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Epidemic threshold : A new spectral and structural approach of prediction

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Abstract

The epidemiological modelling and epidemic threshold analysis in the networks are widely used in the control and prediction of infectious disease spread. Therefore, the prediction of the epidemic threshold in networks is a challenge in epidemiology where the contact network structure fundamentally influences the dynamics of the spread. In this paper, we design and experiment a new general structural and spectral epidemic threshold approach of prediction that more captures the full network structure by using the number of nodes, the spectral radius, and the energy of graph. We drive the simulations overall on 31 different networks types and topologies. The simulations show similar results of the epidemic threshold values compared to the *MF*, *HMF* and *QMF* widely used theoretical benchmarks approaches. With data analytic and data visualization technics, the results show that the new approach is similar to the earlier, further captures the full network structure, and is more accurate than the earlier approaches. The new approach offers a new general and spectral approach to analyse the spreading processes in a network. The results are both fundamental and practical interest in improving the control and prediction of spreading processes in networks. Particularly meaningful to decision-makers in public health.

Keywords

Epidemic threshold ; Energy of graph ; Eigenvalues ; Network structures ; Complex networks ; Infectious disease.

I INTRODUCTION

Networks are ubiquitous in life. However, several real phenomena such as disease spreading, behavior contagion, rumor propagation are described as a spreading process in the complex system [Pastor-Satorras and Vespignani. \(2001\)](#), [Kresge \(2021\)](#). These processes are widely modeled using networks or graphs. Therefore, networks are a great interesting, constitute a fertile, and flexible tools for scientific modeling and analysis of complex systems [Pellis et al. \(2014\)](#) such as an infectious disease spread.

In the study of infectious disease spread, the basic reproduction number R_0 is the average of the expected secondary infections number caused by a primary infectious individual introduced in a fully susceptible host population. R_0 is strongly correlated to the likelihood and extent of an epidemic. Critically R_0 depends not only on the disease but also on the host population structure [Keeling and Rohani \(2008\)](#). Therefore, the network-based models of the epidemiological

contact have emerged as an important tool in understanding and predicting the spread of infectious disease [Bogachev and Smolyanov \(2020\)](#). Understanding the network structure allows for better control of the micro and macro propagation [Keeling and Rohani \(2008\)](#), [Alshahrani et al. \(2020\)](#), and even improves the predictions. Thus, we need more sophisticated tools for analysis and visualization of the network structure: one of these tools is the spectral theory of graph [Biggs \(1993\)](#), [Bogachev and Smolyanov \(2020\)](#). Hence, predicting whether a disease will die out or become an epidemic within a population is known as the *epidemic threshold*.

However, the Epidemic threshold τ is the incidence of a disease at which it can be considered as an epidemic. An epidemic threshold τ is the critical β/γ ratio value beyond which an infection becomes an epidemic [Wang et al. \(2003\)](#). Nevertheless, τ is commonly linked to the R_0 that allows to define the concept of the epidemic threshold [Diekmann et al. \(2012\)](#). τ depends not only on the transmission and recovery rates of a disease but also fundamentally on the network structure [Wang et al. \(2003\)](#). Therefore, the accuracy of the prediction, and understanding of epidemic thresholds on the complex networks is a challenge in the field of network science. To clarify some basic concepts of this work, the table 1 summarises the symbols used in this work.

Symbol	Short description
A	The adjacency matrix of the network.
$\langle k \rangle, \langle k^2 \rangle$	The first (average connectivity) and second moments (connectivity divergence) of the degree distribution.
λ_{max}	The spectral radius (largest eigenvalue) of the matrix A .
β	The infection rate: rate of infection or transmission from an infected individual to a susceptible individual per effective contact.
γ	The recovery rate: rate that an infected individual will recover per unit time (in continuous-time models) or per time step (in discrete time models).
λ	The transmissibility: the infection rate scaled by γ^{-1} so that $\lambda = \beta/\gamma$.
λ_c	The epidemic threshold, critical infection rate.
G	A connected network $G = (V, E)$ with n nodes in V and m edges or links in E .

Table 1: The table of the used symbols

The aim of this paper is to design and experiment a new general structural and spectral epidemic threshold approach of prediction that is similar to those in the literature and more accurately capture the full network structure but not limited by it. Therefore, we propose a new general and spectral approach to analyse the propagation processes in a network.

The layout of this paper is organised as follows: Section 2 reviews the previous approaches and their limitations. Section 3 presents the issue of the epidemic threshold, energy of graph, and the spectral theory of graph. Section 4 describes the proposed new approach, while the section 5 presents the experimentations, results, and discussions. We conclude in section 6.

II THE PREVIOUS APPROACHES AND THEIR LIMITATIONS

There are many successful theoretical approaches of the epidemic threshold in the literature. We denote various benchmark that is generally used to provide an approximation of the epidemic threshold for spreading dynamics in real networks: *Mean-field (MF)*, *Degree-based mean-field (DBMF)* or *Heterogeneous mean-field (HMF)* and *Quenched (QMF)* also called *Individual-based mean-field (IBMF)*.

2.1 The Mean-field (MF) approach

The *Mean-field (MF)* approach is based on the works of *Kephart and White* who adopted a modified homogeneous approach in which the communication among persons is modeled with directed graphs *Kephart and White (1991)*. In a homogeneous network, the epidemic threshold is: $\lambda_c^{MF} = \frac{1}{\langle k \rangle}$, where $\langle k \rangle$ is the first moment of the degree distribution. The *MF* assumes that all nodes in the network are statistically equivalent: the interaction probabilities between any two nodes are the same. Therefore, the structure of the contact network is not considered. However, the *MF* approach can be inaccurate when networks degree distribution is asymmetric, heterogenous.

2.2 The Heterogeneous mean-field (HMF) approach

To more capture network structure, *Pastor-Satorras and Vespignani (2001)* improved the homogeneous *MF* approach to obtain the *Heterogeneous mean-field (HMF)* approach by assumption that the inability for a node or person to infect the node that infected it. Here, the epidemic threshold is: $\lambda_c^{HMF} = \frac{\langle k \rangle}{\langle k^2 \rangle - \langle k \rangle}$, where $\langle k^2 \rangle$ is the second moments of the degree distribution. The *HMF* is more used for uncorrelated networks *Ferreira et al. (2012)*. The *HMF* approach is more useful under the mean field assumption of independence between nodes infectious states. However, due to its parameters and assumptions, the *HMF* approach can be inaccurate for the quenched connections among the nodes. The *HMF* neglects the dynamic correlations among the states of neighbours.

2.3 The Quenched mean-field (QMF) approach

Because neither the *MF* nor the *HMF* approach can capture enough the contact network structure: the *Quench mean-field (QMF)* approach is developed using the adjacency matrix A . This approach is widely used to study the spreading dynamics *Wang et al. (2016)*. In *Wang et al. (2003)*, authors proposed a discrete-time formulation to predict the epidemic threshold problem with any assumption of homogeneous connectivity. However the epidemic threshold is: $\lambda_c^{QMF} = \frac{1}{\lambda_{max}}$, where λ_{max} is the largest eigenvalue of the adjacency matrix A . The *QMF* approach of the epidemic threshold is dependent only on the network structures. The *QMF* is an advanced approach that is more accurate than the *MF* and *HMF*.

The *QMF* approach has many variants such as: the *N-intertwined approach Prasse and Mieghem (2020)*; the *Dynamical Message-Passing (DMP)* using the non-backtracking matrix; the *Simplified DMP (SDMP)*. Nevertheless, in some specific situations, some researches doubt the accuracy of the epidemic threshold value predicted by the *QMF* approach *Ferreira et al. (2012)*.

In the literature, there are many approaches to predict the epidemic threshold. However, we are interested to develop a new general structural and spectral approach of prediction that more captures the full network structure using structural and spectral properties of a network such as the adjacency matrix, eigenvalue, and the energy of graph. This new approach is similar and more accurate to the earlier approaches. It offers a general and spectral approach to analyse the spreading processes in a network.

III THE EPIDEMIC THRESHOLD AND THE SPECTRAL THEORY OF GRAPH

The spectral theory of graph and the network science are used to understand how network topology can predict the dynamic processes *Gutman and Ramane (2020)* like an epidemic threshold

in a complex systems. It analyse the relationships between the graph structure and its eigenvalues. The spectral theory of graph plays a central role in the fundamental understanding of the network [Cvetkovic et al. \(1980\)](#); [Chung \(1994\)](#); [Bogachev and Smolyanov \(2020\)](#). However, a large literature on algebraic aspects of spectral graph theory and these applications is in several surveys, books or monograph such as [Chung \(1994\)](#), [Cvetkovic et al. \(1980\)](#).

3.1 The eigenvalue of graph

Analysis of the eigenvalues allows to get useful information about a graph that might otherwise be difficult to obtain [Chung \(1994\)](#). Eigenvalues have a strong relationship with the structures of graphs. The largest eigenvalue of graph λ_1 or λ_{max} is called the spectral radius.

3.2 The energy of graph

It is a graph-spectrum-based quantity. The original version of graph energy from the year 1978 is based on the eigenvalues of the adjacency matrix [Gutman \(1978\)](#): $E(G) = \sum_{i=1}^n |\lambda_i|$, where λ_i is the i^{th} eigenvalue. However, the energy of graph found unexpected large applications in areas of science and engineering [Gutman and Ramane \(2020\)](#) such in [Mieghem and Bovenkamp \(2015\)](#) with the epidemiological applications.

IV THE PROPOSED NEW APPROACH

In the epidemic threshold study, one of the challenges is to capture the essence of the full network structure with few parameters as possible with accuracy. For any network, we present a new general structural and spectral approach that predict the epidemic threshold. Our approach does not assume homogeneous connectivity or any particular topology in the discrete-time. We assume that during each time interval, an infected node i tries to infect its neighbours with probability β . At the same time, i may be cured with probability γ . Thus, the new epidemic threshold approach λ_c is denoted by Eq. 1.

$$\lambda_c^{KSE} = \frac{kn}{E(G)} e^{-1/\lambda_{max}} \quad (1)$$

Here, $E(G)$ is the graph energy of the network, and k is the real parameter. The λ_c^{KSE} means *K Spectral Energy* approach of the epidemic threshold prediction. In fact, λ_{max} has several applications in science such as chemistry, computer science [Cvetkovic et al. \(1980\)](#). It is proven that more highly connected a network is, the larger is λ_{max} [Tinkler \(1972\)](#), and the smaller is $1/\lambda_{max}$ as an epidemic threshold, that is strongly related to R_0 concept. This can exhibit a basic *exponential decay model* ϕ , where $\phi = e^{\frac{-1}{\lambda_{max}}t}$, $\phi_0 = 1$, with the single parameter λ_{max} . To consider each eigenvalue, we are interesting to the *energy of graph* concept according to its definition. Thus, about the fraction of the energy of graph on each node, we define: $\Delta = \frac{E(G)}{n}$. In the *epidemic threshold* context, according to its salient features like critical or threshold values: we look at the simple *reciprocal model* $y = k(\frac{1}{x})$, where x is a variable and k a constant or *scale parameter*. Hence, the reciprocal of Δ is: $k(\frac{1}{\frac{E(G)}{n}}) = \frac{kn}{E(G)}$. Related to this reciprocal, we have the intuition to observe the rate of ϕ at $t = 1$, over there: $e^{-1/\lambda_{max}} \times \frac{kn}{E(G)} = \lambda_c^{KSE}$. Thus, the new approach to predict the epidemic threshold λ_c^{KSE} is an application that associates each adjacency matrix to a specific decay composition of its eigenvalues relating to Δ .

id	Network	Type	Nodes	Links	kmax	k	k2	den	cc
0	Sociopatterns-infectious	Real social network	410	2765	50	13.488	252.434	0.032978	0.456
1	Airline	Real social network	36	57	20	3.167	33.389	0.090476	0.000
2	Internet	Real social network	40	61	10	3.050	13.000	0.076205	0.154
3	Karate club	Real social network	34	78	17	4.588	35.647	0.139037	0.571
4	Davis Southern Women	Real social network	32	89	14	5.562	39.062	0.179435	0.000
5	Florentine families	Real social network	15	20	6	2.667	8.933	0.190476	0.160
6	Les miserables	Real social network	77	254	36	6.597	79.532	0.086508	0.573
7	Watts Strogatz 1	Generated social network	1000	2000	10	4.000	17.898	0.004004	0.007
8	Watts Strogatz 2	Generated social network	3000	12000	18	8.000	67.741	0.002668	0.008
9	Connected Watts Strogatz 1	Generated social network	1000	2000	11	4.000	17.778	0.004004	0.008
10	Connected Watts Strogatz 2	Generated social network	3000	12000	16	8.000	68.055	0.002668	0.007
11	Newman Watts Strogatz 1	Generated social network	1000	3613	12	7.226	54.172	0.007233	0.157
12	Newman Watts Strogatz 2	Generated social network	5000	36028	23	14.411	211.592	0.002883	0.200
13	Newman Watts Strogatz 3	Generated social network	24	84	9	7.000	49.667	0.304348	0.498
14	Barabasi Albert	Generated social network	1000	4975	150	9.950	211.636	0.009960	0.044
15	Barbell	Generated social network	1005	1010	5	2.010	4.066	0.002002	0.005
16	Random 1	Generated network	1000	3500	17	7.000	56.174	0.007007	0.009
17	Random 2	Generated network	140	6811	111	97.300	9495.843	0.700000	0.700
18	Dense gnm Random	Generated network	1000	3500	16	7.000	56.016	0.007007	0.009
19	Random regular 1	Generated network	1000	1500	3	3.000	9.000	0.003003	0.003
20	Random regular 2	Generated network	1000	4500	9	9.000	81.000	0.009009	0.007
21	Facebook 1	Real social network	52	146	18	5.615	48.692	0.110106	0.462
22	Facebook 2	Real social network	61	270	29	8.852	109.705	0.147541	0.733
23	Facebook 3	Real social network	168	1656	77	19.714	645.321	0.118050	0.534
24	Facebook 4	Real social network	150	1693	57	22.573	680.240	0.151499	0.670
25	Facebook 5	Real social network	333	2519	77	15.129	469.526	0.045570	0.508
26	Facebook 6	Real social network	224	3192	99	28.500	1312.554	0.127803	0.544
27	Facebook 7	Real social network	534	4813	107	18.026	539.884	0.033820	0.544
28	Facebook 8	Real social network	786	14024	136	35.684	2086.852	0.045458	0.476
29	Facebook 9	Real social network	1034	26749	253	51.739	4886.236	0.050086	0.526
30	Facebook 10	Real social network	747	30025	293	60.368	10593.661	0.107759	0.635

Figure 1: The synthesis of the structural information about the networks in the dataset

V EXPERIMENTATIONS, RESULTS AND DISCUSSIONS

With data analytic and data visualisation technics, the simulations are driven to answer the question of how does the new approach is similar and perform in real a good performance than earlier epidemic threshold approaches including the most used QMF with the experimental dataset in the figure 1. We have used the real networks of infectious disease spread and other small-world, random, and regular networks over spreading processes in 31 networks: 17 real social networks, 9 generated social networks, 3 random networks, and 2 regular random networks. With data visualization technics based on numerical and graphical simulations, overall the 31 different networks types and topology: different sets of values MF , HMF , QMF and the new KSE epidemic threshold are been computed, analysed, visualised, and discussed.

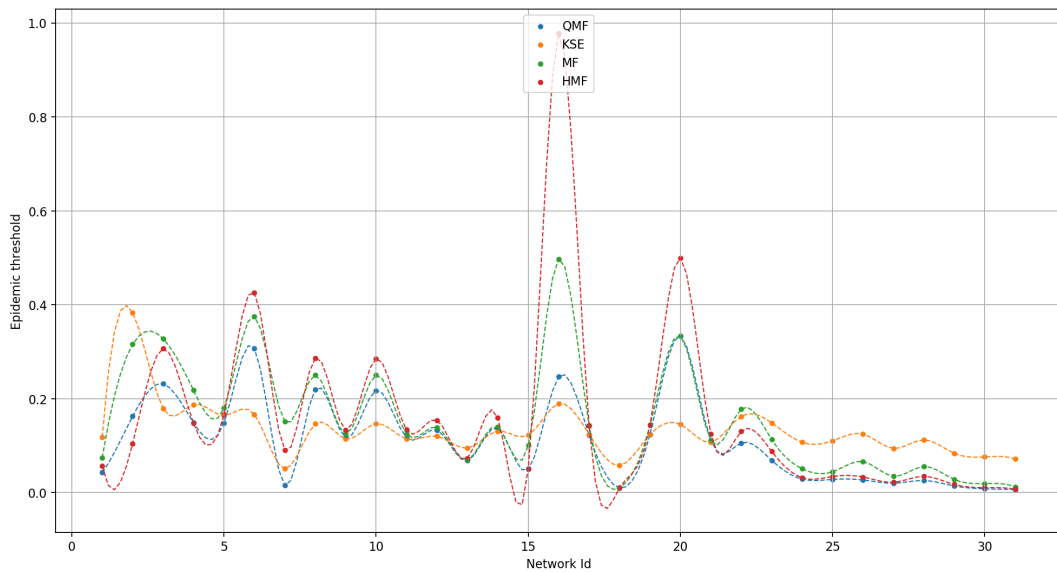


Figure 2: The scatter dashed line visualization of the MF , HMF , QMF and the proposed KSE epidemic threshold

	MF	HMF	QMF	KSE
count	31.000	31.000	31.000	31.000
mean	0.151	0.157	0.110	0.131
std	0.120	0.194	0.091	0.059
min	0.010	0.008	0.006	0.050
25%	0.061	0.034	0.027	0.107
50%	0.125	0.125	0.111	0.122
75%	0.199	0.159	0.149	0.148
max	0.497	0.977	0.333	0.383
IQ	0.138	0.124	0.120	0.040
range	0.487	0.970	0.327	0.332

Table 2: The summary of the descriptive statistic values of the MF, HMF, QMF and the proposed KSE epidemic threshold

In the figure 2, we can show that the network Id 5, 9, 11, 12, 13, 14, 15, 17, 18, 19, and 21 have nearest epidemic threshold values. Hence, the new proposed approach of epidemic threshold *KSE* have similar common features with the earlier approaches, specifically with the widely most used accurate *QMF*. The summary descriptive statistics values of the *MF*, *HMF*, *QMF* and the proposed *KSE* epidemic threshold is built in the table 2. In the table 2, for the most used epidemic threshold in the literature *QMF*, we observed that the new proposed approach *KSE* has the 2nd quantile (Q_2) more similar. The new proposed approach *KSE* is similar for the major descriptive statistic characteristics like: the *mean*, *std*, Q_2 , Q_3 and *range* related to the *QMF*. This means that the new proposed approach of epidemic threshold *KSE* is similar to the earlier and have major common features with the earlier approaches, specifically with the most used accurate *QMF*. Those results come from the eigenvalues concept at the root of *QMF* and *KSE*.

Moreover, the areas, the curve and the shape visualization technic for the values of each epidemic threshold computed can be are observed in the figure 2. We can show that the area of all epidemic thresholds have a similar area, curve and shape over the range of the 31 different experimental networks in the dataset. They share the same shape, curve and sense of variation. This means that the new proposed approach of epidemic threshold *KSE* is similar to the earlier.

The gap or difference between the epidemic threshold values related to the new *KSE* is analysed. The summary of its descriptive statistics is shown in the table 3. Here, for any p, q epidemic threshold, e_{p-q} means the euclidian gap or difference of p to q : $p - q$.

In the figure 3, we can show that scatter and curve of the gap between *QMF* and the new *KSE* is lowest, closest to the x-axis where the difference is zero. In the table3, the *standard deviation* of the gap or the difference between the *QMF* and the *KSE* is 0.078. All the gaps are relatively low. Relatively low related to the earlier approaches particularly lowest to the most used *QMF*. Moreover, the new proposed approach of epidemic threshold *KSE* is similar and have major common features with the earlier approaches, specifically with the most used accurate *QMF*.

	e_MF_KSE	e_HMF_KSE	e_QMF_KSE
count	31.000	31.000	31.000
mean	0.019	0.026	-0.022
std	0.093	0.182	0.078
min	-0.068	-0.279	-0.221
25%	-0.056	-0.066	-0.074
50%	0.010	-0.022	-0.0350
75%	0.025	0.034	0.007
max	0.308	0.788	0.188
IQ	0.081	0.099	0.081
range	0.375	1.066	0.409

Table 3: The summary of the descriptive statistic values of the gap or difference between *MF*, *HMF*, *QMF* approach related to the *KSE*

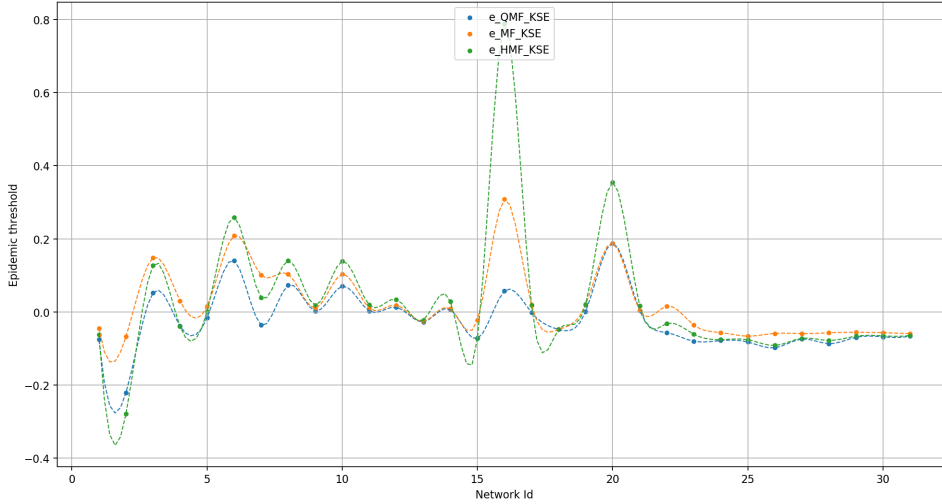


Figure 3: The scatter dashed line visualization of the gap or difference between MF , HMF , and QMF approach epidemic threshold related to the new KSE

Overall, we observed that the new KSE approach of the epidemic threshold prediction is similar to those existing in the literature. It offers a new approach to predict the epidemic threshold by using the spectral radius and the energy of the graph: it constitutes a new general and spectral approach to analyse the spreading processes in a network using structural and spectral properties of a network. In the new approach, conceptually, the eigenvalues concept is at the core.

VI CONCLUSION

In this paper, we address the accurate understanding and prediction of the epidemic threshold on complex networks in the context of the spreading process. Network structure fundamentally influences the dynamics of the spreading processes with a boundary condition for spreading processes over networks called the epidemic threshold. We have designed and experimented a new general structural and spectral approach of epidemic threshold prediction that further captures the full network structure using the nodes number, the spectral radius, and the energy of graph. We have driven the simulations on 31 networks at different topologies: 17 real social networks, 9 generated social networks, 3 random networks, and 2 regular random networks. With data analysis and data visualization techniques, the simulations show that the new KSE approach of epidemic threshold is similar to the earlier MF , HMF , QMF and shares major common features with the earlier approaches, specifically with the most used accurate QMF . The new epidemic threshold approach offers a new general and spectral approach to analyse the spreading processes in a network. The results are both fundamental and practical interest in improving the control and prediction of propagation processes in networks. Particularly meaningful to decision-makers in public health. Future research can examine the case where the epidemic threshold is greater than 1. Also, examine the temporal evolution of a specific infectious disease in a network. As well as to enhance the proposed epidemic threshold approach with other spectral theory of graph concepts.

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