and policymakers, enabling better

pandemic response and risk assessment.

[34]:
```
covid.groupby('severity_level')['transmission_rate'].mean().sort_values
```

[34]:
```
<bound method Series.sort_values of severity_level
Critical    1.684647
Mild        1.724808
Moderate    1.686667
Severe      1.763482
Name: transmission_rate, dtype: float64>
```

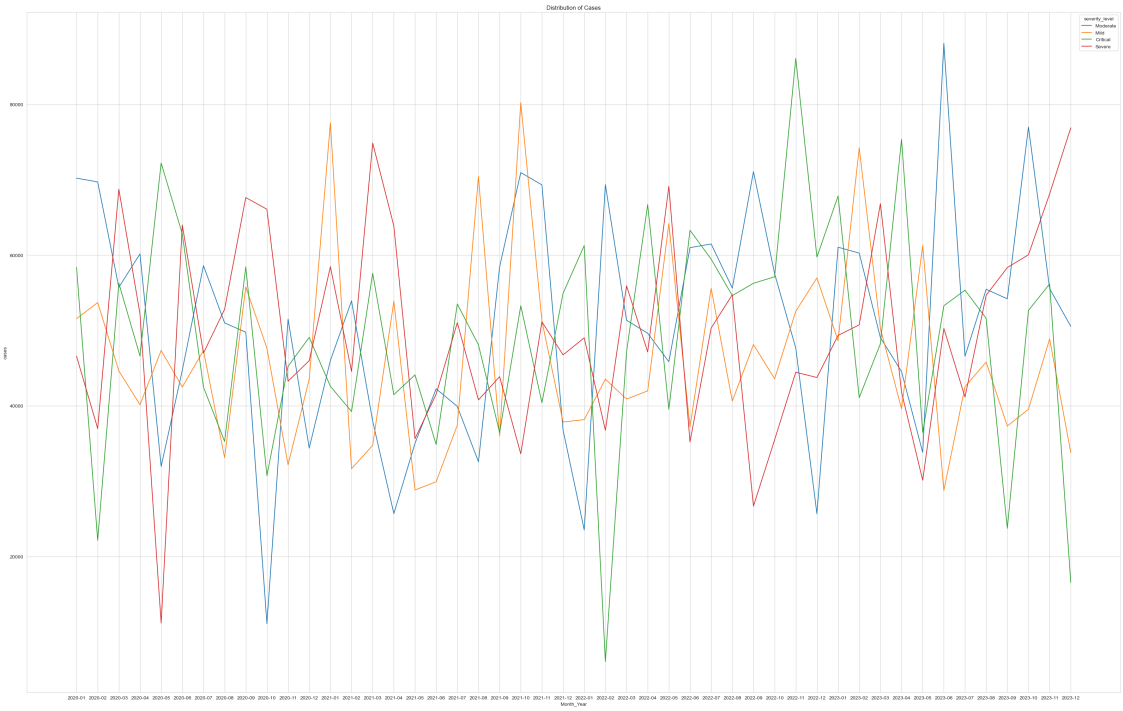
[35]:
```
sns.set_style('whitegrid')

#Boxplot of our feaure
plt.figure(figsize = (8,8))
sns.boxplot(data = covid,
            y = 'severity_level',
            x = 'transmission_rate',
            order = covid.groupby('severity_level')['transmission_rate'].mean().
 ↪sort_values(ascending = False).index)

plt.title("Severity Level Distribution by Cases")
plt.xlabel("transmission_rate")
plt.ylabel("Severity Level")
plt.show();
```



This boxplot helps us to visualize how transmission rate varies across different severity levels of COVID-19 variants. This plot reveals the distribution, median, and outliers of transmission rates for each severity level, allowing us to detect patterns that can improve feature selection in predictive modeling. If higher transmission rates are consistently linked to severe variants, then transmission rate should be included as a key predictor in a machine learning model. This insight enables health organizations to predict which new variants might be severe based on their transmission rate, even before enough hospitalization data is available.

[37]:
```
plt.figure(figsize = (40,25))

sns.lineplot(data = covid,
             x = 'month_year',
             y = 'cases',
```

```
              hue = 'severity_level',
              errorbar =None);

sns.set(style = None)
plt.title('Distribution of Cases')
plt.xlabel('Month_Year')
plt.show();
```



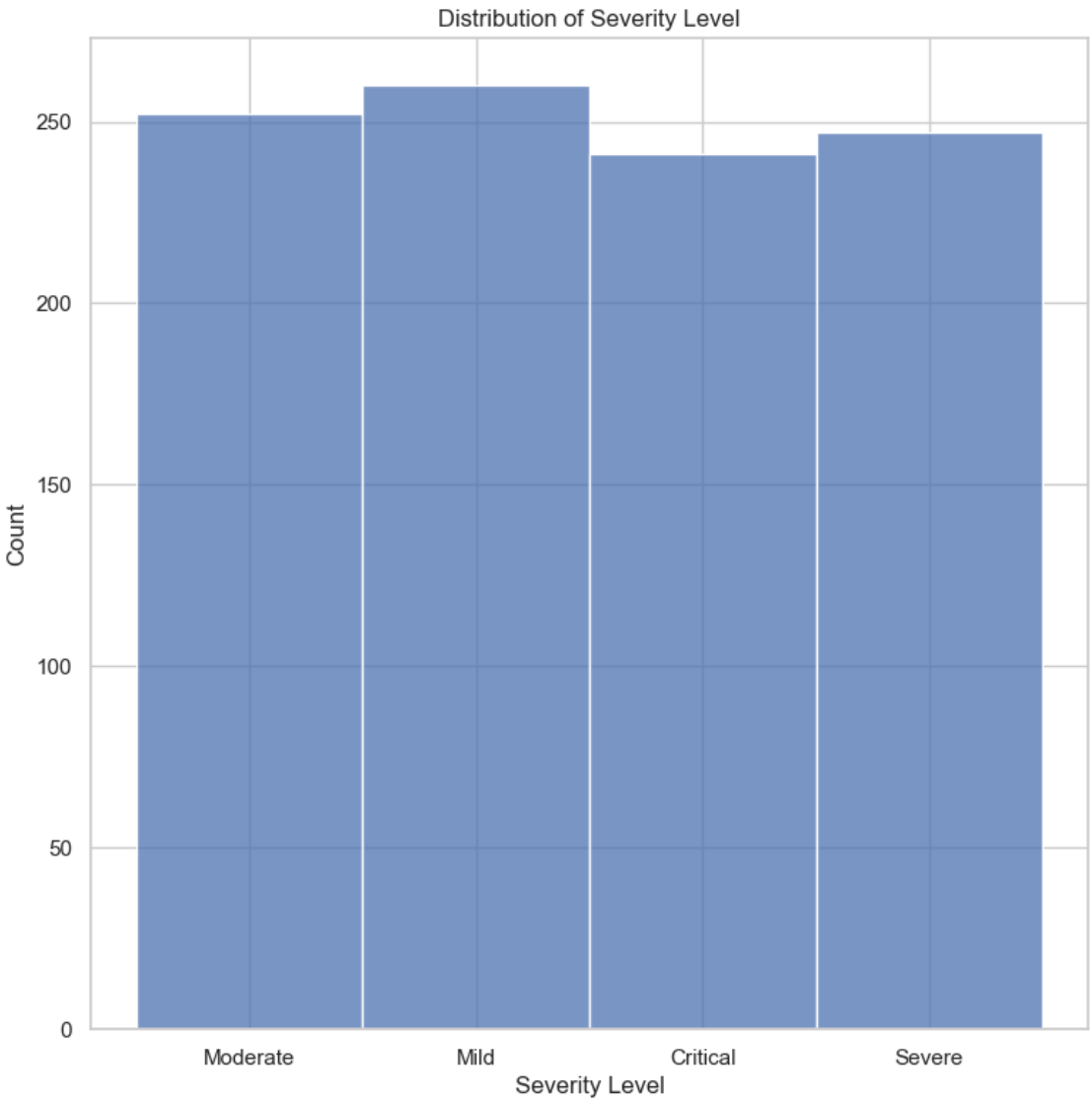
This line plot shows how COVID-19 case trends change over time and how they relate to different severity levels. This highlights time-series trends, showing whether higher case counts correlate with more severe variants, which can improve predictive modeling.

[39]:
```
fig = px.scatter_3d(covid,
                    x = 'cases',
                    y = 'variant_Gamma',
                    z = 'variant_prevalence',
                    color = 'severity_level');

fig.show(renderer='iframe')
```

This 3D scatter plot visualizes how COVID-19 cases, variant prevalence, and variant type (Gamma) relate to severity levels. This helps to identify whether certain variants, like Gamma, are more likely to be severe, guiding public health decisions. This insight allows health experts to track dangerous variants early. Ultimately, this visualization helps both policymakers and data analysts predict variant severity more accurately,

leading to better pandemic response and forecasting.

[41]:
```
plt.figure(figsize = (9,9))
sns.histplot(data = covid,
             x = 'severity_level');

plt.title('Distribution of Severity Level')
plt.xlabel('Severity Level')
plt.show()
```



This histogram shows the distribution of COVID-19 severity levels, helping us understand which severity category is most common. This helps detect class imbalances, which is crucial for training fair and accurate machine learning models

0.4 Baseline Model

[44]:
```
covid.drop(columns = ['country', 'month_year'], inplace = True)
```

[45]:
```
covid['severity_level'].value_counts(normalize = True)
```

[45]:
```
severity_level
Mild        0.260
Moderate    0.252
Severe      0.247
Critical    0.241
Name: proportion, dtype: float64
```

Using our baseline model as a reference point, we are going to determine if our model is learning from the data. We want our model to perform better than **26%** Since the values are close to each other, it suggests that the dataset is relatively balanced across severity levels.

0.5 Train Split Test

[48]:
```
# Encode severity level as a numeric target variable
encoder = LabelEncoder()
y = encoder.fit_transform(covid["severity_level"])
```

[49]:
```
X = covid.drop(columns = 'severity_level')
```

[50]:
```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
↪random_state = 42)
```

[51]:
```
sc = StandardScaler()
```

[52]:
```
#Fit and Transform
X_train_sc = sc.fit_transform(X_train)
X_test_sc = sc.transform(X_test)
```

0.6 Predicting Model

0.6.1 Random Forest Classification

[164]:
```
rf = RandomForestClassifier()
#Fit on training Data
rf.fit(X_train_sc, y_train)
```

[164]:
```
RandomForestClassifier()
```

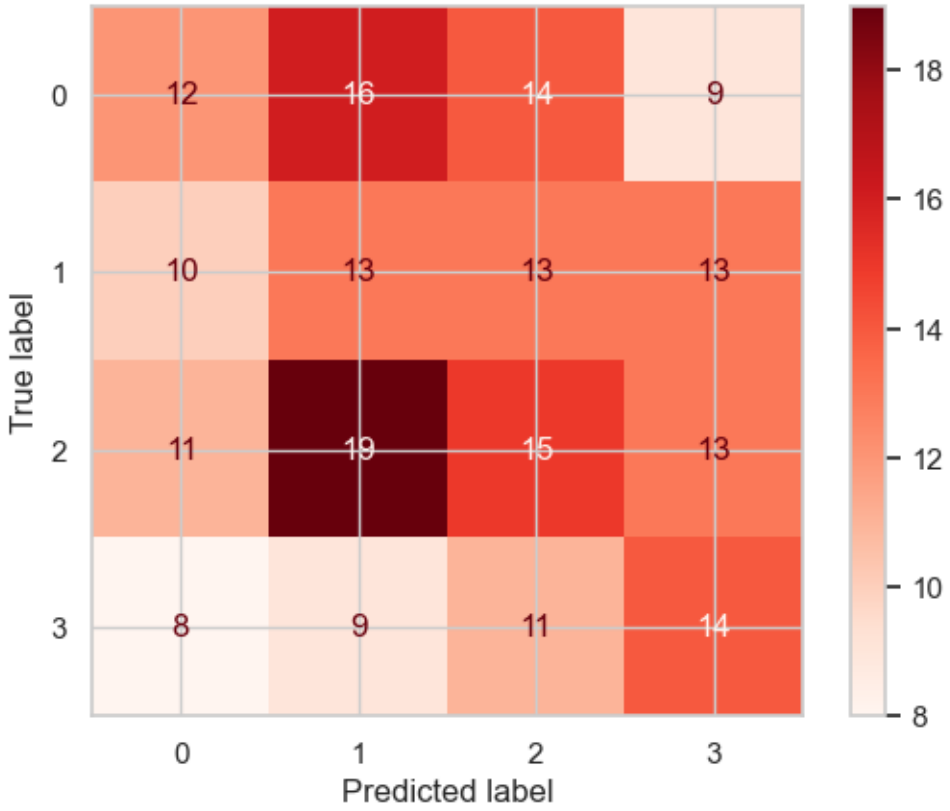
[56]:
```
rf.score(X_train_sc, y_train)
```

[56]:
```
1.0
```

[57]:
```
rf.score(X_test_sc, y_test)
```

[57]: 0.27

[58]:
```
ConfusionMatrixDisplay.from_estimator(rf, X_test_sc, y_test, cmap='Reds');
```



Our train score of 1.0 and test score of 0.27 indicate severe overfitting, meaning the model memorized training data but fails on new data. To fix this, we can reduce model complexity by limiting tree depth and increasing min_samples_split and min_samples_leaf to prevent overly small nodes. Lowering the number of trees (n_estimators) and enabling bootstrap sampling can also improve generalization.

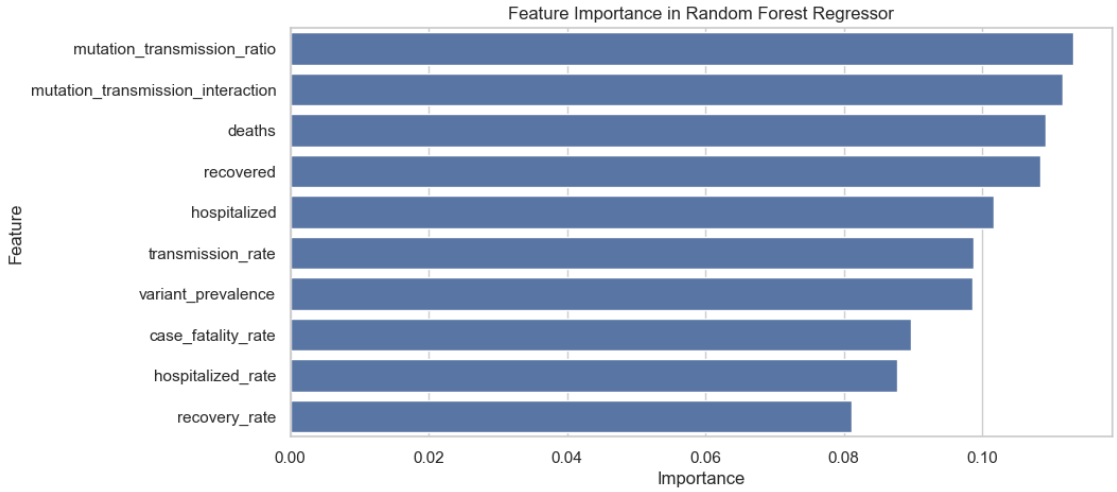
0.6.2 Random Forest Regressor

[252]:
```
model = RandomForestRegressor(n_estimators=100, max_depth= 30, random_state=42)
model.fit(X_train, y_train)

# Make predictions
y_pred = model.predict(X_test)
```

[250]:
```
# Calculate Mean Absolute Error (MAE)
mae = mean_absolute_error(y_test, y_pred)

mae
```

[250]:
```
0.9400499999999999
```

[248]:
```
# Get feature importance
feature_importances = model.feature_importances_
features = X.columns

# Create DataFrame
importance_df = pd.DataFrame({"Feature": features, "Importance":␣
 ↪feature_importances})
importance_df = importance_df.sort_values(by="Importance", ascending=False)

# Plot feature importance
plt.figure(figsize=(10,5))

sns.barplot(x= importance_df["Importance"],
            y=importance_df["Feature"])

plt.title("Feature Importance in Random Forest Regressor")
plt.show()
```



Our Random Forest Regressor model gave a MAE score of 0.95, meaning that the model's severity predictions are off by nearly one severity category on average. To improve accuracy, we can focus on feature selection by identifying the most important factors and removing weak predictors.

0.6.3 Random Forest Regressor (using features)

[268]:
```
features = ["case_fatality_rate", "hospitalized_rate", "variant_prevalence",
            "transmission_rate", "recovery_rate",␣
 ↪"mutation_transmission_ratio","deaths",
            "recovered", "hospitalized", "mutation_transmission_interaction"]
X = covid[features]

encoder = LabelEncoder()
y = encoder.fit_transform(covid["severity_level"])
```

[270]:
```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
 ↪random_state = 42)
```

[272]:
```
model = RandomForestRegressor(n_estimators=100, max_depth= 30, random_state=42)
model.fit(X_train, y_train)

# Make predictions
y_pred = model.predict(X_test)
```

[274]:
```
# Calculate Mean Absolute Error (MAE)
mae = mean_absolute_error(y_test, y_pred)

mae
```

[274]:
```
0.9400499999999999
```

Our Random Forest Regressor still has a MAE of 0.94, suggesting possible overfitting or missing key predictors. To improve performance, we can try scaling the data and reducing model complexity by limiting tree depth and increasing minimum samples per split. Since Random Forest may not capture complex feature interactions, testing **XGBoost** could improve predictions.

[276]:
```
#Calculate the mean squared error and r2 to provide better understanding of␣
 ↪accuracy
mse = mean_squared_error(y_test, y_pred)
r2 = r2_score(y_test, y_pred)

print(f"Mean Squared Error: {mse:.4f}")
print(f"R² Score: {r2:.4f}")
```

```
Mean Squared Error: 1.1815
R² Score: -0.0030
```

Our model is underperforming, with an MSE of 1.1815 and a negative R^2 score (-0.0030), meaning it fails to capture meaningful patterns in this dataset. The R^2 score of -0.0030 indicates that the model is barely better than guessing the mean severity level. This suggests that while the model has reduced its prediction errors, it still struggles to capture meaningful patterns in the data. The goal should be to reduce MSE below 1.0

while improving R^2 closer to 1.0. We can try hyperparameter tuning.

0.6.4 XGBoost Model

[292]:
```
model = xgb.XGBClassifier(objective='binary:logistic', # For binary␣
 ↪classification
                          n_estimators=100,        # Number of boosting␣
 ↪rounds
                          learning_rate=0.1,       # Step size shrinkage
                          max_depth=3)             # Maximum depth of a tree
model.fit(X_train, y_train)
```

[292]:
```
XGBClassifier(base_score=None, booster=None, callbacks=None,
              colsample_bylevel=None, colsample_bynode=None,
              colsample_bytree=None, device=None, early_stopping_rounds=None,
              enable_categorical=False, eval_metric=None, feature_types=None,
              gamma=None, grow_policy=None, importance_type=None,
              interaction_constraints=None, learning_rate=0.1, max_bin=None,
              max_cat_threshold=None, max_cat_to_onehot=None,
              max_delta_step=None, max_depth=3, max_leaves=None,
              min_child_weight=None, missing=nan, monotone_constraints=None,
              multi_strategy=None, n_estimators=100, n_jobs=None,
              num_parallel_tree=None, objective='multi:softprob', …)
```

[294]:
```
y_pred = model.predict(X_test)
```

[296]:
```
accuracy = accuracy_score(y_test, y_pred)
print("Accuracy:", accuracy)
```

```
Accuracy: 0.255
```

Our XGBoost model's accuracy of 25.5% and suggest it struggles to differentiate severity levels and may be predicting randomly. One issue could be class imbalance, so adjusting class weights can help ensure the model does not favor common severity levels.

0.7 Summary

This project aimed to analyze this COVID-19 public health dataset to determine which factors contribute to a variant's severity. Through correlation analysis and feature engineering, we identified key predictors such as Case Fatality Rate, Hospitalization Rate, and Mutation Count as strong indicators of variant severity. We tested multiple machine learning models, including Random Forest and XGBoost, but faced challenges with overfitting and low predictive accuracy. We applied feature selection techniques to improve model performance, but results indicated that severity classification is complex and may require additional data. Ultimately, this analysis provides valuable insights for public health decision-makers, helping them anticipate severe variants and allocate healthcare resources accordingly.