

hw1_50604230

September 16, 2024

1 DIC - Data cleaning and EDA

```
[116]: import pandas as pd
import requests
import re
import numpy as np
from scipy.signal import correlate
import plotly.graph_objects as go
from plotly.subplots import make_subplots
```

```
[117]: url = "https://covid.ourworldindata.org/data/owid-covid-data.csv"
```

2 (a) Load the dataset from the url

```
[119]: df = pd.read_csv(url)
df
```

```
[119]:
```

	iso_code	continent	location	date	total_cases	new_cases	\
0	AFG	Asia	Afghanistan	2020-01-05	0.0	0.0	
1	AFG	Asia	Afghanistan	2020-01-06	0.0	0.0	
2	AFG	Asia	Afghanistan	2020-01-07	0.0	0.0	
3	AFG	Asia	Afghanistan	2020-01-08	0.0	0.0	
4	AFG	Asia	Afghanistan	2020-01-09	0.0	0.0	
...	
429430	ZWE	Africa	Zimbabwe	2024-07-31	266386.0	0.0	
429431	ZWE	Africa	Zimbabwe	2024-08-01	266386.0	0.0	
429432	ZWE	Africa	Zimbabwe	2024-08-02	266386.0	0.0	
429433	ZWE	Africa	Zimbabwe	2024-08-03	266386.0	0.0	
429434	ZWE	Africa	Zimbabwe	2024-08-04	266386.0	0.0	

	new_cases_smoothed	total_deaths	new_deaths	new_deaths_smoothed	\
0	NaN	0.0	0.0	NaN	
1	NaN	0.0	0.0	NaN	
2	NaN	0.0	0.0	NaN	
3	NaN	0.0	0.0	NaN	
4	NaN	0.0	0.0	NaN	

...
429430		0.0	5740.0	0.0	0.0
429431		0.0	5740.0	0.0	0.0
429432		0.0	5740.0	0.0	0.0
429433		0.0	5740.0	0.0	0.0
429434		0.0	5740.0	0.0	0.0

	...	male_smokers	handwashing_facilities	hospital_beds_per_thousand	\
0	...	NaN	37.746		0.5
1	...	NaN	37.746		0.5
2	...	NaN	37.746		0.5
3	...	NaN	37.746		0.5
4	...	NaN	37.746		0.5

...
429430	...	30.7	36.791		1.7
429431	...	30.7	36.791		1.7
429432	...	30.7	36.791		1.7
429433	...	30.7	36.791		1.7
429434	...	30.7	36.791		1.7

	life_expectancy	human_development_index	population	\
0	64.83	0.511	41128772	
1	64.83	0.511	41128772	
2	64.83	0.511	41128772	
3	64.83	0.511	41128772	
4	64.83	0.511	41128772	

...
429430		61.49	0.571	16320539
429431		61.49	0.571	16320539
429432		61.49	0.571	16320539
429433		61.49	0.571	16320539
429434		61.49	0.571	16320539

	excess_mortality_cumulative_absolute	excess_mortality_cumulative	\
0		NaN	NaN
1		NaN	NaN
2		NaN	NaN
3		NaN	NaN
4		NaN	NaN

...
429430		NaN	NaN
429431		NaN	NaN
429432		NaN	NaN
429433		NaN	NaN
429434		NaN	NaN

excess_mortality	excess_mortality_cumulative_per_million
------------------	---

```

0          NaN          NaN
1          NaN          NaN
2          NaN          NaN
3          NaN          NaN
4          NaN          NaN
...
429430      NaN          NaN
429431      NaN          NaN
429432      NaN          NaN
429433      NaN          NaN
429434      NaN          NaN

```

[429435 rows x 67 columns]

3 (b) (i) Displaying the metadata info of columns of the dataset

```
[121]: df.info() # Trying to understand the dataset by its type and how well-built
         ↳ the data is
```

```

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 429435 entries, 0 to 429434
Data columns (total 67 columns):

```

#	Column	Non-Null Count	Dtype
0	iso_code	429435 non-null	object
1	continent	402910 non-null	object
2	location	429435 non-null	object
3	date	429435 non-null	object
4	total_cases	411804 non-null	float64
5	new_cases	410159 non-null	float64
6	new_cases_smoothed	408929 non-null	float64
7	total_deaths	411804 non-null	float64
8	new_deaths	410608 non-null	float64
9	new_deaths_smoothed	409378 non-null	float64
10	total_cases_per_million	411804 non-null	float64
11	new_cases_per_million	410159 non-null	float64
12	new_cases_smoothed_per_million	408929 non-null	float64
13	total_deaths_per_million	411804 non-null	float64
14	new_deaths_per_million	410608 non-null	float64
15	new_deaths_smoothed_per_million	409378 non-null	float64
16	reproduction_rate	184817 non-null	float64
17	icu_patients	39116 non-null	float64
18	icu_patients_per_million	39116 non-null	float64
19	hosp_patients	40656 non-null	float64
20	hosp_patients_per_million	40656 non-null	float64
21	weekly_icu_admissions	10993 non-null	float64
22	weekly_icu_admissions_per_million	10993 non-null	float64

23	weekly_hosp_admissions	24497	non-null	float64
24	weekly_hosp_admissions_per_million	24497	non-null	float64
25	total_tests	79387	non-null	float64
26	new_tests	75403	non-null	float64
27	total_tests_per_thousand	79387	non-null	float64
28	new_tests_per_thousand	75403	non-null	float64
29	new_tests_smoothed	103965	non-null	float64
30	new_tests_smoothed_per_thousand	103965	non-null	float64
31	positive_rate	95927	non-null	float64
32	tests_per_case	94348	non-null	float64
33	tests_units	106788	non-null	object
34	total_vaccinations	85417	non-null	float64
35	people_vaccinated	81132	non-null	float64
36	people_fully_vaccinated	78061	non-null	float64
37	total_boosters	53600	non-null	float64
38	new_vaccinations	70971	non-null	float64
39	new_vaccinations_smoothed	195029	non-null	float64
40	total_vaccinations_per_hundred	85417	non-null	float64
41	people_vaccinated_per_hundred	81132	non-null	float64
42	people_fully_vaccinated_per_hundred	78061	non-null	float64
43	total_boosters_per_hundred	53600	non-null	float64
44	new_vaccinations_smoothed_per_million	195029	non-null	float64
45	new_people_vaccinated_smoothed	192177	non-null	float64
46	new_people_vaccinated_smoothed_per_hundred	192177	non-null	float64
47	stringency_index	196190	non-null	float64
48	population_density	360492	non-null	float64
49	median_age	334663	non-null	float64
50	aged_65_older	323270	non-null	float64
51	aged_70_older	331315	non-null	float64
52	gdp_per_capita	328292	non-null	float64
53	extreme_poverty	211996	non-null	float64
54	cardiovasc_death_rate	328865	non-null	float64
55	diabetes_prevalence	345911	non-null	float64
56	female_smokers	247165	non-null	float64
57	male_smokers	243817	non-null	float64
58	handwashing_facilities	161741	non-null	float64
59	hospital_beds_per_thousand	290689	non-null	float64
60	life_expectancy	390299	non-null	float64
61	human_development_index	319127	non-null	float64
62	population	429435	non-null	int64
63	excess_mortality_cumulative_absolute	13411	non-null	float64
64	excess_mortality_cumulative	13411	non-null	float64
65	excess_mortality	13411	non-null	float64
66	excess_mortality_cumulative_per_million	13411	non-null	float64

dtypes: float64(61), int64(1), object(5)

memory usage: 219.5+ MB

3.1 Trying to understand the data and examine for any unusual data entries (like negative,zero,decimals)

```
[123]: df.describe() # There are no anomalies in the data
```

```
[123]:
```

	total_cases	new_cases	new_cases_smoothed	total_deaths	\
count	4.118040e+05	4.101590e+05	4.089290e+05	4.118040e+05	
mean	7.365292e+06	8.017360e+03	8.041026e+03	8.125957e+04	
std	4.477582e+07	2.296649e+05	8.661611e+04	4.411901e+05	
min	0.000000e+00	0.000000e+00	0.000000e+00	0.000000e+00	
25%	6.280750e+03	0.000000e+00	0.000000e+00	4.300000e+01	
50%	6.365300e+04	0.000000e+00	1.200000e+01	7.990000e+02	
75%	7.582720e+05	0.000000e+00	3.132860e+02	9.574000e+03	
max	7.758668e+08	4.423623e+07	6.319461e+06	7.057132e+06	

	new_deaths	new_deaths_smoothed	total_cases_per_million	\
count	410608.000000	409378.000000	411804.000000	
mean	71.852139	72.060873	112096.199396	
std	1368.322990	513.636567	162240.412419	
min	0.000000	0.000000	0.000000	
25%	0.000000	0.000000	1916.100500	
50%	0.000000	0.000000	29145.475000	
75%	0.000000	3.143000	156770.190000	
max	103719.000000	14817.000000	763598.600000	

	new_cases_per_million	new_cases_smoothed_per_million	\
count	410159.000000	408929.000000	
mean	122.357074	122.713844	
std	1508.778583	559.701638	
min	0.000000	0.000000	
25%	0.000000	0.000000	
50%	0.000000	2.794000	
75%	0.000000	56.253000	
max	241758.230000	34536.890000	

	total_deaths_per_million	...	male_smokers	handwashing_facilities	\
count	411804.000000	...	243817.000000	161741.000000	
mean	835.514313	...	33.097723	50.649264	
std	1134.932671	...	13.853948	31.905375	
min	0.000000	...	7.700000	1.188000	
25%	24.568000	...	22.600000	20.859000	
50%	295.089000	...	33.100000	49.542000	
75%	1283.817000	...	41.500000	82.502000	
max	6601.110000	...	78.100000	100.000000	

	hospital_beds_per_thousand	life_expectancy	human_development_index	\
count	290689.000000	390299.000000	319127.000000	

mean	3.106912	73.702098	0.722139
std	2.549205	7.387914	0.148903
min	0.100000	53.280000	0.394000
25%	1.300000	69.500000	0.602000
50%	2.500000	75.050000	0.740000
75%	4.210000	79.460000	0.829000
max	13.800000	86.750000	0.957000

	population	excess_mortality_cumulative_absolute \
count	4.294350e+05	1.341100e+04
mean	1.520336e+08	5.604765e+04
std	6.975408e+08	1.568691e+05
min	4.700000e+01	-3.772610e+04
25%	5.237980e+05	1.765000e+02
50%	6.336393e+06	6.815199e+03
75%	3.296952e+07	3.912804e+04
max	7.975105e+09	1.349776e+06

	excess_mortality_cumulative	excess_mortality \
count	13411.000000	13411.000000
mean	9.766431	10.925353
std	12.040658	24.560706
min	-44.230000	-95.920000
25%	2.060000	-1.500000
50%	8.130000	5.660000
75%	15.160000	15.575000
max	78.080000	378.220000

	excess_mortality_cumulative_per_million
count	13411.000000
mean	1772.666400
std	1991.892769
min	-2936.453100
25%	116.872242
50%	1270.801400
75%	2883.024150
max	10293.515000

[8 rows x 62 columns]

3.2 Cleaning the dataset

```
[125]: duplicates = df.duplicated() # check for any duplicated row entries
num = duplicates.sum()
print("No. of duplicated rows :", num)
```

No. of duplicated rows : 0

```
[126]: df.isnull().sum() # Lot of incomplete data (NaN values)
```

```
[126]: iso_code          0
continent        26525
location         0
date             0
total_cases      17631
...
population       0
excess_mortality_cumulative_absolute  416024
excess_mortality_cumulative          416024
excess_mortality                     416024
excess_mortality_cumulative_per_million  416024
Length: 67, dtype: int64
```

```
[127]: df.nunique() # Checking for unique values to understand the number of countries
↳ included and other features
```

```
[127]: iso_code          255
continent             6
location            255
date               1688
total_cases        36694
...
population          255
excess_mortality_cumulative_absolute  13205
excess_mortality_cumulative          4218
excess_mortality           5474
excess_mortality_cumulative_per_million  13351
Length: 67, dtype: int64
```

```
[128]: # Converting the date datatype to datetime pandas version
df['date'] = pd.to_datetime(df['date'])
```

4 (b) (ii) Finding the total number of infections and death cases for each country

```
[130]: uniq_code = df['iso_code'].unique()
uniq_coun = df['location'].unique()

# A dict to map each country code to country

coun = dict(zip(uniq_code, uniq_coun))

# Consider only the countries excluding the other unrelavent entries
uniq_noncoun_code = []
```

```

# Utilizing regex to remove the non-countries from country data
pattern = r'OWID\w*'
for code in uniq_code:
    if re.findall(pattern,code):
        uniq_noncoun_code.append(re.findall(pattern,code)[0])

print("Other entries in countries column:\n")
for code in uniq_noncoun_code:
    print(code,coun[code])

print("\n\n")

# separating the non-country entries from list of uncleaned country codes
uniq_coun_code = set(uniq_code) - set(uniq_noncoun_code)
uniq_coun_code = list(uniq_coun_code)

# Finding out the max and min time stamp by each country for normalizing the
↳ constraints to a set date and time
df2 = df.filter(items =
↳ ['iso_code', 'location', 'date', 'total_cases', 'total_deaths', 'total_cases_per_million'],
↳ axis = 1)
df2 = df2[(df2['iso_code'].isin(uniq_coun_code))]
df3 = df2.dropna(subset=['total_cases', 'total_deaths']) #cleaned data without
↳ nulls by dropping the null entries
print(df3)

min_date = df3['date'].min()
max_date = df3['date'].max()

for country in uniq_coun_code:
    if (df3[df3['iso_code'] == country].min()['date'] < min_date):
        min_date = df3[df3['iso_code'] == country].min()['date']
    if (df3[df3['iso_code'] == country].max()['date'] > max_date):
        max_date = df3[df3['iso_code'] == country].max()['date']

# Capturing dataset from the common min and max dates for normalising on the
↳ time period
df3 = df3[(df3['date'] >= min_date) & (df3['date'] <= max_date)]
new_df3 = df3[df3['date'] == max_date]
df6 = new_df3 # for future use
new_df3 = new_df3.
↳ reset_index(drop=True)[['location', 'total_cases', 'total_deaths', 'total_cases_per_million']]
↳ # resetting index for readability and count

```

Other entries in countries column:

OWID_AFR Africa
 OWID_ASI Asia
 OWID_ENG England
 OWID_EUR Europe
 OWID_EUN European Union (27)
 OWID_HIC High-income countries
 OWID_KOS Kosovo
 OWID_LIC Low-income countries
 OWID_LMC Lower-middle-income countries
 OWID_NAM North America
 OWID_CYN Northern Cyprus
 OWID_NIR Northern Ireland
 OWID_OCE Oceania
 OWID_SCT Scotland
 OWID_SAM South America
 OWID_UMC Upper-middle-income countries
 OWID_WLS Wales
 OWID_WRL World

	iso_code	location	date	total_cases	total_deaths	\
0	AFG	Afghanistan	2020-01-05	0.0	0.0	
1	AFG	Afghanistan	2020-01-06	0.0	0.0	
2	AFG	Afghanistan	2020-01-07	0.0	0.0	
3	AFG	Afghanistan	2020-01-08	0.0	0.0	
4	AFG	Afghanistan	2020-01-09	0.0	0.0	
...	
429430	ZWE	Zimbabwe	2024-07-31	266386.0	5740.0	
429431	ZWE	Zimbabwe	2024-08-01	266386.0	5740.0	
429432	ZWE	Zimbabwe	2024-08-02	266386.0	5740.0	
429433	ZWE	Zimbabwe	2024-08-03	266386.0	5740.0	
429434	ZWE	Zimbabwe	2024-08-04	266386.0	5740.0	

	total_cases_per_million
0	0.00
1	0.00
2	0.00
3	0.00
4	0.00
...	...
429430	16577.57
429431	16577.57
429432	16577.57
429433	16577.57
429434	16577.57

[390042 rows x 6 columns]

5 Country-wise total infections/cases & deaths

```
[132]: new_df3
```

```
[132]:
```

	location	total_cases	total_deaths	total_cases_per_million
0	Afghanistan	235214.0	7998.0	5796.468
1	Albania	335047.0	3605.0	118491.020
2	Algeria	272139.0	6881.0	5984.050
3	American Samoa	8359.0	34.0	172831.600
4	Andorra	48015.0	159.0	602280.440
..
228	Vietnam	11624000.0	43206.0	116612.400
229	Wallis and Futuna	3760.0	9.0	326928.100
230	Yemen	11945.0	2159.0	312.509
231	Zambia	349842.0	4077.0	17359.357
232	Zimbabwe	266386.0	5740.0	16577.570

```
[233 rows x 4 columns]
```

5.1 Data analysis by top 10 countries with highest death & infection cases

```
[134]: import plotly.express as px

# Sort by total_deaths and get the top 10
top_deaths = new_df3.sort_values(by='total_deaths', ascending=False).head(10)
top_deaths = \
    top_deaths[['location', 'total_deaths', 'total_cases', 'total_cases_per_million']]

# Sort by total_cases and get the top 10
top_cases = new_df3.sort_values(by='total_cases', ascending=False).head(10)
top_cases = top_cases[['location', 'total_cases']]
```

```
[135]: top_deaths
```

```
[135]:
```

	location	total_deaths	total_cases	total_cases_per_million
221	United States	1193165.0	103436829.0	302859.500
28	Brazil	702116.0	37511921.0	178367.940
95	India	533623.0	45041748.0	31598.860
172	Russia	403188.0	24268728.0	166703.840
132	Mexico	334551.0	7619458.0	59243.242
220	United Kingdom	232112.0	24974629.0	366308.000
163	Peru	220975.0	4526977.0	135232.810
102	Italy	197307.0	26781078.0	449202.940
78	Germany	174979.0	38437756.0	457123.100
72	France	168091.0	38997490.0	606706.000

```
[136]: top_cases
```

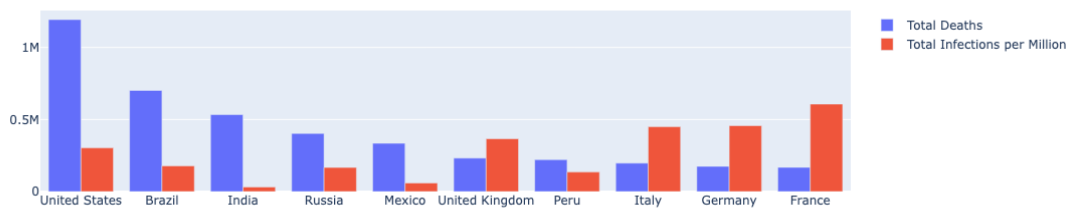
```
[136]:
```

	location	total_cases
221	United States	103436829.0
42	China	99373219.0
95	India	45041748.0
72	France	38997490.0
78	Germany	38437756.0
28	Brazil	37511921.0
196	South Korea	34571873.0
104	Japan	33803572.0
102	Italy	26781078.0
220	United Kingdom	24974629.0

6 Graph Visualisation of top 10 total deaths by country

```
[138]: fig = go.Figure(data=[
    go.Bar(name='Total Deaths', x=top_deaths['location'],
    ↪y=top_deaths['total_deaths']),
    go.Bar(name='Total Infections per Million', x=top_deaths['location'],
    ↪y=top_deaths['total_cases_per_million'])
    # Considering cases per million cz of the scale size
])

fig.update_layout(barmode='group')
fig.show()
```



6.0.1 The above graph depicts the top 10 total deaths by country with thier total infections per million respectively, for understanding how the the infections resulted in death and how hard did the covid impact the world.

7 (b) (iii) Creating graph visualizations to suggest vaccination to old people

```
[141]: # Considering the latest available data of each country for analysis
df4 = df[df['date']== max_date]
df4 = df4[df4['iso_code'].isin(uniq_coun_code)]
df4 =
↳df4[['iso_code','location','total_cases','total_deaths','total_cases_per_million','positive
    'people_vaccinated'],
↳'people_fully_vaccinated','total_vaccinations_per_hundred'],
↳'people_vaccinated_per_hundred',
    'people_fully_vaccinated_per_hundred','median_age'],
↳'aged_65_older','population']]
df4.info()
```

```
<class 'pandas.core.frame.DataFrame'>
```

```
Index: 234 entries, 1673 to 429434
```

```
Data columns (total 15 columns):
```

#	Column	Non-Null Count	Dtype
0	iso_code	234 non-null	object
1	location	234 non-null	object
2	total_cases	233 non-null	float64
3	total_deaths	233 non-null	float64
4	total_cases_per_million	233 non-null	float64
5	positive_rate	0 non-null	float64
6	total_vaccinations	2 non-null	float64
7	people_vaccinated	2 non-null	float64
8	people_fully_vaccinated	2 non-null	float64
9	total_vaccinations_per_hundred	2 non-null	float64
10	people_vaccinated_per_hundred	2 non-null	float64
11	people_fully_vaccinated_per_hundred	2 non-null	float64
12	median_age	197 non-null	float64
13	aged_65_older	191 non-null	float64
14	population	234 non-null	int64

```
dtypes: float64(12), int64(1), object(2)
```

```
memory usage: 29.2+ KB
```

7.1 Grouping the dataset with respect to median age of the population

```
[143]: df3 = df[df['iso_code'].isin(uniq_coun_code)] # Considering all the countries
        ↪only
dft3 = df3.groupby(['median_age']).agg({          # Grouping the data on median age
        ↪for understanding the data on age factor
        'people_vaccinated_per_hundred': 'max',
        'people_fully_vaccinated_per_hundred' : 'max',
        'population': 'max',
        'total_cases_per_million' : 'max',
        'total_deaths_per_million' : 'max'
    }).reset_index()                             # Resetting the index of the
        ↪resultant data entries for graph readability
dft3 = dft3.dropna()
dft3
```

```
[143]:
```

	median_age	people_vaccinated_per_hundred	\
0	15.1	23.84	
1	16.4	42.40	
2	16.7	29.04	
3	16.8	50.99	
4	17.0	17.22	
..	
135	45.5	86.95	
137	46.2	95.62	
138	46.6	77.82	
139	47.9	86.28	
140	48.2	84.47	

	people_fully_vaccinated_per_hundred	population	total_cases_per_million	\
0	20.92	26207982	376.028	
1	27.64	47249588	3638.641	
2	28.33	17723312	417.332	
3	43.57	35588996	3016.162	
4	14.54	99010216	986.445	
..	
135	85.66	47558632	292302.160	
137	86.75	10270857	543733.100	
138	76.24	83369840	457123.100	
139	81.21	59037472	449202.940	
140	83.40	123951696	270433.800	

	total_deaths_per_million
0	12.445
1	76.766
2	10.512
3	76.453

```

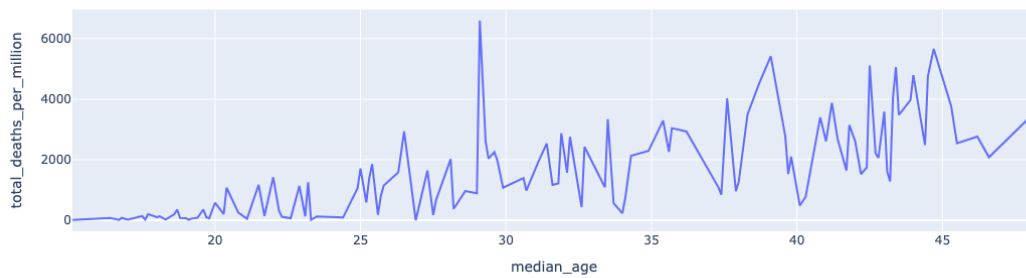
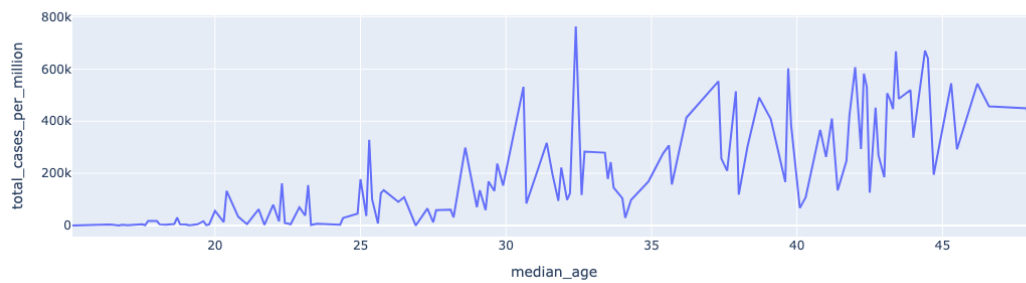
4                14.395
..              ...
135             2547.692
137             2765.556
138             2080.947
139             3309.459
140             597.564

```

```
[131 rows x 6 columns]
```

7.2 The trend of cases and deaths on median aged population

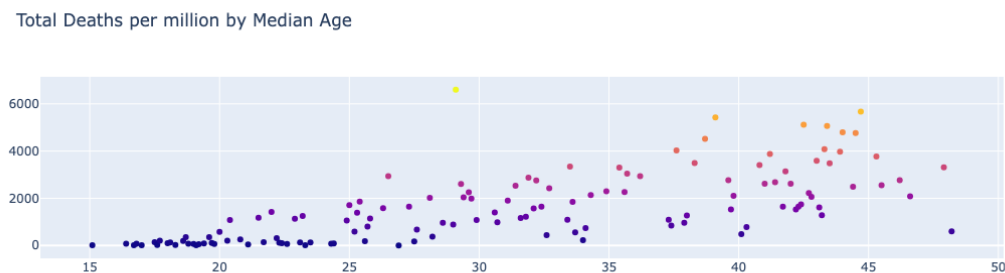
```
[145]: fig = px.line(dft3, x='median_age', y='total_cases_per_million')
fig.show()
fig2 = px.line(dft3, x='median_age', y='total_deaths_per_million')
fig2.show()
```



7.2.1 Above graphs depicts that as age increases the probability of getting infected and death is higher. As observed, people below 32 yrs are less susceptible to infection than the people aged higher. But can be better understood in a scatter plot as shown below which gives a better sense on how death toll increases rapidly with age.

```
[147]: fig = go.Figure(data=go.Scatter(x=dft3['median_age'],
                                     y=dft3['total_deaths_per_million'],
                                     mode='markers',
                                     marker_color=dft3['total_deaths_per_million'],
                                     text=dft3['population'])))

fig.update_layout(title='Total Deaths per million by Median Age')
fig.show()
```



7.2.2 As seen in the above graph, as the median aged population increases, the probability of death due to covid infection rises rapidly.

7.3 Grouping by the % population above 65 yrs as a result targetting the old aged people

```
[150]: dft4 = df.groupby(['aged_65_older']).agg({
    # Grouping the data
    # according to the percentage of population aged 65 or more
    'people_vaccinated_per_hundred': 'max',
    # Considering the max
    # values as we need the most recent data and the attribute is unique to all
    # countries
    'people_fully_vaccinated_per_hundred' : 'max',
    'population': 'max',
    'total_cases_per_million' : 'max',
    'total_deaths_per_million' : 'max',
}).reset_index()
dft4 = dft4.dropna()
```

7.4 The below 2 graphs helps to visualize the impact of covid on older population and suggest them vaccination

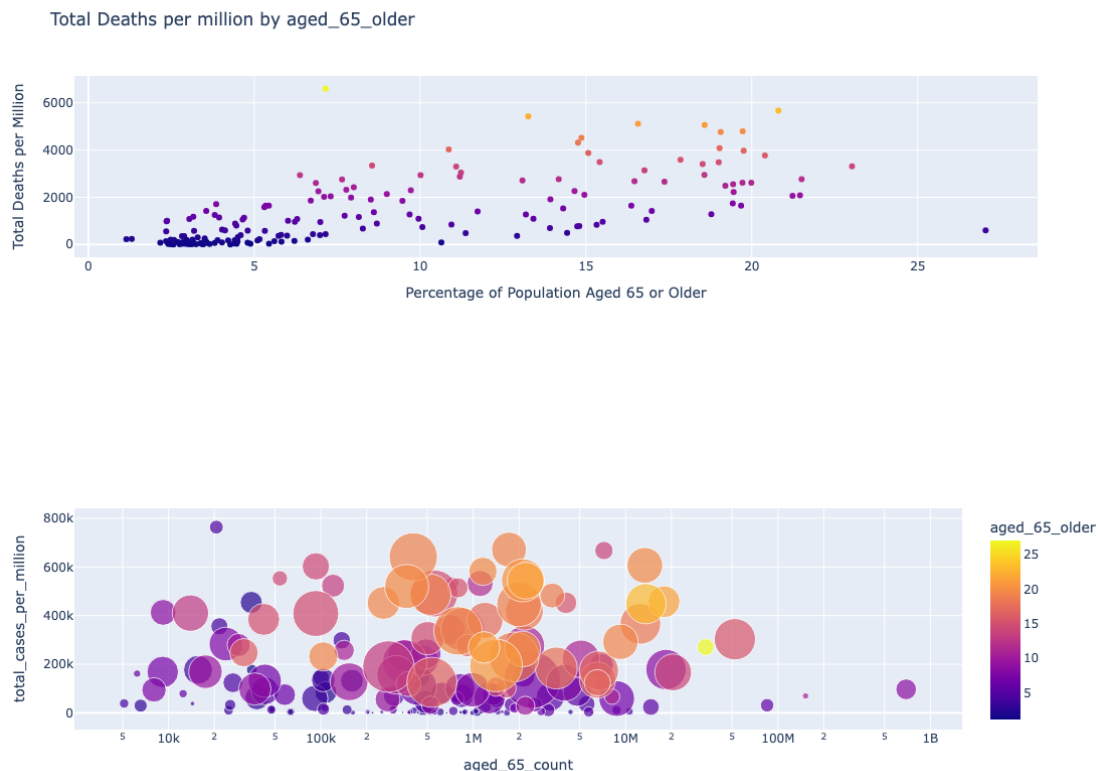
```
[152]: fig1 = go.Figure(data=go.Scatter(x=dft4['aged_65_older'],
                                        y=dft4['total_deaths_per_million'],
                                        mode='markers',
                                        marker_color=dft4['total_deaths_per_million'],
                                        text=dft4['population'])))

fig1.update_layout(title='Total Deaths per million by aged_65_older',
                    xaxis_title='Percentage of Population Aged 65 or Older',
                    yaxis_title='Total Deaths per Million')
fig1.show()

dft4['aged_65_count'] = dft4['aged_65_older']/100 * dft4['population'] #
    ↪ calculating the 65+ yrs aged people out of each country population for
    ↪ better stats

fig2 = px.scatter(dft4, x="aged_65_count", y="total_cases_per_million",
                  size="total_deaths_per_million", color="aged_65_older",
                  hover_name="aged_65_older", log_x=True, size_max=40) # Using
    ↪ log function for better spread of data and visualization
fig2.show()

# For figure 2 : Size of scatter bubbles implies the total deaths per million
```



The 1st graph depicts how the rise in the aged population directly impacts the death cases in the population. If we observe close enough, we are able to draw a conclusion on how the percentage of aged population increasing leads to linear increase in deaths cases, hence deriving to the conclusion that aged people are much more vulnerable to the disease. 2nd graph shows how the age_65_count increases, the size of the bubble(denoting the death cases) and infections increases rapidly with the aged population as seen by the color gradient too.

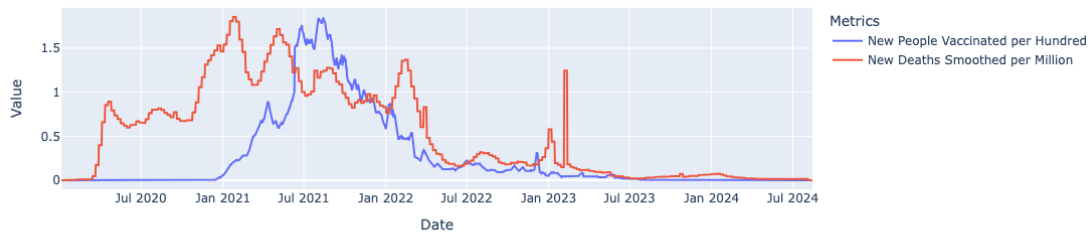
7.5 Utilizing the world data which was provided in the dataset to show the effect of vaccination on new deaths

```
[155]: test_set = df[df['iso_code']== "OWID_WRL"]
com =
    ↳test_set[['date', 'new_deaths_smoothed_per_million', 'total_deaths_per_million', 'new_vaccinat
com = com.fillna(0) # Filling NaN values to zero for graph readability and no
    ↳loss of data rows
fig = px.scatter(com, x="date", y="new_deaths_smoothed_per_million",
                 size="new_deaths_smoothed", color="new_cases_smoothed",
                 hover_name="new_deaths_smoothed", size_max=30)

fig3 = go.Figure()
fig3.add_trace(go.Scatter(x=com['date'],
    ↳y=com['new_people_vaccinated_smoothed_per_hundred']* 7, mode='lines',
    ↳name='New People Vaccinated per Hundred'))
fig3.add_trace(go.Scatter(x=com['date'],
    ↳y=com['new_deaths_smoothed_per_million'], mode='lines', name='New Deaths,
    ↳Smoothed per Million'))
fig3.update_layout(
    title='New Deaths Smoothed per Million and New People Vaccinated per
    ↳Hundred Over Time',
    xaxis_title='Date',
    yaxis_title='Value',
    legend_title='Metrics'
)

# Show the figure
fig3.show()
```

New Deaths Smoothed per Million and New People Vaccinated per Hundred Over Time



The above graph can be used to help the older population understand the importance of vaccination as shown in the graph where the rise of new vaccinated people decreased the death toll. Also, deriving new insights on the data during Jan 2022 & 2023 which were new variants of covid.

8 (b) (iv) Making a visualization to warn your neighborhood about the trend of covid.

```
[158]: df5 = test_set # Considering the world data
fig = make_subplots(rows=1, cols=2,
                    subplot_titles=('New Cases and Deaths Trend', 'Total Cases_
                    ↪and Deaths',
                    'Vaccination Progress', 'Hospitalization_
                    ↪Rates'))

# Add Trend of New Cases and Deaths
fig.add_trace(go.Scatter(x=df5['date'], y=df5['new_cases_smoothed'],
                    ↪mode='lines', name='New Cases'), row=1, col=1)
fig.add_trace(go.Scatter(x=df5['date'], y=df5['new_deaths_smoothed'],
                    ↪mode='lines', name='New Deaths'), row=1, col=1)

fig.update_yaxes(type="log", row=1, col=1) # Applying log to y-axis for more_
                    ↪readable output as scales don't match

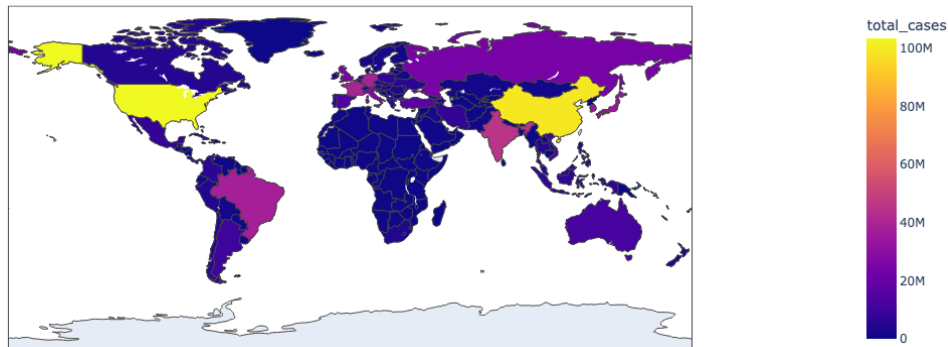
fig.add_trace(go.Scatter(x=df5['date'], y=df5['total_cases'], name='Total_
                    ↪Cases'), row=1, col=2,)
fig.add_trace(go.Scatter(x=df5['date'], y=df5['total_deaths'], name='Total_
                    ↪Deaths'), row=1, col=2)

fig.update_yaxes(type="log", row=1, col=2) # Applying log to y-axis for more_
                    ↪readable output as scales don't match
```

```
fig.update_layout(title_text='COVID-19 Trends and Statistics', showlegend=True)
fig.show()
```



```
[159]: fig = px.choropleth(df6, locations="iso_code",
                           color="total_cases",
                           hover_name="location",
                           color_continuous_scale=px.colors.sequential.Plasma)
fig.update_layout(
    margin=dict(l=20, r=10, t=10, b=10))
fig.show()
```



The above graphs depicts how badly the covid impacted the whole world leading to a total of 776 million infections and 7 million deaths approx. From year 2020 to 2023 end, covid really impacted the whole populations seeing the steady rise of cases and deaths with new variants nullifying the vaccination and crowd control. As seen on the world map, it really reached all corners of the world impacting the world and leading to may countries with higher infection and death rates.

9 (c) How effective is the vaccination?

9.1 (i) Understanding the problem statement, we can apply few conditions and constraints on the dataset to come up with a detailed visualization on how well the vaccine has done in eliminating the chances of infection and its cause of death.

9.1.1 Lets apply the following conditions for deepened visualization and conclusion on the problem statement :

1. Apply time-frame to normalize the data to all origins
2. Key variables being new cases, new deaths, Hospitalisation rates, people vaccinated and population
3. Evaluate based on infection rates, hospitalization rates, mortality rates

9.2 (ii) Explain your approach to your problem statement

Firstly, we need to understand on how to arrive to a conclusion on the problem statement. For that, we need proper analysis and visualization of the dataset on factors mentioned in the above conditions like infection rates before and after vaccination and so on. Secondly, based on the metrics we choose we need to select the data attributes and analyze thier relationship between the problem statement and other attributes.

Then we go on to process the data and clean it in all aspects and set the time frame to analyze the data in a better constraint. After succesful data processing we try to model the effect of vaccination on graphs and do statistical analysis for better understanding of the data to determine if higher vaccination rates are associated with lower case counts and fewer severe outcomes, which helps us to reach our hypothesis.

9.3 (iii) Perform data cleaning to get the pure data for this problem

```
[164]: duplicates = df.duplicated() # check for any duplicated row entries
num = duplicates.sum()
print("No. of duplicated rows :",num,'\n')
df # Consider the dataset to be cleaned
```

No. of duplicated rows : 0

```
[164]:
```

	iso_code	continent	location	date	total_cases	new_cases	\
0	AFG	Asia	Afghanistan	2020-01-05	0.0	0.0	
1	AFG	Asia	Afghanistan	2020-01-06	0.0	0.0	
2	AFG	Asia	Afghanistan	2020-01-07	0.0	0.0	
3	AFG	Asia	Afghanistan	2020-01-08	0.0	0.0	
4	AFG	Asia	Afghanistan	2020-01-09	0.0	0.0	
...	
429430	ZWE	Africa	Zimbabwe	2024-07-31	266386.0	0.0	
429431	ZWE	Africa	Zimbabwe	2024-08-01	266386.0	0.0	
429432	ZWE	Africa	Zimbabwe	2024-08-02	266386.0	0.0	
429433	ZWE	Africa	Zimbabwe	2024-08-03	266386.0	0.0	

429434	ZWE	Africa	Zimbabwe	2024-08-04	266386.0	0.0
--------	-----	--------	----------	------------	----------	-----

	new_cases_smoothed	total_deaths	new_deaths	new_deaths_smoothed	\
0	NaN	0.0	0.0	NaN	
1	NaN	0.0	0.0	NaN	
2	NaN	0.0	0.0	NaN	
3	NaN	0.0	0.0	NaN	
4	NaN	0.0	0.0	NaN	
...	
429430	0.0	5740.0	0.0	0.0	
429431	0.0	5740.0	0.0	0.0	
429432	0.0	5740.0	0.0	0.0	
429433	0.0	5740.0	0.0	0.0	
429434	0.0	5740.0	0.0	0.0	

	male_smokers	handwashing_facilities	hospital_beds_per_thousand	\
0	NaN	37.746	0.5	
1	NaN	37.746	0.5	
2	NaN	37.746	0.5	
3	NaN	37.746	0.5	
4	NaN	37.746	0.5	
...	
429430	30.7	36.791	1.7	
429431	30.7	36.791	1.7	
429432	30.7	36.791	1.7	
429433	30.7	36.791	1.7	
429434	30.7	36.791	1.7	

	life_expectancy	human_development_index	population	\
0	64.83	0.511	41128772	
1	64.83	0.511	41128772	
2	64.83	0.511	41128772	
3	64.83	0.511	41128772	
4	64.83	0.511	41128772	
...	
429430	61.49	0.571	16320539	
429431	61.49	0.571	16320539	
429432	61.49	0.571	16320539	
429433	61.49	0.571	16320539	
429434	61.49	0.571	16320539	

	excess_mortality_cumulative_absolute	excess_mortality_cumulative	\
0	NaN	NaN	
1	NaN	NaN	
2	NaN	NaN	
3	NaN	NaN	
4	NaN	NaN	

```

...
429430      NaN      NaN
429431      NaN      NaN
429432      NaN      NaN
429433      NaN      NaN
429434      NaN      NaN

```

```

      excess_mortality  excess_mortality_cumulative_per_million
0                NaN                NaN
1                NaN                NaN
2                NaN                NaN
3                NaN                NaN
4                NaN                NaN

```

```

...
429430      NaN      NaN
429431      NaN      NaN
429432      NaN      NaN
429433      NaN      NaN
429434      NaN      NaN

```

[429435 rows x 67 columns]

```

[165]: df_cleaned = df[(df['date'] >= min_date) & (df['date'] <= max_date)] #
      ↳ Considering a common time-frame for analysis of data
df_cleaned =
      ↳ df_cleaned[['date', 'iso_code', 'location', 'new_cases_smoothed_per_million', 'new_deaths_smoothed_per_million',
      ↳ 'new_vaccinations_smoothed_per_million', 'new_people_vaccinated_smoothed', 'new_people_vaccinated_smoothed_per_hundred']]
      # Considering the important factor attributes for analysis
df7 = df_cleaned
dft7 = df_cleaned

```

```

[166]: df_cleaned.isnull().sum() # Checking for incomplete data

```

```

[166]: date                0
      iso_code              0
      location              0
      new_cases_smoothed_per_million    20362
      new_deaths_smoothed_per_million    19913
      weekly_icu_admissions_per_million    418307
      weekly_hosp_admissions_per_million    404806
      new_vaccinations_smoothed_per_million    234343
      new_people_vaccinated_smoothed    237188
      new_people_vaccinated_smoothed_per_hundred    237188
      population              0
      people_vaccinated_per_hundred    348266
      dtype: int64

```

```
[167]: # Trying to fill the NaN values by estimation with nearest data points
test11 =
    ↪df_cleaned[['new_cases_smoothed_per_million','new_deaths_smoothed_per_million','weekly_icu_
    ↪
    ↪'new_vaccinations_smoothed_per_million','new_people_vaccinated_smoothed','new_people_vaccin
    ↪interpolate()
test11[['date','iso_code','location']] =
    ↪df_cleaned[['date','iso_code','location']] # because interpolation works on
    ↪numericals only
new_order =
    ↪['date','iso_code','location','new_cases_smoothed_per_million','new_deaths_smoothed_per_mil
    ↪
    ↪'new_vaccinations_smoothed_per_million','new_people_vaccinated_smoothed','new_people_vaccin
test11 = test11[new_order]
test11 = test11.dropna()
test11.reset_index(drop=True, inplace=True) # Resetting the index values for
    ↪each row
test11
```

```
[167]:
```

	date	iso_code	location	new_cases_smoothed_per_million	\
0	2020-04-15	CHL	Chile	20.209	
1	2020-04-16	CHL	Chile	20.209	
2	2020-04-17	CHL	Chile	20.209	
3	2020-04-18	CHL	Chile	20.209	
4	2020-04-19	CHL	Chile	20.479	
...	
357203	2024-07-31	ZWE	Zimbabwe	0.000	
357204	2024-08-01	ZWE	Zimbabwe	0.000	
357205	2024-08-02	ZWE	Zimbabwe	0.000	
357206	2024-08-03	ZWE	Zimbabwe	0.000	
357207	2024-08-04	ZWE	Zimbabwe	0.000	

	new_deaths_smoothed_per_million	weekly_icu_admissions_per_million	\
0	0.336	9.947	
1	0.336	9.896	
2	0.336	9.335	
3	0.336	8.570	
4	0.387	9.182	
...	
357203	0.000	1.892	
357204	0.000	1.892	
357205	0.000	1.892	
357206	0.000	1.892	
357207	0.000	1.892	

	weekly_hosp_admissions_per_million	\
0	28.056	

1	27.903
2	29.484
3	30.861
4	31.525
...	...
357203	1.577
357204	1.577
357205	1.577
357206	1.577
357207	1.577

	new_vaccinations_smoothed_per_million	new_people_vaccinated_smoothed \
0	137.612565	2674.745201
1	138.031414	2683.029668
2	138.450262	2691.314136
3	138.869110	2699.598604
4	139.287958	2707.883072
...
357203	69.000000	332.000000
357204	69.000000	332.000000
357205	69.000000	332.000000
357206	69.000000	332.000000
357207	69.000000	332.000000

	new_people_vaccinated_smoothed_per_hundred \
0	0.013361
1	0.013403
2	0.013445
3	0.013487
4	0.013529
...	...
357203	0.002000
357204	0.002000
357205	0.002000
357206	0.002000
357207	0.002000

	people_vaccinated_per_hundred	population
0	12.844615	19603736
1	12.793846	19603736
2	12.743077	19603736
3	12.692308	19603736
4	12.641538	19603736
...
357203	39.450000	16320539
357204	39.450000	16320539
357205	39.450000	16320539

357206	39.450000	16320539
357207	39.450000	16320539

[357208 rows x 12 columns]

```
[168]: test11.isnull().sum() # Data NaN free
```

```
[168]: date          0
      iso_code      0
      location      0
      new_cases_smoothed_per_million  0
      new_deaths_smoothed_per_million  0
      weekly_icu_admissions_per_million  0
      weekly_hosp_admissions_per_million  0
      new_vaccinations_smoothed_per_million  0
      new_people_vaccinated_smoothed  0
      new_people_vaccinated_smoothed_per_hundred  0
      people_vaccinated_per_hundred  0
      population      0
      dtype: int64
```

```
[169]: dft7 = df_cleaned.dropna() # Dataset cleaned by dropping all NaN
      ↪ values
      dft7.reset_index(drop=True, inplace=True) # Resetting the index values for each
      ↪ row
      dft7
```

```
[169]:
```

	date	iso_code	location	new_cases_smoothed_per_million	\
0	2020-12-25	CHL	Chile	99.166	
1	2020-12-26	CHL	Chile	99.166	
2	2020-12-27	CHL	Chile	109.884	
3	2021-01-04	CHL	Chile	127.916	
4	2021-01-05	CHL	Chile	127.916	
...	
6606	2023-02-15	ESP	Spain	18.142	
6607	2023-02-22	ESP	Spain	18.074	
6608	2023-03-29	ESP	Spain	22.632	
6609	2023-04-26	ESP	Spain	32.458	
6610	2023-05-24	ESP	Spain	32.924	

	new_deaths_smoothed_per_million	weekly_icu_admissions_per_million	\
0	1.863	16.834	
1	1.863	16.834	
2	2.214	16.527	
3	2.338	17.803	
4	2.338	17.905	
...	

6606	0.308	1.766
6607	0.254	1.556
6608	0.284	1.619
6609	0.335	1.998
6610	0.299	2.691

	weekly_hosp_admissions_per_million \
0	61.825
1	63.661
2	66.110
3	73.710
4	79.220
...	...
6606	27.440
6607	29.311
6608	35.136
6609	43.546
6610	39.719

	new_vaccinations_smoothed_per_million	new_people_vaccinated_smoothed \
0	244.0	4779.0
1	202.0	3960.0
2	140.0	2743.0
3	3.0	51.0
4	13.0	250.0
...
6606	258.0	164.0
6607	189.0	137.0
6608	127.0	117.0
6609	50.0	65.0
6610	30.0	68.0

	new_people_vaccinated_smoothed_per_hundred	population \
0	0.024	19603736
1	0.020	19603736
2	0.014	19603736
3	0.000	19603736
4	0.001	19603736
...
6606	0.000	47558632
6607	0.000	47558632
6608	0.000	47558632
6609	0.000	47558632
6610	0.000	47558632

	people_vaccinated_per_hundred
0	0.03

1	0.04
2	0.04
3	0.05
4	0.05
...	...
6606	86.93
6607	86.93
6608	86.94
6609	86.94
6610	86.95

[6611 rows x 12 columns]

9.4 (c) (iv) Implement your approach to this problem and justify your hypothesis

9.4.1 Hypothesis : Higher vaccination rates directly impacts the significant reduction in new COVID-19 cases, hospitalizations, and deaths. Consequently, proving the effectiveness of the vaccine to be really good.

```
[171]: testc = test11.groupby(['date']).agg({                # Grouping the data by date to
    ↪consider the trend over time
        'new_cases_smoothed_per_million' : 'sum',    # Taking the sum to consider
    ↪the world data on a given day
        'new_deaths_smoothed_per_million' : 'sum'
    }).reset_index()

fig = go.Figure()

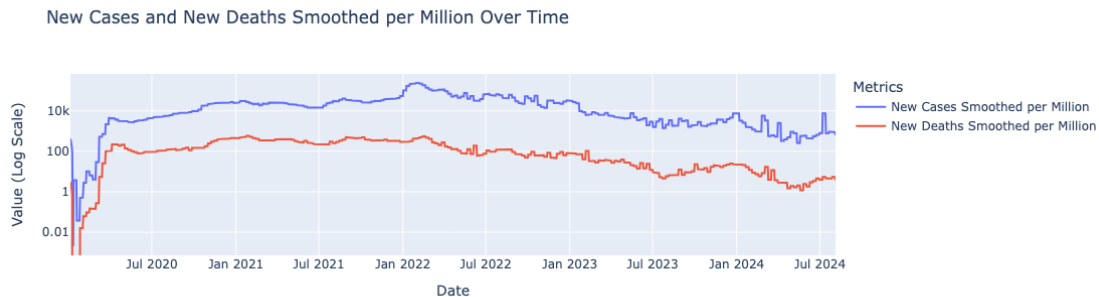
# Add the time series plot with log scale for the y-axis
fig.add_trace(
    go.Scatter(x=testc['date'], y=testc['new_cases_smoothed_per_million'],
    ↪mode='lines', name='New Cases Smoothed per Million')
)

fig.add_trace(
    go.Scatter(x=testc['date'], y=testc['new_deaths_smoothed_per_million'],
    ↪mode='lines', name='New Deaths Smoothed per Million')
)

fig.update_layout(
    title='New Cases and New Deaths Smoothed per Million Over Time',
    xaxis_title='Date',
    yaxis_title='Value (Log Scale)',
    legend_title='Metrics'
)
```

```
fig.update_yaxes(
    type='log'
)

fig.show()
```



The above graph depicts the new cases and deaths smoothed over a week (as the cases and deaths have lag in interpreting the real data). Observing the above trend, the number of new infections decreased by 28 times and death cases by 110 times. Thus, concluding on somekind of measure or vaccine (to verify) effectively worked to bring down the trend in covid.

```
[173]: # considering a time frame for better analysis and lesser data points for less
        ↳ cluttered outputs
start_date = '2021-02-01'
end_date = '2024-01-31'
test12 = test11[(test11['date'] >= start_date) & (test11['date'] <= end_date)]
test12 = test12.groupby(['date']).agg({
    'new_cases_smoothed_per_million': 'sum',
    'new_deaths_smoothed_per_million': 'sum',
    'new_people_vaccinated_smoothed_per_hundred': 'sum',
    'weekly_icu_admissions_per_million': 'sum',
    'weekly_hosp_admissions_per_million': 'sum'
}).reset_index()

# Convert New People Vaccinated Smoothed per Hundred to per Million
test12['new_people_vaccinated_smoothed_per_million'] =
    ↳ test12['new_people_vaccinated_smoothed_per_hundred'] * 10

fig = px.line(
    test12,
    x="date",
    y=[
        'new_cases_smoothed_per_million',
```

```

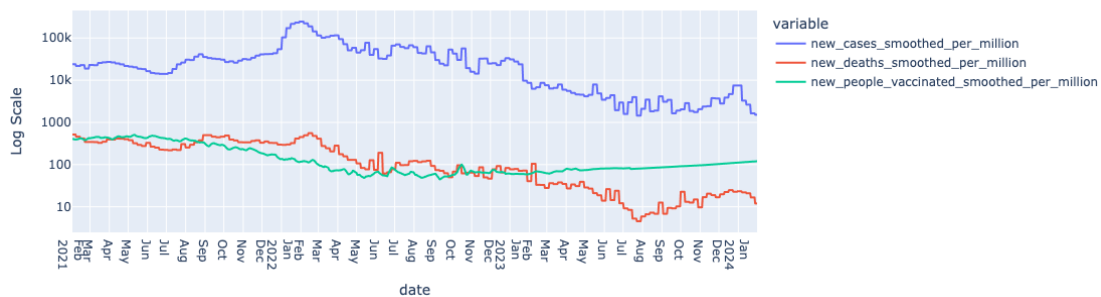
        'new_deaths_smoothed_per_million',
        'new_people_vaccinated_smoothed_per_million'
    ],
    hover_data={"date": "%B %d, %Y"},
    labels={
        'new_cases_smoothed_per_million': 'New Cases Smoothed per Million',
        'new_deaths_smoothed_per_million': 'New Deaths Smoothed per Million',
        'new_people_vaccinated_smoothed_per_million': 'New People Vaccinated_
↪Smoothed per Million'
    }
)

fig.update_xaxes(
    dtick="M1",
    tickformat="%b\n%Y"
)

fig.update_yaxes(
    type='log',
    title_text='Log Scale'
)

fig.show()

```



Checking the possibility of the vaccine being the effective measure taken. We can see that as new people getting vaccinated increases, it lowers the new infections and new deaths, showing its effectiveness.

```

[175]: test13 = dft7.groupby(['date',]).agg({                                # Grouping the data on_
    ↪date for time data
        'weekly_icu_admissions_per_million' : 'sum',                        # sum bcz considering_
    ↪all the data for a given date
        'weekly_hosp_admissions_per_million': 'sum',
        'new_deaths_smoothed_per_million' : 'sum',

```

```

        'new_people_vaccinated_smoothed_per_hundred': 'sum',
        'people_vaccinated_per_hundred' : 'mean'           # mean bcz it tells people
        ↪ vaccinated for every 100 people & as for the whole population
    }).reset_index()

test13['new_people_vaccinated_smoothed_per_million'] =
    ↪ test13['new_people_vaccinated_smoothed_per_hundred'] * 10
test13['daily_hosp_admissions_per_million'] =
    ↪ test13['weekly_hosp_admissions_per_million']/7
test13['daily_icu_admissions_per_million'] =
    ↪ test13['weekly_icu_admissions_per_million']/7

fig2 = px.scatter(test13, x="new_people_vaccinated_smoothed_per_million",
    ↪ y="daily_hosp_admissions_per_million",
                    size="daily_icu_admissions_per_million",
    ↪ color="new_deaths_smoothed_per_million",
                    hover_name="new_deaths_smoothed_per_million", size_max=40)

fig2.show()
test14 = test13

# Set 'date' as index for resampling
test14.set_index('date', inplace=True)

# Aggregate data by month
monthly_data = test14.resample('ME').agg({
    'new_people_vaccinated_smoothed_per_million': 'sum',
    'daily_hosp_admissions_per_million': 'sum',
    'daily_icu_admissions_per_million': 'sum',
    'new_deaths_smoothed_per_million': 'sum'
}).reset_index()

fig = px.bar(
    monthly_data,
    x='date',
    y='new_deaths_smoothed_per_million',
    hover_data={
        'daily_hosp_admissions_per_million': True,
        'daily_icu_admissions_per_million': True,
        'new_deaths_smoothed_per_million': True
    },
    color='new_people_vaccinated_smoothed_per_million',
    labels={'new_deaths_smoothed_per_million': 'New deaths smoothed per
    ↪ million'},
    height=400,

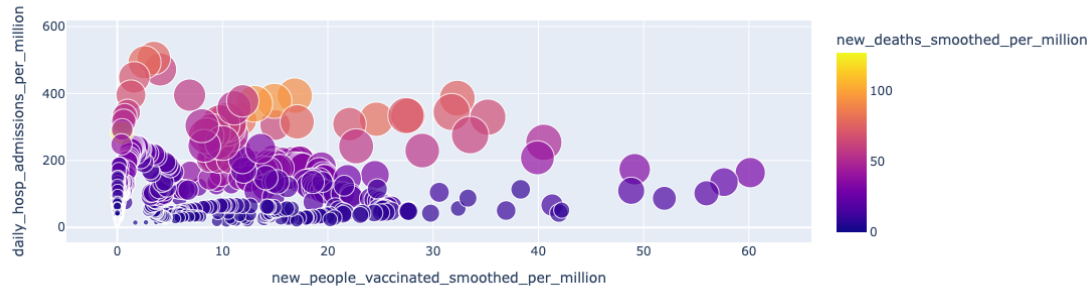
```

```

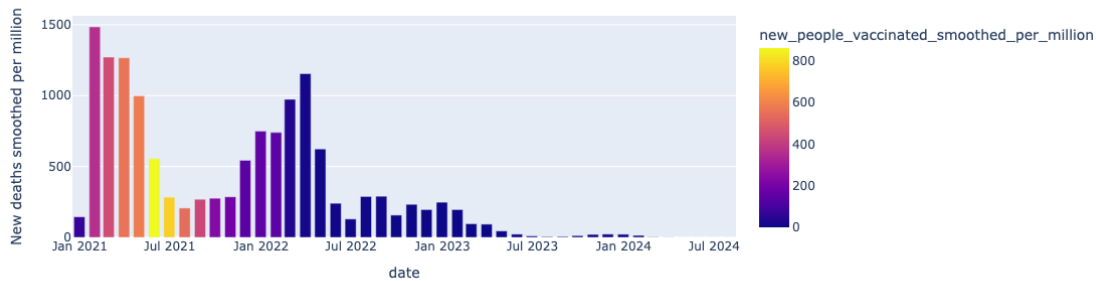
    title='Monthly Vaccination and Admissions Data'
)

fig.show()

```



Monthly Vaccination and Admissions Data



The 1st graph tells the downward trend on daily hospitalizations and icu admits(the size of bubble) as new people get vaccinated. The 2nd graph depicts the new deaths trend by time, observing the new people getting vaccinated wave in Feb 2021 to Jan 2022 leading to the decline in the new deaths, thus succesfully representing the effectiveness of the vaccine on people (The trend from Jan 2022 is the rise of new covid variants).

10 (d) How long does the virus take on average to kill a person if it does kill a person after infection?

10.1 (i) Explain your approach to this problem.

As we need to come up with a certain metric to analyze how long the virus takes to kill a person on infection, we would require the exact dates to compute it. But

our dataset doesn't have those attributes required. But we can approach it the other way by using the new cases and new deaths smoothed to a week to figure out the lag between a new case and a new death for all countries. By calculating the mean lag between each of the countries we would end up with the approximate day average of the virus to kill a person.

10.2 (ii) Perform data cleaning to get the pure data for this problem.

1. Consider only the countries out of the whole dataset
2. Filter out the columns to relevant ones which will be used for the problem
3. Drop the null values out from the data (as very less NaN values for the filtered attributes so dropping will not raise bias)
4. Convert the date column to date-time for easier computation

10.3 (iii) Implement your approach and compute the estimate.

```
[182]: # Filter relevant columns and removing NaN values for cleaning the data
test17 = df[(df['iso_code'].isin(uniq_coun_code))]
test17 = test17[['date', 'location', 'new_cases_smoothed_per_million',
↪ 'new_deaths_smoothed_per_million']].dropna() # Drops the rows with NaN values

# Convert 'date' column to datetime pandas version
test17['date'] = pd.to_datetime(test17['date'])

# Define a function to calculate the lag between new cases and new deaths using
↪ correlation
def estimate_lag(country_df):
    new_cases = country_df['new_cases_smoothed_per_million'].values
    new_deaths = country_df['new_deaths_smoothed_per_million'].values

    # Compute cross-correlation between new cases and new deaths using numpy
    correlation = correlate(new_cases, new_deaths, mode='full')
    lags = np.arange(-len(new_cases) + 1, len(new_deaths))

    # Find the lag with the maximum correlation
    best_lag = lags[np.argmax(correlation)]

    return best_lag

# Group the data by country (location) and apply the lag estimation function
lag_estimates = test17.groupby('location').apply(
    lambda x: estimate_lag(x[['new_cases_smoothed_per_million',
↪ 'new_deaths_smoothed_per_million']]), include_groups=False
)

# Calculate the average lag across all countries
average_lag = lag_estimates.mean()
```



```

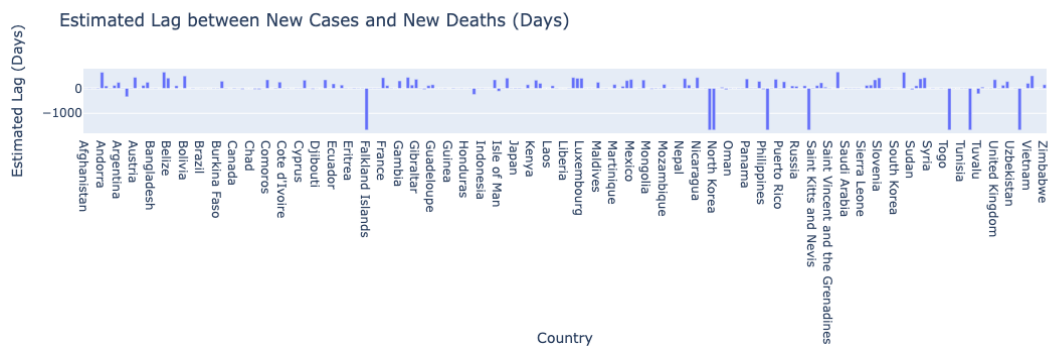
print(f"Average lag between new cases and new deaths across all countries:␣
↳{average_lag:.2f} days")

# Visualize the estimated lags per country
lag_estimates_df = lag_estimates.reset_index(name='lag')
fig = px.bar(lag_estimates_df, x='location', y='lag', title='Estimated Lag␣
↳between New Cases and New Deaths (Days)',
             labels={'lag': 'Estimated Lag (Days)', 'location': 'Country'})

fig.show()

```

Average lag between new cases and new deaths across all countries: 16.84 days



The above graph depicts each countries lag toward the new cases and new deaths. By calculating each countries lag by computing the correlation between them and finding the best correlated data which becomes the best lag for that country, we obtain the mean of all countries to figure out the lag. As “Average lag between new cases and new deaths” refers to the average amount of time it takes a person getting infected with a virus to that person dying from the virus. Thus, after the analysis, we found that a person approximately takes 16.84 days to die from the day of infection on average.

- 11 (e) While understanding the dataset, I came across the attribute stringency index and gdp_per_capita. I was wondering how did each of the countries handle this crisis with limited knowledge and resources. And did the strict rules imposed on the population and being self-sufficient help the countries handle the situation.

11.0.1 Findings/Hypothesis : Increase in stringency index (strict rules imposition) directly impacts in the reduction of deaths and cases. Whereas, availability of much resources and money considering gdp per capita doesnot effect the deaths and cases.

```
[186]: import pandas as pd
import plotly.graph_objects as go
from sklearn.preprocessing import MinMaxScaler

test20 = df[(df['iso_code'].isin(uniq_coun_code))]
test20 = test20[['location', 'gdp_per_capita', 'stringency_index',
    ↪ 'population_density', 'total_cases_per_million',
    ↪ 'total_deaths_per_million']].dropna()

# Normalize population density, deaths, and cases
scaler = MinMaxScaler()
test20[['population_density_scaled', 'total_deaths_scaled',
    ↪ 'total_cases_scaled']] = scaler.fit_transform(
    test20[['population_density', 'total_deaths_per_million',
    ↪ 'total_cases_per_million']]
)

# Group by location and aggregate the values
test20 = test20.groupby(['location']).agg({
    'gdp_per_capita': 'max',
    'population_density': 'mean',
    'total_deaths_scaled': 'sum',
    'total_cases_scaled': 'sum'
}).reset_index()

# Select top 50 countries based on GDP per capita
top_countries = test20.nlargest(50, 'gdp_per_capita')

fig = go.Figure()

fig.add_trace(go.Bar(
    x=top_countries['location'],
    y=top_countries['total_deaths_scaled'],
    name='Total Deaths Scaled',
```

```

        marker_color='crimson'
    ))

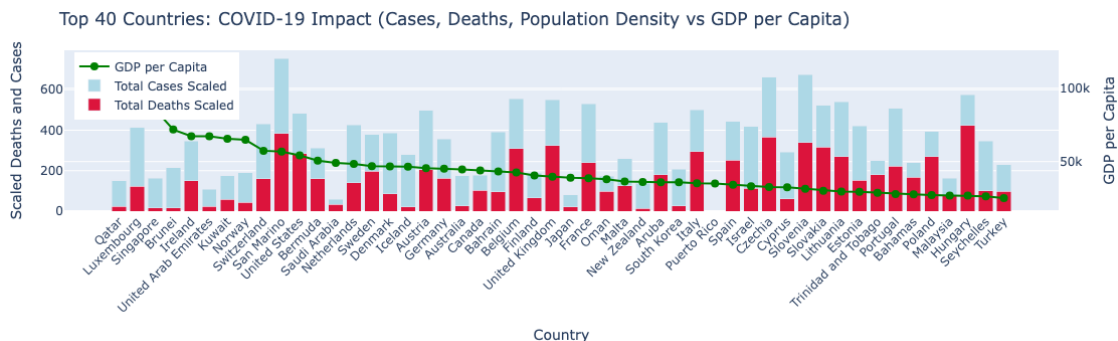
fig.add_trace(go.Bar(
    x=top_countries['location'],
    y=top_countries['total_cases_scaled'],
    name='Total Cases Scaled',
    marker_color='lightblue'
))

# Create a line plot for GDP per capita on a secondary y-axis
fig.add_trace(go.Scatter(
    x=top_countries['location'],
    y=top_countries['gdp_per_capita'],
    mode='lines+markers',
    name='GDP per Capita',
    yaxis='y2',
    line=dict(color='green', width=2),
    marker=dict(size=8, symbol='circle')
))

# Update layout with dual axes and better readability
fig.update_layout(
    title='Top 40 Countries: COVID-19 Impact (Cases, Deaths, Population Density,
    ↪vs GDP per Capita)',
    xaxis=dict(title='Country', tickangle=-45),
    yaxis=dict(title='Scaled Deaths and Cases'),
    yaxis2=dict(title='GDP per Capita', overlaying='y', side='right'),
    barmode='stack',
    legend=dict(x=0.01, y=0.99),
    margin=dict(l=60, r=60, b=150, t=50),
    xaxis_tickfont_size=12
)

fig.show()

```



The above graph depicts the effect of `gdp_per_capita` and availability of resources on the cases and deaths of covid. With the decrease in gdp per capita (referring how rich or poor a country is), some countries do show significant results like lesser deaths and cases with higher `gdp_per_capita` and lower income countries have higher deaths and cases but, many countries with much resources and money are not able to handle pandemic whereas the lowest gdp countries are able to control it. We can visualize it still more clearly in the below graph.

```
[188]: # Filter and aggregate the data
test20 = df[(df['iso_code'].isin(uniq_coun_code))]
test20 = test20[['gdp_per_capita', 'total_deaths_per_million']].dropna()

# Define bin parameters
start_point = test20['gdp_per_capita'].min()
freq = 10000 # Adjust frequency as needed for binning

# Create bins for gdp_per_capita
bins = pd.interval_range(start=start_point,
                        end=test20['gdp_per_capita'].max(),
                        freq=freq)

# Bin the data into intervals
test20['gdp_bin'] = pd.cut(test20['gdp_per_capita'], bins)

# Aggregate data by bins
aggregated_data = test20.groupby('gdp_bin').agg({
    'total_deaths_per_million': 'mean'
}).reset_index()

# Extract bin labels for plotting
aggregated_data['gdp_bin'] = aggregated_data['gdp_bin'].astype(str)

# Create a scatter plot
fig = go.Figure()

# Add total deaths line plot
fig.add_trace(go.Scatter(
    x=aggregated_data['gdp_bin'],
    y=aggregated_data['total_deaths_per_million'],
    mode='lines+markers',
    name='Total Deaths per Million',
    line=dict(color='red', width=2),
    marker=dict(size=10, symbol='circle'),
    text=aggregated_data['total_deaths_per_million'],
    hoverinfo='x+y+text'
```

```

))

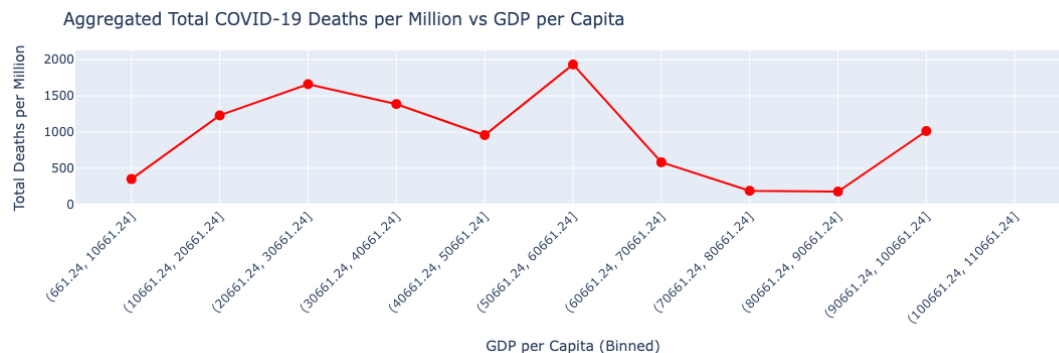
fig.update_layout(
    title='Aggregated Total COVID-19 Deaths per Million vs GDP per Capita',
    xaxis_title='GDP per Capita (Binned)',
    yaxis_title='Total Deaths per Million',
    margin=dict(l=60, r=60, b=50, t=50),
    xaxis=dict(title='GDP per Capita (Binned)', tickangle=-45),
    yaxis=dict(title='Total Deaths per Million'),
    hovermode='closest'
)

fig.show()

```

/var/folders/44/9qj8h9610f9cpmlbsc64dspw0000gn/T/ipykernel_10366/2989387455.py:1
8: FutureWarning:

The default of `observed=False` is deprecated and will be changed to `True` in a future version of pandas. Pass `observed=False` to retain current behavior or `observed=True` to adopt the future default and silence this warning.



From the above graph, it gets clear that better resource availability or money can't control the pandemic's effect on the population. Here, we are segregating the gdp per capita into intervals (bins) such that we can access a better view on it. Few low income countries really managed the pandemic with lower accessibility to resources and funds which few high income countries could not. This explains the importance of managing the existing resources and controlling it such a way that everyone is benefited from it, rather than just having the accessibility to funds and resources.

```

[190]: import pandas as pd
import plotly.graph_objects as go

# Filter and aggregate the data
test20 = df[(df['iso_code'].isin(uniq_coun_code))]

```

```

test20 = test20[['stringency_index', 'total_cases_per_million']].dropna()

# Define the start point and bin frequency
start_point = 15
freq = 3

# Adjust the start and end for binning
bins = pd.interval_range(start=start_point,
                        end=test20['stringency_index'].max(),
                        freq=freq)

test20['stringency_bin'] = pd.cut(test20['stringency_index'], bins)

# Aggregate data by bins
aggregated_data = test20.groupby('stringency_bin').agg({
    'total_cases_per_million': 'mean'
}).reset_index()

# Extract bin labels for plotting
aggregated_data['stringency_bin'] = aggregated_data['stringency_bin'].
    ↪ astype(str)

# Create a line plot
fig = go.Figure()

# Add total cases line plot
fig.add_trace(go.Scatter(
    x=aggregated_data['stringency_bin'],
    y=aggregated_data['total_cases_per_million'],
    mode='lines+markers',
    name='Total Cases per Million',
    line=dict(color='red', width=2), # Line style
    marker=dict(size=8, symbol='circle'), # Marker style
    text=aggregated_data['total_cases_per_million'], # Show the cases number
    ↪ on hover
    hoverinfo='x+y+text'
))

# Update layout for better readability
fig.update_layout(
    title='Aggregated Total COVID-19 Cases per Million vs Stringency Index',
    xaxis_title='Stringency Index (Binned)',
    yaxis_title='Total Cases per Million',
    margin=dict(l=60, r=60, b=50, t=50), # Adjust margins for better spacing
    xaxis=dict(title='Stringency Index (Binned)', tickangle=-45), # Rotate
    ↪ x-axis labels
    yaxis=dict(title='Total Cases per Million'),

```

```

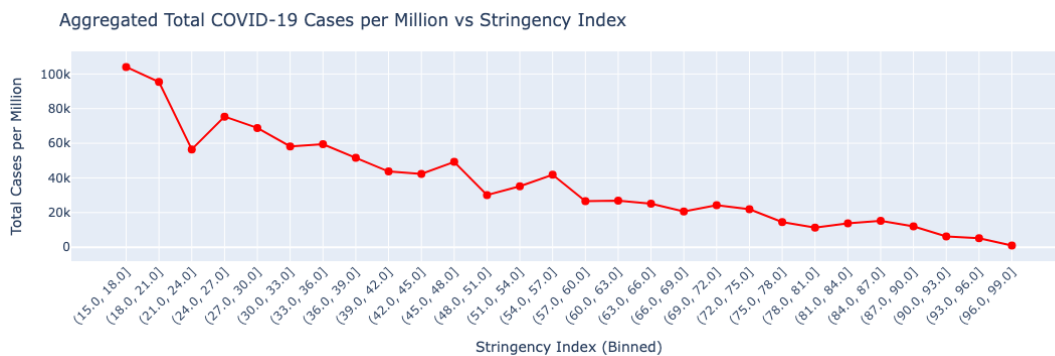
    hovermode='closest' # Ensure closest hover data
)

# Show the figure
fig.show()

```

/var/folders/44/9qj8h9610f9cpmlbsc64dspw0000gn/T/ipykernel_10366/34863613.py:20:
FutureWarning:

The default of `observed=False` is deprecated and will be changed to `True` in a future version of pandas. Pass `observed=False` to retain current behavior or `observed=True` to adopt the future default and silence this warning.



The above graph shows the impact of strict rules (Stringency Index(0-100) ;low value->lenient rules;high value->strict rules; rules such as lockdown, mask rules, no huge crowd gatherings etc.) imposed on the population directly reducing the number of cases. This implies that if governments followed certain protocols and thier implemen-
tation rigidly, it reduced the number of cases drastically. One main reason behind the success of it is, the covid disease being an airborne disease which is directly derived from the above stats. As the people were made aware of the precautionary measures on how covid spreads and the lockdown was in effect, the cases reduced because the virus couldn't find ways to rapidly spread to other uninfected people, which was due to very low human interactivity. Thus, succesfully overcoming and controlling the pandemic.