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# Ameliorated Approach for Identification of Covid-19 Spreaders Using Multiplex Networks Approach

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**ABSTRACT:** In this work, we present a methodology to identify COVID-19 spreaders using the analysis of the relationship between socio-cultural and economic characteristics with the number of infections and deaths caused by the COVID-19 virus in different countries. For this, we analyze the information of each country using the complex networks approach, specifically by analyzing the spreaders countries based on the separator set in 5-layer multiplex networks. The results show that, we obtain a classification of the countries based on their numerical values in socioeconomics, population, Gross Domestic Product (GDP), health and air connections; where, in the spreader set there are those countries that have high, medium or low values in the different characteristics; however, the aspect that all the countries belonging to the separator set share is a high value in air connections.

## I. INTRODUCTION

The COVID-19 pandemic has hit the global at a colossal The COVID-19 pandemic has hit the worldwide at a gigantic scope. With overall announced instances of 5.34 million it seriously affects mankind. Being a profoundly infectious illness, it has given worldwide wellbeing administrations their most serious test. Different nations are battling to limit the misfortunes because of the episode, in any case a typical attribute is implementing lockdown, which has become the primary protection system. Scientists are working nonstop to discover a forward leap in the diagnostics and treatment of the pandemic. Simulated intelligence innovation is valuable for quick medication advancement and treatment. In the beginning period of COVID-19 pandemic, the clinical society in China analyzed the infection utilizing processed tomography (CT) and X-beam pictures because of the limit of testing units. Profound learning neural organization model have additionally been utilized for COVID-19 analysis.

Computer based intelligence helped canny humanoid robots can be utilized to diminish the human contact and spread of COVID-19. In Italy robots have been utilized for estimating pulse, oxygen immersion and temperature of patients. Robots have likewise discovered applications in sanitizing and disinfecting of public spots, COVID-19 testing, food and medication conveyance just as engaging patients in clinics and isolate focuses, accordingly lessening the responsibility of specialists and attendants.

Expectation of the spread of infection and giving the rules or avoidance measures is another AI application in COVID-19. Kaggle and GitHub are the two sites where the ongoing information of COVID-19 is totaled. This incorporates affirmed cases, dynamic cases, restored cases and passings in every country. This informational collection can be utilized for anticipating the dynamic cases across various districts of the world so that proper measure of wellbeing framework can be made accessible to these spots.

Coronavirus' high transmission rate and at first gentle indications makes it almost un-discernible at a beginning phase [1]. The forecast of vulnerable populaces and recognizable proof of asymptomatic transporters of COVID-19 can assist with halting the spread of infection. Past meta-examinations and associate investigations have found illnesses and hidden ailments that has affected a person's probability of COVID-19 diseases and resulting hospitalization. These ailments incorporate those, for example, genuine heart conditions [2], malignancy [3], type 2 diabetes mellitus [4], constant kidney illness [8], weight [9], and persistent obstructive pneumonic infection [2][10]. These outcomes gave helpful experiences into the danger variables of SARS-Cov-2 diseases. Notwithstanding, the vast majority of these examinations just put together their investigation with respect to suggestive and phenotypical examples of COVID-19, rather than their genotypic changes. Expanding on comorbidity designs saw in past research, this examination utilizes Machine Learning with regards to haplotype squares to recognize hereditary variations that can show a person's

helplessness to COVID-19 disease. These COVID-19 hereditary areas of interest, for example, a change recognized by past scientists in the angiotensin-changing over compound 2 (ACE2), exist and fill in as a significant impact to COVID-19 helplessness [5]. In this paper, we initially break down GWAS (Genome-wide Association Studies) information of various illnesses to recognize Single Nucleotide Polymorphism (SNP) that firmly connects with the presence of that specific sickness. Then, at that point, these recognized SNPs are sorted into haplotype blocks. Three co-affiliation esteems are then determined for every haplotype block in each comorbid illness to show how much that haplotype block adds to every one of the seriousness conditions. At last, the outcomes are utilized to prepare an Artificial Neural Network (ANN) and Random Forest (RF) model that can classify people into three classifications: (I) COVID-19 contaminated, (II) hospitalized, and (III) serious conditions

## II. RELATED WORK

- Zhao et al. [27], present an index to calculate the influence of a node based on the number of communities to which it belongs.
- Berahmand et al. [28], propose a local approach based on the detection and expansion of central nodes. The proposed algorithm can detect all the communities of the graph in a network using local information and identify several functions of the nodes.
- Berahmand et al. [29], propose a new measure of semilocal centrality that can assign higher ranges or structural holes as better diffusers in the network; therefore, the proposed centrality avoids the selection of separators that are very close to each other.
- Berahmand et al. [30], demonstrate that, in data sets with a rich-club, it is better to use degree centrality to find influential nodes because it has linear time complexity and uses local information.
- Berahmand et al. [31], propose a new local classification measure to identify the influence of a node, using the propagation capacity of the nodes based on their essential location parameters, such as the degree of the node, the degree of its neighbors, the standard links between a node and its neighbors and the inverse clustering coefficient.
- Wang et al. [32], study the identification of influential spreaders in complex networks based on several centrality indices.
- His et al. [33] and Han et al. [34] propose some node classification algorithms based on the identification of structural holes. A structural hole is known as the phenomenon that occurs when a node connected to multiple local bridges (multiple communities) is removed, and space is produced.
- Li et al. [35], present a classified neighbor algorithm to quantify the nodal propagation capacity. The results show that the proposed algorithm can effectively control the outbreak of epidemics in many real-world systems.
- Wang et al. [36], propose a measure of influence to quantify the propagation capacity of nodes in complex networks.
- Yan et al. [37], propose a method that takes into account several aspects of node properties, including local topological characteristics, central location, propagation characteristics, and ownership of neighboring nodes.

## III. PROPOSED METGODOLOGY

### MATERIALS AND METHODS

In this section, we present the way of model the multiplex networks, and the methodology to analyze and identify the most spreader countries of COVID-19. This study is divided into four phases, which are:

- 1) Data collection: In this phase, we build the data set through a statistical analysis applied to the information obtained from the IMF, WB, WHO and IT.
- 2) Construction of networks: In this phase, based on the similarity of the characteristics for each country, we model the monoplex and multiplex networks.
- 3) Analysis of spreader nodes: For the modeled networks, we use an adaptation of the VSP to identify spreaders countries in multiplex networks.
- 4) Analysis of results: In this phase, we show the study of the countries that are classified as spreaders, which cause the rupture of the multiplex networks.



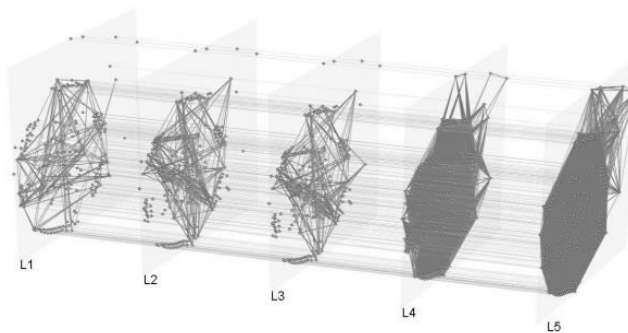


Figure 1: Graph of the GDP multiplex network.

Specifically, in this work, we modeled two 5-layer multiplex networks; where each layer represents the relationship between each pair of countries  $v$  as follows:

- Layer 1 (L1), for Human Development Index and its components.
- Layer 2 (L2), for Human Development Index Trends, 1990-2018.
- Layer 3 (L3), for the Inequality-adjusted Human Development Index.
- Layer 4 (L4), for the air travels (inbound and outbound) between each country.
- Layer 5 (L5), L5.1 for the number of infections and deaths network, and L5.2 for the GDP and health network

#### IV. RESULTS

In this section, we show the results and discussion on the main structural metrics of the modeled networks and the countries that cause the spread of COVID-19.

In Table 1, we present the numerical values for the average, variance and the low and high limits for each structural metric and the closeness and betweenness centralities with 95% level of certainty (for each layer).

TABLE 1: Structural metrics of layers.

ID	Degree	Clust. C.	Triangles	Closeness C.	Betweenness C.	Diam.	Path L.
L1	Av.	35.630	0.933	822.361	0.812	2	1.042
	Var.	421.636	0.012	335328.341	0.042		
	Low L.	34.178	0.921	741.032	0.742		
	High L.	40.083	0.945	921.225	0.842		
L2	Av.	38.761	0.215	823.263	0.815	3	1.099
	Var.	422.462	0.092	383342.402	0.0624		
	Low L.	33.712	0.159	729.631	0.763		
	High L.	43.826	0.271	916.831	0.831		
L3	Av.	37.405	0.946	837.774	0.824	4	1.322
	Var.	423.726	0.015	395358.351	0.064		
	Low L.	34.515	0.929	749.520	0.789		
	High L.	40.294	0.964	926.028	0.860		
L4	Av.	190.342	0.992	20129.969	0.971	2	1.056
	Var.	4.841	0.001	4842.545	0.001		
	Low L.	186.893	0.989	20120.201	0.970		
	High L.	193.257	0.994	20139.736	0.973		
L5.1	Av.	3.437	0.191	5.964	0.203	1	1
	Var.	10.066	0.145	217.914	0.029		
	Low L.	2.991	0.138	3.892	0.146		
	High L.	3.882	0.245	8.036	0.260		
L5.2	Av.	54.869	0.654	1239.767	0.549	3	1.86
	Var.	883.359	0.022	883668.239	0.020		
	Low L.	50.697	0.633	1107.825	0.529		
	High L.	59.040	0.675	1371.709	0.569		

Based on the information presented in Table 1, we can see that L1 to L4 and L5.2, have characteristics of the smallworld model [73], while the layer 5.1 has characteristics of the scale-free model [74]. For example, L3 has a clustering coefficient of 0.952 and an average path length of 1.32, while L5.1 has 0.191 and 1, respectively. On the other hand, for closeness and betweenness centralities, L1 to L4 and L5.2 have high values, while L5.1 has low values.



With using matplotlib we visualizing the total number of covid case(Active, Recovered, Deceased) based on the datasets we have using Matplotlib And then making a plot for the hotspot and death rates in the hotspot for the selected countries.

The MSE, MAE, RMSE are mainly used metrics to evaluate the prediction error rates and model performance in regression analysis.

- MAE (Mean absolute error) represents the difference between the original and predicted values extracted by averaged the absolute difference over the data set.
- MSE (Mean Squared Error) represents the difference between the original and predicted values extracted by squared the average difference over the data set.
- RMSE (Root Mean Squared Error) is the error rate by the square root of MSE. Based on the above equation we are going to find the values of MAE, MSE, RMSE for LGBM, RFR, XGB & Tensorflow with SKLEARN METRICS.

## V. CONCLUSION

In this work, we present an analysis of the countries that are spreaders of COVID-19, based on the main socio-cultural, economic, and connection characteristics, such as GDP, life expectancy, number of air travel, and budget for health, among others.

The results show that the methodology, can cause the rupture of the 5-layer multiplex network and help identify the spreader countries and obtains a classification of the countries based on their characteristics, where, in the spreaders set, the countries have high, medium or low values in the different socio-cultural and economic aspects; however, the characteristic that everyone shares are the high value in air connections.

On the other hand, we can affirm that to mitigate a second outbreak of COVID-19 in the world, the countries that are in the union of both separator sets must reinforce their sanitary measures; in contrast, the countries that are at the intersection of the two separate sets, in addition to improving their sanitary measures, must regulate airflow to contain the spread of the disease. Based on the information collected and modeled (until May 15, 2020), we can affirm that, by changing the relationships of the air flow, the risk of a second outbreak of COVID 19 can be minimized; however, we cannot quantify how much it can help.

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