

## **COVID VACCINES ANALYSIS**

### **DATA ANALYTICS WITH COGNOS -GROUP 2**

#### **INTRODUCTION**

The COVID-19 pandemic has presented an unprecedented global challenge, and the development and distribution of vaccines have emerged as critical tools in the fight against the virus. This project aims to undertake a comprehensive analysis of COVID-19 vaccine data, focusing on three key aspects: vaccine efficacy, distribution, and adverse effects. The analysis is driven by the urgent need to provide evidence-based insights to support policymakers, healthcare authorities, and researchers in making informed decisions regarding vaccine deployment and safety monitoring.

In the following sections, we will outline the step-by-step approach to conducting this analysis, beginning with data collection and preprocessing, followed by exploratory data analysis, statistical modeling, and data visualization. Our ultimate goal is to extract meaningful insights from the available data that can contribute to the development of optimized vaccination strategies, equitable distribution, and enhanced safety surveillance. This project not only addresses the immediate challenges posed by the pandemic but also contributes to the broader knowledge base surrounding vaccine development and deployment in the face of global health crises.

#### **PROBLEM STATEMENT**

The problem is to conduct an in-depth analysis of Covid-19 vaccine data, focusing on vaccine efficacy, distribution, and adverse effects. The goal is to provide insights that aid policymakers and health organizations in optimizing vaccine deployment strategies. This project involves data collection, data preprocessing, exploratory data analysis, statistical analysis, and visualization.

#### **DESIGN THINKING:**

To design a model for your COVID-19 vaccine data analysis project using data analysis techniques, you can follow these step-by-step guidelines:

### 1. Define the Problem:

The problem is to analyze COVID-19 vaccine data to assess vaccine efficacy, distribution patterns, and adverse effects, with the goal of informing evidence-based decision-making for effective pandemic management.

### 2. Data Collection:

Use relevant data from trusted sources, including vaccine efficacy trials, vaccination campaign data, and adverse event reports. Ensure that the data is comprehensive and up-to-date.

### 3. Data Preprocessing:

Clean the data by handling missing values, outliers, and inconsistencies. Normalize or scale numerical features if necessary. Encode categorical variables and create dummy variables. Merge and join datasets as needed to create a consolidated dataset for analysis.

### 4. Exploratory Data Analysis (EDA):

Perform EDA to gain an initial understanding of the data. This includes: Visualizing data distributions with histograms, box plots, and scatter plots. Calculating summary statistics like mean, median, and standard deviation. Identifying correlations and relationships among variables. Detecting outliers and anomalies. Creating geographical or regional visualizations if relevant.

### 5. Hypothesis Formulation:

Based on your EDA findings, formulate hypotheses related to vaccine efficacy, distribution disparities, or adverse effects. These hypotheses will guide your subsequent statistical analyses.

### 6. Statistical Analysis:

Conduct statistical tests and analyses to test your hypotheses. This may include: T-tests or ANOVA for comparing vaccine efficacy rates between groups. Regression analysis to understand factors influencing vaccine

distribution. Chi-squared tests for analyzing associations between adverse effects and demographic variables.

7. Data Visualization:

Create clear and informative data visualizations to communicate your findings. Utilize libraries like matplotlib, seaborn, or Plotly for plotting graphs and charts. Generate geographic visualizations (e.g., choropleth maps) to illustrate regional disparities in vaccine distribution.

8. Documentation:

Document your analysis process thoroughly, including code, data sources, and methodology. Ensure that your work is transparent and replicable.

**DEVELOPMENT PHASE**

IBM NAAN MUDHALVAN

# IMPORT NEEDED LIBRARIES

```
In [1]: import pandas as pd  
import matplotlib.pyplot as plt  
import seaborn as sns
```

# LOAD DATA

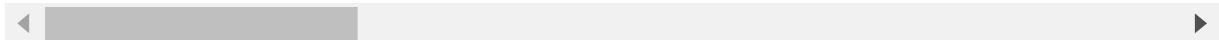
```
In [2]: vaccinations_by_manufacturer = pd.read_csv("D:/ibm naan mudhalvan/country_vaccinations_by_manufacturer.csv")  
vaccinations_data = pd.read_csv("D:/ibm naan mudhalvan/country_vaccinations.csv")
```

In [3]: vaccinations\_data

Out[3]:

	country	iso_code	date	total_vaccinations	people_vaccinated	people_fully_vaccinate
0	Afghanistan	AFG	2021-02-22	0.0	0.0	Na
1	Afghanistan	AFG	2021-02-23	NaN	NaN	Na
2	Afghanistan	AFG	2021-02-24	NaN	NaN	Na
3	Afghanistan	AFG	2021-02-25	NaN	NaN	Na
4	Afghanistan	AFG	2021-02-26	NaN	NaN	Na
...	...	...	...	...	...	...
86507	Zimbabwe	ZWE	2022-03-25	8691642.0	4814582.0	3473523.
86508	Zimbabwe	ZWE	2022-03-26	8791728.0	4886242.0	3487962.
86509	Zimbabwe	ZWE	2022-03-27	8845039.0	4918147.0	3493763.
86510	Zimbabwe	ZWE	2022-03-28	8934360.0	4975433.0	3501493.
86511	Zimbabwe	ZWE	2022-03-29	9039729.0	5053114.0	3510256.

86512 rows × 15 columns



In [4]: vaccinations\_by\_manufacturer

Out[4]:

	location	date	vaccine	total_vaccinations
0	Argentina	29-12-2020	Moderna	2
1	Argentina	29-12-2020	Oxford/AstraZeneca	3
2	Argentina	29-12-2020	Sinopharm/Beijing	1
3	Argentina	29-12-2020	Sputnik V	20481
4	Argentina	30-12-2020	Moderna	2
...	...	...	...	...
35618	European Union	29-03-2022	Oxford/AstraZeneca	67403106
35619	European Union	29-03-2022	Pfizer/BioNTech	600519998
35620	European Union	29-03-2022	Sinopharm/Beijing	2301516
35621	European Union	29-03-2022	Sinovac	1809
35622	European Union	29-03-2022	Sputnik V	1845103

35623 rows × 4 columns

## DATA PREPROCESSING AND EDA

In [5]: `vaccinations_by_manufacturer.info()  
vaccinations_data.info()`

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 35623 entries, 0 to 35622
Data columns (total 4 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   location        35623 non-null    object  
 1   date             35623 non-null    object  
 2   vaccine          35623 non-null    object  
 3   total_vaccinations 35623 non-null  int64  
dtypes: int64(1), object(3)
memory usage: 1.1+ MB
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 86512 entries, 0 to 86511
Data columns (total 15 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   country          86512 non-null    object  
 1   iso_code          86512 non-null    object  
 2   date              86512 non-null    object  
 3   total_vaccinations 43607 non-null  float64 
 4   people_vaccinated 41294 non-null  float64 
 5   people_fully_vaccinated 38802 non-null  float64 
 6   daily_vaccinations_raw 35362 non-null  float64 
 7   daily_vaccinations 86213 non-null  float64 
 8   total_vaccinations_per_hundred 43607 non-null  float64 
 9   people_vaccinated_per_hundred 41294 non-null  float64 
 10  people_fully_vaccinated_per_hundred 38802 non-null  float64 
 11  daily_vaccinations_per_million 86213 non-null  float64 
 12  vaccines          86512 non-null    object  
 13  source_name        86512 non-null    object  
 14  source_website     86512 non-null    object  
dtypes: float64(9), object(6)
memory usage: 9.9+ MB
```

In [6]: `vaccinations_by_manufacturer.rename(columns={'location': 'country'}, inplace=True)`

```
# Convert the 'date' column to datetime
vaccinations_by_manufacturer['date'] = pd.to_datetime(vaccinations_by_manufacturer['date'])
vaccinations_data['date'] = pd.to_datetime(vaccinations_data['date'])

# Check for common columns for merging
common_columns = ['country', 'date']

# Merge the datasets on the common columns
merged_df = pd.merge(vaccinations_data, vaccinations_by_manufacturer, on=common_columns)
```

In [8]: `merged_df.info()`

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 28954 entries, 0 to 28953
Data columns (total 17 columns):
 #   Column           Non-Null Count  Dtype  
---  --  
 0   country          28954 non-null   object  
 1   iso_code          28954 non-null   object  
 2   date              28954 non-null   datetime64[ns]
 3   total_vaccinations_x  27018 non-null   float64 
 4   people_vaccinated  26356 non-null   float64 
 5   people_fully_vaccinated  26442 non-null   float64 
 6   daily_vaccinations_raw  26497 non-null   float64 
 7   daily_vaccinations  28923 non-null   float64 
 8   total_vaccinations_per_hundred  27018 non-null   float64 
 9   people_vaccinated_per_hundred  26356 non-null   float64 
 10  people_fully_vaccinated_per_hundred  26442 non-null   float64 
 11  daily_vaccinations_per_million  28923 non-null   float64 
 12  vaccines           28954 non-null   object  
 13  source_name         28954 non-null   object  
 14  source_website      28954 non-null   object  
 15  vaccine             28954 non-null   object  
 16  total_vaccinations_y  28954 non-null   int64  
dtypes: datetime64[ns](1), float64(9), int64(1), object(6)
memory usage: 4.0+ MB
```

In [9]: `print(vaccinations_data.info())`

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 86512 entries, 0 to 86511
Data columns (total 15 columns):
 #   Column           Non-Null Count  Dtype  
---  --  
 0   country          86512 non-null   object  
 1   iso_code          86512 non-null   object  
 2   date              86512 non-null   datetime64[ns]
 3   total_vaccinations  43607 non-null   float64 
 4   people_vaccinated  41294 non-null   float64 
 5   people_fully_vaccinated  38802 non-null   float64 
 6   daily_vaccinations_raw  35362 non-null   float64 
 7   daily_vaccinations  86213 non-null   float64 
 8   total_vaccinations_per_hundred  43607 non-null   float64 
 9   people_vaccinated_per_hundred  41294 non-null   float64 
 10  people_fully_vaccinated_per_hundred  38802 non-null   float64 
 11  daily_vaccinations_per_million  86213 non-null   float64 
 12  vaccines           86512 non-null   object  
 13  source_name         86512 non-null   object  
 14  source_website      86512 non-null   object  
dtypes: datetime64[ns](1), float64(9), object(5)
memory usage: 9.9+ MB
None
```

```
In [10]: print(vaccinations_by_manufacturer.describe())
```

	total_vaccinations
count	3.562300e+04
mean	1.508357e+07
std	5.181768e+07
min	0.000000e+00
25%	9.777600e+04
50%	1.305506e+06
75%	7.932423e+06
max	6.005200e+08

In [11]: `print(merged_df.describe())`

	total_vaccinations_x	people_vaccinated	people_fully_vaccinated	\
count	2.701800e+04	2.635600e+04	2.644200e+04	
mean	4.145588e+07	2.173495e+07	1.781408e+07	
std	7.839012e+07	3.948117e+07	3.427411e+07	
min	1.000000e+00	1.000000e+00	1.000000e+00	
25%	2.568560e+06	1.526178e+06	1.001473e+06	
50%	1.175507e+07	6.129479e+06	5.180098e+06	
75%	4.690237e+07	2.884636e+07	1.870244e+07	
max	5.601818e+08	2.553624e+08	2.174990e+08	
	daily_vaccinations_raw	daily_vaccinations	\	
count	2.649700e+04	2.892300e+04		
mean	2.011788e+05	1.876768e+05		
std	3.716247e+05	3.296631e+05		
min	0.000000e+00	0.000000e+00		
25%	1.525700e+04	1.749550e+04		
50%	6.908900e+04	7.218400e+04		
75%	2.302590e+05	2.239550e+05		
max	6.586453e+06	3.506960e+06		
	total_vaccinations_per_hundred	people_vaccinated_per_hundred	\	
count	27018.000000	26356.000000		
mean	88.995541	45.428177		
std	67.574722	29.328559		
min	0.000000	0.000000		
25%	23.945000	15.550000		
50%	85.180000	52.430000		
75%	140.610000	71.880000		
max	261.820000	92.960000		
	people_fully_vaccinated_per_hundred	daily_vaccinations_per_million	\	
count	26442.000000	28923.000000		
mean	37.919123	4407.306573		
std	28.897718	3218.155886		
min	0.000000	0.000000		
25%	7.380000	1850.000000		
50%	38.760000	3611.000000		
75%	64.970000	6471.000000		
max	91.530000	19828.000000		
	total_vaccinations_y			
count	2.895400e+04			
mean	1.048228e+07			
std	3.127265e+07			
min	0.000000e+00			
25%	1.349192e+05			
50%	1.162808e+06			
75%	7.418144e+06			
max	3.306080e+08			

```
In [12]: print(vaccinations_data.isnull().sum())
```

```
country          0
iso_code         0
date            0
total_vaccinations 42905
people_vaccinated 45218
people_fully_vaccinated 47710
daily_vaccinations_raw 51150
daily_vaccinations      299
total_vaccinations_per_hundred 42905
people_vaccinated_per_hundred 45218
people_fully_vaccinated_per_hundred 47710
daily_vaccinations_per_million 299
vaccines          0
source_name        0
source_website      0
dtype: int64
```

```
In [13]: print(vaccinations_by_manufacturer.isnull().sum())
```

```
country          0
date            0
vaccine          0
total_vaccinations    0
dtype: int64
```

```
In [14]: print(merged_df.isnull().sum())
```

```
country          0
iso_code         0
date            0
total_vaccinations_x 1936
people_vaccinated 2598
people_fully_vaccinated 2512
daily_vaccinations_raw 2457
daily_vaccinations      31
total_vaccinations_per_hundred 1936
people_vaccinated_per_hundred 2598
people_fully_vaccinated_per_hundred 2512
daily_vaccinations_per_million 31
vaccines          0
source_name        0
source_website      0
vaccine           0
total_vaccinations_y 0
dtype: int64
```

```
In [15]: # Handle missing values
```

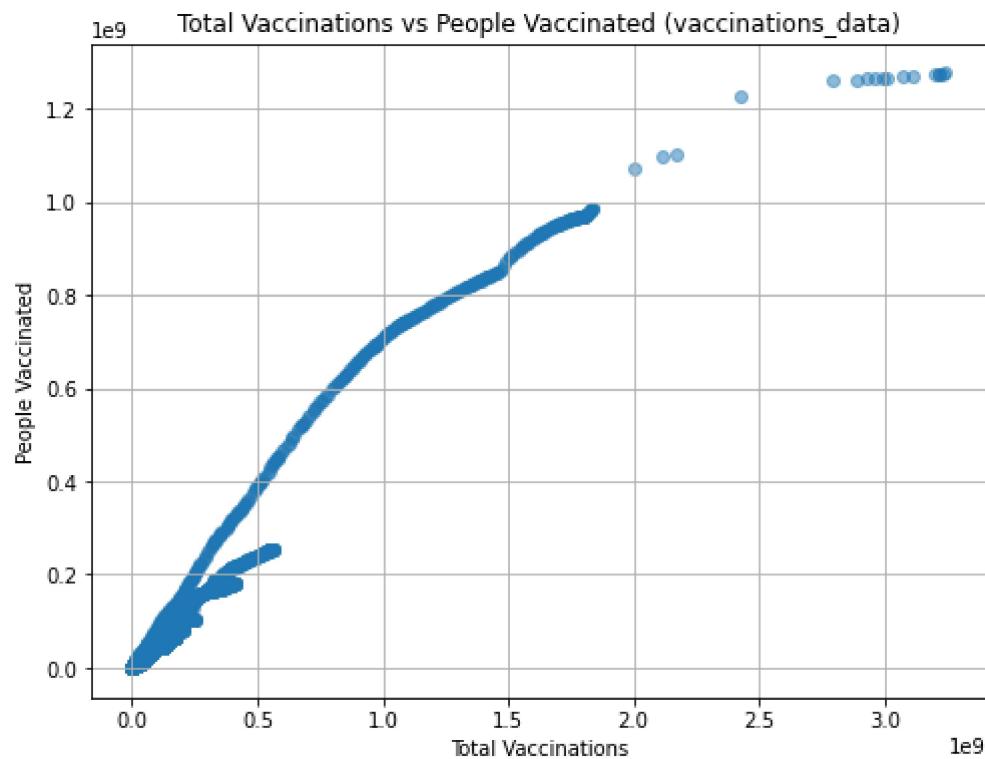
```
merged_df.dropna(subset=['total_vaccinations_x'], inplace=True)
merged_df.fillna(0, inplace=True) # Replace NaN with 0 for certain columns
merged_df.info()
```

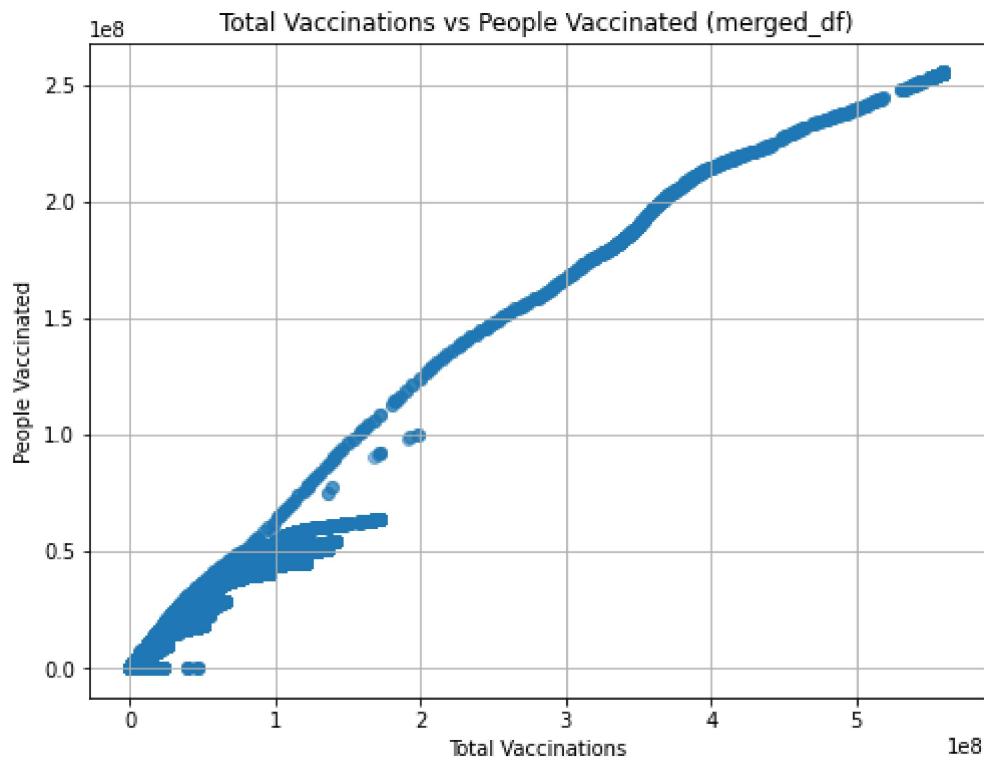
```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 27018 entries, 0 to 28953
Data columns (total 17 columns):
 #   Column           Non-Null Count  Dtype  
---  --  
 0   country          27018 non-null   object  
 1   iso_code          27018 non-null   object  
 2   date              27018 non-null   datetime64[ns]
 3   total_vaccinations_x  27018 non-null   float64 
 4   people_vaccinated  27018 non-null   float64 
 5   people_fully_vaccinated  27018 non-null   float64 
 6   daily_vaccinations_raw  27018 non-null   float64 
 7   daily_vaccinations  27018 non-null   float64 
 8   total_vaccinations_per_hundred  27018 non-null   float64 
 9   people_vaccinated_per_hundred  27018 non-null   float64 
 10  people_fully_vaccinated_per_hundred  27018 non-null   float64 
 11  daily_vaccinations_per_million  27018 non-null   float64 
 12  vaccines           27018 non-null   object  
 13  source_name         27018 non-null   object  
 14  source_website      27018 non-null   object  
 15  vaccine             27018 non-null   object  
 16  total_vaccinations_y  27018 non-null   int64  
dtypes: datetime64[ns](1), float64(9), int64(1), object(6)
memory usage: 3.7+ MB
```

## VISUALIZATION

```
In [16]: # Create a scatter plot for 'total_vaccinations' vs 'people_vaccinated' in 'vaccinations_data'
plt.figure(figsize=(8, 6))
plt.scatter(vaccinations_data['total_vaccinations'], vaccinations_data['people_vaccinated'])
plt.title('Total Vaccinations vs People Vaccinated (vaccinations_data)')
plt.xlabel('Total Vaccinations')
plt.ylabel('People Vaccinated')
plt.grid(True)
plt.show()

plt.figure(figsize=(8, 6))
plt.scatter(merged_df['total_vaccinations_x'], merged_df['people_vaccinated'])
plt.title('Total Vaccinations vs People Vaccinated (merged_df)')
plt.xlabel('Total Vaccinations')
plt.ylabel('People Vaccinated')
plt.grid(True)
plt.show()
```





```
In [17]: relevant_cols_manufacturer = ['total_vaccinations']
relevant_cols_data = ['total_vaccinations', 'people_vaccinated', 'people_fully_vaccinated']

# Create a correlation matrix for 'vaccinations_by_manufacturer'
corr_matrix_manufacturer = vaccinations_by_manufacturer[relevant_cols_manufacturer].corr()

# Create a correlation matrix for 'vaccinations_data'
corr_matrix_data = vaccinations_data[relevant_cols_data].corr()

# Create a figure with subplots
fig, axes = plt.subplots(1, 2, figsize=(14, 6))

# Plot the correlation matrix for 'vaccinations_by_manufacturer'
sns.heatmap(corr_matrix_manufacturer, annot=True, cmap='coolwarm', ax=axes[0])
axes[0].set_title('Correlation Matrix (vaccinations_by_manufacturer)')
plt.tight_layout()

# Plot the correlation matrix for 'vaccinations_data'
sns.heatmap(corr_matrix_data, annot=True, cmap='coolwarm', ax=axes[1])
axes[1].set_title('Correlation Matrix (vaccinations_data)')
plt.tight_layout()

plt.show()

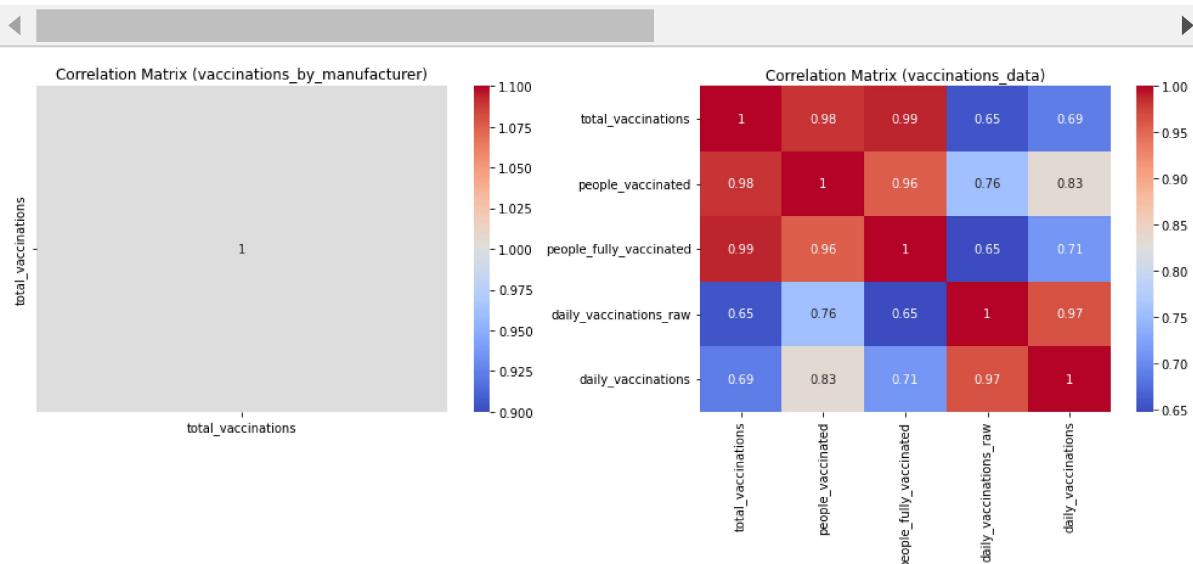
relevant_cols_merged = ['total_vaccinations_x', 'people_vaccinated', 'people_fully_vaccinated', 'daily_vaccinations_raw', 'daily_vaccinations']

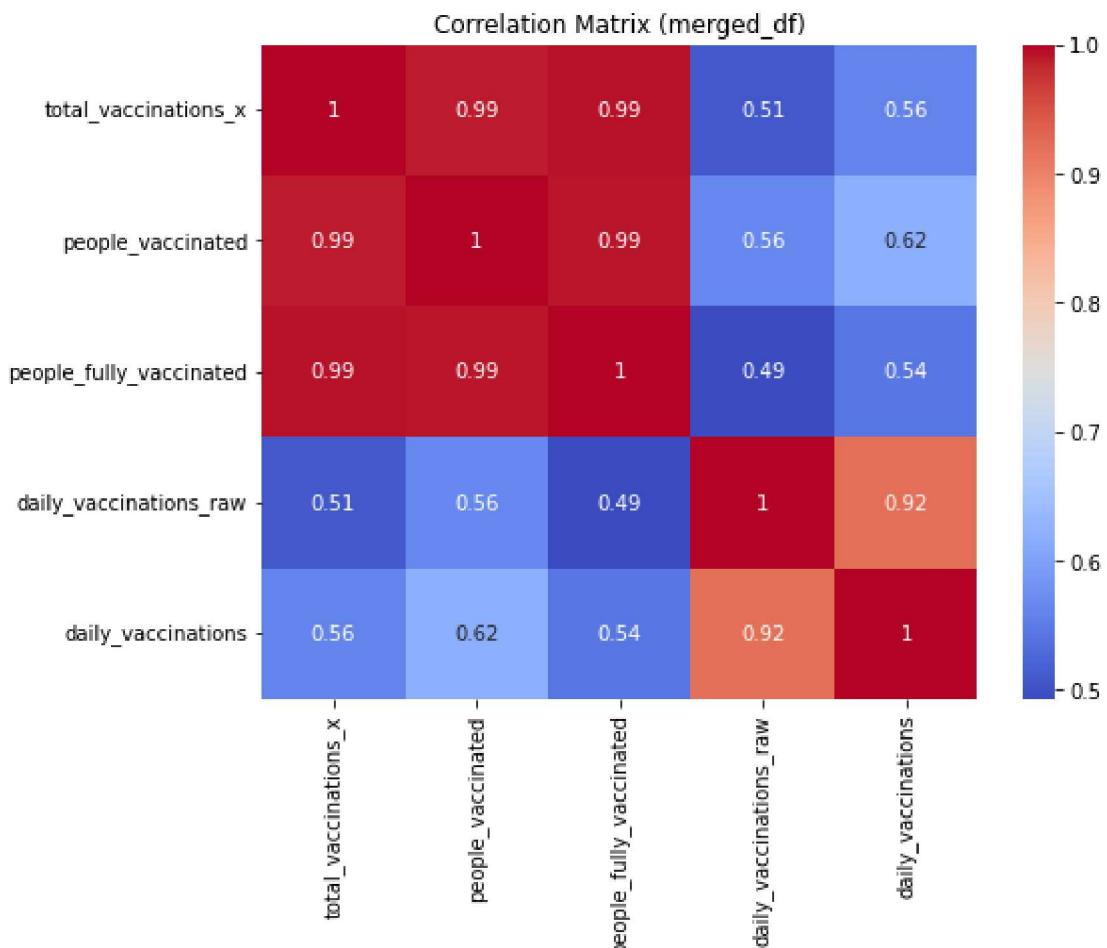
# Create a correlation matrix for 'merged_df'
corr_matrix_merged = merged_df[relevant_cols_merged].corr()

# Create a figure with a subplot
fig, ax = plt.subplots(figsize=(8, 6))

# Plot the correlation matrix for 'merged_df'
sns.heatmap(corr_matrix_merged, annot=True, cmap='coolwarm', ax=ax)
ax.set_title('Correlation Matrix (merged_df)')

plt.show()
```

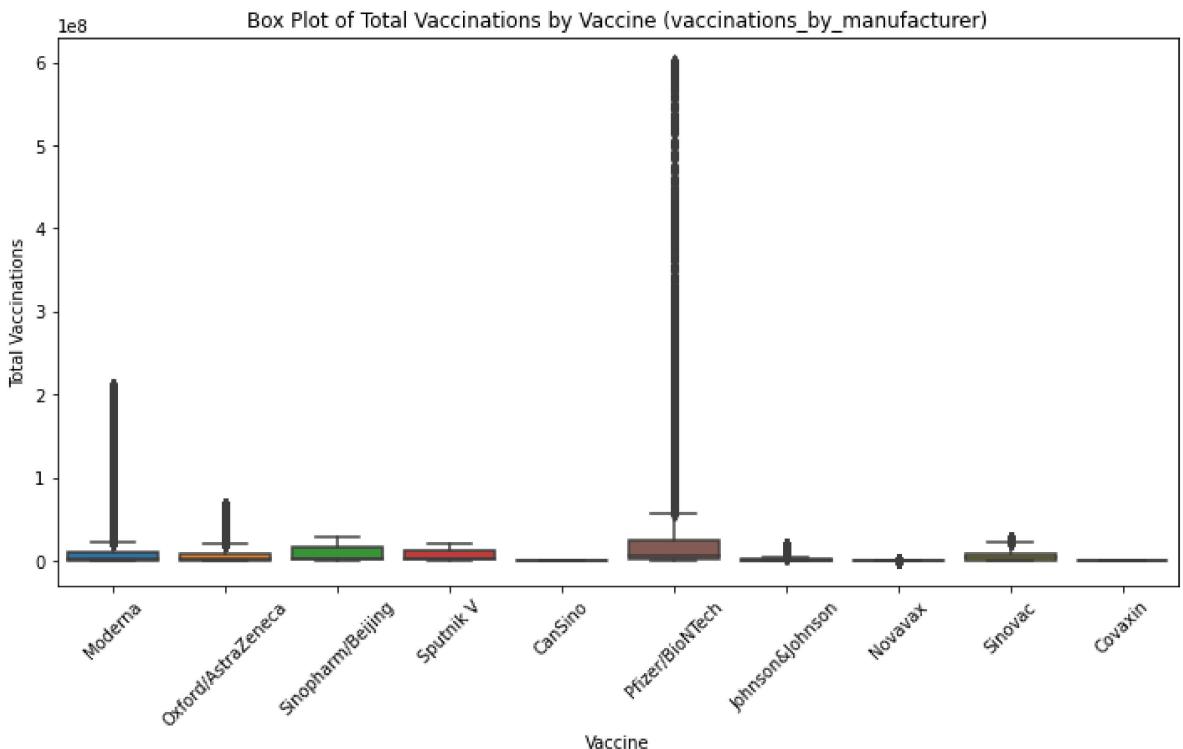
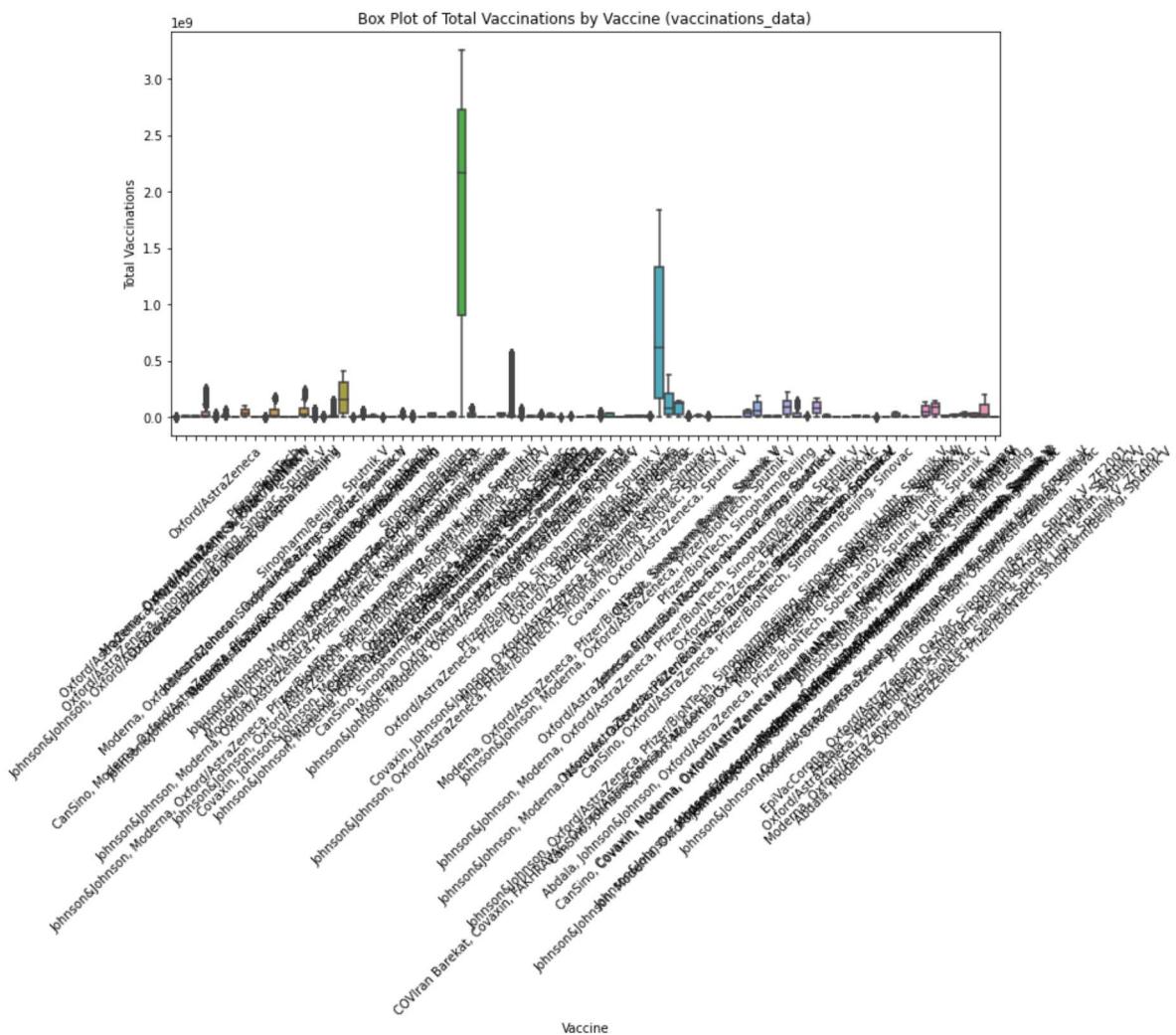


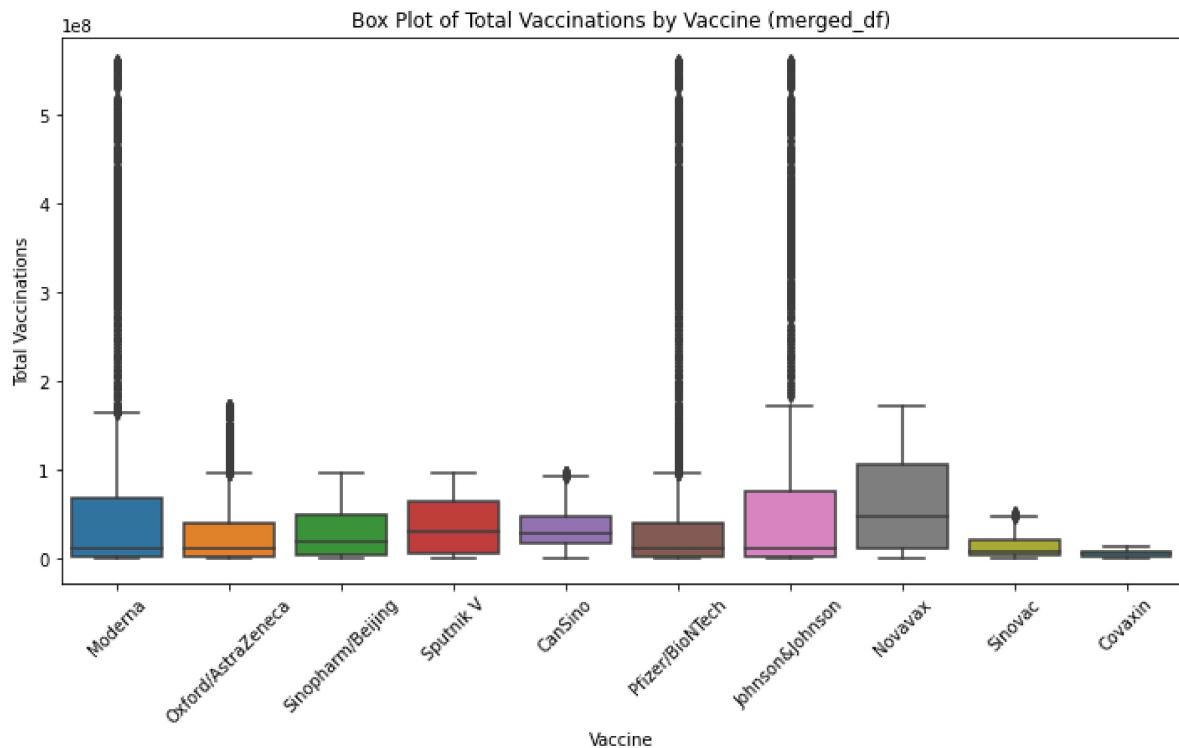


```
In [18]: # Create a box plot to identify outliers for 'total_vaccinations' by vaccine category
plt.figure(figsize=(12, 6))
sns.boxplot(data=vaccinations_data, x='vaccines', y='total_vaccinations')
plt.title('Box Plot of Total Vaccinations by Vaccine (vaccinations_data)')
plt.xlabel('Vaccine')
plt.ylabel('Total Vaccinations')
plt.xticks(rotation=45)
plt.show()

# Create a box plot to identify outliers for 'total_vaccinations' by vaccine manufacturer
plt.figure(figsize=(12, 6))
sns.boxplot(data=vaccinations_by_manufacturer, x='vaccine', y='total_vaccinations')
plt.title('Box Plot of Total Vaccinations by Vaccine (vaccinations_by_manufacturer)')
plt.xlabel('Vaccine')
plt.ylabel('Total Vaccinations')
plt.xticks(rotation=45)
plt.show()

plt.figure(figsize=(12, 6))
sns.boxplot(data=merged_df, x='vaccine', y='total_vaccinations_x')
plt.title('Box Plot of Total Vaccinations by Vaccine (merged_df)')
plt.xlabel('Vaccine')
plt.ylabel('Total Vaccinations')
plt.xticks(rotation=45)
plt.show()
```





In [19]:

```
# Group the data by 'country' and calculate the total vaccinations for each country
country_totals_data = vaccinations_data.groupby('country')['total_vaccinations']

# Sort the data by total vaccinations in descending order
country_totals_data = country_totals_data.sort_values(by='total_vaccinations', ascending=False)

# Create a bar chart for 'total_vaccinations' in 'vaccinations_data'
plt.figure(figsize=(12, 6))
plt.bar(country_totals_data['country'], country_totals_data['total_vaccinations'])

plt.xlabel('Country')
plt.ylabel('Total Vaccinations (vaccinations_data)')
plt.title('Total Vaccinations by Country (vaccinations_data)')

plt.xticks(rotation=90)
plt.show()

country_totals_manufacturer = vaccinations_by_manufacturer.groupby('country')[['total_vaccinations_x']]

country_totals_manufacturer = country_totals_manufacturer.sort_values(by='total_vaccinations_x', ascending=False)

# Create a bar chart for 'total_vaccinations' in 'vaccinations_by_manufacturer'
plt.figure(figsize=(12, 6))
plt.bar(country_totals_manufacturer['country'], country_totals_manufacturer['total_vaccinations_x'])

plt.xlabel('Country')
plt.ylabel('Total Vaccinations (vaccinations_by_manufacturer)')
plt.title('Total Vaccinations by Country (vaccinations_by_manufacturer)')

plt.xticks(rotation=90)
plt.show()

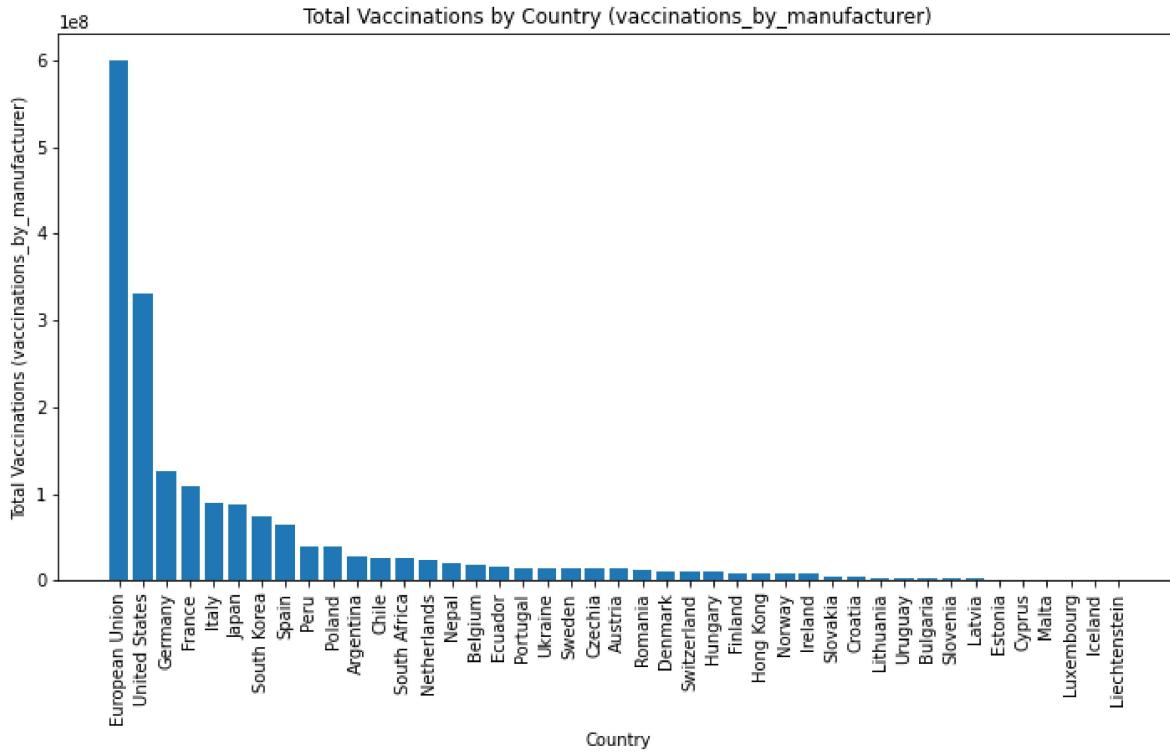
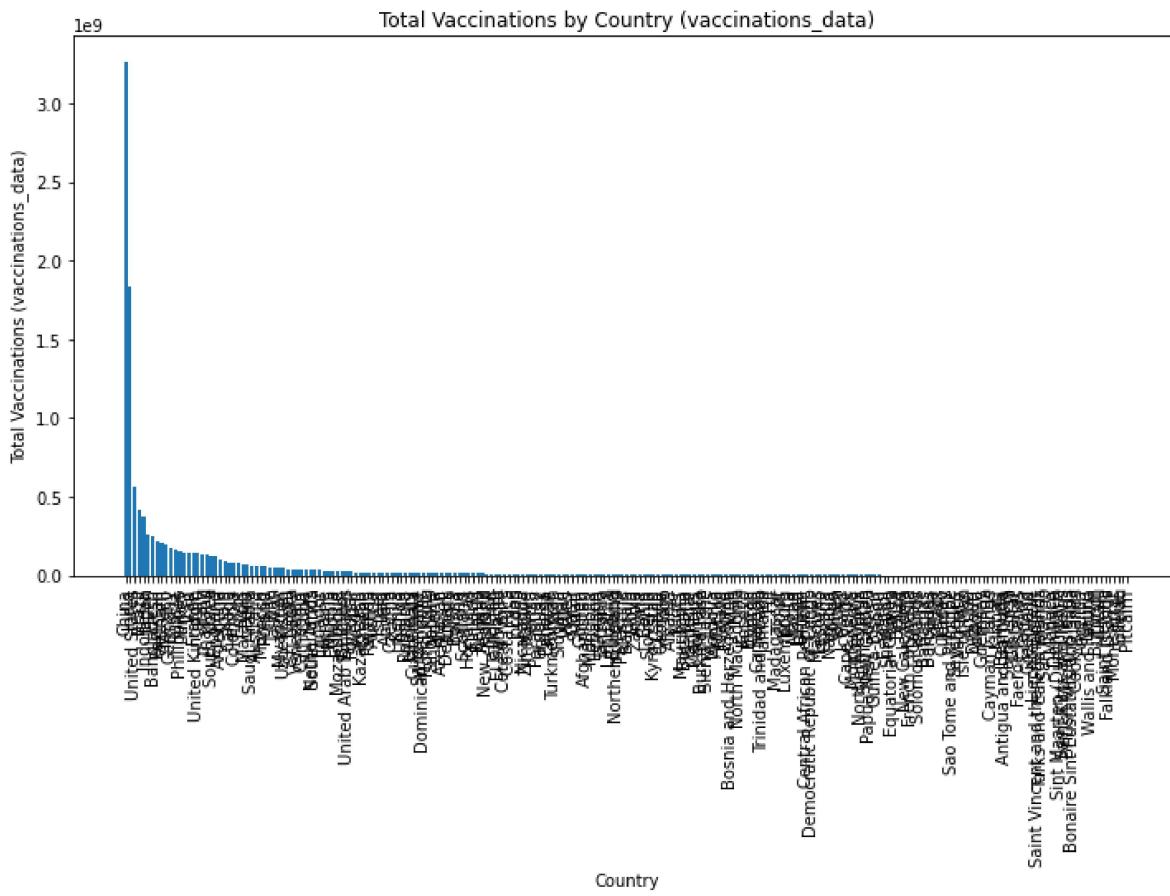
country_totals_merged = merged_df.groupby('country')['total_vaccinations_x'].mean()

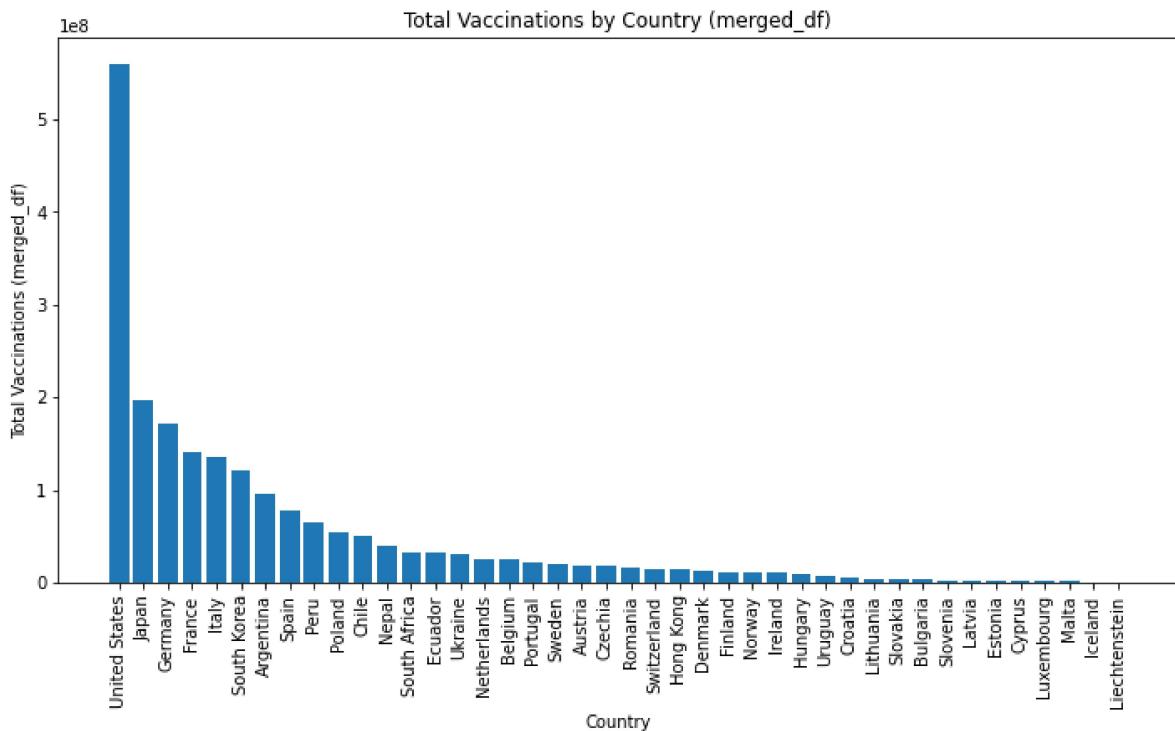
country_totals_merged = country_totals_merged.sort_values(by='total_vaccinations_x', ascending=False)

# Create a bar chart for 'total_vaccinations_x' in 'merged_df'
plt.figure(figsize=(12, 6))
plt.bar(country_totals_merged['country'], country_totals_merged['total_vaccinations_x'])

plt.xlabel('Country')
plt.ylabel('Total Vaccinations (merged_df)')
plt.title('Total Vaccinations by Country (merged_df)')

plt.xticks(rotation=90)
plt.show()
```





## STATISTICAL ANALYSIS

```
In [20]: # Example: T-test for vaccine efficacy comparison

import scipy.stats as stats

vaccine_a_data = vaccinations_data[vaccinations_data['vaccines'] == 'Vaccine A']
vaccine_b_data = vaccinations_data[vaccinations_data['vaccines'] == 'Vaccine B']

# Perform a t-test for comparing the means of "Vaccine A" and "Vaccine B"
t_statistic, p_value = stats.ttest_ind(vaccine_a_data, vaccine_b_data, equal_var=True)

# Print the results
if p_value < 0.05: # You can adjust the significance level (alpha)
    print("There is a significant difference in vaccine efficacy between Vaccine A and Vaccine B.")
else:
    print("There is no significant difference in vaccine efficacy between Vaccine A and Vaccine B.")
```

There is no significant difference in vaccine efficacy between Vaccine A and Vaccine B.

In [21]:

```

country_a = 'Country A'
country_b = 'Country B'

total_vaccinations_country_a = vaccinations_data[vaccinations_data['country'] == country_a]
total_vaccinations_country_b = vaccinations_data[vaccinations_data['country'] == country_b]

# Perform a two-sample t-test to compare the means of the two countries
t_statistic, p_value = stats.ttest_ind(total_vaccinations_country_a, total_vaccinations_country_b)

# Print the t-statistics and p-value
print(f'T-Statistic: {t_statistic}')
print(f'P-Value: {p_value}')

# Print the results
if p_value < 0.05: # You can adjust the significance level (alpha)
    print(f"There is a significant difference in total vaccinations between {country_a} and {country_b}.")
else:
    print(f"There is no significant difference in total vaccinations between {country_a} and {country_b}.")

```

T-Statistic: nan  
P-Value: nan  
There is no significant difference in total vaccinations between Country A and Country B.

## VACCINES EFFICACY

In [22]:

```

# Calculate attack rates
merged_df['attack_rate_vaccinated'] = merged_df['people_fully_vaccinated'] / merged_df['population']
merged_df['attack_rate_unvaccinated'] = (merged_df['total_vaccinations_x'] - merged_df['people_fully_vaccinated']) / merged_df['population']

# Calculate vaccine efficacy
merged_df['vaccine_efficiency'] = (1 - (merged_df['attack_rate_unvaccinated'] / merged_df['attack_rate_vaccinated'])) * 100

# Display the dataset with vaccine efficacy
print(merged_df[['country', 'vaccine', 'date', 'vaccine_efficiency']])

```

	country	vaccine	date	vaccine_efficiency
0	Argentina	Moderna	2020-12-29	-409540.000000
1	Argentina	Oxford/AstraZeneca	2020-12-29	-409540.000000
2	Argentina	Sinopharm/Beijing	2020-12-29	-409540.000000
3	Argentina	Sputnik V	2020-12-29	-409540.000000
4	Argentina	Moderna	2020-12-30	-405690.000000
...	...	...	...	...
28949	Uruguay	Pfizer/BioNTech	2022-03-28	-82.106766
28950	Uruguay	Sinovac	2022-03-28	-82.106766
28951	Uruguay	Oxford/AstraZeneca	2022-03-29	-82.420469
28952	Uruguay	Pfizer/BioNTech	2022-03-29	-82.420469
28953	Uruguay	Sinovac	2022-03-29	-82.420469

[27018 rows x 4 columns]

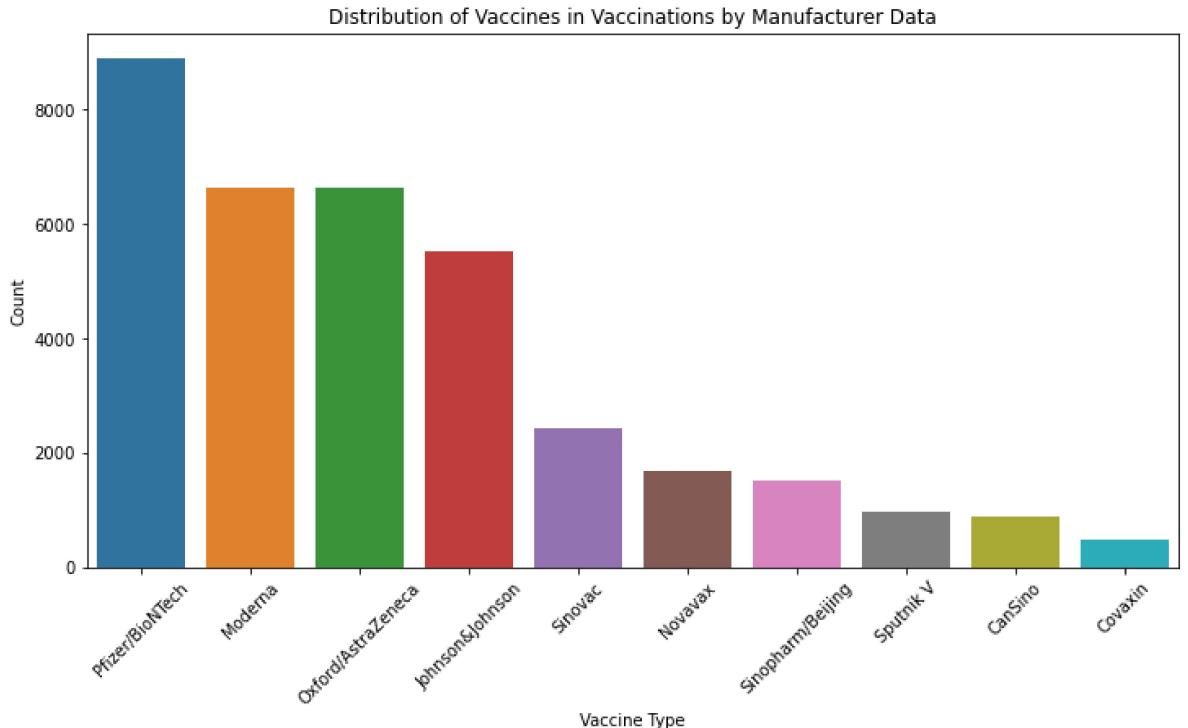
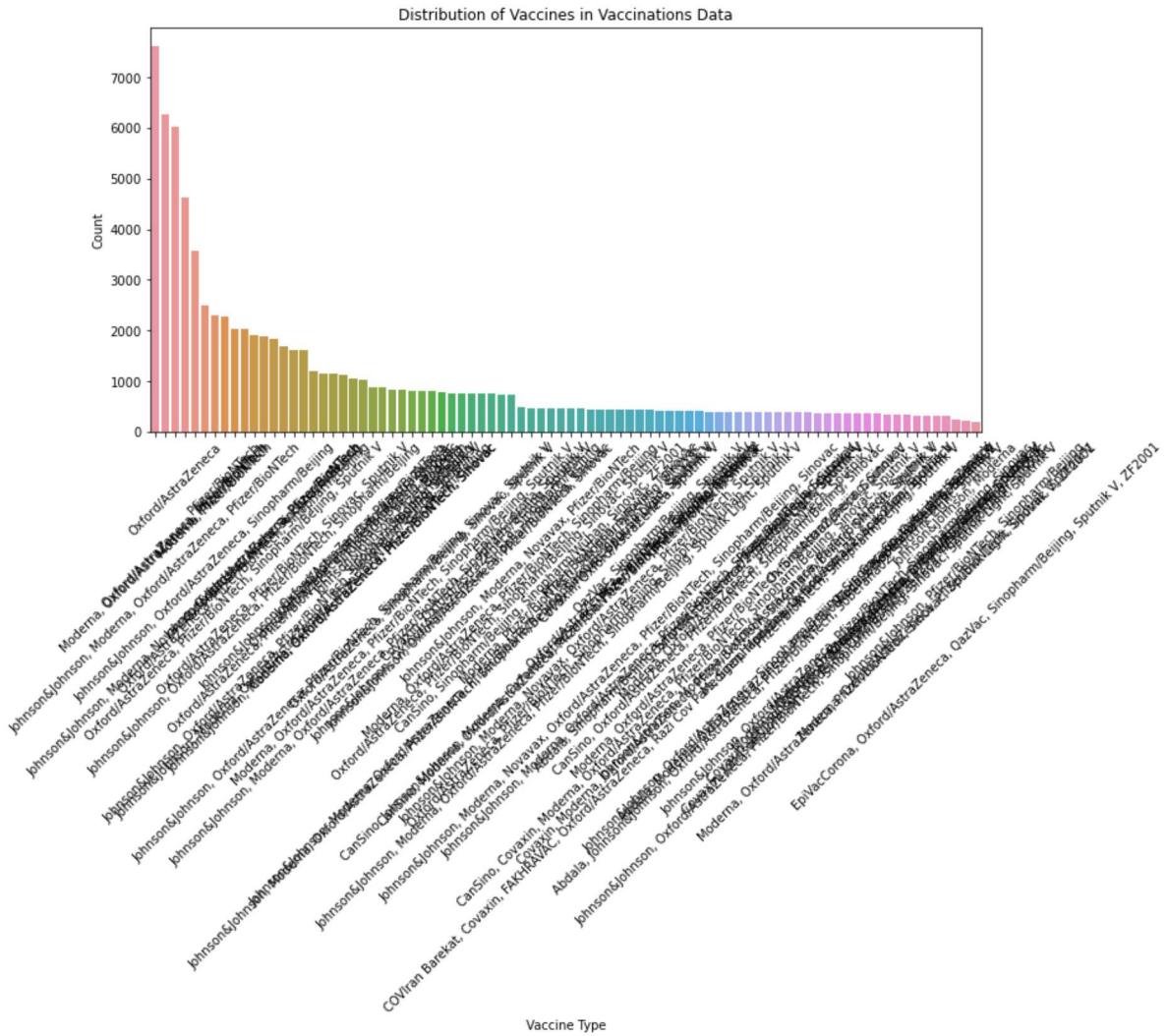
# DISTRIBUTIONS

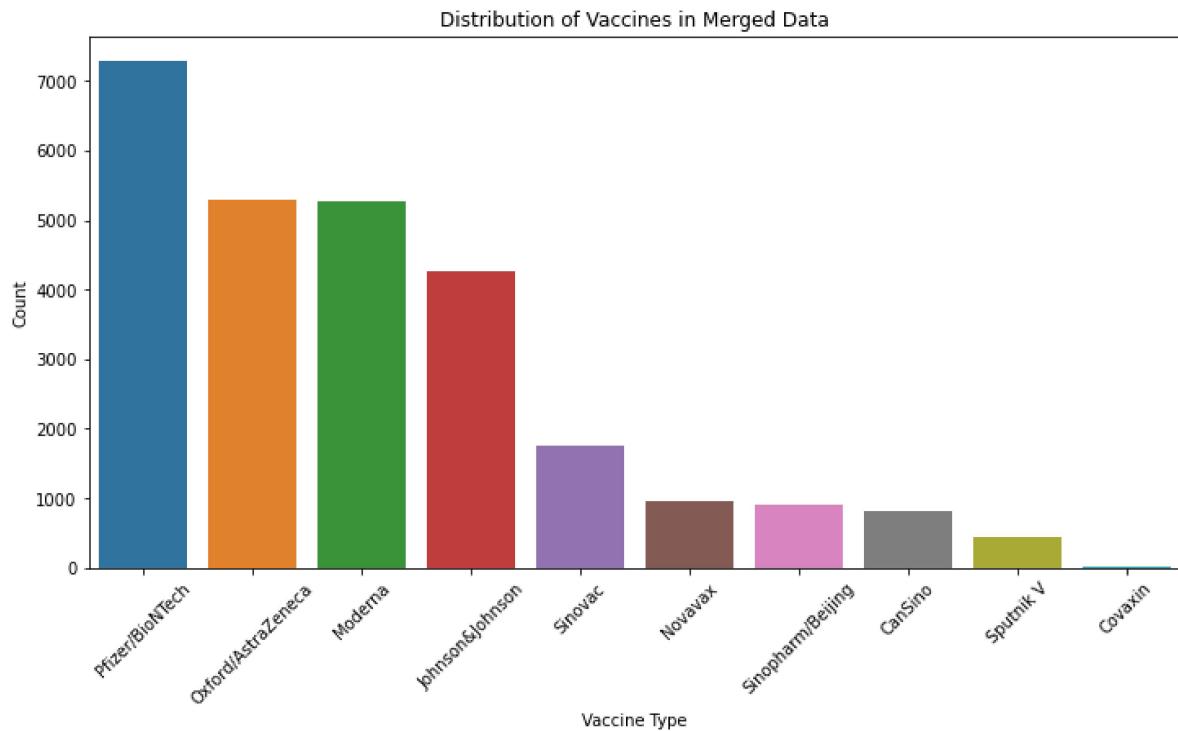
In [23]:

```
# Create a count plot for the distribution of vaccines in 'vaccinations_data'
plt.figure(figsize=(12, 6))
sns.countplot(data=vaccinations_data, x='vaccines', order=vaccinations_data['vaccines'].value_counts().index)
plt.title('Distribution of Vaccines in Vaccinations Data')
plt.xlabel('Vaccine Type')
plt.ylabel('Count')
plt.xticks(rotation=45)
plt.show()

# Create a count plot for the distribution of vaccines in 'vaccinations_by_manufacturer'
plt.figure(figsize=(12, 6))
sns.countplot(data=vaccinations_by_manufacturer, x='vaccine', order=vaccinations_by_manufacturer['vaccine'].value_counts().index)
plt.title('Distribution of Vaccines in Vaccinations by Manufacturer Data')
plt.xlabel('Vaccine Type')
plt.ylabel('Count')
plt.xticks(rotation=45)
plt.show()

# Create a count plot for the distribution of vaccines in 'merged_df'
plt.figure(figsize=(12, 6))
sns.countplot(data=merged_df, x='vaccine', order=merged_df['vaccine'].value_counts().index)
plt.title('Distribution of Vaccines in Merged Data')
plt.xlabel('Vaccine Type')
plt.ylabel('Count')
plt.xticks(rotation=45)
plt.show()
```

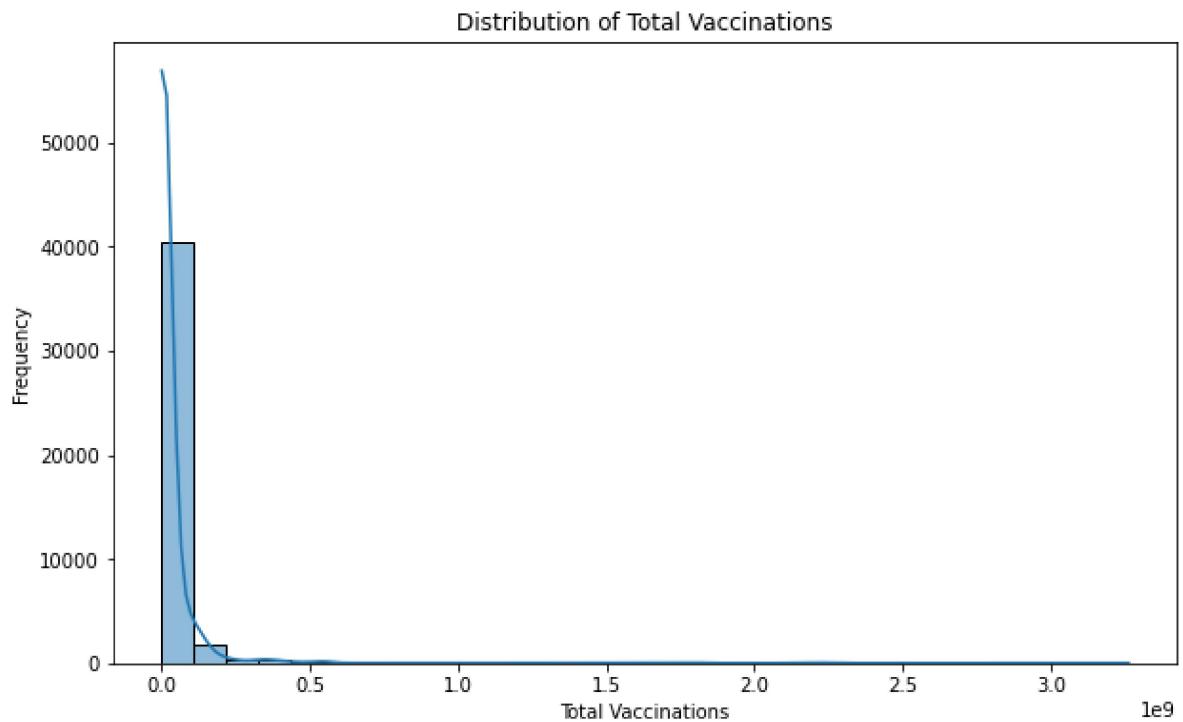




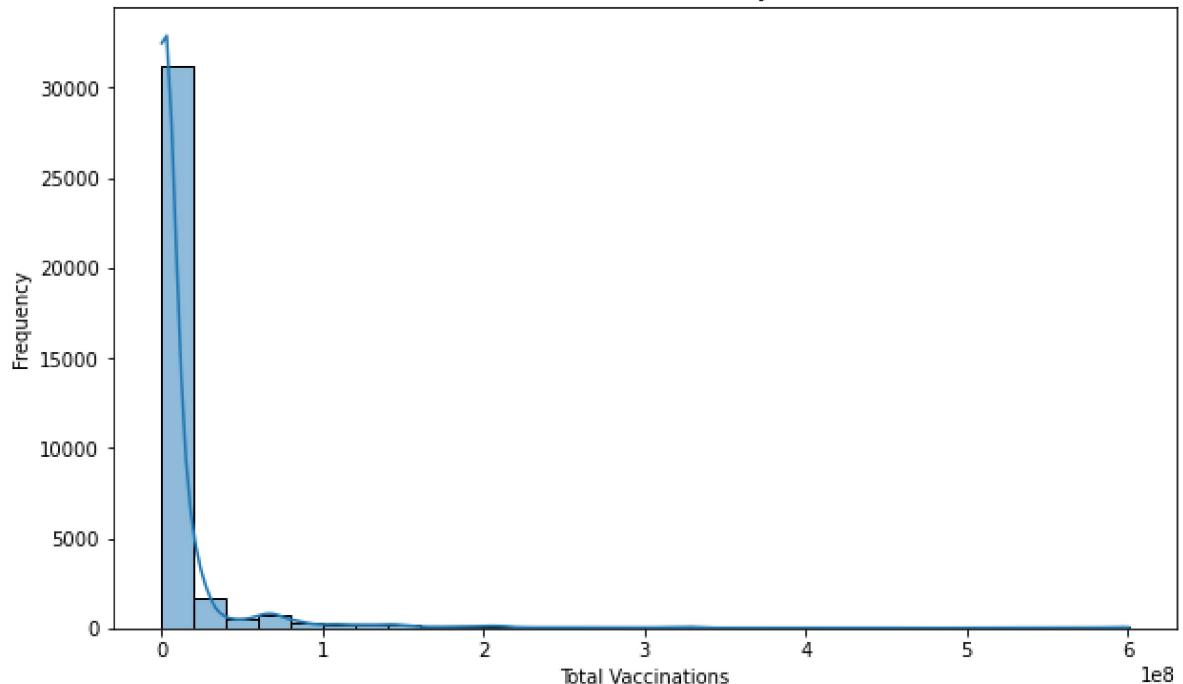
```
In [24]: plt.figure(figsize=(10, 6))
sns.histplot(data=vaccinations_data, x='total_vaccinations', bins=30, kde=True)
plt.title('Distribution of Total Vaccinations')
plt.xlabel('Total Vaccinations')
plt.ylabel('Frequency')
plt.show()

plt.figure(figsize=(10, 6))
sns.histplot(data=vaccinations_by_manufacturer, x='total_vaccinations', bins=30, kde=True)
plt.title('Distribution of Total Vaccinations by Manufacturer')
plt.xlabel('Total Vaccinations')
plt.ylabel('Frequency')
plt.show()

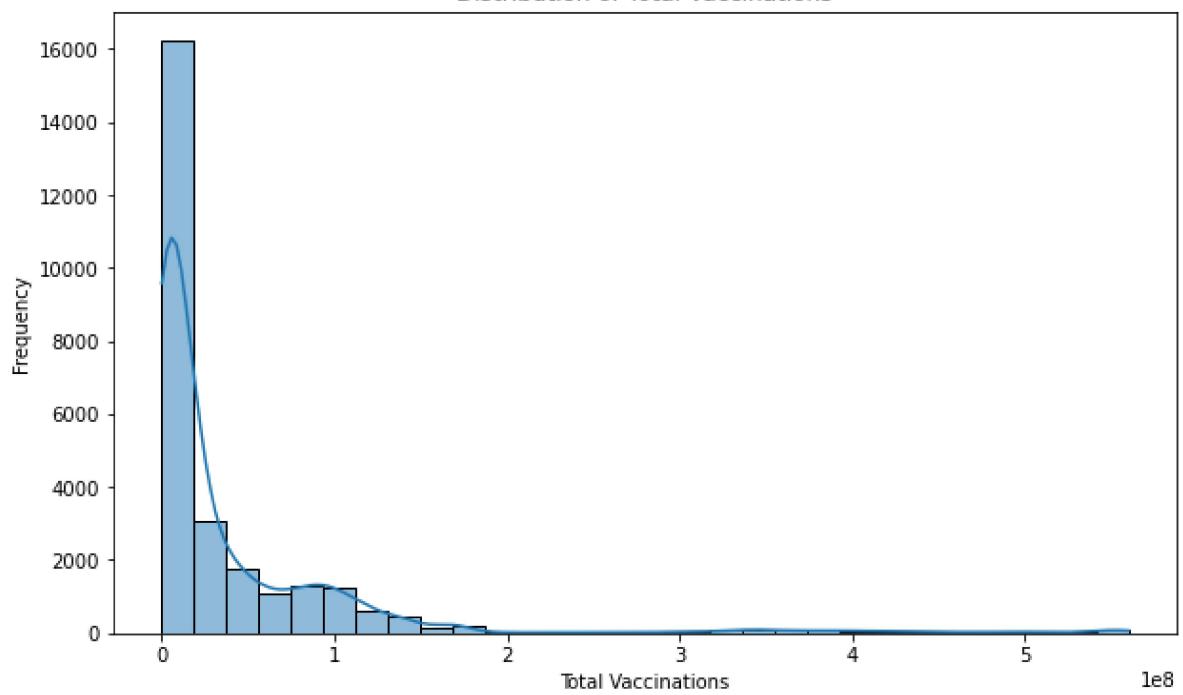
# Create a histogram for 'total_vaccinations' in merged_df
plt.figure(figsize=(10, 6))
sns.histplot(data=merged_df, x='total_vaccinations_x', bins=30, kde=True)
plt.title('Distribution of Total Vaccinations')
plt.xlabel('Total Vaccinations')
plt.ylabel('Frequency')
plt.show()
```



## Distribution of Total Vaccinations by Manufacturer



## Distribution of Total Vaccinations



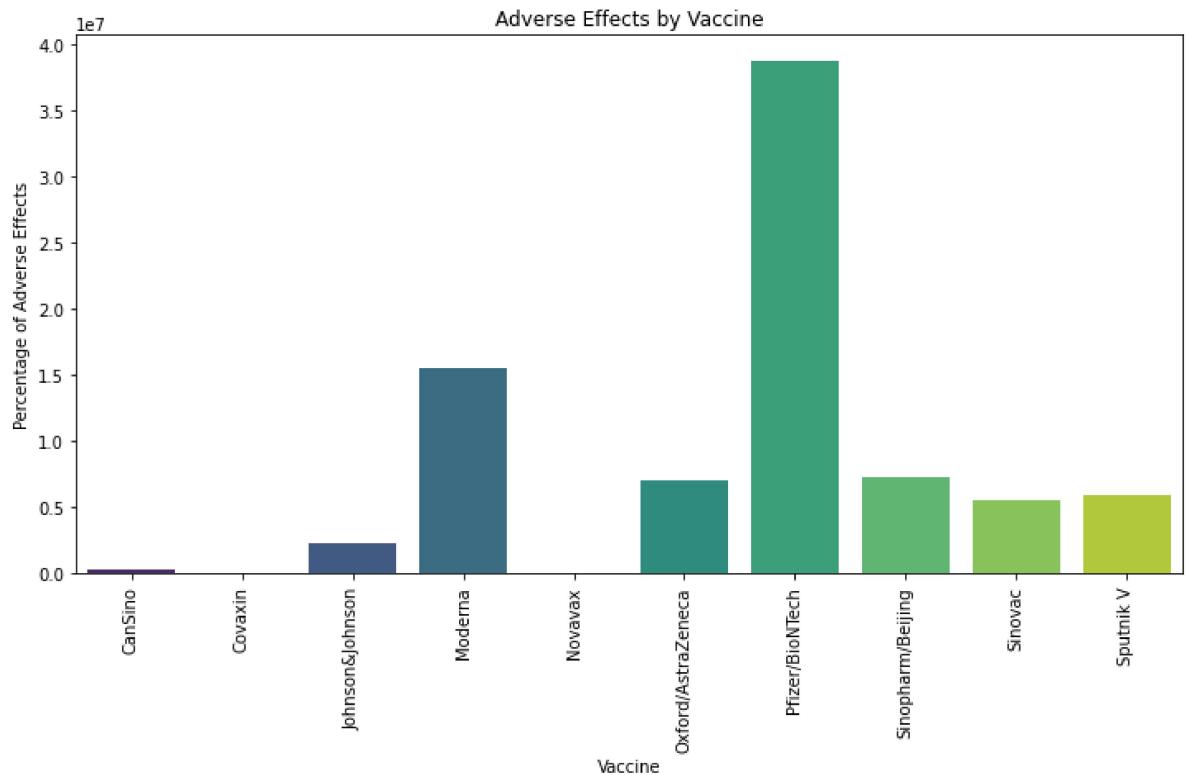
## ADVERSE EFFECTS

```
In [25]: vaccinations_data.rename(columns={'vaccines': 'vaccine'}, inplace=True)
```

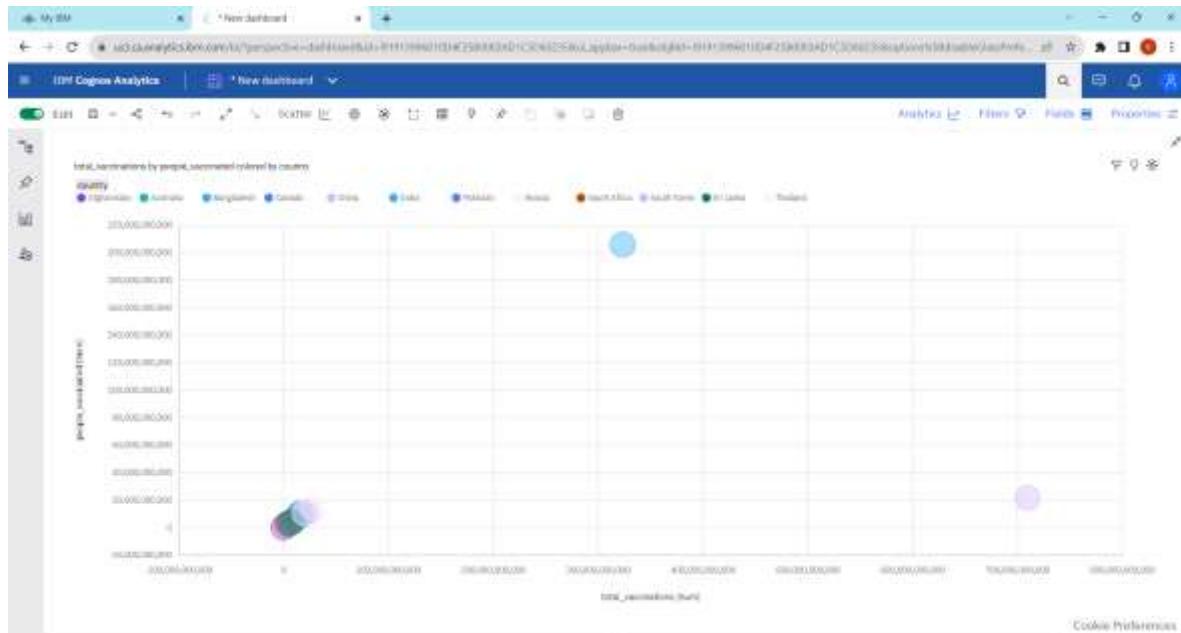
```
In [26]: merged_data_adverse=vaccinations_by_manufacturer.merge(vaccinations_data, on=[

adverse_effects_by_vaccine = merged_data_adverse.groupby('vaccine')['total_vac

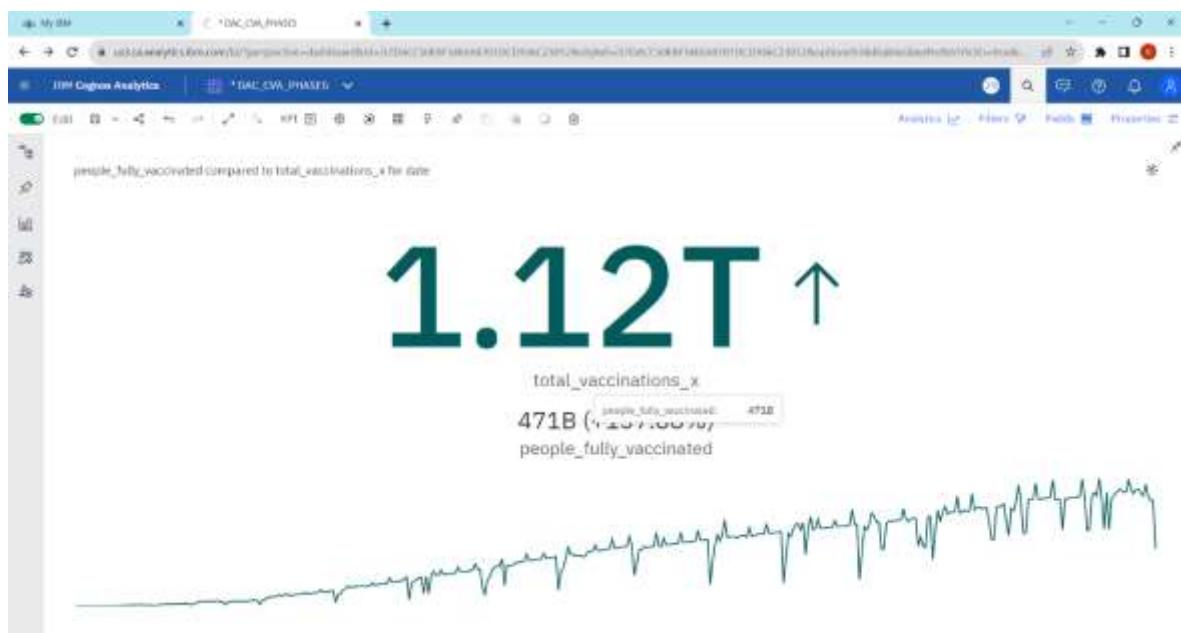
plt.figure(figsize=(12, 6))
sns.barplot(x=adverse_effects_by_vaccine.index, y=adverse_effects_by_vaccine.v
plt.xlabel('Vaccine')
plt.ylabel('Percentage of Adverse Effects')
plt.title('Adverse Effects by Vaccine')
plt.xticks(rotation=90)
plt.show()
```

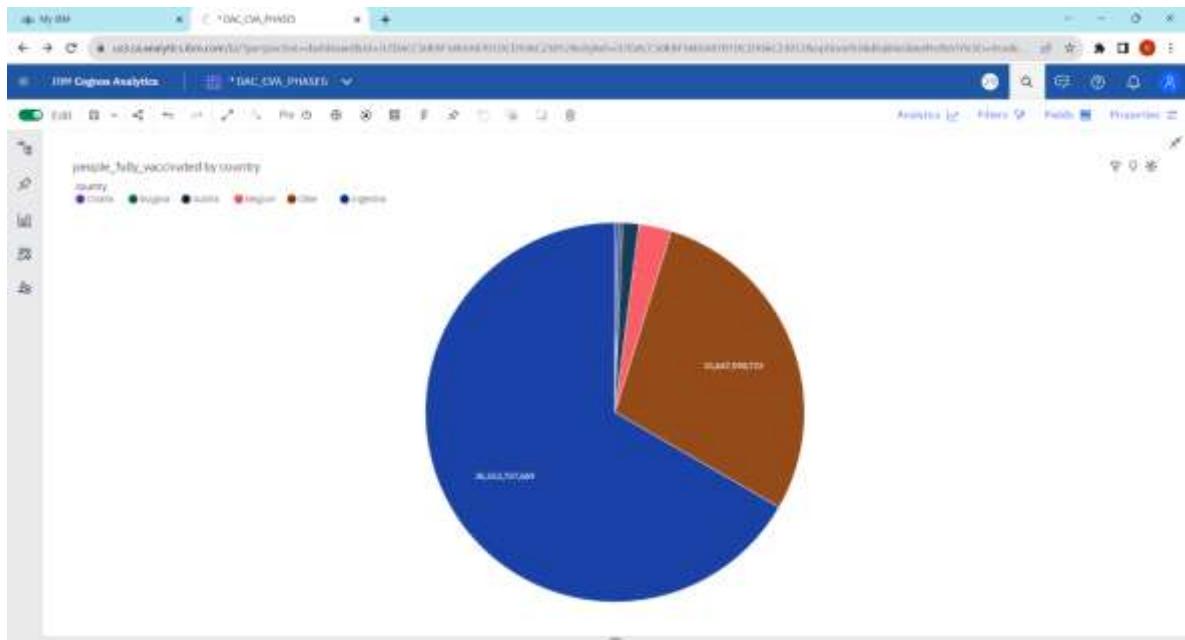


## VISUALIZATION USING IBM COGNOS ANALYTICS



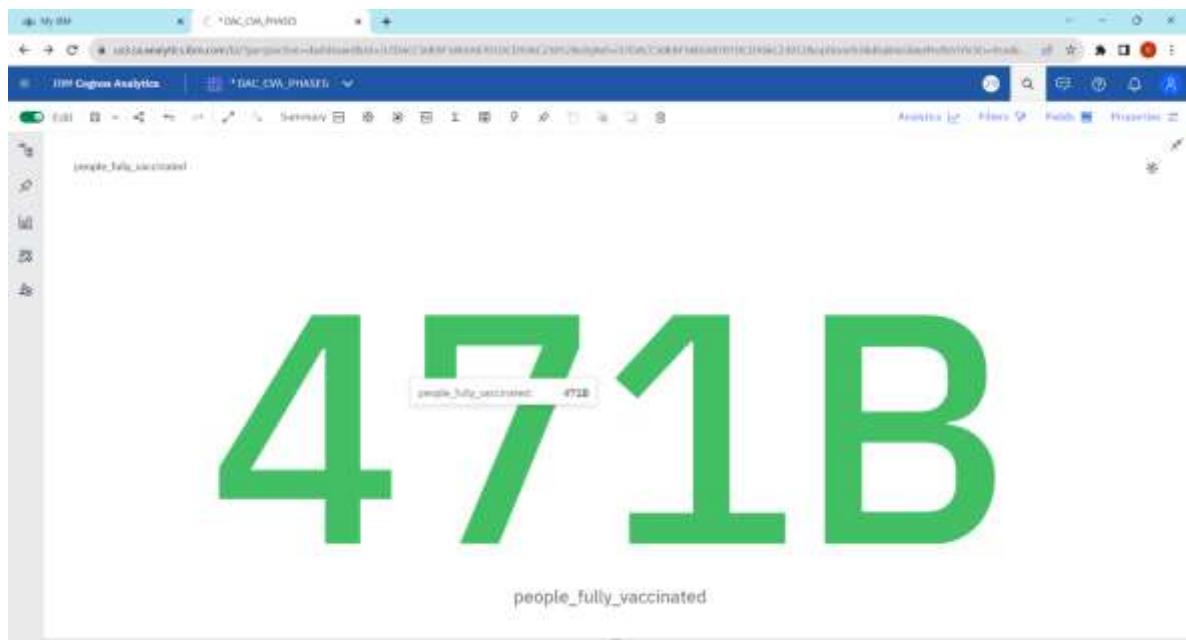
# IBM NAAN MUDHALVAN



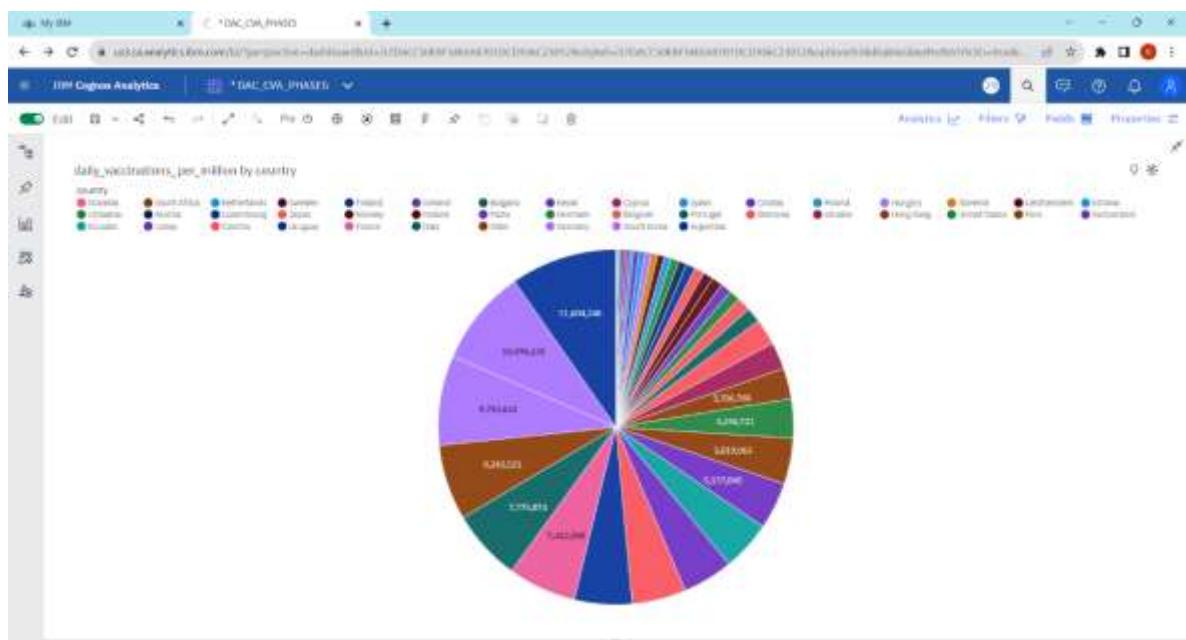


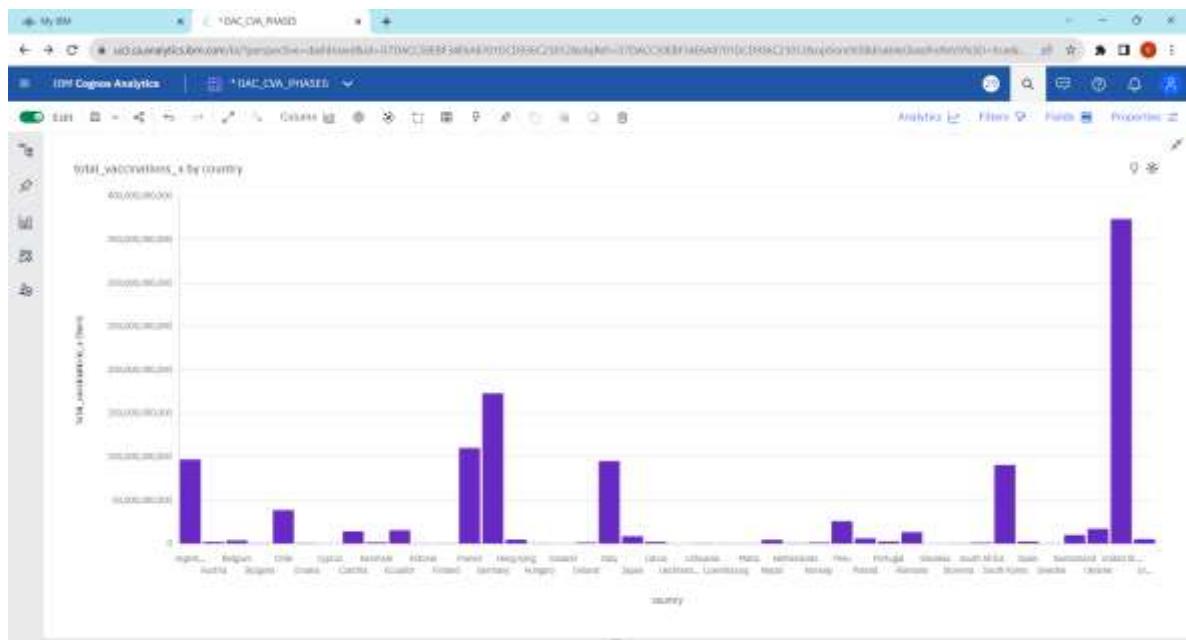
IBM NAAN MUDHALVAN



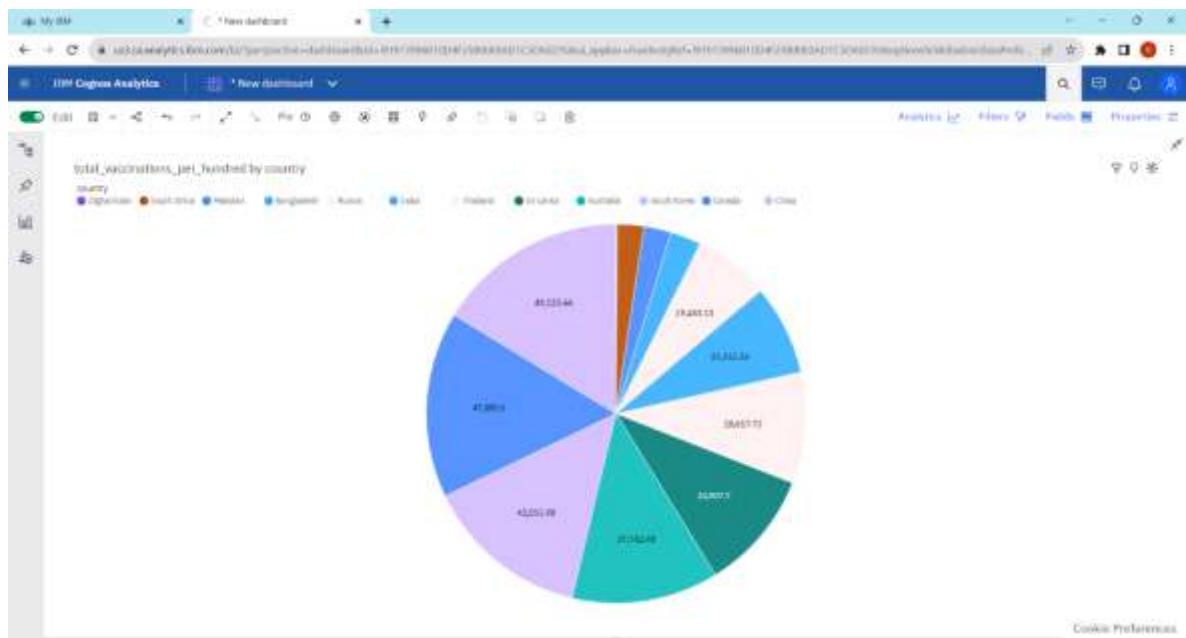


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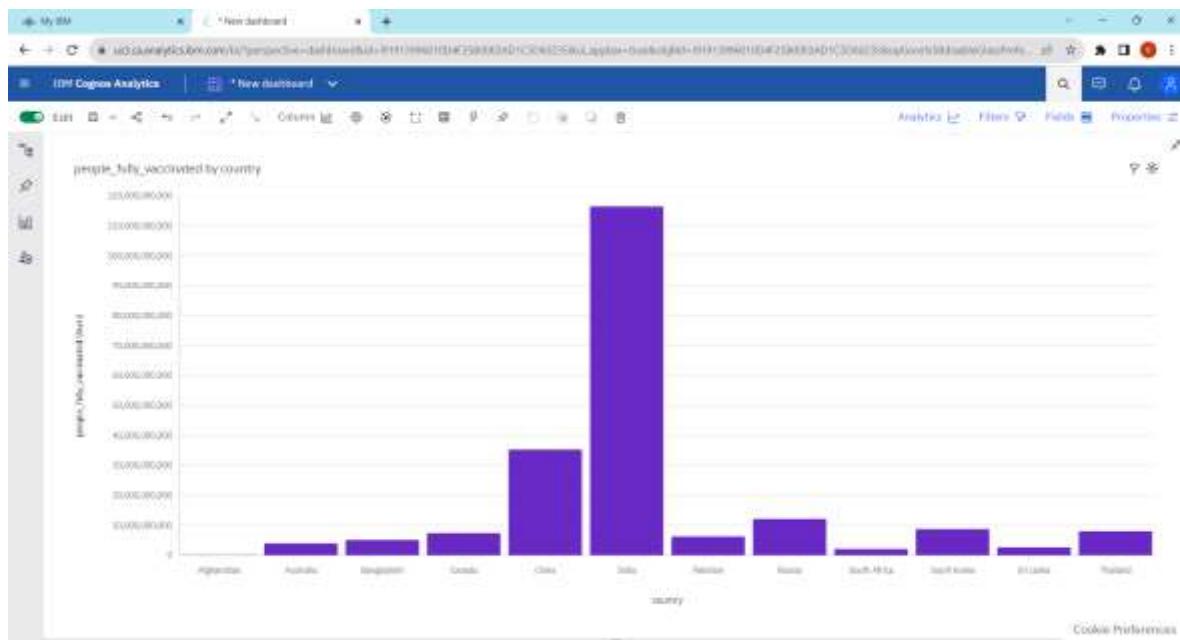




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