



**HAL**  
open science

# Epidemic threshold: A new spectral and structural approach of prediction

Claude Kanyou, Etienne Kouokam, Yves Emvudu

► **To cite this version:**

Claude Kanyou, Etienne Kouokam, Yves Emvudu. Epidemic threshold: A new spectral and structural approach of prediction. CARI 2022, Oct 2022, Yaoundé, Dschang, Cameroon. hal-03714202v2

**HAL Id: hal-03714202**

**<https://hal.science/hal-03714202v2>**

Submitted on 6 Apr 2023 (v2), last revised 30 Nov 2023 (v4)

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - NonCommercial 4.0 International License

## Epidemic threshold : A new spectral and structural approach of prediction

Claude KANYOU<sup>\*1</sup>, Etienne KOUOKAM<sup>2</sup>, Yves EMVUDU<sup>3</sup>

<sup>1,2</sup>Department of Computer Science, Faculty of Science, Université de Yaoundé I, Yaoundé, Cameroon

<sup>3</sup>Department of Mathematics, Faculty of Science, Université de Yaoundé I, Yaoundé, Cameroon

\*E-mail : [kanyouclaude@gmail.com](mailto:kanyouclaude@gmail.com)

DOI : [10.46298/arima.idpermanent](https://doi.org/10.46298/arima.idpermanent)

Submitted on Day Month-in-full-text Year - Published on Day Month-in-full-text Year

Volume : N - Year : YYYY

Special Issue : Title

Editors : First name-1 Last name-1, First name-2 Nom-2,...

---

### Abstract

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 prediction approach of the epidemic threshold. This more captures the full network structure by using the number of nodes, the spectral radius, and the energy of graph. With data analytic and data visualization technics, we drive the simulations overall on 31 different types and topologies networks. The simulations show similar qualitative and quantitative results of the epidemic threshold values compared to the *MF*, *HMF* and *QMF* widely used theoretical benchmark approaches. The results show that the new approach is similar to the earlier one, further captures the full network structure, and is more accurate than the earlier approaches. The new approach offers a new general structural 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 everywhere. Several real phenomena such as disease spreading, behaviour contagion, and rumour propagation are described as a spreading process in the complex system [14]. These processes are widely modelled using networks or graphs. Therefore, networks are

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.
$\lambda_{max}$	The spectral radius (largest eigenvalue) of the matrix $A$ .
$\beta$	The infection rate: rate of infection or transmission from an infected individual to a susceptible individual per effective contact.
$\gamma$	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).
$\lambda$	The transmissibility: the infection rate scaled by $\gamma^{-1}$ so that $\lambda = \beta/\gamma$ .
$\lambda_c$	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: Definition of the used symbols

greatly interesting and constitute fertile, and flexible tools for scientific modelling and analysis of complex systems [17] 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 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 [12]. Therefore, the network-based models of epidemiological contact have emerged as an important tool in understanding and predicting the spread of infectious disease [3]. Understanding the network structure allows for better control of the micro and macro propagation [12], [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 [2], [3]. Hence, predicting whether a disease will die out or become an epidemic is known as the *epidemic threshold*.

The epidemic threshold  $\tau$  is the incidence of a disease at which it can be considered as an epidemic. An epidemic threshold  $\tau$  is the critical  $\beta/\gamma$  ratio value beyond which an infection becomes an epidemic [21]. Nevertheless,  $\tau$  is commonly linked to the  $R_0$  that allows the definition of the concept of the epidemic threshold [6].  $\tau$  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 the symbols 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 is similar to those in the literature and more accurately captures the full network structure but is 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, the energy of graph,

and the spectral theory of the graph. Section 4 describes the proposed new approach, while 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 benchmarks generally used to provide an approximation of the epidemic threshold for spreading dynamics 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[13]. 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 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 *Heterogeneous mean-field (HMF)* approach by the 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 [8]. The *HMF* approach is 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 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 [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:  $\lambda_c^{QMF} = \frac{1}{\lambda_{max}}$ , where  $\lambda_{max}$  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* [19]; 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].

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 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 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. The spectral theory of graph plays a central role in the fundamental understanding of the network [5, 4, 3]. However, a large literature on algebraic aspects of spectral graph theory and these applications are in several surveys, books or monographs such as [4], [5].

#### 3.1 The eigenvalue of graph

Analysis of the eigenvalues allows us to get useful information about a graph that might otherwise be difficult to obtain [4]. Eigenvalues have a strong relationship with the structures of graphs. The largest eigenvalue of graph  $\lambda_1$  or  $\lambda_{max}$  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 [9]:  $E(G) = \sum_{i=1}^n |\lambda_i|$ , where  $\lambda_i$  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  $\beta$ . At the same time,  $i$  may be cured with probability  $\gamma$ . Thus, the new epidemic threshold approach  $\lambda_c$  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  $\lambda_c^{KSE}$  means *K Spectral Energy* approach of the epidemic threshold prediction. In fact,  $\lambda_{max}$  has several applications in science such as chemistry, and computer science [5]. It is proven that the more highly connected a network is, the larger is  $\lambda_{max}$  [11], 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*  $\phi$ , where  $\phi = e^{\frac{-1}{\lambda_{max}}t}$ ,  $\phi_0 = 1$ , with the single parameter  $\lambda_{max}$ . 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 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  $\Delta$  is:  $k(\frac{1}{\frac{E(G)}{n}}) = \frac{kn}{E(G)}$ . Related to this reciprocal, we have the intuition

	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

to observe the rate of  $\phi$  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  $\lambda_c^{KSE}$  is an application that associates each adjacency matrix to a specific decay relative composition eigenvalues relating to  $\Delta$ .

## V EXPERIMENTATIONS, 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 approach is similar and performs in real a good performance than earlier epidemic threshold approaches including the most used *QMF*.

The used dataset contains real networks of infectious disease spread and other small-world, random, and regular networks over spreading processes in 31 different types and topologies 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 these networks: different sets of 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 the nearest epidemic threshold values. Hence, the new proposed approach of epidemic threshold *KSE* has 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 are built in Table 2. Here, for the most used epidemic threshold in the literature *QMF*, we observed that the new proposed approach *KSE* has the 2<sup>nd</sup> 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 has 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 area, curve and shape of each epidemic threshold value can be observed in 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 *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 synthesis of the structural information about the networks in the dataset

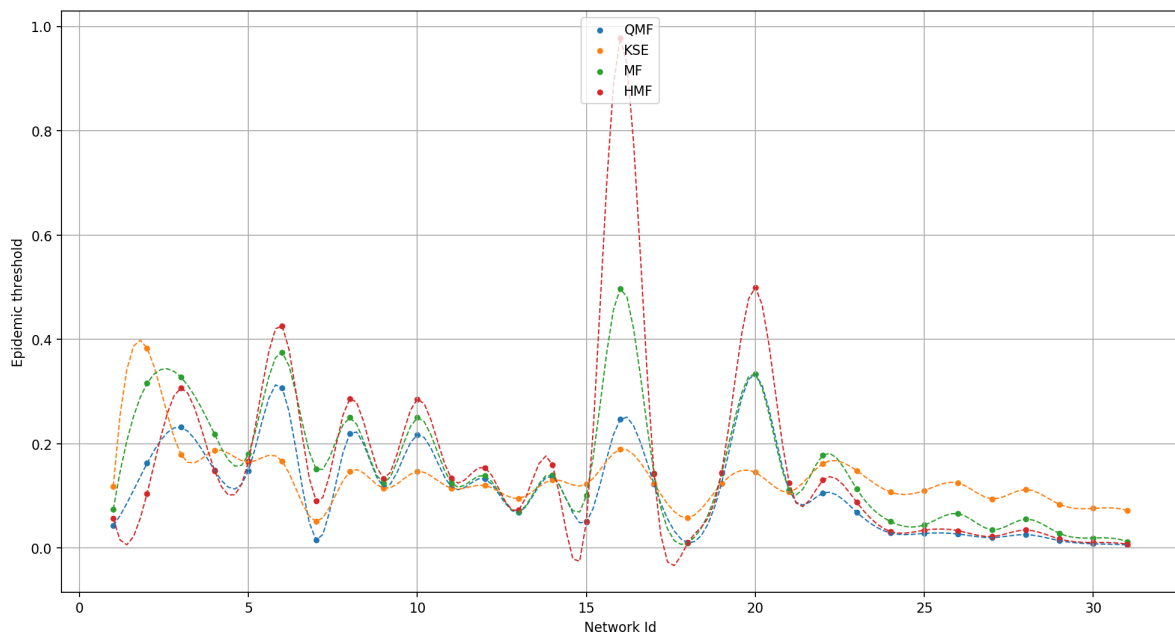


Figure 2: The scatter dashed line visualization of the  $MF$ ,  $HMF$ ,  $QMF$  and the proposed  $KSE$  epidemic threshold

	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* approach related to the *KSE*

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 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*.

In addition, in Figure 3, we can show that scatter and curve of the gap between *QMF* and the new *KSE* is low; relatively close to the x-axis where the difference is zero. The observation is the same as the previous one.

Furthermore, to analyse the statistical difference among those experimental sets of epidemic threshold values, we have used the univariate *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. 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

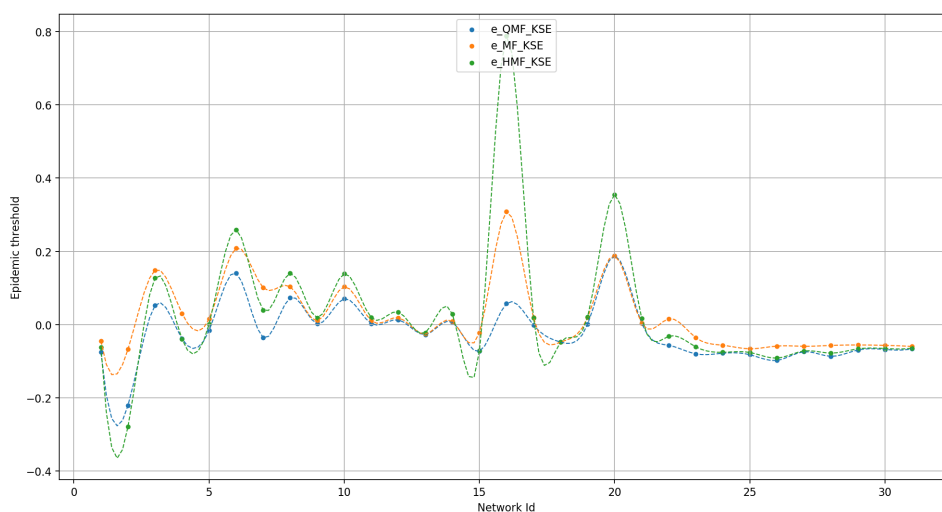


Figure 3: The scatter dashed line visualization of the gap or difference between *MF*, *HMF*, and *QMF* approach epidemic threshold related to the new *KSE*



	$sum_{sq}$	df	F	PR(>F)
$C(epidemic\_threshold)$	0.043670	3.0	0.913627	<b>0.436623</b>
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 approach related to the KSE

Model	Accuracy	Transparency	Flexibility	Parameter
MF	Poor fit: network structure isn't considered.	Easy: single parameter $\langle k \rangle$ .	Poor: due to its assumptions.	The use of a single parameter $\langle k \rangle$ .
HMF	Poor fit: due to its parameters can be inaccurate.	Medium: can assess the role of $\langle k \rangle, \langle k^2 \rangle$ .	Medium: due to its assumptions.	The use of 2 parameters $\langle k \rangle, \langle k^2 \rangle$ .
QMF	Medium fit: captures network structure using only $\lambda_{max}$	Easy: due to it single parameter $\lambda_{max}$ .	Good: due to its assumptions.	The use of a single parameter $\lambda_{max}$ .
KSE	High fit: captures the full network structure using $\{\lambda_{max}, E(G), n, k\}$ .	Medium: parameter assessment in relationship can be complex.	Better: 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 advantages and benefits of the new approach over the earlier: a qualitative comparison between MF, HMF, QMF and the new KSE epidemic threshold prediction

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 approach of the epidemic threshold prediction is similar to those existing in the literature. It offers a new approach to predicting the epidemic threshold using the number of nodes, spectral radius and the energy of the graph. Hence it constitutes a new general and spectral approach to analyse the spreading processes in a network using the structural and spectral properties of a network.

### The advantages and benefits of the KSE new approach compared to the earlier

We established an analytical comparative study in Table 5. However, no model or approach is perfect; the new KSE has an appropriate balance of accuracy, transparency, and flexibility.

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 [18]: *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 [7]:  $\beta = 0.005, \delta = 0.9, \gamma = 0.9$ . 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  $R_0 =$

$\lambda_c \times n$ . So, we obtain the following results in the Table 7. As it happens, the structural  $R_0$

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

Table 7: The results of the different  $\lambda_c, R_0$  by structural approach in comparison

estimation based on  $\lambda_c^{QMF}$  both  $\lambda_c^{KSE}$  are near related to the  $R_0$  using differential equations in [7, 18]. 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 emphasises the usefulness of the network-based structural approach for the prediction of the key epidemiological parameters such as  $\lambda_c, R_0$ .

## 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 prediction approach of the epidemic threshold 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 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 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 who can use these results to improve the control of an infectious disease spread, and also to inform policy for the most 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.

## REFERENCES

- [1] Mohammed Alshahrani, Zhu Fuxi, Soufiana Mekouar, and Sheng Huang. Efficient algorithms based on centrality measures for identification of top-k influential users in social networks. *Information Sciences*, 527, March 2020.
- [2] Norman Biggs. Algebraic graph theory. *Cambridge University Press*, 1993.
- [3] Vladimir Bogachev and Oleg Smolyanov. *Spectral Theory*, pages 279–356. 2020.
- [4] Fan R. K. Chung. Spectral graph theory. *Conference Board of the Mathematical Sciences (CBMS)*, 92, 1994. California State University at Fresno.
- [5] Dragos Cvetkovic, Michael Doob, and Horst Sachs. Spectra of graphs – theory and application. *Academic Press*, 1980. New York.

- [6] Odo Diekmann, J.A.P. Heesterbeek, and Tom Britton. Mathematical tools for understanding infectious disease dynamics. *Mathematical Tools for Understanding Infectious Disease Dynamics*, January 2013.
- [7] Kouokam Etienne, Auger Pierre, Hbid Hassan, and Tchuenté Maurice. Effect of the number of patches in a multi-patch sirs model with fast migration on the basic reproduction rate. *Acta Biotheor*, 56:75–86, 2006. Springer Science+Business Media B.V. 2008.
- [8] Silvio Ferreira, Claudio Castellano, and Romualdo Pastor-Satorras. Epidemic thresholds of the susceptible-infected-susceptible model on networks: A comparison of numerical and theoretical results. *Physical Review E*, 86, October 2012.
- [9] Ivan Gutman. The energy of a graph. *Ber. Math. Statist. Sect. Forschungsz. Graz*, 103:1–22, 1978.
- [10] Ivan Gutman and Harishchandra Ramane. Research on graph energies in 2019. *MATCH Communications in Mathematical and in Computer Chemistry*, 84:277–292, July 2020.
- [11] Tinkler K. J. The physical interpretation of eigenfunctions of dichotomous matrices. *Transactions of the Institute of British Geographers*, 55:17–46, 1972.
- [12] Matt Keeling and Pejman Rohani. *Modeling Infectious Diseases in Humans and Animals*. Princeton University Press, 2008.
- [13] Jeffrey Kephart and Steve White. Directed-graph epidemiological models of computer viruses. In *Proceedings of the 1991 IEEE Computer Society Symposium on Research in Security and Privacy*, pages 343–361, January 1991.
- [14] Keegan Kresge. Analyzing epidemic thresholds on dynamic network structures. *SIAM Undergraduate Research Online*, 14, January 2021.
- [15] Piet Van Mieghem and Ruud Bovenkamp. Accuracy criterion for the mean-field approximation in susceptible-infected-susceptible epidemics on networks. *Physical Review E, Statistical, nonlinear, and soft matter physics*, 91:032812, March 2015.
- [16] Romualdo Pastor-Satorras and Alessandro Vespignani. Epidemic spreading in scale-free networks. *Physical Review Letters*, 86:5252:3200–3203, May 2001.
- [17] Lorenzo Pellis, Frank Ball, Shweta Bansal, Ken Eames, Thomas House, Valerie Isham, and Pieter Trapman. Eight challenges for network epidemic models. *Epidemics*, 10:58–62, 2015.
- [18] Auger Pierre, Kouokam Etienne, Sallet Gauthier, Tchuenté Maurice, and Tsanou Berge. The ross–macdonald model in a patchy environment. *Mathematical Biosciences*, 216:123–131, 2008.
- [19] Bastian Prasse and Piet Mieghem. Time-dependent solution of the nimfa equations around the epidemic threshold. *Journal of mathematical biology*, 81, December 2020.
- [20] Wei Wang, Ming Tang, H. Stanley, and Lidia Braunstein. Unification of theoretical approaches for epidemic spreading on complex networks. *Reports on Progress in Physics*, 80, March 2017.
- [21] Yang Wang, Deepayan Chakrabarti, Chenxi Wang, and C. Faloutsos. Epidemic spreading in real networks: An eigenvalue viewpoint. volume 10, pages 25 – 34, November 2003.