

MINISTRY OF HIGHER EDUCATION AND SCIENTIFIC RESEARCH

ABDELHAMID IBN BADIS UNIVERSITY - MOSTAGANEM



Faculty of Exact Sciences and Computer Science
Department of Mathematics and Computer Science
Sector : Computer Science

PROJECT REPORT

Information Systems Engineering

THEME :

Establishment of a monitoring system for
COVID-19

Students : « **Younsi Ahmed** »

 « **Mekhlouf Mohamed Enadir** »

Supervisor : « Dr. YOUNSI Fatima-Zohra »

Academic year 2020-2021

Abstract

Infectious diseases represent a major public health problem today. With the increase of bacterial resistance, the emergence of new pathogens and the rapid spread of the epidemic, monitoring and surveillance of disease transmission becomes particularly important. In the face of such a threat, society must prepare in advance to respond quickly and effectively if such epidemic is declared. This requires the establishment of monitoring and prevention systems.

In this context, the aim of this work is to propose, discuss and develop a new epidemic system named Susceptible- Exposed-Infected-Quarantined and Recovered based on Scale Free network (SEIQR-SF) to simulate the propagation of the COVID-19 pandemic. Herein, we are interested in compartment models. The decision support system developed generates simulation data, which are displayed in tabular form and social network form. The outputs of SEIQR-SF were discussed in order to better understand their uses in the decision-making process managed by health personal in the face of a health crisis.

Keywords: Mathematical Models, Epidemic monitoring, Decision Making, Spatial Decision Support Systems (SDSS), Geographic Information System (GIS), Compartmental Models ,SEIQR Model.

Résumé

Les maladies infectieuses représentent aujourd'hui un problème majeur de santé publique. Devant l'augmentation des résistances bactériennes, l'émergence de nouveaux pathogènes et la propagation rapide de l'épidémie, le suivi et la surveillance de la transmission de la maladie devient particulièrement importants. Face à une telle menace, la société doit se préparer à l'avance pour réagir rapidement et efficacement si une telle épidémie est déclarée. Cela nécessite une mise en place des dispositifs de suivi et de prévention.

Dans ce contexte, le but de ce travail est de proposer, discuter et développer un nouveau système épidémique nommé Exposed-Infected-Quarantined and Recovered basé sur Scale Free network (SEIQR-SF) pour simuler la propagation de la pandémie de COVID-19. Ici, nous nous intéressons aux modèles à compartiments. Le système d'aide à la décision développé génère des données de simulation, qui sont affichées sous forme de tableau et sous forme de réseau social. Les sorties de SEIQR-SF ont été discutées afin de mieux comprendre

leurs utilisations dans le processus décisionnel géré par les personnels de santé face à une crise sanitaire.

Mots-clés: Modèles mathématiques, Epidémie, Prise de décision, Systèmes d'Aide à la Décision Spatiale (SADS), Système D'information Géographique (SIG), Modèles compartimentaux, Modèle SEIQR.

LIST OF FIGURES

FIGURE 1 : SCHEME OF INFECTION FOR SI MODEL	5
FIGURE 2 : SCHEME OF INFECTION FOR SIR MODEL	5
FIGURE 3 : SCHEME OF INFECTION FOR SIRS MODEL	6
FIGURE 4 : SEIR MODEL.....	7
FIGURE 5 : SCHEME OF INFECTION FOR SEIR/ SEIRS MODEL	7
FIGURE 6 : SCHEME OF INFECTION FOR SEIQR MODEL.....	8
FIGURE 7 : ILLUSTRATION OF A SMALL RANDOM SOCIAL NETWORK	10
FIGURE 8 : THE DECISION-MAKING PROCESS PROPOSED BY SIMON	11
FIGURE 9 : COMPONENTS OF AN IDSS.....	13
FIGURE 10 : RELATIONSHIP BETWEEN GIS, SDSS AND DSS	15
FIGURE 11 : PROPOSED SEIQR-SF SYSTEM.....	20
FIGURE 12 : THE GENERATION OF THE SF NETWORK.....	22
FIGURE 13 : THE GENERATED GRAPH AND THE ADJACENCY LIST	23
FIGURE 14 : SCHEME OF THE SEIQR MODEL.....	23
FIGURE 15 :THE SEIQR-SF MODEL	26
FIGURE 16 : SEQUENCE DIAGRAM OF THE SEIQR-SF SYSTEM.....	27
FIGURE 17 : EVOLUTION OF THE NUMBER OF INFECTED PEOPLE WITH COVID-19.....	28
FIGURE 18 : SCREENSHOT FROM SEIQR-SF SYSTEM FOR COVID-19 SPREAD OVER TIME	30
FIGURE 19 : SCREENSHOT OF ADJACENCY LIST.....	32
FIGURE 20 : SMALL NETWORK CONSISTS OF 52 NODES	32
FIGURE 21 : SCREENSHOT FROM SEIQR-SF SYSTEM FOR THE NETWORK ANIMATION.....	33
FIGURE 22 : SCREENSHOT FROM SEIQR-SF SYSTEM FOR THE NETWORK EVOLUTION OVER TIME.....	33
FIGURE 23 : SCREENSHOT FROM SEIQR-SF SYSTEM FOR DIFFERENT CURVES	34
FIGURE 24 : SCREENSHOT OF DATA COMPARISON.....	34
FIGURE 25 : SCREENSHOT OF DATA OUTPUT: EVOLUTION OF THE COVID-19 OVER TIME.....	35
FIGURE 26 : SCREENSHOT OF DATA COMPARISON.....	35
FIGURE 27 : SCREENSHOT OF DATA COMPARISON.....	36
FIGURE 28 : CARTOGRAPHIC REPRESENTATION.....	37

List of tables

TABLE 1 : SUMMARY OF PARAMETERS AND STATE VARIABLES USED BY SEIQR-SF.....	24
TABLE 2 : THE VALUES OF THE PARAMETERS AND STATE VARIABLES USED BY SEIQR-SF	31
TABLE 3 : CORRELATION BETWEEN NUMERICAL SIMULATIONS SEIQR-SF MODEL OUTPUTS AND REAL DATA	36

List of Abbreviations

SI : Susceptible-Infected.....	3
SIR : Susceptible-Infected-Recovered.....	4
SEIR: Susceptible-Exposed-Infected-Recovered	5
SIRS : Susceptible-Infected-Recovered-Susceptible.....	5
SEIQR : Susceptible-Exposed-Infected-Quarantined-Recovered	7
IDCR : Intelligence-Design-Choice-Review	11
DSS : Decision Support System	12
IDSS : Interactive Decision Support System.....	12
HMI : Human-machine interface.....	13
DMS : database management system	15
GIS : Geographic Information System	15
MBMS : model base management system	15
SDSS : Spatial Decision Support System.....	15

Contents

General introduction	1
Chapter 1 Mathematical models of epidemics	3
1.1 Introduction	3
1.2 The mathematical modeling	3
1.2.1 What is a model ?	3
1.2.2 Mathematical modeling in epidemiology	3
1.2.3 Some mathematical models of disease transmission	4
1.2.3.1 Stochastic model	4
1.2.3.2 Deterministic models	4
2.1 Agent-based modeling for epidemic	9
2.2 Modeling epidemics spread on social contact networks	9
2.3 Conclusion	10
Chapter 2 Decision support system	10
2.1 Introduction	10
2.2 Decision	10
2.3 Decision making process	10
2.4 Decision Support System	12
2.4.1 Interactive Decision Support System	12
2.4.2 Spatial Decision Support System	14
2.5 Decision making in epidemic crisis	15
2.5.1 Decision under Uncertainty	15
2.5.2 Decisions with scientific help	17
2.6 Conclusion	17
Chapter 3 Proposed epidemic spread model	19
3.1 Introduction	19
3.2 Objective of our system	19
3.3 Identifying the problem	19
3.3.1 Disease definition	19
3.3.2 Transmission mechanism	19
3.4 Description of the proposed SEIQR-SF system	20
3.5 The process of applying the SEIQR-SF model	24
3.6 UML modeling	27
3.6 Conclusion	28
Chapter 4 Implementation	29

4.1	Introduction-----	29
4.2	Tools and techniques-----	29
4.2.1	Python-----	29
4.3	Results and Analysis-----	30
4.3.1	The parameter values of the SEIQR-SF system-----	31
4.3.2	Result from the scale free network-----	31
4.3.3	Result from the SEIQR-SF system-----	33
4.3.4	Validation model-----	35
4.3.5	Geographic representation-----	36
4.4	Conclusion-----	37
	General Conclusion -----	38
	Annex-----	39
	Bibliography -----	40

General introduction

Each year, millions of people worldwide die from infectious diseases, some of them, such as chicken pox, usually have mild symptoms and vanish of their own, others like Ebola and SARS, causing countless deaths before disappearing. As an example, in 1346-1353, the Black Death (also known as The Plague), caused about 75–200 million deaths, and the Spanish influenza pandemic of 1918-1919 caused more than 50 million deaths worldwide. These diseases have troubled humanity for decades and put the population and the health systems under stress that led scientists from different fields to combine their efforts to stop the infection and find treatment. One of the solutions is mathematical models, this latter provided much perception into the dynamics of disease epidemics and helped officials make decisions about public health policy.

In order to understand the mechanism of spread of communicable disease, many scientists have developed different models. The first mathematical model in epidemiology was developed by Daniel Bernoulli in 1760 to study the variolation against smallpox in increasing life expectancy [1]. Indeed, in this work, we propose and implement a new decision making system named Susceptible- Exposed-Infected-Quarantined and Recovered based on Scale Free network (SEIQR-SF) to simulate the propagation of the COVID-19 pandemic. The SEIQR-SF is based mainly on Susceptible- Exposed-Infected-Quarantined and Recovered compartmental models and Scale Free social network to understand how COVID-19 spread through relationships between individuals.

Based on the available data on the COVID-19 syndrome, this research study will clarify the model of SEIQR-SF analytically and numerically. Additionally, this proposed study will explore the optimal control to reduce the spread of COVID-19 disease as well as its threshold.

Structure of the manuscript

The manuscript is organized as follows:

The first chapter introduces the role of mathematical modeling along with a review of some models and their properties in the study of diseases transmission.

The second chapter explains the decision-making process and compares between decision support systems (interactive and spatial) and difficulties of decision making during epidemic crisis.

The third chapter present in detail the SEIQR-SF system. The later will be created and investigated using social network concepts and compartiment model. Also, it contains decision making process adapted SEIQR-SF system.

The fourth chapter discuss numerical solutions based on real data for COVID-19 outbreak. Developed software, such as Python will be used to implement and explore the model. The correlation between numerical simulations SEIQR-SF model outputs and real data will be calculated.

Finally, some conclusions will be drawn.

Chapter 1

Mathematical models of epidemics

1.1 Introduction

Interest in mathematical epidemiology has increased in recent years due to the variety of infectious diseases, and it has been studied by many researchers to understand the spread of the disease and if possible make it under control.

In this chapter, we will discuss the basic concepts related to mathematical modeling in epidemiology and we explain some models as well presenting the main properties of each one.

1.2 The mathematical modeling

Mathematical modeling is a set of techniques, tools, and equations that can be adapted to specific disciplines. Before examining the content, some definitions would need further known and understood.

1.2.1 What is a model ?

A model is a description of the reality of a particular phenomenon to help us understand better real-life problems. It could be a graph or diagram, a mathematical or physical model, etc. since the models describe known things for us. They can also help us to understand the unknown or anticipate what could happen by predicting how something will behave in different circumstances. [2]

1.2.2 Mathematical modeling in epidemiology

Epidemic models of infectious diseases date back to Daniel Bernoulli's mathematical analysis of smallpox in 1760 [1]. The models have been developed since the early twentieth century, thanks to the advantages it brings, it can provide an understanding of the mechanisms

of disease transmission, the prediction of the evolution of the disease, suggest effective control and preventive solutions, provide an estimate of the severity of the epidemic, etc.

1.2.3 Some mathematical models of disease transmission

Models that have been proposed to describe the dynamics of infectious diseases can be classified into two types: deterministic and stochastic.

1.2.3.1 Stochastic model

Stochastic models are used when the number of the population is small or in the early stages of epidemics, where infections are still few and stochasticity may play an important role. The first stochastic mathematical model was developed by two researchers L.Reed and W, H. Frost in 1920 called "Reed-Frost model of the epidemic" [3] to describe the spread of disease in populations.

1.2.3.2 Deterministic models

Deterministic models are used in large populations which are divided into groups called compartments (or classes) where each group represents a specific stage of the epidemic. They are used to handling questions like: what fraction of individuals would be infected in an epidemic outbreak? [4]

Deterministic models emerged at the start of the 20th century with the work of Hamer (1906) who assumed that the spread of infection rely on the number of susceptible and infected individuals. [5]

Compartmental models

Compartmental models separate populations into groups and describe how they interact with each other in different compartments using differential equations, these models assume that all individuals in a single compartment are identical to each other. Several variants can be added to make a complex and more realistic model (exposed individuals but not yet infectious, permanent or temporary immunity, etc).

There is a diversity of compartmental models, we present in the following the most known models:

a. The simple SI model

The SI (susceptible, infected) is the first simple dynamic model among all disease models, it was developed by W.H.hamer in 1906 [6]. This model includes two compartments (as shown in Figure 1): individuals likely to be infected (S), infected individuals (I). In the absence of treatment, infected people, never leave the infectious state and become infected for life, for example: herpes and HIV/AIDS.

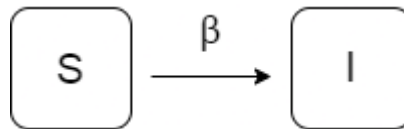


Figure 1 : Scheme of infection for SI model

Transmission of infection occurs through direct contact between susceptible and infective members with infection rate β .

b. The simple SIR model

Kermack and McKendrick [7] created a model in which each individual in a population is assigned to one compartment. In total, we have three compartments (as shown in Figure 2): S (Susceptible) for individuals at risk of infection, I (Infected/Infectious) for individuals who are currently infected and are capable to passing the disease to susceptible, R (Recovered/Removed) for individuals who have recovered from the disease, or have died. They assumed that all individuals are susceptible to the disease, and full immunity is obtained once the infection is cured. The SIR model used to describe a disease, which confers immunity against re-infection.



Figure 2 : Scheme of infection for SIR model

For a given population, we study the size of three sub-populations over time:

- $S(t)$: represents the number of healthy people (susceptible) at time t .
- $I(t)$: the number of infected people.
- $R(t)$: the number of recovered people (removed).

- $N = S(t) + I(t) + R(t)$: represents the total constant population over time.
- β represents the transmission rate, i.e. the rate of healthy people who become infected.
- γ represents the recovery rate.

To these three different states (S, I, R), there are three ordinary differential equations (ODE) that are presented below.

$$\begin{cases} dS/dt = S'(t) = -\beta \cdot S(t) \cdot I(t) \\ dI/dt = I'(t) = \beta \cdot S(t) \cdot I(t) - \gamma \cdot I(t) \\ dR/dt = R'(t) = \gamma \cdot I(t) \end{cases}$$

There is also the SIRS model that is used for some diseases such as cholera. A person's immunity may wane over time (temporary immunity on recovery from infection), so the recovered individuals return to a susceptible state. Figure 3, illustrate the scheme of SIRS model:

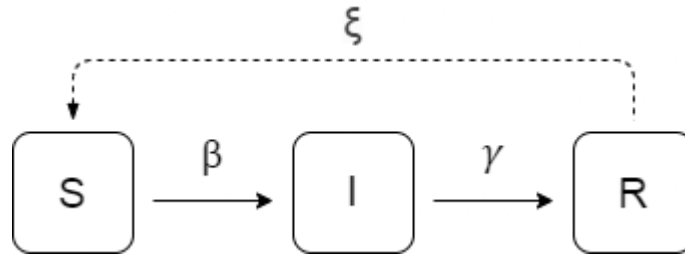


Figure 3 : Scheme of infection for SIRS model

- ξ represents the rate which recovered individuals return to the susceptible state due to loss of immunity.

$$\begin{cases} dS/dt = -\beta \cdot S(t) \cdot I(t) + \xi R \\ dI/dt = \beta \cdot S(t) \cdot I(t) - \gamma \cdot I(t) \\ dR/dt = \gamma \cdot I(t) - \xi R \end{cases}$$

c. SEIR model

The SEIR mathematical model is widely used in the field of epidemiology to analyze infectious diseases, in addition to the SIR model it has a class (E) for those who are exposed to the virus or infected but not yet infectious. In this model there are periods from the time of infection to the end of infectiousness, after the infection, the host doesn't show symptoms and is not capable to transmit the disease to other hosts (latent period). when pathogens multiply and invade the body which in turn reach the target organs, symptoms begin to appear and the host becomes contagious (incubation period). After the infectious period, the infected

individuals gain permanent or temporary immunity (SEIR/SEIRS) [8]. The Figure below shows relations between these periods.

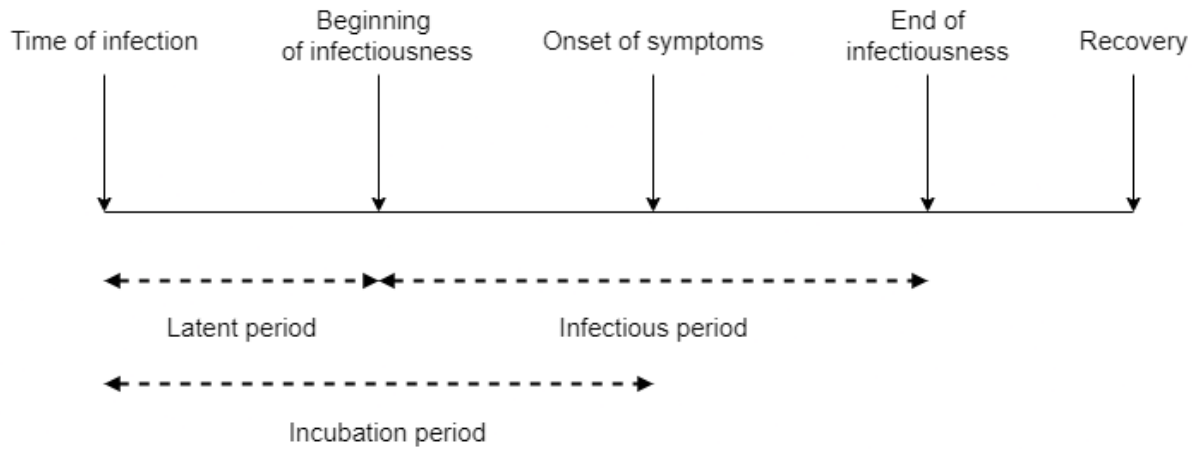


Figure 4 : SEIR model

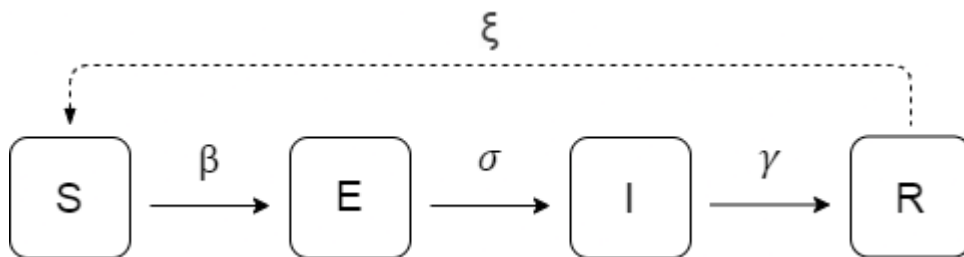


Figure 5 : Scheme of infection for SEIR/ SEIRS model

- $S(t)$: represents the number of susceptible individuals.
- $E(t)$: the number of exposed individuals (those who have been infected but are not yet infectious).
- $I(t)$: the number of infective individuals (those capable of transmitting the disease).
- $R(t)$: the number of recovered people (removed).
- $N = S(t) + E(t) + I(t) + R(t)$: represents the total constant population over time.
- β represents the transmission rate which susceptible individuals become exposed.
- σ represents the transmission rate which exposed individuals become infected.
- γ represents the recovery rate.

The SEIR model is described by the following of differential equations:

$$\begin{cases} \mathbf{dS/dt} = -\beta \cdot \mathbf{S(t)} \cdot \mathbf{I(t)} \\ \mathbf{dE/dt} = \beta \cdot \mathbf{S(t)} \cdot \mathbf{I(t)} - \sigma \cdot \mathbf{E(t)} \\ \mathbf{dI/dt} = \sigma \cdot \mathbf{E(t)} - \gamma \cdot \mathbf{I(t)} \\ \mathbf{dR/dt} = \gamma \cdot \mathbf{I(t)} \end{cases}$$

d. SEIQR model

Some diseases are treated through prevention (such as vaccination) or treatment of patients who have symptoms. For diseases that have no known cure, the solution to controlling them and reducing their transmission is to isolate some infectors and quarantine suspected patients. Over the years, quarantine has been used to reduce the transmission of diseases such as plague, SARS, cholera, and leprosy, in similar cases, instead of using SIR or SEIR models, the most effective one is SEIQR because it contains a class for quarantined people (Q) [9].

SEIQR, SIQR are an improved model of SEIR, SIR for diseases that confer permanent immunity. The SIQR model doesn't take into consideration the latent period, after the infection, susceptible individual instantaneously becomes infectious (I class). While in SEIQR model likely to become exposed. Some exposed individuals stay in class (E) while they are at the latent period and then move to the removed class (R) upon recovery. Others who are at the end of the incubation period will be infected (I class). The infected individuals may recover directly or after transferred into the quarantine class Q [9], [10].

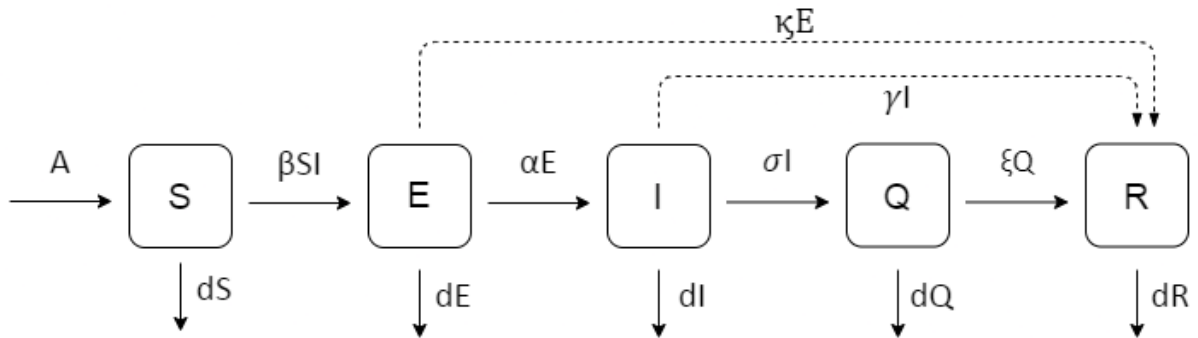


Figure 6 : Scheme of infection for SEIQR model

The model is basically distributed into five compartments :

- The susceptible population $S(t)$ at a given time t .
- The exposed population $E(t)$.

- Infectious population $I(t)$ at time t (this denotes the population that is either asymptomatic or symptomatic).
- Quarantined population $Q(t)$ at time t (the population that has been identified as infected and has been quarantined).
- The population $R(t)$ at time t (the population that has recovered).
- $d, \beta, \xi, \gamma, \sigma, \alpha$ and κ are non-negative constants.
- A represents the recruitment rate of susceptibles corresponding to births and immigration.
- d is the natural mortality rate.
- α and σ are the rates at which individuals leave the exposed and infectious classes respectively.
- κ, γ and ξ are the rates at which individuals recover from the disease or die.

The system of differential equations for the SEIQR model is :

$$\begin{cases} dS/dt = A - \beta \cdot S(t) \cdot I(t) - dS(t) \\ dE/dt = \beta \cdot S(t) \cdot I(t) - (d + \alpha + \kappa) \cdot E(t) \\ dI/dt = \alpha \cdot E(t) - (d + \gamma + \sigma) \cdot I(t) \\ dQ/dt = \sigma \cdot I(t) - (d + \xi) \cdot Q(t) \\ dR/dt = \kappa \cdot E(t) + \gamma \cdot I(t) + \xi \cdot Q(t) - dR(t) \end{cases}$$

2.1 Agent-based modeling for epidemic

For the past twenty years, agent-based modeling has been considered an effective tool in understanding the dynamics of infectious disease outbreak, and it has been increasingly used in order to analyze, model and simulate complex dynamic systems. In agent-based models the process of infectious disease transmission is managed by the behavior of individuals (agents) and interaction between them over space and time. Different from the traditional models (compartmental models), these models represent a heterogeneous population and complex network interactions in the environment. [11]

2.2 Modeling epidemics spread on social contact networks

One of the factors that lead to the rapid spread of infectious diseases is human contact and their interaction in the environment and this varies according to the region and the

population density. Every human being has direct contacts and relationships with others such as friends, neighbors, and family, etc, and this makes him vulnerable to disease or a cause of its spread. This contact network can be presented in the form of a graph made up of nodes, which represent the individuals connected with each other by edges that represent social interactions (as an example shown in Figure 7). [12], [13]

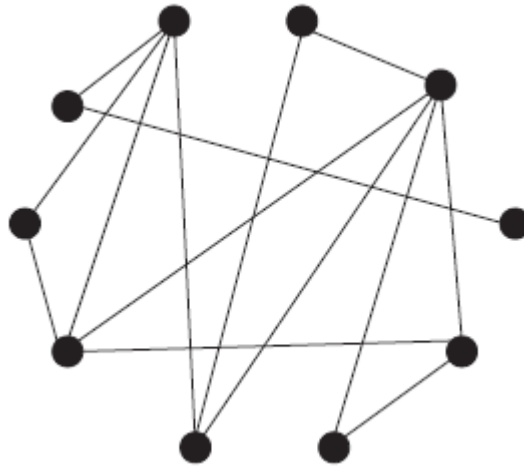


Figure 7 : Illustration of a small random social network

The birth of network modeling based on random networks was in 1959. by The two researchers, Erdős and Rényi which the graph is known by their names (the Erdős-Rényi random graph) This graph is composed of N nodes, and pair of individuals are connected to each other (v_i, v_j) with a probability of $p = \lambda/n$ and the auteurs proposed many models and the most simple model which each node (individual) has $n - 1$ possible connections [14]. The normal (traditional) models ignore the crowding and it's unrealistic so that's why we need an improved model [13]

2.3 Conclusion

In this chapter, first, we discussed mathematical modeling in epidemiology due to the great interest it has received and the importance of its use by researchers and public health officials in recent decades. Then, we presented the most famous models of disease transmission. Finally, we explained the spread of disease in social contact networks as well as their characteristics.

Chapter 2 present an overview of support decision-making system and its extensions.

Chapter 2

Decision support system

2.1 Introduction

While the emergence of a known infectious disease, information and time are available for study, analysis and comparison between alternatives solutions, and this reflects ease in making decisions. However, in the event of a new disease emerging, the process of decision-making will not be easy and simple, which becomes a burden on decision-makers at all levels of crisis management.

In this chapter, we present some definitions related to the decision making and we explain the decision making process.

2.2 Decision

In the literature there are several definitions of a decision, in common parlance, the term decision refers to the result of a process of choice. Roy and Bouyssou believe that the decision is often presented as the act of an isolated individual (decision-maker) who freely exercises a choice between several possibilities of action at a given moment in time [15]. According to Lévine and Pomerol a decision is an action which is taken to face a difficulty or to respond to a modification of the environment, that is to say, to solve a problem which arises with the individual or the organization [16].

2.3 Decision making process

According to baker [17] “ *Efficient decision making involves a series of steps that require the input of information at different stages of the process, as well as a process for feedback*”.

In general, decision-making process is a cognitive way of process that helps people solve problems by finding a solution or alternative solution, and it is a big challenge to make the final decision.

Herbert A. Simon [18] was one of the researchers in the field decision-making, he proposed the IDCR model (Intelligence-Design-Choice-Review) presented in Figure 8. This model is the best known in the field of decision support, it consists of four phases in the decision-making process: information search, design, choice and review :

- 1. Intelligence phase:** In the first phase. It is about defining the problem to be solved, the objectives or goals of the decision-maker, researching and organizing the information needed to make a decision.
- 2. Design phase:** In this phase, the goal is to develop a model, generate and analyze the different possible actions, determine the decision variables, define the criteria of choice and develop possible strategies that allow problem solving. Depending on the complexity of the problem, one or more decision models can be chosen.
- 3. Choice phase:** During this phase, the decision maker chooses between the different solutions. The evaluation of the alternatives and the final choice depend on the type of criteria used (finding the best alternative, i.e. fairly good or satisfying, taking risks or not, etc.). This phase includes research and evaluation of the most suitable solution for the model.
- 4. Review phase:** the purpose of this phase is to evaluate the quality of the decision-making and may involve, if necessary, a return to one of the previous phases.

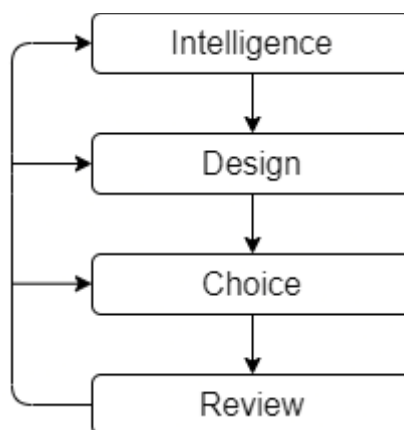


Figure 8 : The decision-making process proposed by Simon

2.4 Decision Support System

A Decision Support System (DSS) is a computer-based information system that helps, supports, facilitates and provides guidance for decision makers by compiling comprehensive information and analyzing massive volumes of data to produce detailed information reports, it consists of software, hardware, data and models and it can either be fully computerized or powered by humans.

2.4.1 Interactive Decision Support System

Interactive Decision Support System (IDSS) would allow the user to evaluate the situation, the various alternatives and their possible impacts, develop his own ideas or points of view. The concept of IDS appeared in the literature in the 1970s [19], [20]. They are tools specifically developed to support decision-making. IDSS are characterized mainly by their interactivity, flexibility and adaptability. The development of such systems involves the use of techniques from various fields such as computer science, operations research, artificial intelligence, software engineering, human-computer interaction and telecommunications. IDSSs are particularly useful in helping to solve complex problems of large dimensions and with objectives that are highly dependent on user preferences.

Among the characteristics associated with IDSS, we mention some of them [21]:

- They mainly help with problems by connecting together human judgments and computed data.
- They provide help for different categories of users or different groups of users.
- They adapt over time and are flexible enough for the decision-maker to be able to adapt them to meet new conditions (add, combine, change and rearrange the variables of the decision process).
- The decision-maker has control over all stages of the decision-making process.
- They use models. Modelling allows different strategies to be experimented with under different conditions.

An IDSS generally consists of four components: a human-machine interface (HMI) or dialogue module, information base (a module containing the data), model base (a module containing calculation procedures or models) and a knowledge base. As shown in Figure 9

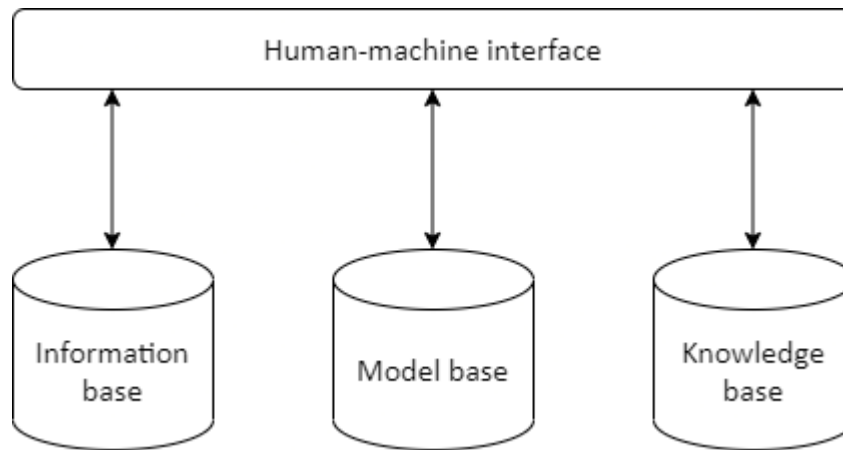


Figure 9 : Components of an IDSS

1. The human-machine interface

The human-machine interface is essential in most interactive programs and systems. It is at the center of the IDSS and it allows the decision maker to interact with the machine, and through it, he can access the data and calculation functions of IDSS. A good dialogue module can display information in different forms (text, 2D or 3D graphics, table or others).

2. The information base

The information base functions as a memory, it stores the data permanently and temporarily and it manages the recording and the erasure of volatile data according to the wish of the user. These volatile data are the results obtained during data processing. The permanent data may be statistical information or other data that describes past and current situations.

3. The model base

The model base consists of a set of models and a system for managing them. The models can be mathematical, optimization, statistical models, analytical techniques, etc. these models assists the user by analyzing the complex data to produce the required information.

4. The knowledge base

The knowledge base brings together a set of knowledge on the models, recognizes the problems and provides help in solving them during all the phases of the process. The knowledge base can also play in certain cases the role of base of models.

2.4.2 Spatial Decision Support System

Spatial Decision Support Systems (SDSS) is an interactive, computer-based system that enables decision-makers to use existing data to solve spatially related issues through a flexible and optimized interface that allows for data analysis, organization and visualization [22]. It combines between the geographic information systems capabilities (GIS), the decision models and optimizing algorithms.

In addition to capabilities of DSS and SDSS provide :

- Spatial data input and cartographic output (maps or other spatial forms);
- Storage of complex structures ;
- Spatial data analytical techniques.

The SDSS is composed mainly of : (i) a database management system (DMS); (ii) which stores and manages spatial data; (iii) a model base management system (MBMS) that contain a set of models and analysis procedures; (iv) graphical and tabular report generators that provide statistical graphics (2D or 3D plots and graphs); (v) cartographic displays, etc; (vi) and a user interface to help communication with the system and aid in outcome analysis.

a. Geographic Information System

A Geographic Information System (GIS) is a computer-based system that is capable of processing, storing, or displaying spatial data in the form of charts and maps. Its core functions are data creation, data management, and data analysis and visualization. During the past 20 years, there has been exponential growth in the use of spatial information in public health studies and increased attention to understanding how place and spatial context are important for many public health issues [23]. The figure 10, shows the relationship between GIS, SDSS and DSS.

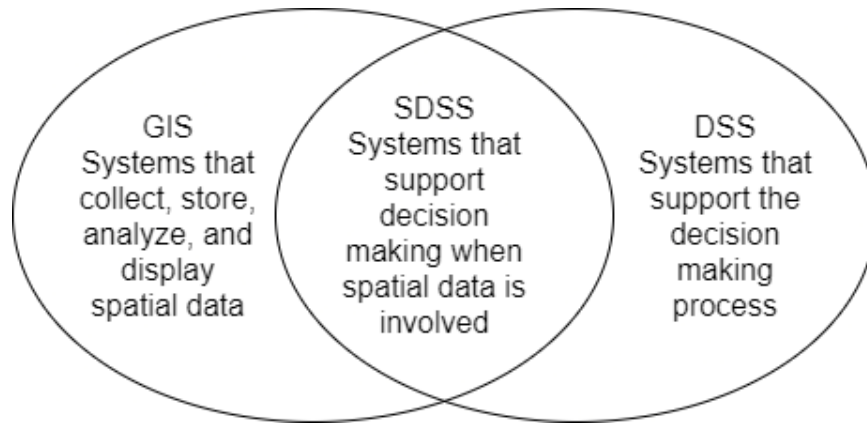


Figure 10 : Relationship between GIS, SDSS and DSS

2.5 Decision making in epidemic crisis

Decision making during an epidemic may be extremely challenging. Because new epidemics continue to emerge and some of them have unprecedented global impacts, decisions are taken during a highly uncertain, complex, and rapidly changing environment. In such a context, within which human lives are in peril, we argue that using ideas and constructs from modern decision theory, even informally, will make decision-making a more responsible and transparent process. Decision-makers are charged with taking actions to protect their population against the disease while lacking reliable information on the virus and its transmission mechanisms, and on the effectiveness of possible measures and their health consequences. The decisions would combine the best available scientific evidence typically provided by expert opinions and modeling studies. However, in an uncertain and rapidly changing environment, the pertinent evidence is extremely unsure, making it challenging to supply scientific predictions of the outcomes course of action. A great deal of attention has been paid to how decision-making has handled uncertainty within the epidemics response [24].

2.5.1 Decision under Uncertainty

The decision-making faced by a high-level government decision-maker during a crisis just like the COVID-19 pandemic is not trivial. Within the first stage, when a new infectious disease appears, the decision-maker may try to contain the outbreak by taking early actions to manage onward transmission (e.g. isolation of confirmed and suspected cases and contact tracing). If this phase is unsuccessful, decision-makers face a second-stage decision problem that consists of determining the acceptable level, timing, and duration of interventions to

mitigate the course of clinical infection, These interventions may include banning mass gatherings, closing schools, and more extreme “lockdown” restrictions [24].

a. Diagnosis

“We have a patient within the local emergency or clinic the patient has certain symptoms of a disease but doesn't have all the symptoms of the epidemic, is that the diagnosis is ruled out of the epidemic infection on this patient ?”

Diagnosis is the process of identifying a disease or condition that explains symptoms and signs of an infected person. It is one of the successful outbreak containment strategies and plays a large and sensitive role in medical decision-making. This is done by collecting information and examination results for ill people, comparing and analyzing them to find out the degree of disease severity, and then taking decisions such as quarantine in the case of a serious illness. wrong test results may negatively affect the decisions taken, for example in the case that symptoms appear late for a person whose test results were negative, this will lead to the spread of the disease. One of the strategies is to learn more about why the test result is negative that's why it's needed to keep the patients under control for a period of time (24 to 48 hours) and test them after to improve the sensitivity and accuracy of the judgment. For this reason, there is some requirement to take into consideration that the tests for the epidemic are not always accurate and there are thresholds in the diagnosis decisions [25].

b. Treatment

“The patient is hospitalized and now has confirmed that has the disease. Now how the patient should be treated ?”

Treatment is a difficult decision-making dilemma, as doctors and public health officials have different opinions about it. The lack or absence of medicines and vaccinations for some diseases, the decisions taken are for example: isolating infected or suspected individuals, and on the contrary, in the new emerging diseases. It takes a long period to make the vaccines due to the few information and the mechanism of the pathogen. In this case, the patients treated with antibiotics with a certain environment and respiratory machines if needed, the decision to use it or not will be difficult due to lack of complete knowledge such as the effects resulting from its use after a period of time [25].

c. Prevention :

“So what's the best protection from the disease ?”

Prevention is a procedure of decisions to take control of infectious diseases. One of these decisions is to, wear masks, wash the hands with hand hygiene and test the temperature for all visitors, doctors, and nurses. However, this prevention alone is not enough, it must be combined with other factors such: proximity distance to the patient at least 1 meter, personal protection equipment, disinfecting the surface of the clinic with chlorine every 4 hours and secure the entrances of building from the infected, these decisions can provide more protection and lower the chance for the doctors and other patients to get infected [26].

2.5.2 Decisions with scientific help

Scientific knowledge is foundational to the prevention, management, and treatment of world catastrophes. These informations helps us brace ourselves for the epidemic, its knowledge came from scientists and their research. A vital part of the scientific evidence comes from quantitative models that mixes what is known normally with what's known about the considered outbreak to provide predictions to assist guide decision-making within the epidemic.

Epidemiological models are accustomed guide decision-making by evaluating what's likely to happen to the transmission of the virus, usually these decisions are made under enormous time pressure and scientific uncertainty, with minimal quality evidence and potential disagreements among experts and models, this leads to quick decisions like closing down schools or wearing masks publically. Models can give decision-makers guidance by helping them understand the fragments from the data available, and eventually determine the suitable decision. Uncertainty within models reflects the risk quality concept. this corresponds, for instance, to the uncertainty of some model parameters, such as the amount of transmission that occurs in different age groups or the infectiousness of people before they show symptoms. Data, if available and reliable, can help examine model inputs. Finally, as models are, it could be incorrectly identified, as an example, they could not mention certain variables that matter, which modelers may be limited in the scope of functional relationships considered, unknown kinds of specification and measurement errors, so forth. It would sometimes be challenging, even for experts, to assess the merits and limits of other models and predictions therefore the decisions [24].

2.6 Conclusion

In this chapter, we discussed some basic concepts about the decision and the process of decision-making. In addition to some systems such as interactive decision, support systems

as well as spatial decision-making systems. These two systems are used to support and facilitate the decision-making by the best possible information available introduced by the systems. Ultimately, we briefly talked about the use of decision-making in epidemics, as well as how scientific knowledge helps this process.

Chapter 3

Proposed epidemic spread model

3.1 Introduction

The emergence of dangerous infectious diseases and their diversity leads to the need for study and analysis to understand the mechanism of their spread in order to control them.

In this chapter, we are interested in modeling the phenomenon of the COVID-19 epidemic transmission in the human population by proposing a new model that helps to understand the mechanism spread.

3.2 Objective of our system

The aim of this study is to model COVID-19 infectious diseases by developing a new model named Susceptible- Exposed-Infected-Quarantined and Recovered based on Scale Free network (SEIQR-SF) to simulate the propagation of the pandemic. Our tool is useful for evaluating hypotheses about the biological systems of the disease. It also enables us to follow the evolution of the epidemic over time, understand the mechanism of spread in the population and the effect of quarantine in reducing infection.

3.3 Identifying the problem

Before starting to explain the model, we will talk about some concepts and definitions. In this work, we are interested in Coronavirus Disease 2019 (COVID-19):

3.3.1 Disease definition

COVID -19 is the disease caused by the emerging coronavirus called Corona-SARS-2. This emerging virus discovered for the first time on December 31, 2019, after a group of viral respiratory illness cases were reported in Wuhan City, China [31]. According to the available evidence, the virus has a natural animal origin and is not a constructed or manipulated virus.

3.3.2 Transmission mechanism

COVID -19 can be transmitted between people in three different ways, namely:

Direct way: when a person meets a person who has respiratory symptoms (such as cough or sneeze), he becomes susceptible to receive disease through droplets and very small particles that contain the virus;

Indirect way: The infection is also transmitted through contact with surfaces or tools used by the infected person;

Through the air: the transmission of the virus through the air can occur in crowded indoor spaces and places for example: restaurants, schools, markets, etc.

3.4 Description of the proposed SEIQR-SF system

In this study, we develop simulation of the COVID-19 spread in human population. The system is mainly based on three components: parameters of the model, the SEIQR epidemic compartment model based on the Scale Free (SF) social network and visualization model. The visualization system shows the simulation results, which are curves (plots), and social networks that show the evolution of each compartment through time, and then are compared with real data. In our case, we used Algeria data. Figure 11 illustrates the global system:

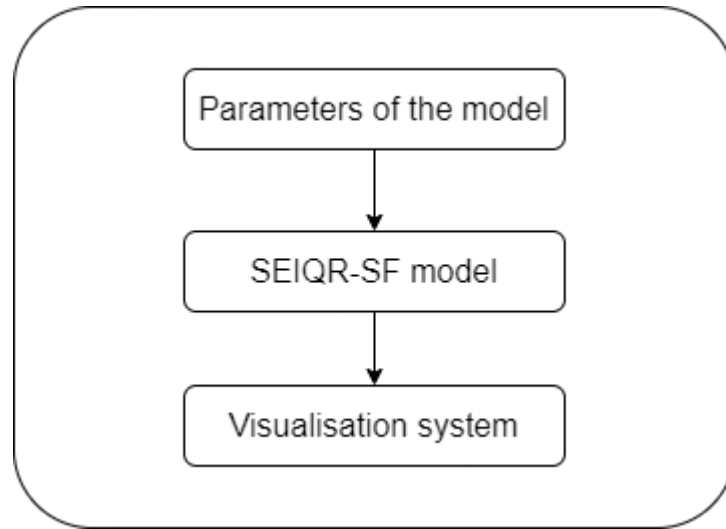


Figure 11 : Proposed SEIQR-SF System

In order to create a social network which is described as a set or groups of people with patterns of contacts or interactions between them, where these interactions allow the disease to spread, we chose a type called scale-free network because it seems to be the closest to represent the real world better than random networks [27]. The nodes in scale-free network aren't randomly or evenly connected, some of them have low connectivity, the others are highly connected, and this is what applies to the real world. The people do not have the same number of relations. The hubs help to know the difference in the speed of the disease spread among individuals, they are referred to as super-spreaders.

a. Basics concept

In order to model social contacts between human populations, we build a SF network by representing individuals by nodes and social relations by links.

A network is described by a graph $G = (V, E)$ made up of a set of vertices (also called nodes) $V = \{v_0, v_1, \dots, v_{n-1}\}$ and a set of links (also called edges) $E = \{e_0, e_1, \dots, e_{m-1}\}$. Each edge 'e' is defined by a pair of vertices $\{v_i, v_j\}$.

In an undirected graph, the degree of a node i represents the node's neighbors, which is the number of connections (links) with the other nodes of the graph, denoted by $k(i)$.

We denote $T = \{ t_0, t_1, \dots, t_m \}$, the sequence of time during which the disease transmits, and $G = \{ G_{t_0}, G_{t_1}, \dots, G_{t_m} \}$ the sequence of networks, where each element represents the state of the network at time t_l .

b. The generation of the SF network

We start by creating a network G with ' n ' nodes (the total number of nodes representing the total population) and ' m ' number of edges to attach from a new node to existing nodes.

We assume that the contact networks will be undirected graphs such that the link between two nodes (source, target) is the same as (target, source). The algorithm to build the network is as follows:

1. creating an initial complete graph by connecting a small number of nodes to each other, the number of initial nodes is given by the parameter ' m_0 ', this step is provided by lines (from 3 to 9).
2. The remaining nodes will be added each one separately and will be connected with the other nodes with the same fixed number ' m ' of new edges based on maximum degree probability $P(k_i) = k_i / \sum_j k_j$.

Where k_i is the degree of node and $\sum_j k_j$ is the total number of edges in the current network.

The figure below present a diagram describing the generation of the SF network:

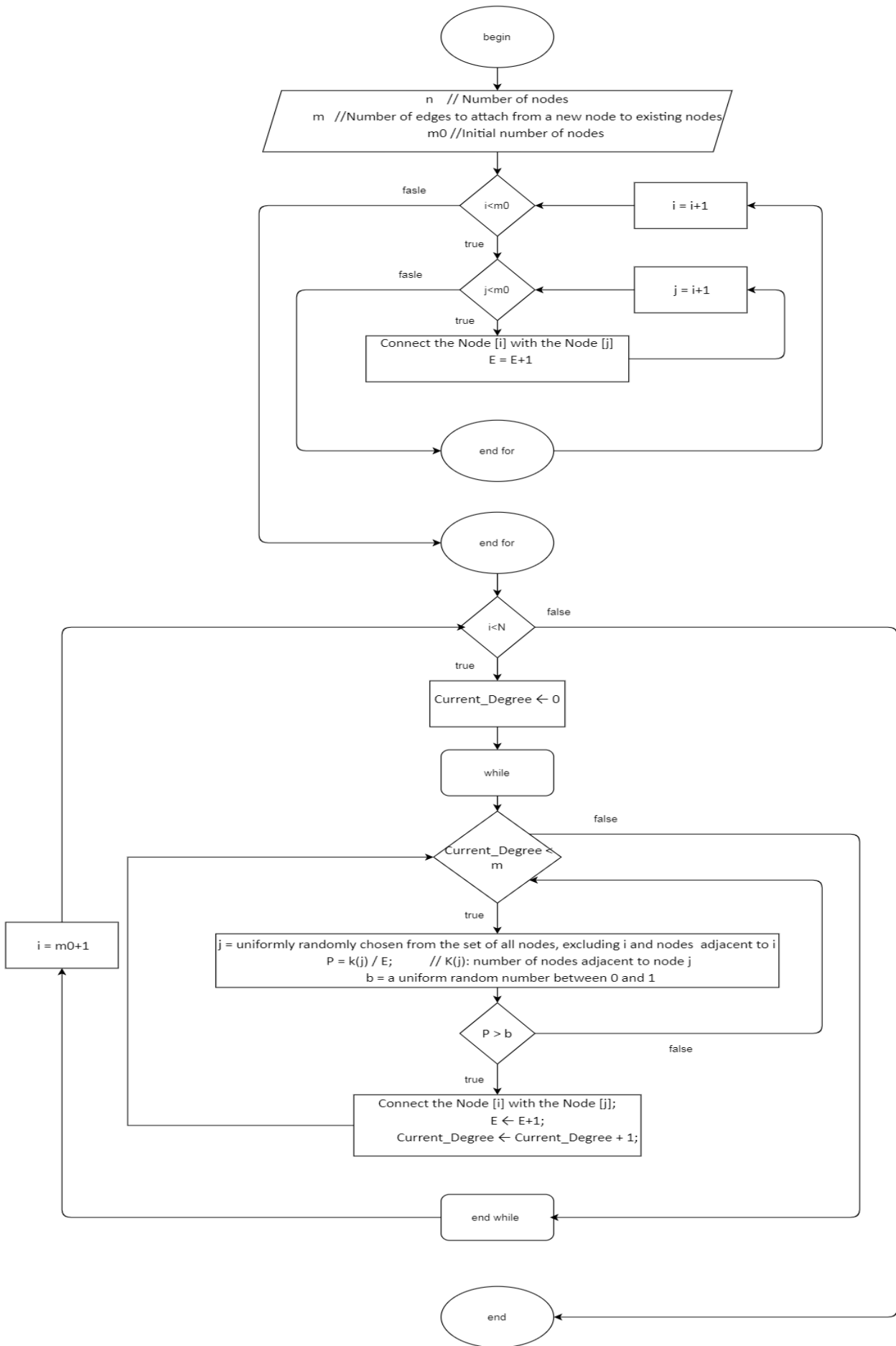


Figure 12 : The generation of the SF network

The execution result of the algorithm provides two lists of nodes: source nodes and target nodes. The representation of the adjacency list is illustrated in Figure 12

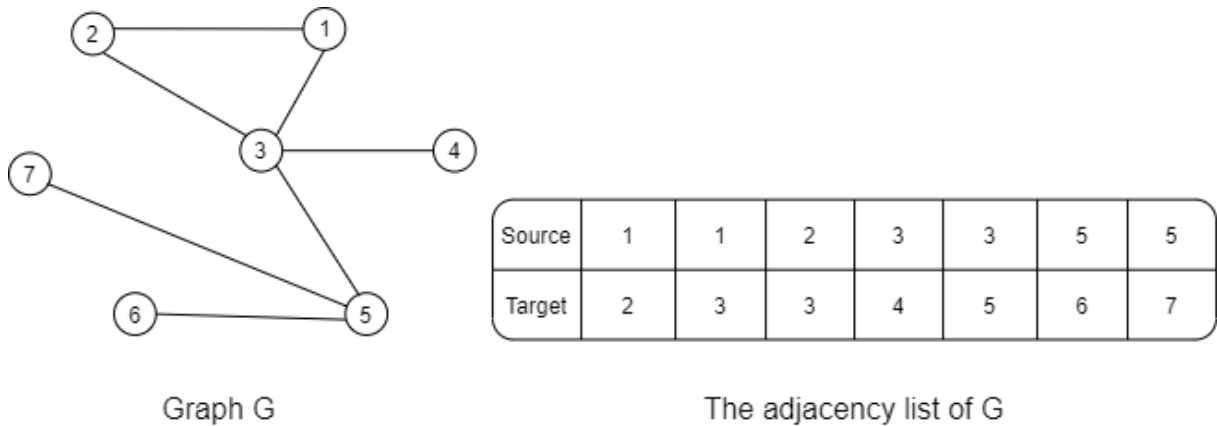


Figure 13 : The generated graph and the adjacency list

c. The SEIQR epidemic model

Among the proposed and known models for studying the spread of infectious diseases such as (SI, SIR, SEIR, etc.), we focused our work on the SEIQR compartment model, which is appropriate to study the transmission of the COVID-19 in a fixed population.

In this model, the population is made up of five classes of individuals: $S(t)$, $E(t)$, $I(t)$, $Q(t)$ and $R(t)$ where the number of individuals is variable over time. These classes are used to represent the health state of individuals as shown in Figure 13.

We didn't consider the effect of the natural death or birth rate so that the total population is affected only by death caused by the disease.

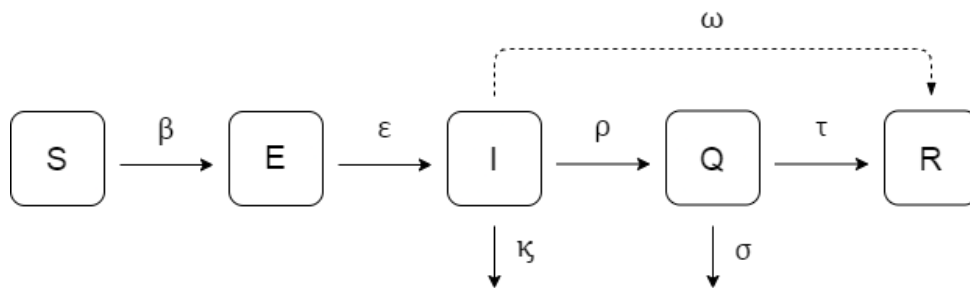


Figure 14 : Scheme of the SEIQR model

- Each susceptible individual moves from the susceptible class to the latent class (E) with a rate β after direct contact with an infected person.
- After the end of the latent period, the person moves from the exposed class to the infected class with a rate ϵ

- ρ and ω are rates at which individuals leave the infected class and move to quarantined and removed classes respectively, or die at a rate κ
- The parameters τ, σ is the rates at which those of the quarantined class pass to the recovered class or die

We assumed that the infection spreads in a direct way between infected and susceptible individuals.

We consider a closed population of individuals who are divided into five groups at all times $t > 0$. At each unit of time t , $N = S + E + I + Q + R$, where N is the total size of population, the initial conditions are $S(0) = S_0$, $E(0) = E_0$, $I(0) = I_0$, $Q(0) = Q_0$ and $R(0) = R_0$, respectively.

Parameters and state variables used by SEIQR-SF shown in Table 1

Table 1 : Summary of parameters and state variables used by SEIQR-SF

State variables	Meaning
S	Number of susceptible individuals
E	Number of exposed individuals
I	Number of infected individuals
Q	Number of quarantined individuals
R	Number of recovered individuals
S_0	Number of susceptible individuals at $t = 0$
E_0	Number of exposed individuals at $t = 0$
I_0	Number of infected individuals at $t = 0$
Q_0	Number of quarantined individuals at $t = 0$
R_0	Number of recovered individuals at $t = 0$
Parameters	Meaning
L	Adjacency list of a node
β	Transmission rate
ε	Latency rate
ρ	quarantine rate
ω	Recovery rate
κ	Death rate
τ	Recovery rate
σ	Death rate

3.5 The process of applying the SEIQR-SF model

During the disease, individuals can have six states: $V = \{\text{Node.S, Node.E, Node.I, Node.Q, Node.R, Node.D}\}$. We defined $S(t)$, $E(t)$, $I(t)$, $Q(t)$, $R(t)$ and $D(t)$ as the lists of individuals for each state and $G(t)$ as a SF network obtained by diagram 1. We considered that 75% of infected people move to quarantine class, while the remain, 24% of them recover directly and 1% die [28].

The general process of the model is as follows:

1. Building a network.
2. A number of initially infected individuals is chosen.
3. The disease spreads through the network G if there is a relation between susceptible and infected individuals.
4. Then each individual will be infected after being exposed.
5. Every infected person either will be cured directly, or after being quarantined, or die.
6. The SF network $G(t)$ evolves to $G(t + 1)$.
7. Plot the results

Steps 3 through 6 will be repeated until no individual is infected.

The figure illustrate the SEIQR-SF creation steps:

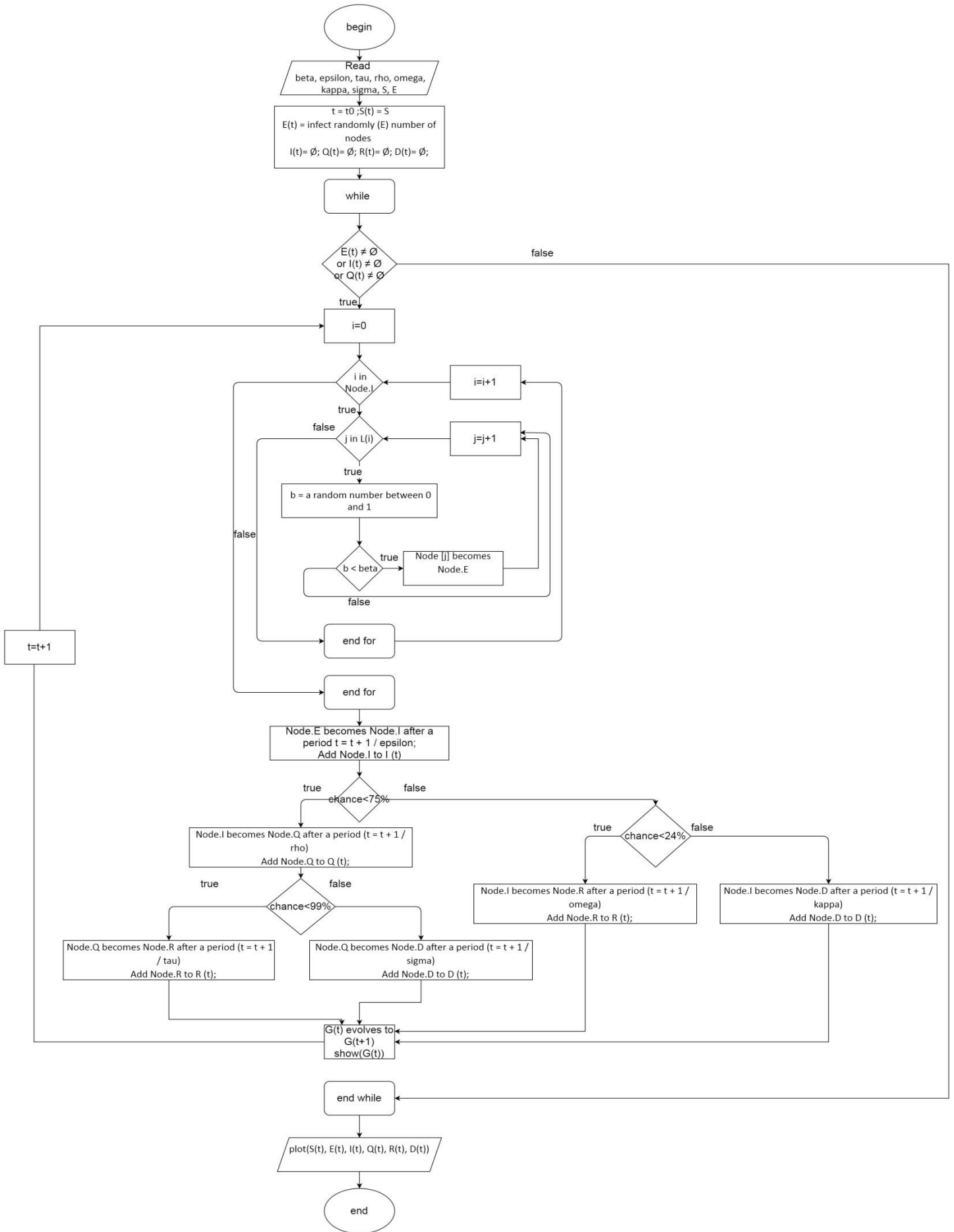


Figure 15 :The SEIQR-SF Model
26

3.6 UML modeling

We choose the UML model, which provides a simplified and planned view of the proposed system. We present the UML diagram corresponding sequences.

Sequence Diagram

The figure 14 shows the sequence diagram of SEIQR-SF:

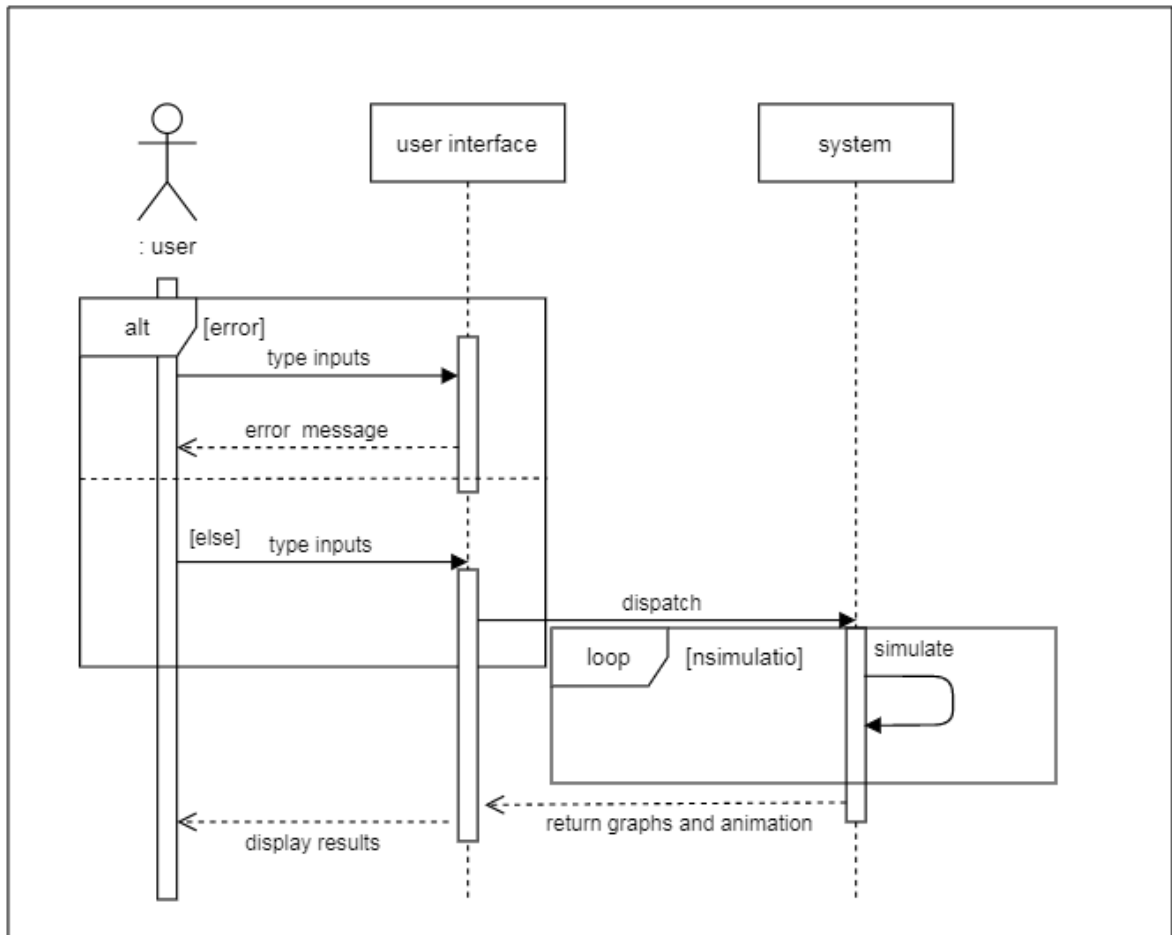


Figure 16 : Sequence diagram of the SEIQR-SF system

Datasets

The database used in this study concerns the COVID-19 disease of 2020 in Algeria. It's made up of 48 tables for all provinces of Algeria. The data contain cumulative confirmed infected cases for each day between 04/01/20 and 10/01/20. Figure 15 represents curves for data of three provinces in the total population.

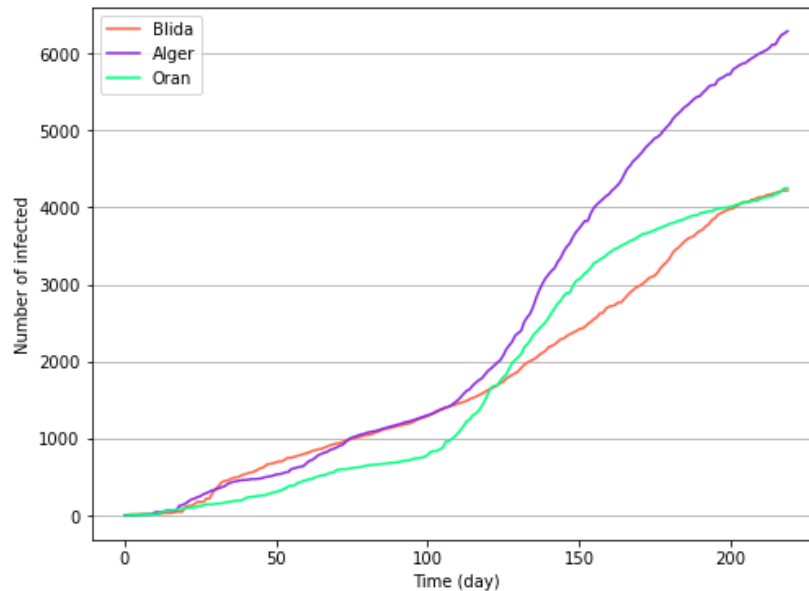


Figure 17 : Evolution of the number of infected people with covid-19

Input and output

In this study, we used a stochastic SEIQR model to simulate the disease transmission, for that, we must begin with the creation of the network and specifying its properties, which are the initial number of the population and the infected people, rates that determine their behavior and the number of the simulations.

The program calculates the average of these simulations and returns a graph that represents data for each class of the model over time (days), a graph showing the cumulative number of infected individuals and an animation illustrating how the illness spreads between the nodes. Finally we compare the results with the real data to obtain disease parameters.

3.6 Conclusion

In this chapter, we describe and detail the SEIQR-SF propagation model that we proposed to control and understand the spread of the COVID-19 epidemic. This model makes it possible to simulate and study the evolution of the epidemic's spread process. The SEIQR-SF system can help healthcare professionals make good decisions.

In the chapter 4, we will give some illustrations and results obtained from SEIQR-SF system.

Chapter 4

Implementation

4.1 Introduction

The interaction between people and digital technology has been thoroughly recorded in recent decades, and it has yet been examined in light of the present worldwide pandemic threat of the COVID-19. Due to these technologies, we can better understand the disease spread.

In this chapter, we explain how disease simulations can help getting an idea of how it spreads by implementing the SEIQR-SF proposed system.

4.2 Tools and techniques

To develop our system, we shall use several tools for testing and analyzing data. In what follow, we present the definition of tools and techniques that we used to achieve this project:

4.2.1 Python

Python is object-oriented, multi-platform, open source and high-level programming language, it is the most widely used among computer scientists. Developing code with Python is easy and fast, because there are no form constraints that occupy time as in other languages, it supports modules and packages, which encourages program modularity and code reuse.

The main uses of Python by developers are programming applications, machine learning, data science, creation of web services, code generation, scripting and automation (interaction with web browsers).

Anaconda

Anaconda is an open source software. It makes it easy to develop python programs in data science and machine learning, it is a toolkit that equips you to work with thousands of open-source packages and libraries. With the help of multiple IDE it's the most popular python distribution platform as it provides utilities to build, distribute, install, update, and manage software in a cross-platform manner. It makes it easy to manage multiple data environments that can be maintained and run separately without interference from each other.

Spyder

Spyder, the Scientific Python Development Environment, is a free integrated development environment (IDE) that is included with Anaconda. It includes editing, interactive testing, debugging, and introspection features.

PyQt5

PyQt is a module, which allows linking the Python language with the distributed Qt library. It allows the creation of graphical interfaces in python. An extension of QtDesigner (graphical utility for creating Qt interfaces) allows you to generate python code for graphical interfaces. It is one of the most powerful and popular cross-platform GUI libraries.

draw.io

Is an open-source diagramming program used to draw diagrams and UML online stores the content of the diagram, which may include text, shapes, icons, and images, along with formatting information. DRAWIO files are used to preserve a variety of diagrams, including organization charts, process diagrams, and flowcharts.

4.3 Results and Analysis

The application consists of a top bar and four pages each representing the main functionalities of SEIQR-SF system. The top bar is the input form of SEIQR-SF system, which is the disease parameters.

The figure below shows the first page, which is the main page. Here, we can found different functionalities of SEIQR-SF system, for example the animation. The later contains a media player that displays the simulation as a video showing the transmission of the disease in the human population during a period.



Figure 18 : Screenshot from SEIQR-SF system for COVID-19 spread over time

First, the user must identify the simulation parameters and initial conditions (in order for the epidemic to start, there should be at least one exposed or one infectious human). The initial conditions are the initial number of population S_0 and the infected I_0 , the rates of the SEIQR model, which were explained in Chapter 3 are shown in Table 1, and the number of simulations. The program runs the simulation n times and calculates the average to obtain result similar to the real data in the best fit.

4.3.1 The parameter values of the SEIQR-SF system

In the SEIQR-SF model, we use different parameters values obtained from different sources. The table 2 shows the different parameter values

Table 2 : The values of the parameters and state variables used by SEIQR-SF

	Parameters	Values 1	Values 2	Source
Population parameters	S_0	8000	5000	Estimated
	I_0	10	10	Database
SF network parameters	Degree of distribution	5	5	Estimated
	Number of simulations	10	10	
Disease parameters	β	0.024	0.021	Estimated
	ε	4	4	[29]
	ρ	3	3	[29]
	ω	14	14	[29]
	κ	8	8	[29]
	τ	15	15	[29]
	σ	4	4	[29]

The values 1 were obtained from the data of the city of Blida and the values 2 were obtained from the data of the city of Oran. This choice is due to the highest confirmed cases of COVID-19 in the two cities.

4.3.2 Result from the scale free network

As results obtained from SEIQR-SF system, we have the generated data of SF network. Figure 17 illustrates the tabular data of SF network it is an adjacency list describes the set of neighbors of each patient.

	A	B	C
1	Patient	neighbor	
2	0	5	
3	0	6	
4	0	8	
5	0	10	
6	0	12	
7	0	13	
8	0	16	
9	0	30	
10	1	5	
11	1	6	
12	1	7	
13	1	8	
14	1	9	
15	1	11	
16	1	12	
17	1	13	
18	1	14	
19	1	15	
20	1	16	
21	1	17	
22	1	18	

Figure 19 : Screenshot of adjacency list

For better readability of the network, we have chosen a small network, which consists of 52 nodes as in Figure below. Here, we use Open Graph Viz Platform to visualize our network. The nodes are colored according to their node degree.

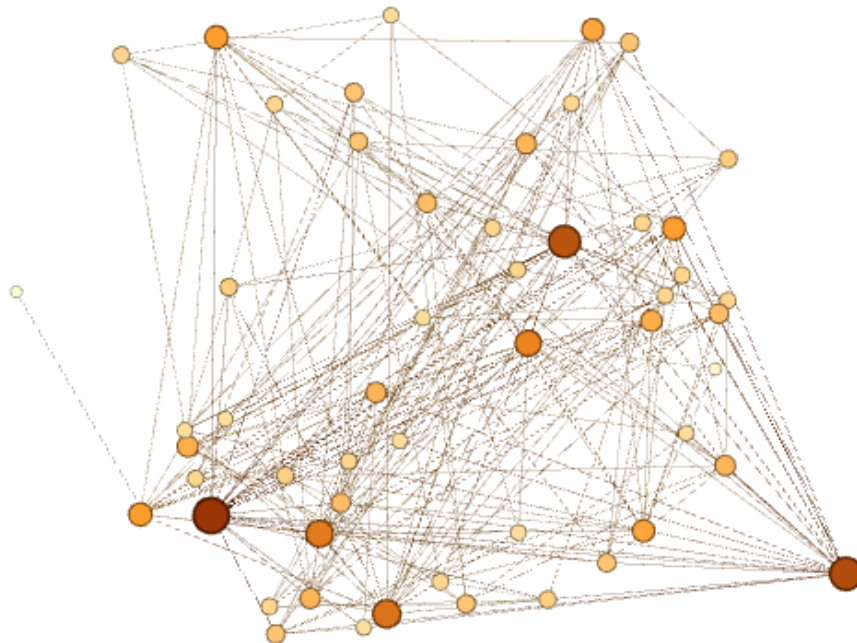


Figure 20 : Small network consists of 52 nodes

4.3.3 Result from the SEIQR-SF system

After launching the simulation, we can follow the COVID-19 spread over time through the animation shown in Figure 19.

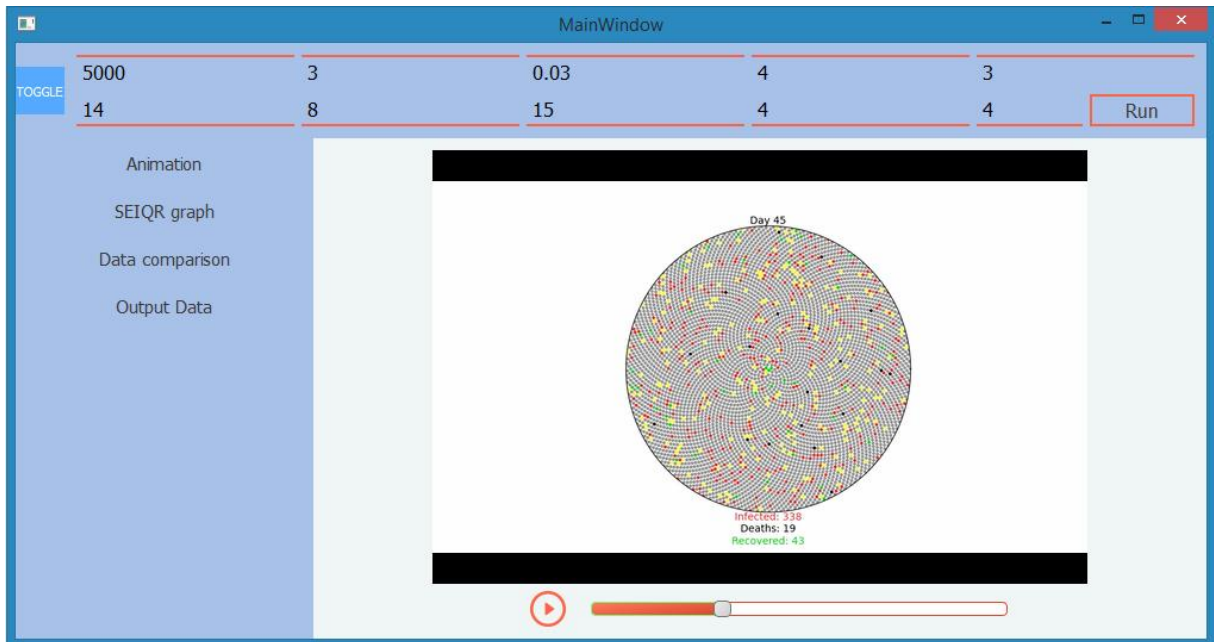


Figure 21 : Screenshot from SEIQR-SF system for the network animation

The animation illustrates how the illness is spreading within the nodes over time (days). We used five colors assigned to each class of the model: the susceptible shown in grey color, the exposed people shown in the yellow color, infected and quarantined shown in the red color, recovered in green and dead in black. The figure 20 shows the evolution of the network over time.

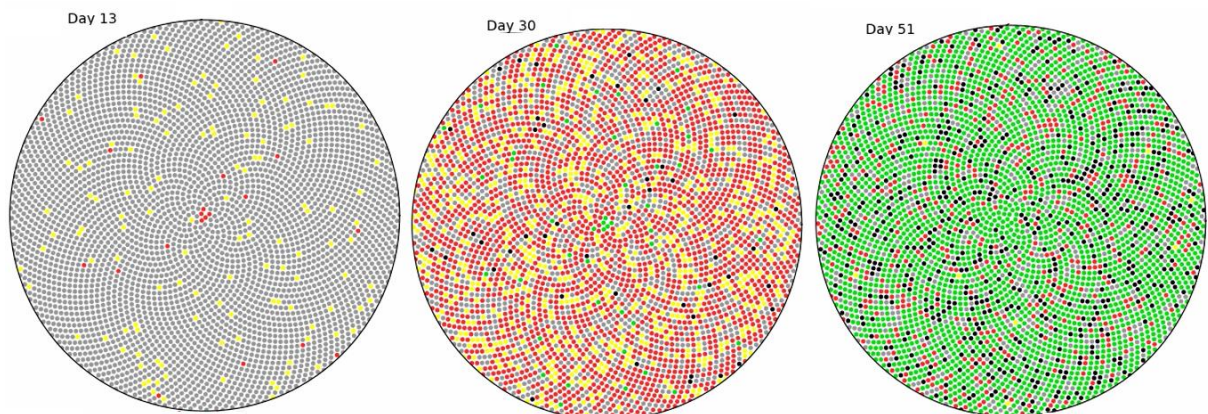


Figure 22 : Screenshot from SEIQR-SF system for the network evolution over time

The second page displays graphs explaining the five components of the model and their behavior from the beginning of the simulation to the end. Figure 21 shows an example of different curves obtained from SEIQR-SF simulation.

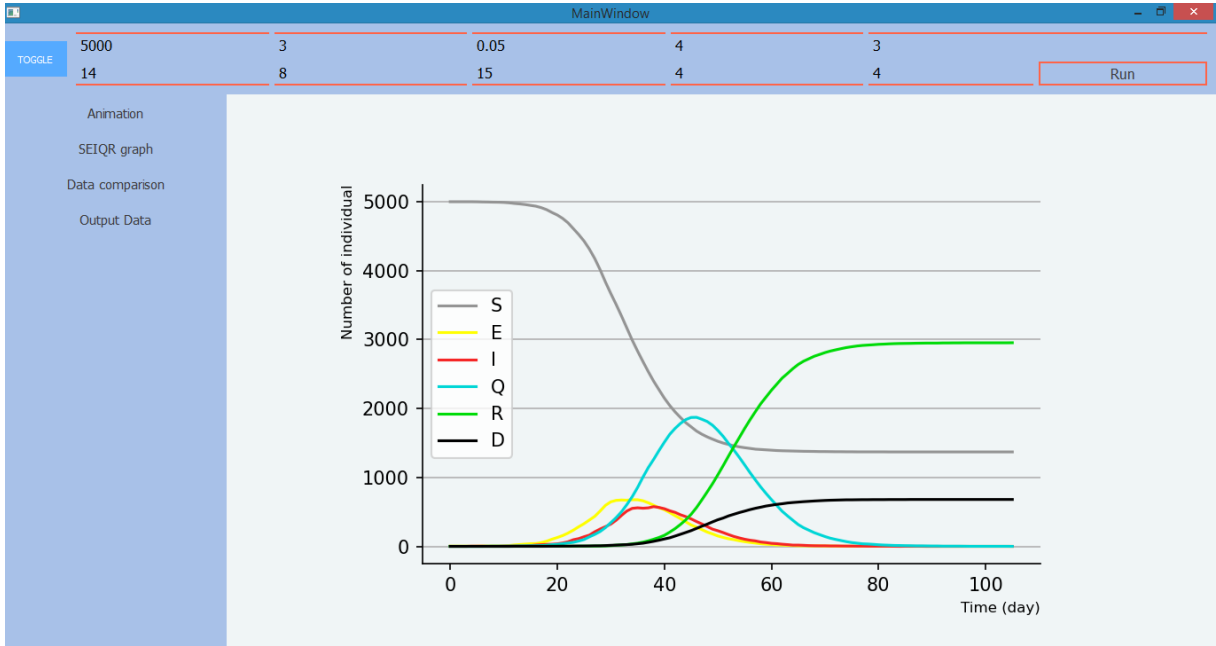


Figure 23 : Screenshot from SEIQR-SF system for different curves

The third page displays a graph containing real data compared with the simulation data, it shows changes in the cumulative number of infected individuals over time. To obtain this graph we must import the data file which is an excel file with data sorted in descending order. As an example we used data of the city Blida of Algeria (Figure 22).

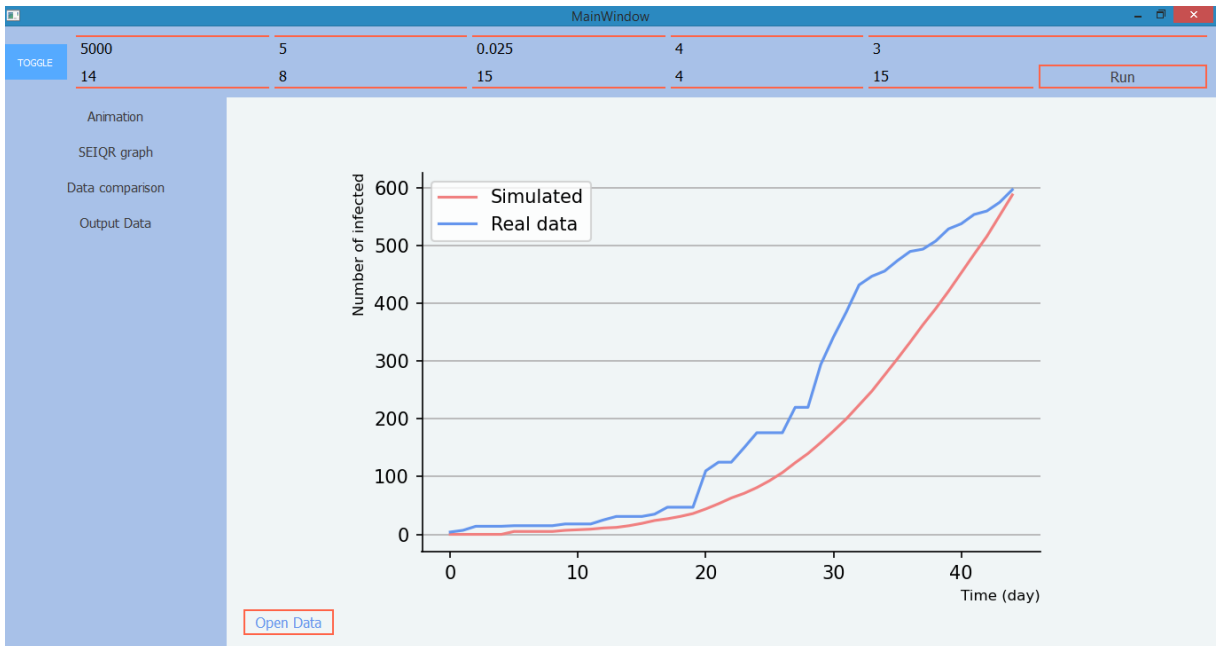


Figure 24 : Screenshot of data comparison

The last page displays the output data for the simulation. This data can help us keep track of and read the evolution of each compartment all the time.

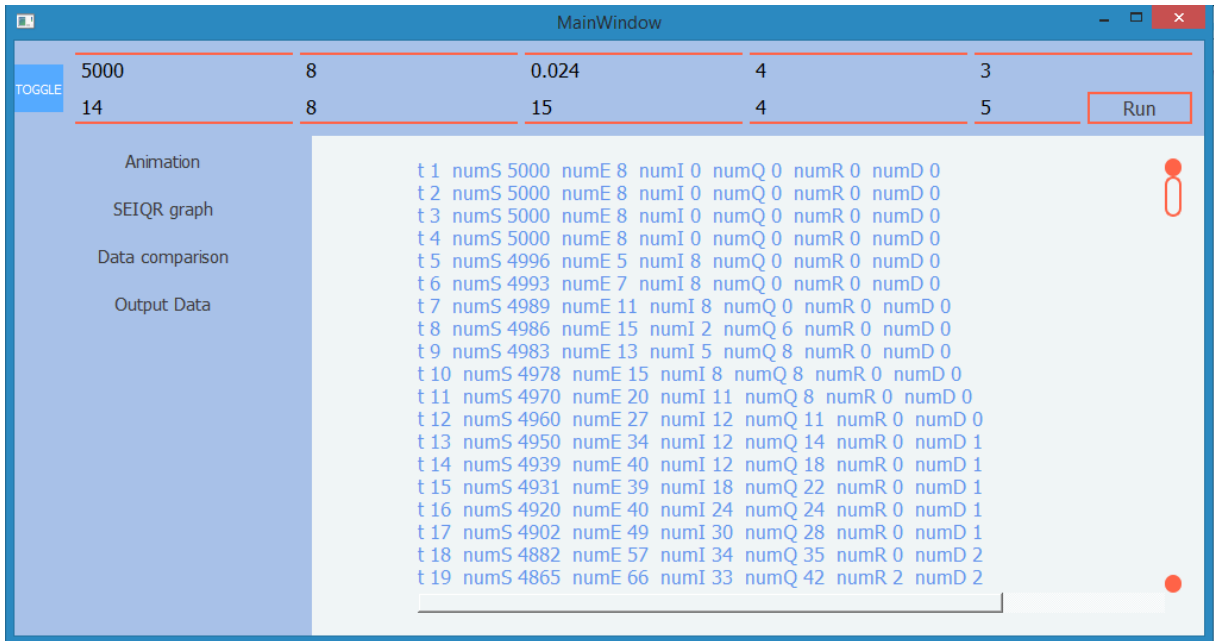


Figure 25 : Screenshot of data output: evolution of the COVID-19 over time

4.3.4 Validation model

To validate our model, we performed simulation with the parameters illustrated by the table above (Table 2). The results obtained are shown in Figure 24 and 25. We compare the evolution of the curves obtained by the model and the COVID-19 data for the two cities of Algeria. We notice that the difference between the two curves in each figure is almost small, this means that the chosen parameters are close to the real parameters.

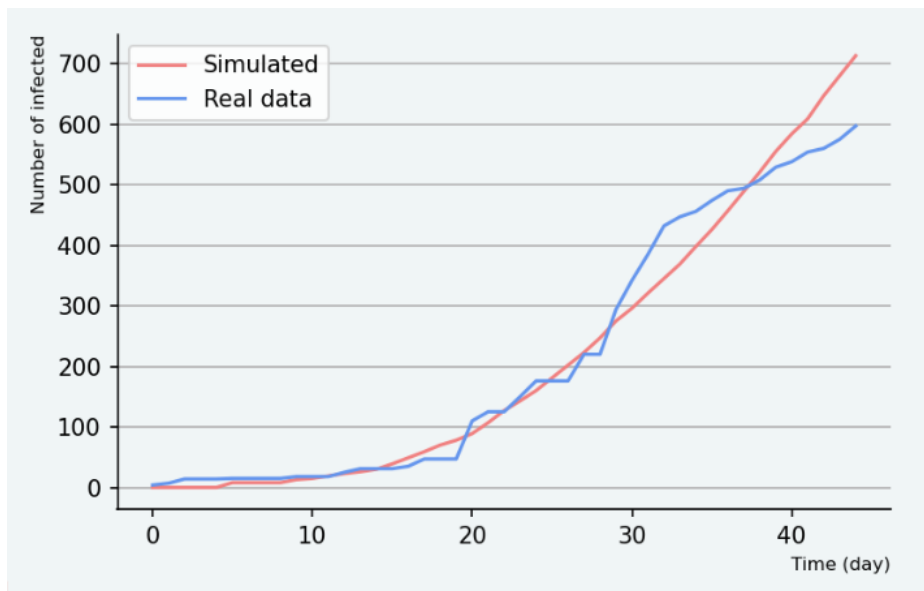


Figure 26 : Screenshot of data comparison

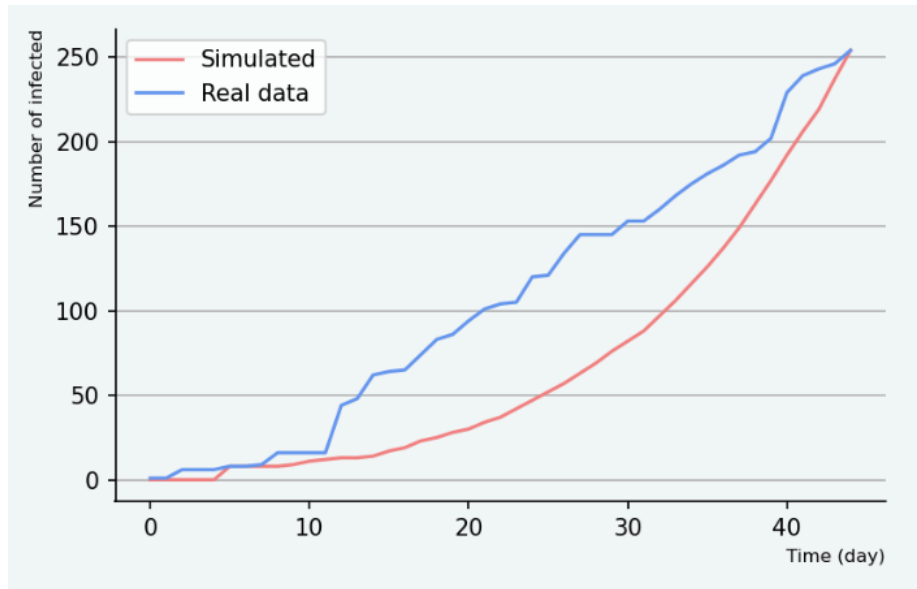


Figure 27 : Screenshot of data comparison

Linear correlation

Correlation is widely used in the sciences as a measure of the degree of linear dependence between two variables [30]. Here, it was used to measure correlation between the SEIQR-SF outputs and real data. A significant positive correlation was found, as shown in Table 3. The SEIQR-SF model accurately modeled the dynamic behavior of observed data used in our study.

Table 3 : Correlation between numerical simulations SEIQR-SF model outputs and real data

	Wilaya of Oran	Wilaya of Blida
Correlation value	0.72	0.9

4.3.5 Geographic representation

One of the ways to analyze the data is to display it on a geographical map, it can help in visualizing and evaluating the geographic distribution of illnesses across time, to make crucial decisions. This method is effective and has been used before in many illnesses and pandemics.

As in our project we obtained results that simulated from a few cities in the region near the capital of Algeria (Alger) and displayed it on the map (Figure 28)

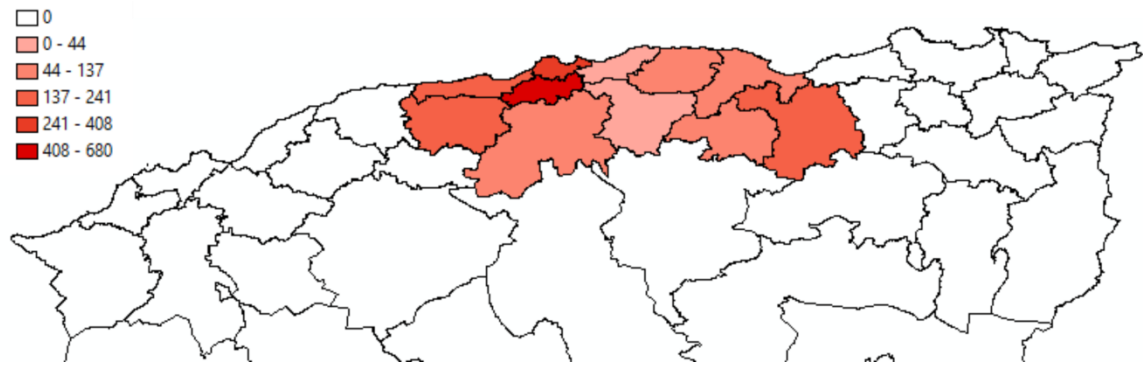


Figure 28 : Cartographic representation

4.4 Conclusion

In this chapter, we presented some illustrations of SEIQR-SF system output. First, we provided a brief description of the tools used. Then, we presented some screenshot from SEIQR-SF system (network visualization and plots). Finally, we performed simulations and compared them with the available data to obtain the significant parameters of the disease.

General Conclusion

According to the World Health Organization (WHO), infectious diseases are responsible for a quarter to a third of all deaths worldwide, it presents a significant morbidity and mortality burden on the population. Moreover, it is crucial to understand how a disease spreads in modern society and identify epidemic outbreak areas. Indeed, faced with such a threat, the society has to get ready in advance to react quickly and effectively if such outbreak is declared. Epidemic models are used extensively in analyzing the spread, and control of infectious diseases qualitatively and quantitatively. Indeed, in the present work, we proposed and discussed a new decision making system for epidemic surveillance. The system named SEIQR-SF is developed to monitor and control COVID-19 spread in human population. The mathematical model SEIQR proposed and the social network free scale in order to understand the mechanism of the virus therefore controlling it and prevention of epidemic spread.

In this manuscript, first, we discussed the most famous epidemic models. We presented the two kinds of them: deterministic and stochastic models. Then, we detailed some compartment models. We defined and introduced the mathematical models precisely the compartmental models and their concept in epidemics and briefly about social contact network. Next, in chapter 2, we detailed the decision-making concepts; we explain the decision support systems, which has significantly changed the decision-making process. It allows decision-makers better managing the mass and complexity of information. In chapter 3, we explained the new proposed system that is based on Scale Free network as well the concept and how the generation of this network work by illustrating two sequence diagrams and detailing each compartment and parameter of this SEIQR-SF model. Finally, in the last chapter we introduced and defined the tools that we worked with, and explaining the input, the parameter values of the system, and the output of the simulation. We closed the chapter by calculating the correlation values of the two-hottest area of the COVID-19 outbreak in Algeria.

Annex

Epidemiology

1. Some definitions

Exposed: An individual is said to be exposed when they have an infectious disease and are not contagious.

Infected: an individual who has been affected by the disease and is contagious.

Susceptible: An individual who has not yet been infected and is exposed to the disease is said to be susceptible.

Quarantined: An individual who is infected and in a quarantine for a certain period

Recovered: An individual who was infected but now cured and in a recover state

Germs: virus, bacteria, parasite, fungus, prions.

COVID-19 : is an infectious disease caused by a newly discovered coronavirus.

2. Epidemiological forms of diseases

Endemic: is the usual presence of disease in an area.

Epidemic: The rapid emergence or spread of an infectious disease, usually by contagion, which affects a large number of people at the same time. This number exceeds the number of cases normally expected.

Pandemic: A pandemic (outbreak or epidemic flush) occurs when a large portion of the world's population is infected with a virus to which the immune system has not yet developed an adequate response.

3. Epidemiological indicators

1. **Mortality indicators:** describe the frequency (rate) of deaths
2. **Morbidity indicators:** describe the frequency of diseases (prevalence and incidence)

Bibliography

- [1] J. H. Klaus Dietz a, "Daniel Bernoulli's epidemiological model revisited," June 2002.
- [2] "Scientific Models: Definition & Examples," [Online]. Available: study.com.
- [3] T. B. Hakan Andersson, "A simple epidemic model: The Reed-Frost model," *Stochastic Epidemic Models and Their Statistical Analysis*, pp. 4, chapter 1.
- [4] A. D. Gwangju, "Deterministic Models in Epidemiology: from Modeling to Implementation," *Institute of Science and Technology*, Institute of Science and Technology March 2013.
- [5] H. W. Hethcote, "The mathematics of infectious diseases," pp. 599-653, *SIAM Rev*, vol 42, no 4, 2000.
- [6] W. H. Hamer, "The Milroy lectures on epidemic disease in England," *the evidence of variability and of persistency of type*, 1906.
- [7] W. O. e. M. A. G. Kermack, "A contribution to the mathematical theory of epidemics," pp. 700–721, volume 115, 1927.
- [8] E. P. Gauthier Sallet, "Mathematical Epidemiology: SEIR model," pp. 41-43, Institut Elie Cartan, UMR CNRS 7502, Université de Lorraine, March 2018.
- [9] "A delayed SEIQR epidemic model with pulse vaccination and the quarantine measure," *Computers & Mathematics with Applications*, pp. 135-145, Volume 58, Issue 1, July 2009.
- [10] "A SEIQR model for pandemic influenza and its parameter identification," *International Journal of Pure and Applied Mathematics*, vol. 52 , no. 2, pp. 247-265, 2009.
- [11] M. C. K. M. K. Melissa Tracy, "Agent-Based Modeling in Public Health: Current Applications and Future Directions," *Annual Review of Public Health*, vol. 39, pp. 77-94, April 2018.
- [12] "Epidemic Spreading in Urban Areas Using Agent-Based Transportation Models Jürgen Hackl and Thibaut Dubernet," pp. 1-2, 8 April 2019.
- [13] H. W. C. W. (. M. I. A. H. F. ZHAOYANG ZHANG1, "Modeling Epidemics Spreading on Social Contact Networks," pp. 1-3, September 2015.
- [14] T. Britton, "Epidemic models on social networks," pp. 2-3, 2015.
- [15] B. D. Roy B, "Aide Multicritère à la Décision," *Méthodes et Cas, Paris, Economica.*, 1993.
- [16] P. L. a. J. Pomerol, "Systèmes interactifs d'aide à la décision et systèmes experts," 1989, Edition

Hermès..

- [17] d. baker, "Guidebook to Decision-Making Methods," January 2001.
- [18] S. H., "The New science of management decision," Prentice hall, New Jersey 1977.
- [19] J. D. Little, "Management Science.," *Models and Managers: The Concept of a Decision Calculus.*, 1970.
- [20] G. A. a. S. S.-M. Gorry, "A Framework for Management Information Systems," Sloan Management Review 13, 1971.
- [21] S. Garlatti, "Multimédia et systèmes interactifs d'aide à la décision en situation complexe," 43th meeting of the european working group, "Multicriteria Aid for Decisions" Brest, Finlande. march 1996.
- [22] R. W. E. & S. M. Beard, "A systematic review of spatial decision support systems in public health informatics supporting the identification of high risk areas for zoonotic disease outbreaks.," *Int J Health Geogr*, vol. 38, no. 17, 2018.
- [23] M. E. Corinna Keeler, " Geographic Information Systems (GIS) in Public Health," 2017.
- [24] B. N. B. V. G. I. H. L. J. C. M. M. S. R. Berger L, "Rational policymaking during a pandemic," 2021, Proceedings of the National Academy of Sciences of the United States of America.
- [25] T. Prentice, "Managing Epidemics : Key Facts about Major Deadly Diseases," 2018.
- [26] A. K. Metlay J, "Clinical Decision Making During the COVID-19 Pandemic," 2021.
- [27] B. A. D and C. Aaron, "Scale-free networks are rare," 2019.
- [28] R. Julia, "Most COVID-19 Cases Come from People Without Symptoms," 2021.
- [29] Y. Hamdy and A. Najat, "Study on the SEIQR model and applying the epidemiological rates of COVID-19 epidemic spread in Saudi Arabia," vol. 6, pp. 678-692, 2021.
- [30] F. Z. Younsi, A. Bounnekar, D. Hamdadou and O. Boussaid, "SEIR-SW, simulation model of influenza spread based on the small world network," *Tsinghua Science and Technology*, vol. 20, no. 5, pp. 460-473, 2015.
- [31] R. Julien and L. A. Christian, "Pattern of early human-to-human transmission of Wuhan 2019 novel coronavirus (2019-nCoV), December 2019 to January 2020," *Eurosurveillance*, vol. 25, no. 4, 2020.

