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Epidemic threshold : A new spectral and structural approach of prediction

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Abstract

Epidemiological modelling and epidemic threshold analysis in the networks are widely used for 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 prediction approach of the epidemic threshold. This more captures the full network structure using the number of nodes, the spectral radius, and the energy of graph. With data analytic and data visualization technics, we drive simulations overall on 31 different types and topologies networks. The simulations show similar qualitative and quantitative results between the new structural prediction approach of the epidemic threshold values compared to the earlier *MF*, *HMF* and *QMF* widely used benchmark approaches. The results show that the new approach is similar to the earlier one, further captures the full network structure, and is also accurate. The new approach offers a new general structural and spectral area 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. So these results can be particularly significant to advise an effective epidemiological control policy.

Keywords

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

I INTRODUCTION

Networks are everywhere. Several real phenomena such as disease spreading, behaviour contagion, and rumour propagation are described as a spreading process in the complex system

Symbol	Short description
A	The adjacency matrix of the network.
$\langle k \rangle, \langle k^2 \rangle$	The first (average connectivity) and second moment (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: Notations

[14]. These processes are widely modelled using networks or graphs. Therefore, networks are greatly interesting and constitute fertile, and flexible tools for scientific modelling and analysis of complex systems [17] such as an infectious disease spread over a contact network.

In the study of infectious disease spread, the basic reproduction number R_0 is the average of expected secondary infection 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 [11]. Therefore, network-based models of epidemiological contact have emerged as an important tool in understanding and predicting the spread of infectious disease [4]. Understanding the network structure allows for better control of the micro and macro propagation [11], [1], 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 [3], [4]. Hence, predicting whether a disease will die out or become an epidemic is known as the *epidemic threshold*.

Epidemic threshold τ denotes 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 [21]. Nevertheless, τ is commonly linked to the R_0 that allows the definition of the epidemic threshold concept [7]. τ depends not only on the transmission and recovery rates of a disease but, also fundamentally on the network structure [21]. Therefore, the accuracy of the prediction and understanding of epidemic thresholds on complex networks is a challenge in the field of network science. To clarify some basic concepts of this work, Table 1 defines some basic notations used in this work.

The aim of this paper is to design and experiment a new general structural and spectral prediction approach of the epidemic threshold. This should be substantially similar to those in the literature and accurately captures the full network structure but is not limited by it. Therefore, we propose a new general and spectral approach to analyse the spreading 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 epidemic threshold, energy of graph, and spectral theory of the graph. Section 4 describes the proposed new approach while section 5 presents the experimentation, results, and discussions. We conclude in section 6.

II THE PREVIOUS APPROACHES AND THEIR LIMITATIONS

In the literature, there are many successful theoretical approaches of the epidemic threshold. We denote various benchmarks generally used to provide an approximation of the epidemic threshold related to the dynamic spreading in real networks. This includes the *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 where directed graphs model the communication among persons [12]. Formally, here, in a homogeneous network, the epidemic threshold is denoted by Eq. 1:

$$\lambda_c^{MF} = \frac{1}{\langle k \rangle} \tag{1}$$

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 contact network structure is not considered. However, *MF* approach can be inaccurate when network degree distribution is asymmetric and heterogeneous.

2.2 The Heterogeneous mean-field (HMF) approach

To more capture network structure, [16] improved the homogeneous *MF* approach to obtain the *HMF* by the assumption of the inability for a node (or person) to infect node that infected it. Here, the epidemic threshold is given by Eq. 2:

$$\lambda_c^{HMF} = \frac{\langle k \rangle}{\langle k^2 \rangle - \langle k \rangle} \tag{2}$$

where $\langle k^2 \rangle$ is the second moment of the degree distribution. *HMF* is more used for uncorrelated networks [8]. It's more useful under the mean-field assumption of independence between node's infectious states. Due to its parameters and assumptions, the *HMF* approach can be inaccurate for the quenched connections among nodes. Moreover, 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 [20]. In [21], authors proposed a discrete-time formulation to predict the epidemic threshold problem with any assumption of homogeneous connectivity. However, the epidemic threshold is given by Eq. 3:

$$\lambda_c^{QMF} = \frac{1}{\lambda_{max}} \tag{3}$$

where λ_{max} is the largest eigenvalue of the adjacency matrix A. The *QMF* approach depends only on the network structures. The *QMF* is an advanced approach that is more accurate than the *MF* and *HMF* [20].

The *QMF* approach has many variants such as the *N-intertwined approach* [18]; the *Dynamical Message-Passing (DMP)* using the non-backtracking matrix; the *Simplified DMP (SDMP)*. Nevertheless, in some specific situations, some research doubts the accuracy of the epidemic threshold value predicted by the *QMF* approach [8].

As it happens, 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 a node number, adjacency matrix, spectral radius, and the energy of graph. This new approach should be substantially similar to the earlier approaches. Moreover, it should be also accurate. Therefore, the new approach offers a general and spectral approach to analyse spreading processes in a network.

III THE EPIDEMIC THRESHOLD AND THE SPECTRAL THEORY OF GRAPH

The spectral theory of graph and network science are used to understand how network topology can predict the dynamic processes [10] like an epidemic threshold in a complex system. It analyses the relationships between the graph structure and its eigenvalues. Thus, the spectral theory of graph plays a central role in the fundamental understanding of the network [6, 5, 4]. However, a large literature on algebraic aspects of spectral graph theory and these applications are in several surveys, books or monographs such as [5], [6].

3.1 The eigenvalue of graph

The analysis of the eigenvalues allows us to get useful information about a graph that might otherwise be difficult to obtain [5]. 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's a graph-spectrum-based quantity. The original version of graph energy from the year 1978 is based on the eigenvalues of the adjacency matrix [9]: $E(G) = \sum_{i=1}^{n} |\lambda_i|$, where λ_i is the i^{th} eigenvalue. However, the energy of graph found unexpected large applications in areas of science and engineering [10] such in [15] 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 as few parameters as possible with accuracy. For any network, we present a new general structural and spectral prediction approach of the epidemic threshold. Our approach does not assume homogeneous connectivity or any particular topology in a discrete time. We assume that during each time interval, an infected node *i* try to infect its neighbours with probability β. At the same time, *i* may be cured with probability γ. Thus, formally, the new epidemic threshold approach λ_c is denoted by Eq. 4:

$$\lambda_c^{KSE} = \frac{kn}{E(G)} e^{-1/\lambda_{max}} \tag{4}$$

Here, $E(G)$ is the energy of graph, and k is a real scale 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, and computer science [6]. It's proven that the more highly connected a network is, the larger is λ_{max} [19], and the smaller is $1/\lambda_{max}$ as an epidemic threshold, which is strongly related to the 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 interested in 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 *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 relative composition eigenvalues relating to Δ.

V EXPERIMENTATION, RESULTS AND DISCUSSIONS

With data analytic and data visualisation technics on the experimental dataset in Figure 1; the simulations are driven to answer the question of how the new prediction approach of the epidemic threshold is substantially similar and performs in real a good performance than earlier approaches including the most used *QMF*.

The dataset describes in Figure 1 contains real networks of infectious disease spread, small-world, random, and regular networks in spreading processes overall 31 different types and topologies networks; 17 real social networks, 9 generated social networks, 3 random networks, and 2 regular random networks. Here, *Id* refers to the network identifier, *kmax* refers to the maximum node degree in a network, *k* denotes the first moment of degree, *k2* the second moment of degree, *den* refers to the density of a network, and *cc* the clustering coefficient. However, with data visualization technics based on numerical and graphical simulations overall these networks: different sets of predicted values *MF, HMF, QMF* and the new *KSE* epidemic threshold are been computed, analysed, visualised, and discussed.

In Figure 2, we can show that the network Id 5, 9, 11, 12, 13, 14, 15, 17, 18, 19, and 21 have nearest predicted values of the epidemic threshold. Thus, the new proposed approach of epidemic threshold *KSE* has substantially 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* are built in Table 2. Here, for the widely used *QMF* approach in the literature, we observed that the new proposed approach *KSE* has the 2^{nd} 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 *KSE* approach is similar to the earlier and shares major features with the earlier, specifically with the widely used accurate *QMF*. Theoretically, those results come from the eigenvalues concept at the root of *QMF* and *KSE* approach.

Moreover, the area, curve and shape of each epidemic threshold value can be observed in Figure 3. Here, we can show that the area of all epidemic thresholds have a substantially 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 *KSE* is similar to the earlier one.

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	0.078205	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	0.086808	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	80.388	10593.861	0.107759	0.635

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

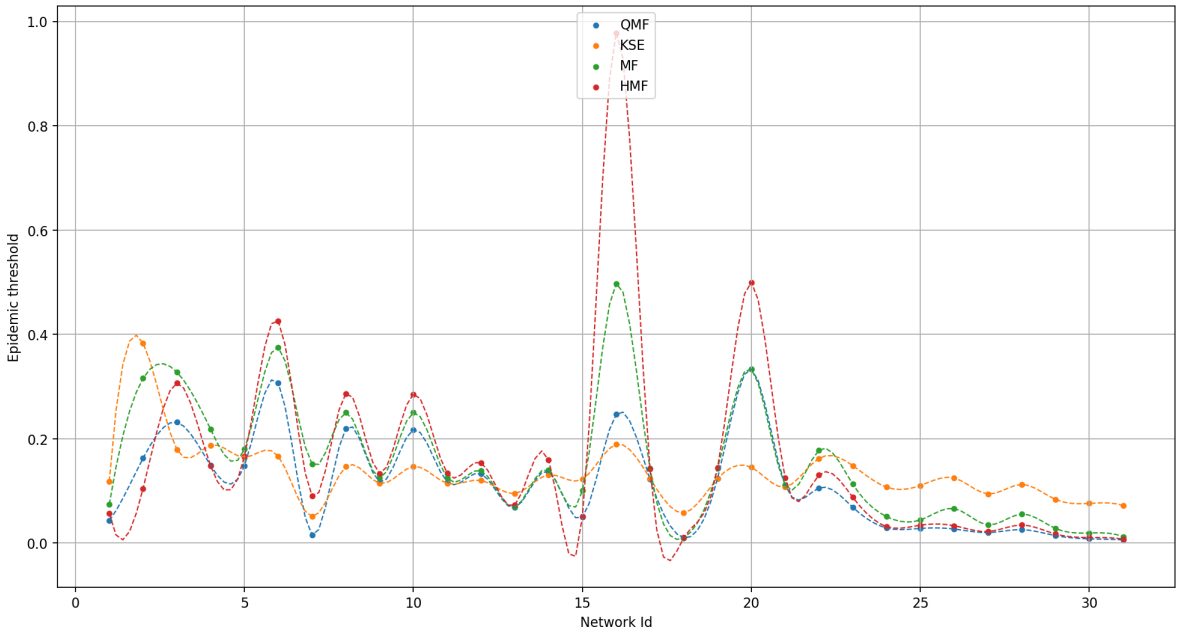

Figure 2: The scatter dashed line visualization of *MF, HMF, QMF* and the proposed *KSE* prediction approach of the epidemic threshold

	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 prediction approach of the epidemic threshold

Furthermore, the gap or difference between predicted values of the epidemic threshold related to the new *KSE* is analysed. The summary of its descriptive statistics is shown in 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 Table 3, 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 is related to the earlier approaches particularly lowest to the most used *QMF*. Moreover, the new *KSE* approach shares major common features with the earlier, specifically with the most used accurately *QMF*.

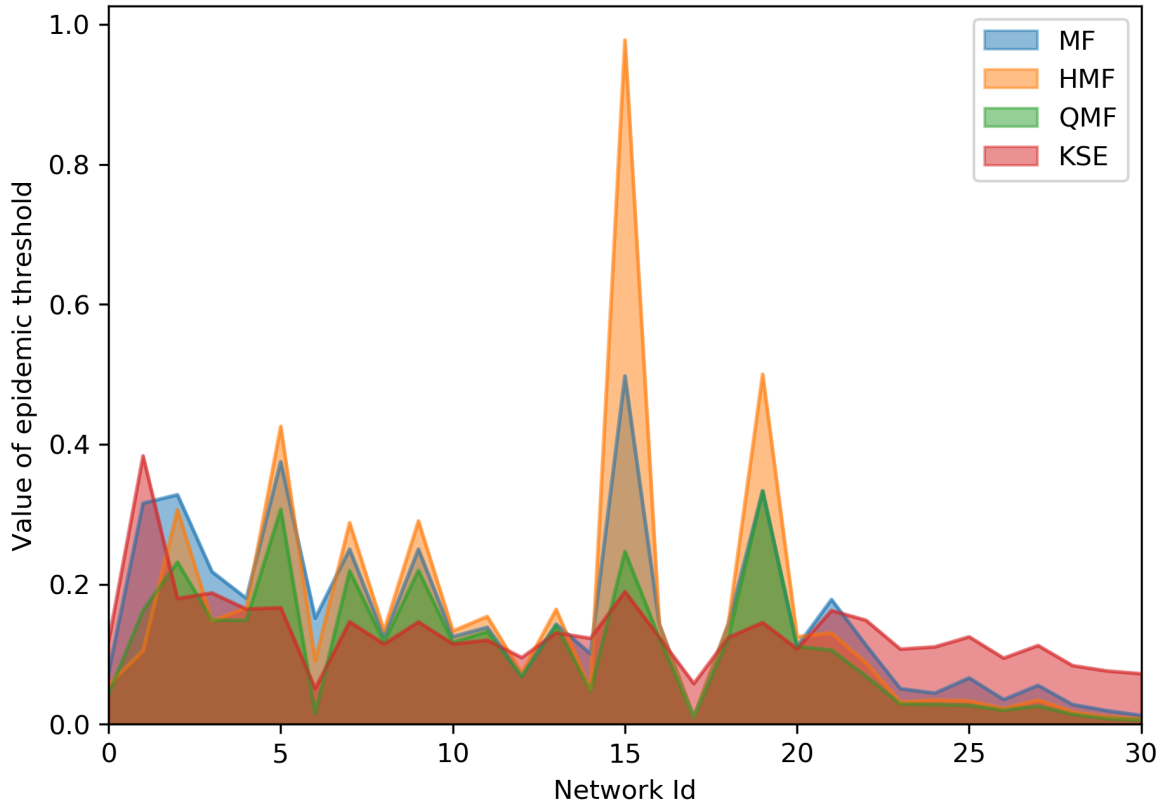

Figure 3: The area visualization of *MF, HMF, QMF* and the proposed *KSE* prediction approach of the epidemic threshold

	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* prediction approach related to the *KSE*

	sum_{sq}	df	F	PR(>F)
$C(epidemic\_threshold)$	0.043670	3.0	0.913627	***0.436623***
Residual	1.911935	120.0	NaN	NaN

Table 4: The *ANOVA F* and *p-value* using the *Ordinary Least Squares* to the *MF, HMF, QMF* prediction approach related to the *KSE*

Furthermore, to analyse the statistical difference among these experimental sets of epidemic threshold predicted values, we have used the univariate *ANalysis Of VAriance (ANOVA)* test using the *Ordinary Least Squares (OLS)* model, or the *Bioinfokit Python* package. We obtain the summarized output of *ANOVA F* and *p-value* in Table 4 where sum_{sq} denotes the sum of squares, *df* denotes the degree of freedom, *F* the F-statistic, and *PR* the P-value. Here, the *p-value* $0.44 > 0.10$. Hence, the *null hypothesis* is accepted. Thus, there is *"not significant"* statistical difference between different sets of epidemic threshold values. So, once again, *ANOVA* shows that the new proposal *KSE* epidemic threshold is similar to the earlier generally used in the literature.

Overall, we observed that the new *KSE* prediction approach of the epidemic threshold is substantially similar to the earlier in the literature. Both *KSE* and *QMF* perform better than the other approaches in terms of « accuracy ». Moreover, *KSE* offers a new approach to predicting the epidemic threshold using nodes number, spectral radius and energy of the graph. Hence it constitutes a new general and spectral approach to analyse the spreading processes in a network through structural and spectral properties of a network.

The potential advantages and benefits of the *KSE* new approach compared to the earlier
We established an analytical comparative study in Table 5. Here, the term *relatively* is related to the context and dataset of this study. This term refers to the possible suggestive theoretical interpretations, or missing formal proofs. Moreover, contextually in Table 5, the criteria *accuracy* refers to the quality to capture the full network structure; *Transparency*, is the quality to assess rule, and function of each parameter in the formula, even the assessment of the parameters in relationship; *Flexibility* refers to the ability to change or be real scale easily; and *parameter*, refers to the quality of parameter(s), its number, also their meaning in the relationship. Nevertheless, no model or approach is perfect; the new *KSE* can have a potential appropriate balance of accuracy, transparency, flexibility, and parameter.

Model	Accuracy	Transparency	Flexibility	Parameter
MF	Relatively poor fit: network structure isn't considered.	Relatively easy: single parameter $\langle k \rangle$.	Relatively poor: due to its assumptions.	The use of a single parameter $\langle k \rangle$.
HMF	Relatively poor fit: due to its parameters can be inaccurate.	Relatively medium: can assess the role of $\langle k \rangle$, $\langle k^2 \rangle$.	Relatively medium: due to its assumptions.	The use of 2 parameters $\langle k \rangle$, $\langle k^2 \rangle$.
QMF	Relatively medium fit: captures network structure using only λ_{max}	Relatively easy: due to it single parameter λ_{max}.	Relatively good: due to its assumptions.	The use of a single parameter λ_{max}.
KSE	Relatively high fit: captures the full network structure using $\{\lambda_{max}$, *E(G), n, k* $\}$.	Relatively medium: parameter assessment in relationship can be complex.	Relatively improved: due to its assumptions, using $\{\lambda_{max}, E(G), n\}$ and a scale k.	The use of $\{\lambda_{max}, E(G), n, k\}$ structural and spectral parameters in *relationship*.

Table 5: The potential advantages and benefits of the new approach over the earlier: a qualitative comparison between MF, HMF, QMF and the new KSE prediction approach of the epidemic threshold

Furthermore, according to the relationship between the epidemic threshold and R_0, we have driven some real case studies related to the previous work in the literature about the R_0:

- The dataset used in [2]: *small-world* networks of the *Newman Watts Strogatz* model for 24 nodes, each of which is connected to 6 nearby nodes, where the probability of an extra link is 1/6.
- The dataset used in [13]: $\beta = 0.005, \delta = 0.9, \gamma = 0.9$. Authors have used these parameters for the simulations, and their differential equations.

Table 6 shows the structural information of the used datasets. However, under the assumption

Id	Network	Type	n	m	$\langle k \rangle$	$\langle k^2 \rangle$	den	cc
1	Newman Watts Strogatz	small-world	24	83	6.916	48.583	0.301	0.536

Table 6: The summary of structural information from the dataset

of a *density-dependent transmission*, by definitions: $R_0 = \beta n/\gamma$, yet $\lambda_c = \beta/\gamma$; thus $\boldsymbol{R_0 = \lambda_c \times n}$. So, we obtain the following results in the Table 7. We can observe that the structural R_0

Id	λ_{max}	λ_c^{QMF}	λ_c^{KSE}	$R_0^{\lambda_c^{QMF}}$	$R_0^{\lambda_c^{KSE}}$	$R_0^{Original}$
1	7.116	0.140	0.133	3.360	3.192	3.268

Table 7: Comparison between different structural λ_c^{QMF}, λ_c^{KSE}, and structural $R_0^{\lambda_c^{QMF}}$, $R_0^{\lambda_c^{KSE}}$ related to the original $R_0^{Original}$ based on differential equations

denoted $R_0^{\lambda_c^{QMF}}$, $R_0^{\lambda_c^{KSE}}$ respectively based on λ_c^{QMF}, and λ_c^{KSE} are very closed to the original value of $R_0^{Original}$ obtained using differential equations in [13, 2]. These results highlight the similar accuracy of the *KSE* related to the earlier approach, specifically to the most used *QMF*. Besides, these results bring nearer the network-based model for the structural approach of R_0 and the mathematical modelling approaches of R_0 using a system of differential equations. This result emphasises the usefulness of network-based structural approach for the prediction of some key epidemiological parameters such as λ_c, R_0.

VI CONCLUSION

In this paper, we address the accurate understanding and prediction of the epidemic threshold on the complex networks in the spreading process context. Here, network structure fundamentally influences the dynamics of the spreading processes with a boundary condition for spreading processes over networks like the epidemic threshold. Therefore, to improve the structural prediction approaches, we have designed and experimented a new general structural and spectral prediction approach of epidemic threshold called *KSE*. The new approach further captures the full network structure using nodes number, spectral radius, and the energy of graph. We have driven simulations on 31 networks at different structures and 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 is similar to the earlier *MF*, *HMF*, *QMF* and shares major features with the earlier, specifically with the most used accurate *QMF* approach. The new prediction approach of the epidemic threshold offers a new general and spectral area to analyse the spreading processes over a network. The results are both fundamental and practical interest in improving the control and prediction of spreading processes over networks. Particularly meaningful to decision-makers in public health who can use these results to improve the control of an infectious disease spread, and also to inform policy to improve the successful mitigation and eradication strategies. Future research can 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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