

shutterstsck\*

• Creating a COVID-19 vaccine analysis program would typically involve data analysis and visualization. Below are examples of Python code snippets using popular libraries like NumPy, Pandas, and Matplotlib to get you started.

### 1.Data Retrieval:

You can fetch COVID-19 vaccine data from sources like the CDC or WHO, or use publicly available datasets. Here's an example using Pandas to read a CSV file:

 import pandas as pd# Read vaccine data from a CSV filevaccine\_data = pd.read\_csv('vaccine\_data.csv')

# 2.Data Exploration:

You might want to explore the dataset by checking for missing values, data types, and basic statistics:

```
# Check for missing values
missing_values =
vaccine_data.isnull().sum()
# Get basic statistics
summary_stats = vaccine_data.describe()
```

## 3.Data Visualization:

Visualize vaccine distribution or coverage using Matplotlib or another plotting library: import matplotlib.pyplot as plt

```
# Plot vaccine coverage over time plt.figure(figsize=(10, 6)) plt.plot(vaccine_data['Date'], vaccine_data['Coverage']) plt.xlabel('Date')plt.ylabel('Vaccine Coverage (%)')plt.title('COVID-19 Vaccine Coverage Over Time')plt.show()
```

## 4.Data Analysis:

You can perform specific analyses, like calculating the average vaccine coverage or identifying regions with lower coverage:

```
# Calculate average vaccine
coverage
avg coverage =
vaccine data['Coverage'].mean()
# Find regions with lower coverage
low_coverage_regions =
vaccine_data[vaccine_data['Coverage'] < 50]</pre>
```

# • 5. Machine Learning (Optional):

If you have enough data, you can build predictive models. Here's a simple linear regression example using scikit-learn:

from sklearn.model\_selection import train\_test\_split from sklearn.linear\_model import LinearRegression

- # Split the data into training and testing sets
- X = vaccine\_data[['Population']]
- y = vaccine\_data['Coverage']
- X\_train, X\_test, y\_train, y\_test = train\_test\_split(X, y, test\_size=0.2, random\_state=42)
- # Create and train a linear
- regression model
- model = LinearRegression()model.fit(X\_train, y\_train)

 Relation between Total Vaccinations and Total Vaccinations per Hundred:

```
fig = px.scatter(new_df,x =

'total_vaccinations',y='total_vaccinations_per_hundred',

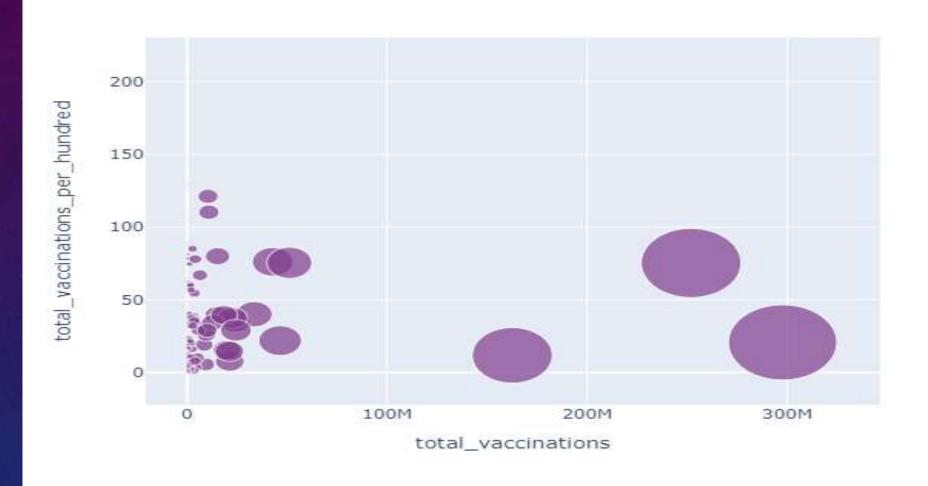
size='total_vaccinations', hover_name = 'country',size_max

= 50, title="Total vs Total vaccinations per hundred grouped

by Vaccines", color_discrete_sequence =

px.colors.qualitative.Bold) fig.show()
```

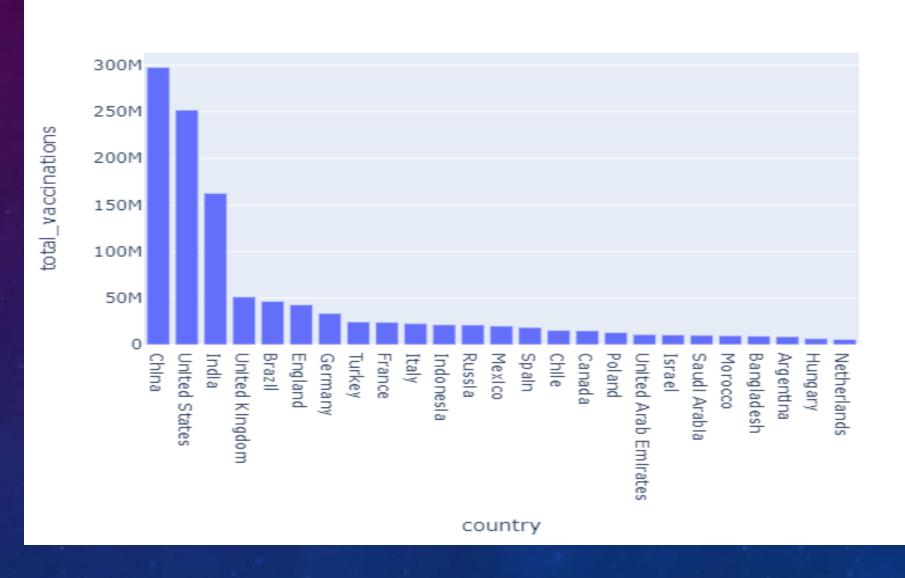
### Total vs Total vaccinations per hundred grouped by Vaccines



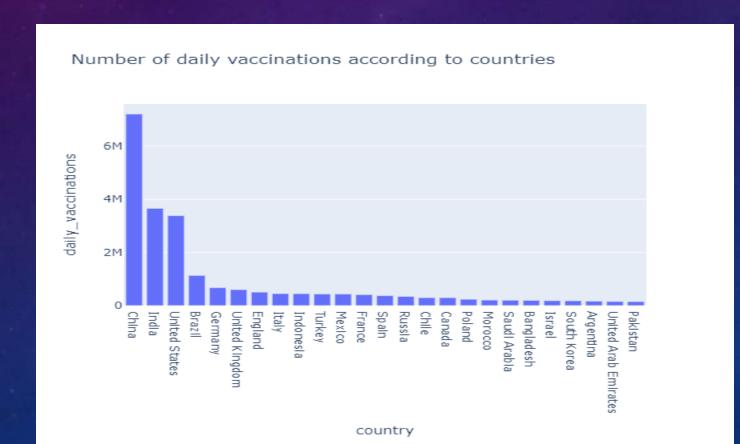
 What is the number of total vaccinations & daily vaccinations according to countries?

```
data =
new_df[['country','total_vaccinations']].nlargest(2)
5, 'total vaccinations') fig = px.bar(data, x =
'country',y = 'total vaccinations',title="Number of
total vaccinations according to countries",)
fig.show()
```

#### Number of total vaccinations according to countries



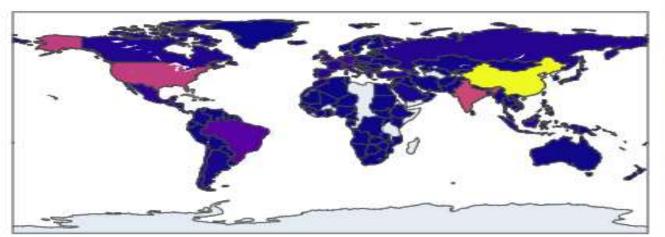
data =
 new\_df[['country', 'daily\_vaccinations']].nlargest(25, 'daily\_vaccinations') fig = px.bar(data, x = 'country', y =
 'daily\_vaccinations', title="Number of daily vaccinations according to countries",) fig.show()



# Daily Vaccinations per Countries:

```
fig = go.Choropleth(locations =
new df["country"],locationmode = 'country names', z
= new df['daily vaccinations'], text=
new df['country'],colorbar = dict(title= "Daily
Vaccinations")) data = [fig] layout = go.Layout(title =
'Daily Vaccinations per Countries') fig = dict(data =
data, layout = layout) iplot(fig)
```

### Daily Vaccinations per Countries





• The conclusions from the available data up to that point indicated that COVID-19 vaccines:

1.Are effective in preventing COVID-19 infection.

2. Significantly reduce the risk of severe illness, hospitalization, and death.

 3.Contribute to herd immunity, slowing the spread of the virus.

• 2. Have demonstrated safety profiles, with side effects typically being mild and temporary.

• 3. May require booster shots for ongoing protection due to the emergence of new variants.