PROJECT

Complex Network Dynamics

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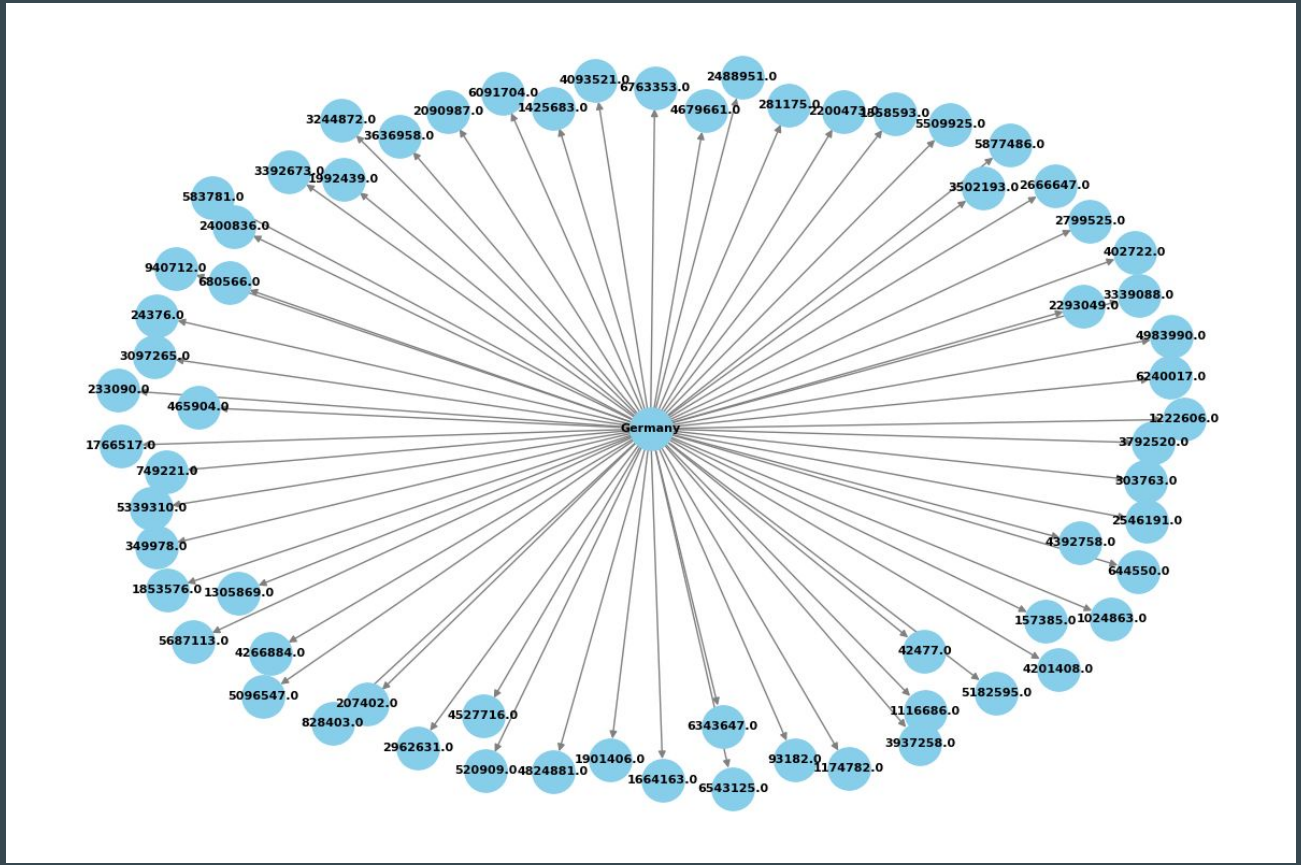
COVID-19 VACCINATION PROGRESS NETWORK

Abstract:

This project delves into the intriguing dynamics of global COVID-19 vaccine choices, specifically exploring homophily in vaccine adoption based on countries' degrees. Using network analysis, we examine how nations with similar external degrees exhibit analogous patterns in vaccine selection. Each edge in our analysis represents the adoption of the same vaccine. Clusters of countries with comparable degrees, shedding light on the shared decision-making processes shaping global vaccination strategies. This research provides valuable insights into the interplay between external degrees and vaccine preferences.

Approach

The initial step in this study involved working with a CSV dataset named "country_vaccinations.csv," which contained information on the vaccination status of each country along with the types of vaccines administered. Leveraging the pandas library in Python, I performed an initial exploration to gain insights into the vaccination landscape globally. The script for this task is demonstrated in "import pandas as pd.py."


Germany
4093521.0
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2488951.0
6091704.0
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1425683.0
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3636958.0
5509925.0
5877486.0
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3339088.0
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24376.0
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233090.0
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1222606.0
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749221.0
303763.0
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2546191.0
349978.0
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42477.0
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3937258.0
2962631.0
93182.0
520909.0
4824881.0
1901406.0
1174782.0
1664163.0
6543125.0

Subsequently

to visually represent the relationships between countries and their vaccine types, I employed the NetworkX library in Python. The script for creating graphs can be found in the script labeled "script_projected.py." This script utilizes the power of NetworkX to generate meaningful graphs based on the dataset, shedding light on the interconnectedness of countries and their vaccine preferences.

To further enhance the understanding of these relationships, I harnessed the capabilities of the itertools library. By grouping the dataset by country and using itertools.product, I created pairs of countries along with their respective vaccine types. This process was applied individually for each country and executed through the terminal.

from the projected graph I extract a small instance

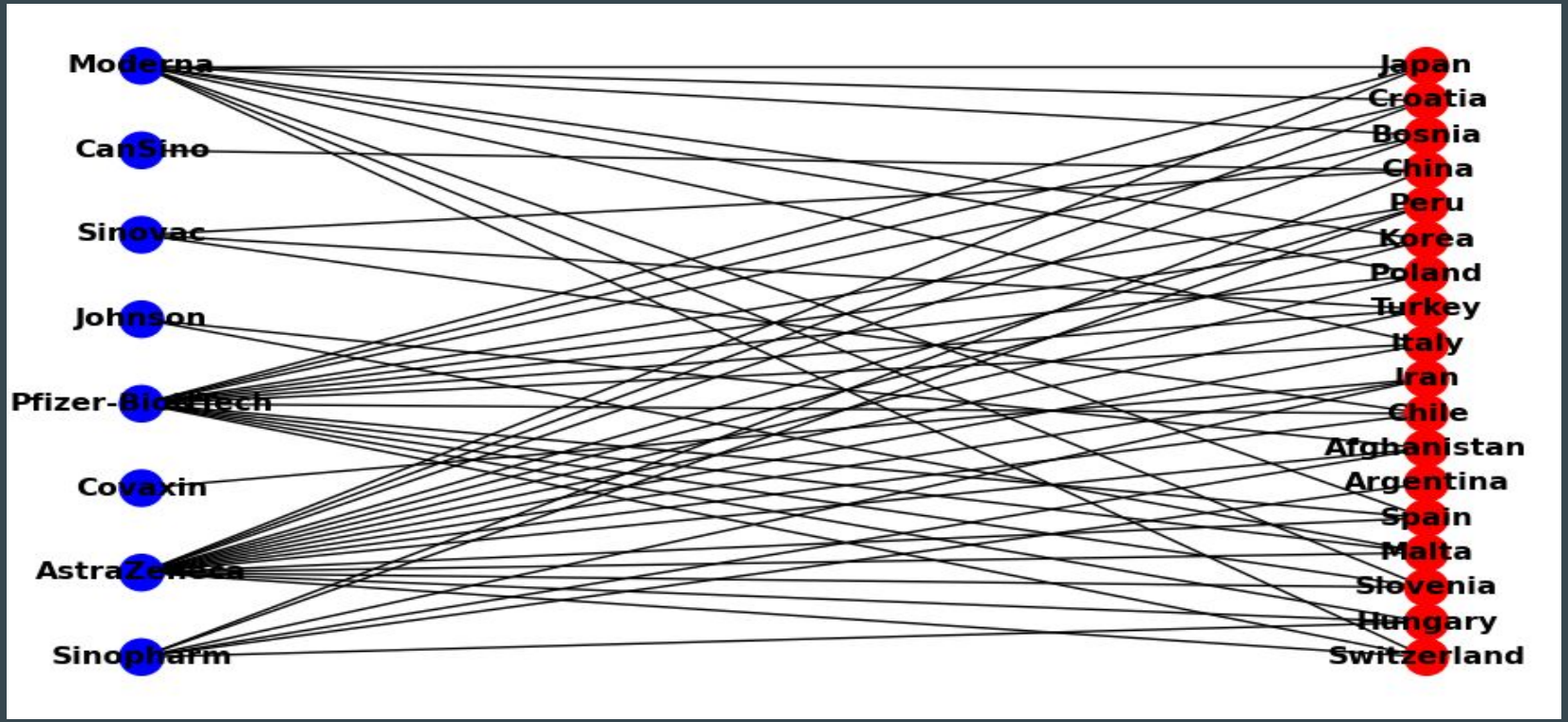
```
PROBLEMS  OUTPUT  DEBUG CONSOLE  TERMINAL  PORTS

Name: country, Length: 84, dtype: object
PS C:\Users\xrist\Desktop\hy345\assignment1\assignment1> & C:/Users/xrist/anaconda3/python.exe "c:/Users/xrist/Desktop/import pandas as pd.py"
vaccines
Abdala, Johnson&Johnson, Oxford/AstraZeneca, Pfizer/BioNTech, Soberana02, Sputnik Light, Sputnik V                                [(Nicaragua, Nicarag
ua), (Nicaragua, Nicaragua...
Abdala, Moderna, Oxford/AstraZeneca, Pfizer/BioNTech, Sinopharm/Beijing, Sputnik V                                                 [(Vietnam, Vietnam),
 (Vietnam, Vietnam), (Viet...
Abdala, Sinopharm/Beijing, Sinovac, Soberana02, Sputnik Light, Sputnik V                                                           [(Venezuela, Venezue
la), (Venezuela, Venezuela...
Abdala, Soberana Plus, Soberana02                                                                                                  [(Cuba, Cuba), (Cuba
, Cuba), (Cuba, Cuba), (Cu...
COVIran Barekat, Covaxin, FAKHRAVAC, Oxford/AstraZeneca, Razi Cov Pars, Sinopharm/Beijing, Soberana02, SpikoGen, Sputnik V    [(Iran, Iran), (Iran
, Iran), (Iran, Iran), (Ir...
```

Graph visualization

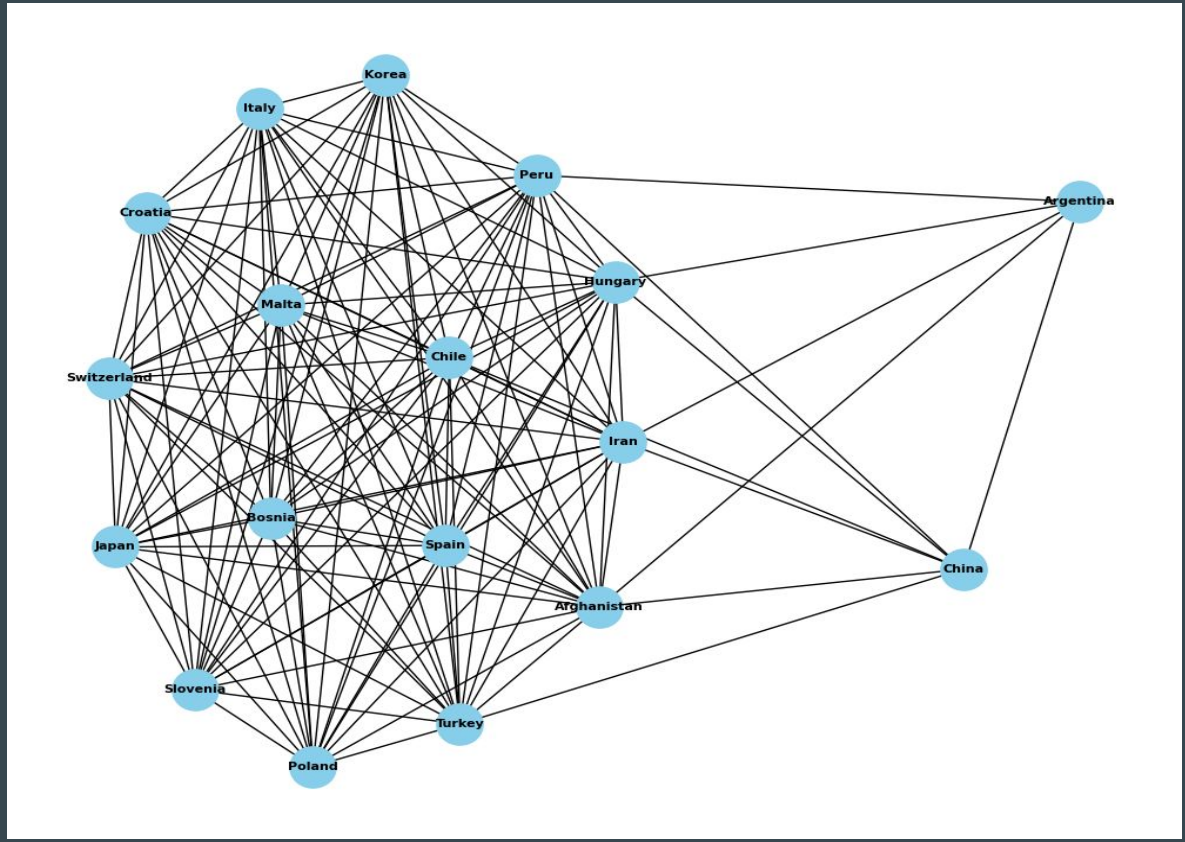
To facilitate a more focused analysis and clearer visualization, a subset of countries was selected for the final step. This subset was carefully chosen to ensure ease of interpretation and noticeability of key observations.

This approach, combining data manipulation, network analysis, and visualization techniques, aims to provide a comprehensive understanding of global COVID-19 vaccination dynamics.

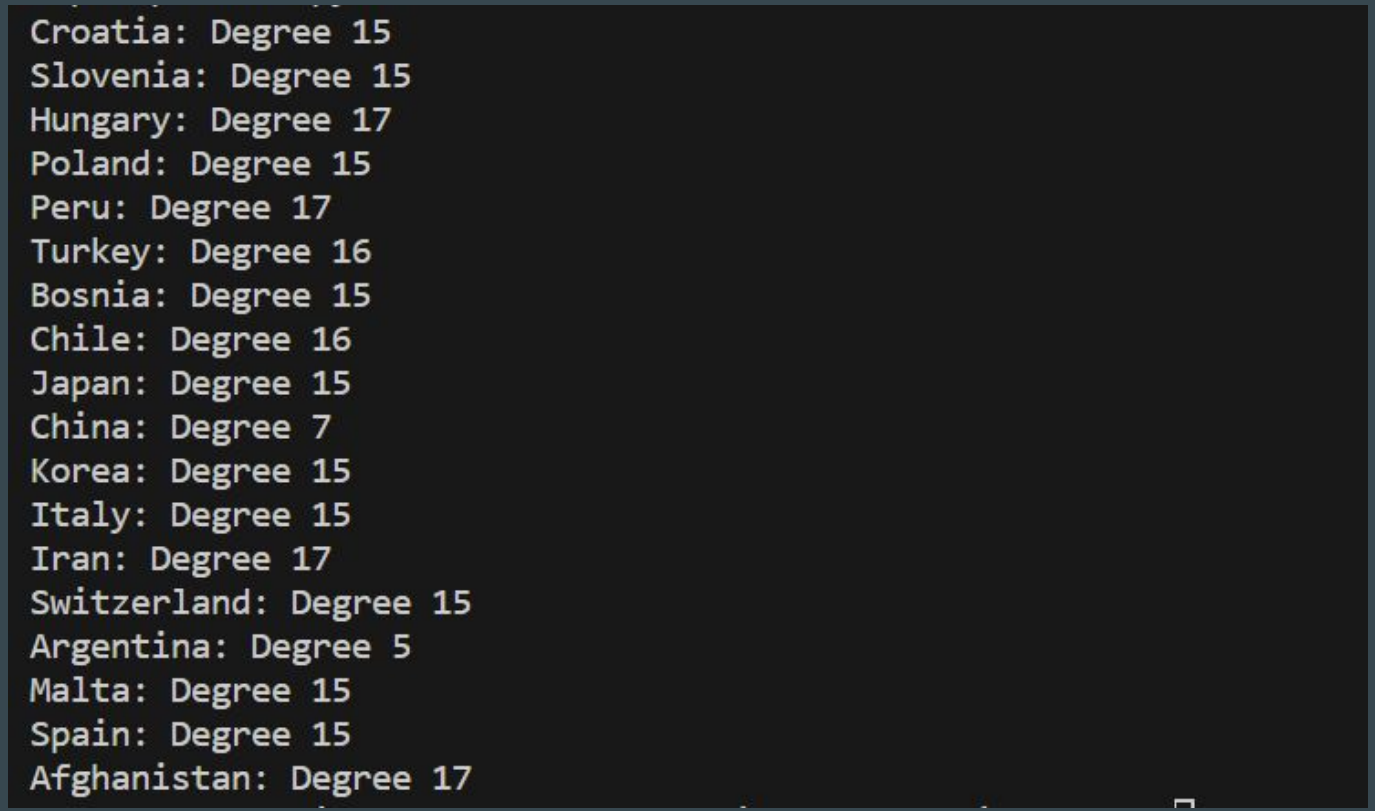
Affiliation graph



Projected graph



Counted the degree of each country



Observations

Each edge is the same vaccine .

Homophily is noticed in the countries with the same degree having same rates

Countries with similar degrees are likely to have a common set of vaccine affiliations. They are connected because they share at least one vaccine affiliation

Homophily in countries with similar degrees might be influenced by regional or cultural factors. Countries within the same region or with similar cultural backgrounds may have more shared interests in terms of vaccine choices.

Similar degrees and homophily may reflect a shared interest in specific vaccines or vaccine technologies. This could lead to increased scientific collaboration, joint research initiatives, or technology transfer among countries.

dataset :

https://www.kaggle.com/datasets/gpreda/covid-world-vaccination-progress?resource=download