Epidemiological Complex Networks: A Survey

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Abstract

In this review paper, several research studies were surveyed to assist future researchers to identify available techniques in the field of infectious disease modeling across complex networks. Infectious disease modelling is becoming increasingly important because of the microbes and viruses that threaten people's lives and societies in all respects. It has long been a focus of research in many domains, including mathematical biology, physics, computer science, engineering, economics, and the social sciences, to properly represent and analyze spreading processes. This survey first presents a brief overview of previous literature and some graphs and equations to clarify the modeling in complex networks, the detection of societies and their medical information, the identification of nodes, the method of communication with individuals and their spread, the analysis of their transmission through complex networks, and the detection of mathematical methods over the past century. Secondly, the types of epidemiological models and complex networks and the extent of their impact on humans are presented.

Keywords: complex network, community detection, Epidemiological, metadata, covid-19

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مراجعة نمذجة الأوبئة في الشبكات المعقدة

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الخلاصة

في ورقة المراجعة هذه، تم مسح العديد من الدراسات والأبحاث لمساعدة الباحثين المستقبليين على تحديد التقنيات المتاحة في مجال نمذجة الأمراض المعدية عبر الشبكات المعقدة، تزداد أهمية نمذجة الأمراض المعدية بسبب الميكروبات والفيروسات التي تهدد حياتهم وتهدد المجتمعات من جميع النواحي. لطالما كان محورًا للبحث في العديد من المجالات، بما في ذلك البيولوجيا الرياضية والفيزياء وعلوم الحاسوب والهندسة والاقتصاد والعلوم الاجتماعية، لتمثيل وتحليل عمليات الانتشار بشكل صحيح. يقدم هذا الاستطلاع أولاً، لمحة موجزة عن المؤلفات السابقة وبعض الرسوم البيانية والمعادلات لتوضيح النمذجة والشبكات المعقدة، واكتشاف المجتمعات ومعلوماتها الطبية، وتحديد العقد، وطريقة التواصل مع الأفراد وانتشارهم، وتحليل انتقالها عبر شبكات معقدة واكتشاف الأساليب الرياضية خلال القرن الماضي، وثانيًا أنواع النماذج الوبائية وأنواع الشبكات المعقدة ومدى تأثيرها على الإنسان.

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1. Introduction

Observations of real networks inspire the study of dynamic networks. In fact, complex networks enable us to understand different real systems from biological networks. To ensure our survival, for example, we require a network of neurons linked by synapses with the ability to understand this information; relationships govern our bodies' thousands of cells [1]. Networking infrastructures Routers and computers work together to form networks, such as the Internet cables and optical fibers. Culture is made up of human friendship and other mutual partnerships. For example, collaborations with friends or colleagues keep us together. These systems are referred to as complex systems because their individual components' aggregate actions cannot be predicted. However, having a mathematical understanding of these structures allows one to predict if they can be monitored and communicated with [2]. The greatest technological challenges of our day play a significant role in our daily lives when it comes to the distinctions between dynamic systems that are found in nature and those found in civilization. Hence, the processes of these systems are relatively similar because they are governed by the same principles. Nowadays, the most prominent models for representing epidemics and their impact on health and society, including the model of common epidemics exposed to Susceptible Infection and Recovering (SIR), is the Corona virus (COVID-19). Also, in the segmentation of medical pictures, deep neural networks (DNN) are successfully used to meet the demand for a dependable and precise organ segmentation system, which has grown with the COVID-19 epidemic [3].

The study of complex networks has been impacted by experimental research on real networks. They are one of the most essential scientific issues because of the impact they have on our daily lives. Complex networks, in particular, help us understand a wide range of real-world processes, including technical networks, biological networks, cultures, illnesses, rumors, and more [4]. In general, there are basic models of complex networks that are shown in Table 1 that have been used in the study and application of epidemics in communities [5]. Companies consist of people with social linkages such as friendship, familiarity, or technological cooperation, while epidemics are diseases that propagate through contacts and combinations of humans or animals, such as measles disease and AIDS [6]. These systems are referred to as complex systems because the overall behavior of their elements cannot be predicted. However, the statistical description of these systems can be understood, anticipated, and theoretically managed due to the various networks and the methods of synchronization between nodes. Also, understanding how viruses move in transportation networks allowed for the prediction of the 2009 H1N1 pandemic and the new coronavirus year 2019/2020 [7].

Table 1: The basic models in complex networks [5]

| Type models of complex network	
1.	*Scale-free networks*
2.	*The Random Graph*
3.	*Small-world networks*
4.	*Spatial networks*
5.	*Generalized Random Graphs*
6.	*Networks with Community Structure*
7.	*Geographical Models (GN)*

2. Related Work

The scientists have many subjects for complex networks, epidemiological and community detection. According to [8], a series of algorithms are clarified for discovering network groups. Furthermore, the consistency of community detection in networks under degree-corrected stochastic block models was suggested. The first feature proposed iteratively removing edges from the network in order to split it into groups using inter-layer steps. The second feature recommended recalculating the inter-metrics objectively with each edge removed. The aim of these calculations is to find the shortest path between all pairs of vertices and to count the number of nodes along each vertex.

This process yields a constant multiplied by the number of edges inside clusters, which is less than the number predicted in a parabolic grid of randomly positioned edges. A new community-detection algorithm was created to perform better than earlier general-purpose algorithms in terms of consistency of results and execution speed. Also, it can evaluate any larger network with millions of vertices and edges. The effective and exact segmentation findings improve the prediction and diagnosis of diseases [8].Then, in [9], a GN algorithm is suggested for removing the group structure from a network with a large speed benefit in comparison to previous algorithms that are complete.

There is also an equivalence between the maximization of modularity and maximum liability. All populations have statistically similar properties. Models of stochastic networks produce modular networks, random graphs, and non-scale networking modularity. They clarify that the complex networks need to be made more modular. The mechanism that could boost modularity would be sufficiently wide and based on the assumption that random graphs have low modularity. The modularity approach is often considered to expand the validated technique to maximize modularity that is widely applied in undirected networks to test group structuring. Three classes of the suggested approaches can be defined for population identification. The last class of such methods is classified as hypothesis-driven methods based on a probabilistic model for a community network. Figure 1 shows data from political blogs. The area of each node is proportional to its degree's logarithm, and the colors represent community labels [10].

Social distance and disconnections may reduce the scale of the outbreak. The initial step of the SIR can be approximated using conjugation techniques as the population size becomes large, as shown in Figure 2.
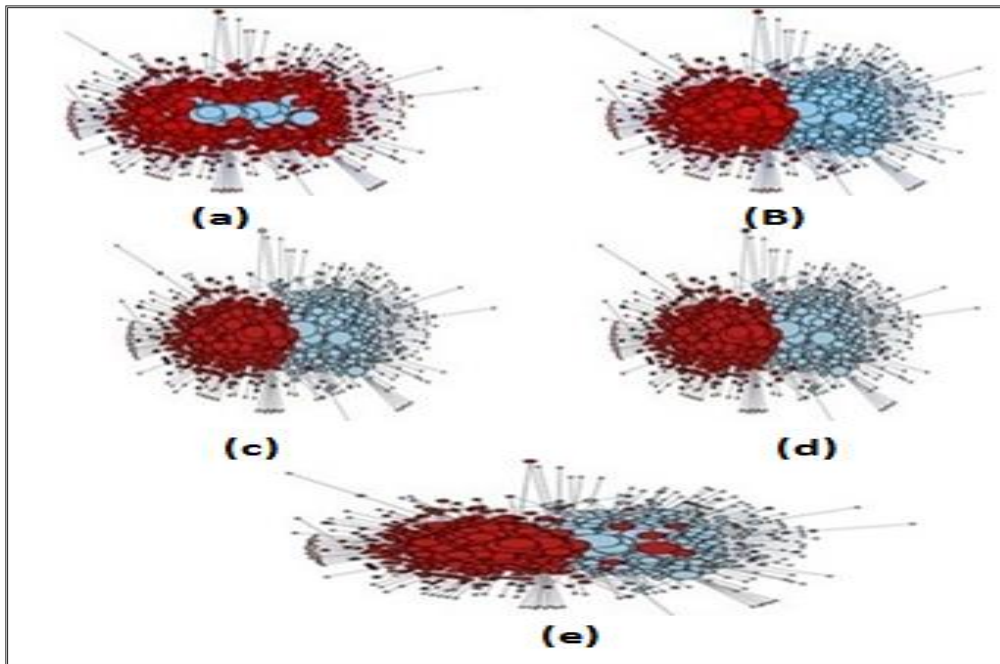
Figure 1: (a- block model b- The degree-corrected stochastic block model c- The degree-corrected stochastic block model d- Newman-Girvan Modularity e-true labels).
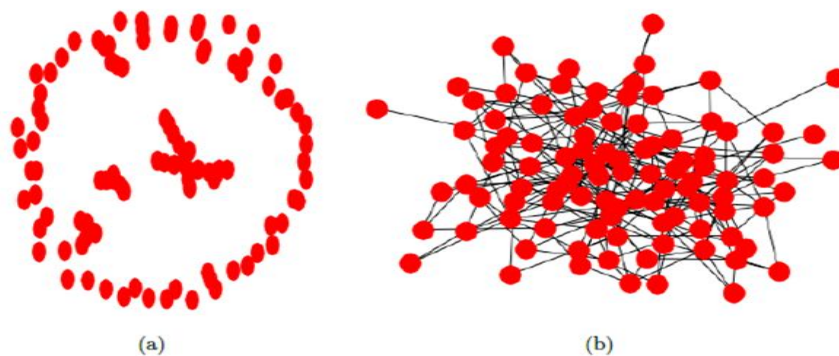
Figure 2: (Rényi Graph with (a) c = 0.9, (b) c = 5 using n = 100 vertices).

In [11], the study of graph models for complex networks is based on kernel functions over metric spaces. These are mixtures of microscopic models that take network semantics into account and macroscopic random graph models for complex networks. Kernel random graphs are a brand-new class of complex network models that give standard random graphs meaning for their nodes and links. A kernel random graph model creates a graph of n nodes for any given number of network nodes n. Also, the conceptual, analytical, and implementation clarity of random graph models is preserved by kernel-based models. Network nodes and links are given explicit semantics by kernel-based models. These semantics are capable of capturing fundamental elements of machine learning and information retrieval primitives such as hierarchy and clustering, which are more frequently seen in actual complex networks than in pure random graphs.
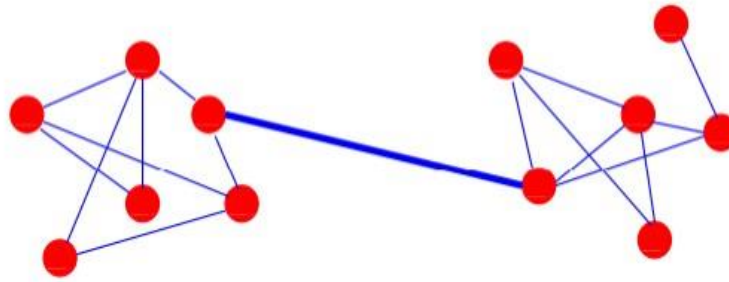
Figure 3: (The highest edge connecting edge connecting between communities).

In [12], the study of complex systems is advanced due to the study of networks in contemporary science. In system graphs, vertices are grouped into groups with many borders joining the heads of one group and relatively few edges linking the vertices of different groups. System graphs play a similar role in the human body's issues or the organs.

Community detection is very important for locating modules and the boundaries of those modules, which enables vertices to be categorized based on their structural position within the modules. Because it is much simpler to assemble the smallest subparts first and then use them as building blocks to create larger structures until the entire system is assembled, the generation and evolution of an organized system in interrelated stable subsystems occurs much more quickly than in an unstructured system.

This makes it far more challenging for mistakes to happen throughout the process. Identifying the modules and their hierarchical organization is the goal of community detection in graphs, which relies solely on the data encoded in the graph topology. For example, in Figure 3, edges are chosen based on the results of an edge centrality measure, while assessing the significance of edges is based on a feature or activity occurring on the graph. Firstly, all an edge's centralities are calculated, and then the highest centrality is removed in cases of ties with other edges.

In [13], the study illustrates a network as a device that can communicate with other systems and can be represented as a graph that is made up of elements such as nodes or vertices, as well as a collection of linking connections (edges) that reflect their relationships with one another using a variety of statistical and computing methods. A network can be represented by an adjacent matrix A from a mathematical point of view. The adjacency matrix of a graph with N vertices is N×N. The elements Aij of this matrix can be used to describe the boundaries. The ready-to-use Zakary Karate Club dataset, which provides genuine values for a variety of applications such as group recognition, was used as a well-known and enduring example from a social network. For example, in Figure 4, there is a greater chance that an edge will form between two people in a network made up of pairs of people if they have more than one friend in common [13]. In 1971 to 1972, the connections of 34 founders who met outside of the club, where this social network was investigated, were documented.
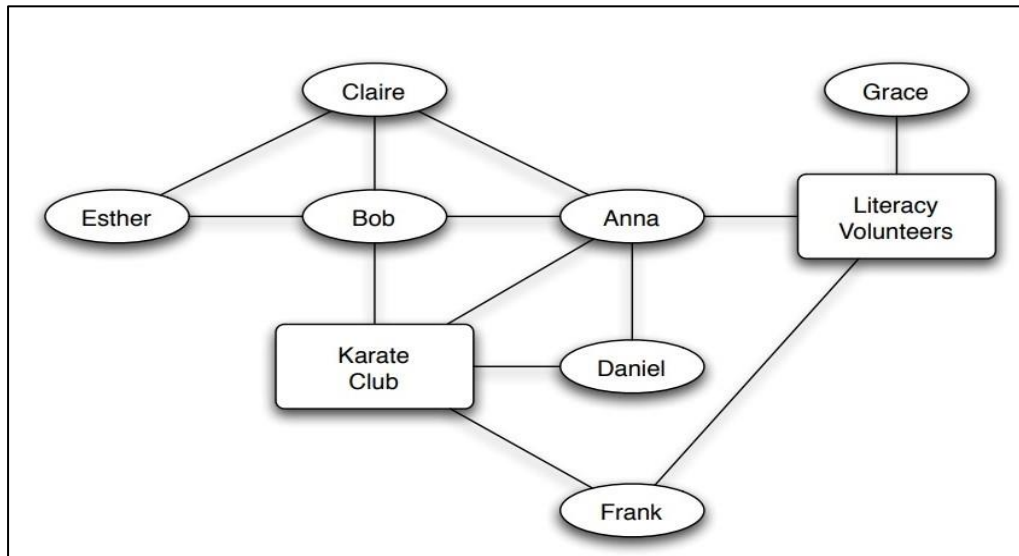
Figure 4: (a network reflection of a group's social experiences within the same karate club).

In [14], a high-dimensional SBM model has been developed for spectra aggregation, where the disclosures of the underlying group design of dynamic and cross-disciplinary networks have become a key subject in many applications. By studying the close effects of spectral clustering, the prophetic vectors were found to converge under the more general latent space model. A consistent spectrum was added, as spectral clustering is a fast and common algorithm for network clusters that allows presenting and grouping flexible options into SBM with optimized full data capabilities. The results of collective extraction spectroscopy are interpreted using random-block models. The use of specified clustering on a matrix near the network has been proven to successfully restore hidden groups.

Networks have been proposed to be dominated in a number of areas, including economics, genetics, neuroscience, and informatics. The borders are semantically asymmetrical since the source node transfers those qualities to the destination but not the other way around because graphs are frequently arranged to have guidance on the edges. This is because nodes are very similar in the same society, while nodes in present communities have poor similarity. Then, in [15], the homogenous network theory of Cannistraci-Hebb is presented as a recent development in network scientific research. It has a variety of real uses, such as the suggestion of social network friendships.

The modeling of the agent-functional class clusters in complex networks is shown by block model pictures and diagram nodes that depict the key communications patterns and the network functions. Then the grid's match is measured to every picture diagram that allows objective hypothesis testing. The optimum compatibility characteristics allow us to directly find the most appropriate picture scheme from the network and to have a standard for avoiding overcasting. Different types of connections can be handled simultaneously in two-mode and single-mode results, guided and indirect networks, and weighted networks. Then, in [16], eight state-of-the-art and five regular algorithms are analyzed and checked for overlap and population segmentation recognition.

They also applied two finely tailored group recognition algorithms, working to improve the quality of the population by splitting and merging certain community networks. These algorithms are precisely tuned based on modularity maximization. The results were used in social and biological network generative models. The classical modular maximization formula was used to provide convex programming relaxation using the double average median

technique. It has been shown that the approximate clustering results for approximate clusters and ideal clubs are minimally sensitive to non-asymptotic theoretical guarantees.

In [17], a strong new technology known as action-based modeling is introduced. A brief overview of the solutions to the disease prevalence problem was provided, including the use of filtration in dynamics, the use of epidemiology in a diverse population, and the multi-layered network of outbreaks by complex hierarchical modelling. The first section suggested that the deployment of bond filters in a single network should be studied and compared. The second section discusses when a site-infiltration, site bond, or geo-filtering analysis is conducted, and links are included in small-world networks.

In [18], the models that can help in understanding pandemics that spread quickly, like COVID-19, must be proposed where a variety of pandemics, including SARS, H1N1, and the current new coronavirus (COVID-19), have affected humanity. Scientists have created vaccinations; however, once the epidemic enters a territory, the distribution of the local population is crucial. They suggest two variations of our mobility-based SIR model: fully mixed and complex networks, which pay particular attention to interactions that occur in real-world settings.

The best model is the first of its type, taking into account data on network connectivity of individuals as well as statistics on population distribution and connectivity of various geographic regions throughout the world. Extensive simulations utilize synthetic data that has been undertaken in addition to presenting the mathematical evidence of proposed models to show how generalizable they are. They show the expanded capabilities of the suggested model applied to forecasting COVID-19 cases at the county level in Estonia and at the regional level in France's Rhône-Alpes region. In [19], waning immunity is clarified as having a crucial role in basic epidemic models on networks; however, it is underestimated in actual epidemic outbreaks.

When using the Susceptible-Infected-Recovered-Susceptible (SIRS) epidemic model on networks, they found that the mean-field technique was more accurate at describing the dynamics of the epidemic. On large networks with various degrees of heterogeneity, two types of mean-field theories are based on Recurrent Dynamical Message-Passing (RDMP) and Pair Quenched Mean-Field theory (PQMF) are contrasted. On power-law networks with degree distribution, RDMP outperforms PQMF theory for waning immunity times that are more than or equivalent to the recovery time. According to the real epidemic's localization patterns, improved theoretical frameworks are required to comprehend the SIRS dynamics, which lie between the two mean-field theories.

3. *Epidemiological model on networks*
3.1. *Types of epidemic models*
I. *Stochastic*
   "Stochastic" means to be a random variable or to have it. A stochastic model is a tool that allows a random change of a single or more inputs across time to estimate probability distributions of probable results. Stochastic models depend on the risk fluctuations in exposure, disease, and other dynamics of disease [20].

II. *Deterministic*
   Deterministic or compartmental mathematical models are frequently employed when dealing with big groups such as TB. In a deterministic model, distinct subgroups that reflect a

specific epidemic stage are allocated to people in the population. The transition rates from class to class are theoretically stated as derivatives; therefore, the model is developed by means of differential equations. In developing such models, the population number in a cell must be considered to be distinguishable from time and that the epidemic is deterministic. In other words, only the history used to create the model can compute changes in the population of a compartment [20].

3.1.1. *Regular Lattices*

Grid models are the most basic kinds of networks. They are used in cellular automata and agent-based models in science [21]. Each position in a normal network may indicate, for example, a person positioned in a typical network of points. They just have contact with their immediate. Since all locations have the same number of contacts, regular clamps are homogeneous. It has been widely applied to the study of complex processes in general, such as the diffusion reaction and disease dynamics [22]. However, in comparison to real systems, its generalized topology is impractical. The ease of thoroughly solving analytical problems, such as the Ising model, is a benefit of this form of the network [23].

3.1.2. *Random Regular Network*

Another simple grid prototype was examined by the Erdos-Rényi (ER) model, which was one of two closely related models for generating random graphs. In its initial form, the graph is created starting from a set of N nodes, and all edges between them have the same probability. This resulted in a homogeneous graph in which the heads have a number of neighbors not much different from the mean (k) score, with a conductivity distribution like Poisson, as shown in Figure 5 [5].
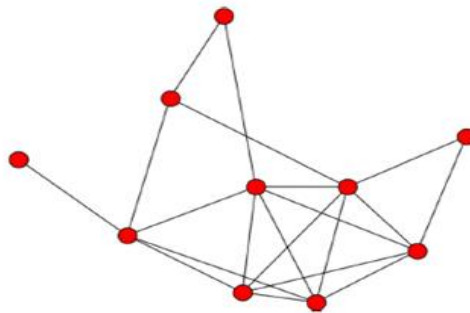
Figure 5: (Random Regular Network for nodes=10,period=0.5).

3.1.3. *Small-World Networks*

The world's smallest model is being developed as a more tangible social networking model. At first, N vertices are organized into a one-dimensional network with regular boundaries, and each vertex has m relations in WS networks with its nearest neighbors. When peaks are visited in a clockwise fashion, the edges of the clock ways are rejoined with the p probability. Rewiring establishes connected networks while maintaining consistent edge counts (k = m). Even with a modest p, the occurrence of shortcuts between remote nodes substantially lowers the average distance. This program generates a network with small-world characteristics using an energy law model; however, it cannot produce a heterogeneous distribution of degrees [24]. As shown in Figure 6, a Watts-Strogatz network of size N = 20 in which the network gets increasingly random as the p-value rises. In the first instance, p = 0, while in the second case p = 1, and in the third case p = 0.1 [5].
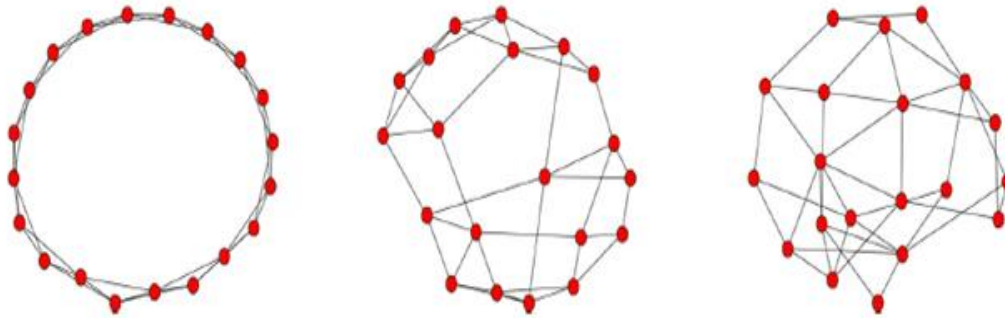
Figure 6: (Small-World Networks).

3.1.4. *Bar´abasi-Albert*

A preferential correlation model was adequate, which has been suggested to simulate the temporal development of many actual networks. New headers are introduced to the procedure at every stage of this model. Every new pinnacle has a likelihood which is proportionate to its current level with existing network nodes [25]. The creation and choosing of networking features enables the modelling of real-world networks such as the Internet and the World Wide Web [13]. The form shows the presence of graphs with the distribution of a force law degree, [$P(k) \sim k^{-y}$], where $\gamma = 3$ and micro-world properties. While considering adding new nodes, this network is considered to be static when dealing with a dynamic process since it evolved first, and then the dynamics ran across the substrate, as shown in Figure 7 [5]. A smaller network image (left side) and a larger ($N = 106$) network connection distribution (right side). We can see that there are hubs with a high degree of distribution in power-law. The sloping line is an eye guide with pitch $P(k) \sim k^{-3}$.
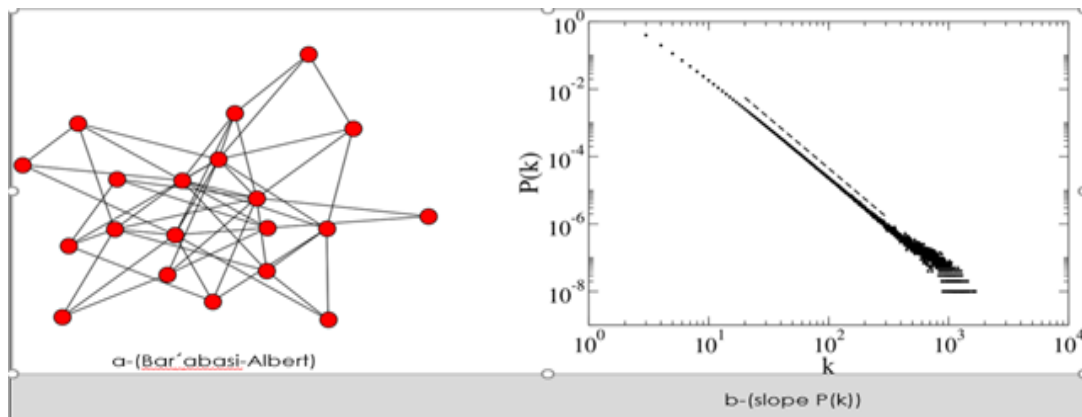

Figure 7: (a-Bar´abasi-Albert b- slope P(k)).

3.1.5. *Uncorrelated Random Networks*

Actual networks describe the presence of grade correlations in their conditions, in addition to their power-law distributions. $P(k^{\wedge}/|k)$ for uncorrelated networks can be estimated as the probability that any edge points to a vertex with degree $⟦k⟧^{\wedge}/$, leading to

$p_{unc}(k^{/}|k) = k^{/}p^{(k^{/})}/_{(k)}$, thus, the average nearest neighbor degree becomes in equation (1) as

$$k_{nn}^{unc}(k) = \frac{(k^2)}{(k)^2} \qquad\qquad \dots\dots\dots\dots (1)$$

That is independent on the degree of k.

From the behavior of dynamic systems, whose theoretic solution is only possible if no correlation can be assessed, unlinked random graphs from a numerical point of view are important despite correlations in most real networks [25].

3.1.6. *Networks with Euclidean Distance*

The related Euclidean distance between nodes is not taken into account in the majority of scale-free networks. Real-world structures, on the other hand, exist on top of a geographical vacuum. A food chain ecological network is integrated into 3-dimensional space and city streets that may be mapped as a square grid.

A feature of Euclidean distance Physical contact is an important element in forming social bonds. In interactive media networks, formation takes place using a network model that accounts for geographical proximity [26].

They see a square grid substratum and start with one node at an arbitrary origin in space. The network's second node is entered and connected to the first. At a distance of r, its position is chosen at random from the first node. This r-distance has a random distribution.

3.1.7. *Metapopulation Model*

Meta populations are characterized as a set of nodes corresponding to the intra-population level in each node. A metapopulation network consists of a number of networks that are not individuals but connected populations [27]. The internal structure might be a heterogeneous group of people. If we look at the transmission of rumors, we may split the individuals into three groups (spreaders, stiflers, and ignorant): (1) the spreaders of the news; (2) the stiflers who know the truth but are not participating in its share; and (3) the ignorant. As a basic example of a metapopulation network that is depicted into groups of people who may get ill, susceptible or healed if an outbreak is spreading, as it is shown in Figure 8 [22] [5].
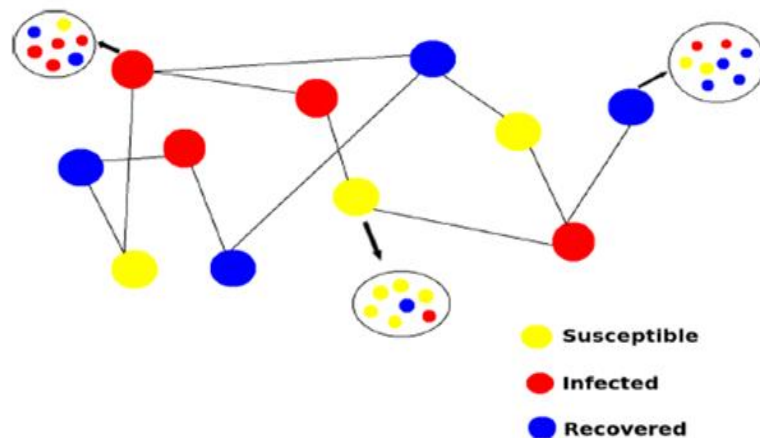
Figure 8: (a metapopulation network).

The dynamic spread happens in each population throughout the metapopulation, but because of the movements of people, the interaction between populations occurs [28]. For example, since movement is a significant factor in the dissemination of human diseases, this model is widely used. For example, a pandemic of Sars-Cov-2 and vector-borne farm diseases [29].

3.1.8. *Multilayer Networks*

In most real-world systems, a collection of components is linked in a number of ways. Multilayer systems with different architectures as networking tiers tend to be a major approach for describing these systems. Each layer has the same nodes as in the other levels, or the dynamic mechanism may be widened vertically in various ways or horizontally [30]. A vector is used to transfer several infectious illnesses between individuals. Insects are the most popular disease vectors, such as malaria, dengue, and the zika virus [31]. As shown in Figure 9, an example of a multilayer network created with the Python package payment [5].
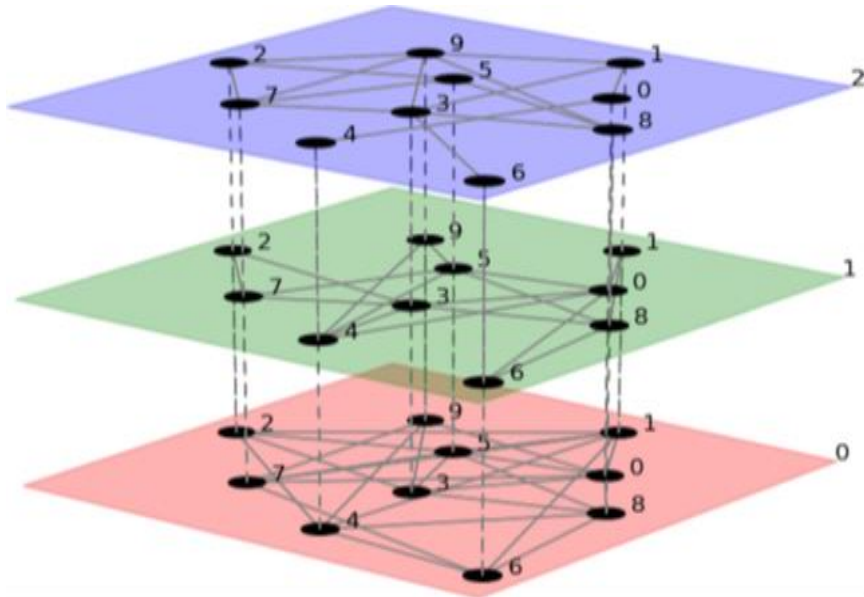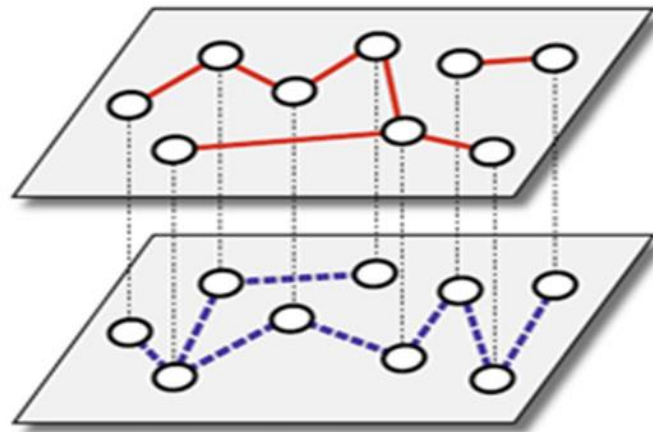

Figure 9: (an example of a multilayer network).

Consequently, we may shape this process with two layers, one of which represents human life and motion and the other represents insects. An insect bites an infected person; subsequently, this bite infects a healthy person; the transmission of disease takes place exclusively inside these layers. Social encounters are another example. We may envision a multi-layer network that serves Facebook, Twitter, and Instagram social media sites. Each node symbolizes an individual who can log into all social media sites, such as Instagram, but not Facebook or Twitter. Furthermore, connections with a person on a website may differ from their friendships in other networks.

3.1.9. *Multiplex Networks*
Multiplex networks are just specific instances of multi-layered networks in which every node has the same number of nodes in each of the levels. Multiplex networks provide the best framework to explore the dynamic interactions of different dynamic processes in the same node-set. For any dynamic mechanism under consideration, multiplicity allows the integrating of distinct network layers in such a way. The interference issue between the spread of two distinct diseases can, therefore, be resolved in a single-layer network. An epidemic model for two SIR illnesses is built on a single-layer network; for example, Figure 10 shows a schematic depiction of a nine-layer multiplex network: the red (solid) and the blue (dashed) layer. The dotted line indicating an identity relationship denotes the knots and their replication [32].

Figure 10: (an example of a nine-layer multiplex network).

The first pathogen's threshold behavior is preserved; however, the second pathogen is unable to spread, and certain agents who have recovered from the first illness are now immune to the second. As a result, even in scale-free networks, the illness breakout threshold is nonzero. The concept of separate transmission channels for different illnesses is a natural extension of competing epidemics to multiplex networks [33]. This takes into account a two-layer multiplex network and an SIR model in which the disease spreads sequentially.

The initial spreading takes place on one of the network levels, leaving the model with a number of repaired nodes. Before the second spread in the second layer, these nodes were already configured to be retrieved in the other layer. The assortative degree of correlation is increased by the degree of connection between nodes in both levels. The network is resistant to the second spread in terms of increasing the effective epidemic threshold to decrease the coexistence of both epidemics. The effects of delay between two spreading systems, as well as complete and partial immunity, may be investigated in a generalized scenario with two SIR epidemics propagating simultaneously [34]. The SIS model has also been used to study interacting epidemics [35].

3.1.10. *Temporal Networks*
It is possible to enhance network architecture by understanding the behavior of complex networks. The edges are not always involved. Edges in e-mail networks, for example, display a series of instant communications [32]. Agents should not form associations in the system while attending closed gatherings of people, such as schools or conferences [33].The fundamental temporal evolution of a network, similar to network topology, may affect system dynamics such as disease contagion or information distribution [36]. Indeed, in contrast to what has been observed in static networks, this mixing of time scales may lead to new phenomena in temporal network dynamics. Furthermore, the temporal evolution of time-network communications, which is characterized by long periods of inactivity followed by intense activity, may trigger a slow dynamic in propagation processes such as epidemics, diffusion, or synchronization.

3.2. *Concepts and Statistical Characterization of Networks*
3.2.1. *Mean-Field Approaches Using Nodes*
The midfield concept was the first theoretical technique for analyzing epidemiological dynamics in complex networks [37]. This technique divides the population in terms of not only the state of the individuals but also the degree of the node. The basic concept is that all nodes with the same statistical features have the same statistic. Therefore, nodes of the same degree

may be grouped together. Using this method, the structure of the network topology can be easily taken into account [38].

Where any node in grade k, p (I | k) symbol represents the same probability (chance) as any node in grade I. The relative densities are the focus of mid-field models based on nodes; for example, of K- class people in particular classes (s_k) or infectious compartment (p_k) that shown in equation (2).

$$S_K = \frac{S_K}{N_K}, P_K = \frac{I_K}{N_K} \qquad \ldots\ldots\ldots\ldots (2)$$

The SIS model means the probability of a person having a degree of k in the S, sensor, or infectious compartment. The SIS model describes the relative density of infected nodes in which the infection rate is commensurate with the infection level and the probability that an infectious node would have a random edge [39]. The SIS dynamic equation for k was derived as shown in equation (3).

$$\frac{dp_k(t)}{dt} = -p_k(t) + \lambda\, k[1 - p_k(t)] \sum_{lp}\big((l|k)p_l(t)\big) \qquad \ldots\ldots\ldots\ldots (3)$$

Where any node in grade k, λ is the effective rate of infection for the solution in equation (4). In a study of the pandemic limit, which is

$$\lambda_c = \frac{1}{\Lambda_m} \qquad \ldots\ldots\ldots\ldots (4)$$

where Λ_m is the largest eigenvalue of the connectivity matrix C [40], whose elements are $C_{Kl} = K_P(l|k)$. In the case of uncorrelated networks, they give the specific form of the epidemic threshold, where p (lk) =l p (l)/k and k are the average degree of the network. Thus, in uncorrelated networks $C_{kl} = klp(l)/\langle k\rangle$, and the broad expression of uncorrelated networks' epidemic threshold in equation (5)

$$\lambda_c = \frac{\langle k\rangle}{\langle k^2\rangle} \qquad \ldots\ldots\ldots\ldots (5)$$

It must be noted that multiple versions of an epidemic threshold exist for certain decisions of degree p(k). For example, the problem is solved using integral approximations for the distribution of form by a power law; therefore, they show that the SIS model does not have a non-null pandemic threshold in the networks without scale [41].

The analysis above is the general case of the epidemic model on networks, especially for the epidemic spreading on heterogeneous networks. Since $\langle k^2\rangle = \langle k\rangle$ holds for a homogeneous network, the generation expression of epidemic threshold recovers the result $\lambda_c = {}^1/_{\langle k\rangle}$ in the network is homogeneous. Also, a strict global study was carried out of the SIS model to demonstrate the aforesaid result [42].

The SIR transmission model may be used with this intermediate field technique [43], so the predicted final size may be derived during the whole transmission operation, in addition to a variety of others, including different degrees of distributions, which are generalized with this modeling technique, and complex network immunization [44].

More globally, analysis was performed using the generated function approach to analyze the propagation of epidemic risks in asymmetry networks, the dynamics of mid-field equations on guided networks, and the threshold of epidemic breakout. The epidemic model for SIS infection was created on the basis of semi-directed networks, which aims to represent the coexistence of

direct and undirected connections. In Table 2, we clarify the basic models of epidemiological modeling and their concepts [45].

The propagation of sexually transmitted diseases on two-party graphs depicts heterosexual and gay networks of contacts [46]. In [47], the researcher developed a methodology to take into account the impact of vectors, such as mosquitoes, and calculate a reproductive number that may be used to evaluate the vector's impact on the spread of the epidemic. In Figure 11, the population is split into distinct classes that vary with time. Susceptible (S) refers to disease susceptibility, and infections (I) refer to infections that can spread the illness to those who are healthy. While Recovered (R) refers to an immune system that has recovered.
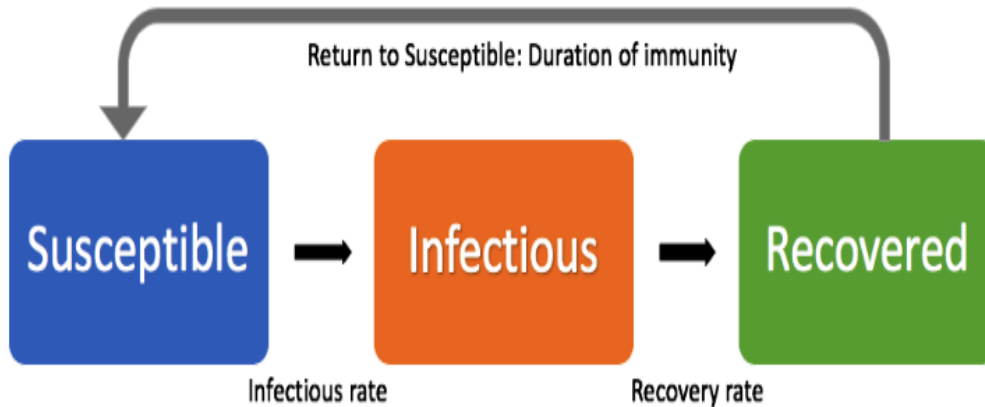
Figure 11: (the basic SIR model).

The examined population has a constant size N, which is big enough to allow continuous variables to be considered for each class.
- If the model involves vital dynamics, births and naturally-occurring deaths are considered to be equivalent.
- There is a uniform mixture in the community, and the sort of direct or indirect contact suitable for transmission depends on the particular illness.

Table 2: The basic models of epidemiological modeling [47]

The basic model		
	Type	*Concept*
1.	SIS model	*The model is termed the SIS model if the recovery doesn't offer immunity. Certain germs, such as meningitis and plague, are suitable.*
2.	SIR model	*The model is named the SIR. It is a suitable model because when the individual recovers, it will accept permanent immunity like measles, smallpox, and mumps.*
3.	SIRS model	*If people go back temporarily such that they become sensitive again eventually, then it is suitable for the SIRS model.*
4.	The SEIS model	*The SEIS model takes the exposed or latent time of the illness into account and offers an extra compartment, E (t).*
5.	The SEIR model	*In this approach, the four divisions: sensitive, exposed, infected and recovered, are included.*
6.	The MSIR model	*A person is born with a passive immunity from the mother to numerous illnesses.*
7.	The MSEIR model	*The MSEIR model is used in the event of a disease with passive immunity components and latency.*
8.	The MSEIRS model	*A MSEIRS model is similar to the MSEIR, except R-class immunity would be transitory, thus people would regain their sensitivity at the conclusion of the temporary immunity.*

The proposed model was expanded to include both homogenous and heterogeneous connections simultaneously through a global homogenous mixture and via a contact network [48] to extend this technique to efficient models of network diseases. The SIS epidemic model has solved the limitations by extending this technique to efficient models of network diseases [49]. An infectious person with one transmittable link can pass on to numerous susceptibles before they recover. An efficient degree model tackles the Pastor-Satorras and the Vespignani SIS problems, overestimating the threshold of epidemic transmission. In addition, a node epidemic model was created on dynamic networks in relation to the static network epidemic model, which may examine the influence of demography on the transmission of diseases [50].

3.2.2. *Edge-Based Mean-Field Approaches*

Field edge-based epidemiological models are presented in order to understand how communication networks impact disease propagation and the edge's effect on disease propagation. The advantages and disadvantages of various models of edge-based infectious diseases, as well as their differences from edge-based models of node-based epidemics, are discussed. The marital epidemic model is an alternate method aimed at describing the impact of the edges, which is based on the method of a marital approach and aims to assess the proportion of the infection rate of vulnerable persons to the number of partnerships between susceptible persons and damaged persons [51].

In the population, the predicted number of susceptible and infected susceptible relationships may be described in the same way as SS, SI, and the other types of partnership. The rate of infection was then shown to be based on the number of susceptible partnerships, which SI can reflect in the presentation of the medium-scale model. There is an inflow between SI and SS as infected people recover (Susceptible and Infected Susceptible SIS model) and people who are vulnerable to another relationship. Eddy and SEIRS pair model discovered action for studying children's epidemics [52]. The SIR model is presented in pairs using homogenous networks. This might allow a broader framework and neighboring architecture to characterize the behavior of spatial models as normal differential equations [53]. The following are the equations for the SIR model that are shown in equations (6).

The flow of this model is the following: S→I→R
S: number of sensitive persons S′: S change rate of S
I: number of people affected I′: I change rate I
R: number of people retrieved R′: R change rate R′

$$\frac{dS}{dt} = -\beta . I . \frac{S}{N}$$
$$\frac{dI}{dt} = \beta . I . \frac{S}{N} - r . I$$
$$\frac{dR}{dt} = r . I \qquad\qquad \dots\dots\dots\dots (6)$$

The basic disease model known by the name Kermack–McKendrick proved the following:
1. There is a simple replication number R_0, because if R_0 is less than one, the disease dies out, whereas if R_0 is greater than one, an outbreak occurs.
2. As t increases, the number of infective approaches is zero, and the number of susceptible exceeds a positive limit.

3. There is a relationship between the number of reproductions and the epidemic's final size, which is equal if no disease deaths occur.
Indeed, these properties remain true for disease models with more complex compartmental structures [54].

As shown in Figure 12, where R_0 represents the number of instances of a disease that an infected individual will go on to produce, and the more contagious leads to the higher the R_0 number as in equation (7). It is sometimes handled as a time-varying variable and utilized as a metric to make lockdowns go more smoothly. R_0 is the first parameter in the SIR model.

$$R_0 = \frac{\beta}{\gamma} \qquad \qquad \ldots \ldots \ldots \ldots (7)$$

R_0 calculates the number of individuals infected due to the interaction with a single sick person before he/she dies or recovers. In the Table 3, that clarify the basic reproductive number in the global world for the most popular diseases [55]. The dimensionless basic reproductive number R_0 is a feature of a population with infectious illness. The total population of a person's meetings, the disease's transmissible, and the average infectious time are included in R_0, which decides whether the epidemic infiltrates the populace, how many people are infected during the outbreak, how many infectious individuals are infected, and how many people would be vaccinated to preserve herd immunity in the SIR model [56].

Figure 12: (How the R_0 numbers of COVID-19 variants and other diseases compare).

The SIR model is adapted to describe the spread of infectious diseases to take into account non-infection births and deaths. Temporary immunity may also be modelled with a R_0 response that represents immunity loss. To simulate an endemic balance, the illness persists indefinitely in the population and is known as an epidemic [57]. For the diseases of more than the usual percentage of a certain population, the rate (v) rises in order to decrease epidemics below a particular threshold which future modelers might predict. This is predicated on the premise that

the action affects v alone. Other therapies may influence both (S) susceptible groups and (I) infectious communities, such as selected vaccinations [31].

Table 3: The basic reproductive number in the global world

	Basic reproductive number		
	Diseases	*Transmission*	R_0
1.	*Measles*	*Inhaling*	*12-18*
2.	*Pertussis*	*Drops of inhalation*	*12-17*
3.	*Diphtheria*	*Saliva*	*6-7*
4.	*Smallpox*	*Social connection.*	*5-*
5.	*Polio*	*oral-faecal route*	*5-7*
6.	*Rubella*	*Drops of inhalation*	*5-7*
7.	*Mumps*	*Drops of inhalation*	*4-7*
8.	*HIV/aids*	*Sexual connection*	*2-5*
9.	*Sars*	*Drops of inhalation*	*2-5*
10.	*Chick pox*	*Aerosol*	*12-18*
11.	*Ebola (2014 outbreak)*	*Body fluids*	*1.78 (1.44–1.80)*
12.	*Influenza common cold (1918 strain)*	*Drops of inhalation*	*2-3*
13.	*Sars-cov-2*	*Drops of inhalation*	*2-3 (71)*
14.	*Covid-19 (delta variant)*	*Aerosol and respiratory droplets*	*5-8*
15.	*Covid-19 (alpha variant)*	*Aerosol and respiratory droplets*	*4-5*
16.	***Covid-19 (ancestral strain)***	***Aerosol and respiratory droplets***	*2.87 (2.39-3.44)*

• *SIS model*

The SIS model may simply be calculated by assuming that individuals are immediately susceptible following recovery without immunity to disease. S →I→ S.
Where S: symbol to Susceptible, I symbol to Infective, t time.

The following differential equations (8-10) may be derived by eliminating the equation representing the population recovered from the SIR model and by bringing the population eliminated to the vulnerable.

$$\frac{dS(t)}{dt} = -\beta S(t)I(t) \qquad \qquad \ldots\ldots\ldots\ldots (8)$$

$$\frac{dI(t)}{dt} = \beta S(t)I(t) - \mu I(t) \qquad \qquad \ldots\ldots\ldots\ldots (9)$$

$$\frac{dR(t)}{dt} = \mu I(t) \qquad \qquad \ldots\ldots\ldots\ldots (10)$$

4. *Comparison of SIR, SIS, and SEIR models*
Table 4 displays a comparison of the three most popular models SIR, SIS and SEIR.

Table 4: A comparison of the most popular models

criteria	Comparing of most popular models		
	SIR	**SIS**	**SEIR**
Abbreviation	*It is a simple basic epidemiological study compartmental model*	*It is a fundamental SIR derivative where immunity does not give a longer-term immunity after recovery.*	***It is a variant of the standard SIR model that is subjected to an extra bay that contains those affected but not yet afflicted.***
Attributes	*Three as S, I and R*	*Three as S, I and S*	***Four as S, E, I and R***
Modelling of a standard	*Basic model*	*A derivative of SIR model*	***A derivative of SIR model***
Latency of model	*No, addition of a latency period*	*No, addition of a latency period*	***Yes, addition of a latency period***
Progress of model	*Progress from infection-prone to recovery*	*Progress against susceptibility to infections*	***Progress from exposure to recovered infections***
Population target	***N= S+I+R is the total population***	***N=S+I+S is the total population***	***N=S+E+I+R is the total population***

5. Conclusion

An overview of the complex networks is presented in the current study. The overview here took this area to a larger audience with the aim of summarizing the complex network tools, models, forms, and domains involved in modeling epidemics and diseases in societies.

Wide lists of citations have been compiled for those interested in learning more about this issue. Furthermore, these models should be reviewed and the extent to which knowledge can be expanded on epidemics that directly affect people's lives should be determined.

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