

Pandemics and Networks: the Case of the Mexican Flu

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Abstract—The recent widespread of the new Mexican flu and *SARS* show the high dependency on contemporary traveling patterns. The air transport network is recognized as an important channel of epidemic propagation for different diseases. In order to predict epidemic spreading and the influence of protection measures, a mathematical model of the Susceptible - Infected - Susceptible (*SIS*) type is used. We compare three different networks, namely the air transport network (in the USA and Europe), Erdős-Rényi (*ER*) graphs and complete bi-partite networks in the light of graph theoretical results based on the *N*-intertwined model. Using the spreading parameters of the Mexican flu estimated in Mexico City, we determine the necessary speed of countermeasures such that the epidemic is stopped. Restructuring of the air transport in the case of the USA transport network does not improve protection, while in the case of the European transport network the number of infected nodes is reduced for 10%.

Keywords: *pandemics, networks, phase transition, Mexican flu*

1 Introduction

When an epidemic spreads across a large region, a continent or even planetary, it is called a pandemic. Some widely known examples are the Black Death (plague) in Europe in the 1300s, the smallpox in the New World in the 1500s [1], measles and diphtheria.

Influenza is one of the most common human and animal diseases which can easily become a pandemic. In our recent history, several different influenza pandemics emerged [29]: 'Spanish' influenza (1918), 'Asian' (1957), 'Hong Kong' (1968) and the 'Russian' influenza (1977). Finally, we were witnesses of the pandemic of the Mexican flu [2].

In order to predict epidemic spreading and the influence of protection measures, mathematical models are applied. The mathematical theory of epidemics has evolved from simple models with two states (Susceptible Infected Susceptible (*SIS*)) or three states (Susceptible Infected Removed (*SIR*)) described by deterministic equations with

homogeneous mixing assumption [10] to highly complex, multiscale models [3]. The additional complexity caused by traveling patterns and social structures has introduced different approaches such as diseases realism, metapopulation grouping and agent-based numerical simulations [7]. Unfortunately, the power of analysis decreases with increased complexity. We will use simplified assumptions in order to keep the model analytically tractable.

Population movement is the main cause of pandemics. The recent widespread of the new Mexican flu and of *SARS* show the high dependency on contemporary traveling patterns. Due to changes in life style, namely increased travel volumes and global shift of population to urban centers, pandemics are becoming a realistic threat to human society [33].

One of the most important novelties in epidemic modeling is the introduction of a network of contacts and traveling patterns. The homogeneous mixing assumption was shown not to be adequate [20]. Great attention is given to epidemics on different networks from random graphs [4], small-world graphs [28], to scale-free networks [31]. Generalization of the epidemic modeling to any network structure was recently proposed by Ganesh *et al.* in [15] and Newman [30]. Social networks as well as transportation networks exhibit a non-local, small-world effect, which makes these network an excellent propagation media [17], [14], [19].

From the first research by Rvachev and Longini [32] and Baroyan *et al.* [5], the air transport network is recognized as an important channel of epidemic propagation for different diseases from influenza [17], the recent pandemic of the Mexican flu [21] to HIV [14]. The worldwide air transportation network is found to be scale-free and small-world [18]. It was shown that contrary to the prediction of scale-free models the most connected cities are not the most central in the sense of shortest path betweenness. Several authors have studied the reduction of disease spreading using air line restrictions [13], [23], [16]. Due to the multicomunity structure of the network with hubs not being the most central nodes, the optimal strategy for flight cancellation is not the removal of nodes (cities), but the removal of intercommunity flights, which introduced an increase in spreading time [23] by 81% for the *SI* model. The international travel restrictions

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showed to introduce a delay of maximum 3 weeks [13] for the Susceptible Exposed Infected Recovered (SIER) model. The robustness of the air transportation network against virus spread is a complex problem and the network as a whole has to be considered.

Large population centers are ideal for the spread of disease. The deployment of vaccines in large areas can exceed 6 or 8 months [8] and for some diseases, a vaccine does not exist. Thus, it is interesting to consider applications of quarantine and similar measures to stop or slow down the spread. If the disease spread is stopped in one city by the means of quarantine, new carriers of infection can still arrive to the city infecting the susceptible population. The effectiveness of quarantine and of similar defenses depends on the introduction of new carriers in the population. We model a city as a node which can have infection introduced over the air transportation network from other cities with rate β per link and the deployment of protection measures can stop the spread after some exponentially distributed random time with rate δ per city. For this scenario, a *SIS* model is adequate, which has some theoretical results similar to the *SIR* model.

In *SIS* and *SIR* models, epidemics can be stopped if the application of measures against the virus are faster than the reproduction of the virus. The epidemic thus exhibits threshold behavior. The threshold can be defined as follows: for effective spreading rates τ (rate of spread divided by rate of protection $\tau = \beta/\delta$) below some critical value τ_c the virus in the network with N nodes dies out before a large population is infected with a mean epidemic lifetime of order $O(\log N)$. For effective spreading rates above the critical value τ_c , the epidemic persists and the number of infected nodes is large, with a mean epidemic lifetime [15] of order $O(e^{N^\alpha})$ for *SIS* model. The epidemic threshold is equal to the largest eigenvalue of the adjacency matrix of the underlying topology [15] and similar results exist for the *SIR* model [12], [10].

We will examine the influence of the air transport network on epidemic spreading in the light of graph theoretical results based on the N -intertwined model [26].

2 Epidemic model

We will model the epidemic spread using the N -intertwined *SIS* model introduced and discussed in [26].

An air transport network with N cities is modeled as a connected graph specified by a symmetric adjacency matrix A . We will model a city population as a single node in the network, such that it is assumed to be in an *infected* state, if there are carriers of infection among the population. If the infection is isolated from the rest of the population, the city is assumed to be *susceptible*, because new carriers can enter the city. The probability of infection is denoted by $v_i(t) = \Pr[X_i = 1]$, and that of

the susceptible state by $1 - v_i(t)$. The sum of the probabilities of being infected and susceptible are equal to 1 because a node can only be in one of these two states. The state of a city i is specified by a Bernoulli random variable $X_i \in \{0, 1\}$: $X_i = 0$ for a susceptible node and $X_i = 1$ for an infected node. We assume that the curing process per node i is a Poisson process with rate δ , and that the infection rate per link is a Poisson process with rate β which is imminent for all nodes and thus constant in the network. For a node i , we can formulate the following differential equation

$$\frac{dv_i(t)}{dt} = \beta(1 - v_i(t)) \sum_{j=1}^N a_{ij}v_j(t) - \delta v_i(t)$$

where a_{ij} is the element of the adjacency matrix A and it is equal to 1 if the nodes i and j are connected, otherwise it is 0. A node is not considered connected to itself, i.e., $a_{ii} = 0$. The probability of a city being infected depends on the probability that it is not infected $(1 - v_i(t))$ multiplied with the probability that a neighbor j is infected $a_{ij}v_j(t)$ and that it tries to infect the city i with the rate β . Detailed derivations are given in [26] and [25].

In the steady-state, where $\frac{dv_i(t)}{dt} = 0$ and $\lim_{t \rightarrow \infty} v_i(t) = v_{i\infty}$, for each node $1 \leq i \leq N$, we have that

$$v_{i\infty} = \frac{\beta \sum_{j=1}^N a_{ij}v_{j\infty}}{\beta \sum_{j=1}^N a_{ij}v_{j\infty} + \delta} \quad (1)$$

The model has a threshold value $\tau_c = \frac{\beta}{\delta}$ below which the epidemic extincts and the number of infected nodes in the meta-stable steady-state is 0. The threshold [26] is equal to

$$\tau_c = \frac{1}{\lambda_{\max}(A)}$$

where $\lambda_{\max}(A)$ is the maximal eigenvalue of the matrix A . If $\tau < \tau_c$, the epidemic will eventually be stopped, and for $\tau > \tau_c$ the infection will persist with the average number of infected cities equal to $y_\infty = \frac{1}{N} \sum_{j=1}^N v_{j\infty}$.

For example, the largest eigenvalue of a path graph (nodes on a line) is $\lambda_{\max}(A) \simeq 2$, while that of a star topology (all the nodes are connected to one central node) is $\lambda_{\max}(A) = \sqrt{N-1}$. These two graphs are interesting examples, as both have the same number of links $L = N-1$. Thus, a star topology is much more prone to an epidemic than a path graph.

For a general epidemic *SIR* model, similar threshold results exist [11], [12], [10]. If the ratio of the death to

infection rate is larger than the largest eigenvalue of the adjacency matrix of the graph $\lambda_{\max}(A)$, and the initial infected population is small, then the final infected population is also small. If the ratio is smaller than $\lambda_{\max}(A)$, the final population size is large.

3 Results and discussion

One of the most exciting facts about the threshold is that, if the curing ratio δ is increased such that the threshold is reached, the epidemic can be stopped. The threshold of an epidemic depends on the underlying network of contacts and travel patterns. The spreading effectiveness depends on the spreading and protection ratio. To illustrate the influence of traveling patterns on virus spread, we have used the direct airport-to-airport American traffic network maintained by the U.S. Bureau of Transportation Statistics and the European direct airport-to-airport traffic network obtained from the European commission for statistics Eurostat. The networks are not weighted; however, the model is extendable to heterogeneous settings [25]. The USA network consists of $N = 2188$ airports and $L = 31331$ connections or links. The European network consists of $N = 1247$ airports and $L = 22830$ connections or links. The N -intertwined model can be applied to many other air transport networks used in epidemiological research, as well.

The model gives a prediction for the threshold of a specific network structure. A network can be restructured such that it performs better with respect to virus spread. In order to estimate the air transport network's performance, we have compared the threshold for 3 different graphs with the same number of nodes and a similar number of links: namely, the air transport network (European, USA), the ER random graph and the complete bipartite graph. For large number of nodes, the ER random graph [6] is close to a regular graph, where all the nodes have the same number of neighbors. The complete bi-partite graph consists of two sets of nodes with 15 and 2173 for the USA network and 9 and 1238 for the European, which are connected to all of the nodes from the opposite set and not inside the set. Therefore, we compare the air transport network with a non-hierarchical structure and with a highly hierarchical structure. The epidemic threshold is given in the Tables 1 and 2.

In order to stop the pandemic spread over the air transportation network with $\tau_c = 6 \cdot 10^{-3}$, measures applied against the virus need to be $6 \cdot 10^{-3}$ faster than the infection process.

In the case of the recent the Mexican flu, parameters of the spread were estimated for Mexico City [9]. The spreading rate per contact, when recalculated for the N -intertwined model and applied to the air transport network is estimated to be $\beta = 0.0199 \text{ day}^{-1}$, while the recovery rate is $\gamma = 0.33 \text{ day}^{-1}$. If the epidemic is left

without intervention ($\gamma = \delta$) it can quickly spread with effective spreading rate of $\tau = \frac{\beta}{\gamma} = 0.0603$. In the case of the USA network, 30% of the cities will have the infection introduced, while for the same parameters the ER network will have 35% and the complete bi-partite graph 45%. The restructuring of the air transportation network into the bi-partite and the ER random graph would not help in the case of the USA network. In the Europe air transport network, 25% of the nodes are infected, while only 16% of the nodes are infected for the same parameters in the ER graph and 33% in the complete bi-partite graph. In order to stop the epidemic spread through air transport networks, either flights need to be reorganized - restructuring the network such that the threshold τ_c increases or faster measures need to be applied. Van Mieghem *et al.* show in [27] that disassortative degree-preserving rewiring increase the threshold. In case of the Mexican flu, the curing rate has to be higher than $\delta = 199 \text{ day}^{-1}$, which is a reaction of the order of a couple of minutes. In the case of a more homogeneous network structure as a ER random graph, the curing rate can be up to 10 times lower.

The largest eigenvalue of a graph $\lambda_{\max}(A)$ is always larger than the average degree d_{av} . In case of a regular graph, $\lambda_{\max}(A)$ is equal to the average degree [24]. This means that the smallest possible eigenvalue is equal to 2 for a cycle, while the largest possible threshold τ_c for any connected graph is equal to 0.5. From the point of view of an epidemiologist, the reduction of the air transport graph to a path graph is an excellent way to stop the pandemic, however, economists and tourists would disagree. A combined method of flight restriction hand in hand with efficient protection strategies seems to be the right way to address the problem. If additional measures are applied, they have to be fast.

Figures 1 and 2 show the number of infected nodes in the steady-state as a function of the effective spreading rate τ for the three different networks. Although the air transportation network has a low threshold, the number of infected nodes grows much more slowly with τ , than in case of the other two networks. Therefore, it is wise to be careful and take the whole range of the effective spreading rate τ into account when restructuring [22].

4 Conclusion

We have presented the N -intertwined epidemic model for pandemic spread over an air transport network. Based on the parameters estimated in the case of the Mexican flu in Mexico City [9], we have discussed whether an epidemic threshold can be reached and how a pandemic can be stopped. Because of the very small threshold and the necessity of traveling in contemporary world, a combination of flight restrictions together with an introduction of efficient protection strategies seems to be the best strategy

Table 1: Networks comparison, USA air transportation network.

	Air transport	Random ER	Complete bi-partite
N	2188	2188	2188
L	31331	31298	32595
d_{av}	28.6389	28.6088	29.7943
$\lambda_{\max}(A)$	144.6112	29.5880	180.5409
τ_c	0.0069	0.0338	0.0055

Table 2: Networks comparison, European air transportation network.

	Air transport	Random ER	Complete bi-partite
N	1247	1247	1247
L	22830	22786	22284
d_{av}	18.3079	18.2727	17.8701
$\lambda_{\max}(A)$	80.9576	19.3552	105.5557
τ_c	0.0124	0.0517	0.0095

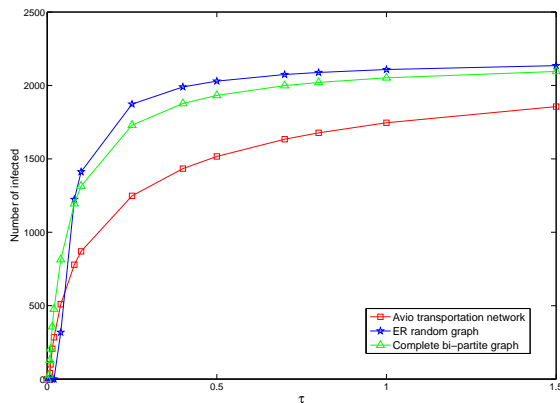


Figure 1: USA air transportation network compared with complete bi-partite and ER random graph topologies.

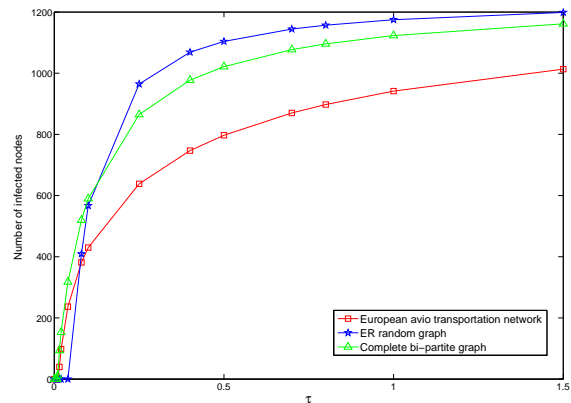


Figure 2: European air transportation network compared with complete bi-partite and ER random graph topologies.

to reach the threshold. Further, we compare the threshold of two air transport networks with 2 structurally different networks, namely the ER random graph and the complete bi-partite graph with the same number of nodes and a similar number of links. Although, the ER network is more robust against epidemic spreading for values of effective spreading rate τ close to the threshold τ_c , for larger values of τ it exhibits worse behavior than the air transport network.

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