C19-TraNet: an empirical, global index-case transmission network of SARS-CoV-2

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Abstract

Originating in Wuhan, the novel coronavirus, severe acute respiratory syndrome 2 (SARS-CoV-2), has astonished health-care systems across globe due to its rapid and simultaneous spread to the neighboring and distantly located countries. To gain the systems level understanding of the role of global transmission routes in the COVID-19 spread, in this study, we have developed the first, empirical, global, index-case transmission network of SARS-CoV-2 termed as C19-TraNet. We manually curated the travel history of country wise index-cases using government press releases, their official social media handles and online news reports to construct this C19-TraNet that is a spatio-temporal, sparse, growing network comprising of 187 nodes and 199 edges and follows a power-law degree distribution. To model the growing C19-TraNet, a novel stochastic scale free (SSF) algorithm is proposed that accounts for stochastic addition of both nodes as well as edges at each time step. A peculiar connectivity pattern in C19-TraNet is observed, characterized by a fourth degree polynomial growth curve, that significantly diverges from the average random connectivity pattern obtained from an ensemble of its 1,000 SSF realizations. Partitioning the C19-TraNet, using edge

betweenness, it is found that most of the large communities are comprised of a heterogeneous mixture of countries belonging to different world regions suggesting that there are no spatial constraints on the spread of disease. This work characterizes the superspreaders that have very quickly transported the virus, through multiple transmission routes, to long range geographical locations along with their local neighborhoods.

Keywords

SARS-CoV-2, COVID-19, infectious disease, global transmission routes, spatio-temporal network, pandemic

Introduction

Recent outbreak of COVID-19 has been emerged due to a new species of human infecting coronaviruses (HCovs), namely, SARS-CoV-2¹ that was isolated from a cluster of pneumonia cases in Wuhan, capital city of Hubei Province, China² in December 2019. It rapidly spread across the globe and was declared as a Public Health Emergency of International Concern (PHEIC) on January 30, 2020³, and was later declared a pandemic on March 11, 2020 by the World Health Organization (WHO)⁴. As of June 25, 2020, more than 9.1 million confirmed cases, and more than 0.47 million deaths have been reported due to COVID-19 in 216 countries/territories⁵. The outbreak is attributed to a zoonotic transmission of SARS-CoV-2 from primordial or intermediate host to humans, it could have further propagated through human-to-human contacts^{6,7}. Globalization of transport systems *via* air, sea and land routes has resulted in drastic decrease in journey time alongwith an unprecedented increase in transport volume of passengers. Although global transport has played a pivotal role in world's economic growth, it has also facilitated the disease causing agents to move to remote and otherwise unreachable places very quickly⁸, and therefore has enhanced the potential of any endemic to become a pandemic⁹.

In the past five centuries the world has witnessed several major pandemics, like, plague ¹⁰ (caused by Yersinia pestis), cholera¹¹ (Vibrio cholera), influenza ¹² (influenza virus), HIV/AIDS ¹³ (HIV), SARS ¹⁴ (SARS-CoV) etc., that had badly affected most of the world population as well as economy. All these pandemics had been originated in localized regions and had different means of human-to-human transmission, however, they were transported to distant geographical locations by human movements via air, land or sea transport ^{15–18}. There are many other emerging, reemerging infections, with varying consequences in terms of severity, morbidity, mortality, which the world continues to confront ¹⁹. Different epidemiological strategies, like, modeling disease dynamics, spread, mitigation and other epidemiological parameters of different outbreaks have been applied successfully in the past ^{20–22}. Network theoretic approaches have also been successfully utilized to gain understanding about the topology of different epidemiological disease transmission networks ^{23–26}. Topological understanding of infection transmission networks provides us critical insights about infection growth and distribution. Furthermore, knowledge of potential transmission routes allows us to devise effective control strategies to contain infection ²⁷.

Due to lack of specific medication for SARS-CoV-2, non-pharmaceutial containment based intervention methods have become indispensable tools to grapple with the infection. A large number of studies are being published to investigate important metrics, like, CFR, basic reproduction rate (R_0) , spread kinetics etc., however, a comprehensive study investigating the transmission routes of the virus across countries is still lacking. The actual structure (topology) underlying the global spread of the SARS-CoV-2 is also less explored. To prevent virus re-invasion in the countries/territories/regions (from where the virus has been eradicated) considering large incubation period of SARS-CoV-2, at this stage of outbreak, it is crucial to gain insights about the short range human-to-human contacts as well as long range geographically separated country-to-country global transmission pathways. It may have implications in making SARS-CoV-2 prevention policies as well as better prepare ourselves to fight against future outbreaks. In this study, we have constructed an empirical

global transmission network of SARS-CoV-2 and explored its topological space to explore the mechanism of global spread of infection. Increased topological knowledge will provide us the understanding about the epidemiological dynamics of the virus invading remote geographical locations.

Methods

Network construction

In this work, we have constructed the index-case empirical global transmission network of SARS-CoV-2 by manually going through the daily situation reports published by WHO. government press releases of various countries, their official social media handles (facebook, twitter), and other online news reports providing relevant information regarding the travel history of the patients for a period of 84 days ranging from January 13, 2020 to April 5, 2020. The transmission network is a dynamic network having the potential to grow on daily basis. Countries comprise the nodes of this network, while infected index-case individuals carrying the infection from a given country X to some other country Y connect these two countries with a directed link with X as the source node and Y as the target node. The direction of an edge indicate the flow of virus infection across borders. The connection between two countries have been placed on the basis of travel history of the patient. Any foreign national reported to be corona positive in any country has been considered as a carrier of virus to that country irrespective of his home nation. For the countries reporting more than one patient as their index-cases, if the reported patients had different travel histories we first observed the timeline to find the countries in which virus had been already spread out and if the the virus had already reached in the source countries then we placed a link between all these source countries with the target country. On the other hand for the source countries where the virus had yet not reached, we considered that the patient has contracted the virus enroute and did not place link between them.

Stochastic scale free (SSF) random network models

SARS-CoV-2 or any other outbreak that spread through human-to-human contacts will follow a peculiar spread pattern where the infection starts from a source area and then gradually spreads across other countries/areas/regions. To model this specific spread pattern, we are proposing a novel algorithm, namely, stochastic scale free (SSF). SSF is developed as an extension of the basic Barabási-Alberts (BA) model of scale free network. In the proposed SSF algorithm, network grows stochastically over time with number of nodes and their associated edges both being drawn from an appropriate distribution. The algorithm follows three basic steps: (i) The infection spread is unidirectional i.e. from source to target, new nodes (targets) attach preferentially with already existing nodes (source) and have linkage probabilities proportional to source degree. (ii) At every time step, any number of nodes $(0, 1, 2, \ldots, maximum-nodes)$ can be incorporated into the network. (iii) Every node can bring one or more number of links $(1, 2, 3, \ldots, maximum-nodes)$ with it. The key purpose of stochastically adding both nodes and edges is to model the index-case of SARS-CoV-2 infection across various countries as a growing transmission network. In this network, the index-case import in various countries may have two different scenarios, namely, (i) more than one country can import their index-case on any given day i.e. more than one nodes may be added at a single time step. (ii) a country can receive their index-case from more than one countries *i.e.* an incoming node may have more than one in-degree.

The main characteristic of the growth of C19-TraNet is that initially very few new countries get infection so the probability of infection transmission to new countries at any given day is very low, however, this probability increases very rapidly with increase in number of infected countries. Therefore, while generating an SSF model of C19-TraNet, to obtain the number of nodes and links associated with them at a unit time interval t (one day), we have used beta distribution that is given by $f(x; \alpha, \beta) = \frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)\Gamma(\beta)}x^{\alpha-1}(1-x)^{\beta-1}$ where Γ is a gamma function, and α , β are two non-zero parameters that control the shape of this distribution. The scaling parameters at any time interval t were computed as $\beta_t = \frac{Max-time-Current-time}{Max-time}$

and $\alpha_t = 1 - \beta_t$, where Max-time is the number of days for which the infection is to be modeled (84 in the current study) and Current-time is the t^{th} time step. On the other hand, scaling parameters $\alpha = 0.05$ and $\beta = 0.95$ were qualitatively selected to draw the number of edges associated with the incoming nodes. The small value for α and a high value for β are deliberately selected considering a very low average connectivity (≈ 2.1) of C19-TraNet. The maximum number of nodes (maximum-nodes) that can be incorporated into the network at a discrete time step is given by maximum-nodes = $\langle k_{in+out} \rangle + 1\sigma$, while maximum number of edges that a node can bring along with it was computed as maximum-nodes = $\langle k_{out} \rangle + 1\sigma$. Values obtained were truncated to retain only the integer part. Corresponding to the manualy curated C19-TraNet, we constructed an ensemble of 1,000 stochastic scale free random networks having same number of nodes, and approximately same number of edges.

Global network metrics and community detection

Four global network metrics, namely, (i) degree (k) distribution, (ii) network density (ρ) , (iii) average clustering coefficient (C), and (iv) average path length (L) were estimated for C19-TraNet and compared with the corresponding 1,000 SSF random network models generated via proposed SSF algorithm. The degree of a node is the number of edges connected with it. In a directed network, the number of edges incident on a particular node constitute its indegree (k_{in}) , while the number of edges extending outward constitute its oudegree $(k_{out})^{28}$. The in and out degree distributions of a network are defined as fraction of nodes having k incoming or outgoing links. Furthermore, we computed the density of network that is defined as a fraction of existing edges in the network to the all possible edges i.e. $\rho = \frac{m}{\binom{n}{2}}$. We also enumerated clustering coefficient for every node that is defined as the number of edges existing between first neighbors of the node i to the total possible edges existing between the first neighbors, averaged over all the nodes i^{29} . If N_i is the set of nodes directly

connected to node i then its clustering coefficient for a directed network is defined as

$$C_i = \frac{|\{e_{jk} : v_j, v_{\in} N_i, e_{jk} \in E\}|}{|N_i|(|N_i| - 1)}$$

, where E is the edge set of network G(V, E). Average path length of a network is the average of geodesic paths between all possible pairs of nodes in the network ²⁹ and is defined as

$$L = \frac{2}{n(n-1)} \sum_{a=1}^{n-1} \sum_{b=a+1}^{n} \delta_{ab}$$

. We identified communities based on edge betweenness, where the network is partitioned into node sets by removing high betweenness edges³⁰. We generated 1,000 random realizations of SSF models and Mann-Whitney U test was performed on distributions of average outdegree obtained at different time steps for both real and random networks³¹.

Results and Discussion

The dynamic effects of heterogeneous communication routes has been central to the propagation of many diseases³², hence the interplay between them and the underlying transmission network of SARS-CoV-2 across different countries/territories/areas is the focus of this study. We catalogued the first person diagnosed to have contracted SARS-CoV-2 virus for 187 countries. By investigating the travel history of index-cases from government press releases, their official social media handles and other online news reports, we inferred a probable source (country where the patient contracted the virus) and the target (country confirming COVID-19 infection in the diseased) of each edge to be incorporated in the empirical COVID-19 global transmission network (C19-TraNet). The constructed C19-TraNet is comprised of 187 nodes and 199 directed edges specifying the route of infection transmission from the source country to the target country (1a). The final network is a combined snapshot representing SARS-CoV-2 transmission across the countries that has grown over a

period of 84 days from January 13, 2020 to April 5, 2020.

SARS-CoV-2 global transmission routes

The outbreak originated from China (Western Pacific region) December 30, 2019 and within two months (by February 25, 2020) the virus had been spread to at least one country of all the six WHO regions. By the end of January, the contagion had been reported in five WHO regions, namely, Western Pacific Region (45%), South-East Asia Region (40%), European Region (13.33), Region of Americas (5.56%) and Eastern Mediterranean (4.54%). The numbers in parentheses indicate percentage of infected countries per region. Except Malaysia and Spain, which imported virus from Singapore and Germany, respectively, all the other 23 countries imported it from China. Global transmission of SARS-CoV-2 can broadly be attributed to two tidal waves, namely, (i) a Chinese wave, from the date of origin of outbreak till the end of January, 2020 and (ii) a European wave that took off from mid February and continued until almost all the countries got infection. The major reason for this quick spread is, (i) emergence of China as an economic globaliser in past few decades that has increased international business and trade, and (ii) expansion of highly connected local and global travel systems ³³.

Travel data suggests that approximately 3 billion people traveled through trains or flights during the Chunyun (Lunar New Year) holidays³⁴. Also, a large volume of passengers have been estimated to travel within³⁵ and outside China³⁶ through land and air routes from previous travel data. These studies suggest a significant relation between transport volume and likelihood of imported cases of SARS-CoV-2. Although ban was implemented in Wuhan city on January 23, 2020, which was followed by travel restrictions to 14 of its neighboring cities of Hubei Province on January 24, 2020, however, by this time the virus had been transmitted to other Chinese cities as well as to 9 different countries belonging to four WHO regions³⁷. From these sources, the virus kept on spreading locally as well as outside China till the end of January when the results of containment measures became visible

with overall decrease in cases exported from China³⁸ (diminishing the effects of Chinese wave). Then from mid of February, second tidal wave took off from European Region and circulated the infection to most parts of the globe. Italy, Iran and Spain were among the super spreaders which aggressively spread the contagion. Owing to large incubation period of SARS-CoV-2 along with lack of necessary infrastructure, sophisticated testing facilities, herd immunity, a large number of undocumented asymptomatic or presymptomatic cases passed undetected into susceptible populations of different countries/territories/areas, thus provided unprecedented routes to virus transmission^{39,40}. These large number of possible routes also increased the strength of second wave by providing opportunities to circulate the virus to most of the uninfected countries belonging to different regions. Therefore, we may infer that a large incubation period, high movement and multiple routes helped global circulation of the disease.

Global topological metrics of C19-TraNet

The final network is sparse with a very low density (0.01). This is expected, as we constructed only the index-case transmission network. Average connectivity of the network is found to be 2.128, computed by ignoring the edge directions. Average or characteristic path length (APL) of a network represents closeness in the network, so lesser the magnitude of APL closer the nodes are. The characteristic path length of C19-TraNet is found to be 1.56, while its diameter and radius are found to be 4 and 1, respectively. As per APL, most of the countries are infected by one or two transmission events. Network diameter suggests that most distant country in the network is infected by a maximum of four transmission events. These short path related metrics explain the quick global spread of virus, *i.e.* the virus got access to those countries which have a wider reach on the globe that helped in propelling the infection across the world in a very short span of time. Short APL and a very small network diameter also indicate that there are some long range connections connecting distant geographical locations bringing an element of small worldness to the network. There are some hub nodes (very few)

with a large number of edges in C19-TraNet. Plotting the degree distribution on log-log scale, we obtained a straight line (with scaling exponent -1.63) indicating that C19-TraNet follows power law degree distribution and possess the property of scale freeness (Fig. 1b). The power law pattern of degree distribution has a simple interpretation that only few countries in the network are responsible for spreading the virus to most other countries. It has been reported that for any scale free disease transmission networks with scaling exponent less than 3, the virus reproduction number (R_0) is greater than 1 *i.e.* very few nodes (super spreaders) are sufficient to maintain virus load in the susceptible populations ⁴¹. Its main implications lie in designing control strategies, like, targeting the super spreaders by implementing the basic containment strategies *e.g.* prohibit transport, sanitization etc..

Global infection exportation potential (GIEP)

Emergence of a large number of countries in C19-TraNet as leaf nodes (having very low average clustering coefficient) implies that the infection was not equally spread by all the countries, rather only a few countries were responsible for its spread. We observed that only 38(≈ 20%) countries among 187 have at least one edge projecting outward. Among them, only seven countries are found to have an outdegree of 10 or more, with Italy at the top of the tally contributing a total of 47 exportation events followed by china (29) and Iran (16) (see Table 2). Furthermore, infection import to every target node in C19-TraNet would have occurred in two possible ways, either a domicile of the target country has brought the virus from a source country, or a foreign national visiting a source country has spread the infection to the target country. To investigate the proportion of these two cases in the global spread of infection, we enlisted the nationalities of SARS-CoV-2 carriers and found that most of the index-cases are local nationals who contracted the infection in some source country and then brought it to their home nations.

A total of $131 (\approx 65\%)$ out of 202 index-cases were found to be local nationals. Here we mentioned 202 index-cases because some countries, like, Kuwait, Aruba, Kazakhstan had

reported more than one cases on the same day (Supplementary Table 1). Remaining 71 (45%) index-cases were foreign nationals belonging to 22 countries. Among these foreign nationals, 19 are found to be Chinese followed by 14 Italians (see Table 3). To estimate the global infection exportation potential (GIEP) per country, we further normalized the number foreign nationals belonging to each of the source country by the total number of exportation events (71) carried out by foreign nationals (Fig. 2). Above data clearly suggests that although most of the infections are imported to the target countries by their domiciles, however, a significant proportion of countries are infected by foreign nationals. As an example, the number of virus transmission events (47) that took place from Italy is very high, however, there were only 14 Italians involved in these transmission events. Thus, in the light of above data, it can be inferred that highly robust and efficient transportation system has played a huge role in spreading the infection across international borders. Therefore, more caution is required specially from aviation departments regarding individual's health at international transportation junctions.

Connectivity dynamics modeling and analysis of C19-TraNet

Since the pandemic evolves with time, so exploring the connectivity of growing C19-TraNet at different instances of time (t) can provide critical insights about the network topology and growth mechanisms. Keeping that in mind we computed average out-degree of C19-TraNet for each of the 84 days. Further, 1,000 random networks using SSF model corresponding to C19-TraNet were generated and average out-degree vectors for all these random networks were computed which were further averaged to yield a single vector. We then performed Mann-Whitney U test to verify the null hypothesis (H_0) that the two outdegree distributions (of real network and average of 1,000 random networks) are equal, which is refuted by a very low p - value = 3.041e - 09. Distributions of average outdegree per unit time (days) for both real and average of SSF models are shown in Fig 3a. We fitted four distributions viz. linear, logarithmic, exponential and, polynomial (up to order four), among which 4^{th}

order polynomial curve is found to have the highest adjusted coefficient of determination (Adj. R^2) for both the real and SSF distributions (Table 4).

In the initial growth phase (i.e. till the end of January, 2020), both the curves followed same trend, however, from February onwards a peculiar phase of no growth (for about a fortnight) is observed in C19-TraNet which is absent in the random networks (Fig 3a). This delay emerges due to implementation of Wuhan ban and can be attributed to the border control measures including local and international travel ban, quarantine, symptom screening at airports etc. simultaneously adopted by China and other countries. As stated earlier, most of the infections in Chinese wave are disseminated from China, therefore the two consecutive travel bans implemented by China substantially reduced the rapid local and international flow of virus 42,43. The second surge in average connectivity (starting from the end of February, 2020) marks the onset of European wave which can be attributed to passage of undocumented pre- or asymptomatic infected people from countries other than China where restrictions were not that much strict ^{39,43}. Though the contagion invaded most of the world, however, our model suggests that these containment measures have delayed the global transmission of virus by 51 days. If the growth had continued to follow the initial trends, the virus would have invaded South Sudan (187^{th} country to be infected) on February 13, 2020. We obtained similar trend, in reverse order, characterized by a phase of no growth for approximately same period when density is plotted against time (see Fig 3b). Network density peaked when the network was very small. With the passage of time, addition of new countries brought small increase in network size in comparison to the network order resulting in an overall decrease in network density.

Community structure of C19-TraNet

We explored the structure of C19-TraNet by leveraging edge betweenness, in which high betweenness nodes were recursively removed to identify sparsely connected 'node sets' (communities) whose members are densely connected among themselves ³⁰. Communities provide

an insight about the local connectivity patterns in C19-TraNet by partitioning the network into densely connected, small sub-graphs. A total of 23 different communities (Fig. 4a) were obtained with the largest set consisting of 39 countries followed by 16 countries in the second community and 14 in the third set (Table. ??). Most of the communities were small sized, while very few consisted of large number of countries (hubs), indicating that few countries (having high volume of international traffic) have acted as super spreaders. We further grouped the countries into six geographical regions as per WHO, namely, European Region (ER), Western Pacific Region (WPR), South-East Asia Region (SEAR), Eastern Mediterranean Region (EMR), Region of the Americas (RA), African Region (AR) and enumerated the country share of each region per community.

As shown in Fig. 4b, most of communities are composed of a heterogeneous mix of countries from different regions. Most of the communities are comprised of countries from more than one region among which larger regions (in terms of number of countries) including ER, RA and AR are the major contributors. Approximately 62% of the countries in Community_0 belongs to ER followed by a relatively few countries of RA (15%) and AR ($\approx 13\%$) regions. Similarly, Community_1 is also comprised mostly of countries from two regions, ER (42%) and EM ($\approx 53\%$) (Fig. 4b). These results indicate that there is not any kind of positional constraint imposed on the spread of infection, *i.e.*, infected countries from a given region have spread the infection to their neighboring countries (short range interactions) as well as across non neighboring countries or territories which are geographically far away from them (long range interactions).

Summary and Conclusion

In this study, we have constructed the an empirical index-case global transmission network of infection caused by SARS-CoV-2. Our main objective here is to develop a systems level understanding of emergence and growth of COVID-19 from a local outbreak into a global

pandemic. To achieve this goal, we relied on the travel history of index-case patients obtained from various reliable sources. It allowed us to map multiple transmission routes through which the virus intruded into different geographical locations.

We observe that, after its origin in China, the global transmission of SARS-CoV-2 can be attributed to two waves, namely, the Chinese wave and the European wave. Initially, during Chinese wave, the virus invaded to a large number of neighboring as well as distantly located countries from China due to a large volume of international traffic. By the end of January, 2020, the effect of Chinese wave started to diminish due to implementation of various border control measures within and outside China. However, soon after a small stagnation phase, the virus started to spread from other infected countries mainly from European Regions. The main reason of this European wave was that a large number of asymptomatic patients (local or foreign nationals) passed undetected to different countries and by the time we responded, it had already victimized the whole world.

Topological structure of C19-TraNet is found to be sparse, however, its degree distribution follows a power law distribution, *i.e.*, it possess scale free property suggesting that few countries have played the role of super spreaders in virus transmission. Considering the C19-TraNet as an evolving network, we further modeled the temporal growth of its average outdegree and found a delay of 51 days in virus transmission that can be attributed to different border control measures. Data suggests that large incubation period, free flow of international traffic and lack of coordinated action at international level in implementing various control strategies have played a vital role in global transmission of the virus. Exploration of community structure of the network revealed that large communities are not comprised of countries from a single region, however, they are heterogeneous composition of countries from different regions suggesting the presence of local transmission, to neighboring countries of the same region, as well as long range transmission to countries belonging to different regions. These multiple transmission paths allowed the virus to rapidly invade susceptible subpopulations located in distant geographical regions. This conclusion emphasizes

the imposition of travel restrictions which although implemented, however, lack coordinated actions from different countries. It suggests that a coordinated action plan is needed to put in places to fight with any future outbreak.

The stochastic scale free (SSF) algorithm, proposed in this work to model the first case global transmission network of SARS-CoV-2, can be implemented very easily to model other human-to-human transmission disease networks with minor changes. The main advantage of the proposed algorithm is that the probability of infecting new nodes changes with change in number of infected nodes, that increases continuously until the network order approaches saturation.

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Author Contributions

 VS^* conceptualized and designed the research framework. VS^{\dagger} performed the computational experiments. VS^{\dagger} and VS^* analyzed the data and interpreted results. VS^{\dagger} and VS^* wrote and finalized the manuscript.

Conflict of Interests

The authors declare that they have no conflict of interests.

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Table 1: Number of countries per region present in individual community.

Community	European	Western	South-	Eastern	Region of	African
	Region	Pacific	East Asia	Mediter-	the Ameri-	Region
		Region	Region	ranean	cas	
				Region		
1	24	0	2	2	6	5
2	8	1	0	10	0	0
3	2	5	2	2	3	0
4	0	1	2	0	10	3
5	3	1	0	1	1	8
6	1	0	0	0	7	6
7	5	1	0	1	3	3

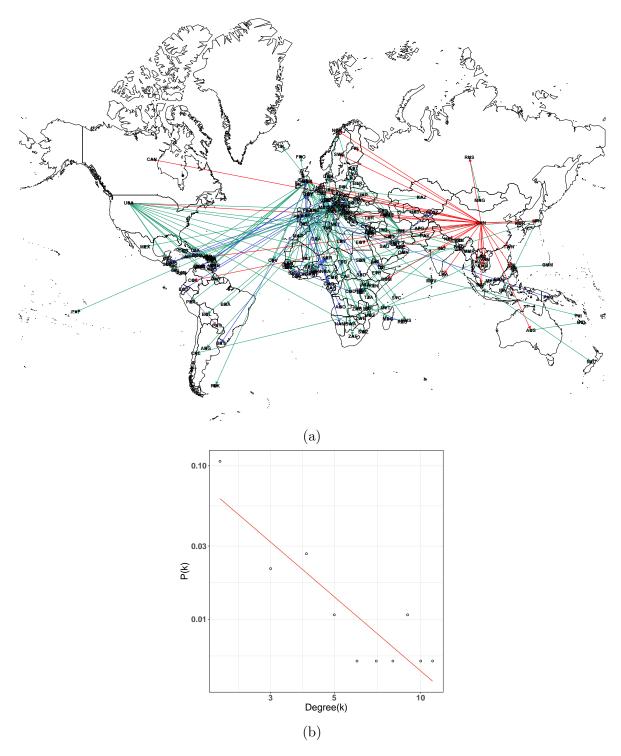


Figure 1: (a) Empirical global COVID-19 transmission network (C19-TraNet) with edges highlighted as per the distance of source nodes from the country where the first COVID-19 patient was reported, into three colors: red (primary spreader, i.e. China), green (secondary spreaders) and blue (tertiary spreaders). (b) Degree distribution of C19-TraNet with a power law fit having exponent -1.63.

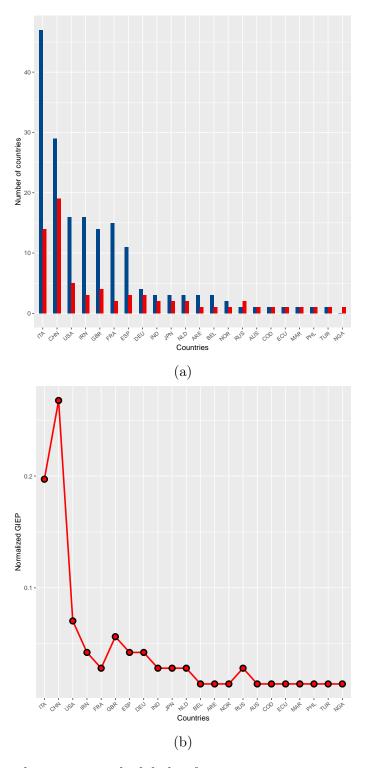


Figure 2: Outdegree histogram and global infection exportation potential (GIEP) of 22 source countries: (a) Total number of index-case exportation events from a source country (blue), and the number of such events carried out by its domiciles (red). (b) Global infection exportation potential (GIEP) that is defined as the ratio of index-case exportation events from the domiciles of a source country to the total number of such events (71). It may be noted that China has the largest GIEP followed by Italy and USA.

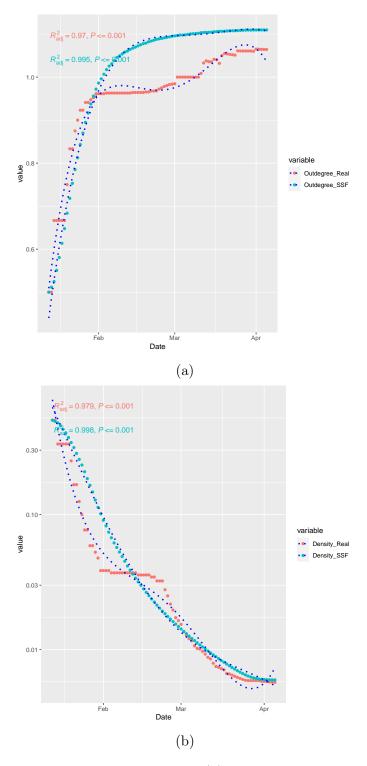


Figure 3: Disease dynamics of SARS-CoV-2. (a) Comparison of daily reported average outdegree (red circles) of growing C19-TraNet with the average of outdegree (cyan circles) obtained from an ensemble of 1,000 stochastic scale free realizations, modeled using parameters $\alpha = 0.05$, $\beta = 0.95$, maximum-nodes = 6 and maximum-nodes = 5. Blue colored dotted line indicates 4^{th} order polynomial curve fit. (b) Comparison of daily reported average density of C19-TraNet with average density obtained from 1,000 SSF models.

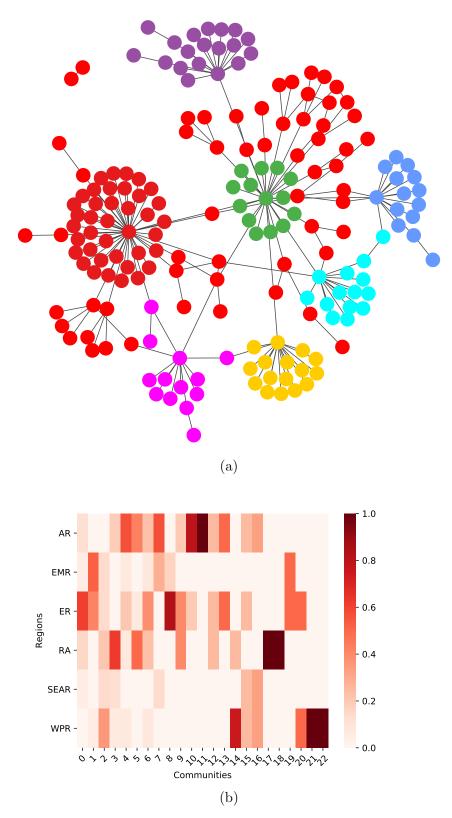


Figure 4: (a) Top seven communities of C19-TraNet based on edge betweenness. (b) Percentage of countries shared by individual region per community.

Table 2: Network metrics of countries with at least one outdegree.

Country	k_{in}	k_{out}	L
Italy	1	47	1.2034
Spain	1	11	1.1538
Iran	1	16	1.1111
French Republic	1	15	1.1176
United States of America	1	16	1.0000
United Kingdom	1	14	1.0667
Germany	1	4	1.8824
Switzerland	1	4	1.0000
Netherlands	1	3	1.0000
Portugal	2	1	1.0000
Japan	1	3	1.0000
United Arab Emirates	1	3	1.0000
India	1	3	1.2500
Belgium	1	3	1.2500
Singapore	1	2	1.3333
Ecuador	1	1	1.0000
Norway	1	2	1.3333
Ghana	2	1	1.0000
Greece	1	2	1.0000
Malaysia	1	1	1.0000
Dominican Republic	1	1	1.0000
Morocco	1	1	1.0000
Saudi Arabia	1	1	1.0000
Hungary	1	1	1.0000
Cameroon	1	1	1.0000
Thailand	1	2	1.0000
CÃťte dâĂŹIvoire	1	1	1.0000
Australia	1	1	1.0000
Philippines	1	1	1.0000
Russian Federation	1	1	1.0000
Democratic Republic of the Congo	1	1	1.0000
Rwanda	1	1	1.0000
Mauritius	1	1	1.0000
Togo	1	1	1.0000
Burkina Faso	1	1	1.0000
China	0	29	1.9836
Turkey	0	1	1.5000
Panama	0	1	1.0000

Table 3: Number of domiciles of source country spreading infection to target countries and global infection exportation potential (GIEP) obtained by normalizing individual number by total out degree.

Countries	Number of domiciles of source country	GIEP
	spreading	
	the infec-	
	tion	
China	19	0.4043
Italy	14	0.2979
United States of America	5	0.1064
United Kingdom	4	0.0851
Germany	3	0.0638
Iran	3	0.0638
Spain	3	0.0638
French Republic	2	0.0426
India	2	0.0426
Japan	2	0.0426
Netherlands	2	0.0426
Russian Federation	2	0.0426
Australia	1	0.0213
Belgium	1	0.0213
Democratic Republic of the Congo	1	0.0213
Ecuador	1	0.0213
Morocco	1	0.0213
Nigeria	1	0.0213
Norway	1	0.0213
Philippines	1	0.0213
Turkey	1	0.0213
United Arab Emirates	1	0.0213

Table 4: R adjusted (R_{adj}) and p-values obtained by fitting different models on outdegree and density obtained from both C19-TraNet and corresponding SSF models (for comparison, average of 1,000 SSF models is used.)

	Outdegree			Density				
	Real		\mathbf{SSF}		Real		\mathbf{SSF}	
	$ m R_{adj}$	$p ext{-}value$	$ m R_{adj}$	$p ext{-}value$	$ m R_{adj}$	$p ext{-}value$	$ m R_{adj}$	$p ext{-}value$
Linear	0.623	2.80E-19	0.599	3.58E-18	0.441	3.54E-12	0.567	9.09E-17
Quadratic	0.762	1.01E-24	0.906	2.24E-37	0.725	5.95E-19	0.889	5.14E-34
\mathbf{Cubic}	0.887	6.54E-35	0.987	8.93E-70	0.882	1.96E-29	0.984	1.02E-64
Quartic	0.97	1.44E-55	0.995	2.14E-84	0.957	2.12E-44	0.994	1.72E-81
Quintic	0.977	1.02E-59	0.995	1.19E-84	0.972	5.75E-51	0.994	3.29E-81
Log	0.906	4.97E-44	0.911	5.16E-45	0.822	1.20E-32	0.896	3.00E-42
Exponential	0.536	1.50E-15	0.54	1.11E-15	0.906	4.57E-44	0.929	5.17E-49