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Modeling and simulation of traffic flow and epidemic spreading in scale free networks.

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DEDICATED

To

In the token of love, affection and gratitude,
I would like to dedicate this work to all those who were
of great help and assistance to me.

& Particularly to

My mother Khadija

My father Moustapha

My brothers: Mohamed & Mohssine

All other members of my family

All my colleagues

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Abstract

Network science has acquired much interest from researchers. In fact, complex networks are involved in various fields and disciplines. However, studies that have been conducted in this area, had revealed a great discovery, the scale-free nature represents many real networks.

For a given network topology, the main goal of most studies carried out in this domain, is to understand various dynamical processes on complex networks. Two types of dynamical processes that have been studied extensively are : epidemic spreading and traffic dynamics.
Traffic dynamics is one of the most popular processes on complex networks, the objective of which is to enhance the traffic flow without extra-technical and monetary costs. While, epidemic spreading which is also considered an important issue, its aim is to describes how infections spread throughout a network and how to control the prevalence of infection.

Following this logic, in epidemic spreading, we propose a restricted scale-free network topology more resistible to the spread of epidemics. After that, we studied the effect of different routing algorithm schemes (shortest path "SP", efficient path "EP" and global dynamic "GD") on epidemic spreading in complex networks, which allows us, to proposed a new method of anti-virus vaccination that helps us to still use performant algorithms routing strategies (EP and GD), our method maintains an acceptable level of protection against virus spreading without affecting the traffic transport efficiency.
Concerning the traffic dynamics, we studied the effect of routing algorithm strategies in interconnected networks. We proposed an optimal routing algorithm schemes useful in interconnected complex networks "border routing algorithms". Our routing schemes has a similar performance comparing with the global routing schemes, without extra cost and the load of global routing protocols.

Despite the network architecture, we believe that the results of our works may be applied in several network systems. For example, biological, economical, social, transportation and airline networks ….

keywords

Complex networks; Epidemic spreading; Traffic dynamics ; Restricted scale-free network; Vaccination; Routing algorithms.

Résumé

Nombreux systèmes dans le monde réel peuvent être représentés comme des réseaux complexes. Les recherches montrent que la majorité des réseaux réels sont de nature dite : "sans échelle".

Le défi majeur d'une architecture d'un réseau, est de comprendre les phénomènes qui apparaissent dans les réseaux complexes. Dans la littérature il y a deux phénomènes qui sont largement étudiés: la propagation des virus et le trafic.
L'objectif de l'étude du trafic sur les réseaux complexes est l'augmentation de la capacité du trafic sans frais supplémentaires au niveau technique et économique. En outre, l'étude de la propagation des virus dans les réseaux complexes est de connaître la dynamique de cette dernière et la méthode efficace pour contrôler la prévalence de l'infection. L'objectif de cette thèse est d'étudier les deux phénomènes mentionnés ci-dessus et la relation entre eux.

D'une part, nous avons proposé une architecture de réseau qui permet de résister à la propagation des virus dans les réseaux complexes; cette architecture nommée "Restricted scale-free network". D'autre part, nous avons étudié l'impact des stratégies de routage (shortest path "SP", efficient path "EP" et global dynamic "GD") sur la propagation des virus dans les réseaux complexes. Cette étude nous a permis de proposer une nouvelle méthode de vaccination anti-virus pour utiliser des algorithmes de routage performants (EP et GD) avec un niveau de protection convenable pour combattre la propagation des virus sans aucun effet sur l'efficacité du trafic.
A l'égard du trafic, nous avons étudié l'impact des algorithmes de routage dans les réseaux interconnectés et nous avons proposé des algorithmes optimales, très utiles et efficaces "Border routing algorithms". Nos stratégies ont donné des performances similaires par rapport aux stratégies de routage globales sans charges de trafic ni de frais supplémentaires.

Les résultats de nos travaux pourront être appliquer dans plusieurs domaines: la biologie, l'économie, sciences sociales et d'autres ….

Mots clés

Réseaux complexes; Trafic; Propagation des virus; Réseau sans échelle restreint; Vaccination; Algorithmes de routage.

Résumé détaillé

De nos jours, l'étude de la science des réseaux devient nécessaire et importante, car de nombreux systèmes dans le monde réel peuvent être représentés par des réseaux complexes et les exemples les plus illustratifs ce sont: les réseaux internet, les réseaux sociaux, les réseaux de transport et d'autres. En plus, ces réseaux nous entourent dans notre vie quotidienne. Donc, ils doivent être étudiés.

Dans la dernière décennie, l'accroissement du nombre d'utilisateurs actifs dans ces réseaux ne cesse pas d'augmenter de façon redoutable, ce qui déclenche des problèmes comme la congestion du trafic et la propagation des virus et ce qui influence aussi la qualité des services fournis aux clients. Pour surmonter ces problèmes, les études scientifiques sont focalisées essentiellement sur des méthodes capables de limiter la propagation des virus, et sur la conception des stratégies efficaces de routage capables de rester à la hauteur des progrès rapides des réseaux en satisfaisant les demandes des utilisateurs.

L'intérêt de cette thèse est d'étudier les phénomènes qui apparaissent dans les réseaux complexes et notamment la propagation des virus, le trafic et la rapport entre les deux dans les réseaux de type sans échelle « scale-free ». L'objectif du trafic est d'augmenter sa capacité sans frais supplémentaires au niveau technique et économique. En outre, l'étude de la propagation des virus est faite pour connaître sa dynamique afin de trouver des méthodes efficaces pour contrôler la prévalence de l'infection. Alors, nous proposons ci-dessous les résumés des chapitres constituant cette thèse.

Chapitre *I*

Au début de ce chapitre, nous avons introduit quelques notions importantes qui sont fréquemment utilisées dans la science des réseaux, également elles sont empruntées de la théorie des graphes.

Ensuite, nous avons étudié les caractéristiques les plus intéressantes qui sont détectées dans des réseaux réels, et nous avons exposé une étude concernant la modélisation des réseaux complexes existés dans la réalité, afin de justifier le choix d'un réseau sans échelle modélisé par Barabási-Albert, comme une plateforme du trafic et propagation des virus.

Chapitre *II*

Dans le deuxième chapitre, nous avons présenté les phénomènes qui apparaissent dans les réseaux complexes. En effet, il existe deux types de processus dynamiques qui ont été étudiés profondément, à savoir la propagation de virus et la dynamique du trafic.

Dans la première partie, nous avons défini les principaux concepts du trafic. Ensuite, nous avons entamé une revue globale sur les stratégies de routage les plus utilisées pour améliorer la capacité du trafic des données, tout en distinguant la politique derrière chaque approche et en précisant les avantages et les inconvénients de chaque stratégie.

Nous avons consacré la deuxième partie pour étudier la propagation des virus. D'abord, nous avons commencé par les définitions fondamentales de la propagation des virus. Ensuite, nous avons présenté les méthodes les plus mémorables et les plus utilisables par les chercheurs pour comprendre la dynamique de la propagation des virus dans les réseaux complexes.

Chapitre *III*

Dans ce chapitre, nous avons étudié la propagation des virus dans un réseau sans échelle proposé par Barabasi-Albert avec ses différentes topologies et nous avons proposé un réseau sans échelle restreint (RSF) plus résistant à la propagation des virus. Notre idée est basée sur l'influence de degré de la connectivité des noeuds k. Dans notre travail, nous avons déterminé un degré maximal critique (K_c). Dans le cas où ($k < K_c$), la propagation des virus est limitée dans le réseau. Cependant, la proportion des noeuds infectés continue d'augmenter lorsque ($k > K_c$).

De plus, nous avons constaté que certaines propriétés des réseaux tels que la taille peuvent influencer la propagation des virus. En effet, La proportion des noeuds infectés augmente selon la taille de réseau.

Chapitre *IV*

En réalité, même lorsqu'il existe un lien entre deux noeuds, la propagation de l'infection ne se produit pas, sauf s'il y a une sorte de trafic dans le réseau capable de transporter physiquement le virus d'un noeud à un autre. Pour cette raison, dans ce chapitre nous nous sommes focalisés sur l'étude de lien entre la propagation de l'épidémie et le processus de transport. Également nous avons étudié les effets des stratégies de routage sur la propagation des virus dans les réseaux complexes.

Nos résultats ont montré que dans la phase d'écoulement libre, les algorithmes de routage performants ("efficient path (EP)" et "global dynamic (GD)") qui sont utilisés pour surmonter le problème de congestion, eux-mêmes favorisent la propagation des virus plus que dans le cas de "shortest path (SP)". Dans la phase de la congestion et a cause d'une faible probabilité d'infection, tout le réseau devient infecté par tous les algorithmes de routage étudiés.

Les algorithmes de routage performants (EP et GD) favorisent la propagation des virus en comparaison avec la stratégie SP, et au lieu d'une vaccination aléatoire, nous avons proposé une nouvelle méthode de vaccination qui nous permet de continuer à utiliser des stratégies de routage performantes avec un niveau de protection acceptable pour lutter contre la propagation des virus et sans affecter l'efficacité du trafic.

Chapitre *V*

Concernant notre travail sur le trafic présenté dans le chapitre V, nous sommes concentrés sur le problème du trafic dans les réseaux interconnectés. Nous avons étudié les effets des stratégies de routage sur les réseaux interconnectés.

Dans une situation réelle, les réseaux interconnectés ont des politiques de routage différentes. Malheureusement, ces politiques sont à l'origine des problèmes et des difficultés au niveau de l'échange et de la mise à jour des informations dans les sous-réseaux. Pour surmonter ces problèmes, l'Internet a utilisé un protocole de routage bien connu entre les différents systèmes autonomes (AS), appelé "Border Gateway Protocol" (BGP). Pourtant, dans notre cas, nous avons utilisé la version simple de ce protocole, elle se base sur la séparation entre les deux autorités administratives implémentées dans chaque réseau et introduit des règles de routage pour l'échange des informations entre les deux réseaux. Nous avons proposé des stratégies de routage qui donnent des performances similaires par rapport aux stratégies de routage globales sans charges de trafic ni de frais supplémentaires.

Contents

NOMONCLATURE

SW	:	Small world.
WS	:	Watts and Strogatz.
SF	:	Scale free.
BA	:	Barabási and Albert.
ER	:	Erdös and Rényi.
RSF	:	Restricted scale free.
SP	:	Shortest path.
EP	:	Efficient path.
GD	:	Global dynamic.
UAA	:	Unique administrative authority.
MAA	:	Multi-administrative authorities.
BAA_1	:	Border administrative authority 1.
BAA_2	:	Border administrative authority 2.
AS	:	Autonomous systems.
PS	:	Policy strategy.
$FIFO$	:	First-in-first-out.
SI	:	Susceptible-Infected.
SIS	:	Susceptible-Infected-Susceptible.
SIR	:	Susceptible-Infected-Removed.
SIE	:	Susceptible-Infected-External.
SV	:	Selective vaccination.
RV	:	Random vaccination.

INTRODUCTION

Context

Many systems taking the form of networks abound in the world. Different artificial and natural systems can be represented as network [1, 2]. Indeed, networks are all around us, and ourselves, as individuals, the units of a network of social relationships of different kinds, the biological systems, the electric power grids, the Internet, highways or subway systems, neural networks, metabolic networks, food webs, distribution networks, blood vessels or postal delivery routes, networks of citations between papers, and many others considered to be application of networks [3–8].

The scientists used to ignore that the majority of practical networks have actually complex structure, they believed that these networks have homogeneous and relatively simple architecture. This idea was the result of the absence of sufficient real data acquisition which makes it impossible to determine with certitude the structure of these networks. Consequently, regular networks, then intuitively random graphs were the first network models used to study real networks for over a century [9, 10]. However, driven by the computerization of data acquisition, scientists had finally access to huge databases related to various real networks of complex topologies. Such topological information is increasingly available, raising the possibility of understanding the dynamical and topological stability of large networks [11–13].

The analysis of networks from different fields and the huge amount of available data have produced a series of unexpected and dramatic results. Indeed, this analysis has been crowned with significant discoveries in graph theory and network science. The research on complex networks begun with the effort of defining new concepts and measures to characterize the topology of real networks. As a result, the researchers come to identify a series of unifying principles and common statistical properties to most of the real networks considered. Which were crowned with the discovery of the small-world phenomenon by Watts and Strogatz in 1998 [14, 15] and the scale-free characteristic by Albert and Barabási in 1999 [13, 16].

The small-world is a concept in simple terms describes the fact that despite their often large size, in most networks there is a relatively short path between any two nodes. The Small world concept includes two popular manifestations. The first one refers to the distance between two nodes, and defined as the number of edges along the shortest path connecting them [17, 18]. For example, in a friendship network, a friend of my friend is more likely a friend of mine too. The second is "the six degree of separation" by the social psychologist Stanley Milgram

(1967) [11], who concluded that there was a path of acquaintances with a typical length of about six between most pairs of people, which means that two individuals can be linked in relativity short path.

The other important discovery so-called the scale-free (SF) concept, means that the number of connections that got each node of the network is not homogeneous as in regular and random graphs [16]. As example, in friendship network, this is reflected by the fact that we do not have the same number of friends. More than that, the number that has each one of us does not oscillate around an average. The reality is that few of us have very large number of friends and the majority has few numbers of friends. In network science, those very popular people are called "hubs". In general, with respect to the network nature, a hub is a node with large number of connections, greatly above the average. The presence of such nodes as long with other properties is literally a signature of a complex topology or SF networks [19].

In other context, networks rarely seen in isolation in reality, are subject of interact with each other [20]. For example, in epidemiology; diseases can propagate through populations but can also propagate to other populations [21, 22]. In order to model the interactions between real world networks, several coupled network models have been developed, such as interconnected networks, multiplex network ....
Multiplex network refer to class of networks introduced as a better model of such systems. In this class of networks the same set of nodes are connected via more than one type of links. Each type of links in multiplex network constitutes the network layer [23, 24]. Therefore, Multiplex networks are networks of networks in which the identity of the nodes is the same across different networks but the links are different. Multiplex social networks tend to describe a person who participates in multiple social networks. For example, despite the actors will be the same, the networks of phone communication and email communication between individuals will have different topologies [25, 26].
In this thesis, we consider the case of only two isolated networks that are connected by some links, which can provide path for traffic between them(interconnected networks) which were studied in [27–29].

The study of complex network is not limited to understand and modeling only the structure of complex networks, but it includes the dynamic processes that has been proving to be interesting and vital importance, such as the traffic dynamics [30–40] and epidemic spreading [41–50].

Epidemic spreading is to understand how the infections spread in the network and propose effective measures to overcome this issue. Traffic dynamics is concerned mainly with how information or "packets" can be delivered efficiently from one location to another on a network and the conditions under which congestion may emerge.

In order to alleviate traffic congestion and enhance the traffic capacity of complex networks, researchers proposed various improved strategies [51], which can be classified into "hard" and "soft" strategies. The hard strategies are about optimizing network topological structures by removing some links or nodes, or by adding some links between nodes with long distance or nodes in the same neighborhood of large-degree nodes [52]. It is called "hard strategy" because it operates on the underlying network structure. In the second strategy, which is referred as "soft strategy", the network structure is kept intact and only routing protocols are meant to alleviate the traffic flow and improve the transmission efficiency [53, 54]. The hard strategies can remarkably enhance the network performance. However, they are very expensive and not practical speaking of the implementation problem. In the other hand, soft strategies are more

flexible, they are not much costly, and more applicable to real-world communication networks. For these reasons, scientists devoted more attention to soft strategies.

Inspired by previous works on traffic dynamics and the interconnected networks [55–58], we proposed a routing schemes to optimize the traffic flow in interconnected complex networks.

The importance of the study of complex networks is justified by the different phenomena that occur on these networks, such that epidemic spreading. Indeed, the human society has suffered from various viruses that have to do with human nature; such as AIDS, $H1N1$ influenza and viruses that have to do with technological development such as computer viruses. Modeling, analysis and control of the infectious diseases have become a relevant problem of an interdisciplinary nature [49, 59, 60].

The research of infectious diseases has always been a high issue, many mathematical models were proposed to model and understand how infections spread throughout a real world networks [43,61–63]. Indeed, there are two main mathematical approaches: deterministic models based on differential equations and stochastic models that employ Markov chains, branching and diffusion processes, etc. Both deterministic and stochastic models play a significant role in epidemiology [64, 65].

The majority of these Mathematical models are usually assumed the propagation is to be driven by reaction processes, in which that every infected node transmits diseases to all its neighbors at each time step, producing a diffusion of the epidemics in the population. However, in many realistic situations, even when there is a link connecting two nodes, infection will not propagate unless some kind of traffic happens between the nodes. For example, a computer virus can spread over Internet via email-exchanges. In the absence of such data packet transmission, even if there is a path linking two computers, an infected computer will not be able to infect the other one [59, 60, 66].

After we have seen the modeling and analyzing of the epidemic spreading in complex networks, the turn comes to see the control of epidemic spreading [50]. Indeed, in the field of epidemic spreading, one of the most important issues in the study of epidemic spreading is to control the prevalence of infection. Indeed, the control plays an important role to maintain the security of complex networks [42, 44, 67–70].

Following this way, and inspired from previous works which studied the epidemic spreading, we have propose some strategies to model, analyze and control the epidemic spreading in complex networks.

Contribution of the thesis

To overcome the problems that complex networks suffer from, such as traffic congestion and epidemic spreading, we propose in this thesis, different strategies. On the one hand, a strategy devoted to minimize the traffic congestion, on the other hand, a strategies devoted to solve the problem of epidemic spreading in complex networks.

In the first part, we studied the virus spreading in scale free network with different topologies. We focused on the proportion of infected nodes in these networks. For this reason, we proposed a restricted scale-free (RSF) network more resistible to the spread of virus. Our idea is based on the influence of the degree of connectivity nodes k.

We devoted the second part also, to study the virus propagation in complex networks and

specifically on traffic-driven epidemic spreading and studied the effects of routing algorithm strategies, which has been ignored and has not received an adequate attention. This reason motivated us to get along to study this topic.
It is well known that more performant routing algorithm strategies are used to overcome the congestion problem. However, our main result shows unexpectedly that these algorithms favor the virus spreading more than the case where the shortest path based algorithm is used. We proposed a new method of anti-virus vaccination that helps us to still use performant routing algorithms with an acceptable level of protection against virus spreading without affecting the traffic transport efficiency.

In the third part, we have focused on the traffic problem in interconnected networks. Inspired by previous studies of traffic congestion in isolated networks and the newly developed works of interconnected networks. In addition, we noticed that the effect of routing algorithms strategies on interconnected networks has not received an adequate attention. This reason encourage us to study this topic.
In real situation, the interconnected networks have different administrative routing policies. Unfortunately, these policies present some problem; such as difficulty of exchanging and updating information about the subnetworks for all routers, and information exchange has also a high economic cost. To overcome this drawback, the Internet used a well-know routing protocol between different Autonomous Systems (AS). This routing protocol is called the Border Gateway Protocol (BGP) [71]. However, in our case, we used a simplified model version of this protocol, which keeps separated the two administrative authorities implemented in each network separately and introduce rules for the exchange of information between the two networks.

Organization of the thesis

The rest of this manuscript will be divided into five chapters.

- **The first chapter** is devoted to studying in general, the structure of complex networks.
- **The second chapter** deals with the presentation of the processes taking place on complex networks, such as traffic dynamics and epidemic spreading.
- **The third chapter** introduces the study of effects of maximum node degree on computer virus spreading in scale-free networks.
- **The fourth chapter** focuses on the study of the effect of the routing algorithm strategies on the traffic driven epidemic spreading in complex networks, and suggested a new anti-virus vaccination method.
- **The fifth chapter** concentrates on the study of effect of routing algorithm strategies in interconnected networks.

Finally, this thesis will be ended by drawing conclusions and some perspectives for future works.

CHAPTER I
STRUCTURE OF COMPLEX NETWORKS

I.1 Classification of real networks

Before get deep in structure of complex network, we shall consider the different application of real world networks. In this section, we recall briefly : the social networks, the information networks, the technological networks, and the biological networks.

- **Social networks:** a social network refers to a set of people with some manner of contacts and interactions between them [3]. For instance, the patterns of friendships between individuals [72], business relationships between companies [73], and intermarriages between families [74].
  The social sciences have a long history of the substantial quantitative study of real-world networks. Indeed, among the early works on the subject, we find : Moreno's networks of friendships within small groups [75]. Another important set of experiments is the famous "small-world" experiments of Milgram [11, 12, 76].

- **Information networks:** the second network category is the information networks which also called "knowledge networks". For instance, the network of citations between academic papers is the classic example of an information network [77]. Indeed, Most learned articles cite previous works by others on related topics. Hence, these citations form a network in which the vertices are articles and a directed edge from article A to article B, which indicates that A cites B (Fig. I.1). The structure of the citation network reflects then the structure of the information stored at its vertices. Therefore, the term "information network" although certainly there are social aspects to the citation patterns of papers too. The World Wide Web is another very important example of an information network (Fig. I.1). That is to say that the network of Web pages containing information linked together by hyper links from one page to another [78].

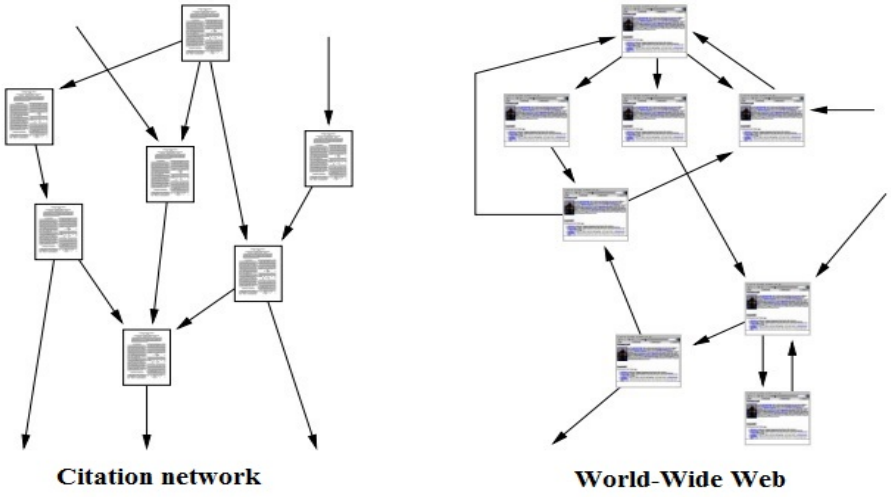

Figure I.1: Two examples of the information networks [1]

- **Technological networks:** are the third class of networks. These networks are designed typically for distribution of some commodity or resource. Electricity and information are good examples. The electric power grid is a network of high-voltage three-phase transmission lines that spans a country or a portion of a country (as opposed to the local low-voltage AC power delivery lines that span individual neighborhoods). Other distribution networks that have been studied include the network of airline routes [4], the networks of roads [79] and railways [5]. The telephone network and delivery networks such as those used by the post office or parcel delivery companies also fall into this general category. Another example studied in technological network, is the Internet, i.e., the network of physical connections between computers.

- **Biological networks:** a plenty of biological systems can be represented as networks. For instance, the network of metabolic pathways, which is a representation of metabolic substrates and products with directed edges joining them if a known metabolic reaction existed that acts on a given substrate and produces a given product [6, 7].
  Food also is another much-studied example of a biological network in which the vertices represent species in an ecosystem and a directed edge from species A to species B indicates that A preys on B [8, 80].

I.2 Preliminaries on network and graph

In the reference [81], the terms graph and network are used indistinctly. Indeed, in this branch, we will reserve the term graph for the concept mathematical abstract, and the term network is representing real-world objects in which the nodes represent entities of the system and the edges represent the relationships among them (Fig. I.2). The network can be used to represent different systems in the real world.

For example, one could describe the Internet as a network where the nodes are computers or other devices and the edges are physical connections between the devices or wireless. The

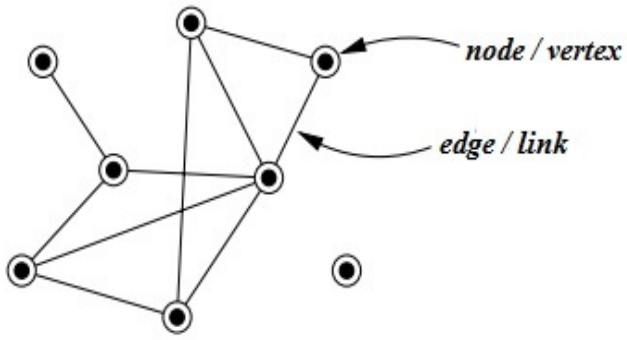

Figure I.2: Example of network with eight vertices and ten edges

World Wide Web is a huge network where the pages are nodes and links are the edges. Therefore, it is clear that we will refer to the system of individuals and their interactions as a "social network" and not as a "social graph". However, they should can have same meaning.

The graph theory includes the mathematical area studying complex networks; it is a symbolic representation of a network and of its connectivity. It implies an abstraction of the reality so it can be simplified as a set of linked nodes. Another key point; a complex network can be represented as a graph; as follow: $G = (V,E)$, where $V = v_1, v_2 .... v_n$ a non-empty set that is represents the vertices (nodes) and $E = e_1, e_2 .... e_n$ is all the pairs of vertices which are linked (edges).
The size N or the cardinality $|G|$ of the graph refers to the number of vertices. Two nodes i and j sharing the same link are called adjacent or neighboring. The link is said to be incident in nodes i and j or to join the two nodes $[1, 81, 82]$.
In the table below, we represent a "dictionary" between graph theory terms and complex network terms. In the next, we will usually adopt the complex network terminology.

Table I.1: Graph/ Network dictionary

Graph theory term	Complex network term
Graphs	Networks
Vertices	Nodes
Edges	Links
Cycles	Loops
loops	Tadpoles

I.3 Different representation of network

Generally, it is not sufficient to model natural or artificial networks using a simple network model (Fig. I.2). Indeed, in some complicated network systems, identical nodes and edges do not sufficient to reflect the reality of the systems. Unlike, there are alternative ways to represent graphs, notably adjacency matrix.
Considering a graph G with n vertices and m edges. Its adjacency matrix is a table denoted A with n rows and n columns. The entry $A[i, j]$ is the number of edges joining vertices v_i and v_j.

In the following, we will consider firstly the undirected networks, then the directed, and finally the weighted.

I.3.1 Undirected networks

A undirected network is defined as a network of finite order that contains only undirected edges, has no parallel edges, and no self-loops [83].
The adjacency matrix of a simple network is $N \times N$ matrix A of elements

$$A_{ij} = \begin{cases} 1 & \text{if node } j \text{ is linked to node } i \\ 0 & \text{otherwise} \end{cases}$$

Since in an undirected network if node j is linked to node i also node i is linked to node j, the adjacency matrix of this network is always symmetric (Fig. I.3). In an undirected network there are no tadpoles, then the diagonal matrix elements are equal to zero.

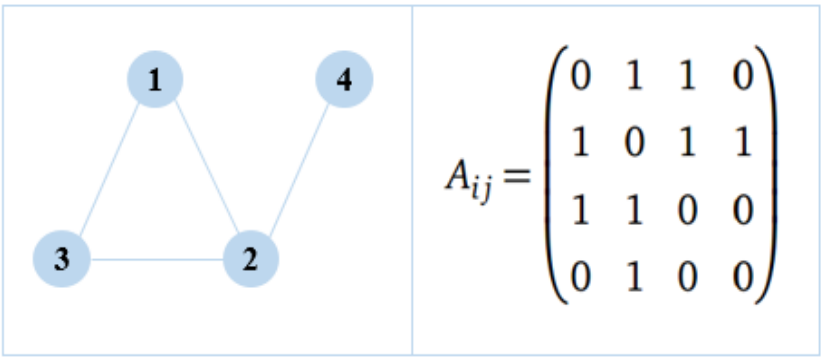

Figure I.3: Directed network.

I.3.2 Directed networks

In directed networks a link can be either directed or undirected. A directed link indicates an interaction between nodes that is not symmetrical.
The directed graph (or digraph) is a graph where edges have a direction associated with them. Unlike of an undirected network, a directed network means that the interaction between two adjacent nodes is not reciprocal [81–83].
In the graphic representation, links are typically drawn as arrows indicating the direction of the interaction as illustrated in Fig. I.4. For example, in a social network two individuals might be connected if one calls the other one by mobile phone. This is a case of directed interaction, since it is not guaranteed that if j calls i then i calls j in the given time window over which the network is aggregated. The adjacency matrix of a directed network is a $N \times N$ matrix, denoted A, the A_{ij} elements are defined as :

$$A_{ij} = \begin{cases} 1 & \text{if node } j \text{ points to node } i \\ 0 & \text{otherwise} \end{cases}$$

The adjacency matrix of a directed network is asymmetric. In fact, if node j points to node i it is not involve that node i points to node j (Fig. I.4).

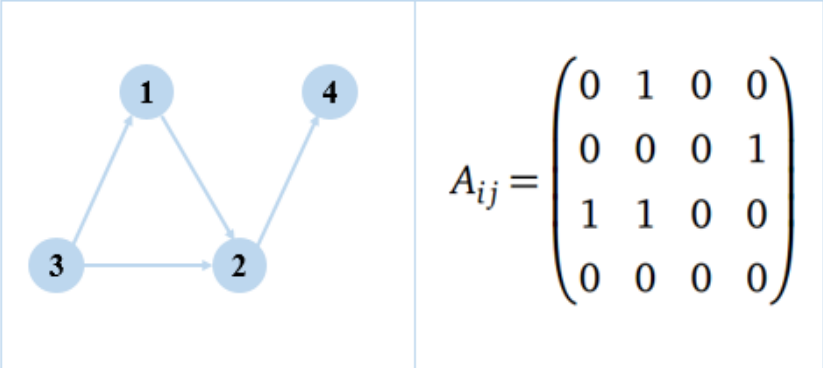

Figure I.4: Directed network.

I.3.3 Weighted networks

The Links in these networks are weighted. The weight of the link is a integer that reflects the situation in which different interactions have different intensities [83, 84].
In many applications, mainly in the weighted, it is prerequisite to determine a numerical value to each edge in a graph. The weights of edges are usually positive integers (Fig. I.5).
Weighted graphs can be either directed or undirected. The weight of an edge is often referred to the "cost" of the edge. For example, when modeling a railway network as a graph, railway stations are naturally represented the vertices, whereas two stations are connected by means of an edge. We then assign a weight of an edge by the distance between those two stations.
The adjacency matrix of a weighted network is a $N \times N$ matrix, A, of elements A_{ij} defined as follows (Fig. I.5):
Undirected weighted network

$$A_{ij} = \begin{cases} w_{ij} & \text{if node } j \text{ is linked to node } i \text{ with a link of weight} \\ 0 & \text{otherwise} \end{cases}$$

Directed weighted network

$$A_{ij} = \begin{cases} w_{ij} & \text{if node } j \text{ points to node } i \text{ with a link of weight} \\ 0 & \text{otherwise} \end{cases}$$

The adjacency matrix of an undirected weighted network is symmetric. However, the adjacency matrix of a directed weighted network is asymmetric.

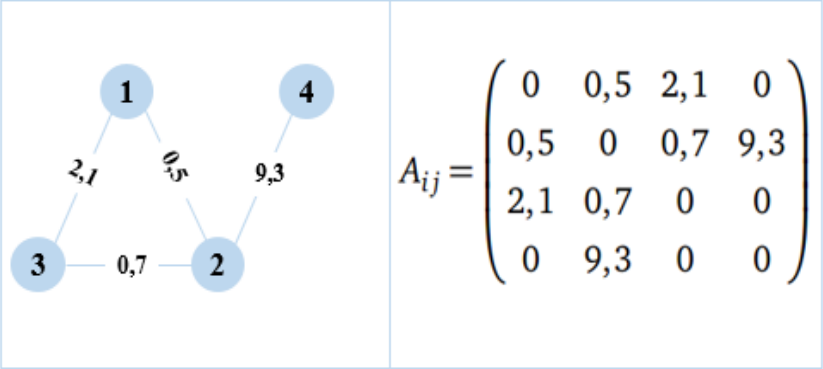

Figure I.5: Weighted network.

I.4 Characteristics of network

In addition to what we have seen above, it exists many other non visible characteristics of a network that we can get by performing some calculations. Generally speaking, these network measurements are divided into two sets. First, it can be specific to the node and defines its influence in the network. Second, it can be global, which means that, it concerns the whole network. Moreover, we present some global measurements that we intend to use in the next subsection to describe real networks topology features. These properties are compared to that of network models in order to determine the closest model to the reality.

I.4.1 Degree, average degree and degree distribution

A key property of each node is its degree, representing the number of links it has to other nodes. The degree can represent the number of mobile phone contacts an individual has in the call graph (i.e. the number of different individuals the person has talked to), or the number of citations a research paper gets in the citation network.

Degree

We denote with k_i the degree of the i^{th} node in the network. For example, the undirected networks shown in Fig. I.3, we have $k_1 = 2$, $k_2 = 3$, $k_3 = 2$, $k_4 = 1$. In an undirected network the total number of links, S_{link}, can be expressed as the sum of the node degrees:

$$S_{link} = \frac{1}{2}\sum_{i=1}^{N} k_i \tag{I.1}$$

Here the $1/2$ factor corrects for the fact that in the sum each link is counted twice.

Average degree

An important property of a network is average degree, which for an undirected network is:

$$\langle k \rangle = \frac{1}{N}\sum_{i=1}^{N} k_i = 2\frac{S_{link}}{N}, \tag{I.2}$$

In directed networks we distinguish between incoming degree, k_i^{in}, representing the number of links that point to node i, and outgoing degree, k_i^{out}, representing the number of links that point from node i to other nodes (Fig. I.6). Finally, a node's total degree,k_i, is given by:

$$k_i = k_i^{out} + k_i^{in}, \tag{I.3}$$

The total number of links in a directed network is:

$$S_{link} = \sum_{i=1}^{N} k_i^{in} = \sum_{i=1}^{N} k_i^{out} \tag{I.4}$$

the factor $1/2$ seen in equation $(I.1)$ is now absent, as for directed networks the two sums in equation $(I.4)$ separately count the outgoing and the incoming degrees. The average degree of a directed network is

$$\langle k^{in} \rangle = \frac{1}{N}\sum_{i=1}^{N} k_i^{in} = \langle k^{out} \rangle = \frac{1}{N}\sum_{i=1}^{N} k_i^{out} = \frac{S_{link}}{N}. \tag{I.5}$$

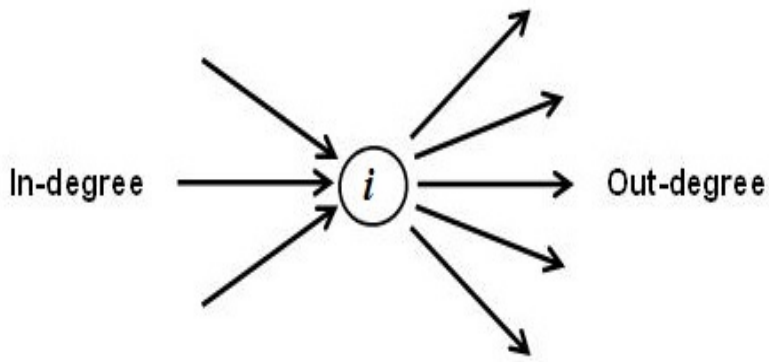

Figure I.6: Example of the degree of a node in directed graph

Degree distribution

The degree distribution, P_k, provides the probability that a randomly selected node in the network has degree K. Since p_k is a probability, it must be normalized, i.e.

$$\sum_{k=1}^{\infty} p_k = 1, \tag{I.6}$$

For a network with N nodes the degree distribution is the normalized histogram (Fig. I.7), which given as follow :

$$p_k = \frac{N_k}{N}, \tag{I.7}$$

where N_k is the number of degree k nodes. Hence the number of degree k nodes can be obtained from the degree distribution as $N_k = N p_k$. The degree distribution has assumed a central role in network theory following the discovery of scale free networks [13]. One reason is that the calculation of most network properties requires us to know p_k. For example, the average degree of a network can be written as

$$\langle k \rangle = \sum_{k=1}^{\infty} k p_k. \tag{I.8}$$

In Fig. I.7, represents the degree distribution of a network is provided by the ratio ($Eq.\ I.7$). For the network in (a) with $N = 4$ the degree distribution is shown in (b). We have $p_1 = 1/4$ (one of the four nodes has degree $k_1 = 1$), $p_2 = 1/2$ (two nodes have $k_3 = k_4 = 2$), and $p_3 = 1/4$ (as $k_2 = 3$). As we lack nodes with degree $k > 3$, $p_k = 0$ for any $k > 3$. A one dimensional lattice presented in (c) for which each node has the same degree $k = 2$, its degree distribution is shown in (d).

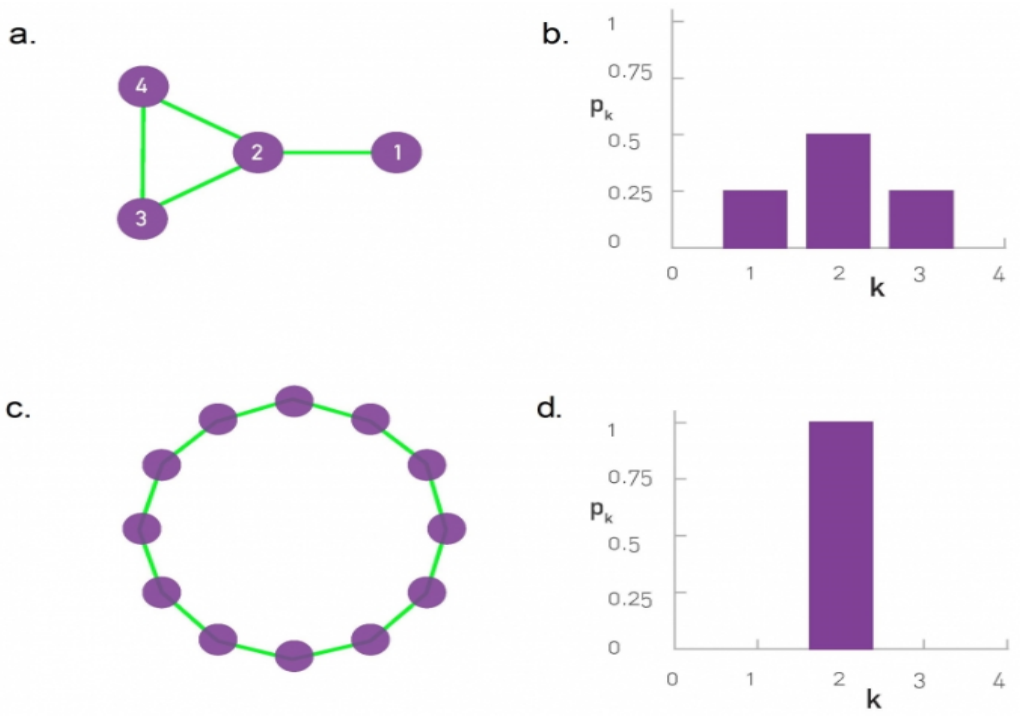

Figure I.7: Example of the degree distribution for two different networks.

I.4.2 Paths and distance

Physical distance plays a key role in determining the interactions between the components of physical systems. For example the distance between two atoms in a crystal or between two galaxies in the universe determine the forces that act between them.

In networks distance is a challenging concept. Indeed, what is the distance between two web pages, or between two individuals who do not know each other ? The physical distance is not relevant here: Two web pages could be sitting on computers on the opposite sides of the globe, yet, have a link to each other. At the same time two individuals that live in the same building may not know each other.
In networks physical distance is replaced by path length. A path is a route that runs along the links of the network. A path's length represents the number of links the path contains.

Distance

The distance (often called shortest path) between two nodes, labeled i and j denoted as d_{ij}, can be defined by any metrics. Indeed, the distance between two nodes is equal to the total number of edges that connect them through a shortest route.

The diameter of a network, denoted by D, is defined to be a largest of all distances in the graph [2]:

$$D = \max d_{ij}. \tag{I.9}$$

Average Path Length

The average path length or The average distance, denoted by $\langle d \rangle$, is the average distance between all pairs of nodes in the network. For an undirected network of N nodes, $\langle d \rangle$ is [85]:

$$\langle d \rangle = \frac{2}{N(N-1)} \sum_{i<j} d_{ij}. \tag{I.10}$$

Example: Fig. I.8 shows an example of a network with 5 nodes and 5 edges, where:
$D = d_{45} = 3$ and $\langle d \rangle = \frac{16}{10} = 1.6$,
$d_{12} = 1$
$d_{13} = 1$ and $d_{23} = 1$
$d_{14} = 2$, $d_{24} = 1$ and $d_{34} = 2$
$d_{15} = 1$, $d_{25} = 2$, $d_{35} = 2$ and $d_{45} = 3$.

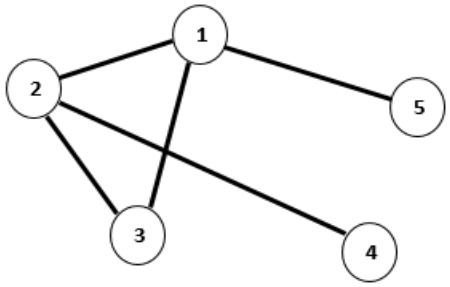

Figure I.8: Example of a graph with 5 nodes and 5 edges

I.4.3 Clustering coefficient

The clustering coefficient (or the transitivity) measures the degree of presence of clusters or triangles in a graph. In a friendship network, two friends of someone may or may not be friends themselves. This example refers to the concept clustering.
In a graph, let i be a node with k_i edges connecting to other k_i nodes, which are called neighbors of node i. It is simple to verify that there are at least $\frac{k_i(k_i-1)}{2}$ edges among these k_i neighbors. Let E_i be the number of the actual edges existing among these k_i nodes. Then, the ratio between the actual and the possible numbers of edges in the cluster of these k_i nodes is defined to be the clustering coefficient of node i, denoted as C_i [2]; namely,

$$C_i = \frac{2E_i}{k_i(k_i-1)}. \tag{I.11}$$

Again we consider the **example** shown in Fig. I.8, where:
Node-1 has 3 neighbors, $E_1 = 1$, so $C_1 = 2 \times \frac{1}{(3\times 2)} = \frac{1}{3}$;
Node-2 has 3 neighbors, $E_2 = 1$, so $C_2 = 2 \times \frac{1}{(3\times 2)} = \frac{1}{3}$;
Node-3 has 2 neighbors, $E_3 = 1$, so $C_3 = 2 \times \frac{1}{(2\times 1)} = 1$;
Node-4 has 1 neighbors, $E_4 = 0$, so $C_4 = 0$;
Node-5 has 1 neighbors, $E_5 = 0$, so $C_5 = 0$;

I.4.4 Closeness centrality

For graphs (networks), there are various measures named as centrality of a node within a graph, which indicates the relative importance of the node in the graph. For instance, it measures how important a person is within a social network. Generally speaking, a more "central" node has a stronger influence on other nodes in the same network.
Closeness refers to a measure of the velocity to spread information from a node to all other nodes sequentially. In a graph, a useful concept is closeness centrality. The farness of a node in the graph is defined as the sum of its distances to all other nodes, while its closeness is defined as the inverse of the farness [2].
For instance in Fig. I.8, Node 1 has farness $1+1+2+1=5$ and closeness $1/5$.

I.4.5 Betweenness centrality

Node betweenness
In a graph of size N, the node-betweenness of node i is defined by [2, 85, 86]:

$$B(i) = \sum_{j\neq l\neq i} \frac{L_{jl}(i)}{L_{jl}}, \tag{I.12}$$

Where L_{jl} is the number of all existing shortest paths from node j to node l, and $L_{jl}(i)$ is the number of all shortest paths from node j to node l that actually pass through node i.
The node-betweenness may be normalized by dividing with the total number of pairs of nodes

not including node i as an end-node, which is $(N-1)(N-2)/2$.

Edge betweenness

For an edge e_{ij} connecting node i and node j, the edge-betweenness of e_{ij} is similarly defined:

$$B(e_{ij}) = \sum_{(l,q)\neq(i,j)} \frac{L_{lq}(e_{ej})}{L_{lq}}. \tag{I.13}$$

Where L_lq is the number of all existing shortest paths from node l to node q, and $L_{lq}(eij)$ is the number of all shortest paths from node l to node q that actually pass through edge e_{ij}. The edge-betweenness can also be normalized, by dividing with the total number of edges not including e_{ij}, which is $\frac{1}{2}N(N-1)-1$.

For **example**, we consider the graph shown in Fig. I.9.

The betweenness of node 1 is:

$$B(1) = \frac{(5,1,4)}{(5,1,4)} + \frac{(5,1,2)}{(5,1,2)+(5,3,2)} + \frac{(4,1,2,3)+(4,1,5,3)}{(4,1,2,3)+(4,1,5,3)} + \frac{(4,1,2)}{(4,1,2)}$$

$$B(1) = 1 + \frac{1}{2} + 1 + 1 = \frac{7}{2}$$

.

Or $B(1) = \frac{7/2}{(N-1)(N-2)/2} = 7/12$ after normalization, where (i,l,q,j) is the path from node i to node j passing though node l and node q successively.

The betweenness of edge e_{12} is:

$$B(e_{12}) = \frac{(5,1,2)}{(5,1,2)+(5,3,2)} + \frac{(4,1,2,3)}{(4,1,2,3)+(4,1,5,3)} + \frac{(4,1,2)}{(4,1,2)} + \frac{(3,2,1)}{(3,2,1)+(3,5,1)}$$

$$B(e_{12}) = \frac{1}{2} + \frac{1}{2} + \frac{1}{1} + \frac{1}{2} = \frac{5}{2}$$

. Or $B(e_{12}) = \frac{5/2}{N(N-1)/2-1} = 3/8$ after normalization.

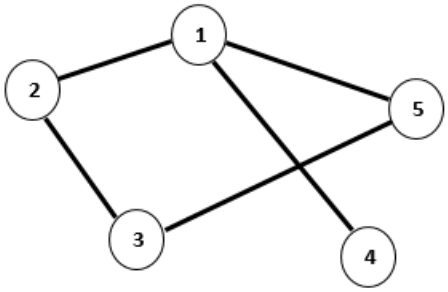

Figure I.9: Example for calculating betweenness.

I.5 Properties of real world networks

In order to model real world networks, it is primordial to understand firstly what does their topology looks like. Empiric data result reveals that the main characteristics shared between many natural and artificial complex networks are the Small World property (SW) and the Scale-Free (SF) degree distribution. Knowing real networks features will allow thereafter the comparison between different network models and judge their reliability.

I.5.1 Small world property

In most of the real networks, despite of their often large size, there is relatively short path between any two nodes. This feature is so-called the small world property, it is mathematically characterized by an average shortest path length. This property was first investigated, in the social context, by Milgram in the 1960s. Milgram had done a series of experiments to estimate the actual number of steps in a chain of acquaintances [12, 17, 87]. In these experiments, Milgram asked randomly selected people in Nebraska to send letters to a distant target individual in Boston, using as intermediate people that they know. Although the common guess was that it might take hundreds of these steps for the letters to reach their final destination, Milgram's surprising result was that the number of links needed to reach the target person had an average value of just six. This experience have given rise to a myth known as "the Six Degrees of Separation" in its popular version [12, 18].
Fig. I.10 shows an example of this experience. According to six degrees of separation two individuals, anywhere in the world, can be connected through a chain of six or fewer acquaintances. This means that while Sarah does not know Peter, she knows Ralph, who knows Jane and who in turn knows Peter. Hence Sarah is three handshakes, or three degrees from Peter. In the language of network science six degrees, also called the small world property, means that the distance between any two nodes in a network is unexpectedly small. Indeed, this property has been observed in a variety of other real networks, including biological and technological ones [88, 89].

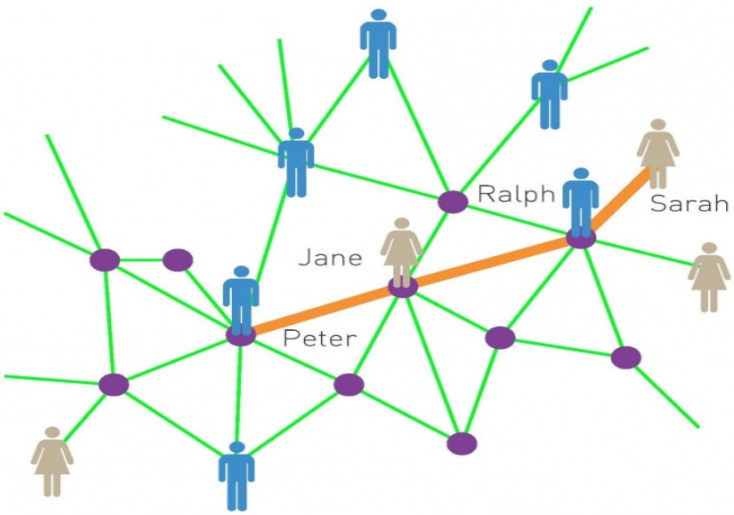

Figure I.10: Example of six degree of separation.

I.5.2 Scale free property

Homogeneous networks were the usual case in Science until few years ago. Homogeneity in the interaction structure means that almost all nodes are topologically equivalent. Indeed, a great range of real networks such as social networks, communication networks and cellular networks, were thought to have homogeneous degree distribution, like regular lattices and random graphs. In these latter ones, for example, each of the $N(N-1)/2$ possible links are presented with equal probability, and hence the degree distribution is binomial or Poisson [13, 90].

When the scientists approached the study of real networks from the available databases, it was considered reasonable to find degree distributions localized around an average value [13, 91]. In contrast with all the expectancies, it was found that most of the real networks display power law shaped degree distribution $P(k) \sim ak^{-\gamma}$, with exponent γ varying in the range $2 < \gamma < 3$. This means that the majority of network vertices have low connectivity rate while few of them are highly connected and form what we call hubs (see Fig. I.11). Such networks are named scale-free (SF) or scale invariant networks.

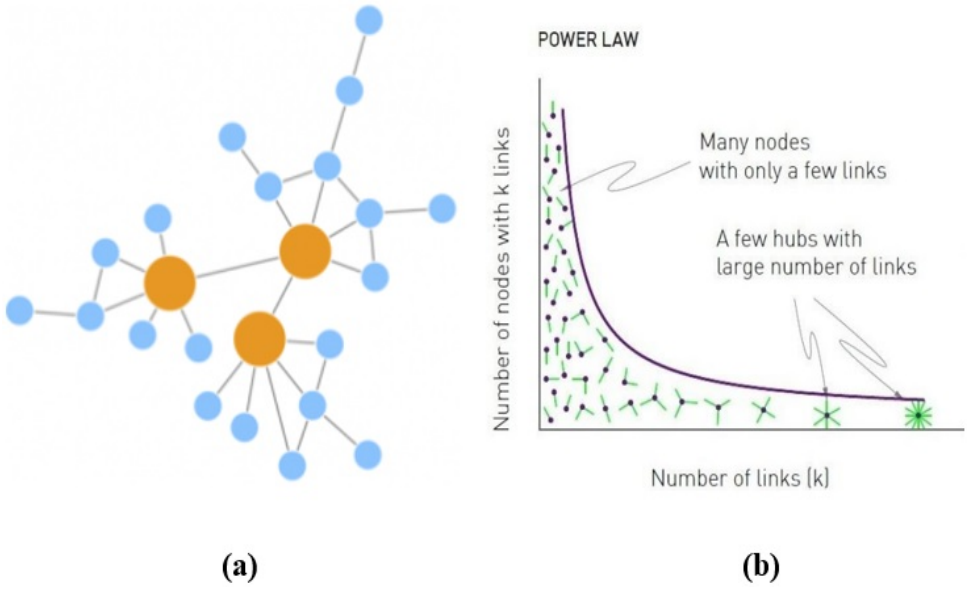

Figure I.11: Example of a SF network (a) and The degree distribution of SF network follows a power law (b).

Origin of the term "scale free"

The idea behind the name of scale-free is related to spread of the nodes for enormous network size. In general, for any normal distribution the degree of a randomly chosen node is typically bounded considering the relation between the average $\langle k \rangle$ and standard deviation σ_k as:

$$k = \langle k \rangle \pm \sigma_k$$

For instance, in the case of random graph, the degree distribution follows a poisson function. The scare root of the variance $\sigma_k = \langle k \rangle^{1/2}$ is always smaller than $\langle k \rangle$. As results all the nodes degree are in the range $k = \langle k \rangle \pm \langle k \rangle^{1/2}$, we say that the average degree $\langle k \rangle$ can be a scale of the random network. On the other side, for SF networks, the calculation the scare root of the

variance $\sigma^2 = \langle k^2 \rangle - \langle k \rangle^2$ of the degrees it has been proved that this quantity diverges when $N \to \infty$. This brought to conclude that the fluctuations around the average can be arbitrary large. In other words, if we pick randomly a node from the network, its degree could be either too small or extremely high. As the term "scale free" would suggest, the degree of the randomly chosen node has no limiting bound :

$$k = \langle k \rangle \pm \infty$$

Contrarily to the random graph where the degrees fluctuate around the average regular graphs where they have the same degree ($\sigma = 0$).

Real example

In Fig. I.12, we address some examples of degree distributions of real complex networks extracted from empiric data analysis; namely the Internet, the collaboration network and the protein interactions where nodes represent computers, scientists and molecules respectively [19].

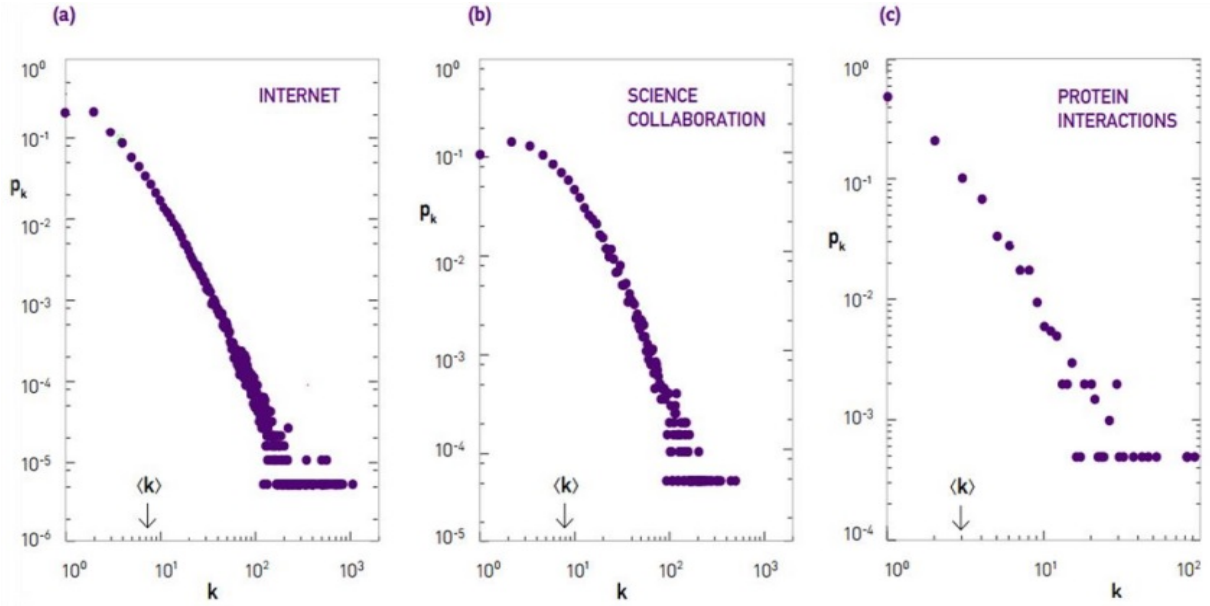

Figure I.12: The degree distribution of the Internet (a), science collaboration network (b), and protein interaction network (c) [19].

One can see that despite the fact that these networks belongs to various domains, they all share the same appearance of the degree distribution. Indeed, for each network it that can be approximated with a power law function.

I.6 Complex network models

In this section, we will focus on the mathematical modelling of networks, with the intent of studying the topological properties of real networks, in fact, several network models have been proposed. Some of these models have become subject of great interest, including random

networks Erdös-Rényi (ER), the small world networks Watts-Strogatz (WS) and the scale free networks Barabási-Albert (BA).

Firstly, we recall briefly the origin of complex network. Thereafter, we shall review a number of interesting and important findings not only for the classical Erdös-Rényi model but also for two more recent models, namely the Watts-Strogatz, and the one by Barabási-Albert. Especially the last model of these will be used extensively in our later work.

I.6.1 Complex network concept

Complex network research has a long history. The study of networks, in the form of mathematical graph theory, is one of the fundamental pillars of discrete mathematics. Its roots go back to 1735 in Königsberg, the capital of Eastern Prussia, a thriving merchant city of its time. The trade supported by its busy fleet of ships allowed city officials to build seven bridges across the river Pregel that surrounded the town. Five of these connected to the mainland the elegant island Kneiphof, caught between the two branches of the Pregel. The remaining two crossed the two branches of the river (Fig. I.13). This peculiar arrangement gave birth to a contemporary puzzle: Can one walk across all seven bridges and never cross the same one twice ? Despite many attempts, no one could find such path. The problem remained unsolved until 1735, when Leonard Euler, a Swiss born mathematician, is celebrated solution of the Königsberg bridge problem is often cited as the first true proof in the theory of networks [2, 92].

The origin of the graph theory can be traced to Leonhard Euler who devised in 1735 a problem that came to be known as the "Seven Bridges of Königsburg". In this problem, Euler proved that there is no solution to represent it as a set of nodes and links. This led to the foundation of the graph theory and there variants.
Euler had a good idea to describe this real world problem by an abstract graph, using four points A, B, C, D to represent the four pieces of lands separated by the river in town, with lines a, b, c, d, e, f, g to represent the seven bridges that connected the four points together (Fig. I.14). Thus, Euler was able to convert the physical problem to the following mathematical problem: starting from any point is there a possible loop leading back to the starting point such that it passes all seven lines once and once only. Furthermore, Euler derived a necessary and sufficient condition for the existence of such a loop, Euler observed that if a point (A, B, C, D) has one incoming edge then it should also have one outgoing edge. Therefore, it is necessary for each point to have an even number of edges. However, the graph shown in Fig. I.14 does not satisfy this condition, therefore the problem has no solution.
Euler's proof was the first time someone solved a mathematical problem using a graph. For us the proof has two important messages: The first is that some problems become simpler and more tractable if they are represented as a graph. The second is that the existence of the path does not depend on our ingenuity to find it. Rather, it is a property of the graph. Indeed, given the structure of the Königsberg graph, no matter how smart we are, we will never find the desired path. In other words, networks have properties encoded in their structure that limit or enhance their behavior.
The contribution of Euler had gone far beyond this simple seven-bridge problem, it has opened up a new branch of mathematics: graph theory. Thereafter, Euler has been named the father of graph theory, and the picture shown in Fig. I.14 was called an Eulerian graph.

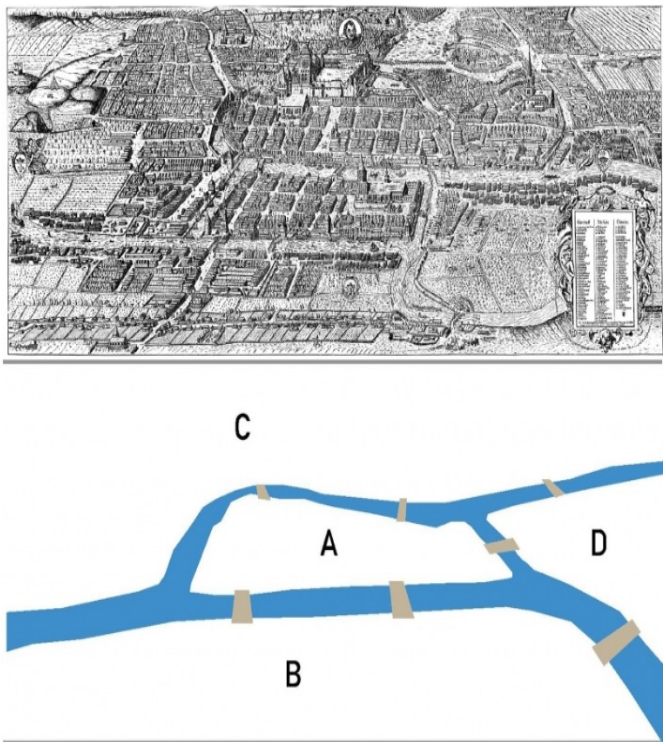

Figure I.13: The town Königsberg and the seven bridges in 1736.

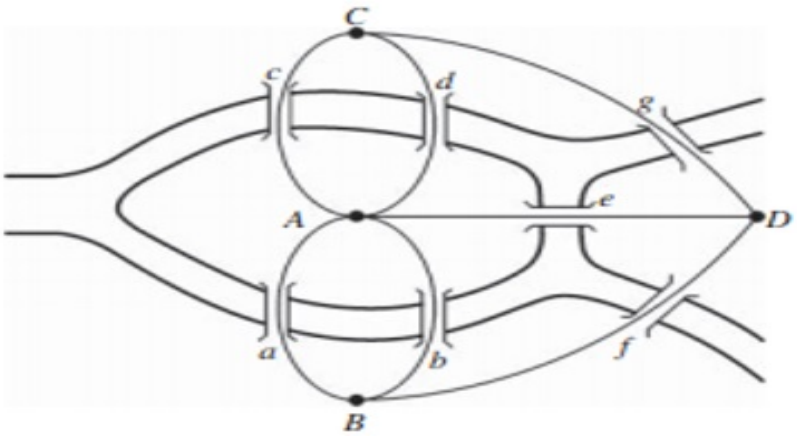

Figure I.14: Graph of the Königsberg seven bridges problem.

I.6.2 Regular graphs

Due to their simplicity, regular graphs or lattices were the traditional models to be studied in graph theory. Indeed, lattices represent very simple topologies in which nodes are linked following some strict and periodic topological rules (regular polygons).

The name regular network here does not necessarily refer to the mathematically defined concept of regular graph. One of the most typical regular networks is a fully connected network (complete graph) [1]. In such a network, between every pair of nodes there exists an edge connecting them together (Fig. I.15(a)), a fully connected network has the average path length $[L]_{full} = 1$, and the average clustering coefficient $C_{full} = 1$. Note also that although fully connected networks can describe the fact that many real world networks possess high clustering and small world features, they are nevertheless too regular to be realistic. In particular, such a network with a periodic boundary connectivity condition is a ring-shaped network (Fig. I.15(b)). Assume that in a large-scale ring-shaped network, with a large enough number N of nodes, if each node is connected to $2k$ nearest neighbors, then the clustering coefficient can be asymptotically approximated by :

$$C_{ring} \approx \frac{3(k-1)}{2(2k-1)} \longrightarrow 3/4(k \longrightarrow \infty).$$

Another typical regular network is the star-shaped network, which has a center, and all the other nodes are connected to, and only connected to the center (Fig. I.15(c)).

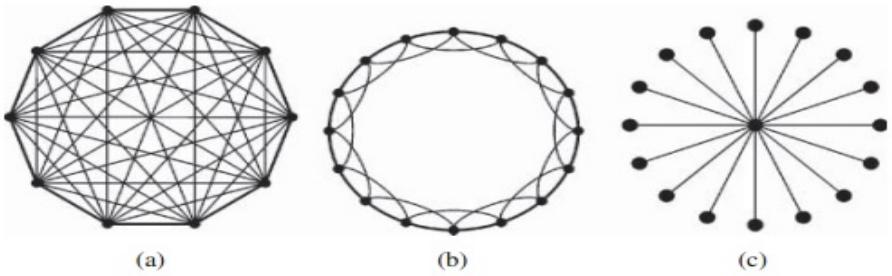

Figure I.15: Some simple networks : fully-connected network (a), ring-shaped network (b), and star-shaped network (c).

I.6.3 Random networks: The Erdös-Rényi (ER) model

Network science aims to build models that reproduce the properties of real networks.
From a modeling perspective a network is a relatively simple object, consisting of only nodes and links. The real challenge, however, is to decide where to place the links between the nodes so that we reproduce the complexity of a real system. In this respect the philosophy behind a random network is simple: We assume that this goal is best achieved by placing the links randomly between the nodes. The extremely opposite to the regular networks are completely random networks [10, 16].
Two mathematicians Erdös and Rényi in 1959, have played an important role in understanding the properties of the random networks or random graphs. In their honor a random network is called Erdös-Rényi model (ER).

I.6.3.1 Generation of ER model

To construct a random network we follow these steps:

1. Start with N isolated nodes.
2. Select a node pair and generate a random number between 0 and 1. If the number exceeds p, connect the selected node pair with a link, otherwise leave them disconnected.
3. Repeat step (2) for each of the $N(N-1)/2$ node pairs.

The figure below (Fig. I.16) shows an example of some random graphs generated of different values of p.

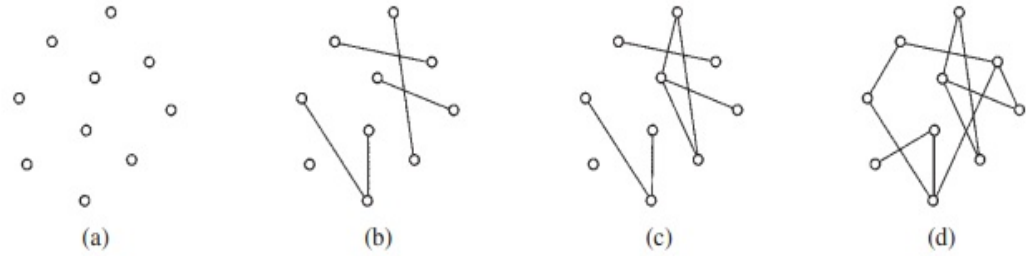

Figure I.16: Some random graphs generated with different values of p: $p = 0$ (a), $p = 0,1$ (b), $p = 0,15$ (c), and $p = 0,25$ (d).

I.6.3.2 Characteristics of ER model

we should mention that the features of random graphs, appear quite suddenly. Hence, the study of random graphs strives fundamentally the determination of the connection probability p with that a particular property appears. Since many properties of such graph have probabilistic form. Erdös and Rényi state that a graph has a given property Q if and only if the probability of having Q tends to 1 when N tends to the infinity. Taking in consideration this, we can explore thereafter some random network properties to see the difference from real networks.

The degree distribution: The average degree in random graph refers to a function of the network size. It is equal to :

$$\langle k \rangle = \frac{2m}{N} = p(N-1) \approx pN,$$

Where m is the total number of the edges. Now let's consider an Erdös-Rényi (ER) graph with connection probability p. It has been confirmed that the degree distribution of a random graph follows a binomial distribution [16]:

$$p(k) = C_{N-1}^{k} p^{k} (1-p)^{N-1-k},$$

Where p^k is the probability of k edges, C_{N-1}^{k} is the number of possibilities and $(1-p)^{N-1-k}$ is the complementary probability of the existence of additional edges. When N is large this

distribution could be replaced by Poisson distribution [19] (see Fig. I.17):

$$p(k) \approx e^{pN} \frac{(pN)^k}{k!} = e^{-\langle k \rangle} \frac{\langle k \rangle^k}{k!}.$$

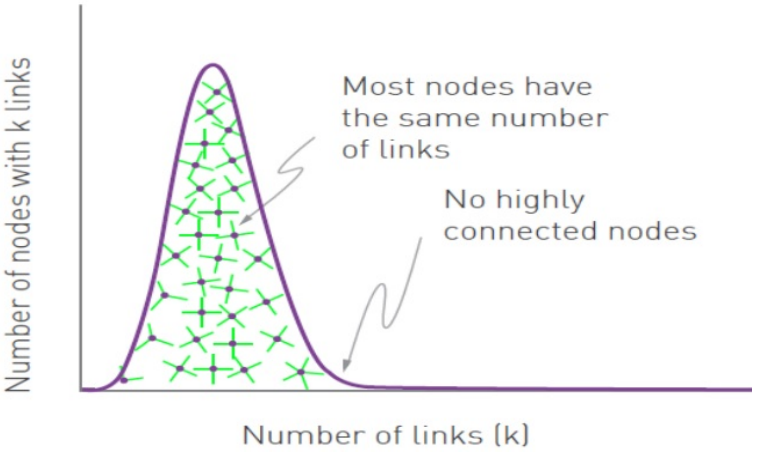

Figure I.17: Degree distribution of random graphs

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As we can observe, this degree distribution is far from the power law distribution that we noticed in real network. This distribution indicates that the degrees of nodes fluctuate around an average highly connected nodes are absent.

The clustering coefficient: We have observed that a high clustering coefficient is a characteristic appeared in many real networks. This means that there is a high probability to find two neighbors of the same node connected in order to forme a triangle. In a random graph, this probability is equal to the probability of picking randomly two nodes and find that they are connected. Hence, the expression of the clustering coefficient in a random graph is as follows :

$$C_{ER} = p = \frac{\langle k \rangle}{N}.$$

Fig. I.18 presents a comparison between the ratio of the ER clustering coefficient and the ratio of the clustering coefficient of real world as a function of the sizes. Contrarily to the ER graph expectation real networks appeared to be independent of N and the fraction $\frac{C}{\langle k \rangle}$ doesn't decrease as $\frac{1}{N}$.

The average path length: The average path length between any pair of node in a ER graph scales with the number of nodes N is given as [16]:

$$L_{ER} \sim \frac{\ln(N)}{\ln(\langle k \rangle)}.$$

In this thesis, we focused in the comparison between the prediction given by the equation above and some real networks average path lengths given in [16]. From Fig. I.19, it is obvious that

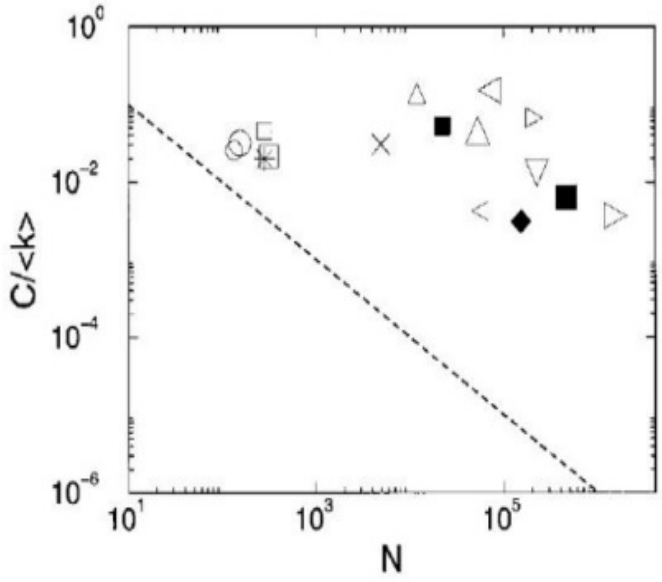

Figure I.18: Comparison between the clustering coefficient of real networks (symbols) and random graphs dashed line [16].

the average path length of ER graph is close to that of real world networks with the same size N.

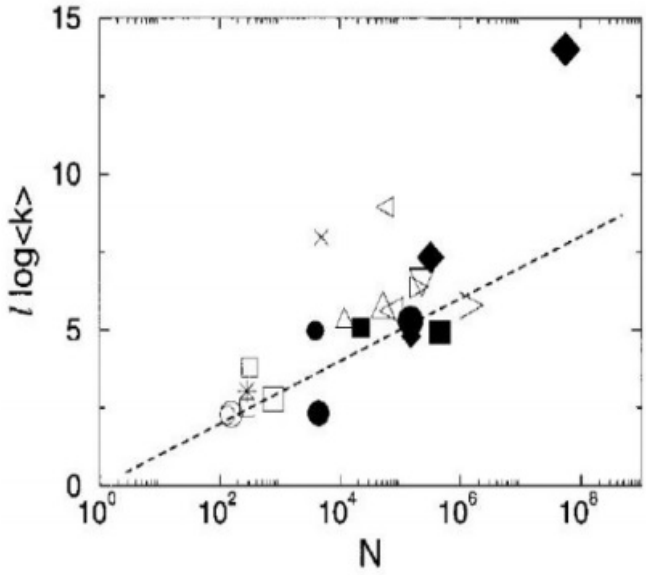

Figure I.19: Comparison between the average path lengths of real networks (symbols) and the prediction of random graph theory (dashed line) [16].

I.6.4 Small world networks: The Watts-Strogatz (WS) model

As mentioned above, a regular ring-shaped network has a large clustering coefficient and a random network has a short average path length.
Are there any kinds of networks that have both high clustering coefficient and short average

path length ? The answer is yes, which are the so called small world networks discovered by Watts and Strogatz in 1998, which named The Watts-Strogatz Model.

Based on the small world theory, in 1998 Watts and Strogatz have proposed a network model which is an intermediate network between the classical random graphs and the regular graphs [14, 15]. This model was the first successful random model manifesting both the high clustering and the small average path characteristics encountered in many real world networks. Watts and Strogatz were inspired from social networks.

I.6.4.1 Generation of WS model

The idea behind generating graphs with small world character is to start from ordered graph and transmit to randomize graph a bit [16].
Starting with order allows for the relatively high clustering coefficient, yet randomizing, to rewiring some edges which create "long distance shortcuts". These shortcuts are responsible for the relatively low average path length. This process is depicted in Fig. I.20. The rewiring probability p passes from 0, corresponding to the initial regular graph, via a phase between order and complete randomness (where "local" clusters are connected via a few long range connections), to 1 which complete randomness. The graph obtained with ($p = 1$) is corresponding to an Erdös-Rényi graph.

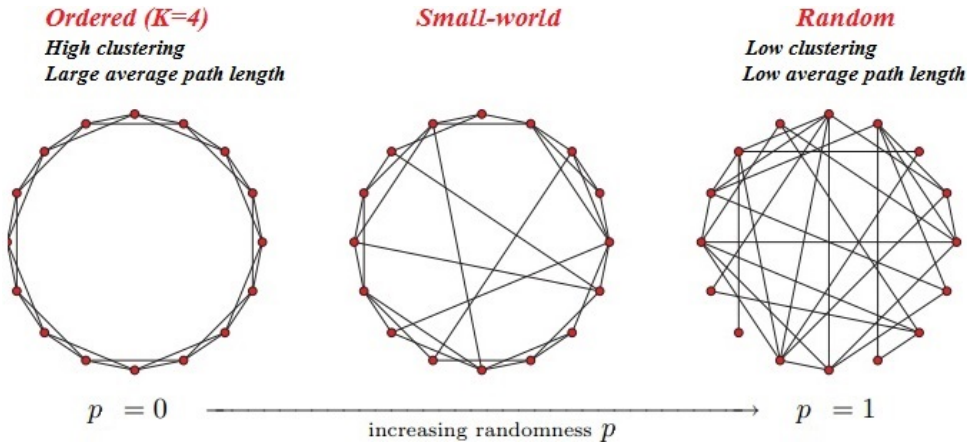

Figure I.20: Waths Strogatz model, transition from order to randomness through rewining; we start with $N = 16$ nodes, each node is linked to its first K=4 neighbors.

I.6.4.2 Characteristics of WS model

The clustering coefficient and the average path length : To understand this, we consider the example above (Fig. I.20), the expression of the clustering coefficient of the regular lattice is:

$$C = \frac{3(K-2)}{4(K-1)}.$$

For very large coordination number K. This equation converge to $C(p=0) \cong \frac{3}{4}$. Indeed, this lattice doesn't have a short path despite its small size $L((p=0) \cong \frac{N}{2K} >> 1)$. On the other hand, random graphs have a short path ($L(1) \sim \frac{\ln(N)}{\ln(K)}$), but also a small clustering coefficient

($C(p=1) \sim \frac{K}{N}$).
The fact that the model of Watts and Strogatz is an intermediate state between regular and totally random networks doesn't indicate exactly the coexistence of small path and the high clustering in this SW model [93]. To clarify this, we chase down the variation of this two measures as a function of the rewiring probability. Fig. I.21 shows the normalized values of $L(p)$ and $C(p)$ by $L(0)$ and $C(0)$, respectively. We observed that for small rewiring probability, the network characteristic regarding the clustering coefficient stays nearly the same as the initial regular graph ($C(p) \sim C(0)$). This points out that the transition to the small world is barely detectable at local level. However, the average path length drops rapidly to arrive already almost the same order of a random graph for small rewiring probability $p(L(p) << L(0))$.

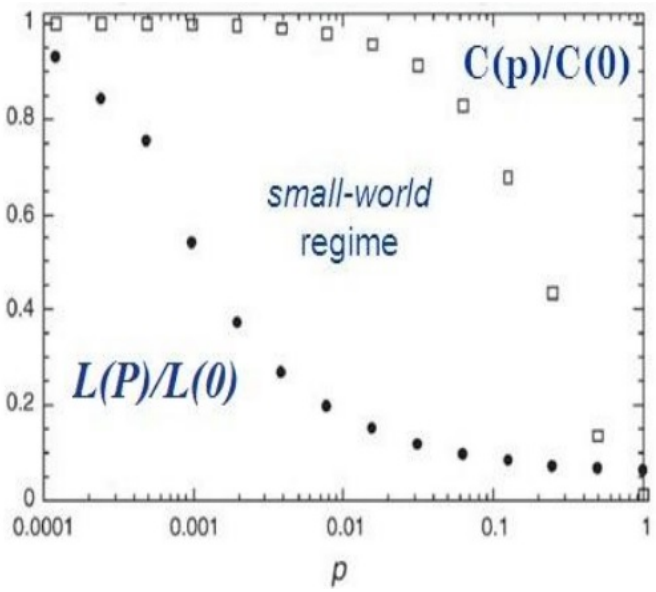

Figure I.21: Path length $L(p)$ and the clustering coefficient $C(p)$ for Watts-Strogatz model. The data are normalized by the values $L(0)$ and $C(0)$ [16]

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The degree distribution : In the WS model, for $p > 0$, every node i at least $K/2$ connections, in the end of the rewiring process. The expression of the node degrees can be written as [16,93]:

$$k_i = \frac{K}{2} + c_i \tag{I.14}$$

where c_i can be divided into two parts: $c_i^1 \leq K/2$ edges have been left in place (with probability 1-p), while $c_i^2 = c_i - c_i^1$ edges have been rewired towards i, each with probability $1/N$.
The probability distributions of c_i^1 and c_i^2 are:

$$P_1(c_i^1) = C_{K/2}^{c_i^1}(1-p)^{c_i^1} p^{k/2-c_i^1} \tag{I.15}$$

and

$$P_2(c_i^2) = C_{pNK/2}^{c_i^2}\left(\frac{1}{N}\right)^{c_i^2}\left(1-\frac{1}{N}\right)^{pNK/2-c_i^2} \approx \frac{(pK/2)^{c_i^2}}{c_i^2!}e^{-pK/2} \tag{I.16}$$

From the equation above, it has been proved that the analytic expression of the degree distribution of WS network for large N is

$$P(k) = \sum_{j=0}^{f(k,K)} C_{K/2}^{j} (1-p)^{j} p^{K/2-j} \frac{\left(pK/2^{k-K/2-j}\right)}{(k-K/2-j)!} e^{-pK/2}. \tag{I.17}$$

where $f(k,K) = \min\left(k-\frac{K}{2}, \frac{K}{2}\right)$.
Fig. I.22 displays the degree distribution of WS network, $K = 4$ as function of different values of p. One can draw that all the degrees are superior or equal to $K/2$ ($k \geq K/2$). We observed that the degree distribution is the same to that of a random graph. $P(k)$ grows up to a peak at $\langle k \rangle = K$ followed by an exponential decay for high K. We conclude that the vertices have almost the same number of edges, specifically, the degree distribution is relatively homogeneous which is not consistent with what seen in reality.

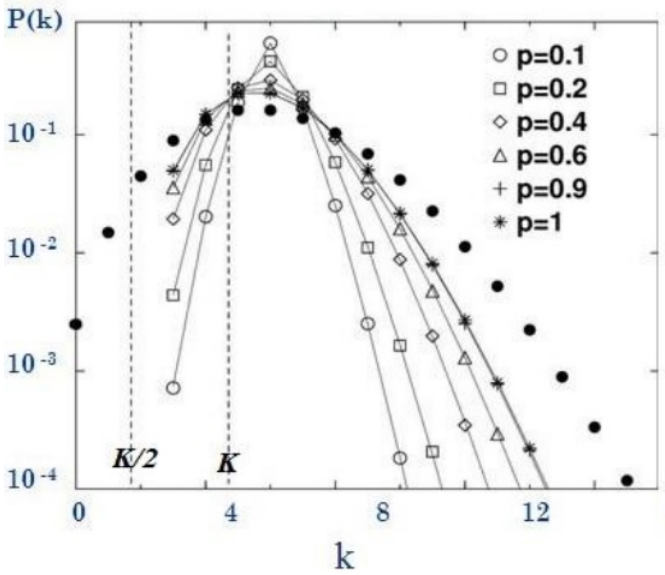


Figure I.22: Degree distribution of Watts-Strogatz model for K and various p [16].

I.6.5 Scale-free networks: The Barabási-Albert (BA) model

Based on real networks observation, the scientists Albert László Barabási and Réka Albert came up with a successful mechanism to construct of a SF network in 1999 [13]. The Barabási-Albert a proved that the SF phenomena observed in many real networks is a consequence of two generic aspects that are actually manifested reality and neglected in all the former models: Growth and preferential attachment [13, 16]. However, what it should take in consideration, that Price [94] is ground breaking in scale free networks, he is the first one who conduct works about this field, while; Barabàsi-Albert have been the driving force behind much of the recent works in this area.

In the next, we will introduce the Price model and then get deep concerning Barabási-Albert model.

I.6.5.1 Introduction to Price model

Derek de Solla Price described in 1965 probably the first example of what known now a scale-free network. Indeed, he studied the network of citations between scientific papers, and discovered that both in- and out-degrees (number of times a paper has been cited and number of other papers a paper cites) have power law distributions [94, 95]. Based on ideas developed in 1950*s* by Herbert Simon [96], who showed that power-law arise when "the rich get richer", when the amount you get goes up with the amount you already have. Price published another paper, that offered what is now the accepted explanation for power Law distribution.
The work of Price was an important contribution. Indeed, he took the idea of Simon and apply them to the growth of a network. Since Simon was thinking of wealth distributions in his work, and although he later gave other applications of his idea, none of them was to networked systems. However, Price appeared to have been the first to discuss cumulative advantage in the context of networks, and particularly in the context of the network of citations between papers and its in-degree distribution. His idea was that the rate at which a paper gets new citations should be proportional to the number that it already has.

I.6.5.2 Generation of BA model

The Barabási-Albert (BA) network model is based on two basic rules: growth and preferential attachment [13].

- **Growth:** is the first aspect which reflects the fact that the real world networks are in continuous expansion and not fixed as it was assumed. In the BA model this aspect is taken into account; we start from small number m_0 of fully connected vertices. Then, at each time step one new node is added to the network and establish m links with different nodes already present in the network. Since neither double connections to the same node not loops are tolerated, we have to start from a number of nodes are superior or equal to the number of links that we are going to add at each time step ($m_0 \geq m$). At t time, the total number of the node in the network is $N(t) = t + m_0 - 1$ (the new node is not counted yet). The processes continues until that we reach the desired network size N.
  Fig. I.23 shows an example of the first nine steps of generating a scale free graph using the Barabási-Albert model. Starting with $m_0 = 1$ node and adding $m = 1$ edge with each newly introduced node.

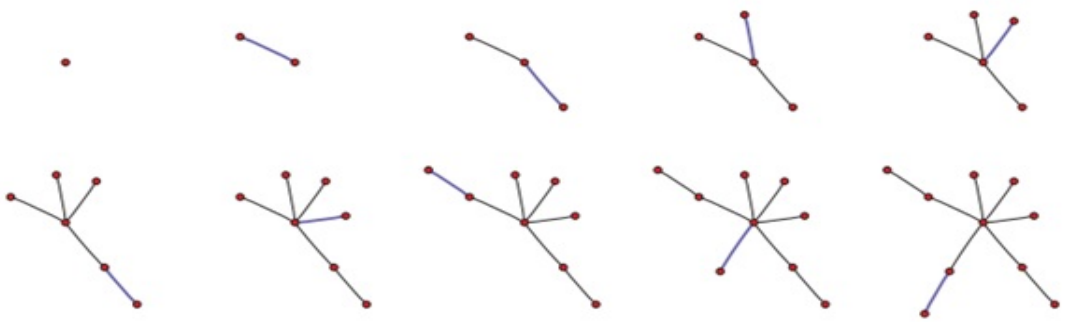


Figure I.23: Growth of scale-free graph using the Barabási-Albert model.

- **Preferential attachment:** is the second aspect which is not expressed in random models means that the new node establishes its connections with the old nodes with non uniform probabilities. In the *BA* model this probability is assumed to be depending on the degrees of the old nodes. The expression of probability p that a new node will be connected the node i whom k_i is the degree is :

$$p(k_i) = \frac{k_i}{\sum_{j=1}^{N(t)} k_j} \tag{I.18}$$

Fig. I.24 is an illustration of the preferential attachment mechanism. It shows for each already existing node, the probability that a new node i joining the network at $t = t_i$ would link to it.

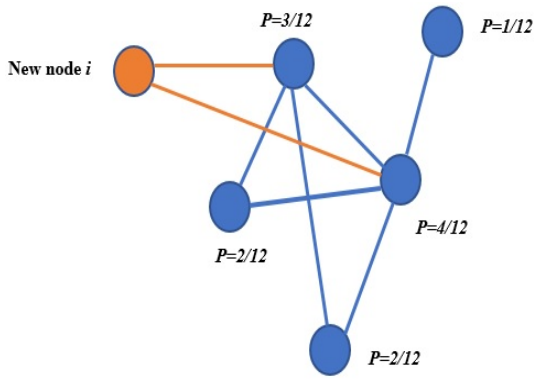


Figure I.24: Illustration of preferential attachment.

In this example, we have five old nodes and a total of ten connections distributed as follow: one node has only one link, two others have two links, one node has three links and one node has four links. Thus, the probability that the new node links to one of the old nodes is equal to the number of connection that it has divided by ten. Thus, the most connected vertices have greater a probability of receiving new vertices. This is known as "the rich get richer" paradigm.

I.6.5.3 Characteristics of BA model

Despite that, BA model generates a SF network, it does not mean that it responds perfectly to all the properties observed in real networks. In this sub-section, we are going to display BA characteristics to notice which of them matches with real networks features specifically the coexistence of high clustering coefficient and short path lengths.

Average path length: In [16] a comparison between the average path length of BA network and a random graph with the same size and average degree $\langle k \rangle = 4$ has been performed.

Fig. I.25 demonstrates the average path length versus the network size N for both network types. One can describe that the average path length is smaller in the BA model than in a

random graph for all network sizes. This result proves that the heterogeneous SF networks are more successful in making the nodes close than random graphs [16].

The average path length of the BA model tends to increases approximately logarithmically with N:

$$L = A\ln(N-B)+C.$$

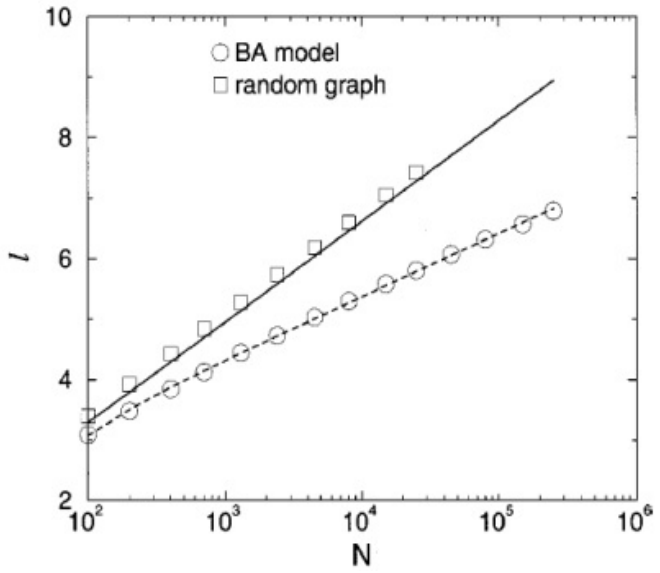


Figure I.25: The path length L versus the size N in BA model (circles) with $\langle k\rangle = 4$, compared with random graph with the same size and average degree (Squares) [16].

Clustering coefficient: Numerical results confirm that comparing to the random graphs with the same size and average degree. That is, due to the absence of analytical prediction for the BA clustering coefficient, the clustering coefficient of the BA network is about five times higher [16].

However, the clustering coefficient decays slowly with the network size, this behavior is completely different from that of SW model where the clustering coefficient is independent of N (Fig. I.26).

Degree distribution The distinguishing feature of the networks generated by the BA model is their power law degree distribution presented in Fig. I.27. This figure shows p_k for a single network of size $N = 100,000$ and $m = 3$. It shows both the linearly-binned (purple) and the log-binned version (green) of p_k. The straight line is added to guide the eye and has slope $\gamma = 3$, corresponding to the network's predicted degree exponent.

The analytical calculations predict that the BA model generates a scale-free network with degree exponent $\gamma = 3$ [16]. The degree exponent is independent of the m and m_0 parameters ([19] for more detail). Furthermore, the degree distribution is stationary (i.e. time invariant), explaining why networks with different history, size and age develop a similar degree distribution.

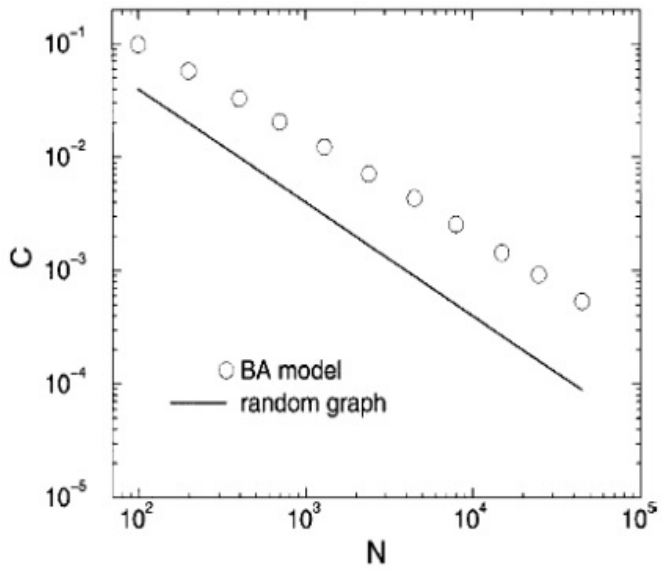


Figure I.26: Clustering coefficient versus N of BA network ($\langle k \rangle = 4$), compared to that of random graphs [16].

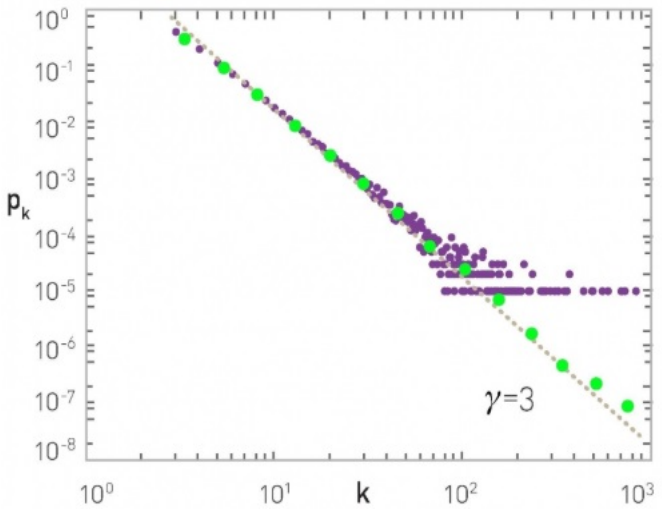


Figure I.27: Degree distribution of a BA network with $N = 100.000$, $m = 3$ [19]

I.7 Network of Network

In the field of network science, networks rarely appear in isolation, in which objects interact with each other. For instance, in epidemiology, diseases can propagate through populations but can also propagate to other populations, from different gender. Another example, in transportation networks, there are different means, mainly highway, bus, train and airplane, these means are covering the same areas but acting in different way [20, 97].

There are different types of networks of networks, such as interconnected networks and multiplex networks.

I.7.1 Interconnected networks

In this type of network of network, we consider the case of only two isolated networks that are connected by adding some links. These links provide path for traffic between them. Which named these links interconnected N_i. For instance, Fig. I.28 illustrates a schematic of real interconnected social networks in the world.
The majority of the conducted works on interconnected networks, exposed three different kinds between interconnected networks; as describe as follow [27, 56]:

- **Assortative coupling:** Considering two networks denoted A and B. Nodes are first sorted in networks A and B, both in descending order of load. If different nodes share the same load, we sort them at random. Connect the first node in network A with the first node in network B, and then connect the second node in network A with the second node in network B, and so on. Repeat this process until N_i interconnected links are added.

- **Disassortative coupling:** Nodes are first sorted in network $A(B)$ in descending (ascending) order of load. If different nodes share the same load, we sort them at random. Connect the first node in network A (with the heaviest load) with the first node in network B (with the lightest load), and then connect the second node in network A with the second node in network B, and so on. Repeat this process until N_i interconnected links are added.

- **Random coupling:** Randomly choose a node in network A and a node in network B. If neither of them has an interconnected link, then connect them. Repeat this process until N_i interconnected links are added.

I.7.2 Multiplex networks

Multiplex networks are networks of networks in which the identity of the nodes is the same across different networks but the links are different (see Fig. I.29). Moreover, multiplex networks were tend to describe a person who participates in multiple social networks [23]. For example, despite the actors will be the same, the networks of phone communication and email communication between individuals will have different topologies [26]. Another example, each online social network shares the same individuals, despite this, the network topologies will be very different depending on the community that the social network represents.
In Fig. I.30, people in a society interact via their friendship, family relationship, and/or more formal work related acquaintanceship, etc.

Figure I.28: Representation of social interconnected networks around the world

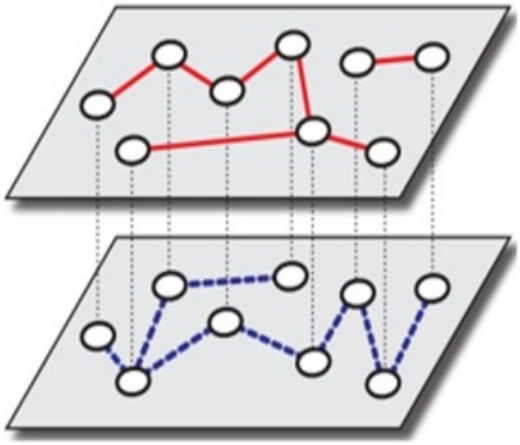


Figure I.29: An illustrative example of the multiplex network of nine nodes with two layers, the red (solid) and the blue (dashed) layer.

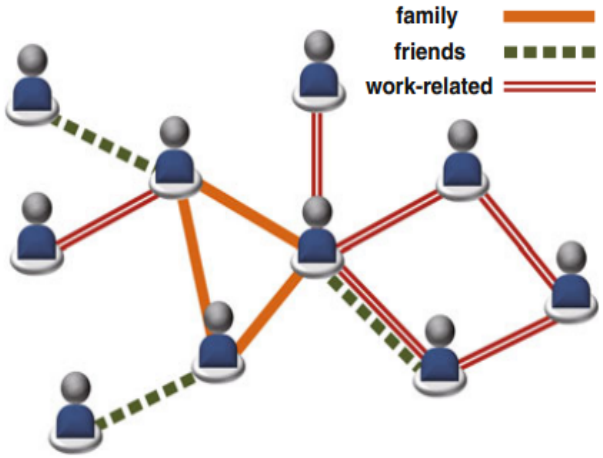


Figure I.30: Example of multiplex social network as a triplex network consisting of friend ship, family, and work related acquaintanceship layers

I.8 Conclusion

In the beginning of this chapter, we have introduced some important notions, frequently used in network science, mostly borrowed from graph theory.
We have also seen some important characteristics of nodes, which determine their influence in the network. We will cast light on these measures, in the next chapter, which will be useful for the implementation of phenomena occurring in complex networks (traffic and epidemic spreading).
After that, we have studied the most important features detected in real networks, and compared them to the known models. We concluded that the most appropriate model and the closest to the reality is the scale free network modeled by Barabási-Albert. For this reason, we will use this model to imitate the infrastructure, the behavior of processes taking place on networks.

CHAPTER II

PROCESSES TAKING PLACE ON NETWORKS

For a given network topology, understanding various dynamical processes on complex networks is a central theme in modern network science. Two types of dynamical processes that have been studied extensively : epidemic spreading and traffic dynamics.

II.1 Traffic dynamics

Traffic dynamics is one of the most important processes involved in networks. The prototypes of traffic dynamics on networks are mass transfer by chemical reactions in a cell, packet transfer on the Internet, airplane traffic between airports, and so on.

II.1.1 Basic concepts

The traffic is defined by several parameters. Here, we summarize these parameters, this later will be used in what follows.

- **Data packets :** Typically, a data packet is a unit of data made into a single package that navigates along a digital network path such as the Internet. However, it can represent travelling items in other kinds of networks. Indeed, regarding the networks nature, that could be vehicles in roadways, airplanes in airlines and so on.
- **Packet generation rate :** Packet generation rate indicates the number of packets added to the network per time step.
- **Packet delivering capacity :** The node packet delivering capacity, that is, the number of packets a node can deliver to other nodes in each time step, it is assumed to be a constant or proportional to the node's degree in most previous works. For a basic traffic simulation this quantity is uniform and it is equal to $C = 1$ for all the network routers.
- **Traffic Queues :** Packets form queues when two or more packets are at same node at the same time; The queue length at node i at time t is denoted by $Q_i(t)$.
- **Queuing Discipline:** This vocabulary determines the order in which packets leave a queue.

- **Free Flow Regime:** Refers to the free (uncongested) flow of packets.
- **Congested Regime:** Corresponds to a partial or complete jamming in networks when packets can get stuck for an indefinite time.
- **Traffic routing :** Traffic routing refers to the mechanism of selecting a path for traffic items in networks (links to follow in order to reach the destination). The process is governed by the routing protocol used. It is performed for many networks types that we often call traffic networks.

II.1.2 Traffic dynamics model

Once the network is generated, it remains fixed, and the traffic dynamics is modeled on top of it. Typically, in standard model it would include the following steps:

1. R packets generated in the system, with randomly chosen sources and destination.
2. Newly created packets queue up at the nodes at which they are generated.
3. Each node forwards only one packet to one of its neighbors according to the First-In-First-Out policy ($FIFO$).
4. The transmitted packet is placed at the end of the queue of the hosting node.
5. Packets are removed from the system once they reach their destinations.

Notice :

- The next destination of the packets is defined by the routing strategy used in the simulation.
- In our study, nodes are equally considered as hosts and routers, they all could generate and deliver packets.
- The buffering capacity of the nodes is supposed to be unlimited as well as the bandwidth.

II.1.3 Methods of measuring the traffic efficiency

In order to describe the phase transition of traffic flow in the network, they are so many methods to perform this transition, in this section we will focus on the famous ones:

II.1.3.1 Average travel time

The travel time or also the transport time of packet is defined as the total time that the packet spends in the network from the creation until reaching its destination [98]. It could be also defined as the total waiting time at the queues of nodes along the packet trajectory plus the path length (number of the nodes along the path).
The average traveling time is established by summing and averaging the travel time of all the packets that manage to arrive to their destinations [99].

II.1.3.2 Average path length

As for the average traveling time, the average path length concerns only the packets removed from the system. It is equal to the sum of the packets path lengths divided by the number of removed packets. Where the path length means the number of hops that the packet performs from the source to the destination. Notice that the path length is nothing but the travel time minus the waiting time [99].

II.1.3.3 The network capacity

The network capacity is the maximal quantity of traffic information that can the network handle successfully without transiting to the jam state. In other word it is critical packet generation rate R_c also called the congestion threshold, at which the system jumps from the free flow phase to the jamming of phase. In a traffic simulation, this important measurement can be determined experimentally.

Experimental estimation (The order parameter): The order parameter allowing to distinguish between the free flow and congested phases. In traffic simulation, the order parameter is defined as follows [51, 100]:

$$\eta = \lim_{t\to\infty} \frac{1}{R} \frac{<\Delta Q>}{\delta t} \tag{II.1}$$

R is the packet generation rate and $Q(t)$ is the total number of packets in the network at t. i.e. packets that have not reached yet their destinations at time t, or equivalently the total queue length of all the nodes; $\Delta Q = Q(t+\Delta t) - Q(t)$ and $<\cdots>$ denotes the average over time window of width Δt (observation time).

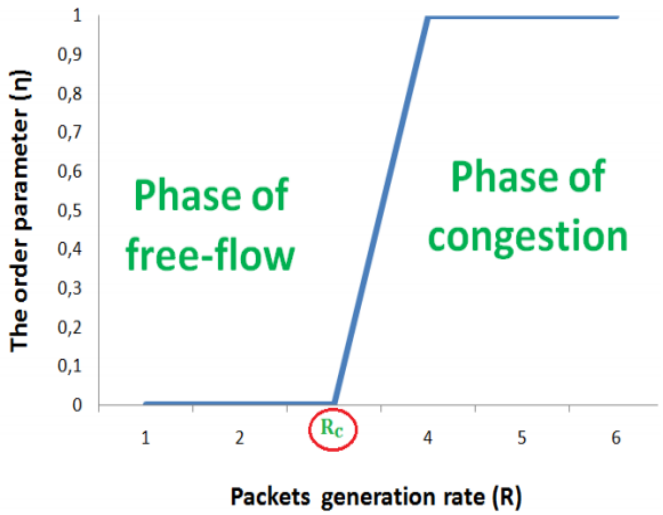


Figure II.1: Phase of transition.

At the beginning, $\eta(R) = 0$, which means that the generated and the removed packets are in balance. The traffic is then in the free flow phase. With increasing number of introduced packets, at start point, packets start to accumulate in the network. This leads to the loss of this balance and the system ends up in the congested phase $\eta(R) > 0$ (see Fig. II.1).

II.1.4 Traffic routing protocols

The goal of network traffic study is to alleviate traffic congestion and to improve the transportation efficiency of networked traffic system. Indeed, some studies have focused on the design of efficient routing strategies, on one hand, to provide a short delivery times and, on the other hand, to avoid the onset of the congested state in which the load of packets in the system increases, thus causing the failure of information flow [37, 39, 53, 101–103].

Here, we follow the classification proposed in [51], in which strategies can be classified into "hard" strategy and the other is called "soft" strategy, in order to alleviate traffic congestion and enhance the capacity of networks. Designing efficient routing strategies is considered to be "soft" strategies, because it does not require any topological changes. Making changes to network structure is considered to be "hard" strategies, because it requires topological changes. One can add a few links to existing networks or delete a few links from existing networks to realize the modification of network structure.

For each strategy, we provide examples from the most prominent propositions in literature. Meanwhile, we are going to distinguish the policy behind each approach.

II.1.4.1 Hard strategies

The hard strategies are about optimizing network topological structures by removing some links or nodes, or by adding some links between nodes with long distance or nodes.

Removing some links: Removing links from networks is usually easy to be implemented to the low cost. For instance, in a highway network system, some roadways are usually closed at rush hours in order to alleviate congestion, specifically, when crowds of people are heading to their offices in the morning or coming back home in the afternoon. Traffic administrators need only to block the entries to the roadways, which is easy to be implemented, to realize the closure of roadways. In [104], the authors pointed out that the removals of nodes or links could alleviate or even mitigate cascades of overloading on networks. Another example is the Internet; network administrators can easily isolate some connections among computers through computer software. In fact, the link removal strategy has been widely studied in order to enhance or optimize dynamics of different kinds on complex networks. In [105], the link-removal strategy was applied in the metabolic network. The authors stated that the removals of metabolic reactions, which represent links in the metabolic network, could improve metabolic performances and rescue defective metabolic networks. In [106], the authors found that the removals of links could also help to enhance synchronization in complex networks of dynamical systems.

Adding some links: Adding or rewiring links strategy have been also considered [107, 108]. However, if new nodes and links are added to an existing network in an improper way, the new links may not be helpful for enhancing transport efficiency while packets are generated on both existing nodes and new nodes, which may aggravate congestion in the network. More links then need to be added into the networks to alleviate congestion with extra cost. Hence, it is necessary to investigate how to add nodes and links in an efficient way so that the traffic capacity can be enhanced maximally.

In [52], the authors proposed a strategy that can effectively enhance the traffic capacity by the process of adding nodes and links. They consider two cases:

1. the number of nodes is kept unchanged and only the number of links is allowed to be increased.

2. Both nodes and links are allowed to be added to the existing network. Furthermore, the authors pointed out, that shortcut links are added among nodes that have the longest shortest path lengths. The shortcut links are placed in proper positions to avoid packets flowing through hub nodes so that there are not too many packets accumulated on hub nodes.

II.1.4.2 Soft strategies

The "soft" strategy is more economical and more flexible, compared with the costly "hard" strategy. Moreover, compared to the hard strategies in real situation that is often costly or even impossible to modify the network topological structures, the soft strategies are various routing protocols more applicable to real world communication networks.

Here, we present the some examples of these strategies in literature :

Routing by flooding:

The flooding routing method occurs when source packets (without routing data) is transmitted to all attached network nodes, since nodes create copies of the packet and forward them to all their neighbors [51, 109].

The advantage of this routing strategy is being simple to implement, Because it does not require any routing table update or prior knowledge of the network structure. Besides, it guarantees that at least one copy of the packet has arrived to the destination in case of topological change. So it is recommended for very dynamic networks. However, because of unnecessary traffic that it produces, flooding based routing consumes a lot the network resources (Fig. II.2).

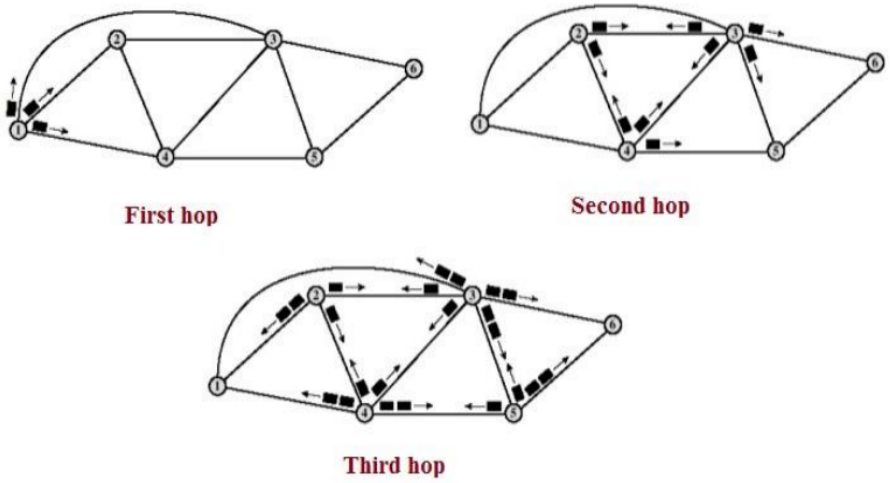


Figure II.2: The principal of routing by flooding

Random walk:

Random walk is a mathematic model which is deeply present in various multitude disciplines

such as economy, biology, physics, computer science, etc [39, 110].
The random walk means a stochastic process describing a sequence that consists of a succession of uncorrelated random steps. In mathematics, this process is referred to as the Markov process. As a routing technique, it has been extensively studied [40, 41, 45, 111, 112]. Due to its wide application and fundamental dynamics, which can be explained by theoretical analysis [112]. Random walk shares many characteristics with the routing by flooding, they both have high resilience against topological changes, and also the simplicity of implementation. However, the limitation of this technique emerge when packets get trapped in very limited network area for a long time visiting the same locations repeatedly. Which leads to the accumulation of packets in the network and cause the increases of the packets travelling time. Besides, it does not represent completely the reality of real traffic systems.

Traffic minimal model as an example

The model mimics the probabilistic events taking place in nodes buffers by a stochastic equation. The events that could occur which lead to the increase or the decrease of the queue length of a node i are:

- A creation of a new packet with a probability p.
- A successful delivery of a packet to a neighbor j with a probability $(1-\eta)$ where η is the rejection probability.
- A packet removal from the system with the probability μ.

Taking these events into account, we introduce the expression of the time discrete Markov chain regarding in the queue length of the node at the next time step for the minimal traffic model as [112]:

$$q_i^{t+1} = q_i^t + p + \sum_{j=1}^{N} \frac{\Theta(q_j^t) A_{ij}}{k_j}(1-\mu)(1-\eta) - \Theta(q_i^t) \sum_{j=1}^{N} \frac{A_{ij}}{k_i}(1-\eta). \tag{II.2}$$

Where A_{ij} is the value $A(i,j)$ of the adjacency matrix, $\theta(x)$ is the Heaviside function [$\theta(x)=1$ if $x>0$ and $\theta=0$ otherwise] and k_i represent the degree of the node i.
The authors studied the enhancement of the traffic flow by assigning to the node individual rejection rate [40, 112]. Opting for rejection rate based on global traffic information enhanced significantly the network resilience to the congestion. However, it demands the exchange of traffic information between routers which consume the bandwidth.
Fig. II.3 presents the behavior of the order parameter ρ by taking the rate of packet creation p as the control parameter. As observed in this figure, the transition from free-flow to congestion occurs in a smooth way at low values of p being the critical point $p_c = 0.02$ for $\eta = 0$ (no rejection). However, as the rejection rate η increases the value of p_c decreases and ρ increases faster.

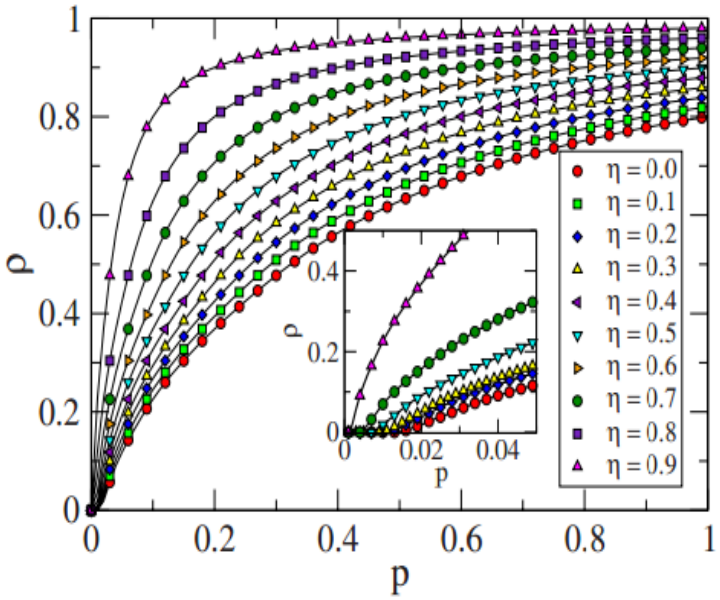


Figure II.3: Phase diagrams of the minimal traffic model using different values of rejection rate η [112].

The shortest path scheme:
In this strategy, The routing rules allow each node to have the whole network's topological information. The shortest path routing strategy indicates that each packet is always transported along the topological shortest path between the packet's source and destination [113–115]. Different from routing strategies with stochastic factors, under the shortest path routing strategy, once the network is constructed. Each packet has a fixed delivering path. Therefore, the shortest path routing strategy is widely used in real communication systems, due to its economical and technical costs [116].
However, this routing strategy has very limited network capacity. In fact, in the shortest path routing strategy, packets are easy to pass through hub nodes, this kind of movement can easily lead to congestions on hub nodes [54, 117]. This fact encourage and motivates the designing of many other efficient routing strategies.

Traffic awareness strategy:
It has been pointed out that, if packets are always transported along the shortest path from source and destination, then networks cannot handle heavy traffic. In fact Many research conducted works in order to improve transport efficiency of packets in the network.
In [36, 101, 118], the authors proposed a strategy called traffic awareness strategy, in which the factor of waiting time at the neighboring nodes is also considered in addition to the fact of shortest path length from the neighboring node to destination. The waiting time is regarded as the number of packets in the queue at a neighboring node at the time of decision. Moreover, they investigated the maximal time $< T_{max} >$ it takes a packet to travel from its source to destination and the traffic capacity ρ_c in complex heterogeneous networks. Results reveal that compared to the shortest path routing strategy, $< T_{max} >$ is shortened and ρ_c is enhanced by using the traffic awareness strategy. According to [119], efficient routing strategy is based on the projected waiting time along the shortest path from a neighboring node to the destination.

Strategies based on local information:

The routing strategies mentioned above, allow each node to have the whole network's global topological information, which may be practical for small or medium size networks but not for large real communication such as the Internet, urban transportation system. However, strategies based on local information (each node only knows the information of its neighbors) are favored in large networks, due to heavy communication cost on searching global information in networks [39]. In [39, 102], they present a traffic model in which packets are routed only based on local topological information with a single tunable parameter α The optimized value of α was sought out to maximize the traffic capacity. In this model, each node performs a local search among its neighbors. If the packet's destination is within the searched area, it is delivered directly to its destination. Otherwise, it is forwarded to a node i, one of the neighbors of the searching node, according to the preferential probability :

$$\Pi_i = \frac{(k_i)^\alpha}{\sum_j (k_j)^\alpha}. \tag{II.3}$$

Where the sum runs over all neighbors of the searing node i, k_i is the degree of node i, and α is a tunable parameter. With the delivering capacity of each node set as a constant C, the simulation results show that the optimal performance of the system corresponds to $\alpha = -1$, which can be observed from Fig. II.4. Theoretical analyses for the optimal value $\alpha = -1$ were obtained in [39]. In this later, The authors pointed out that choosing the optimal $\alpha = -1$ not only maximizes the traffic capacity but also minimizes the average delivering time. When the delivering capacity of each node is proportional to its degree k, the optimal value of α changes to $\alpha = 0$, as demonstrated in Fig. II.5.

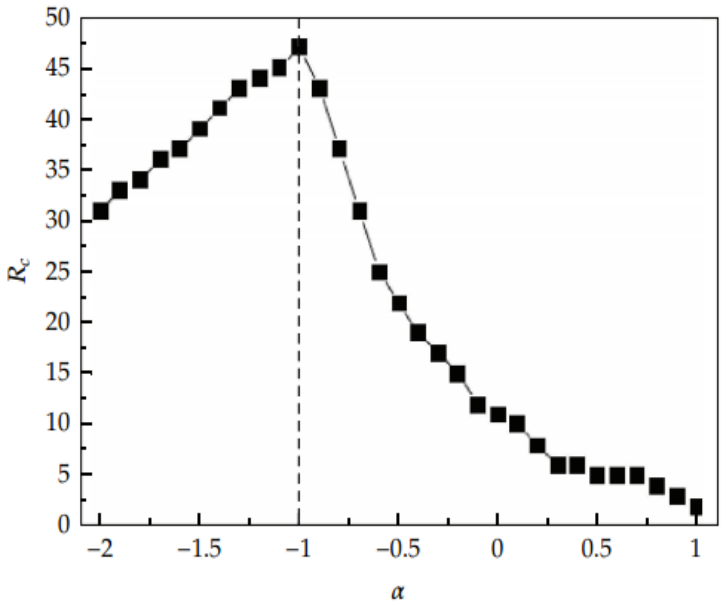


Figure II.4: R_c versus α on a scale-free network with network size $N = 1000$ and constant delivery capacity of each node $C = 10$. The maximal of R_c corresponds to $\alpha = -1$ marked by a dotted line.

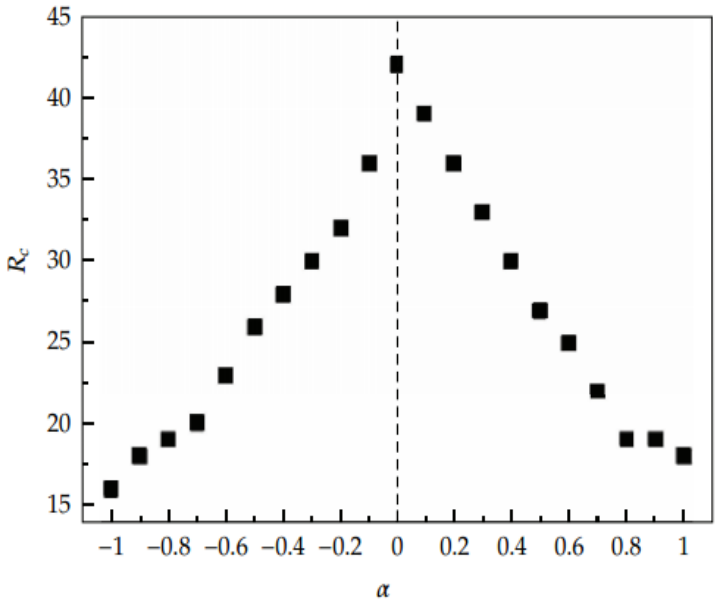


Figure II.5: R_c as a function of α, with $C_i = k_i$, size of network $N = 1000$. The maximum of R_c corresponds to $\alpha = 0$ marked by a dotted line.

In [54], the authors incorporated both the global shortest path length information and local degree information in the transport process of traffic, via two tunable parameters, α and β, to guide the routing of packets. Indeed, at each time step, all packets move from their current position, i, to the next node in their path, j, with a probability Q_{ij} defined as

$$Q_{ij} = \frac{\left(k_j\right)^{\alpha} \exp\left[-\beta(q_{it} - d_{jt} - 1)\right]}{\sum_{l \in \Omega_i} (k_l)^{\alpha} \exp[-\beta(q_{it} - d_{lt} - 1)]} \tag{II.4}$$

Where Ω_i is the set of neighboring nodes of i, k_j is the degree of node j, and d_{it} is the shortest path length between node i and node t. The parameters α and β are tunable parameters with varying range $\alpha \in]-\infty, \infty[$ and $\beta \in [0, \infty[$. Through numerical simulations, they showed that with appropriate selection of the tunable parameters [54], concerning the strategy proposed in [54], authors pointed out that this strategy is superior to the shortest path routing strategy in enhancing the traffic capacity.

Strategies based on local and dynamical information:
Another strategy, based on local static and dynamical information in scale-free networks [103]. In the routing model of this strategy, it was assumed that each node has an identical delivering capacity C. A packet is directly delivered to its destination, if the destination is one of the direct neighbors of the searing node l. Otherwise, the probability of a neighbor node i to which the packet will be delivered is :

$$P_{l \to i} = \frac{k_i (n_i + 1)^{\beta}}{\sum_j k_j (n_j + 1)^{\beta}} \tag{II.5}$$

Where the sum runs over all neighbors of the searching node i, n_i is the number of packets in the queue of i and β is a tunable parameter. Fig. II.6 shows that in the case of no delay, the traffic capacity is considerably reduced when decreasing β until $\beta \approx -3$. The maximal traffic

capacity is only 23 when choosing $C = 5$ under the case of only adopting local topological information [39, 102]. Results show that the traffic capacity is further improved by using the strategy in [103]as compared to the strategy in [39, 102].

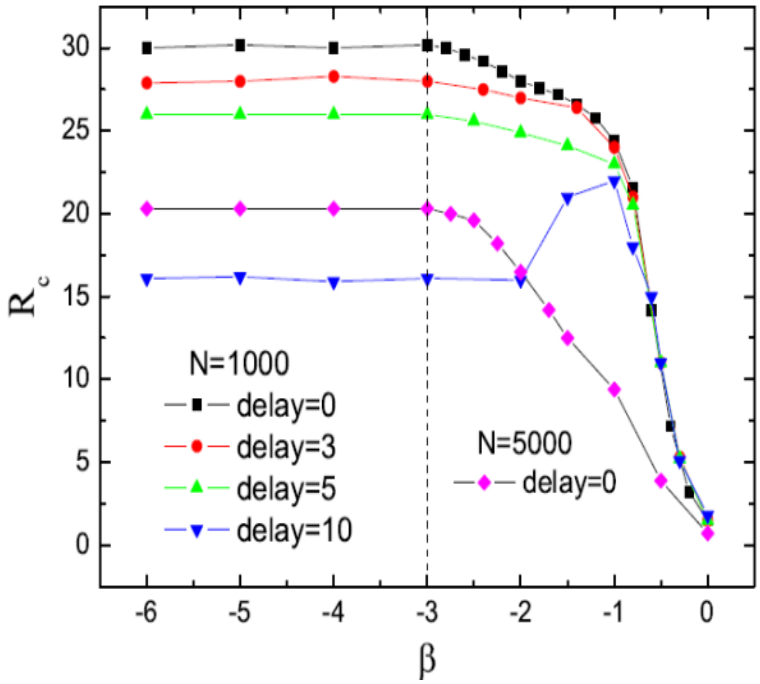


Figure II.6: R_c versus parameter β for different time delay and for different network size N, with $C = 5$.

II.2 Epidemics spreading

Epidemic spreading is one of the most popular dynamics on complex network, which describes how infections spread throughout a network. A part from one side, Infectious diseases have always been the great enemy of human health. The other side is that, applications based on computer networks are becoming more and more popular in our daily life. While bringing convenience to us, computer networks are exposed to various threats.

In fact, modeling, analyzing and controlling the spreading of information and infectious diseases have become a relevant problem of an interdisciplinary nature.

II.2.1 Basic concepts

- **Epidemiology:**
  There are many different definitions of the term epidemiology. A simple and useful definition is epidemiology is the study of disease in populations. In branches of medicine, are mostly interested in to find cures for diseases in individuals already affected.

- **Epidemic diseases:**
  The Centers for Disease Control and Prevention on 2012 [120], defined epidemic disease as the occurrence of more cases of disease, injury or other health condition than expected in a given area or among a specific group of persons during a particular period.

- **Computer virus:**
  Computer viruses are pernicious codes or programs, which can copy themselves and spread by wired or wireless networks. With the large number of Internet applications, computer viruses have become a great threat to our Work and daily life, this threat should be taken in consideration, due to the damage that may cause.

- **Computer anti-virus:**
  Antivirus software was originally developed to detect and remove computer viruses, hence the name. However, with the proliferation of other kinds of malware, antivirus software started to provide protection from other computer threats.

- **Vaccination:**
  In the field of computer virus, the term vaccination is often used to describe the process of installing the newest-version antivirus software in an uninfected computer. As a result, a newly vaccinated computer can acquire temporary immunity.

II.2.2 A brief history of epidemics spreading

Generally speaking, the history of humans is a history of struggle with all kinds of diseases, indeed, they are several diseases, from the Black Death in medieval Europe to the recently notorious severe acute respiratory syndrome [121], avian influenza [122], swine influenza [123], etc.

Since the first mathematical approach to the spread of a disease by Daniel Bernoulli (1760), epidemic models Depend on the core of our understanding about infectious diseases. The acclaimed work of Kermack and McKendrick (1927), defining the modern mathematical modeling

of infectious diseases, has improved through the years in an impressive body of work, whose culmination is well represented by the monumental summary of Anderson and May (1992). At the same time, the epidemic modeling metaphor has been introduced to describe a wide array of different phenomena. The spread of information, cultural norms, and social behavior can be conceptually modeled as a contagion process [124].

Cohen [125] and Murray [126] suggested exploiting the mathematical techniques developed in the epidemiology of infectious diseases to study the spread of computer viruses, inspired by the compelling analogies between computer viruses and their biological counterparts. Like its biological counterpart, computer virus epidemiology is intended to understand how computer viruses spread on networks and, thereby, to work out policies of inhibiting their prevalence.

Following Cohen and Murray work, Kephart and White [127] founded the first epidemic model of computer viruses. The so-called homogeneous model. This model is called homogeneous because every node of the network has the same probability of interaction with other nodes. Using a rate of infection and a death rate, they were able to calculate the infection threshold. Unfortunately, this model fails to capture real-world complexity. Data available show that real-world computer networks are not homogeneous and, instead, follow a power law structure in the number of connections of the nodes [13, 128].

After Kephart and White model, multifarious epidemic models have been proposed based on the fully-interconnected assumption of the Internet, with focus on their complex dynamical properties [47, 48, 129, 130]. The finding at the end of last century that the Internet topology asymptotically follows a power-law degree distribution [13] has greatly stimulated the interest in understanding the effect of network topology on virus spreading, leading to the surprising result that a virus could spread across an infinite-sized scale-free network even when the infection probability is vanishingly small [49]. Most previous work toward this direction, for example: the SI model [131], the SIS model [132], and the SIR model [133].

II.2.3 Types of epidemic models

In general, epidemic models can be classified into two main mathematical approaches: deterministic models based on differential equations and stochastic models that employ Markov chains, branching and diffusion processes, etc.

Here is the definition of the two approaches [65]:

Stochastic: means being or having a random variable. A stochastic model is a tool for estimating probability distributions of potential outcomes by allowing for random variation in one or more inputs over time. Stochastic models depend on the chance variations in risk of exposure, disease and other illness dynamics.

Deterministic: When dealing with large populations, as in the case of tuberculosis, deterministic or compartmental mathematical models are often used. In a deterministic model, individuals in the population are assigned to different subgroups or compartments, each representing a specific stage of the epidemic. Letters such as S, E, I, and R are often used to represent different stages.

The differences between deterministic and stochastic epidemic models [64, 134]:

- The own random nature of the disease dynamics which leads to differences and fluctuations where the deterministic model will often predict an unvarying equilibrium solution.

- The fact that eventually stochastic solutions converge to the disease-free event though the corresponding deterministic solution converges to an endemic equilibrium
- Stochastic models allow to calculate the probability of an outbreak, the final size distribution of an epidemic, the length of the time to extinction and the quasi-stationary regime.
- Knowledge about uncertainty in estimation (e.g. standard errors) requires to deal with a stochastic model.

II.2.4 Epidemic modeling

The overwhelming majority of disease models are based on an existence of "compartments" into which individuals in a population are divided, the two most common compartments that exist in essentially every epidemic model are susceptible (S) and infected (I) [131]. S represents individuals who are healthy but susceptible to becoming infected, and I represents individuals who are infected but are able to recover or remove R (Fig. II.7(a)). In addition, based on the homogeneous mixing hypothesis (also called fully mixed or mass action approximation) assumes that each individual has the same chance of coming into contact with an infected individual (Fig. II.7(b)). This hypothesis eliminates the need to know the precise contact network on which the disease spreads, replacing it with the assumption that anyone can infect any one else.

From this basic compartmentalization and homogeneous mixing, there are numerous ways that interactions within the population can be modeled.

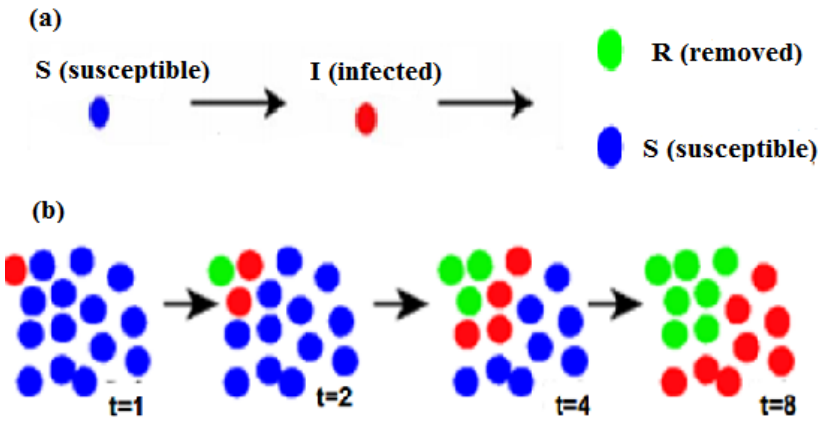


Figure II.7: Illustration of two fundamental hypotheses in epidemic spreading. Compartmentalization (a) and the homogenous mixing (b)

II.2.4.1 Mathematical model

There are many models of epidemic spreading, we explore in this section the dynamics of three frequently used epidemic models, the so-called SI, SIS and SIR models, that help us understand the basic building blocks of epidemic modeling.

Susceptible-Infected (SI) model

The SI model consists of two populations; the first is the Susceptible means that all individuals in this group can acquire the infection, when there is a contact with an infected individual. While the second is the infected denoted that all individuals in this group carry and spread the infection and never leave this situation ($S \rightarrow I$), with β is the infection probability (see Fig. II.8).
The dynamic equations for the populations S, I are:

$$\begin{cases} \frac{ds}{dt} = -\beta si \\ \frac{di}{dt} = \beta si. \end{cases} \tag{II.6}$$

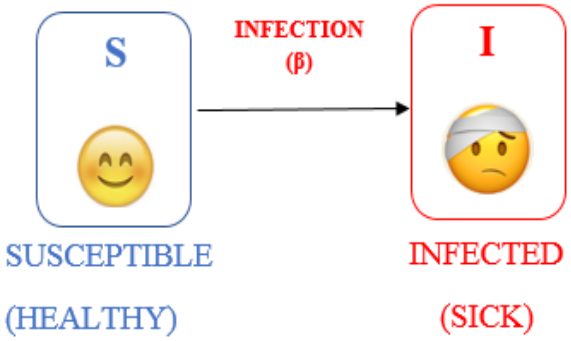


Figure II.8: Schematic representation of an SI model with infection probability β

Susceptible-Infected-Susceptible (SIS) model

The SIS model is One of the simplest two-state compartmentalization, with only two possible transitions: The first one occurs when a susceptible individual interacts with an infectious individual and becomes infected ($S \rightarrow I$). The second transition occurs when the infectious individual recovers from the disease and returns to the pool of susceptible individuals ($I \rightarrow S$). with the recovery probability γ (see Fig. II.9).
The differential equations for this model are:

$$\begin{cases} \frac{ds}{dt} = \gamma i - \beta si \\ \frac{di}{dt} = \beta si - \gamma i. \end{cases} \tag{II.7}$$

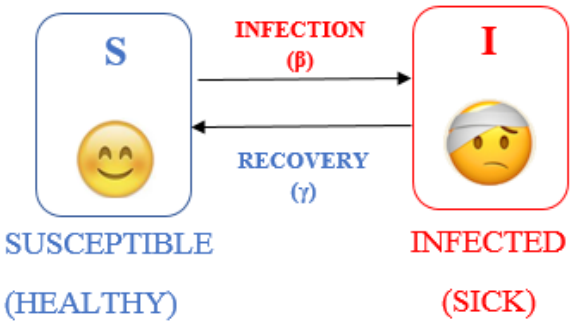


Figure II.9: Schematic representation of an SIS model with infection probability β and recovery probability γ

Susceptible-Infected-Removed (SIR) model

Another basic model called the classic three-state SIR model has two transitions. In the first transition, susceptible individuals become infected when they have contact with infected individuals. Contacts between individuals are assumed to happen at an average rate β per person as before. In the second transition, infected individuals recover (or die) at some constant average rate γ (see Fig. II.10). The equations for the SIR model are:

$$\begin{cases} \frac{ds}{dt} = -\beta si \\ \frac{di}{dt} = \beta si - \gamma i \\ \frac{dr}{dt} = \gamma i. \end{cases} \tag{II.8}$$

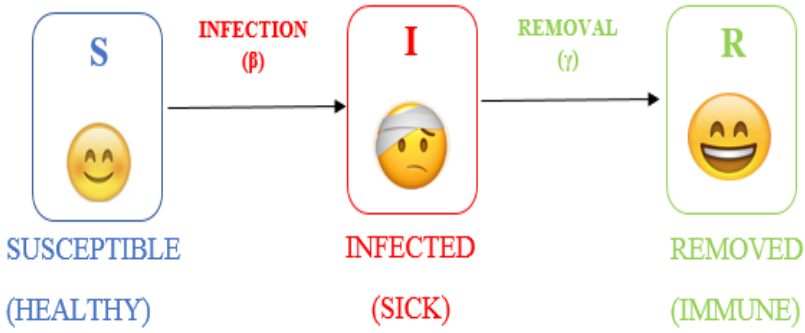


Figure II.10: Schematic representation of an SIR model with infection probability β and recovery probability γ

II.2.4.2 Basic results

The classic understanding of epidemic dynamics is based on taking the continuous-time limit of difference equations for the evolution of the average number of individuals in each com-

partment, despite the fact that epidemic spreading is best described as a stochastic reaction-diffusion process. However, deterministic approach depends on the homogeneous mixing approximation, that assumes that the individuals in the population are well mixed and interact with each other completely at random, in such a way that each member in a compartment is treated similarly and indistinguishably from the others in that same compartment. This approximation, which is essentially equivalent to the mean-field approximation commonly used in statistical physics [135].

Following this approximation, full information about the state of the epidemics is encoded in the total number N^α of individuals in the compartment α or, analogously, in the respective densities $\rho^\alpha = \frac{N^\alpha}{N}$, where N is the population size. By deterministic differential equations, the time evolution of the epidemics is described, which are constructed applying the law of mass action, stating that the average change in the population density of each compartment due to interactions is given by the product of the force of infection times the average population density.

The deterministic equations for the SIR and SIS processes are obtained by applying the law of mass action and read as:

$$\begin{cases} \dfrac{d\rho^I}{dt} = \beta\rho^I\rho^s - \mu\rho^I. \\ \dfrac{d\rho^s}{dt} = -\beta\rho^I\rho^s + \chi\rho^I. \end{cases} \tag{II.9}$$

Where $\chi = \mu$ for the SIS process and $\chi = 0$ for the SIR model, and the force of infection is $\alpha = \beta\rho^I$. These equations are complemented with the normalization conditions $\rho^R = 1-\rho^s-\rho^I$ and $\rho^s = 1-\rho^I$ for the SIR and SIS models, respectively. If we consider the limit $\rho^I \approx 0$, generally valid at the early stage of the epidemic, we can linearize the above equations obtaining for both the SIS and SIR models the simple equation

$$\frac{d\rho^I}{dt} \simeq (\beta-\mu)\rho^I. \tag{II.10}$$

whose solution :

$$\rho^I(t) \simeq \rho^I(0)e^{(\beta-\mu)t} \tag{II.11}$$

represents the early time evolution. Equation (II.12) clarifies one of the key concepts in the classical theoretical analysis of epidemic models. The number of infectious individuals grows exponentially if

$$\beta-\mu > 0 \Longrightarrow R_0 = \frac{\beta}{\mu} > 1. \tag{II.12}$$

This result permits to define the concept of epidemic threshold. This concept is very general and the analysis of different epidemic models shows in general the presence of a threshold behavior. This threshold is similar to the concept of phase transition. A phase transition characterized by qualitatively different properties, is defined as an abrupt change in the state (phase) of a system, and that is experienced varying a given control parameter λ. The transition is characterized by an order parameter (ρ), which takes (in a system of infinite size) a nonzero value in one phase, and a zero value in another (see Fig. II.11). The phase transition takes place at a particular value of the control parameter, the so-called transition point λ_c , in such a way that for $\lambda > \lambda_c$ we have $\rho > 0$, while for $\lambda \leq \lambda_c$, $\rho = 0$. A part from the determination of the transition point, the interest in physics lies in the behavior of the order parameter a round λ_c, which in continuous

or critical phase transitions takes a power-law form $\rho(\lambda) \sim (\lambda - \lambda_c)^{\beta_{crit}}$, defining the critical exponent β_{crit}.

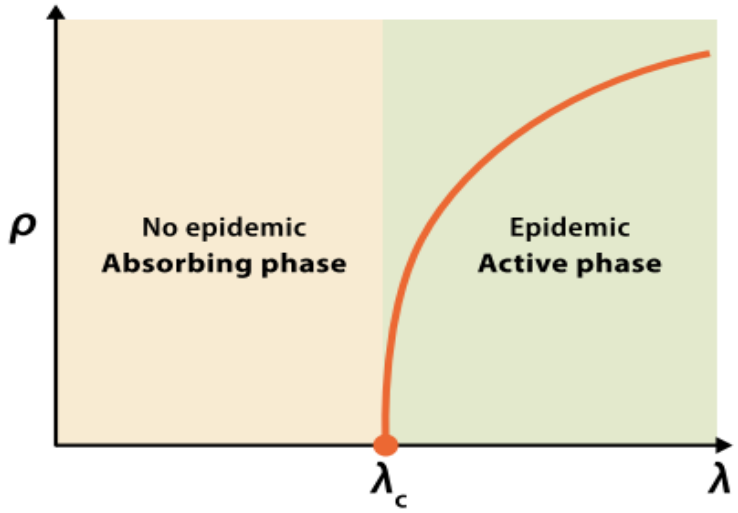


Figure II.11: The order parameter

II.2.5 Network epidemics

The ease of air travel, allowing millions to cross continents on a daily basis, has dramatically accelerated the speed with which viruses travel around the world. Therefore, to understand and predict the precise patterns that viruses follow as they spread around the globe.

The epidemic models discussed in the previous section do not incorporate the structure of the contract network that facilitates the spread of a virus. Instead they assume that any individual can come into contact with any other individual (homogeneous mixing hypothesis) and that all individuals have comparable number of contacts,$< k >$. Both assumptions are false: Individual can transmit a virus only to those they come into contact with, hence viruses spread on a complex contact network. Furthermore, these contact networks are often scale-free, hence $< k >$ is not sufficient to characterize their topology. In this section, we present the Susceptible-Infected (SI) model in a network.

Susceptible-Infected (SI) model on a network

If a virus spreads on a network, individuals with more links are more likely to be in contact with an infected individual, hence they are more likely to be infected. Therefore the mathematical formalism must consider the degree of each node as an implicit variable. This is achieved by the degree block approximation, that distinguishes nodes based on their degree and assumes that nodes with the same degree are statistically equivalent. These, written as :

$$i_k = \frac{I_k}{N_k}, \tag{II.13}$$

The fraction of nodes with degree k that are infected among all degree k nodes in the network. The total fraction of infected nodes is the sum of all infected degree k nodes.

$$i = \sum_k p_k i_k, \tag{II.14}$$

Given the different node degrees, the SI model is [19]:

$$\frac{di_k}{dt} = \beta(1-i_k)k\theta_k. \tag{II.15}$$

With β is the rate of infection, the fraction of degree k nodes that are not yet infected, which is $(1-i_k)$ and the density function θ_k represents the fraction of infected neighbors of a susceptible node k.

II.2.6 Immunization strategies

Immunization strategies specify how vaccines, treatments or drugs are distributed in the population. Ideally, should a treatment or vaccine exist, it should be given to every infected individual or those at risk of contracting the epidemic. Yet, often cost considerations, the difficulty of reaching all individuals at risk, and real or perceived side effects of the treatment prohibit full coverage. Given these constraints, immunization strategies aim to minimize the threat of a pandemic by most effectively distributing the available vaccines or treatments.

This part exposes three typical effective immunization strategies, specifically, Random Immunization (or, Uniform Immunization), Targeted Immunization (or, Selected Immunization), and Acquaintance Immunization.

Random immunization

Random immunization refers to a process in which nodes selected randomly from the network to immune [136]. Random immunization, the large nodes and small nodes has an equal chance to be chosen for immunization, despite that the large nodes have higher risk to be infected comparing to the small nodes which can be relatively safe. Casting light on heterogeneous networks, it seems obviously that the random immunization for heterogeneous networks is ineffectual, since such a network have a small fraction of large-degree nodes (hubs) whereas, the majority of nodes have small degrees, hence, random immunization approach will likely immune only small-degree nodes that have less effect on the whole network.

Targeted immunization

Since the scale free network are heterogeneity, in this case, the targeted immunization strategy can be adopted, indeed this strategy targeted and immune the most highly connected nodes that are likely received the diseases from, and spread the diseases to many other nodes in the network. At the time that these nodes are immunized, conceptually their edges are removed, losing connections with the other nodes, hence reducing or even completely blocking the way of virus spreading over the network.

Acquaintance immunization

The Acquaintance immunization is a localized strategy. It means randomly select a fraction f of nodes from the population of N nodes and then randomly select one of its neighbors or select the bigger node among its neighbors, for immunization [137]. This strategy only demand information about the randomly selected node and its neighbors, but not the global network. In a scale free network, it is probably the first that would be selected at random is small nodes, but then since most small nodes are connected to big nodes it is relatively easier to find a big node from among its neighbors to immunize.

II.3 Conclusion

In this chapter, we have presented the behavior of processes that takes a place on networks. Indeed, there are two types of dynamical processes that have been studied extensively, which are the epidemic spreading and traffic dynamics.

In the first part of this chapter we have presented analysis of traffic dynamics on complex networks. In order to enhance transport efficiency so that traffic congestions on complex networks can be alleviated. We have exposed the most memorable methods that researchers had used to implement efficient routing protocols. We clarified their principle and also shed some light on the differences between each routing strategy in order to understand which one is the most appropriate according to the context.

We devoted the second part of this chapter, to study the epidemic spreading. We have displayed the most memorable methods that researchers had used to understand the dynamical process of epidemic spreading on complex networks. Besides, modeling and controlling methods of the epidemic spreading.

CHAPTER III

EFFECTS OF MAXIMUM NODE DEGREE ON COMPUTER VIRUS SPREADING IN SCALE-FREE NETWORKS.

III.1 Introduction

Because of the globalization and development of communication, networks have made computers more present in our daily life, the increasing use of computers allows the appearance of large numbers of computer virus, this is an important risk factor for corporations and individuals [125].

A general computer virus, including the defined virus is code or a malicious software program that can duplicate itself and spread on the network across the internet [63]. It is called virus because, it shares some traits of biological virus, and it can pass from one computer to others like the spread of biological virus between persons [125].

Many mathematical models were proposed to investigate the epidemic behaviors of computer virus. For instance, some classical models for the propagation of computer virus, such as the dynamic models [138], stochastic models are Susceptible-Infected-Susceptible (SIS) [127], Susceptible-Infected-Removed-Antidotal (SIRA) [61], Susceptible-Infected-Recorved-Susceptible (SIRS) [47], and in order to study the influence of external computers, there are other epidemic models describing the spread of computer viruses under the influence of external computers (specially external infected computers connected to the internet). As the Susceptible-Infected-External (SIE) model [63] and Susceptible-Infected-External-Susceptible (SIES) model [62].

In the field of computer virus, anti-virus software plays an important role to maintain the security of computer networks. Indeed, the development of anti-virus software comes always after virus propagation [139, 140].

Recently, computer virus in complex networks have been greatly concerned and generally investigated. Many numerical simulations of computer virus in scale-free network were proposed to analyze the spread of computer virus in real environment. In [141], the authors show that the epidemic spread in varying complex network with the diffusion of exponent γ (γ characterizes the degree distribution scaling in the network) influence on the network structure. In [49], the authors have incorporated the importance of scale-free network topology in the theoretical description of infections; they worked on a threshold of epidemic and its associated critical behavior. In [142] the authors studied the effects of community structure in spread of

the epidemic. In another work [143], the authors worked on the impact of external computers and network topology on a scale-free network. In [43] the authors proposed a new model for computer virus attacks and recovery at the level of information packets in scale free network. Furthermore, the effects of node degree have been studied in [144].

In this chapter, we study the spread of viruses in a scale-free network with different topologies. We proposed a restricted scale-free (RSF) network more resistible to the spread of virus. Our idea is based on the influence of the degree of connectivity nodes k. In our work, we determined a critical maximum node degree (K_c), below which the virus spread in the network is limited. However, the infected nodes increased when $K > K_c$. Moreover, we compare our RSF with Erdös and Rényi (ER) network [9]. Finally, we see the influence of the network size with different topologies on the spread of virus.
In order to study the effects of the RSF to the spread of virus, we have focused on the SIE model, with the nodes that are classified into three states (susceptible-infected-external) [63].

III.2 Model and methods

Networks are described by a graph in which the nodes represent the computers and the edges account for the communication links between computers. Each time step, each node can be internal or external according to the connection to the internet. In addition, internal nodes may be susceptible or infected and all external nodes are susceptible [63, 143].

III.2.1 Network structure

In this chapter, to construct our network, we use the scale-free network proposed by Barabàsi-Albert (BA).

To construct the Barabàsi-Albert model, we start with a clique of $m_0 = 3$ nodes fully connected and stops when the desired total number of node N is reached. It is a model based on two concepts (growth and preferential attachment).

Implementation of BA model:
Here, we are going to explain how the two BA model ingredients (growth and preferential attachment) are implemented in a program. The output of our simulation program is the adjacency matrix $A(i, j)$ of the BA network.
Initially, all the elements of the adjacency matrix are equal to zero except the m_0 nodes which are fully connected:

$$A_{ij} = \begin{cases} 1 & \text{if } i \neq j \leq m_0 \\ 0 & \text{otherwise} \end{cases}$$

According to the BA model, at each time step a new node joins the network and attached preferentially to already well-connected nodes.
Each old node has an attachment probability that it updated whenever a new node is added to the network. The update takes into account the new added node as well as the new degrees of all nodes. The sum of all the probabilities is always equal to one.
The total simulation time is $T = N - m_0$. In order that the index of the current simulation time indicates at the same time the total number of the nodes in the evolving network at the end of the time step, we set $t_1 = m_0 + 1$.

In an interval $I=[0,1]$, we assign to each node an interval belonging to I ranked by creation order starting from zero. Therefore we split the interval I to $(t-1)$ subintervals whom widths equal to the attachment probabilities of the nodes that they represent (see the illustration in Fig. III.1). For example, the subinterval $[0,P(1)]$ represents the node N_1, and $[P(1),P(2)]$ stands for the node N_2, and so on.
At each time t :
At the beginning, I includes m_0 uniform subintervals and at the end of each time step the num-

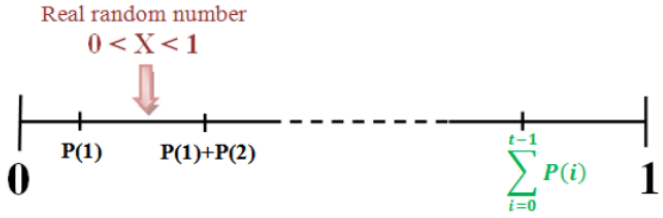


Figure III.1: Method of implementing of the preferential attachment in simulation program.

ber and the width of the subintervals are updated to take into account the current probability attachments of each node.
To decide the nodes that a new node will establish links with, we generate m times (or more if necessary) a different random real number between 0 and 1. At each time we spot the subinterval that includes the value of X and we link the new node to the old node that it represents. For instance, in the illustrative example Fig. III.1, the value of X is included in the second subinterval so the new node (number t) will be connected to the node number $2(N_2)$.
The adjacency matrix is updated as:

$$A(t,2)=A(2,t)=1$$

We repeat the same process until we reach the network size N.

Restricted Scale Free (RSF):
Among the characteristics of the network, there is the degree of connectivity. Each node is characterized by its degree of connectivity k, equal to the number of connections that are attached to it. A hub is a node that stands out by high degree of connectivity, it is a very important component in the network. For example, in social networks, the node with the higher degree of connectivity is represented by the person of great influence (a lot of friends) on the network. In internet networks, the fundamental problem is the spread of viruses, the hubs are more susceptible to infection than others, because they are the most influenced nodes in internet network [84]. In [70], the authors proposed a method to suppress traffic-driven epidemic outbreak by properly removing some edges in a network. For this reason, we will try to build a network that does not have hubs that have very high degrees by limiting the maximum number of links that a particular node can acquire. This network is called "Restricted scale-free" (RSF), it is constructed by changing the SF model and adding a conditional constraint to the preferential attachment mechanism, which limits the number of links of the hubs in the RSF. In other word, by fixing a maximum node degree K. Such that: New node tends to create links with nodes having a higher degree k of connectivity, proportional to the preferential attachment probability P_i (see Eq. I.18). Moreover, the degree of the chosen node is not allowed to

exceed K.

Degree distribution of RSF:
We have plotted in Fig. III.2 the probability of degree distribution $p(k)$ as a function of node degree, to prove that the restricted scale-free network (RSF) has still a scale-free character, and it is clear from the slope of the fitting curve that it behaves as a power law.

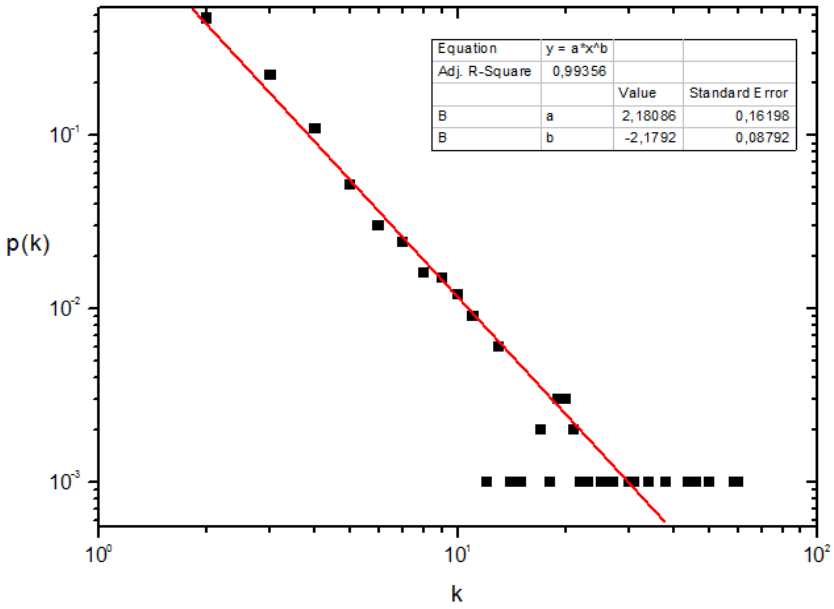


Figure III.2: The probability $p(k)$ as a function of node degree. With the fit to a power law, $N = 1000$, $m = 2$ and $m_0 = 3$.

III.2.2 Epidemic spreading

In this work, we use the SIE model [63]. A computer is called internal or external depending on whether it is connected to the Internet or not. For this purpose, internal computers are further classified into the following two compartments:

- S-nodes, i.e., susceptible or uninfected internal computers,
- I-nodes, i.e., infected internal computers.
- E-nodes, i.e., external computers, which could be connected to the Internet.

Besides, the following notations, most of which are dependent on time t, are introduced.

- Δ : the maximum node degree of the Internet.
- $S_k(t)$: the number of k-degree S nodes.
- $I_k(t)$: the number of k-degree I nodes.
- $E_k(t)$: the number of k-degree E nodes.
- $N_k(t)$:the total number of k-degree nodes, i.e., $N_k(t) := S_k(t) + I_k(t) + E_k(t)$

- $s_k(t)$: the relative density of k-degree S-nodes, i.e., $s_k(t) := S_k(t)/N_k(t)$
- $i_k(t)$: the relative density of k-degree I-nodes, i.e., $i_k(t) := I_k(t)/N_k(t)$
- $e_k(t)$: the relative density of k-degree S-nodes, i.e., $e_k(t) := E_k(t)/N_k(t)$
- $s(t) := (s_1(t), ..., s_\Delta(t))$
- $i(t) := (i_1(t), ..., i_\Delta(t))$
- $e(t) := (e_1(t), ..., e_\Delta(t))$

Moreover, the authors in this model are based on the following hypotheses (also can see in Fig. III.3):
($H1$) Due to the fact that external computers are constantly connected to the internet, each E-node becomes an S-node or I-node at constant rate $\eta_2 > 0$ or $\eta_1 > 0$, respectively.
($H2$) Each S-node (respectively, I-node) is disconnected from the internet at constant rate $\alpha_2 > 0$ (respectively, $\gamma_1 > 0$).
($H3$) Each S-node is infected by an I-node at constant rate $\alpha_1 > 0$.
($H4$) Due to the effect of treatment, each I-node becomes an S-node at constant rate $\gamma_2 > 0$.
($H5$) Every computer dies out with probability $\mu = 0$, and $E_k(t)$ increases at rate $\mu N_k(t)$. This implies that $N_k(t)$ is conservative.
($H6$) The probability, denoted by $\Theta(i(t))$, that a link has an I-node as one endpoint, does not depend on the degree of the other endpoint of the link, so $\theta(i(t)) = \frac{1}{\langle k \rangle} \sum_k kp(k)i_k(t)$, where $\langle k \rangle$ stands for the average node degree, $\langle k \rangle := \sum_k kp(k)$; $p(k)$ stands for the probability that a computer chosen randomly from the Internet is of degree k.

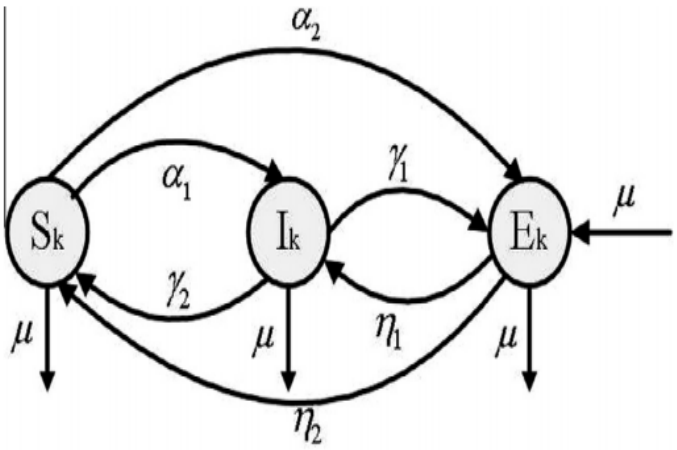


Figure III.3: Schematic representation of an SIE model.

By applying the mean-field technique to the above hypotheses, the dynamical model for each degree class k is formulated as:

$$\begin{cases} \dot{S_k}(t) = \gamma_2 I_k(t) + \eta_2 E_k(t) - \alpha_1 k S_k(t)\Theta(i(t)) - \alpha_2 S_k(t) - \mu S_k(t) \\ \dot{I_k}(t) = \alpha_1 K S_k(t)\Theta(i(t)) + \eta_1 E_k(t) - \gamma_1 I_k(t) - \gamma_2 I_k(t) - \mu I_k(t) \\ \dot{E_k}(t) = \mu N_k + \alpha_2 S_k(t) + \gamma_1 I_k(t) - \eta_1 E(t) - \eta_2 E_k(t) - \mu E_k(t). \end{cases} \quad \text{(III.1)}$$

with initial conditions $S_k(0), I_k(0), E_k(0) \geq 0, 1 \leq k \leq \delta$.
It follows from $(H5)$ that $N_k(t) := S_k(t) + I_k(t) + E_k(t)$ is conservative. Then system $(III.1)$ could simplify to the following equivalent system:

$$\begin{cases} \dot{i_k}(t) = \alpha_1 k(1 - i_k(t) - e_k(t))\Theta(i(t)) + \eta_1 e_k(t) - (\gamma_1 + \gamma_2 + \mu) i_k(t) \\ \dot{e_k}(t) = \mu + \alpha_2(1 - i_k(t) - e_k(t)) + \gamma_1 i_k(t) - (\eta_1 + \eta_2 + \mu) e_k(t). \end{cases} \tag{III.2}$$

with initial conditions $i_k(t), e_k(t) \geq 0$, and $i_k(t) + e_k(t) \leq 1$, $1 \leq k \leq \Delta$

III.3 Results and discussion

In our simulation, we considered a scale-free network (proposed by Barabàsi-Albert) of size $N = 1000$. We start our network with $m_0 = 3$ nodes. At each time steep, a new node is added to the network with $m = 2$ links with the already existing nodes according to preferential attachment, the new node connected more likely to the node with higher degree than lower degree. The obtained network will have an average degree $< k >= 4$. All nodes are considered as computers and the links between them represent the corresponding communication channel [16]. The total number of computers is compartmentalized into three sets: S: susceptible internal computers, I: infected internal computers and E: external computers. In our simulation, we used the SIE model [63].

In this chapter, we used the parameters of the model (III.2), which taken as the same values used in [63]: $\eta_1 = 0.1$, $\eta_2 = 0.2$, $\gamma_1 = 0.2$, $\gamma_2 = 0.01$, $\gamma = 2.48$, $\alpha_1 = 0.04$, $\alpha_2 = 0.3$, $\mu = 0.001$, $I(0) = 0.3$, $E(0) = 0.2$. Fig. III.4 illustrates the evolution of the proportion of infected $I(t)$ and external $E(t)$ nodes in the entire SF network at each time-step. In this figure, the proportion of infected nodes increases, until it reaches its maximum. After that, it decreases and tends to a constant value. This can be explained by several factors; like the algebraic form or the network topology [49]. These results are in the good agreement with those obtained in [63].

In the following graph, we will investigate a restricted topology (RSF), where we try to reduce the infected nodes and limit the virus propagation. Fig. III.5 shows the comparison between the SF and RSF. In the first case (SF), the proportion of infected nodes presents a peak (maximum) for low times. This peak disappears in the case of RSF. Moreover, $I(t)$ decreases and remains constant for intermediate and high times in both cases. Hence, the RSF can reduce the virus propagation in a remarkable manner in the low and high times.

For more explanation of this result, we plotted in the Fig. III.6 the impact of the maximum node degree K on the virus propagation. By manipulating the maximum node degree K, can build a restricted scale-free topology more resistible to virus propagation. We can see clearly that the peak which appears in the low time regime decreases with decreasing K until it is disappears for $K = K_c = 62$. The virus computer cannot expand in the whole network, because the proportion of infected node does not exceed the starting value of 30%, but decrease rapidly with time.

For more details, we present in Fig. III.7, the phase diagram of the system in the parameter space (K, I_{max}) of the maximum node degree K and the maximum proportion of infection I_{max}. The phase diagram is a very important tool that allows us to determine how the system varies depending on the control parameters and show the states of a system. In our case, we have a line separating two areas. In the first region $K \leq 62$, the system is resistible to the infection of

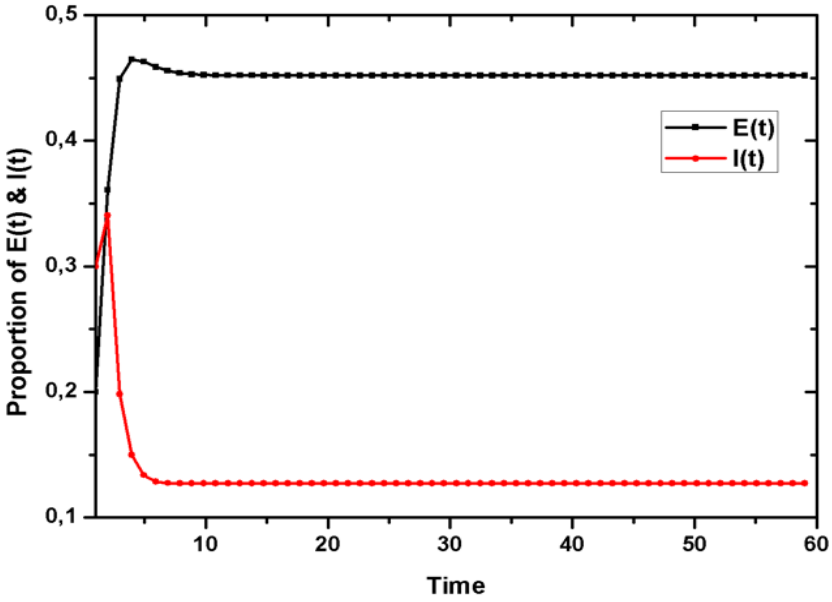


Figure III.4: The evolution of the proportion of infected and external node ($I(t)$ and $E(t)$) in all networks as a function of time t.

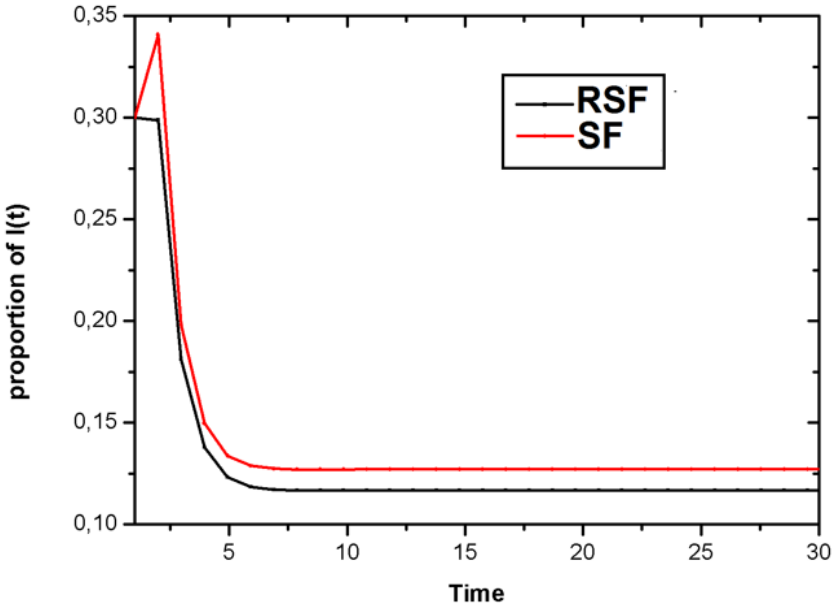


Figure III.5: The evolution of the proportion of infected nodes in two topologies of SF networks as a function of time t.

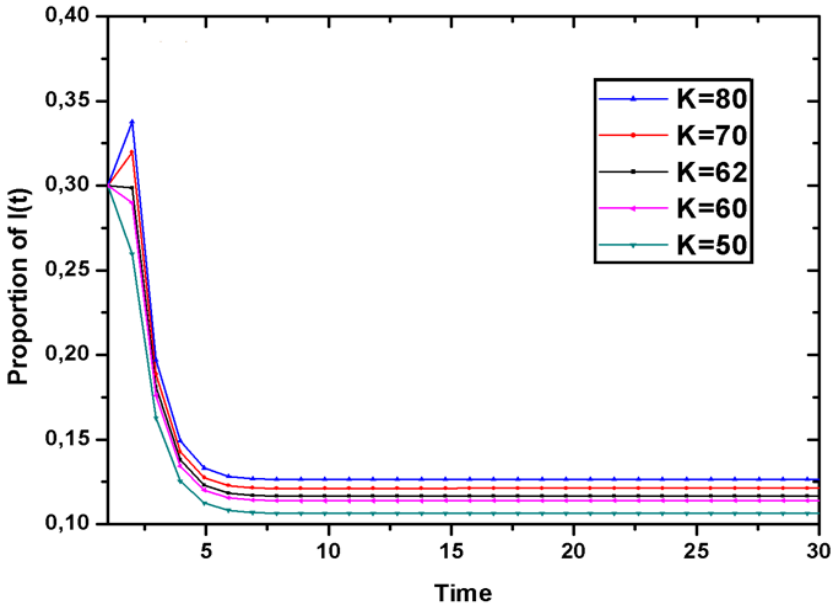


Figure III.6: Impact of variation of maximum node degree (k) on the infected nodes in all networks as a function of time t.

new nodes that are connected to the Internet. $I(t)$ stay constant at a low value. In the second region $K > 62$, the proportion of infected nodes augments with further nodes degree. In this zone the system is more susceptible to infection.

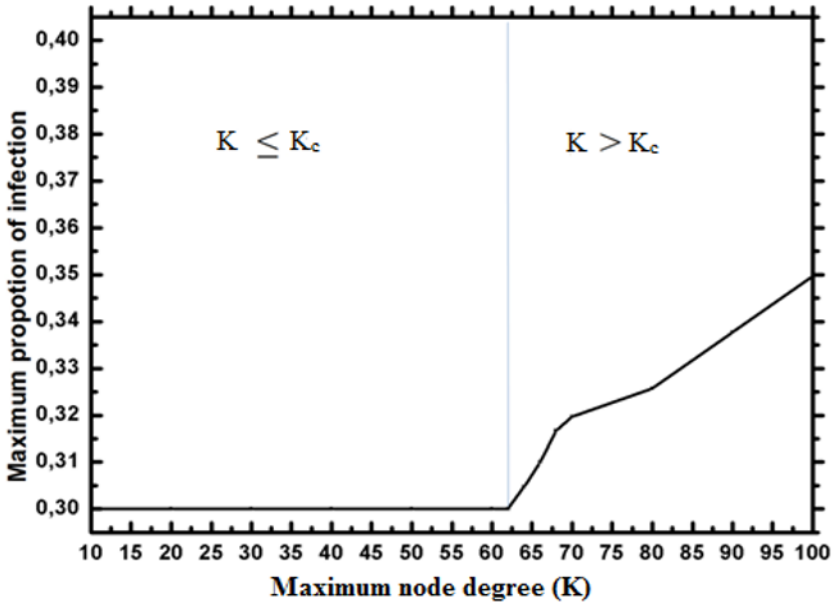


Figure III.7: Phase diagram in the space parameters (K, I_{max}), showing the maximum proportion of infected nodes as a function of maximum node degree K.

Fig. III.8, shows a comparison of virus spreading in the both RSF and ER network with the same size and average nodes degree ($N = 1000, < k >= 4$). On the one hand, the both RSF and ER allow us to reduce the proportion of $I(t)$. On the other hand, the infected nodes in ER are smaller than that in RSF at each time steps. This is can be explained by the fact that RSF

network is more connected than the *ER* network in average nodes degree $< k >= 4$. Moreover, In *ER* model all nodes play roughly the same role [145,146]. In fact, real networks are heterogeneous, when the same nodes have a few connections (peripheral) while some others have a very large number of connections (hubs), which is taken in consideration in the *RSF* model.

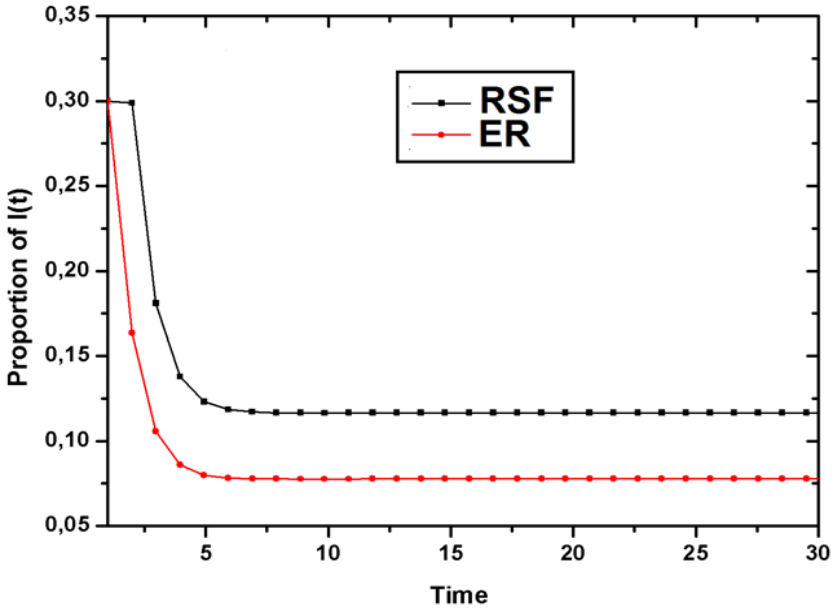


Figure III.8: Comparison between *RSF* and the topology of *ER* network.

Another perceptible result of our study shows that the virus spreading depends strongly on the network size. Fig. III.9(a), shows the maximum infected nodes as a function of the network size. The proportion of infected nodes increases with increasing of the network size. This result can be explained by the fact that high node degrees (hubs) acquire more new links where the network size is increased with more connections between them, which favor the proportion of infected nodes. In addition, Fig. III.9(b) displays the relation between network size and K_c. The fit indicates the existence of a strong relationship between the two parameters, where the dependence is almost linear. Hence, the network with low size is more effective to reduce the proportion of infected nodes.

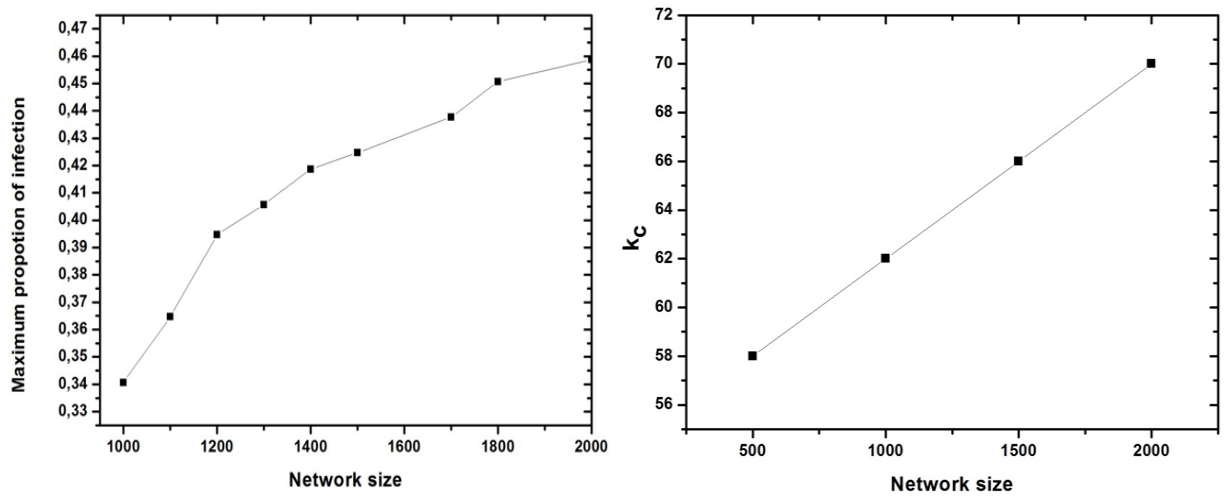


Figure III.9: The impact of network size on the proportion of infected nodes. Maximum proportion of infection versus size network (a), K_c versus size network (b).

III.4 Conclusion

In summary, we studied the virus spreading in SF network with different topologies. We have focused on the proportion of infected nodes in these networks. For this reason, we used a restricted scale-free network (RSF) based on the limitation of the higher node degree (k).

The main result shows that the network topology influences the virus spreading, where, the nodes with higher degrees are more susceptible to the infection than others. To resolve this problem, we determined a critical maximum value of nodes degree (K_c), below which the virus computer cannot expand in the whole network. Moreover, we find that certain properties of networks like size can influence the virus spreading. The proportion of infected nodes increases with increasing the network size.

CHAPTER IV

SELECTIVE EPIDEMIC VACCINATION UNDER THE PERFORMANT ROUTING ALGORITHMS

IV.1 Introduction

Thanks to the increasing attention to large communication networks, the transportation in communication networks such as the Internet and urban networks may be considered of practical importance, despite the problems that remain unresolved in different complex networks. Finding efficient strategies for traffic routing is considered to have significant issues we have to address. The traffic jamming transition in the Internet was first observed and analyzed in 1996 [147]. It has been found that both structural characteristics of the underlying network [148] and the routing algorithm of traffic [30–33, 37–39, 111, 114, 149–151] influence the performance of transportation. Indeed, the optimal performance of transportation relies robustly on the two characteristics mentioned above. These characteristics are more beneficial compared with the high cost of changing the infrastructure of a network.

In order to enhance the traffic flow and avoid the traffic congestion in large growing communication networks, many traffic models have focused on developing better packet routing strategies. These traffic models have been presented to describe real traffic systems by introducing the concepts of packet generating rate R, with randomly selected sources and destinations of packets [113, 152]. At the critical packet generating rate R_c, a continuous phase transition from free flow state to congested state occurs. In the free flow phase, the numbers of created and delivered packets are balanced, leading to a steady state; while in the congested phase, the number of accumulated packets increases with time, due to the limited delivering capacity or finite queue length of each node. In those works, packets mainly are forwarded according to two broad classes of routing strategies. In the first class, the packets are forwarded based only on local information: the local routing strategy [39, 149]. In contrast, the second class deals with information from the whole network such as: the shortest path strategy [39, 149, 150, 153], the efficient path strategy [37] and global routing strategy [38].

The importance of the study of complex networks is justified by the different phenomena that occur on these networks, such that epidemic spreading. Indeed, The Human society has suffered from various viruses that have to do with human nature; such as AIDS, $H1N1$ influenza and viruses that have to do with technological development such as computer viruses [127].

Much researches have been done to understand the dynamic process of epidemic spreading on complex networks [43, 49, 67, 154–159].

Many works have been concentrated on the traffic driven and epidemic spreading. The first work on the traffic-driven epidemic spreading was achieved by Meloni et al. [59, 60], who found that the behavior of agents influences the disease spreading. Meanwhile, Yang et al. in [66] treated the relation of outbreak time associated with traffic-driven epidemic on the complex network. In a different work, they observed that the epidemic spreading can be totally under control by two strategies; the local routing strategy [68] and the efficient routing protocol [69]. In [70], the authors proposed a method to delete the traffic-driven epidemic spreading by properly removing some edges in the network. Furthermore, another research [160] mentioned the effects of the exponent of the power-law degree distribution on the traffic-driven epidemic spreading.

The effect of routing algorithm strategies on epidemic spreading in complex networks has been ignored and has not received an adequate attention. This reason motivated us to get along to study this topic. In this chapter, we studied the effect of the different routing algorithm strategies on epidemic spreading in complex networks. Our results have shown that the performant routing algorithms mainly: efficient path (EP) strategy and global dynamic (GD) routing strategy favor the virus spreading more than the case where the shortest path algorithm (SP) is used especially in the free flow phase. For the congested phase, even a small value of the infection probability rate β, the whole network becomes globally infected with all the studied routing algorithms.

Since the performant algorithms routing favor the propagation of virus more than the SP strategy and instead of a random vaccination, we proposed a new method of anti-virus vaccination that helps us to still use performent algorithms routing strategies with an acceptable level of protection against virus spreading without affecting the traffic transport efficiency.
We noted that some previous studies [68, 69], have tried to modify the routing rules to limit the virus spreading, but the negative point of these attempts is, the reduction of the traffic transport efficiency. And our method proposed a solution to overcome this drawback, by limiting the virus spreading without impacting the efficiency of the traffic capacity.

IV.2 Model and methods

IV.2.1 Network structure

In this chapter, we use the famous model of Barabàsi-Albert to generate a scale free network. In this model, we start to build the network with m_0 nodes fully connected. Then at each time step, we add a new node. The network develops continuously over time (the growth concept), and set up m new links with the existing nodes according to the preferential attachment (see Sect. I.6.5). It is well know that this procedure generates a scale free network with a power law degree distribution characterized by the existence of high degree nodes (called hubs) and low degree nodes (called peripheral nodes).

IV.2.2 Traffic dynamics

In a given network, at each time-step, R new packets are generated with randomly chosen sources and destinations, and each node can deliver at most C packets towards their destinations (we set $C = 1$). Packets are forwarded according to a given routing algorithm protocol. The queue length of each node is assumed to be unlimited. The first-in-first-out principle applies (FIFO) to the queue. Each newly generated packet is placed at the end of the queue of its source node. The packet is removed from the system when it reaches its destination.

Routing schemes:

In this work, we consider three routing schemes:

Shortest path (SP) routing algorithm "Dijkstra problem":

The most popular algorithm that allows the determination of a unique SP between two nodes in directed/undirected weighted graphs (with positive cost) is Dijkstra algorithm. However, many other algorithms are meant to solve the problem of the SP in a given graph [161, 162]. For instance, the Bellman-Ford algorithm that tolerates negative weights unlike Dijkstra algorithm, the Floyd-Warshall Algorithm and the Genetic Algorithm which is based on biological evolution and that may give different solution at each execution which might be an advantage over the others [163–165].

Since we are not interested in negative weight costs, and due to the acceptable execution time of Dijkstra algorithm, we have implemented this algorithm to find when needed the SP in our simulation programs.

Dijkstra problem:

To explain how Dijkstra algorithm does works, let's consider the weighted graph $G(V,E)$ and $w : E \rightarrow R$ is the corresponding weights function $w(e)$ associating each edge $e = (u;v)$ between two nodes u and v, to a real positive value weight.

We define the two following terms:

- **The length of the path :** $p = \langle v_0; v_1; ...; v_k \rangle$ is the sum of the weights of its constituent edges :

$$lengh(p) = \sum_{i=0}^{k} w(u,v)$$

- **The distance :** The shortest distance or simply the distance from a vertex u to another vertex v, denoted $\delta(u,v)$ is equal to infinity.

The problem :

Given a weighted graph with positive edge weights $G = (V;E)$ and a distinguished source vertex, $(s \in V)$, we aim to determine the distance and the SP from the source s to every other node in the graph G.

1. Initialisation
   At the beginning, we have to set the following tables:
   $d[v]$: which is an estimation of the length $\delta(s,u)$ of the SP for each vertex v from s, in other words it is the shortest known between the source s and the vertex v. Initially, $d[s] = 0$ and $d[v] = \infty$ for all other vertices, and at the end of the algorithm the estimation should match with the actual distance such as :

$$d[v] = \delta(s,v); \forall v \in V$$

$Prev[v]$: The previous, the predecessor or parent array; it is the previous node to reach u from s through the shortest known (discovered) path. Notice, that $Prev[v]$ is also the next step from v if we are going in the opposite direction i.e. from the node v to the node s. Initially, we don't have this information as result, we set $Prev[v] \equiv None;\ v \in V$.
$Visit[v]$: When the algorithm is seeking for the SP, this table indicates whether the node v was visited or not visited yet; it takes the value "Yes" if it has been already visited and "No" if not. Initially $Visit[v] \equiv No; \forall v \in V$.

2. The progress
In order to establish the SP and the distance to any v from s, the algorithm will visits and treats the nodes one by one in some order; we start the proceeding of the vertices from the closest vertex to the source. It is simply the neighbor $\in Adj[s]$ which is linked to s with the minimum weight. Then we treat all remaining neighbors from the nearest to the furthest (minimum to the maximum weight).
Once all the adjacent vertices have been explored, we move to the next neighbors and treat them following the same order priority i.e. beginning always from the closest. We continue until all the nodes are visited.
Visiting a node u means that when its turn comes, we compare the old known estimated path with the path passing through that node u. If it is better than the current value (lower cost), we update the distance $d[v]$ and that of all the other neighbors of u if necessary. The process by which an estimated distance is updated is called relaxation.

The relaxation
To decide whether we update $d[v]$ or not, we have to compare the current value of $d[v]$ and total weight of the path from s to u, plus the weight of the link $[u,v]$. We do the relaxation only if the new path from s to v is shorter than $d[v]$. if it is the case, then we replace the old path $\langle s;....;x;v\rangle$ with the new SP $\langle s;....;u;v\rangle$ and u becomes the previous node to v from s instead of x (see Fig. IV.1)
If

$$d[u] + w(u,v) < d[v]$$

then

$$d[v] = w(u,v) + d[u]$$

and

$$Prev[v] == u$$

formerly

$$Prev[v] == x$$

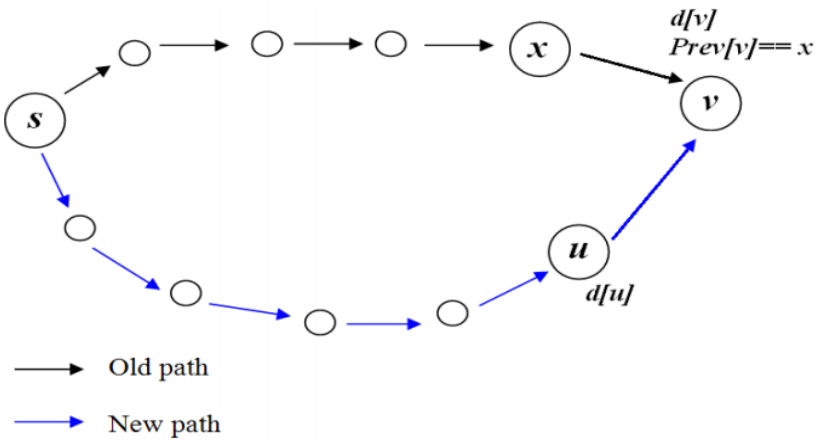


Figure IV.1: Illustration of the relaxation proceeding performed when discovering new path with less cost.

Remark: During the algorithm process, always the estimation $d[v] \geq \delta(s,v)$ and $d[v]$ equals to the length of the shortest discovered path.

3. End of the algorithm
   When all vertices have been treated, for all the vertices the estimation is validated as being the real shortest distance. Thus, $d[v] = \delta(s,v)$ and no further relaxations are done. Of course if s and v aren't connected $d[v] = \delta(s,v) = \infty$.
   $Pred[v]$ now indicates the closest neighbor of u to the source s. Which means that the table $Prev[v]$ gives the shortest sequence of nodes from s to u and vice versa.

Efficient path (EP) routing algorithm:
The EP routing scheme is a routing model proposed by Gang Yan et al [37], which can reach a very high capacity compared to the SP strategy.
In this model, can be as redistributing traffic load in central nodes (hubs) to other non-central nodes (peripheries). The authors define "the efficient path" as any path between node i and node j as $P(i \longrightarrow j) := i \equiv x_0, x_1, \cdots, x_{n-1}, x_n \equiv j$, define :

$$L(P(i \longrightarrow j) : \beta) = \sum_{i=0}^{n-1} k(x_i)^{\beta} \tag{IV.1}$$

Where $k(x_i)$ is the degree of node x_i and β is a tunable parameter. The efficient path between i and j is corresponding to the route that makes the sum $L(P(i \longrightarrow j) : \beta)$ minimal. It is clear that $L(\beta = 0)$ recovers the shortest path routing strategy. It is expected that the system behave better under the routing rule with $\beta > 0$ than under the shortest path routing strategy. As well as, they concerned how R_c, that is, the critical number of generated packets at each time step, varies with β. Here, $R_c = N\rho_c$. The simulation results for the critical value R_c as a function of β on BA scale-free networks are illustrated in Fig. IV.2. It can be found that R_c firstly increases with β and then decreases, with the maximal R_c corresponding to $\beta = 1$. As compared to the shortest path routing strategy ($\beta = 0$), the traffic capacity is greatly improved, from $R_c \approx 4$ when $\beta = 0$ to $R_c \approx 45$ when $\beta = 1$, more than ten times.

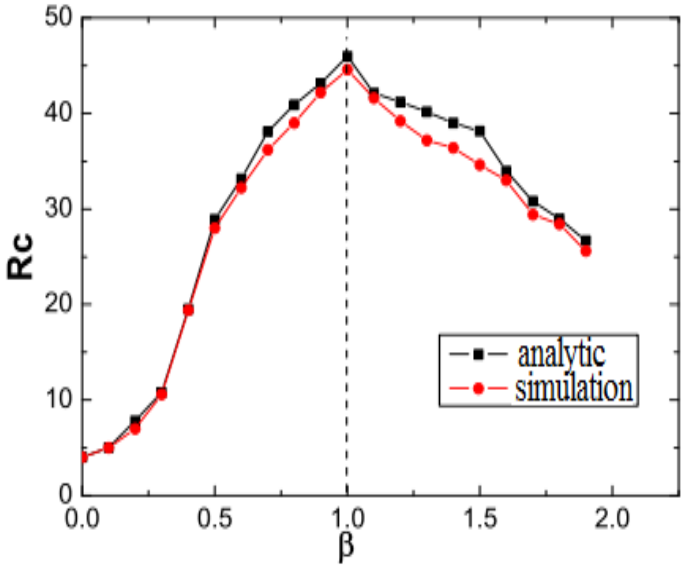


Figure IV.2: The critical R_c as a function β for scale-free networks with size $N = 1225$. Both simulation and theoretical analysis indicate that the maximal value of R_c corresponding to $\beta \approx 1$. The data shown here is the average over 10 independent runs [37].

Global dynamic (GD):

The GD routing scheme is a routing model proposed by Xiang Ling et al [38]. That can reach a very high capacity compared to the SP strategy and the EP. In fact, under this strategy, the capacity of handling the traffic is much larger than other previously known routing methods. In this model, packets are forwarded through the path with the least traffic charge; the path between the source i and the destination j of a packet is denoted as :

$$P(i \longrightarrow j) = min \sum_{i=0}^{l} [1 + q(x_m)] \tag{IV.2}$$

Where $q(x_m)$ is the queue length of the node x_m and l is the path length. Notice that when the traffic load tends to zero the model degenerates to the minimum hop routing (SP). All the results and the figures presented in this subsection are taken from [38].
In order to prove the efficiency of this routing over other routing strategies, the authors compare between the performance of the traffic in BA networks, using the SP, the EP and the GD as routing protocols under the same conditions; the network size $N = 500$ and average degree $\langle k \rangle = 4$.

The Figs. IV.3(a), IV.3(b) and IV.3(c) displays the total number of the packets within the network as a function of time step for the three routing protocols (SP, EP and GD) respectively. In accordance with the definition of the critical packets generation rate R_c, the number of packets information is still in balance at $R = R_c$ (The small red triangles graphs). This balance is automatically lost at $R = R_c + 1$ (blue scares graphs). In Fig. IV.3(d) represents the order parameter η versus the packets generation rate under the three routing strategies. Clearly, the network capacity under the SP is the smallest ($R_c = 3$), followed by that of the EP ($R_c = 20$) and on top, the GD with a very high capacity ($R_c = 41$), this capacity exceeds the double of the capacity under the EP (Fig. IV.3(d)).

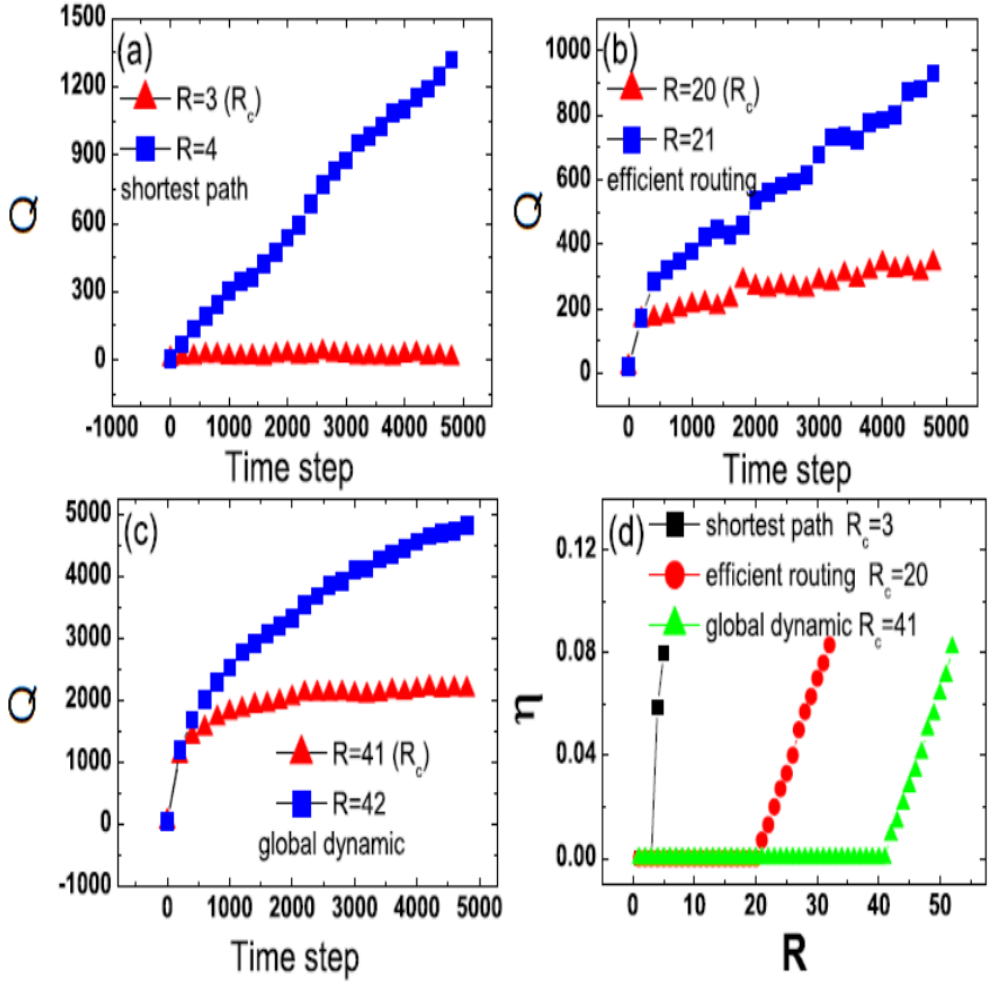


Figure IV.3: Evolution of the packet number in the network under different routing strategies. (a) SP, (b) EP, (c) GD. (d) The order parameter η versus R under the three routing strategies [38].

The authors demonstrate also that the network capacity increases with increasing connectivity rate as well as with increasing network size for all the three routing methods. As we can see from the Fig. IV.4, the ranking of the network capacity remains the same ($GD > EP > SP$) for both cases i.e. increasing the connectivity rate or the network size.

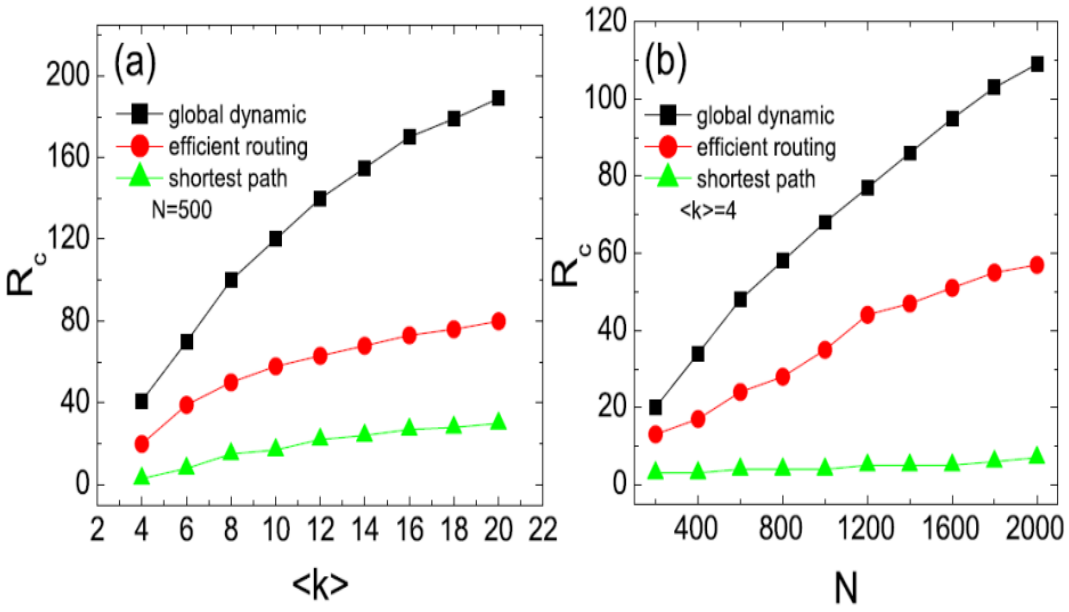


Figure IV.4: The network capacity R_c vs the average degree $\langle k \rangle$ under the three routing strategies (a). The network capacity R_c vs the network size N with the same average degree $\langle k \rangle = 4$ (b) [38].

IV.2.3 Epidemic spreading

The interest of the previous studies on the Epidemic spreading was mainly on how the network topology affects the epidemics [42, 142]. Indeed, the typical approach is to assign a certain probability of infection to each link originating from an infected node. In many realistic situations, even when there is a link connecting two nodes, the infection will not propagate unless some kind of traffic happens between the nodes. Following this logic, we have implemented the Susceptible-Infected (SI) model in which the nodes can be divided into two states: either susceptible (S) or infected (I). Beginning with an initial proportion of infected nodes $i_0 = I_0/N$, the infection spreads in the network through packet exchange. The entire packets in an infected node are infected and similarly all the packets in a susceptible node are uninfected. Once a susceptible node receives a packet from an infected neighbor node, it has the probability β of being infected (Fig. IV.5).

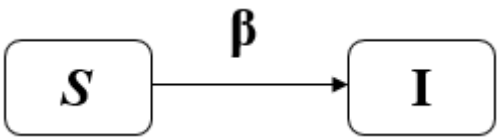


Figure IV.5: Schematic representation of an SI model with an infection probability β

On the other hand, and in order to study the vaccination process, we have implemented the Susceptible-Infected-Susceptible (SIS) model (Fig. IV.6). In this model, the node can be in two states, Susceptible (S) or Infected (I), we target the infected nodes by vaccinated them with anti-virus. In our model, the non-infected nodes are not vaccinated and can be reinfected after a potential vaccination. We assumed that a vaccinated node can transform again to a susceptible node at a rate μ (we set μ=1, one node is disinfected per unit time). To vaccinate our

network, we distinguish between two types of vaccination intervention: a random vaccination (RV) which is generally used in the literature [60, 66, 68–70] where the nodes to be vaccinated are chosen at random with μ=1, and a selective vaccination (SV) where we select nodes to be vaccinated from a preferential distribution probability:

$$P_i = \frac{k_i^\alpha}{\sum_j k_j^\alpha} \tag{IV.3}$$

Where k_i is the degree of node i and α is a control parameter. The choice of the nodes to be vaccinated is done under the constraint of an average rate $\mu = 1$ per unit time.

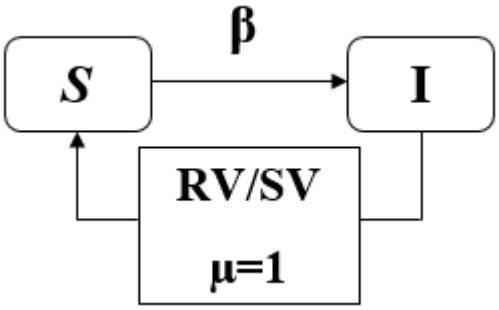


Figure IV.6: Schematic representation of the SIS model with the two adopted vaccination methods: random vaccination (RV) and selective vaccination (SV) with an average vaccination rate $\mu = 1$.

IV.3 Results and discussion

In our simulations, we applied the traffic driven epidemic spreading using the Barabási-Albert network with size $N = 500$. We started our network with $m_0 = 3$ nodes. At each time step, a new node is added to the network with $m = 2$ links with the already existing nodes according to preferential attachment. We considered three routing algorithm strategies: Shortest path (SP) [164], Efficient path (EP) with the optimal parameter value ($\alpha = 1$) [37] and Global dynamic (GD) [38].
For the three routing schemes, we have done simulations with $R = 4$ packets corresponding to the free flow phase and $R = 50$ for the congested phase.

IV.3.1 The SI model

We used the SI model (Fig. IV.5) to study the effect of virus spreading in the network with fixed size $N = 500$ constructed according to the procedure described above, with different routing algorithms.

In Fig. IV.7, we have plotted the evolution of the proportion of the infected nodes (i) for different routing algorithm strategies in all the network as a function of time, in the free flow phase ($R = 4$), by taking different values of β. We can notice in the three graphs (Figs. IV.7(a), IV.7(b) and IV.7(c)), that the infection proportion is higher in the EP strategy compared to the two others strategies (SP, GD); and it is possible to say that in both the EP and the GD schemes,

the viruses spread more rapidly than in the SP algorithm.
This fact can be explained by the following reason. In the SP algorithm, packets try to navigate from source to destination following the shortest paths by traversing a minimum number of intermediate nodes. In contrast, when either the EP and GD algorithms are used, packets try to avoid congested nodes by using more intermediate noncongested nodes following longer paths. As a result, the infected packets have the chance of being in contact with a great number of uninfected nodes. So, the virus will have more opportunity to spread in the network. Indeed, the results of many authors show that the average path length and the average packet travel time of performant algorithms are larger than those of SP scheme. As an example, we cite the results of the following algorithms: EP [37], GD [38], OR [151] and the SAPR algorithm [30, 31]. Hence, as an important result, we can say that the performant algorithms (EP and GD) which are supposed to avoid congestion, are actually more sensible to epidemic spreading.

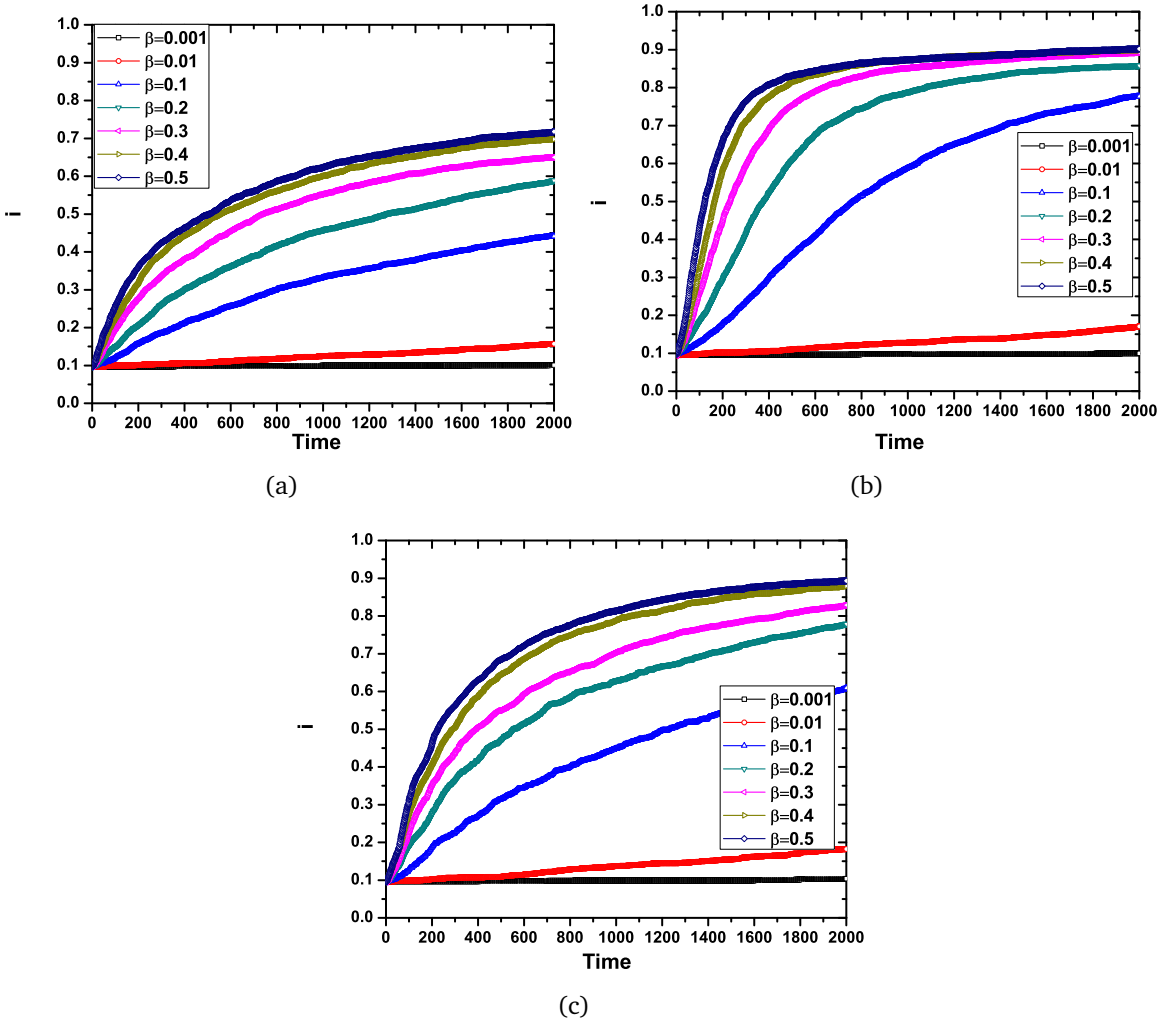
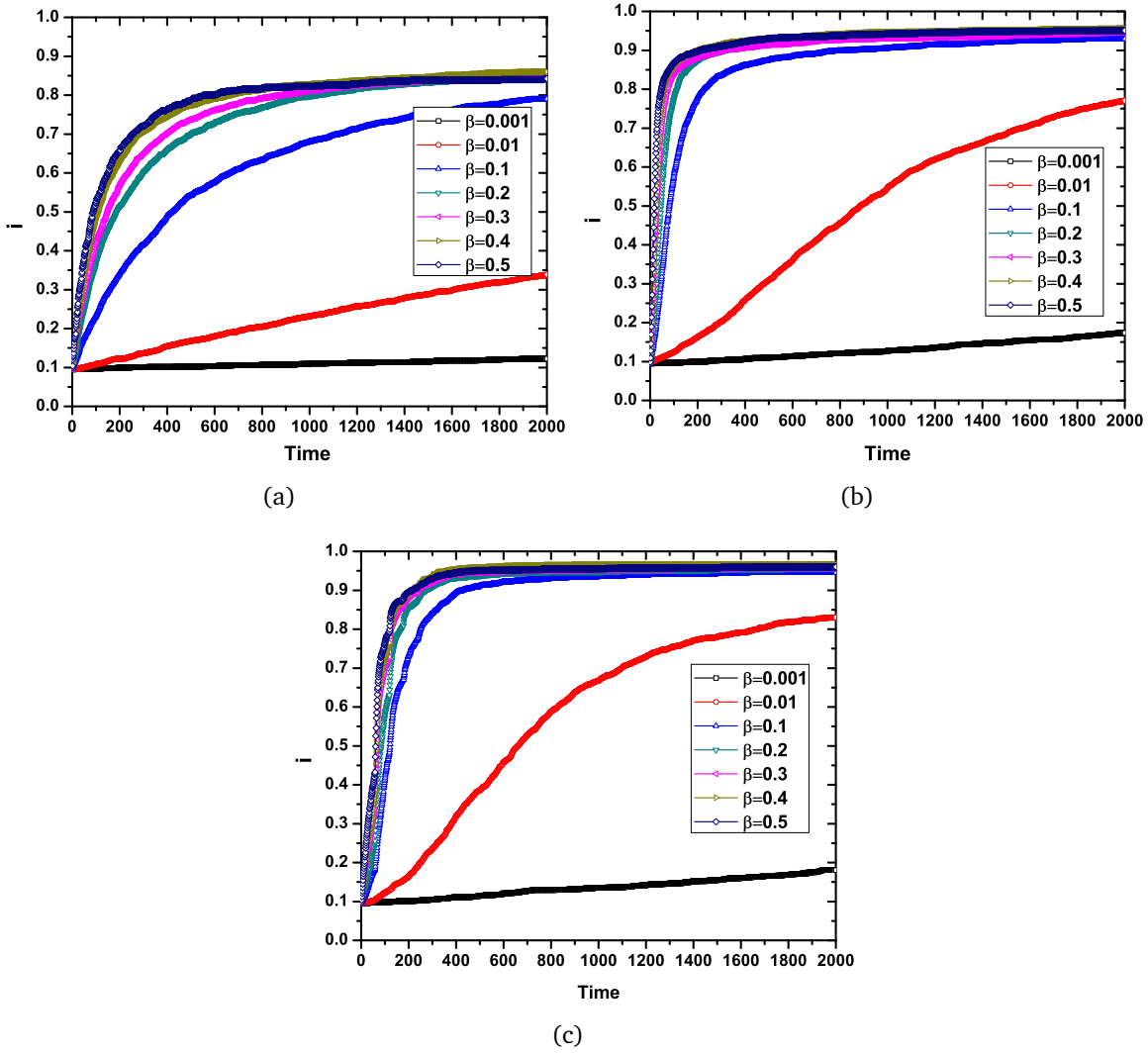


Figure IV.7: The proportion of infected nodes (i) in the whole network as a function of time in free flow phase, for $R = 4$, with an initial proportion of infected nodes $i_0 = 0.1$ in the framework of the SI model using the routing algorithms: SP (a), EP (b), GD (c).

In the congested phase ($R = 50$), Fig. IV.8 illustrates the evolution of the proportion of infected nodes (i) for different routing algorithm strategies in all the network as function of time, for different values of β. Fig. IV.8 shows that in the congested phase, the three algorithms favor

the virus spreading, and we also remarked that the epidemic spreading is more pronounced in the free flow phase, especially for the (EP and GD) schemes. Moreover, we can see that for low values of the infection probability β, the virus propagates more slowly (the same remark holds also for the free flow phase (Fig. IV.7)).



(a) (b)

(c)

Figure IV.8: The proportion of infected nodes (i) in the whole network as a function of time in the congested phase, for $R = 50$, with an initial proportion of infected nodes $i_0 = 0.1$ in the framework of the SI model using the routing algorithms: SP (a), EP (b), GD (c).

In order to see the effect of the infection probability β on the virus propagation, we have presented in the IV.9, the proportion of infected nodes as a function of β, at a given observation time ($t = 1200$) in the two phases (free flow and congestion phases).
We see clearly in Fig. IV.9 that the EP (Fig. IV.9(b)) and GD (Fig. IV.9(c)) algorithms have a similar behavior in contrast to SP algorithm (Fig. IV.9(a)), where the maximum proportion of infected nodes saturates at lower values in both free flow and congested traffic phases. We also noticed in GD and EP algorithms that the proportion of infected nodes saturated for small values of β compared to the SP algorithm. This result shows that the two performant algorithms (EP and GD) are very sensitive to small values of the infection probability β compared to the SP scheme.

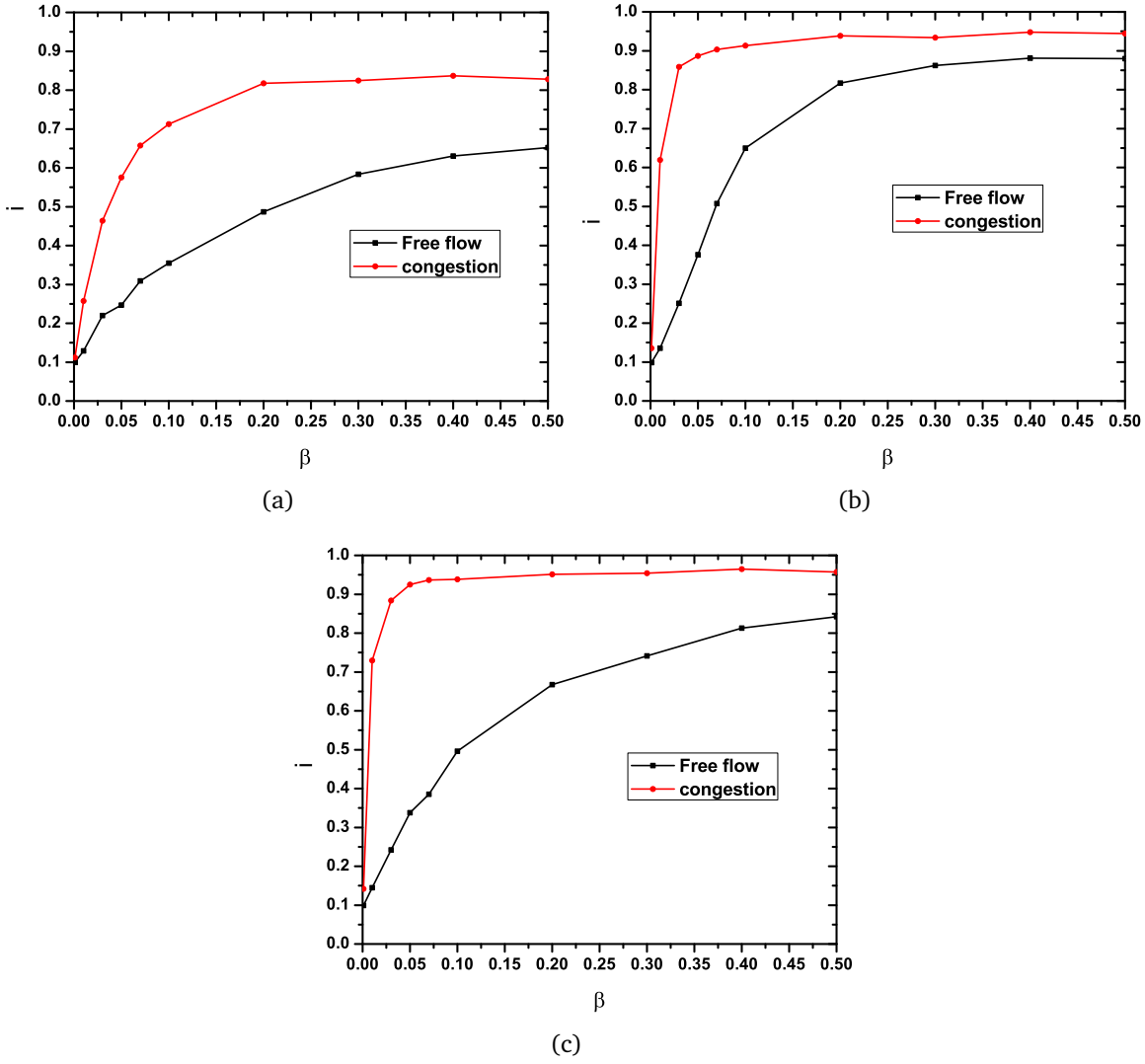


Figure IV.9: The proportion of infected nodes (i) as a function of infection probability β for different phase at observation time ($t = 1200$), with initial proportion of infected nodes $i_0 = 0.1$ under the SI model using the following routing algorithms: SP (a), EP (b), GD (c).

After investigating how the virus spreads in the whole network using different routing algorithm strategies (SP, EP, GD), the question now is how we can limit the propagation of the virus. For this end, the natural model to use is the SIS model(see Fig. IV.6).

IV.3.2 The SIS model

This model is based on the SI model accompanied with anti-virus which operates on the network nodes. We assumed that nodes are vaccinated at a rate $\mu = 1$. Each vaccinated node becomes again susceptible. Moreover, if we have an infected node, this means that all the packets in this node are assumed to be infected and the same principal holds for susceptible nodes.

According to the previous results, we can conclude that the performant routing algorithms (EP, GD) present qualitatively the same behavior with respect to virus propagation. So, in the following, we will concentrate just on the comparison between the SP and the EP algorithms. Our simulation will be limited to the free flow phase, because our aim is to try to stop the virus spreading in the entire network at its first appearance. To vaccinate the network, we will use the two methods mentioned in the model: random and selective vaccination (RV and SV).

IV.3.2.1 Random vaccination (RV)

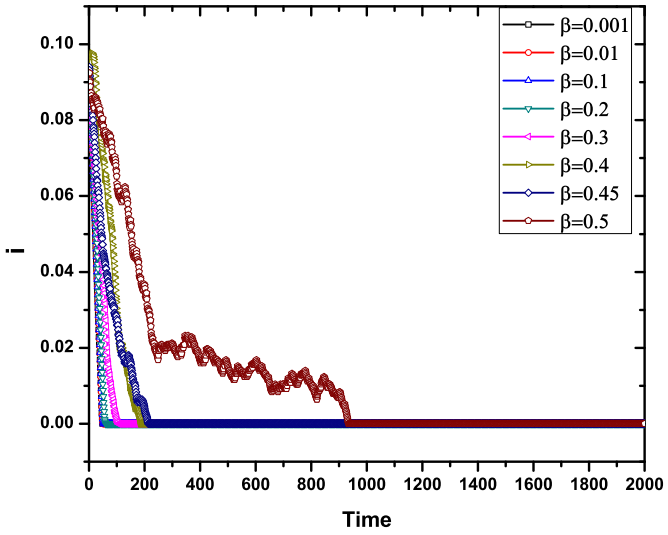
In the literature, most authors [60, 66, 68, 70] have used the random vaccination. And to our knowledge, no work has been performed on selective vaccination, which we will try to prove that it is more effective when used in conjuction with more performant routing algorithms such as EP and GD schemes.

In Fig. IV.10, we have presented the proportion of infected nodes as a function of time in the whole network, with different values of infecftion rate β, by using random vaccination within the framework of the SIS model.
In Fig. IV.10(a), we see clearly that for the SP algorithm, after a transient time, the virus is completely removed from the network. This disinfection time increases with the infection probability β. In contrast, the EP algorithm succeded in removing the virus only for small values of the infection rate $\beta < 0.4$; while for larger infection rates, the virus continues spreading in the network and the random vaccination fails to eradicate the virus (Fig. IV.10(b)).

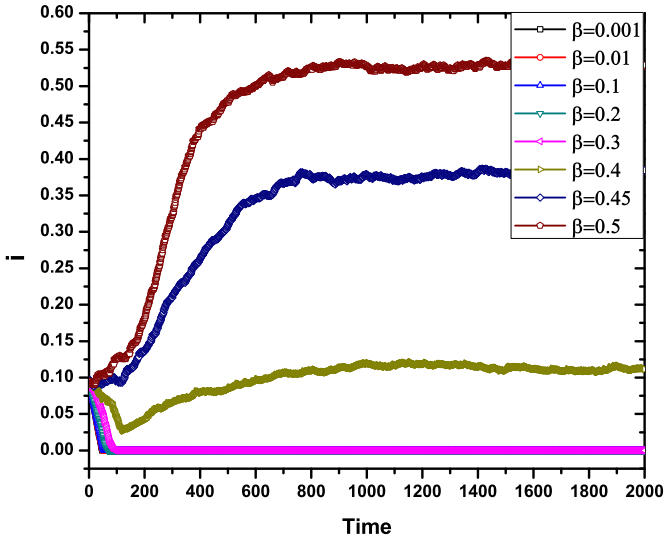
Hence, the random vaccination in the network is efficient in removing the virus only when used in conjuction to the shortest path routing strategy. But when one tries to use a more efficient routing protocol such as the efficient path routing strategy, a simple random vaccination is clearly inefficient and can't suppress the virus, except for the trivial case of small infection rates. Now, our goal in the next subsection is to find an optimal method of vaccination that is better than random vaccination which can be used with performant routing protocols.

IV.3.2.2 Selective vaccination (SV)

A selective vaccination refers to a process, in which we choose an infected node to be vaccinated by using a suitabe preferential probability distribution (see Eq. IV.3) with a tunable parameter whose value is to be chosen such that to target specific types of node. For $\alpha > 0$, we targetted the high degree nodes (hubs) in the network, and when $\alpha < 0$, the peripheral nodes are targetted instead. And if $\alpha = 0$, the SV reduced to the random vaccination (RV) procedure. The selection



(a)

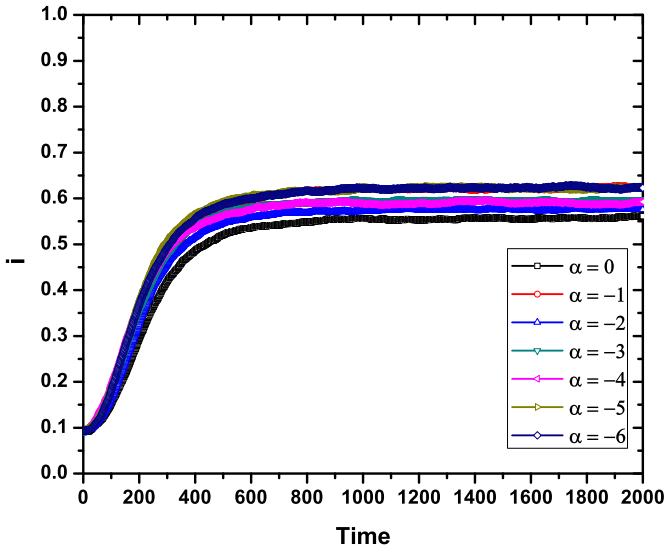


(b)

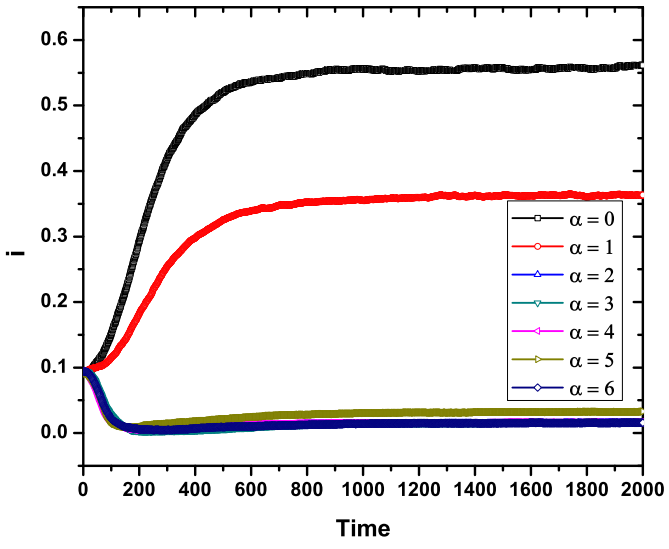
Figure IV.10: The proportion of infected nodes (i) in the entire network as a function of time in free flow phase, for $R = 4$, $i_0 = 0.1$, by using the random vaccination within the SIS model using the two routing protocols: SP (a), EP (b).

of nodes to be vaccinated is done under the overall constraint of average $\mu = 1$ vaccinated node per unit time.

Our simulation results are shown in Fig. IV.11 where we plotted the proportion of infected nodes (i) as a function of time, by fixing the probability of infection $\beta = 0.5$, with different value of the control parameter α using selective vaccination (SV) within the SIS model.
We see clearly in Fig. IV.11(a) that when the vaccination targetted the peripheral nodes ($\alpha < 0$), the proportion of infected nodes is comparable to the random vaccination (RV) case ($\alpha = 0$); that is the virus continues spreading in the network. In the other hand, when we targetted the hubs in the network, the proportion of infected nodes is strongly limited for $\alpha < 2$, and completely removed for $\alpha \geq 2$ (Fig. IV.11(b)). To get more insight into this result, we presented in



(a)



(b)

Figure IV.11: The proportion of infected nodes (i) as a function of time, using the EP strategy in fee flow phase, for an initial proportion of infected nodes $i_0 = 0.1$, $\beta = 0.5$, using the selective vaccination within the SIS model: targetting the peripheral ($\alpha < 0$) (a), targetting the hubs ($\alpha > 0$) (b).

Fig. IV.12 the proportion of infected nodes as a function of the control parameter α, for a given

observation time ($t = 1200$) and infection rate $\beta = 0.5$.
When we targetted the peripheral nodes ($\alpha < 0$), no noticeable difference is observed compared to the random vaccination case. In contrast, when the vaccination targetted the hubs ($\alpha > 0$), we see a very ramarkable drop of the proportion of infected nodes towards a very nonsignificant value indicating that the virus is succefully suppressed from the whole network with the vaccination process.
As a conclusion, we can say that a preferential vaccination oriented towards the hubs is more suitable for eradicating the virus when using an EP algorithm. We notice also that we obtained similar results for the GD algorithm.

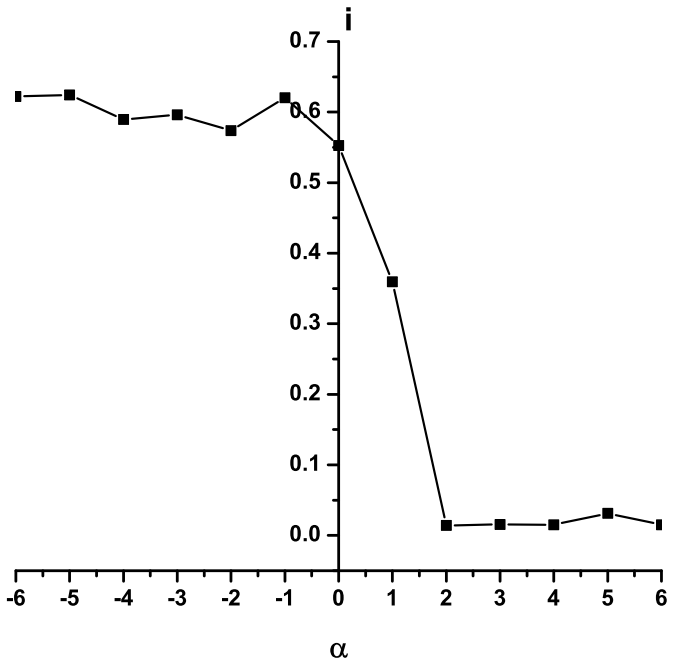


Figure IV.12: The proportion of infected nodes (i) as a function the control parameter α by used EP algorithm in the free flow phase, for an initial proportion of infected nodes $i_0 = 0.1$, an infection rate $\beta = 0.5$, at time $t = 1200$, by using the selective vaccination within the SIS model.

In the previous works that concentrated on the control of the virus spreading mentioned in [68,69], the authors proposed some methods that have the ability to limit the virus spreading, but as a drawback, they reduced the traffic capacity efficiency. For example, in [68], the authors used the efficient path scheme to suppress the virus in the network by modifying a routing parameter. But, they propose another optimal tunable parameter γ that leads to a maximal epidemic threshold. As a consequence, they automatically reduced the network capacity of the efficient path algorithm. The reason why they are constrained to do so because is that there exists no value of γ where they can obtain in the same time a traffic efficiency and a virus suppression optimality. Through our proposed method with a selective vaccination, we could limit the virus spreading when we use the efficient path scheme, without any modification in the parameter γ that gives an optimal traffic capacity.

We conclude that our method of vaccination is useful for virus removal when used along with a performant routing algorithm without the drawback of reducing the capacity of transport efficiency. This result is not limited to these two protocols, but is general for the performant

algorithms as they share the commun feature of using longer but efficient paths for sending information traffic.

IV.4 Conclusion

To sum up, we have focused on the propagation of virus in complex networks and specifically on traffic-driven epidemic spreading and have studied the effects of routing algorithms strategies.

Our main result has shown that the performant routing algorithms (EP and GD) strategies which are used to overcome the congestion problem, favor in fact the virus spreading. We found that the performant routing algorithms favor the virus spreading more than the case where the shortest path algorithm (SP) is used. To eradicate the virus spreading, we used the SIS model in the free flow regime.

Our results show that a random vaccination succeeded in suppressing the virus for the SP scheme and fails for the EP algorithm. However, when we used a preferential selective vaccination, which targets the hubs, we arrive at eradicating the virus for some preferential control parameter α. With this procedure, we recover the performance of the EP (and also the GD) algorithms without the drawbacks of its sensibility to virus spreading and without affecting the traffic transport efficiency.

CHAPTER V

BORDER ROUTING IN INTERCONNECTED NETWORKS

V.1 Introduction

In reality, networks rarely appear in isolation. For example, in epidemiology, diseases can spread within populations but can also transition to other populations, even to different species. In transportation networks, there are typically highway, bus, train and airplane networks covering the same areas but behaving differently [97]. Moreover, the way in which one network affects another is not trivial and often specific nodes in one network interact with specific nodes in another network. This leads to the concept of interacting networks in which links exist between nodes within a single network as well as across networks.

Although many studies has been conducted on the problem of traffic congestion, the focus of most previous work has been on isolated networks over the past decade [33–35, 41]. However, many infrastructure networks in the real world are actually coupled together or interacting with each other. In order to model the interactions between real-world networks, several coupled network models have been developed [28, 29, 58, 166]. In [167], the authors proposed a theoretical model of interdependent networks. As another kind of coupling model, the interconnected networks contains coupling links that are physical links between networks and provide paths for traffic transmission [56, 168]. In another works concerning the traffic congestion, in [57] the authors show the effect of interconnections on traffic congestion in interconnected Barabási-Albert scale free networks. Moreover, in [58], the authors analytically prove that the structure of multiplex networks can induced congestion for flows that otherwise would be decongested if the individual layers were not interconnected.

Inspired by previous studies of traffic congestion in isolated networks and the newly developed works of interconnected networks. In addition, we notice that the effect of routing algorithms strategies on interconnected networks has not received an adequate attention. This reason motivated us to get along to study this topic. In real situation, the interconnected networks have different administrative routing policies [21]. Unfortunately, these policies present some problems; such as difficulty of exchanging and updating information about the subnetworks for all routers, and information exchange has also a high economic cost. To overcome this drawback, the Internet used a well know routing protocol between different Autonomous Systems (AS). This routing protocol is called the Border Gateway Protocol (BGP) [71]. In this paper, we to use a simplified model version of this protocol, which keeps separated the

two administrative authorities implemented in each network separately, and introduce rules for the exchange of information between the two networks. Our main results show that approximately similar performance is obtained without the extra cost and load of global routing protocols between the border routing strategies and the global routing algorithms.

V.2 Model and methods

V.2.1 Network structure

Many real world systems are modeled by the classical network topology "scale free networks (SF)". To build a SF network that was developed by Barabàsi-Albert (BA), we start with m_0 fully connected nodes. Then at each time step, we add a new node, the network continues to develop over time (the growth concept), and establish m new links with the existing nodes according to the preferential attachment at each time step. This process manufactures a scale free network with a power law degree distribution characterized by the existence of high degree nodes (called hubs) and low degree nodes (called peripheral nodes) Sect. I.6.5.

In our work, we consider the case of only two BA scale free networks labeled A and B. These two separate networks are linked to each other, by adding some links, which can supply paths for traffic between them. This system known as (Global network). We define N_{int} is the number of links interconnecting the subnet A and subnet B.
Following a process of connection, we choose a node in network A and, a node in network B, then connect them. Repeat this process until N_{int} interconnected links are added. Nodes of subnet A (respectively subnet B) connected to subnet B (respectively subnet A) are called **border nodes**.

V.2.2 Traffic dynamics

In a given Global network, at each time-step, R new packets are generated, with randomly chosen sources and destinations (in subnet A or subnet B), and each node can deliver at most C packets towards their destinations (we set $C = 1$). The queue length of each node is assumed to be unlimited. The first-in-first-out ($FIFO$) principle applies to the queue. Each newly generated packet is placed at the end of the queue of its source node. The packet is removed from the system when it reaches its destination. In our model, the packets are forwarded according to different network administrative authorities:

- **Unique Administrative Authority** (UAA)**:**
  In this case, there exists a unique policy strategy (PS) of routing for the whole global networks. Since there is a uniform policy strategy, so there is no difference whether the packet belongs to subnet A or to sub-net B. In this work, we choose the shortest path routing strategy as the PS in the global network.

- **Multi-Administrative Authorities** (MAA)**:**
  In this case, there exists two policy strategies PS_A and PS_B, and each network has its own policy strategy; subnet A has policy strategy PS_A, and subnet B has policy strategy PS_B.
  Each packet belongs to the sub-net A forwarded with policy strategy PS_A in the global

network. And the same for each packet belongs to sub-net B. In this work, PS_A is shortest path routing Strategy, and PS_B is efficient path routing scheme.

In the both models above, in order to construct optimal shortest path between any source and destination across the two sub-nets, the strategy requires that every node in the network knows a global information about the network structure. Clearly, this procedure is not economical in terms of the extra traffic load, that required to exchange and update information about the status of the network.
In this respect, nodes on every subnet are classified in two categories: interior nodes are connected only to other nodes in the same subnet and border nodes that are in addition connected to the other subnet.

- **Border Administrative Authority** (BAA_1)**:**
  In this strategy, every interior node on each subnet possesses global information only about its proper subnet. Border nodes possess in addition information about all the other border nodes (see Fig. V.1). Policy strategy A (PS_A) (respectively the policy strategy B (PS_B)) is used as a routing algorithm inside subnet A (respectively B) separately. However, in this across subnets A and B, the packets are forwarded randomly from one border node to the other in the destination subnet.
  If the packet is generated with the source and destination, belonging to subnet A, in this case the packet is forwarded only according to PS_A. The same procedure holds for packets generated with source and destination in subnet B using a PS_B.
  If the packet is generated with source belonging to subnet A and destination belonging to subnet B, in this case, the packet is forwarded according to PS_A, until it reaches a border node of subnet A, and is then randomly sent to a border node of subnet B, that it will follow strategy PS_B inside subnet B towards its destination. The same procedure holds for packets generated with source in subnet B and destination in subnet A.

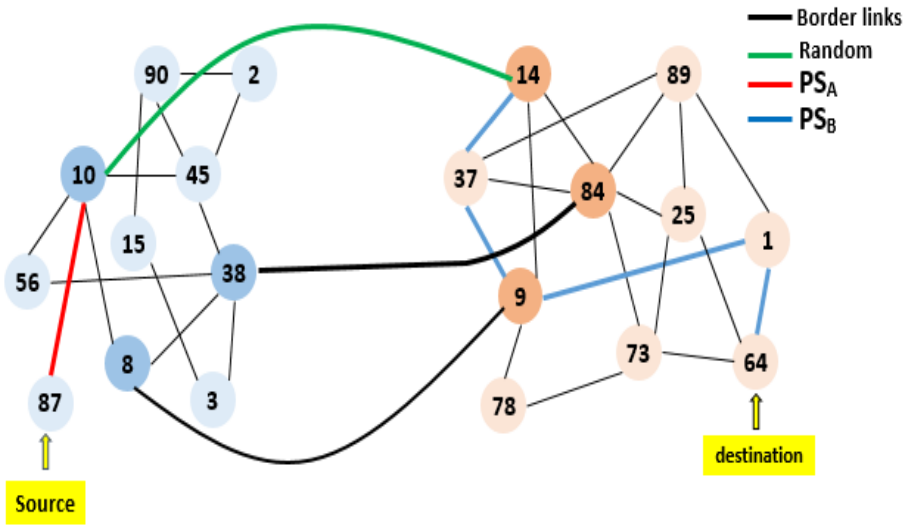


Figure V.1: Schematic represents a border Administrative Authority (BAA_1) with no routing at the border.

- **Border Administrative Authority** (BAA_2):
  In this strategy, the information about a subnet is not shared by all the nodes in the two subnets, as in BBA_1 with the addition that the border nodes do have information about the two subnets (see Fig. V.2).
  The two subnets A and B have different policy strategies PS_A and PS_B respectively. And when subnet A send information to subnet B, we use the Border nodes, as intermediate between them.
  If the packet is generated with the source and destination, belonging to subnet A, in this case the packet is forwarded only according to PS_A. The same procedure holds for packets generated with the source and destination in subnet B using a PS_B.
  If the packet is generated with source belonging to subnet A and destination belonging to subnet B, in this case , the packet is forwarded according to PS_A and then follows an optimal path leading to a border node in subnet B. When arrived at this node, it follows PS_B. The same procedure holds for packets generated with source in subnet B and destination in subnet A.

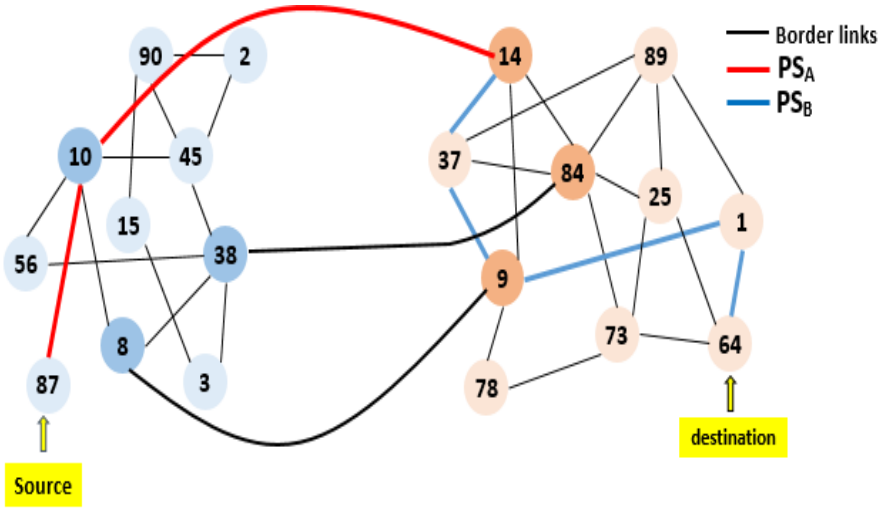


Figure V.2: Schematic represents a border Administrative Authority (BAA_1) with routing at the border.

V.3 Results and discussion

In this section, we investigate the effect of routing schemes in interconnected networks.
For this simulation, we used two BA networks, labelled A and B. We assumed that these two networks have the same size $N = N_A = N_B = 500$ and the same average degree $\langle k_A \rangle = \langle k_B \rangle = 4$, the number of links interconnecting the two subnets is $N_{int} = 5$. We choose the border nodes in both networks, with preferential attachment.

Given the whole network, Fig. V.3 shows how the traffic capacity is affected by the different routing algorithms in interconnected networks.
In figures Fig. V.3(a), V.3(b),V.3(c) and V.3(d), we have plotted traffic capacity ρ as a function of the number of packets R under different network administrative authorities.

We used in Fig. V.3(a), the unique routing algorithm (shortest path: SP) in the whole network, and in Fig. V.3(b), we used the multi routing algorithms (SP for subnet A and efficient path: EP for subnet B). These two routing strategies described in Figs. V.3(a) and V.3(b), requires that every node in the subnet knows a global information about the network structure. We noticed in these two figures, that the traffic capacity ρ increases when the packets number R increases, but the main observation is that the EP losses its advantages, concerning the enhancement traffic capacity.
In Figs. V.3(c) shows the results for the BAA_1 strategy, we used two different routing algorithms for the two subnets (SP for subnet A and EP for subnet B) separately, and the packets transmission between the two sub-net is done randomly, while in Figs. V.3(d) is devoted to BAA_2 strategy where we used two different routing algorithms for the two subnets (SP for subnet A and EP for subnet B), knowing that the subnet A has information about the border nodes of the subnet B, and the same thing is for the subnet B. In these two network administrative authorities, every node knows only information about the network that it belong to. We see in these two figures, that the traffic capacity ρ increases when the packets number R increases, and EP keeps its advantages compared with the administrative authorities that used the global routing algorithms.

To sum up, the strategies in Figs. V.3(a) and V.3(b) are not economical because of terms of extra traffic load. However, our proposed strategies Figs. V.3(c) and V.3(d) give approximately similar performance without extra cost and traffic load.

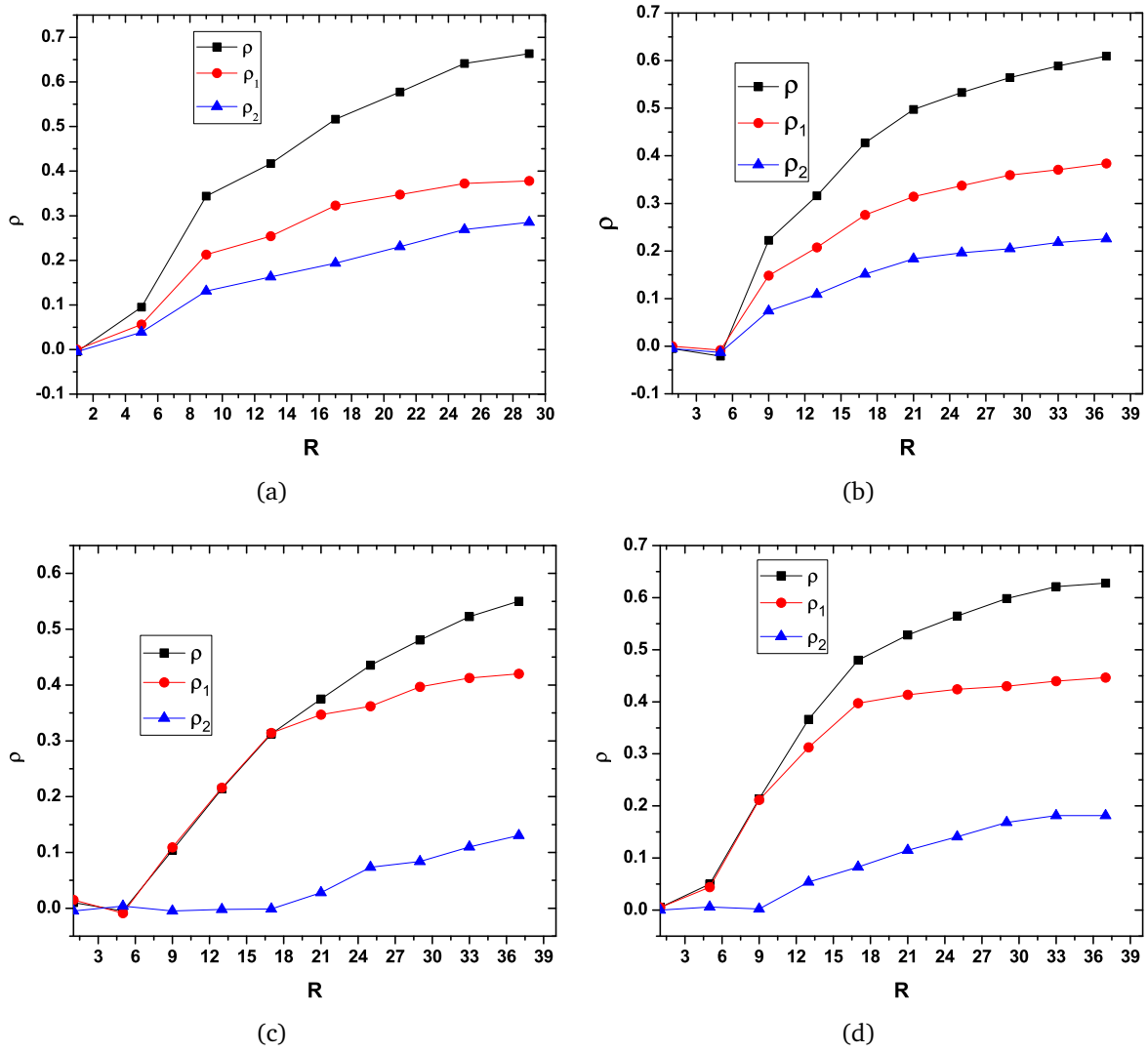


Figure V.3: Evolution the order parameter ρ as a function of packets number R under different network administrative authorities. UAA (a), MAA (b), BAA_1 (c) and BAA_2 (d)

V.4 Conclusion

In this chapter, we investigate the effect of routing schemes in interconnected networks.

For interconnected BA scale-free networks, it is found that the proposed routing rules "border routing schemes" can effectively give similar performance compared with the global routing protocols, without extra cost and load of the global routing protocols.

Additionally, This result is not useful uniquely in the context of two interconnected networks but can also be very useful in the case of a large network, where the traffic cost of a global routing protocol is very large. In this case, we can divide the network into two interconnected subnets and use our different authorities as in the BAA_1 and BAA_2 strategies. Then as we noted in [169], the number of interconnection should be kept as small as possible. In this respect, we can suggest to use a dedicated algorithm such as **Kernighan-Lin** algorithm for graph partitioning.

CONCLUSIONS & PERSPECTIVES

In our life, society depends greatly on the efficient operation of many critical networked infrastructures such as power grids, the Internet, transportation networks, and so on. In fact, the importance of the study of complex networks is justified by the different phenomena that occur on these networks, such as the traffic flow and epidemic spreading. The main reason to study these processes dynamics is how to reduce the traffic congestion by designing efficient algorithms, and understanding and limiting the virus propagation.

This thesis is based on some important results concerning the phenomena that take place in the complex network domain and is crowned by the following results:

In chapter VI, we studied the spread of viruses in a scale-free network (proposed by BA) with different topologies. In this way, we proposed a restricted scale-free (RSF) network more resistible to the spread of virus. Our idea is based on the influence of the degree of connectivity of nodes k. In our work, we determined a critical maximum node degree (K_c), below which the virus spread in the network is limited. However, the infected nodes increased when $k > K_c$. Moreover, we compared our RSF with the random network (proposed by $Erds$ and $Rnyi$). Finally, we found that certain properties of networks like size can influence the virus spreading. Indeed, the network size with different topologies influences the spread of virus. The proportion of infected nodes increases with increasing of network size.

In chapter V, we have focused once again on the propagation of virus in complex networks, but from the side of traffic-driven epidemic spreading and we have studied the effects of routing algorithms strategies in complex networks. Our results have shown that the performant routing algorithms mainly: efficient path (EP) strategy and global dynamic (GD) routing strategy which are used to overcome the congestion problem, favor the virus spreading more than the case where the shortest path algorithm (SP) is used especially in the free flow phase. For the congested phase, even a small value of the infection probability rate β, the whole network becomes globally infected with all the studied routing algorithms. Since, the performant algorithms routing favor the propagation of virus more than the SP strategy and instead of a random vaccination, we proposed a new method of antivirus vaccination that helps us to still use performant algorithms routing strategies with an acceptable level of protection against virus spreading without affecting the traffic transport efficiency. Our results show that a random vaccination succeeded in suppressing the virus for the SP scheme and fails for the EP algorithm. However, when we used a preferential selective vaccination, which targets the hubs, we arrive at eradicating the virus for some preferential control parameter α. With this procedure, we recover the performance of the EP (and also the GD) algorithms without the drawbacks and

without affecting the traffic transport efficiency. We noted that some previous studies, have tried to modify the routing rules to limit the virus spreading, but the negative point of these attempts is, the reduction of the traffic transport efficiency. however, our method proposed a solution to overcome this drawback, by limiting the virus spreading without affecting the efficiency of the traffic capacity.

Concerning our work in traffic dynamics presented in chapter VI. We have studied the effects of routing algorithms strategies on interconnected networks. Inspired from previous studies of traffic congestion in isolated networks and the newly developed works of interconnected networks, and in real situation, the interconnected networks have different administrative routing policies. These policies however, have some inconvenient, such as difficulty of exchanging and updating information about the subnetworks for all routers, and information exchange has also a high economic cost. To overcome these drawbacks, the Internet used a well-knowing routing protocol between different Autonomous Systems (AS). This routing protocol is called the Border Gate Way Protocol (BGP). We use a simplified model version of this protocol, which keeps separated the two administrative authorities and introduce rules for the exchange of information between the two networks. Our main results show that approximately similar performance is obtained without the extra cost and load a global routing protocol between two routing schemes global and border.

Although this work has achieved the proposed goals and objectives, much remains to be further studied. Some areas for future work include the following:

- Thanks to the increasing attention given to this subject from network science, they are many questions have been answered. However, there are many open questions that raise up. Indeed, for some questions that still raise up, we will propose more strategies and control methods to limit the virus spreading in complex networks and designing an effective routing strategies to overcome the traffic congestion in complex networks.

- All the results presented in this thesis are concerning the complex networks regardless the domain of application, in the following works, we will try to implement our results in the biological networks and the traffic road.

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List of Figures

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Résumé

Nombreux systèmes dans le monde réel peuvent être représentés comme des réseaux complexes. Les recherches montrent que la majorité des réseaux réels sont de nature dite : "sans échelle".

Le défi majeur d'une architecture d'un réseau, est de comprendre les phénomènes qui apparaissent dans les réseaux complexes. Dans la littérature il y a deux phénomènes qui sont largement étudiés: la propagation des virus et le trafic.

L'objectif de l'étude du trafic sur les réseaux complexes est l'augmentation de la capacité du trafic sans frais supplémentaires au niveau technique et économique. En outre, l'étude de la propagation des virus dans les réseaux complexes est de connaître la dynamique de cette dernière et la méthode efficace pour contrôler la prévalence de l'infection. L'objectif de cette thèse est d'étudier les deux phénomènes mentionnés ci-dessus et la relation entre eux.

Mots-clefs : Réseaux complexes ; Trafic ; Propagation des virus ; Réseau sans échelle restreint ; Vaccination ; Les algorithmes de routage.

Abstract

Network science has acquired much interest from researchers. In fact, complex networks are involved in various fields and disciplines. However, studies that have been conducted in this area, had revealed a great discovery, the scale-free nature represents many real networks.

For a given network topology, the main goal of most studies carried out in this domain, is to understand various dynamical processes on complex networks. Two types of dynamical processes that have been studied extensively are epidemic spreading and traffic dynamics.

Traffic dynamics is one of the most popular processes on complex networks, the objective of which is to enhance the traffic flow without extra-technical and monetary costs. While, epidemic spreading which is also considered an important issue, its aim is to describes how infections spread throughout a network and how to control the prevalence of infection. The main goal of this thesis is to study the two phenomena mentioned above and the relationship between them.

Key Words : Complex networks ; Epidemic spreading ; Traffic dynamics ; Restricted scale-free networks ; Vaccination ; Routing algorithms.