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Stochastic epidemic models on dynamic networks

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Introduction

The main aim of mathematical epidemiology is to gain a better understanding of the spreading of infectious disease. In order to achieve this goal, when approaching an epidemic, two fundamental and challenging problems need to be solved.

Firstly, a good modelling of the epidemic's transmission mechanism has to be found. Secondly, those features that are most influential in the spread have to be identified. Only after overcoming those challenges, scientists are able to make reliable predictions and evaluate the effectiveness of control strategies. Unfortunately, this whole procedure is easier said than done: both due to the lack of available data and to computational limits, scientists have often been forced to oversimplify their models through approximations and unrealistic assumptions.

One of the most common simplifications is to assume *homogeneous mixing* of the population, which means that at any time each individual can come into contact with any other individual of the population. Even more sophisticated non-homogeneous network models often present a strong limitation, since it is common to assume that the network is static, i.e. that there is no temporal evolution on humans' contact. Complications do not arise only when addressing modelling of the spreading, because measuring infection dynamics over time also pose significant challenges. For instance, still nowadays many studies aim to describe the evolution of an epidemic by the so-called *basic reproduction number* R_0 , which is defined as “the average number of secondary infections that one single case would produce in a completely susceptible population”. Unfortunately, recent papers (see, for example, [1]) have highlighted the weakness of this approach. One possible solution is to consider the more general concept of *replacement number* R_t , which is defined as “the average number of secondary infections produced by a typical individual who becomes infective at time t ”. However, even studies based on the replacement number often lead to distorted predictions since they estimate R_t from the *generation interval* GT , which is “the time between the infection time of an infected individual and the infection time of his infector”, without taking into account the time-variation of GT ([5]).

The main aim of this thesis is to implement and analyze an in-vitro epidemic model which takes into account both the non-homogeneous mixing of the population and

the time-evolution of humans' contacts. Particularly, the analysis are focused on founding similarities and discrepancies between the mathematical properties of our and more classical models, and on confirming the fact that, even in a simple abstract model, some epidemiological quantities are strongly biased.

The first three chapters address different epidemic models, following both a chronological order and an ascending level of complexity.

In Chapter 1 we present some examples of *compartmental models*, originally introduced by W. O. Kermack and A. G. McKendrick in 1927 ([19]) and still representing a landmark for mathematical epidemiology. The rationale behind these model refers in splitting the population in labeled compartments, assuming the existence of an ODEs' system which rules the flows between them.

Chapter 2 is devoted to the stochastic epidemic models introduced by L. Allen ([2]-[3]-[4]). They are compartmental models either, with the exception that here the spreading is randomly described by Markov chains. We start from a discrete time model, and then we generalize the results in continuous time, underlying an almost equal behaviour in both the cases.

Chapter 3 introduces epidemic models in static networks. In the first section we describe a generating function approach which has been extensively studied, for example, by M. Newman ([11]). This approach links the early stage of an epidemic with percolation. In the second section, we discuss the relation between network models and deterministic models, following the work by F. Brauer ([7]-[8]). Particularly, we prove that under certain hypothesis on the graph and in the limit of infinite population, network epidemic models can be approximated with the more classical deterministic models. We end this chapter by deriving the N -intertwined epidemic model which has been studied in detail by P. Van Mieghem ([26]). In this model, each node of the graph follows a dynamic given by a 2-states continuous time stochastic process, which can be faced with usual Markov theories by making a mean field approximation.

In Chapter 4 we propose our original model, which is an epidemic model in a simple dynamic network. In the first section we give the mathematical description of the model, whereas in the second section we focus on its implementation. The last section is dedicated to simulations performed by different choices on the graph topology or on model's parameters. We start discussing the homogeneous case, in which each contact rate λ_{ij} is equal to a constant c . Here we underline relations between some of the main epidemiological quantities, but also their dependence on the constant c . Three interesting results are discussed:

- The basic reproduction number reaches a steady-state which doesn't correspond to a stop on the growing of the speed of the spreading.
- There is a different time-evolution of the generation time w.r.t the topology of the graph.

- When the contact rate is sufficiently large, the probability of an outbreak overlaps with the final size.

A first insight on the heterogenous case is also given: what we found is that the discrepancies with the homogeneous case are mainly quantitative.

Finally, Appendix A provides an insight of all the mathematical tools exploited more or less explicitly during the dissertation. A brief recap on Markov chain theory and graph theory is provided, with particular emphasis on Poisson processes and on computations for specific graphs, which are the key instruments in our model. Then, we make an excursus on some non-standard Linear Algebra's notions that are used in Chapter 2. Finally, Appendix B contains the whole Python code we wrote in order to implement our model and make simulations.

Chapter 1

Compartmental models in epidemiology

Mathematical epidemiology has a long history, going back to the smallpox model of Daniel Bernoulli in 1760. A massive development of this research area has occurred between 1900 and 1935, especially thanks to the work of Karmack and McKendrick on compartmental models ([19]), which are the simplest way to describe the spread of infectious disease. The idea behind those models is to split the whole population in labeled compartments, then assume that in some way people may progress between them. The most classical example, when referring to compartmental models, is the *SIR* model, in which a population is made of susceptible, infectious and recovered individuals: the aim of this chapter is to provide the main definitions and results of such a model, and then discuss some of its possible generalizations. We will follow very closely [7] and [22].

1.1 The SIR model without vital dynamics

Let us consider a population of $N = N(t)$ individuals and suppose for the moment that it is *closed* (SIR model without demography), i.e. that there are neither arrivals nor departures from the population, which size $N(t) \equiv N$ is consequently constant. From an epidemiological point of view, this simplification could be justified thinking that the time duration of the disease that we are considering is sufficiently small to avoid considering births and deaths. As we anticipated, the whole population is splitted in three compartments:

- **Susceptible:** individuals who have no immunity to the infectious agent, so might become infected if exposed.
- **Infectious:** individuals who are currently infected and can transmit the infection to susceptible individuals who they contact.
- **Recovered:** individuals who are recovered from the disease and are consequently immune to the infection. Since those individuals could neither infect nor been infected from other individuals, they don't affect in any way the transmission dynamics: for this reason, many authors call "Removed" the individuals of this compartments.

For the sake of brevity, we will indicate with S, I and R respectively the number of susceptible, infectious and recovered individuals. Those quantities must be integers, of course, but we can assume that the size of the population N is large enough to treat them as continuous variables. In this way, we can explain how S, I and R change over time in terms of a system of differential equations:

$$\begin{cases} \frac{dS}{dt} = -\beta SI \\ \frac{dI}{dt} = \beta SI - \gamma I \\ \frac{dR}{dt} = \gamma I \end{cases} \quad (1.1)$$

Here β is the transmission rate (per capita) and γ is the recovery rate, so that the mean infectious period can be explicitly calculated: let us consider the cohort of members who were all infected at one time and let $u(s)$ denote the number of these who are still infective s time units after having been infected. If a fraction γ of these leaves the infective class in unit time, then

$$u' = -\gamma u \Rightarrow \quad (1.2)$$

$$\Rightarrow u(s) = u(0)e^{-\gamma s} \quad (1.3)$$

Thus, the fraction of infectives remaining infected after s units time after having been infected is $e^{-\gamma s}$, so that the lenght of the infective period is distributed exponentially with mean $\int_0^{+\infty} e^{-\gamma s} ds = \frac{1}{\gamma}$.

Since it holds that:

$$R(t) = N - I(t) - S(t) \quad \forall t \in \mathbb{R}_+ \Rightarrow \quad (1.4)$$

$$\Rightarrow \frac{dR}{dt} = -\left(\frac{dI}{dt} + \frac{dS}{dt}\right) \quad (1.5)$$

the third equation in Syst. (1.1) is ridondant, to confirm the fact that R has no effect on the transmission dynamics.

Before trying to solve the above system, we can learn a great deal with the following qualitative approach. We firstly observe that the model makes sense only so long as $S(t)$ and $I(t)$ are strictly positive: if either $S(t)$ or $I(t)$ reaches zero, we consider the system to have terminated. We have that:

$$S' < 0 \quad \forall t \in \mathbb{R}_+ \quad (1.6)$$

$$I' > 0 \Leftrightarrow S > \frac{\gamma}{\beta} \quad (1.7)$$

which jointly implie that I ultimately decreases approaching to zero:

$$I_\infty := \lim_{t \rightarrow +\infty} I(t) = 0 \quad (1.8)$$

More precisely, we can have those two cases:

- $S_0 := S(0) < \frac{\gamma}{\beta}$: $I(t)$ monotonically decreases to zero (no epidemic)
- $S_0 := S(0) > \frac{\gamma}{\beta}$: $I(t)$ first increases to a maximum attained when $S = \frac{\gamma}{\beta}$ and then decreases to zero (epidemic)

If (almost) everyone is initially susceptible, i.e. $S_0 \simeq N$, then a newly introduced infected individual can be expected to infect other people at rate βN during his infectious period which lasts $\frac{1}{\gamma}$. Thus, this first infective individual can be expected to infect:

$$R_0 = \frac{\beta N}{\gamma} \quad (1.9)$$

individuals. The number R_0 is called *basic reproduction number*, and it is undoubtedly one of the key parameter when analyzing the spread of an infectious disease, as we will see soon. ¹

1.1.1 Qualitative analysis of the model

From Syst. (1.1), we deduce that:

$$\frac{dI}{dS} = -1 + \frac{\gamma}{\beta S} \quad (1.10)$$

which can be easily integrate to find the orbits (curves in the (S, I) -plane):

$$I(S) = -S + \frac{\gamma}{\beta} \ln(S) + c \quad (1.11)$$

Another way to describe the orbits is to define the function

$$V(S, I) = S + I - \frac{\gamma}{\beta} \ln(S) \quad (1.12)$$

and note that each orbite is a curve implicitly given by the equation $V(S, I) = c$ for some constant c .

An explicit expression of the constant c is given by:

$$c = V(S_0, I_0) = S_0 + I_0 - \frac{\gamma}{\beta} \ln(S_0) \quad (1.13)$$

¹To avoid ambiguity, we have to provide some clarifications. The basic reproduction number R_0 is precisely defined as “the average number of secondary infections that occur when one infective is introduced into a completely susceptible host population”. Obviously, once that the virus starts spreading, the host population can’t be considered fully susceptible anymore: this means that R_0 is well defined only at the time invasion. Thus, it has become necessary to define the so-called *replacement number* $R = R_t$ as “the average number of secondary infections produced by a typical infective during the entire period of infectiousness”. The quantities R_0 and R are equal at the beginning of the spread of an infectious disease, when the entire population (except the infective invader) is susceptible, whereas after the invasion it clearly holds that $R \leq R_0$.

which allows us to rewrite Eq. (1.11) as:

$$I(S) = I_0 + S_0 - S + \frac{\gamma}{\beta} \ln \left(\frac{S}{S_0} \right) \quad (1.14)$$

Even if Eq. (1.14) is an exact solution, it gives I as a function of S and not as a function of t : particularly, it doesn't give any indication of the time taken to reach any particular points on the orbits. Unfortunately, despite the simplicity of the SIR model, it is impossible to obtain an exact solution for $I(t)$: it is therefore necessary to find an accurate numerical solution. The simplest approach to achieve this goal is the Euler's method, that we will now briefly mention.

Assuming to have a sufficiently small time interval Δt , we make the approximation $\frac{dS}{dt} \simeq \frac{\Delta S}{\Delta t}$, where $\Delta S = S(t + \Delta t) - S(t)$. If we now solve for the number of susceptibles a time Δt in the future, we obtain:

$$S(t + \Delta t) = S(t) - \beta S(t)I(t)\Delta t \quad (1.15)$$

and similarly for the number of infectious:

$$I(t + \Delta t) = I(t) + \beta S(t)I(t)\Delta t - \gamma I(t)\Delta t \quad (1.16)$$

To get approximating solutions of the basic SIR model, it is now enough to decide a suitable time step Δt , and then specify the parameter values and initial conditions I_0, S_0 .

Going back to the phase portrait, it is important to observe that orbits never reach the I -axis, which means that $S(t) > 0 \ \forall t \in \mathbb{R}_+$. Thus:

$$S_\infty := \lim_{t \rightarrow \infty} S(t) > 0 \quad (1.17)$$

which implies that part of the population escapes infection.

Now, for a given orbit $V(S, I) \equiv \bar{c}$ we have $V(S_0, I_0) = V(S_\infty, 0)$; if we keep considering $S_0 \simeq N, I_0 \simeq 0$, this relation implies

$$N - \frac{\gamma}{\beta} \ln(S_0) = S_\infty - \frac{\gamma}{\beta} \ln(S_\infty) \Leftrightarrow \quad (1.18)$$

$$\Leftrightarrow \frac{\beta}{\gamma} = \frac{\ln \left(\frac{S_\infty}{S_0} \right)}{S_\infty - N} \Leftrightarrow \quad (1.19)$$

$$\Leftrightarrow R_0 \left(1 - \frac{S_\infty}{N} \right) = \ln(S_0) - \ln(S_\infty) \quad (1.20)$$

which is a rewriting of the key parameter R_0 in terms of the final size relation. Since the left hand-side of Eq. (1.20) is finite, the right hand-side is finite too: this

confirms the correctness of the limit in Eq. (1.17), which we informally proved before. However, the real importance of this relation lies in the fact that, contrary to the contact-rate β , the quantities S_0 and S_∞ may be estimated with a quite good accuracy by serological studies. From these data one can then estimate R_0 using Eq. (1.20). It is important to underline that, however, this estimate of R_0 is a retrospective one, which can be determined only after the epidemic has run its course.

An alternative approach to avoid extracting β from data, is to approximate the second equation in Syst. (1.1) with:

$$I' = (\beta N - \gamma) I \quad (1.21)$$

From this approximation, which is valid only in the early period of the spreading, we immediately get:

$$I(t) = I_0 \cdot e^{(\beta N - \gamma)t} \quad (1.22)$$

which means that, initially, the number of infectives grows exponentially with initial *exponential growth rate*

$$r = \gamma (R_0 - 1) \quad (1.23)$$

Since r may be determined experimentally when an epidemic begins, and N, γ may be measured as well, also β can be indirectly calculated as

$$\beta = \frac{r + \gamma}{N} \quad (1.24)$$

At this point a brief excursus is needed. Even if both R_0 and r provides a strength's measure of the spreading, they are significantly different. While R_0 is an unitless quantity, and consequently it doesn't provide any information about time, r is basically a measure of how fast the spreading runs in time. A natural question which then arises is the following one: how R_0 and r can be linked? The answer besides in the concept of *generation time* (GT), which is "the amount of time between an individual is infected by an infector, and the time that the infector was infected" ([13]). Indeed many authors have provided mechanical ways to link those three quantities, as for example with the relation ([1]):

$$R_0 = 1 + r \cdot GT \quad (1.25)$$

Many problems arise with those relation, either practical and theoretical. Firstly, in order to obtain precise relations, often many limiting assumptions have to be made. For instace, it is often assumed that GT doesn't vary in time, which is a too strong assumption, as we will see even in our simple model. Secondly, in practice, generation times are difficult to calculate since a detailed contact-tracing is needed.

In order to avoid this problem, one introduces the so-called *serial interval* which is defined as the time between when an infector and an infectee become symptomatic. Often this notion is used interchangeably with GT , leading to misunderstanding of how these intervals link r with R_0 ([6]). In Chapter 4 we will suggest that also in our simple and in-vitro model this inference is quite difficult. We now shall return to the main discussion.

We have already said that R_0 is one of the key parameters when analyzing the spread of a disease: the reason of its importance lies in the following theorem, which is merely a rewriting of what we have just proved.

Theorem 1.1.1. *Let $(S(t), I(t))$ be the solution of the Syst. (1.1), and let us define the susceptible/infectious fraction: $s(t) := \frac{S(t)}{N}$, $i(t) := \frac{I(t)}{N}$. If $R_0 \leq 1$, then $i(t)$ decreases to 0 as $t \rightarrow +\infty$. If $R_0 > 1$, then $i(t)$ first increases up to a maximum value $i_{max} = i_0 + s_0 - \frac{\gamma}{\beta} (1 + \ln(R_0))$, and then decreases to 0 as $t \rightarrow +\infty$. The susceptible fraction $s(t)$ is a decreasing function and the limiting value s_∞ is the unique root in $(0, \frac{\gamma}{\beta})$ of the equation*

$$i_0 + s_0 - s_\infty + \frac{\gamma}{\beta} \ln \left(\frac{s_\infty}{s_0} \right) = 0 \quad (1.26)$$

The results in theorem are epidemiologically reasonable: if enough people are already immune so that a typical infective initially replaces itself with no more than one new infective, the infectives decrease and there is no epidemic. On the contrary, if a typical infective initially replaces itself with more than one new infective, then infectives initially increase so that an epidemic occurs. The speed at which an epidemic progresses depends on the characteristics of the disease.

1.2 Some generalizations of the SIR model

The simplicity of the *SIR* model that we have just introduced is exactly its strength. Sometimes it is however useful to make the model more complicated, in order to give a better representation of the reality. Aim of this section is to introduce and briefly describe the most common generalizations of the basic SIR model.

1.2.1 SIR model with vital dynamics

If the outbreak's duration is quite long, we can take into account births and deaths in our model. If B is the number of births per unit time and μ is a natural²

²It is important to observe that we are not considering the possibility that someone dies due to the disease. The fatality of the disease would indeed make the model much more complicated.

mortality rate, such a model is described by:

$$\begin{cases} \frac{dS}{dt} = B - \beta SI - \mu S \\ \frac{dI}{dt} = \beta SI - \gamma I - \mu I \\ \frac{dR}{dt} = \gamma I - \mu R \end{cases} \quad (1.27)$$

Generally, it is assumed that the birth rate depends on the total population size, i.e. $B = \Lambda(N)$. If $\Lambda(N) \neq \mu N$, this model allows the total population size to grow exponentially or die out exponentially, since it holds:

$$N' = \Lambda(N) - \mu N \quad (1.28)$$

At this point, it is necessary to introduce some basic definitions and result to describe the qualitative behavior of solutions of this differential equation, since is not possible to solve it analytically.

Definition 1.2.1. The *carrying capacity* of the population is the limiting population size K , satisfying

$$\Lambda(K) = \mu K, \quad \Lambda'(K) < \mu \quad (1.29)$$

The condition $\Lambda'(K) < \mu$ assures the asymptotic stability of the equilibrium population size K . It is reasonable to assume that K is the only positive equilibrium, so that

$$\Lambda(N) > \mu N \quad \forall 0 < N < K \quad (1.30)$$

Frequently it is assumed that $\Lambda(0) = 0$: in this case we require $\Lambda'(0) > \mu$, otherwise there wouldn't be any positive equilibrium and the population would die out even in the absence of disease. From what we have just said, we immediately deduce the following limit:

$$\lim_{t \rightarrow +\infty} N(t) = K \quad (1.31)$$

It is easy to verify that in the new settings the reproduction number R_0 satisfies

$$R_0 = \frac{\beta K}{\mu + \gamma} \quad (1.32)$$

because a single infective introduced into a fully susceptible population of size K causes βK new infections in unit time, and the mean infective period corrected for natural mortality is $\frac{1}{\mu + \gamma}$. In literature, it is often assumed that births balance deaths, i.e. $\Lambda(N) = \mu N$. This choice implies that the population is constant, i.e. $N(t) \equiv N \Leftrightarrow N' \equiv 0$.

We will now try to make a qualitative analysis of the model given by Syst. (1.27) with $B = \Lambda(N) = \mu N$. The first stage of the analysis is to note that the model is

well posed, in the sense that it has a unique solution which remains non-negative (so that it has epidemiological meaning). That is, since $S = 0 \Rightarrow S' \geq 0$ and $I = 0 \Rightarrow I' \geq 0$ we have that $S, I \geq 0 \forall t \geq 0$. Moreover, $N = K \Rightarrow N' \leq 0$ so that $N \leq K \forall t \geq 0$. Summing up, it holds that the solution always remains in the biologically realistic region $\{(S, I, N) \mid S \geq 0, I \geq 0, 0 \leq N \leq K\}$ if it starts in this region. Our approach will now consists in identifying equilibria and then determining the asymptotic stability of each equilibrium.

To find equilibria (S_∞, I_∞) we set both the right sides in the first two equations of Syst. (1.27) equal to zero. Starting from the second of the resulting equations, we find out two alternatives:

1. $I_\infty = 0 \Rightarrow S_\infty = \frac{\Lambda(N)}{\mu} = K$. It is a disease-free equilibrium.
2. $S_\infty = \frac{\gamma + \mu}{\beta} \Rightarrow I_\infty = \frac{\Lambda(N)}{\mu + \gamma} - \frac{\mu}{\beta}$. It will give an endemic equilibrium provided that $\gamma + \mu < \beta K$.

We now linearize about an equilibrium (S_∞, I_∞) by letting $y = S - S_\infty, z = I - I_\infty$, writing the system in terms of y, z and retaining only the linear terms in Taylor expansions. We obtain:

$$\begin{cases} y' = -(\beta I_\infty + \mu)y - \beta S_\infty z \\ z' = \beta I_\infty y + (\beta S_\infty - \mu - \gamma)z \end{cases} \quad (1.33)$$

which means that the coefficient matrix of the linearized system is:

$$J = \begin{bmatrix} -(\beta I_\infty + \mu) & -\beta S_\infty \\ \beta I_\infty & \beta S_\infty - \mu - \gamma \end{bmatrix} \quad (1.34)$$

We then look for solutions whose components are constant multiplies of $e^{\lambda t} \Leftrightarrow \lambda$ is an eigenvalue of J . The condition that all solutions of the linearization at an equilibrium tend to zero as $t \rightarrow \infty$ is that $\text{Re}(\lambda) < 0 \forall \lambda \in \sigma(J)$.

At the disease-free equilibrium, the coefficient matrix becomes:

$$J^{\text{DF}} = \begin{bmatrix} \mu & -\beta K \\ 0 & \beta K - \mu - \gamma \end{bmatrix} \quad (1.35)$$

whose eigenvalues are μ and $\beta K - \mu - \gamma$. Thus, the disease-free equilibrium is asymptotically stable if $\beta K < \mu + \gamma$, and it is unstable otherwise.

At the endemic equilibrium, Eq. (1.34) becomes:

$$J^{\text{EN}} = \begin{bmatrix} -(\beta I_\infty + \mu) & -(\gamma + \mu) \\ \beta I_\infty & 0 \end{bmatrix} \quad (1.36)$$

Since the following holds:

$$\begin{cases} \det(J^{EN}) = (\gamma + \mu)\beta I_\infty \geq 0 \\ \text{Tr}(J^{EN}) = -(\beta I_\infty + \mu) \leq 0 \end{cases} \quad (1.37)$$

we have that $\text{Re}(\lambda) < 0 \ \forall \lambda \in \sigma(J^{EN})$, thus the endemic equilibrium, if there is one, is always asymptotically stable.

What we have said can be written in a more comfortable way in terms of the reproduction number

$$R_0 = \frac{\beta K}{\mu + \gamma} = \frac{K}{S_\infty} \quad (1.38)$$

If $R_0 < 1$, then the system has only the disease-free equilibrium which is a (global) asymptotically stable equilibrium, i.e. the disease die out.

On other hand, if $R_0 > 1$, then the disease-free equilibrium is unstable but there is an endemic equilibrium which is asymptotically stable, which means that the disease will be endemic. As we did in the previous section, we now collect all the results that we have exposed in a single theorem.

Theorem 1.2.2. *Let $(S(t), I(t))$ be the solution of (1.27) where it is assumed that the population remains constant, i.e. $B = \mu N$. Let us define the susceptible/infectious fraction: $s(t) := \frac{s(t)}{N}$, $i(t) := \frac{i(t)}{N}$.*

If $R_0 = \frac{\beta N}{\mu + \gamma} < 1$ or $i_0 := i(0) = 0$, then solution paths approach the disease-free equilibrium $(s, i) = (1, 0)$.

If $R_0 > 1$, then all solution paths with $i_0 > 0$ approach the endemic equilibrium given by $(s_e, i_e) = \left(\frac{\gamma + \mu}{N\beta}, \mu \left(\frac{1}{\mu + \gamma} - \frac{1}{N\beta} \right) \right) = \left(\frac{1}{R_0}, \mu \left(\frac{R_0}{\beta N} - \frac{1}{(\mu + \gamma)R_0} \right) \right)$

1.2.2 Models with different compartments

Even if the SIR model is the most used compartmental model, some well-known diseases show different dynamics. For this reason, in literature there are many variations of the SIR model: we will now present some of them without getting into the details.

Some viruses, like the flu one, can change their genes very easily: just as our immune system kill off one version of the virus, another emerges that our immune system doesn't recognize. This means that an infectious individual who recovers from the disease becomes another time susceptible, instead of getting immunity. In terms of compartmental models, what we have just described is the so-called *SIS* model. Here, the whole population is splitted in only two compartments:

- **Susceptible:** individuals who might become infected for the first time if exposed and individuals who are recovered from the disease and could consequently being infected another time.

- **Infectious:** individuals who are currently infected and can transmit the infection to susceptible individuals who they contact.

The simplest SIS model is given by the following system:

$$\begin{cases} \frac{dS}{dt} = -\beta SI + \gamma I \\ \frac{dI}{dt} = \beta SI - \gamma I \end{cases} \quad (1.39)$$

Since $N = S + I$ is constant, the system reduces in a logistic differential equation:

$$\frac{dI}{dt} = (\beta N - \gamma)I \left(1 - \frac{1}{N - \frac{\gamma}{\beta}}\right) = rI \left(1 - \frac{1}{K}\right) \quad (1.40)$$

where $r := \beta N - \gamma$ and $K := N - \frac{\gamma}{\beta}$. This equation, jointly with the initial condition I_0 can be easily solved with separation of variables getting

$$I(t) = \frac{KI_0}{I_0 + (K - I_0)e^{-rt}} \Rightarrow \quad (1.41)$$

$$\Rightarrow \lim_{t \rightarrow +\infty} I(t) = \begin{cases} K, & \text{if } I_0 > 0 \text{ and provided } r, K > 0 \\ 0, & \text{if } r, K < 0 \end{cases} \quad (1.42)$$

Thus, if $R_0 := \frac{\beta N}{\gamma} < 1$ then all solutions with non-negative initial value approach the limit zero as t tends to ∞ , while if $R_0 > 1$ then all solutions with non-negative initial values except the constant solution $I \equiv 0$ approach the limit $N - \frac{\gamma}{\beta}$.

Also the SIS model has a version with vital dynamics and birth rate depending on the size population N . This model is determined by:

$$\begin{cases} \frac{dS}{dt} = \Lambda(N) - \beta SI - \mu S + \gamma I \\ \frac{dI}{dt} = \beta SI - \gamma I - \mu I \end{cases} \quad (1.43)$$

The qualitative analysis of this model is very similar to the one we made for the SIR model with demography. In this case $R_0 = \frac{\beta K}{\mu + \gamma}$ where K is the carrying capacity of the population, and the main result is that:

- Endemic equilibrium, which exists if $R_0 > 1$, is always asymptotically stable.
- If $R_0 < 1$ the system has only the disease-free equilibrium which is asymptotically stable.

A middle ground between *SIS* and *SIR* model is the so-called *SIRS* model, in which we assume that, after an infectious period, an individual recovers and get a temporary immunity to the virus. When this temporary immunity fails, the individual comes back to the susceptible class. In this case we have only to

introduce the rate of loss immunity (per capita) ρ , then add a term $-\rho R$ in the equation involving R and a term $+\rho R$ in the one involving S , no matter what variations of the SIR model we are considering. Both in the SIR and in the SIS model, we are not telling the whole story. We already know that the infection of a disease begins when an infectious agent is successfully transmitted from one host to another. What we didn't mention before is that, after pathogens enter the body of the new host, they take a period of time to overcome the immune response of the body and to replicate, and only when the pathogens become sufficiently numerous the host becomes capable of transmitting pathogens to others. This motivates the following definition.

Definition 1.2.3. The time interval between when an individual is infected and when he or she becomes infectious is called *latent period*

The following model will take into account the presence of a new compartment E comprehending all the individuals in their latent period.

The $SEIR$ model without vital dynamics is described by the following ODEs' system:

$$\begin{cases} \frac{dS}{dt} = -\beta SI \\ \frac{dE}{dt} = \beta SI - \epsilon E \\ \frac{dI}{dt} = \epsilon E - \gamma I \\ \frac{dR}{dt} = \gamma I \end{cases} \quad (1.44)$$

where ϵ^{-1} is the mean value of the latent period, which is exponentially distributed. While $N = S + E + I + R$ and $N' = 0$, once again the equation involving R is useless. Let us consider a solution (S, E, I) of Syst. (1.44) and define, as we have already done before, the respective fractions $s(t) := \frac{S(t)}{N}$, $e(t) := \frac{E(t)}{N}$, $i(t) := \frac{I(t)}{N}$. Thus, what could be proved is that the tetrahedron in the (s, e, i) -phase-space given by

$$T = \{(s, e, i) \mid s \geq 0, i \geq 0, s + e + i \leq 1\} \quad (1.45)$$

is positively invariant and unique solutions exist for all $t \geq 0$, i.e. that the model is mathematically and epidemiologically well posed. Moreover, the following qualitative result holds.

Theorem 1.2.4. If $R_0 := \frac{\beta N}{\gamma} < 1$, then $e(t)$ and $i(t)$ decrease to zero as $t \rightarrow \infty$. Otherwise, if $R_0 > 1$, then $e(t) + i(t)$ first increases up to a maximum $e_{max} + i_{max} = e_0 + i_0 + s_0 - \frac{\gamma}{\beta} \ln(s_0)$ and then decreases to zero as $t \rightarrow \infty$. The susceptible fraction $s(t)$ is a decreasing function and the limiting value s_∞ is the unique root in the interval $(0, \frac{\gamma}{\beta})$ of the equation

$$e_0 + i_0 + s_0 - s_\infty + \frac{\gamma \ln\left(\frac{s_\infty}{s_0}\right)}{\beta} = 0 \quad (1.46)$$

In the same way as before, we can take into account births and deaths also in the SEIR model. We omitt the details for the sake of brevity

Let us now make a consideration concerning vital dynamics. If a mother infected (or recovered) gives birth, she transfers some IgG antibodies across the placenta to her fetus, so that her newborn infant has temporary passive immunity to an infection. Only when these passive antibodies are gone, the infant becomes susceptible to the disease, moving from the passively immune state M to the susceptible state S with rate (per capita) δ . Infants who do not have any passive immunity, because their mothers weren't infected, enter directly in the class S of susceptible individuals, so they can immediately be infected. We want to take into account this feature in a SEIR model with vital dynamics, constant population (μ = rate of births = rate of mortality) and temporary immunity. The result is the so-called MSEIR model, which dynamics is described by the following system.

$$\begin{cases} \frac{dM}{dt} = \mu(N - S) - (\delta + \mu)M \\ \frac{dS}{dt} = \delta M - \beta SI + \rho R \\ \frac{dE}{dt} = \beta SI - (\epsilon + \mu)E \\ \frac{dI}{dt} = \epsilon E - (\gamma + \mu)I \\ \frac{dR}{dt} = \gamma I - (\rho + \mu)R \end{cases} \quad (1.47)$$

It is convenient to convert this system in differential equations for the fractions in the epidemiological classes by dividing all the quantities for the population size N and eliminating the linear-dependent equation involving s by using the fact that $s = 1 - m - e - i - r$. The differential equations for the *MSEIRS* are:

$$\begin{cases} \frac{dm}{dt} = \mu(e + i + r) - \delta m \\ \frac{de}{dt} = \beta i(1 - m - e - i - r) - (\epsilon + \mu)e \\ \frac{di}{dt} = \epsilon e - (\gamma + \mu)i \\ \frac{dr}{dt} = \gamma i - (\rho + \mu)r \end{cases} \quad (1.48)$$

A suitable domain is clearly

$$D = \{(m, e, i, r) \mid m \geq 0, e \geq 0, i \geq 0, r \geq 0, m + e + i + r \leq 1\} \quad (1.49)$$

which is positively invariant because no solution paths leave through any boundary. While the right sides of the equations in Syst. (1.48) are smooth, initial value problems have unique solutions on maximal intervals; but since solutions cannot leave D , they exist for all positive times. Thus, the *MSEIRS* model is mathematically and epidemiologically well posed. The correct expression for the reproduction number is now

$$R_0 = \frac{\beta N \epsilon}{(\gamma + \mu)(\epsilon + \mu)} \quad (1.50)$$

where the term $\frac{\epsilon}{\epsilon+\mu}$ is the fraction of exposed people surviving the latent class E . The $MSEIR$ model always has a disease-free equilibrium given by $m = e = i = r = 0$ and consequently $s = 1$. If $R_0 > 1$ there is also a unique endemic equilibrium in D given by

$$\begin{cases} m^{en} = \frac{\mu}{\delta+\mu} \left(1 - \frac{1}{R_0}\right) \\ e^{en} = \frac{\delta(\gamma+\mu)(\rho+\mu)}{(\delta+\mu)[(\rho+\mu)(\gamma+\epsilon+\mu)+\gamma\epsilon]} \left(1 - \frac{1}{R_0}\right) \\ i^{en} = \frac{\delta\epsilon(\rho+\mu)}{(\delta+\mu)[(\rho+\mu)(\gamma+\epsilon+\mu)+\gamma\epsilon]} \left(1 - \frac{1}{R_0}\right) \\ r^{en} = \frac{\delta\epsilon\gamma}{(\delta+\mu)[(\rho+\mu)(\gamma+\epsilon+\mu)+\gamma\epsilon]} \left(1 - \frac{1}{R_0}\right) \end{cases} \quad (1.51)$$

which together imply that $s^{en} = \frac{1}{R_0}$. A qualitative behaviour of the $MSEIRS$ is described by the following result.

Theorem 1.2.5. *If $R_0 \leq 1$, then the disease-free equilibrium $(m, e, i, r) = (0, 0, 0, 0)$ is globally asymptotically stable in D . Otherwise if $R_0 > 1$, then the disease-free equilibrium is unstable and the endemic one $(m^{en}, e^{en}, i^{en}, r^{en})$ is asymptotically stable, and the system is said to be **uniformly persistent**, in the sense that*

$$\lim_{t \rightarrow \infty} i(t) \geq c \quad \exists c > 0 \quad (1.52)$$

for all initial points such that $e_0 + i_0 > 0$.

We end this section by saying that the models we presented are only few of the many ones which can be defined and studied. For instance, many model we have not treated could be defined without adding new compartments to the five we have used: $SI, SEI, SEIS, MSIRS$ are example of such models. Moreover, when a particular disease requires it, any useful compartment could be created and implemented in preexisting model. Talking about the infamous COVID-19, it taught us the importance of quarantine and isolation measures when no vaccine is available: it is not surprising that in literature we find a model $SEQIJR$, where a class Q of quarantined members and a class J of isolated members are introduced. On other hand, to protect against infection like the annual influenza, vaccination is a form of treatment available and commonly used: in [7] we find a $SITR$ model in which a fraction per unit time of infectives is selected for treatment, and the treatment reduces infectivity by a certain factor.

Chapter 2

Stochastic epidemic models

In Chapter 1 we have seen compartmental models in their original form, which is a deterministic one. This feature makes those models quite simple to treat both analytically and computationally. The downside is that those models couldn't be very realistic, since lifelike phenomena as inter-human contacts are often ruled by randomness. Those considerations have led mathematicians to develop stochastic counterparts of the epidemiological models we have presented in the previous chapter. The aim of this chapter is to formulate two Markov-chain based epidemic models and illustrate some techniques to analyze them. The most interesting things about those models, is that under the same hypothesis they can show a different asymptotical behaviour from their deterministic counterpart. We will follow closely the works done by L. J. S. Allen in [2], [3], [4] and [7].

2.1 Discrete time epidemic models

2.1.1 SIS Model

We start with a discrete time markov chain (DTMC) model based on the *SIS*. Again the state variables are the number of susceptible and infectious individuals $\mathcal{S} = \mathcal{S}(t)$ and $\mathcal{I} = \mathcal{I}(t)$: here the choice of the calligraphic letters is to stress the fact that those are now random variables. We assume that the population size N is constant, so that it holds $\mathcal{S}(t) = N - \mathcal{I}(t)$, i.e. there is only one independent random variable $\mathcal{I}(t)$. In order to have a discrete-time Markov chain, we split the time interval \mathbb{R}_+ in a countable number of small disjoint intervals:

$$\mathbb{R}_+ = \bigcup_{n \in \mathbb{N}} [n\Delta t, (n+1)\Delta t[\quad (2.1)$$

and we focus on the extremes of those intervals, i.e. we choose $t \in \mathbb{N}\Delta t := \{n\Delta t : n \in \mathbb{N}\} = \{0, \Delta t, 2\Delta t, \dots\}$, where $\Delta t > 0$ is sufficiently small (we will be more precise about that in a moment). The stochastic process $\{\mathcal{I}(t)\}_{t \in \mathbb{N}\Delta t}$ has an associate probability function,

$$p_i(t) := \mathbb{P}(\mathcal{I}(t) = i) \quad (2.2)$$

where $i \in \{0, \dots, N\}$. Obviously, for every fixed $t \in \mathbb{N}\Delta t$ it holds

$$\sum_{i \in \{0, \dots, N\}} p_i(t) = 1 \quad (2.3)$$

Let us denote with $p(t) = (p_0(t), p_1(t), \dots, p_N(t))$ the probability vector associated to $\mathcal{I}(t)$. The stochastic process has the Markov property iff

$$\mathbb{P}(\mathcal{I}(t + \Delta t) = i \mid \mathcal{I}(t) = j, \dots, \mathcal{I}(\Delta t) = i_1, \mathcal{I}(0) = i_0) = \mathbb{P}(\mathcal{I}(t + \Delta t) = i \mid \mathcal{I}(t) = j)$$

For the sake of brevity, we will use the following standard notation

$$p_{ij}(t, t + \Delta t) := \mathbb{P}(\mathcal{I}(t + \Delta t) = j \mid \mathcal{I}(t) = i) \quad (2.4)$$

Since the deterministic *SIS* model is autonomous, its stochastic counterpart is time homogenous: thus, the left hand-side of Eq. (2.4) does not depend on t . We will use the shorter notation $p_{ij}(\Delta t)$ to underline this fact. We have just said that Δt must be sufficiently small. What we meant was that Δt is so small that the number of infected individuals changes by at most one during the time interval Δt , that is

$$\mathcal{I}(t) = i \Rightarrow \mathcal{I}(t + \Delta t) = \begin{cases} i + 1, & \text{with probability } p_{i,i+1}(\Delta t) \\ i, & \text{with probability } p_{ii}(\Delta t) \\ i - 1, & \text{with probability } p_{i,i-1}(\Delta t) \end{cases} \quad (2.5)$$

where no other transitions can happen, i.e. $p_{i,i+1} + p_{ii} + p_{i,i-1} = 1$. It is important to observe that there are four events which can cause the transition: a new infection, a birth, a death or a recovery. Using the rates introduced in Syst. (1.43) considering $\Lambda(N) = \mu N$, we can calculate explicitly the probability of a transition in a time-interval Δt :

$$p_{ij}(\Delta t) = \begin{cases} \beta i(N - i)\Delta t, & j = i + 1 \\ (\mu + \gamma)i\Delta t, & j = i - 1 \\ 1 - [(\beta(N - i) + \mu + \gamma)i]\Delta t, & j = i \\ 0, & j \in \{0, \dots, N\} \setminus \{i, i + 1, i - 1\} \end{cases} \quad (2.6)$$

To relate this model with a birth-death process and to lighten the discussion, we will use the following notation:

$$b(i) := \beta i(N - i), \quad d(i) := (\mu + \gamma)i \quad (2.7)$$

What we are saying is that $b(i)\Delta t$ is the probability that the number of infectious increases from i to $i + 1$ in the time interval Δt , and $d(i)\Delta t$ is the probability that

the number of infectious decreases (due to a death or a recovery) from i to $i - 1$ in the time interval Δt . We can use this shorter notation to rewrite Eq. (2.6) as

$$p_{ij}(\Delta t) = \begin{cases} b(i)\Delta t, & j = i + 1 \\ d(i)\Delta t, & j = i - 1 \\ 1 - [(b(i) + d(i))\Delta t], & j = i \\ 0, & j \in \{0, \dots, N\} \setminus \{i, i + 1, i - 1\} \end{cases} \quad (2.8)$$

Since all those quantities must be probabilities, an explicit inequality involving Δt holds:

$$\max_{i \in \{0, \dots, N\}} \{[b(i) + d(i)]\Delta t\} \leq 1 \quad (2.9)$$

Using the Markov property jointly with the preceding transition probabilities we can find an explicit relation between the probability vector $p(t + \Delta t)$ and the probability vector $p(t)$:

$$\begin{aligned} p_i(t + \Delta t) &= p_{i-1}(t)b(i-1)\Delta t + p_i(t)(1 - [b(i) + d(i)]\Delta t) + p_{i+1}(t)d(i+1)\Delta t \\ &= p_i(t) + (p_{i-1}(t)b(i-1) - p_i(t)[b(i) + d(i)] + p_{i+1}(t)d(i+1))\Delta t \end{aligned}$$

From what we have just said we deduce the form of the transition matrix

$$\begin{bmatrix} 1 & 0 & 0 & 0 & \dots & 0 & 0 & 0 \\ d(1)\Delta t & 1 - (b + d)(1)\Delta t & b(1)\Delta t & 0 & \dots & 0 & 0 & 0 \\ 0 & d(2)\Delta t & 1 - (b + d)(2)\Delta t & b(2)\Delta t & \dots & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & 0 & \dots & d(N-1)\Delta t & 1 - (b + d)(N-1)\Delta t & b(N-1)\Delta t \\ 0 & 0 & 0 & 0 & \dots & 0 & d(N)\Delta t & 1 - d(N)\Delta t \end{bmatrix}$$

We rename this matrix $M(\Delta t) \in M_{N+1}(\mathbb{R})$. It is important to observe that we have used the compact notation: $(b + d)(i)$ instead of $(b(i) + d(i))$. The data of the transition matrix $M(\Delta t)$ jointly with an initial probability vector $p(0)$ fully determine the dynamics of the stochastic process $\{I(t)\}_{t \in \mathbb{N}\Delta t}$ (see App. A.1.1). Particulary, given $t = n\Delta t$:

$$p(t + \Delta t) = p(0)M^{n+1}(\Delta t) \quad (2.10)$$

Since the probability vectors $p(\cdot) \in \mathbb{R}^{N+1}$, and $M(\Delta t) \in M_{N+1}(\mathbb{R})$, the right hand-side of Eq. (2.10) belongs to \mathbb{R}^{N+1} as the left hand-side does, so the equality is well-defined.

The following theorem establish a link between the solution of the stochastic *SIS* model and its deterministic counterpart.

Theorem 2.1.1. *Let $I(t)$ and $\mathcal{I}(t)$ be respectively the solution of the differential Syst. (1.43) and the random variable representing the number of infectious individuals at time t in the SIS stochastic model. Then the following inequality holds:*

$$\mathbb{E}(\mathcal{I}(t)) \leq I(t) \quad \forall t \in \mathbb{R}_+ \quad (2.11)$$

Proof. We can find a difference equation for the first moment of $\mathcal{I}(t)$ starting from the difference equation which links $p_i(t + \Delta t)$ and the probability vector at the preceding step $p(t)$:

$$\begin{aligned} \mathbb{E}(\mathcal{I}(t + \Delta t)) &= \sum_{i=0}^N i p_i(t + \Delta t) \\ &= \sum_{i=1}^N i p_{i-1}(t) b(i-1) \Delta t + \sum_{i=0}^N i p_i(t) - \sum_{i=0}^N i p_i(t) b(i) \Delta t - \\ &\quad - \sum_{i=0}^N i p_i(t) d(i) \Delta t + \sum_{i=0}^{N-1} i p_{i+1}(t) d(i+1) \Delta t \\ &= \mathbb{E}(\mathcal{I}(t)) + \sum_{i=1}^{N-1} p_i(t) b(i) \Delta t - N p_N(t) b(N) \Delta t - \sum_{i=1}^N p_i(t) d(i) \Delta t \end{aligned}$$

We now write $\beta i(N-i)$ instead of $b(i)$ and $(\mu + \gamma)i$ instead of $d(i)$ in order to get:

$$\begin{aligned} \mathbb{E}(\mathcal{I}(t + \Delta t)) - \mathbb{E}(\mathcal{I}(t)) &= \sum_{i=1}^{N-1} p_i(t) \beta i(N-i) \Delta t - \sum_{i=1}^N p_i(t) (\mu + \gamma) i \Delta t \\ &= \sum_{i=0}^N [p_i(t) \beta i(N-i) \Delta t - p_i(t) (\mu + \gamma) i \Delta t] \\ &= \sum_{i=0}^N [p_i(t) i (\beta N - (\mu + \gamma)) - p_i(t) i^2 \beta] \Delta t \\ &= (\beta N - (\mu + \gamma)) \mathbb{E}(\mathcal{I}(t)) \Delta t - \beta \mathbb{E}(\mathcal{I}^2(t)) \Delta t \end{aligned}$$

which ultimately implies:

$$\begin{aligned} \frac{\mathbb{E}(\mathcal{I}(t + \Delta t)) - \mathbb{E}(\mathcal{I}(t))}{\Delta t} &= (\beta N - (\mu + \gamma)) \mathbb{E}(\mathcal{I}(t)) - \beta \mathbb{E}(\mathcal{I}^2(t)) \\ &\leq (\beta N - (\mu + \gamma)) \mathbb{E}(\mathcal{I}(t)) - \beta \mathbb{E}^2(\mathcal{I}(t)) \end{aligned} \quad (2.12)$$

As $\Delta t \rightarrow 0$ Eq. (2.12) becomes:

$$\begin{aligned} \frac{d\mathbb{E}(\mathcal{I}(t))}{dt} &\leq (\beta N - (\mu + \gamma)) \mathbb{E}(\mathcal{I}(t)) - \beta \mathbb{E}^2(\mathcal{I}(t)) \\ &= \beta (N - \mathbb{E}(\mathcal{I}(t))) \mathbb{E}(\mathcal{I}(t)) - (\mu + \gamma) \mathbb{E}(\mathcal{I}(t)) \end{aligned} \quad (2.13)$$

What we see now is that the right hand-side of Eq. (2.13) is exactly the same as the differential equation for $I(t)$ in Syst. (1.43), if in the deterministic SIS model we replace $I(t)$ with $\mathbb{E}(\mathcal{I}(t))$ and $S(t)$ with $N - \mathbb{E}(\mathcal{I}(t))$. Thus, the differential inequality precisely implies the thesis, i.e. the mean of the random variable $\mathcal{I}(t)$ in the stochastic SIS epidemic process is less than the solution $I(t)$ to the deterministic differential equation of the deterministic SIS model in Syst. (1.43). \square

Remark 2.1.2. With the same procedure as the one we used in the proof, we could find difference equations for higher order moments. However, whereas $\mathbb{E}(\mathcal{I}(t))$ depends on the second moment, higher order moments depend on even higher order moments. Therefore, these equations cannot be solved unless some additional assumptions are made regarding the higher order moments.

The following result shows how different the asymptotic behaviour of the stochastic SIS model is from the asymptotic behaviour of its deterministic counterpart.

Theorem 2.1.3. *Let be $p(t)$ the probability vector associated to $\mathcal{I}(t)$ where $t = n\Delta t$ for some $n \in \mathbb{N}$. Then it holds:*

$$\lim_{t \rightarrow +\infty} p(t) := \lim_{n \rightarrow +\infty} p(n\Delta t) = (1, 0, 0, \dots, 0) \quad (2.14)$$

i.e. the population approaches the disease-free equilibrium regardless of the magnitude of the basic reproduction number.

Proof. Looking at the transition matrix M we see that the zero state is an *absorbing state*, i.e. beginning from state 0 no other state can be reached. Thus, $\{0\} \subseteq \{0, \dots, N\}$ is a finite closed class, which implies that it is also a recurrent class:

$$\mathbb{P}_0(T_0 < \infty) = 1 \quad (2.15)$$

where T_i is the random variable representing the *first passage time* to state i . The class of all the states different from zero $\{1, \dots, N\}$ is a communication class, i.e. $\forall i, j \in \{1, \dots, N\}$ there exists a path included in $\{1, \dots, N\}$ and with a strictly positive probability which link them. Thus, from Th. A.1.11 it is enough to show that one state of this class is transient to establish that all the class is made of transient states. Let us consider for instance the state 1. Since $\alpha_{10} = d(1)\Delta t > 0$ and 0 is an absorbing state, it holds:

$$\mathbb{P}_1(T_1 < \infty) = 1 - \mathbb{P}_1(T_1 = \infty) \leq 1 - p_{10} < 1 \quad (2.16)$$

which exactly means that 1 is a transient state, then that $\{1, \dots, N\}$ is a transient class.

Using the reverse implication of the *potential matrix criterion* (Th. (A.1.12)), we

find the following property: if $M^n = (\alpha_{ij}^{(n)})$ is the n th power of the transition matrix M , then it holds

$$\lim_{n \rightarrow \infty} \alpha_{ij}^{(n)} = 0 \quad (2.17)$$

for any state i and any transient state j . Since the set of stochastic matrices is closed under the multiplication in $M_{N+1}(\mathbb{R})$, we have that $M^\infty := \lim_{n \rightarrow \infty} M^n$ is stochastic, thus we must have $\lim_{n \rightarrow \infty} \alpha_{i0}^{(n)} = 1 \ \forall i \in \{0, \dots, N\}$. Summing up the limit transition matrix becomes:

$$M^\infty = \begin{bmatrix} 1 & 0 & 0 & \cdots & 0 & 0 \\ 1 & 0 & 0 & \cdots & 0 & 0 \\ 1 & 0 & 0 & \cdots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 1 & 0 & 0 & \cdots & 0 & 0 \\ 1 & 0 & 0 & \cdots & 0 & 0 \end{bmatrix} \quad (2.18)$$

Thus the probability of absorption is given by:

$$\lim_{n \rightarrow \infty} \mathbb{P}(\mathcal{I}(n\Delta t) = 0 | \mathcal{I}(0) = i) = (M^\infty)_{i1} = 1, \ \forall i \in E \quad (2.19)$$

and the limit distribution (which is also a stationary distribution) is given by:

$$\lim_{t \rightarrow \infty} p(t) = (\alpha_{11}^\infty, \alpha_{22}^\infty, \dots, \alpha_{NN}^\infty) = (1, 0, 0, \dots, 0) \quad (2.20)$$

which is exactly the thesis. \square

2.1.2 SIR model

In the DTMC *SIR* model we have two independent random variables $\mathcal{I}(t)$ and $\mathcal{S}(t)$ which represent respectively the number of infectious/susceptible individuals at time t . Since we keep assuming that the population size is constant, the random variable of the number of recovered individuals \mathcal{R} is clearly dependent from \mathcal{I}, \mathcal{S} . Thus, we have a bivariate process $\{\mathcal{I}(t), \mathcal{S}(t)\}_{t=0}^\infty$ with joint probability function given by

$$p_{(s,i)}(t) = \mathbb{P}(\mathcal{S}(t) = s, \mathcal{I}(t) = i) \quad (2.21)$$

Since in this section we are still considering a discrete-time Markov chain, we should have specified that the times t are of the form $n\Delta t$ for $n \in \mathbb{N}$, as in the previous section. What is more interesting is that this process is again an homogenous markov chain. In order to define the transition probabilities, we have to choose $\Delta t > 0$ so small that at most one change¹ in state occurs during the time

¹No matter if it is a birth, a death, a new infection or a recovery

interval Δt . With this extra assumptions, we can define transition probabilities which are denoted as follows:

$$p_{(s+k, i+j)}(\Delta t) = \mathbb{P}((\Delta \mathcal{S}, \Delta \mathcal{I}) = (k, j) \mid (\mathcal{S}(t), \mathcal{I}(t)) = (s, i)) \quad (2.22)$$

where k, j are integers and $\Delta \mathcal{S}, \Delta \mathcal{I}$ are respectively the variations in the number of susceptible/infectious individuals which occurs in the time interval Δt , i.e.

$$\Delta \mathcal{S} := \mathcal{S}(t + \Delta t) - \mathcal{S}(t), \quad \Delta \mathcal{I} := \mathcal{I}(t + \Delta t) - \mathcal{I}(t) \quad (2.23)$$

The explicit computation of those probabilities is based on the *SIR* deterministic formulation, but first we can immediately observe that as long as $k, j \notin \{-1, 0, 1\}$ we have that $p_{s+k, i+j}(\Delta t) = 0$ whatever s, i are. The probability that one transition from $\mathcal{S} \rightarrow \mathcal{I}$ happens during Δt can be computed as follows:

$$\begin{aligned} p_{s-1, i+1}(\Delta t) &= \mathbb{P}\{\text{One infective contact during } \Delta t \mid (\mathcal{S}(t), \mathcal{I}(t)) = (s, i)\} \\ &= \beta si \Delta t \end{aligned} \quad (2.24)$$

In the same way, the probability that a transition $\mathcal{I} \rightarrow \mathcal{R}$ happens in Δt , assuming that at the beginning of the time interval the number of infectious is equal to i , is given by $\gamma i \Delta t$. In the same way all other transition probabilities can be computed in order to have this compact expression:

$$p_{s+k, i+j}(\Delta t) = \begin{cases} \beta si \Delta t, & (k, j) = (-1, 1) \\ \gamma i \Delta t, & (k, j) = (0, -1) \\ \mu i \Delta t, & (k, j) = (1, -1) \\ \mu(N - s - i) \Delta t, & (k, j) = (1, 0) \\ 1 - [\beta si + \gamma i + \mu(N - s)] \Delta t, & (k, j) = (0, 0) \\ 0, & (k, j) \notin \{-1, 0, 1\} \times \{-1, 0, 1\} \end{cases} \quad (2.25)$$

It is important to note that in the computation of this probabilities we have take into account the fact that births compensate deaths: for instance, a death of an immune individual is accompanied by a birth of a susceptible one. As in the *SIS* stochastic model, Δt must be chosen sufficiently small so that all the entries in Eq. (2.25) belong to $[0, 1]$. In this case, the transition matrix is quite complicated, so we avoid to write it down. Applying the Markov property, it is however possible to get a difference equation satisfied by the probability $p_{s,i}(t + \Delta t)$:

$$\begin{aligned} p_{s,i}(t + \Delta t) &= p_{s+1, i-1}(t) \beta(s+1)(i-1) \Delta t + p_{s, i+1}(t) \gamma(i+1) \Delta t + \\ &+ p_{s-1, i+1}(t) \mu(i+1) \Delta t + p_{s-1, i}(t) \mu(N - (s-1) - i) \Delta t + \\ &+ p_{s,i}(t) \{1 - [\beta si + \gamma i + \mu(N - s)] \Delta t\} \end{aligned} \quad (2.26)$$

From Eq. (2.26) we can find out difference equation for the mean and higher order moments just substituting $p_{s,i}(t + \Delta t)$ in those expressions:

$$\mathbb{E}(\mathcal{I}(t + \Delta t)) = \sum_{i=0}^N i p_{s,i}(t + \Delta t) \quad (2.27)$$

$$\mathbb{E}(\mathcal{S}(t + \Delta t)) = \sum_{s=0}^N s p_{s,i}(t + \Delta t) \quad (2.28)$$

Since those equations cannot be solved explicitly due to their dependence on higher order moments, we will not go into more detail. Even if we don't have a friendly expression neither for the transition matrix nor for the difference equations regarding moments, an important qualitative result can be deduced.

Theorem 2.1.4. *Let be $p(t)$ the probability vector associated to the jointed state variable $(\mathcal{S}(t), \mathcal{I}(t))$ which means that the entries of the vector $p(t)$ are all the probabilities $p_{(s,i)}(t)$ with $s, i \in \{0, \dots, N\}$ and $0 \leq s + i \leq N$:*

$$p(t) := (p_{(N,0)}(t), p_{(N-1,1)}(t), p_{(N-1,0)}(t), \dots, p_{(N-i,i)}(t), p_{(N-i,i-1)}(t), \dots, p_{(N-i,0)}(t), \dots, p_{(1,N-1)}(t), \dots, p_{(1,0)}(t), p_{(0,N)}(t), \dots, p_{(0,0)}(t)) \quad (2.29)$$

Then it holds:

$$\lim_{t \rightarrow +\infty} p(t) = (1, 0, 0, \dots, 0, 0) = \begin{cases} 1, & (s, i) = (N, 0) \\ 0, & \text{otherwise} \end{cases} \quad (2.30)$$

i.e. asymptotically all sample paths are absorbed into the disease-free state $(N, 0)$ regardless of the magnitude of the basic reproduction number.

Proof. Looking at the transition probabilities in Eq. (2.25) we observe that $(N, 0)$ is an absorbing state, since starting from this state the only non-zero transition probability is the one with both the increments k, j equal to zero, which is consequently equal to 1. The set of all the other states is a finite communication class, and the state $(N - 1, 1)$, which belongs to this class, is transient since the transition $(N - 1, 1) \rightarrow (N, 0)$ has probability $\mu \Delta t > 0$. Thus we can split the set of all states in the disjoint union of one transient class and one absorbing recurrent state. The conclusion follows from exactly the same reasoning that we made in the proof of Theorem 2.1.1. \square

2.2 Continuous time epidemic models

Another stochastic approach to epidemic models is to consider a continuous time Markov chain (CTMC) where the time $t \in \mathbb{R}_+$ is continuous and the states $\mathcal{S}(t), \mathcal{I}(t), \mathcal{R}(t)$ are discrete, i.e. they belong to $E = \{0, \dots, N\}$.

2.2.1 SIS Model

In the CTMC *SIS* model the stochastic process depends on the collection of discrete random variables $\{\mathcal{I}(t)\}_{t \in \mathbb{R}_+}$ and their associated probability functions $p(t) = (p_0(t), \dots, p_N(t))$. The stochastic process has the *markov property* in the sense that:

$$\mathbb{P}(\mathcal{I}(t+\Delta t) = j \mid \mathcal{I}(t) = i, \mathcal{I}(t_{n-1}) = i_{n-1}, \dots, \mathcal{I}(t_0) = i_0) = \mathbb{P}(\mathcal{I}(t+\Delta t) = j \mid \mathcal{I}(t) = i)$$

for all $i_0, \dots, i_{n-1}, i, j \in E$, all $0 \leq t_0 < t_1 < \dots < t < t + \Delta t$ and all $n \in \mathbb{N}$. Since the right hand-side of the last expression depends only in the time interval Δt and not on t , the markov chain is said to be *homogenous*. Let then be

$$S(\Delta t) = (\alpha_{ij}(\Delta t))_{i,j \in E} \quad (2.31)$$

where

$$\alpha_{ij}(\Delta t) = \mathbb{P}(\mathcal{I}(t + \Delta t) = j \mid \mathcal{I}(t) = i) \quad (2.32)$$

$S(t)$ is called the *transition semigroup* of the stochastic process $\{\mathcal{I}(t)\}_{t \in \mathbb{R}_+}$ (see App. A.1.2), and apart from the $o(\Delta t)$, it is exactly the same transition matrix we found for the DTCM *SIS* model. Moreover, it satisfies the following properties:

$$\begin{cases} \sum_{j=1}^{N+1} \alpha_{ij}(\Delta t) = 1, \quad \forall \Delta t \in \mathbb{R}_+ \\ S(t + \Delta t) = S(t)S(\Delta t), \quad \forall t, \Delta t \in \mathbb{R}_+ \\ S(0) = \mathbb{1} \end{cases} \quad (2.33)$$

We can easily see that the semigroup is also continuous at the origin, i.e.

$$\lim_{\Delta t \rightarrow 0^+} S(h) = S(0) = \mathbb{1} \quad (2.34)$$

This assumption implies continuity at any time t , i.e.

$$\lim_{\Delta t \rightarrow 0^+} \alpha_{ij}(t + \Delta t) = \alpha_{ij}(t), \quad \forall i, j \in E \quad (2.35)$$

which is enough to state the following analytical result:

Theorem 2.2.1. *For any state $i \in E$ there exists*

$$q_i := \lim_{\Delta t \rightarrow 0} \frac{1 - \alpha_{ii}(\Delta t)}{\Delta t} \quad (2.36)$$

and for any pair i, j of different states there exists

$$q_{ij} := \lim_{\Delta t \rightarrow 0} \frac{\alpha_{ij}(\Delta t)}{\Delta t} \quad (2.37)$$

If we let now $q_{ii} := -q_i$ we obtain a matrix $Q = (q_{ij})_{i,j \in E} \in M_{N+1}(\mathbb{R})$ which is called the *infinitesimal generator* of the process (see App. A.1.2). It is quite easy to calculate the *local characteristics* q_{ij} in order to get the explicit expression for Q , which is the following

$$\begin{bmatrix} 0 & 0 & 0 & 0 & \cdots & 0 & 0 & 0 \\ d(1) & -(b+d)(1) & b(1) & 0 & \cdots & 0 & 0 & 0 \\ 0 & d(2) & -(b+d)(2) & b(2) & \cdots & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & 0 & \cdots & d(N-1) & -(b+d)(N-1) & b(N-1) \\ 0 & 0 & 0 & 0 & \cdots & 0 & d(N) & -d(N) \end{bmatrix}$$

Directly from the expressions of the local characteristics we can deduce that

$$Q = \lim_{\Delta t \rightarrow 0} \frac{S(\Delta t) - S(0)}{\Delta t} \quad (2.38)$$

i.e. Q is the derivative at 0 of the matrix function $t \mapsto S(t)$. Since $|E| < \infty$, Q is both *stable* and *conservative*, i.e.

$$q_i = -q_{ii} < \infty, \quad q_i = \sum_{j \in E \setminus \{i\}} q_{ij} \quad (2.39)$$

thus, we can pass to the limit in the following equation

$$\begin{aligned} \frac{S(t + \Delta t) - S(t)}{\Delta t} &= S(t) \frac{S(\Delta t) - \mathbb{1}}{\Delta t} = \frac{S(\Delta t) - \mathbb{1}}{\Delta t} S(t) \xrightarrow{\Delta t \rightarrow 0} \\ &\xrightarrow{\Delta t \rightarrow 0} \frac{dS(t)}{dt} = S(t)Q = QS(t) \end{aligned} \quad (2.40)$$

which are the so-called *Kolmogorov's backward/forward* differential systems (see Eq. (A.11)). One consequence of Eq. (2.40) is that it holds

$$\begin{cases} \frac{dp_i(t)}{dt} = p_{i-1}(t)b(i-1) + p_{i+1}(t)d(i+1) - p_i(t)[b(i) + d(i)], & i = 1, \dots, N \\ \frac{dp_0(t)}{dt} = p_1(t)d(1) \end{cases}$$

which can be expressed in matrix form as:

$$\frac{dp(t)}{dt} = Qp(t), \quad p(t) = (p_0(t), \dots, p_N(t)) \quad (2.41)$$

We are now able to establish a relation between CTMC *SIS* model and its deterministic counterpart:

Theorem 2.2.2. *Let be $I(t)$ and $\mathcal{I}(t)$ respectively the solution of the *SIS* deterministic model and the random variable of the CTMC *SIS* model. Then yields:*

$$\mathbb{E}(\mathcal{I}(t)) \leq I(t), \quad \forall t \in \mathbb{R}_+ \quad (2.42)$$

Proof. We multiply by i the first equation of Syst. (2.41), then we sum on i . What we get is:

$$\begin{aligned} \frac{d\mathbb{E}(\mathcal{I}(t))}{dt} &= \sum_{i=1}^N p_{i-1}(t)ib(i-1) + \sum_{i=1}^{N-1} p_{i+1}(t)id(i+1) - \sum_{i=1}^N p_i i [b(i) + d(i)] \\ &= \sum_{i=0}^N p_i b(i) - \sum_{i=1}^N p_i d(i) \\ &= \sum_{i=0}^N \{p_i(t)i[\beta N - \mu - \gamma] - p_i(t)i^2\beta\} \\ &= [\beta N - \mu - \gamma]\mathbb{E}(\mathcal{I}(t)) - \beta\mathbb{E}(\mathcal{I}^2(t)) \\ &\leq \beta[N - \mathbb{E}(\mathcal{I}(t))]\mathbb{E}(\mathcal{I}(t)) - (\mu + \gamma)\mathbb{E}(\mathcal{I}(t)) \end{aligned} \quad (2.43)$$

Reasoning as the theorem for the DTCM *SIS* model, the conclusion follows. \square

The most important result of this section is that, once again, the distribution of $\mathcal{I}(t)$ converges to the disease-free equilibrium:

Theorem 2.2.3. *Let be $p(t)$ the probability vector associated to the number of infectious individual at time t , namely $\mathcal{I}(t)$. Thus the following convergence holds:*

$$\lim_{t \rightarrow +\infty} p(t) = (1, 0, 0, \dots, 0, 0) \quad (2.44)$$

i.e. the population approaches the disease-free equilibrium regardless of the magnitude of the basic reproduction number.

Proof. The vector $\pi = (1, 0, 0, \dots, 0, 0)$ is an an eigenvector of 0-eigenvalue for Q :

$$\pi Q = 0 \quad (2.45)$$

where Q is the infinitesimal generator of the process which we have defined above. Let us now define $\forall i \in \{1, \dots, N+1\}$

$$\begin{aligned} R_i(Q) &:= \sum_{j=1, j \neq i}^{N+1} q_{ij} \\ &= d(i-1) + b(i-1) \end{aligned} \quad (2.46)$$

and

$$\begin{aligned} K_i &= \{z \in \mathbb{C} : |z - q_{ii}| \leq R_i(Q)\} \\ &= \{z \in \mathbb{C} : |z + (b+d)(i-1)| \leq (d+b)(i-1)\} \end{aligned} \quad (2.47)$$

The *Gershgorin's circle theorem* A.2.2 tells us that

$$\sigma(Q) \subset \bigcup_{i=1}^{N+1} K_i(Q) \quad (2.48)$$

where $\sigma(Q)$ is the spectrum of Q . In particular Eq. (2.47) implies that

$$|z| \leq 0, \quad \forall z \in \sigma(Q) \cap \mathbb{C} \quad (2.49)$$

but since the submatrix \tilde{Q} of Q obtained by deleting the first row and the first column of Q is non singular (i.e. $\det(\tilde{Q}) > 0$) it follows that all the eigenvalues different from zero are negative or they have negative real part. Thus π is the only one eigenvector of Q , and it represents a stationary distribution. Furthermore, since the Markov chain is a finite state space HMC, we can always assume that it has an uniform structure, thus it has the same absorption probabilities than the correspondent discrete-time Markov chain has (see [9] pp. 364-365). This conclude the proof. \square

2.2.2 SIR model

The CTMC *SIR* model can be derived in the same way in which we have derived the *SIS* model, taking into account that the *SIR* epidemic process is a bivariate stochastic process $\{(\mathcal{S}(t), \mathcal{I}(t))\}$ while $\mathcal{R}(t) = N - \mathcal{S}(t) - \mathcal{I}(t)$. We define firstly a joint probability function associated to the pair $(\mathcal{S}, \mathcal{I})$:

$$p_{(s,i)}(t) = \mathbb{P}\{(\mathcal{S}(t), \mathcal{I}(t)) = (s, i)\} \quad (2.50)$$

The Kolmogorov's backward differential system admits implies the following differential equation:

$$\begin{aligned} \frac{dp_{(s,i)}(t)}{dt} &= p_{(s+1,i-1)}(t)\beta(s+1)(i-1) + p_{(s,i+1)}(t)\gamma(i+1) + \\ &+ p_{(s-i,i+1)}(t)\mu(i+1) + p_{(s-1,i)}(t)\mu(N-s+1-i) - \\ &- p_{(s,i)}(t) [\beta si + \gamma i + \mu(N-s)] \end{aligned} \quad (2.51)$$

From this equation we can deduce differential equations for the moments of \mathcal{S} and \mathcal{I} . However, as it happens in the discrete time case, in those equations each successive moment depends on higher order moments, so it is necessary to make more assumptions on higher moments and to introduce closure techniques to approximate the solutions to these equations. The *SIR* model is actually a Markovian and time-homogeneous process. In particular, the disease-free $(N, 0)$ is an absorbing state.

2.3 Main properties of stochastic epidemic models

We have already proved that the asymptotic behaviour of stochastic models always coincides with the disease-free equilibrium. However, many other interesting properties distinguish stochastic models from their deterministic counterpart: the probability of an outbreak, the final size distribution and the expected duration of an epidemic are three of those properties.

2.3.1 Probability of an outbreak

When studying the spreading of a disease, it is important to see **if** an outbreak actually occurs, i.e. the number of infectious individuals escalates. This event doesn't always happen: for instance, the reader can think about a *SIR* model in which the first infectors recover before infecting other susceptible individuals. The aim of this section is to use a simple random walk or a birth and death process on the set $E = \{0, 1, 2, \dots\}$ to estimate the probability of an outbreak. Let then be $X(t)$ the random variable for the position on E at time t in a random walk model. According to previous models, here 0 is an absorbing state whereas all the remaining states are transient. If $X(t) = x$, then in the next time interval there is either a move to the right $x \rightarrow x + 1$ with probability p or a move to the left $x \rightarrow x - 1$ with probability q . Since $|E| = |\mathbb{N}|$, either the process approaches the absorbing state or approaches to infinity. In particular, the following result holds:

Proposition 2.3.1. *Let $X(t) = x_0 > 0$, then*

$$\lim_{t \rightarrow +\infty} \mathbb{P}\{X(t) = 0\} = \begin{cases} 1, & p \leq q \\ \left(\frac{q}{p}\right)^{x_0}, & p > q \end{cases} \quad (2.52)$$

For the proof we refer to [3] and [4]. The above identity is also valid for birth and death process in which $b(i) = \beta i$ and $d(i) = \delta i$, where the infinitesimal probability to increment/decrement by 1 a population of size i in a time interval Δt are

respectively given by $\beta i \Delta t$ and $\delta i \Delta t$. In this case, Eq. (2.52) holds with β replacing p and δ replacing q . We will use this fact to approximate the probability of an outbreak in DTMC and CTMC *SIS* and *SIR* models, where we call outbreak the persistence of the infectious population. Suppose, as usual, that the initial number of infected individuals i_0 is very small compared to the size of the population $N \gg 0$. Thus, the birth and death functions in the previous models are given by

$$b(i) = \beta i(N - i) \approx \beta N i \quad (2.53)$$

$$d(i) = (\mu + \gamma)i \quad (2.54)$$

Moreover we observe that the ratio $\frac{q}{p} = \frac{\mu + \gamma}{\beta N}$ is equal to $\frac{1}{R_0}$. Thus, Eq. (2.52) becomes

$$\mathbb{P}(\mathcal{I}(t) = 0) \approx \begin{cases} 1, & R_0 \leq 1 \\ \left(\frac{1}{R_0}\right)^{i_0}, & R_0 > 1 \end{cases} \quad (2.55)$$

Therefore the probability of an outbreak O is obtained by passing at the complementary event:

$$\mathbb{P}(O) \approx \begin{cases} 0, & R_0 \leq 1 \\ 1 - \left(\frac{1}{R_0}\right)^{i_0}, & R_0 > 1 \end{cases} \quad (2.56)$$

It is important to underline that estimates in Eq.(2.56) apply both to *SIS* and *SIR* stochastic models but only for a range of times (which strongly depends on N and i_0), because eventually $\lim_{t \rightarrow +\infty} \mathbb{P}(\mathcal{I}(t) = 0) = 1$ because zero is an absorbing state.

2.3.2 Final size of an epidemic

In the deterministic framework it is possible to compute explicitly the *final size* of an epidemic, which is the number of all individuals who go through the disease during the whole duration of the epidemic. For instance, in the *SIR* model with vital dynamics we can calculate the final size, since it is equal to $R_\infty = N - S_\infty$, and we have an explicit description of S_∞ in terms of the parameters β, μ, γ and K . In the stochastic *SIR* model things are much more complicated, since there is a distribution associated with the final size of the epidemic. Let us denote (s, i) the ordered pairs of value for the susceptible and infected individuals in the CTMC *SIR* model. We are interested to make a study at the end of the epidemic, i.e. when $\mathcal{I}(t) = 0$: when this happens, the random variable of susceptible individuals ranges from 0 to $N - \mathcal{I}(0) = N - i_0$ and the set $\{(s, 0)\}_{s=0}^{N-i_0}$ is absorbing:

$$\lim_{t \rightarrow \infty} \sum_{s=0}^{N-i_0} p_{(s,0)}(t) = 1 \quad (2.57)$$

Let us now describe an approach to find the distribution $\{P_n\}$ of the ultimate size of the epidemic, where

$$P_n := \lim_{t \rightarrow +\infty} p_{N-n,0}(t) \quad (2.58)$$

indicates the probability that n of the initial susceptibles become infected at some stage during the epidemic. We recall that the **embedded markov chain** of a CTMC is a regular homogeneous DTMC with same values of those of the original CTMC but transitions which represent the conditional probabilities of **jumping** from state i to state j (see App. A.1.2). If $Q = (q_{ij})$ is the infinitesimal semigroup of the CTMC associated to a process $\{X(t)\}_{t \in \mathbb{R}_+}$, then the transition matrix $T = (t_{ij})$ of the respective embedded chain is given by

$$t_{ij} = \frac{q_{ij}}{q_i}, \text{ if } q_i > 0, i \neq j \quad (2.59)$$

and if we define

$$\pi_{ij} = \mathbb{P}((X(t) = j \exists t \mid X(0) = i)) \quad (2.60)$$

then the forward Kolmogorov equations for the jump chain give the relation

$$\pi_{ik} = t_{ik} + \sum_{j \neq k: t_{jk} > 0} \pi_{ij} t_{jk} \quad (2.61)$$

Since all quantities in the right hand-side of this equation are positive, it is quite easy to use this relation to calculate the probability of reaching the absorbing state k starting from the state i . An embedded markov chain for the CTMC *SIR* model with i_0 initial infectors and without vital dynamics (i.e. $\mu = 0$) takes place on the finit region

$$\chi_N = \{(s, i) : s = 0, 1, \dots, N, i = 0, 1, \dots, N - s\} \quad (2.62)$$

For $(s, i) \in \chi_N$ the only non-zero one-step transition probabilities are given by:

$$t_{(s,i),(s-1,i+1)} = \frac{\beta s i}{\beta s i + \gamma i} = \frac{s}{s + \rho} = p_s \quad (2.63)$$

$$t_{(s,i),(s,i-1)} = \frac{\gamma i}{\beta s i + \gamma i} = \frac{\rho}{s + \rho} = 1 - p_s \quad (2.64)$$

where $\rho = \frac{\gamma}{\beta}$. Moreover, it holds:

$$\pi_{(s,i),(N-i_0,i_0)} = \begin{cases} \pi_{(s+1,i-1),(N-i_0,i_0)} p_{s+1} + \pi_{(s,i+1),(N-i_0,i_0)} (1 - p_s), & i \geq 2 \\ \pi_{(s,i+1),(N-i_0,i_0)} (1 - p_s), & i = 0, 1 \end{cases} \quad (2.65)$$

where on the right hand-side $\pi_{s,i} = 0$, $\forall (s, i) \notin \chi_N$. In particular,

$$\pi_{(s,0),(N-i_0,i_0)} = \lim_{t \rightarrow +\infty} p_{s,0} = P_{N-s} \quad (2.66)$$

In matrix notation, this means that given the initial distribution $p(0)$ for the states, then the distribution for the final size of the epidemic can be found from the first $N + 1$ entries of

$$\lim_{t \rightarrow \infty} p(0)T^t \quad (2.67)$$

where the states of T are in the following order:

$$(s, i) \in \{(N, 0), (N - 1, 0), \dots, (0, 0), (N - 1, 1), (N - 2, 1), \dots, (0, 1), \dots, (0, N)\}$$

i.e. the first $N + 1$ states are the absorbing ones.

Example 2.3.2. Suppose that the (constant) size of the population is equal to $N = 3$. Thus, the states of the region χ_3 are ten:

$$\chi_3 = \{(3, 0), (2, 0), (1, 0), (0, 0), (2, 1), (1, 1), (0, 1), (1, 2), (0, 2), (0, 3)\}$$

and the first four states of this list are the absorbing ones. The transition matrix of the embedded chain has the following form

$$T = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 - p_2 & 0 & 0 & 0 & 0 & 0 & p_2 & 0 & 0 \\ 0 & 0 & 1 - p_1 & 0 & 0 & 0 & 0 & 0 & p_1 & 0 \\ 0 & 0 & 0 & 1 - p_0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 - p_1 & 0 & 0 & 0 & 0 & p_1 \\ 0 & 0 & 0 & 0 & 0 & 1 - p_0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 - p_0 & 0 \end{bmatrix}$$

and it is a stochastic matrix, since $1 - p_0 = 1$. Given the initial distribution $p(0)$, which is a vector with ten entries, we need to calculate the first four entries of $\lim_{t \rightarrow +\infty} p(0)T^t$ since the remaining are all equal to zero. Now, for one moment we treat T just as a linear application which sends a vector space (V, \mathcal{B}) in itself. Thus $V \cong R^{10}$ and we can take the canonical basis $\mathcal{B} = \{e_1, \dots, e_{10}\}$. In this notation it

is straightforward to see what happens reiterating T :

$$\begin{aligned}
e_1 &\xrightarrow{T} e_1 \xrightarrow{T^2} e_1 \xrightarrow{T^3} \dots \\
e_2 &\xrightarrow{T} e_2 + (1 - p_2)e_5 \xrightarrow{T^2} e_2 + (1 - p_2)e_5 \xrightarrow{T^3} \dots \\
e_3 &\xrightarrow{T} e_3 + (1 - p_1)e_6 \xrightarrow{T^2} e_3 + (1 - p_1)e_6 + (1 - p_1)^2 e_8 \xrightarrow{T^3} e_3 + (1 - p_1)e_6 + \\
&\quad + (1 - p_1)^2 e_8 + (1 - p_1)^2 p_2 e_5 \xrightarrow{T^4} e_3 + (1 - p_1)e_6 + (1 - p_1)^2 e_8 + (1 - p_1)^2 p_2 e_5 \xrightarrow{T^5} \dots \\
e_4 &\xrightarrow{T} e_4 + e_7 \xrightarrow{T^2} e_4 + e_7 + e_9 \xrightarrow{T^3} e_4 + e_7 + e_9 + p_1 e_6 + e_{10} \xrightarrow{T^4} e_4 + e_7 + e_9 + p_1 e_6 + e_{10} \\
&\quad + p_1(2 - p_1)e_8 \xrightarrow{T^5} e_4 + e_7 + e_9 + p_1 e_6 + e_{10} + p_1(2 - p_1)e_8 + p_1(2 - p_1)p_2 e_5 \xrightarrow{T^6} \dots \\
e_5 &\xrightarrow{T} 0 \xrightarrow{T^2} 0 \xrightarrow{T^3} \dots \\
e_6 &\xrightarrow{T} (1 - p_1)e_8 \xrightarrow{T^2} (1 - p_1)p_2 e_5 \xrightarrow{T^3} 0 \xrightarrow{T^4} \dots \\
e_7 &\xrightarrow{T} e_9 \xrightarrow{T^2} p_1 e_6 + e_{10} \xrightarrow{T^3} p_1(1 - p_1)e_8 + p_1 e_8 \xrightarrow{T^4} p_1(2 - p_1)p_2 e_5 \xrightarrow{T^5} 0 \xrightarrow{T^6} \dots \\
e_8 &\xrightarrow{T} p_2 e_5 \xrightarrow{T^2} 0 \xrightarrow{T^3} \dots \\
e_9 &\xrightarrow{T} p_1 e_6 + e_{10} \xrightarrow{T^2} p_1(1 - p_1)e_8 + p_1 e_8 \xrightarrow{T^3} p_1(2 - p_1)p_2 e_5 \xrightarrow{T^4} 0 \xrightarrow{T^5} \dots \\
e_{10} &\xrightarrow{T} p_1 e_8 \xrightarrow{T^2} p_1 p_2 e_5 \xrightarrow{T^3} 0 \xrightarrow{T^4} 0
\end{aligned}$$

which means that we don't really have to compute $\lim_{t \rightarrow \infty} T^t$ since the limit converges by time $t = 2N - 1$. The limit matrix T^∞ is then equal to T^5 , so that

$$T^\infty = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 - p_2 & (1 - p_1)^2 p_2 & p_1(2 - p_1)p_2 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 - p_1 & p_1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & (1 - p_1)^2 & p_1(2 - p_1) & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix} \quad (2.68)$$

Thus, if we start with a initial probability distribution $p(0) = (p_1(0), p_2(0), \dots, p_{10}(0))$, then the final size epidemic can be calculated from $v = p(0)T^5$ which has the following expression:

$$v_i = \begin{cases} p_1(0), & i = 1 \\ p_2(0) + (1 - p_2)p_5(0), & i = 2 \\ p_3(0) + (1 - p_1)^2 p_2 p_5(0) + (1 - p_1)p_6(0) + (1 - p_1)^2 p_8(0), & i = 3 \\ p_4(0) + p_1(2 - p_1)p_2 p_5(0) + p_1 p_6(0) + p_7(0) + p_1(2 - p_1)p_8(0) + p_9(0) + p_{10}(0), & i = 4 \\ 0, & 5 \leq i \leq 10 \end{cases}$$

Now we use the fact that $P_n = v_{n+1}$ for $n \in 0, 1, 2, 3$. For instance, if we take $i_0 = 1$ (so that $s_0 = 2$) thus $p(0) = (0, 0, 0, 0, 1, 0, 0, 0, 0, 0)$ and in this case the probability of a final size epidemic equal to $n \in \{0, \dots, 3\}$ is equal to

$$P_n = \begin{cases} 0, & n = 0 \\ 1 - p_2, & n = 1 \\ (1 - p_1)^2 p_2, & n = 2 \\ p_1(2 - p_1)p_2, & n = 3 \end{cases} \quad (2.69)$$

which is actually a distribution. In many real disease the reproduction number R_0 stands between 2 and 3: in our example, this happens if, for instance, $\gamma = 1$ and $\beta = \frac{3}{4}$. For this value we have $p_1 \approx 0.4$ and $p_2 \approx 0.6$. With those value the distribution of the final size can be explicitly computed:

$$P_n \approx \begin{cases} 0, & n = 0 \\ 0.4, & n = 1 \\ 0.2, & n = 2 \\ 0.4, & n = 3 \end{cases} \quad (2.70)$$

2.3.3 Persistence time of an epidemic

While we saw that all stochastic models converge to the disease-free equilibrium, it is not clear how many they need to reach it, i.e. it is not clear what is the first time $T \in \mathbb{R}_+$ such that $\mathcal{I}(T) = 0$. In this section our aim is to derive a system of equations that can be solved in order to find the expected time until absorption for the stochastic *SIS* model. The most interesting fact is that, while the convergence to the disease-free equilibrium holds regardless of the value of R_0 , depending on N, i_0 and R_0 the persistence time of an epidemic can be very short or very long. Let then be T_i the random variable describing the time until absorption beginning with $i_0 = i$ infectors, where $i = 0, 1, \dots, N$, and let denote with τ_i its expected value: $\tau_i := \mathbb{E}(T_i)$. A first trivial observation is that no persistence occurs if there are no infectors, i.e. $\tau_0 = 0$. Using the *first step analysis* we see that the mean persistence time in the DTMC *SIS* model with time step of lengths Δt satisfies the following differential equation:

$$\tau_i = b(i)\Delta t (\tau_{i+1} + \Delta t) + d(i)\Delta t (\tau_{i-1} + \Delta t) + (1 - [b(i) + d(i)] \Delta t) (\tau_i + \Delta t)$$

Simplyfing and multiplying by Δt^{-1} both the sides of the expression, it can be rewritten as:

$$d_i \tau_{i-1} - [b(i) + d(i)] \tau_i + b(i) \tau_{i+1} = -1 \quad (2.71)$$

It is important to observe that, even if we are treating the DTMC *SIS* model, Eq. (2.71) holds also for the CTMC *SIS* model: indeed, in continuous time, τ_i satisfies the same equation as τ_i expect for an extra term $o(\Delta t)$. Multiplying by Δt^{-1} and taking the limit $\Delta t \rightarrow 0$, we find again Eq. (2.71). We can express what we have just said in matrix form. Let be $\tau = (\tau_1, \dots, \tau_N)$. Then Eq. (2.71) is equivalent to:

$$\tau D = (1, 1, \dots, 1) \quad (2.72)$$

where:

$$D = \begin{bmatrix} -[b+d](1) & d(2) & 0 & \dots & 0 & 0 \\ b(1) & -[b+d](2) & 0 & \dots & 0 & 0 \\ 0 & b(2) & 0 & \dots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & 0 & d(N) \\ 0 & 0 & 0 & \dots & 0 & -d(N) \end{bmatrix} \quad (2.73)$$

Since this matrix is an *irreducibly diagonally dominant* matrix (see Def. A.3.5), it is not singular ([24],[25]): the solution τ to Eq. (2.72) is unique. Since the matrix is also *tridiagonal* (see Def. A.3.7), we can find explicetely the solution using the *Thomas algorithm* (see App. A.3.2):

$$\tau_i = \begin{cases} \frac{1}{d(1)} \sum_{k=2}^N \frac{b(1) \dots b(k-1)}{d(1) \dots d(k)}, & i = 1 \\ \tau_1 + \sum_{k=s}^{i-1} \left[\frac{d(1) \dots d(s)}{b(1) \dots b(s)} \sum_{h=s+1}^N \frac{b(1) \dots b(h-1)}{d(1) \dots d(h)} \right], & i = 2, \dots, N \end{cases} \quad (2.74)$$

Chapter 3

Network models in epidemiology

The next step in the modelling of an epidemic is to consider network models. In these models, contrary to what happens in deterministic and stochastic models, the whole population is made of single individuals instead of compartments and this fact allows to consider interactions different from the classical *homogeneous mixing*, in which every person enters in contact with any other individuals of the population. Individual-level models make analysis difficult and simulations computationally intensive, but they offer a totally different way of describing biological populations which seems to fit better epidemiological data taken from the real-world. Since there are many different approaches to construct network models in epidemiology, we present here only some of them. The first section presents the so-called *generating function approach*, which basically links the early stage of an epidemic to percolation: for this part we refer to [7],[8],[11] and [23]. In the second section we will establish a relation between network model and simple deterministic model, that is always due to F. Brauer ([8]). Finally, in Sec. 3, we will derive the so called *N-intertwined model* which has been largely studied by P. Van Mieghem ([12],[26]): here the model is described by (a family of) continuous time processes that can be studied with usual Markov chain theory under a mean field approximation. We refer to App. A.2 for the main definitions and results on graph theory.

3.1 Network model for the early stage of an epidemic

In the simplest epidemic network models, nodes of the (undirected and unweighted) graph represent individuals and an edge (i, j) depicts an interaction between i and j that could potentially lead to transmission of infection. This is enough to understand how important the topology of the network is: for instance, an isolated node could not spread the virus, while a node with high degree can infect many people becoming a so-called *super-spreader*. If an edge (i, j) represents a contact between two individuals, we could argue that the graph should be dynamic, since interactions between people change over time and the changing pattern of social contacts can have an huge impact on transmission. However, the importance of the

dynamic aspects of network structure depends on the timescale over which disease dynamics are of interest. For rapidly spreading infections, it is common to assume that the network is static, since it suffices for the description of the spreading. In more general situations, network static models are also useful to describe the first phase of the spreading. Since this assumption leads to considerable simplifications, much of the recent work has focused on static network settings.

From now on we will consider a configuration model, i.e. a graph $G = (V, E)$ in which every node $i \in V$ has a predetermined degree k_i (see App. A.2.4). Moreover, we will take G as a static graph, assuming that we are describing just the beginning of the spreading. This allows us to do not give much importance at the kind of model ($SIR, SIRS, SEIR$) we are taking into account.

3.1.1 Excess degree distribution

From now on we indicate with $\{p_k\}$ the *degree distribution*, i.e. the fraction of nodes having degree equal to k : clearly, it holds $\sum_{k=0}^{\infty} p_k = 1$.

When a disease is introduced into a network, we think of it as starting from a single infective node i_0 . This node is chosen randomly from V , so that it has a random degree k_{i_0} , and it represents the only individual who becomes infected without any infective transmission. In word, we are assuming that the first infector has been infected by a contact outside of the population. Moreover, we assume that individuals make contacts independently of one another and, for the moment, that every contact leads to a transmission.

The distribution p_k tells us the probability that a vertex chosen randomly from V has exactly k neighbours. Suppose instead that we take a vertex i and follow one of its edges (assuming it has at least one) to the vertex j at the other end of the edge. What is the probability that j has degree k ? In some way we are conditioning the probability for j of having k neighbours to the fact of being linked to i . This is enough to understand that this new probability we are searching for couldn't be equal to p_k again: for instance, an isolated node j can't be reached by following an edge in this way, so if j is isolated the probability we are trying to compute would be $0 \neq p_0$. For the general formula we proceed as follows: first of all, let us call k_i the the degree of the vertex i . We have

$$\sum_i k_i = 2m, \quad m \in \mathbb{N} \quad (3.1)$$

Now, since we start from i and then we follow the edge (i, j) , when analyzing the behaviour of j we know that $2m - 1$ edges remain, and k of them are clearly attached to a vertex with degree k . We know that p_k is the fraction of vertex with degree k , where the set of all nodes is V , and for the sake of brevity we can rename

$|V| = N$. Thus, the probability of our edge (i, j) attaching to any vertex of degree k is equal to:

$$\frac{k}{2m-1} N p_k \quad (3.2)$$

Now, in the limit of large network size, m becomes very large and $2m-1$ can be approximated with $2m$, and since the degrees are pre-assigned the average degree $\langle k \rangle$ is equal to the arithmetic mean $\frac{1}{N} \sum_i k_i = \frac{2m}{N}$. This allows us to rewrite Eq. (3.2) in a more useful way:

$$\frac{k}{2m} N p_k = \frac{k p_k}{\langle k \rangle} \quad (3.3)$$

Thus, the probability that we reach a vertex of degree k upon following an edge in this way is proportional to $k p_k$ instead of p_k . This result has a funny, counterintuitive consequence: since the right hand-side of Eq. (3.3) is the probability for a node reached following an edge of having k neighbours, we can compute the average degree of a neighbor as

$$\sum_k k \frac{k p_k}{\langle k \rangle} = \frac{\langle k^2 \rangle}{\langle k \rangle} \quad (3.4)$$

If we want to make a comparison between the average degree of a neighbor and the average degree of a typical node in V , we found that:

$$\frac{\langle k^2 \rangle}{\langle k \rangle} - \langle k \rangle = \frac{1}{\langle k \rangle} (\langle k^2 \rangle - \langle k \rangle^2) = \frac{\sigma_k^2}{\langle k \rangle} \quad (3.5)$$

where we indicated with σ_k^2 the variance of the degree distribution. Since both σ_k^2 and $\langle k \rangle$ are positive numbers, it follows that the average degree of a neighbor is greater or equal to the one of a typical node of the graph: in colloquial terms “your friends have more friends than you do”. From now on, we will be interested not in the total degree of the vertex at the end of an edge, but in the number of edges attached to that vertex other than the one we arrived along. This quantity is called the *excess degree* of the vertex, and it is just one less than the total degree. Of course the excess degree is greater or equal to zero, since, by definition, a vertex reached by following an edge must have at least total degree equal to 1. We will indicate with $\{q_k\}$ the distribution of the excess degree, i.e. q_k is the probability, for a vertex j reached by following an edge (i, j) , of having k other neighbors different from i .

Proposition 3.1.1. *The following formula for q_k holds:*

$$q_k = \frac{(k+1)p_{k+1}}{\langle k \rangle} \quad (3.6)$$

Proof. Let j be a node of V reached by following an edge (i, j) . The probability that j has excess degree equal to k is exactly equal to the probability that it has total degree equal to $k+1$. Using Eq. (3.3) with $k+1$ instead of k we conclude. \square

Let us now define the *generating function* of the degree distribution $\{p_k\}$ as :

$$g(t) = \sum_{k=0}^{\infty} p_k t^k \quad (3.7)$$

Now, $p_k \leq 1$, $\forall k \in \mathbb{N}$, thus the series is dominated by the geometric series $\sum_{k=0}^{\infty} t^k$: this prove that the series converges for $0 \leq t \leq 1$ and could be differentiated term by term. Thus

$$p_k = \frac{g^{(k)}(0)}{k!} \quad (3.8)$$

The generating function has the following properties:

1. $g(0) = p_0$
2. $g(1) = 1$
3. $g'(t) > 0$
4. $g''(t) > 0$
5. $\langle k \rangle = g'(1)$

which can be proved by direct computations. We can define the generating function also for the distribution of the excess degree:

$$\begin{aligned} \tilde{g}(t) &= \sum_{k=0}^{\infty} q_k t^k = \sum_{k=0}^{\infty} \frac{(k+1)p_{k+1}}{\langle k \rangle} t^k \\ &= \sum_{h=1}^{\infty} \frac{h p_h}{\langle k \rangle} t^{h-1} = \frac{g'(t)}{\langle k \rangle} \end{aligned} \quad (3.9)$$

From this generating function we can extract an explicit formulation of the mean excessive degree $\langle k_e \rangle$:

$$\begin{aligned} \langle k_e \rangle &= \sum_{k=0}^{\infty} k q_k = \sum_{k=0}^{\infty} \frac{k(k+1)p_{k+1}}{\langle k \rangle} \\ &= \frac{1}{\langle k \rangle} \sum_{h=1}^{\infty} h(h-1)p_h = \frac{1}{\langle k \rangle} \left[\sum_{h=1}^{\infty} (h^2 p_h - h p_h) \right] \\ &= \frac{\langle k^2 \rangle}{\langle k \rangle} - 1 = \tilde{g}'(1) \end{aligned} \quad (3.10)$$

The importance of the mean excessive degree is that it coincides with the mean number of secondary cases by patient zero, which is the basic reproduction number as usually defined. For this reason, from now on we will rename $\langle k_e \rangle = \tilde{g}'(1) = R_0$

3.1.2 Probability of an outbreak

As we did for stochastic models, we want now to calculate the probability that an outbreak actually occurs, or equivalently the probability that the infection die out without developing into a major epidemic. It is important to underline another time that all those analysis are confined to the initial stage of the spreading, in which the portion of infectious individuals remains small compared to the whole population: with epidemic we mean a situation in which the growth of infectious becomes exponential in this stage. The main result in this sense is given by the following

Theorem 3.1.2. *If $R_0 < 1$, then the probability that the infection will die out is 1. On other hand, if $R_0 > 1$ there is a \tilde{g} -fixed point $z_\infty > 0$, i.e. an element satisfying*

$$\tilde{g}(z_\infty) = z_\infty \quad (3.11)$$

and there is a positive probability $1 - g(z_\infty)$ that the infection will persist and lead to an epidemic.

Proof. Let $i_0 \in V$ be the first infectors and let us suppose that k_{i_0} is its correspondent degree. Suppose that i_0 infects a contact with degree k through an edge of E . Let z_n be the probability that this infection dies out within the n -th generation. Now, we observe that the infection starting from the first infectors dies out in n th generations if, and only if, each secondary infection dies out in $n - 1$ generations: let us denote with z_{n-1}^k the probability of this event. Thus, z_n can be decomposed as follows:

$$z_n = \sum_{k=0}^{\infty} q_k z_{n-1}^k \quad (3.12)$$

which means that the probability that the infection dies out in n -th generation starting from the first infector is the sum over all possible degree k of the probability that all secondary infections starting from nodes with degree equal to k die in $n - 1$ generations, weighted with the probability of having an excess degree equal to k . Eq. (3.12) can be rewritten in terms of the generating functions as

$$z_n = \tilde{g}(z_{n-1}) = \frac{g'(z_{n-1})}{\langle k \rangle} \quad (3.13)$$

Since we have proved that g has first and second derivatives strictly positive, it follows from Eq. (3.13) that z_n is an increasing sequence, thus it has a limit z_∞ which is the probability that the infection will die out eventually. Since z_∞ is the limit as $n \rightarrow \infty$ of the solution of the difference equation:

$$\begin{cases} z_n = \tilde{g}(z_{n-1}) \\ z_0 = 0 \end{cases} \quad (3.14)$$

it follows that z_∞ must be an equilibrium for the difference equation, that is, a fixed point for $\tilde{g}(z)$. Let now be ω the smallest positive fixed point of \tilde{g} , i.e.

$$\omega = \inf\{t \in (0, 1) : \tilde{g}(t) = t\} \quad (3.15)$$

Since \tilde{g} is itself increasing, the following chain holds:

$$t \leq \tilde{g}(t) \leq \tilde{g}(\omega) = \omega, \quad \forall 0 \leq z \leq \omega \leq 1 \quad (3.16)$$

In particular, since $z_0 = 0 \leq \omega$ and $z_{n-1} \leq \omega$, it holds by induction that:

$$\begin{aligned} z_1 &= \tilde{g}(z_0) \leq \tilde{g}(\omega) = \omega \\ z_2 &= \tilde{g}(z_1) \leq \tilde{g}(\omega) = \omega \\ &\vdots \\ z_\infty &\leq \omega \end{aligned} \quad (3.17)$$

which ultimately implies that $z_\infty = \omega$ since z_∞ is a fixed point. Now, since $\{q_k\}$ is a distribution, it holds that $\tilde{g}(t) = t$ has a root $t = 1$. Now, let us define

$$f(t) := \tilde{g}(t) - t \quad (3.18)$$

We can prove that the second derivative of f is positive in the open interval $(0, 1)$:

$$f''(t) = \left(\frac{g'(t)}{\langle k \rangle} \right)'' = \frac{g^{(3)}(t)}{\langle k \rangle} = \sum_{k=0}^{\infty} k(k-1)(k-2)p_k t^{k-3} > 0 \quad \forall t \in (0, 1)$$

thus, $f'(t) = \tilde{g}'(t) - 1$ is a strictly increasing function on $(0, 1)$ and it has at most one zero in this interval, i.e. there are at most two roots of $\tilde{g}(t) = t$ in $[0, 1]$. Now, if $R_0 < 1$, $f(t)$ has a negative first derivative $f'(t)$:

$$f'(t) = \tilde{g}'(t) - 1 \leq \tilde{g}'(1) - 1 = R_0 - 1 \quad (3.19)$$

and the equation $g(t) = t$ has only one root $t = 1$. On other hand, if $R_0 > 1$, the function $f(t)$ is positive for $t = 0$ and negative near $t = 1$ since it is zero at $t = 1$,

and its derivative $f'(t)$ is positive both for $t < 1$ and t near 1. Thus, equation $\tilde{g}(t) = t$ has a second root $z_\infty < 1$. The probability that the disease outbreak will die out eventually is the sum over k of the probabilities that the initial infection in a vertex of degree k will die out, and this is

$$\sum_{k=0}^{\infty} p_k z_\infty = g(z_\infty) \quad (3.20)$$

This can be expressed equivalently by saying that, if $R_0 > 1$, there is a probability equal to $1 - g(z_\infty)$ that an epidemic occurs. \square

3.1.3 Transmissibility

Until now we have assumed that each contact between an infectious and a susceptible leads to an infection. In the real world this does not happen, and there is just a **probability** that a contact causes an infection. Moreover, the aim of preventive interventions such as the use of mask are exactly made in order to decrease this probability. From now on we will continue to assume that there is a network whose degree distribution is fully described by the generating function g , but in addition we will consider that there is a probability of transmission equal to α . The following definition will be useful:

Definition 3.1.3. Suppose i, j are two vertex of G , linked through the edge $(i, j) \in E$. If the link corresponds to an infection, we say that (i, j) is *occupied*.

The importance of this definition besides in the fact that, at any time, the cluster of vertices connected to the first infectors i_0 through path made by occupied edges represents exactly the size of the epidemic at that time. The probability that a node of degree k infects exactly $m \leq k$ of its neighbours is given by:

$$r_m^k = \binom{k}{m} \alpha^m (1 - \alpha)^{k-m} \quad (3.21)$$

Now, let us indicate with $h(z, \alpha)$ the generating function for the distribution of the number of infections caused by a randomly chosen node of V , which is also equal to the distribution for the number of occupied edge attached to that node. Observe that h depends on α , since it is not necessary to consider the transmissibility fixed during the computation. As we did for \tilde{g} , even for h admits an explicit rewriting in terms of the generating function for the distribution of the degree g :

Proposition 3.1.4. *The generating function h admits the following expression:*

$$h(t, \alpha) = \sum_{m=0}^{\infty} g(1 + \alpha(t - 1)) \quad (3.22)$$

Proof. By definition, the generating function $h(t)$ is the sum over all possible $m \in \mathbb{N}$ of t^m weighted with the probability that a random chosen node is exactly linked to m occupied edges; now, since the degree of the random chosen node is unknown, this probability is in turn equal to the sum on all degree k of $p_k r_m^k$, i.e:

$$\begin{aligned} h(t, \alpha) &= \sum_{m=0}^{\infty} \sum_{k=0}^{\infty} p_k r_m^k t^m \\ &= \sum_{m=0}^{\infty} \left[\sum_{k=0}^{\infty} p_k \binom{k}{m} (t\alpha)^m (1-\alpha)^{k-m} \right] \end{aligned} \quad (3.23)$$

Now, we recall that according to the binomial theorem, it holds:

$$(x + y)^n = \sum_{k=0}^n \binom{n}{k} x^k y^{n-k} \quad (3.24)$$

we can apply this result to Eq. (3.23) in order to get:

$$h(t, \alpha) = \sum_{k=0}^{\infty} p_k (1 + \alpha(t-1))^k = g(1 + \alpha(t-1)) \quad (3.25)$$

□

With direct computations, we get the following corollary

Corollary 3.1.5. *The generating function h has the following properties:*

1. $h(0, \alpha) = g(1 - t)$
2. $h(1, \alpha) = 1$
3. $h'(t, \alpha) = \alpha g'(1 + \alpha(t-1))$

Proof. Property 1 follows just by a substitution in Eq. (3.25). We have that $h(1, \alpha) = g(1)$ and we have already seen that $g(1) = 1$ since p_k is a distribution. Property three follows by direct computations. □

Along the lines of the previous section, we might calculate the generating function $\tilde{h}(t, \alpha)$ for the distribution of the number of infections caused by a vertex reached by following an edge starting from a random chosen vertex. Again, we need to use the concept of excess degree. What we obtain is given by the following:

Proposition 3.1.6. *The generating function for secondary infections $\tilde{h}(t, \alpha)$ satisfies the following equality:*

$$\tilde{h}(t, \alpha) = \tilde{g}(1 + \alpha(t-1)) \quad (3.26)$$

Proof. The probability that a node j reached by following an edge starting from a random chosen node i_0 infects exactly m other nodes is obtained by summing on all possible degree k of the secondary node j the probability that a node of degree k infects m of its neighbours, namely r_m^k weighted by the probability q_k that j has actually degree k . Briefly:

$$\tilde{h}(t, \alpha) = \sum_{m=0}^{\infty} \sum_{k=0}^{\infty} q_k r_m^k t^m \quad (3.27)$$

We now proceed similarly to what we have done for Proposition 3.1.4:

$$\begin{aligned} \tilde{h}(t, \alpha) &= \sum_{m=0}^{\infty} \left[\sum_{k=0}^{\infty} q_k \binom{k}{m} (t\alpha)^m (1-\alpha)^{k-m} \right] \\ &= \sum_{k=0}^{\infty} q_k (1 + \alpha(t-1))^k \\ &= \tilde{g}(1 + \alpha(t-1)) \end{aligned} \quad (3.28)$$

□

As we did for h , some easy properties can be deduced from \tilde{h} .

Corollary 3.1.7. *The generating function \tilde{h} satisfies the following properties:*

1. $\tilde{h}(0, \alpha) = \tilde{g}(1 - \alpha)$
2. $\tilde{h}(1, \alpha) = \tilde{h}(1) = 1$
3. $\tilde{h}'(t, \alpha) = \alpha \tilde{h}'(1 + \alpha(t-1))$

Again, the importance of the generating function for the excess degree besides in the fact that it is strictly related to the basic reproduction number, because

$$R_0 = \alpha \tilde{g}'(1) = \tilde{h}'(1, \alpha) \quad (3.29)$$

The calculation of the probability that an infection will die out before becoming a real epidemic follows the same arguments of Th. 3.1.2. The following theorem holds:

Theorem 3.1.8. *If $R_0 = \alpha \tilde{g}'(1) = \tilde{h}'(1, \alpha) < 1$, the probability that the infection will die out is 1. On other hand if $R_0 > 1$ there are a \tilde{h} -fixed point $z_{\infty}(\alpha) > 0$ and a positive probability $1 - h(z_{\infty}(\alpha), \alpha) > 0$ that the infection will persist and lead to an epidemic.*

Remark 3.1.9. It is important to observe that there isn't a sharp distinction for different values of R_0 , as there was in the deterministic case. For instance, if $R_0 > 1$ it is not sure that an epidemic will happen, since there is a positive probability $h(z_\infty(\alpha), \alpha)$ that the spreading will stop before having a real outbreak.

The theorem motivates the following definition:

Definition 3.1.10. We will call *critical transmissibility* the quantity α_c defined as

$$\alpha_c = \frac{1}{\tilde{g}'(1)} \quad (3.30)$$

The importance of α_c is that it is the transmissibility that makes the basic reproduction number equal to 1: thus, if the mean transmissibility α of an epidemic can be decreased low the α_c , then the epidemic can be prevented. This result is quite interesting for the study of preventive actions to avoid acute outbreaks.

3.1.4 Final size of the epidemic

Let us begin with another generating function: we define $f(t, \alpha)$ to be the generating function for the distribution of outbreak sizes corresponding to a random chosen vertex, where with outbreak sizes we mean the number of vertices who become infected during an epidemic started from a first infectors i_0 . As usual, we are interested also in generating function of secondary properties, so we define also $\tilde{f}(t, \alpha)$ as the generation function for the sizes of the clusters of connected vertices reached by following a randomly chosen edge attached to i_0 . The following important result holds:

Proposition 3.1.11. *Let be $f(t, \alpha)$ and $\tilde{f}(t, \alpha)$ the generating functions above defined. Then the following rewriting in terms of the generating function $h(t, \alpha)$ and $\tilde{h}(t, \alpha)$ yields:*

$$f(t, \alpha) = t \cdot h(\tilde{f}(t, \alpha), \alpha) \quad (3.31)$$

$$\tilde{f}(t, \alpha) = t \cdot \tilde{h}(\tilde{f}(t, \alpha), \alpha) \quad (3.32)$$

Proof. It is enough to prove Eq. (3.32), since the proof for the other equation is analogous. The epidemic starts following an edge attached to the so-called *patient-zero* i_0 , so that we can argue that i_0 infects an element j which forms the generation one. The member of generation one has degree k with probability q_k and turn causes independently a new set of m infections distributed according to \tilde{f} . If in the final count we want to take into account also the initial infections caused by j , we must increase the exponent of the series by 1 and we do that

simply multiplying by t . In formulas:

$$\begin{aligned}
\tilde{f}(t, \alpha) &= t \sum_{m=0}^{\infty} \left[\sum_{k=0}^{\infty} q_k \binom{k}{m} \alpha^m (1 - \alpha)^{k-m} \right] (\tilde{f}(t, \alpha))^m \\
&= t \sum_{k=0}^{\infty} \left[\sum_{m=0}^{\infty} q_k \binom{k}{m} (\alpha \tilde{f}(t, \alpha))^m (1 - \alpha)^{k-m} \right] \\
&= t \sum_{k=0}^{\infty} q_k \left(1 + \alpha(\tilde{f}(t, \alpha) - 1) \right)^k \\
&= t \tilde{g}(1 + \alpha(\tilde{f}(t, \alpha) - 1))
\end{aligned} \tag{3.33}$$

which implies the thesis. \square

The importance of this proposition is that it makes possible an explicit computation of the mean size of the disease outbreak, i.e. the mean number of individuals who take the virus during the epidemic.

Theorem 3.1.12. *The final size of the epidemic depends on $R_0 = \alpha \tilde{g}'(1)$ since there are three possible situations:*

1. *If $R_0 < 1$ almost surely an epidemic will not occur, and the final size is given by*

$$1 + \frac{\alpha g'(1)}{1 - R_0} \tag{3.34}$$

2. *If $R_0 = 1$ a discontinuity on the final size of the outbreak occurs.*
3. *If $R_0 > 1$ the fraction of the individuals affected by the infection is equal to the probability that the outbreak will develop into a major epidemic which*

$$1 - h(z_{\infty}, \alpha) \tag{3.35}$$

where $z_{\infty} > 0$ is a \tilde{h} -fixed point.

Proof. By construction the mean size of the disease outbreak is $f'(1, \alpha)$. We can calculate explicitly this quantity by differentiating both the expressions for f and \tilde{f} in the previous proposition. Differentiating Eq. (3.32) gives

$$\begin{aligned}
\tilde{f}'(t, \alpha) &= \tilde{h}(\tilde{f}(t, \alpha), \alpha) + t \tilde{h}'(\tilde{f}(t, \alpha), \alpha) \tilde{f}'(t, \alpha) \Rightarrow \\
\Rightarrow \tilde{f}'(t, \alpha) &= \frac{\tilde{h}(\tilde{f}(t, \alpha), \alpha)}{1 - t \tilde{h}'(\tilde{f}(t, \alpha), \alpha)}
\end{aligned} \tag{3.36}$$

whereas implicit differentiation of Eq. (3.31) jointly with Eq. (3.50) gives

$$\begin{aligned} f'(t, \alpha) &= h(\tilde{f}(t, \alpha), \alpha) + th'(\tilde{f}(t, \alpha), \alpha)\tilde{f}'(t, \alpha) \\ &= h(\tilde{f}(t, \alpha), \alpha) + th'(\tilde{f}(t, \alpha), \alpha) \frac{\tilde{h}(\tilde{f}(t, \alpha), \alpha)}{1 - t\tilde{h}'(\tilde{f}(t, \alpha), \alpha)} \end{aligned} \quad (3.37)$$

Now, \tilde{f} is a probability generating function so that

$$\tilde{f}(1, \alpha) = 1 \Rightarrow \begin{cases} h(\tilde{f}(1, \alpha), \alpha) = h(1, \alpha) = 1 \\ \tilde{h}(\tilde{f}(1, \alpha), \alpha) = \tilde{h}(1, \alpha) = 1 \end{cases} \quad (3.38)$$

thus the mean size of the outbreak reduces to

$$\begin{aligned} f'(1, \alpha) &= 1 + \frac{h'(1, \alpha)}{1 - \tilde{h}'(1, \alpha)} \\ &= 1 + \frac{\alpha g'(1)}{1 - \alpha \tilde{g}'(1)} \\ &= 1 + \frac{\alpha g'(1)}{1 - R_0} \end{aligned} \quad (3.39)$$

It is important to observe that this expression is consistent if $R_0 < 1$. For $R_0 = 1$ there is a discontinuity (phase transition) that has the epidemiological meaning of the appearance of a giant component which leads to a major epidemic. If $R_0 \geq 1$ we exclude the giant component of the graph in the definition of $\tilde{f}(t, \alpha)$ so that $\tilde{f}(1, \alpha) < 1$. Now, we have that

$$\tilde{f}(1, \alpha) = \tilde{h}(\tilde{f}(1, \alpha), \alpha) \quad (3.40)$$

therefore $\tilde{f}(1, \alpha) < 1$ is a \tilde{h} -fixed point, i.e. it is the second root $z_\infty(\alpha)$ of

$$\tilde{h}(t, \alpha) = t \quad (3.41)$$

We can thus apply Th. 3.1.8 to deduce that, in this case, there is a positive probability $h(z_\infty, \alpha)$ that there will be only a small disease outbreak whereas $1 - h(z_\infty, \alpha)$ is the probability that the infections will persist and lead to epidemic. For the same reason, if $R_0 < 1$ we have that $\tilde{f}(1, \alpha) = 1$, thus $z_\infty(\alpha) = 1$ and the probability of an epidemic is equal to zero.

Let us now suppose to have an epidemic, i.e. R_0 is above the threshold quantity 1. We define $FS(\alpha)$ as the fraction of the graph affected by the infection, i.e. the final size of the epidemic. It holds:

$$f(1, \alpha) = 1 - FS(\alpha) \quad (3.42)$$

from which we can rewrite the final size as

$$FS(\alpha) = 1 - f(1, \alpha) = 1 - h(\tilde{f}(1, \alpha), \alpha) = 1 - h(z_\infty(\alpha), \alpha) \quad (3.43)$$

which implies the thesis. \square

3.2 Relation with deterministic models

Until now we have used only a *branching process* without referring to any compartmental model, because we confined our attention to the early stage of the spreading. Aim of this section is to expand the time interval we want to study, and immerse a simple compartmental model on a network. To avoid complications, we will consider the basic *SIR* model on a static configuration network, in which the probability that a node has degree k is equal to p_k where $\sum_{k=0}^{\infty} p_k = 1$. The degree generating function is then the same as the one introduced in the previous section:

$$g(t) = \sum_{k=0}^{\infty} p_k t^k \quad (3.44)$$

and it is well defined when $0 \leq t \leq 1$. We assume that at any time each node of the network can be in three possible states: susceptible, infectious or recovered. The transition from the susceptible to the infectious class happens with a certain rate β when a susceptible individual is linked through an edge of the network to an infected node. On other hand, the transition from the susceptible to the removed class occurs at a rate α . If we denote with $s(t)$, $i(t)$ and $r(t)$ respectively the fraction of susceptibles, infectious and recovered individuals, it is easy to found a differential equation satisfied by r :

$$r'(t) = \alpha i(t) \quad (3.45)$$

Since $s(t) + i(t) + r(t) = 1$, $\forall t \in \mathbb{R}_+$ we only need to found an equation for s in order to fully describe the model. We underline that r is the only one deterministic quantity of the three mentioned. From an epidemiological point of view, it is reasonable to assume that the more contacts we have the more we expose ourselves to being infected. From a mathematical point of view this means that the hazard of infection for a susceptible node i is proportional to its degree, that we shall indicate with k_i . If we denote with $\phi_I(t)$ the probability that a neighbour of the susceptible node i is infective at time t , we obtain the following expression for the i 's hazard of infection at time t :

$$\lambda_i(t) = k_i \beta \phi_I(t) \quad (3.46)$$

Let us now change the notation and consider i as a randomly chosen node. We are interested in computing the probability that, at time t , i belongs to the susceptible class. In order to do that, we introduce $\theta(t)$ as the probability that a random neighbor of i hasn't transmitted the infection to i at time t . It is easy to deduce that the event " i is susceptible at time t " coincides with the intersection of the events " j hasn't transmitted the infection to i " where j are all the potential infective

neighbours of i . Then, the probability that the random chosen node i is still susceptible at time t is given by $\theta(t)^{k_i}$. If we now want to know what is the fraction of susceptible at time t , namely $s(t)$ we should average over all nodes the probability that a node is still susceptible at time t , i.e.

$$s(t) = \sum_{k=0}^{\infty} p_k \theta(t)^k = g(\theta(t)) \quad (3.47)$$

In order to proceed we now make the following observation. The fact that a random neighbor j of a susceptible individual i hasn't transmitted to him the infection at time t can be splitted in three disjoint subevent:

1. The random neighbor j is still susceptible at time t . This happens with a probability $\phi_S(t)$.
2. The random neighbor j is infective at time t , but he hasn't transmitted the virus to i . We have already introduced this event and we called $\phi_I(t)$ its probability.
3. The random neighbor j is recovered at time t , and during the period in which he was infective he didn't infect i . This happens with a probability $\phi_R(t)$.

The following equality follows:

$$\theta(t) = \phi_S(t) + \phi_I(t) + \phi_R(t) \quad (3.48)$$

On other hand, the probability that the random neighbor j has transmitted to i the virus at time t is equal to $1 - \theta(t)$. The following proposition provides a differential relation involving θ .

Proposition 3.2.1. *Let be $\theta(t)$, α , β and $g(t)$ as above defined. Thus the following differential equation holds:*

$$\theta'(t) = -\beta\theta(t) + \beta \frac{g'(\theta(t))}{g'(1)} + \alpha(1 - \theta) \quad (3.49)$$

Proof. We have already observed that r satisfies Cond. (3.45). Since infected neighbors recover at rate α , the flux from ϕ_I to ϕ_R satisfies an analogous relation:

$$\phi'_R(t) = \alpha\phi_I(t) \quad (3.50)$$

Since edges which link an infectious and a susceptible node transmitt infections at rate β , we can argue that the flux from ϕ_I to $(1 - \theta(t))$ is given by:

$$(1 - \theta(t))' = \beta\phi_I \Leftrightarrow \theta'(t) = -\beta\phi_I(t) \quad (3.51)$$

To obtain ϕ'_I we need to study separately each flux into and out of its correspondent compartment. Firstly, we have an incoming flux from ϕ_S to ϕ_I which is represented by the neighbours of i who get the infections. Secondly, we have two outgoing flows: the flux from ϕ_I to $(1 - \theta)$, which happens with rate β , and the flux from ϕ_I to ϕ_R , which happens with rate α . The total outgoing flux from ϕ_I is then equal to $(\alpha + \beta)\phi_I$. In order to determine precisely the incoming flux from ϕ_S to ϕ_I , we proceed as follows. Let us consider a random neighbor j of i : Eq. (3.3) tells us that the probability that j has degree equal to k is equal to $\frac{kp_k}{\langle k \rangle}$. If we now assume that j has degree k , it follows that it has $k - 1$ neighbours who can potentially be infectious (the k -th neighbor is i , that is susceptible by hypothesis). Thus, as we have already seen, the probability that j is susceptible is given by θ^{k-1} . In order to get the probability that a random neighbor of i is susceptible, we need to average over all k the probability that a neighbor of i with degree k is susceptible, i.e.:

$$\phi_S(t) = \sum_{k=0}^{\infty} \frac{kp_k}{\langle k \rangle} \theta(t)^{k-1} = \frac{g'(\theta(t))}{g'(1)} \quad (3.52)$$

Now, from Eq. (3.50-3.51) we deduce that the flux from ϕ_I to ϕ_R and the one from ϕ_I to $(1 - \theta)$ are proportional with a proportional constant equal to $\frac{\alpha}{\beta}$. By construction we have that

$$(1 - \theta(0), \phi_R(0)) = (0, 0) \quad (3.53)$$

which then implies

$$\phi_R(t) = \frac{\alpha}{\beta} (1 - \theta(t)) \quad (3.54)$$

from which the thesis follows:

$$\begin{aligned} \theta'(t) &= -\beta\phi_I(t) \\ &= -\beta[\theta(t) - \phi_S(t) - \phi_R(t)] \\ &= -\beta\theta(t) + \beta\frac{g'(\theta(t))}{g'(1)} + \alpha(1 - \theta(t)) \end{aligned} \quad (3.55)$$

□

Remark 3.2.2. The previous proposition enables us to give a formal definition of the *SIR* model on a static configuration network, in the sense that it is fully described by the following differential system:

$$\begin{cases} \theta'(t) = -\beta\theta(t) + \beta\frac{g'(\theta(t))}{g'(1)} + \alpha(1 - \theta(t)) \\ s(t) = g(\theta(t)) \\ r'(t) = \alpha i(t) \\ s(t) + i(t) + r(t) = 1 \end{cases} \quad (3.56)$$

The following theorem establish a relationship between the *SIR* model on a static configuration network (Syst. 3.56) and the simpler *SIR* model without vital dynamics given by Syst. (1.1).

Theorem 3.2.3. *Let be $G = (V, E)$ a network which has the following property:*

$$|k_i - \langle k \rangle| \rightarrow 0 \text{ as } \langle k \rangle \rightarrow \infty, \forall i \in V \quad (3.57)$$

*i.e. G is a graph in which all the degrees are close to the average degree $\langle k \rangle$ when $\langle k \rangle$ gets higher, i.e. when $N := |V|$ grows. Then the *SIR* model in the network G can be approximatively reduced to a deterministic *SIR* model, in the sense that the following equation for the fraction of susceptible individuals holds :*

$$s'(t) = \beta \langle k \rangle s(t)i(t) \quad (3.58)$$

Proof. From the above computations it follows

$$s'(t) = -\beta g'(\theta(t))\phi_I(t) \quad (3.59)$$

We now prove the theorem making the extra assumption that every individual of the population has the same number of contact equal to $C \leq N - 1$. Thank to this hypothesis, it follows that

$$s(t) = \sum_{k=0}^{\infty} p_k \theta(t)^k = g(\theta(t)) = \theta(t)^C \Leftrightarrow \quad (3.60)$$

$$\Leftrightarrow \frac{d}{dt} g(\theta(t)) = \frac{Cs(t)}{\theta(t)} s'(t) \quad (3.61)$$

which jointly with Eq. (3.59) implies

$$s'(t) = -\beta \frac{Cs(t)}{\theta(t)} \phi_I(t) \quad (3.62)$$

We now let $C \rightarrow \infty$, which clearly implies that $N \rightarrow \infty$, in such a way that

$$\tilde{\beta} = \beta C \quad (3.63)$$

remains constant and therefore bounded as C grows, which basically happens iff

$$\beta = \mathcal{O}(C), \quad C \rightarrow \infty \quad (3.64)$$

Now, if we start from a node i , the probability that an edge that links i with one of its random susceptible neighbors j doesn't correspond to an infection is equal to θ . We have already seen that at each time t the quantity $\theta(t)$ is decomposable

in three factors, ϕ_S, ϕ_I, ϕ_R . When $C, N \rightarrow \infty$ those factors approach respectively their correspondent fractions of individuals:

$$(\phi_S(t), \phi_I(t), \phi_R(t)) \rightarrow (s(t), i(t), r(t)) \quad (3.65)$$

Thus, it follows that $\theta(t)$ converges to 1 when C tends to ∞ . An easy consequence of those facts is that the ratio $\frac{\phi_I(t)}{\theta(t)}$ is approximatively equal to $i(t)$ when the contacts get higher. We can resume all what we have just said by saying that

$$s'(t) \simeq -\tilde{\beta}s(t)i(t) \quad (3.66)$$

when the number of contacts per-node (thus, the number of nodes) get very high. The same conclusion holds in the general case, by adapting the proof and substituting C with the more general expression $\langle k \rangle$. \square

3.3 Markov chain epidemic model on a network

Another possible approach to epidemic models on networks is to make use of Markov chains. We end this section by describing one example of this approach, which consists in deriving a continuous-time *SIS* model on network and then making a mean-field approximation in order to solve it. We will limit the discussion to the derivation of some results on such a model, whereas for more detailed analysis we refer to [26].

Let us consider that the virus spread in a undirected static graph $G = (V, E)$ which is fully described by a symmetric adjacency matrix $A = (a_{ij})_{i,j \in V}$ where:

$$a_{ij} = a_{ji} = \begin{cases} 1, & \text{if } (i, j) \in E \\ 0, & \text{otherwise} \end{cases} \quad (3.67)$$

We associate to each node $i \in V$ a state function $X_i(t) \in \{0, 1\}$, where $X_i(t) = 1$ means that at time t node i is infectious and $X_i(t) = 0$ means that at time t node i is healthy. If an infectious node i is linked to a susceptible one j , we assume that the arrival of the infection through the edge (i, j) is a Poisson process with rate β which is independent from the specific edge (i, j) . At the same time, the infectious node i recovers according to another Poisson process, independent to the previous one, with rate δ . Since we are considering a *SIS* model, it holds:

$$\mathbb{P}(X_i(t) = 1) + \mathbb{P}(X_i(t) = 0) = 1, \quad \forall i \in V, \forall t \in \mathbb{R}_+ \quad (3.68)$$

By separately observe each individuals of the population i and applying the usual Markov chains' tools, we deduce that the infinitesimal generator $Q_i(t)$ of the two-state continuous time Markov chain $\{X_i(t)\}_{t \in \mathbb{R}_+}$ is equal to:

$$Q_i(t) = \begin{bmatrix} -q_1^i & q_1^i \\ q_2^i & -q_2^i \end{bmatrix} \quad (3.69)$$

It is easy to deduce that the element q_2^i is exactly equal to the recovery rate δ . For the element q_1^i we proceed as it follows. At any time, the node i is linked to a some other nodes. The probability that one of those nodes infects i at time t is proportional both to the transmissibility of the virus β and to the number of neighbours of i that are actually infected at time t . Summing up we end with the following expression:

$$q_1^i = \beta \sum_{j=1}^N a_{ij} \mathbb{1}_{\{X_j(t)=1\}} \quad (3.70)$$

Directly from the meaning of the infinitesimal generator, it follows that:

$$\mathbb{P}(X(t + \Delta t) = 1 | X(t) = 0) = q_1^i \Delta t + o(\Delta t) \quad (3.71)$$

The crucial consequence of Eq. (3.70) is that q_1^i are random variables, and not number as in ordinary Markov chain theory. If we want to applicate continuous-time Markov chain theory, we can replace the actual random infection rate q_1^i by an average infection rate, which is a real number. This is basically a mean field approximation. In formula, this means that we replace q_1^i with its average $\mathbb{E}(q_1^i)$. We can also have an explicit expression for the average:

$$\begin{aligned} \mathbb{E}(q_1^i) &= \beta \sum_{j=1}^N a_{ij} \mathbb{E}(1_{\{X_j(t)=1\}}) \\ &= \beta \sum_{j=1}^N a_{ij} \mathbb{P}(X_j(t) = 1) \end{aligned} \quad (3.72)$$

This leads to this expression for the effective infinitesimal generator:

$$Q_i(t) = \begin{bmatrix} -\mathbb{E}(q_1^i) & \mathbb{E}(q_1^i) \\ \delta & -\delta \end{bmatrix} \quad (3.73)$$

Let us now denote $v_i(t) := \mathbb{P}(X_i(t) = 1)$, i.e. $v_i(t)$ is the probability that the node i is infectious at time t . It clearly holds that the probability that i is still susceptible at time t is given by $\mathbb{P}(X_i(t) = 0) = 1 - v_i(t)$.

Lemma 3.3.1. *Let us denote with $S = S(t)$ and $Q = Q(t)$ respectively the transition matrix and the infinitesimal generator related to a continuous-time markov chain process $\{X(t)\}_{t \in \mathbb{R}_+}$. If we define the probabilities:*

$$p_k(t) = \mathbb{P}(X(t) = k) \quad (3.74)$$

the following differential equation for p_k holds:

$$p'_k(t) = -q_k p_k(t) + \sum_{j=1, j \neq k}^N q_{jk} p_j(t) \quad (3.75)$$

Proof. If $p(t)$ is the probability vector for the state of the process at time t , we know that it holds:

$$p(t+h) = p(t)S(h) \quad (3.76)$$

from which we can deduce that

$$\begin{aligned} p_k(t+h) &= \sum_{j=1}^N p_j(t)S_{jk}(h) \Leftrightarrow \\ \Leftrightarrow \frac{p_k(t+h) - p_k(t)}{h} &= \frac{\sum_{j=1}^N p_j(t)S_{jk}(h)}{h} - \frac{p_k(t)}{h} \\ &= \frac{\sum_{j=1, j \neq k}^N p_j(t)S_{jk}(h)}{h} + p_k(t) \frac{S_{kk}(t) - 1}{h} \end{aligned} \quad (3.77) \quad (3.78)$$

which in the limit for $h \rightarrow 0$ becomes the differential equation we are looking for. \square

Applying this result to our process, we obtain a differential equation for $v_i(t)$ which is non linear:

$$v'_i(t) = \beta \sum_{j=1}^N a_{ij}v_j(t) - v_i(t) \left(\beta \sum_{j=1}^N a_{ij}v_j(t) + \delta \right) \quad (3.79)$$

Now, we can proceed in this way for each node of the grap, so that we obtain a system of differential equations analogous to Syst. (3.79):

$$\begin{cases} v'_1(t) = \beta \sum_{j=1}^N a_{1j}v_j(t) - v_1(t) \left(\beta \sum_{j=1}^N a_{1j}v_j(t) + \delta \right) \\ v'_2(t) = \beta \sum_{j=1}^N a_{2j}v_j(t) - v_2(t) \left(\beta \sum_{j=1}^N a_{2j}v_j(t) + \delta \right) \\ \vdots \\ v'_i(t) = \beta \sum_{j=1}^N a_{ij}v_j(t) - v_i(t) \left(\beta \sum_{j=1}^N a_{ij}v_j(t) + \delta \right) \\ \vdots \\ v'_N(t) = \beta \sum_{j=1}^N a_{Nj}v_j(t) - p_N(t) \left(\beta \sum_{j=1}^N a_{Nj}v_j(t) + \delta \right) \end{cases} \quad (3.80)$$

It is now convenient to introduce the following shorter notation:

$$V(t) = (v_1(t), v_2(t), \dots, v_N(t))^T \quad (3.81)$$

The Syst. (3.80) can be rewritten in matrix form as:

$$V'(t) = \beta AV(t) - \text{diag}(v_i(t)) (\beta AV(t) + \delta u) \quad (3.82)$$

where u is the column vector which N entries are all equal to 1. We can obviously rewrite $V(t)$ as $V(t) = \text{diag}(v_i(t))u$ in order to obtain:

$$\begin{aligned} V'(t) &= \beta AV(t) - \text{diag}(v_i(t)) (\beta AV(t) + \delta u) \\ &= (\beta A - \delta \mathbb{1})V(t) - \beta \text{diag}(v_i(t))AV(t) \\ &= (\beta \text{diag}(1 - v_i(t))A - \delta \mathbb{1})V(t) \end{aligned} \quad (3.83)$$

It is important to underline that this model can be easily modified in order to take into account significant generalizations. As an example, one can think about non constant infection and curing rates described by the vectors $\beta = (\beta_1, \beta_2, \dots, \beta_N)$ and $\Delta = (\delta_1, \delta_2, \dots, \delta_N)$. To consider this generalization it is enough to rewrite Eq. (3.82) as

$$V'(t) = A \text{diag}(\beta_i)V(t) - \text{diag}(v_i(t)) (A \text{diag}(\beta_i(t))V(t) + \Delta) \quad (3.84)$$

Assuming that the steady-state exists, one can calculate the steady-state probabilities of infection for each node. Since the steady-state $v_{j\infty}$ implies:

$$v'_j(t)|_{t \rightarrow \infty} = 0 \quad (3.85)$$

we have that for all nodes $j \in V$ it holds:

$$\beta \sum_{j=1}^{\infty} a_{ij}v_{j\infty} - v_{i\infty} \left(\beta \sum_{j=1}^N a_{ij}v_{j\infty} + \delta \right) = 0 \quad (3.86)$$

from which it can be proved that it holds

$$v_{i\infty} = 1 - \frac{1}{1 + \tau \sum_{j=1}^N a_{ij}v_{j\infty}} \quad (3.87)$$

where $\tau = \frac{\beta}{\delta}$ is the effective transmissibility of the virus. The right hand-side in Eq. (3.87) is equal to the steady-state probability in the two-state Markov chain. We can observe that Eq. (3.87) has a trivial solution $v_{i\infty} = 0$ for all $i \in V$, which means that eventually all nodes will be healthy. On other hand if the recovery rate δ is equal to 0, then all $v_{i\infty}$ are equal to 1, i.e. almost surely all nodes will eventually be infected. A part from trivial solutions, the non-linearity gives a second solution which can be interpreted as the fraction of time that a node is infected while there is a long-living epidemic, i.e. while the system is in a metastable state. The main results in [26] is that this second solution has an explicit expression as a continuous fraction:

Theorem 3.3.2. *For any effective spreading rate $\tau \geq 0$, the nonzero steady-state infection probability of any node i can be expressed as:*

$$v_{i\infty} = 1 - \frac{1}{1 + \tau d_i - \tau \sum_{j=1}^N \frac{a_{ij}}{1 + \tau d_j - \tau \sum_{k=1}^N \frac{a_{jk}}{1 + \tau d_k - \tau \sum_{q=1}^N \frac{a_{kq}}{\ddots}}}} \quad (3.88)$$

where $d_i = \sum_{j=1}^N a_{ij}$ is the degree of node i . Particularly, the exact steady-state infection probability of any node i is bounded by

$$0 \leq v_{i\infty} \leq 1 - \frac{1}{1 + \tau d_i} \quad (3.89)$$

Let $y(t)$ be the (average) fraction of infected nodes in the network at time t :

$$y(t) = \frac{1}{N} \left[\sum_{j=1}^N \mathbb{1}_{\{X_j(t)=1\}} \right] = \frac{1}{N} \sum_{j=1}^N v_j(t) \quad (3.90)$$

and let us define

$$y_\infty = \frac{1}{n} \sum_{i=1}^N v_{i\infty} \quad (3.91)$$

i.e. y_∞ is the fraction of infected node in the steady-state. Summing Eq. (3.79) over all i is equivalent to right multiplication of $V(t)$ by the all one vector u^T , because

$$\sum_{i=1}^N v_i(t) = u^T V(t) \quad (3.92)$$

then we find:

$$\begin{aligned} \frac{du^T V(t)}{dt} &= u^T (\text{diag}(1 - v_i(t))\beta A - \delta I) V(t) \\ &= \beta(u^T - V(t))AV(t) - \delta u^T V(t) \end{aligned} \quad (3.93)$$

which allows to deduce a relation for $y_\infty \in [0, 1)$ in terms of V_∞ :

$$Ny_\infty = u^T V_\infty = \tau(u - V_\infty)^T A V_\infty \quad (3.94)$$

Now, if D is the vertex containing the degrees of the nodes, the following hold:

$$u^T A = D^T \quad (3.95)$$

$$D = \Gamma u := \text{diag}(d_1, \dots, d_N)u \quad (3.96)$$

From those relations, and introducing the *Laplacian* $Q := \Gamma - A$ one can express y_∞ as a quadratic form in terms of Laplacian:

$$y_\infty = \frac{\tau}{N} ((u - V_\infty^T \Gamma V_\infty + V_\infty^T Q V_\infty)) \quad (3.97)$$

where it can be proved that V_∞ follows the governing equation:

$$V_\infty = \tau \text{diag}(1 - v_{i\infty}) A V_\infty \quad (3.98)$$

In epidemic models often the existence of an epidemic threshold τ_c is mentioned. If the effective spreading $\tau = \frac{\beta}{\delta} > \tau_c$, the virus persists and a non-zero fraction of nodes are infected, whereas if $\tau < \tau_c$ the epidemic dies out. The fundamental result in this model is that there exists a threshold value τ_c such that for $\tau < \tau_c$ there is only the trivial steady-state solution $V_\infty = 0$ whereas there is a non-zero second solution for each $\tau > \tau_c$. The most interesting thing is that this threshold quantity τ_c depends on the *spectral radius* of the graph λ_1 , which is the largest absolute value of the eigenvalues of its adjacency matrix. This fact has a practical consequence that we now discuss.

Let us suppose that a network G with adjacency matrix A is given. Moreover, let β and δ be respectively the infection rate and the nodal curing rate. Thus, if δ is kept above $\beta\lambda_1$, we can maintain the network virus-free. This fact is quite important when it is reflected in real-world network which are actually modifiable by several prevention measures, because it gives a measure of how those measures must decrease the spectral radius in order to prevent an outbreak.

Chapter 4

SIR model on a dynamic network

All the models that we have presented in previous chapters are static, in the sense that they don't take into account human dynamics. This simplification is very useful especially for two reasons:

- From a computational point of view, epidemic models which consider time-evolving humans' interactions bring heavy computations even for small population.
- Modelling humans' interactions is very challenging, and until few years ago it was almost impossible due to the lack of available data.

However recent events are changing the situation: on the one hand recent technologies are making the processing power everyday stronger, on the other hand specific apps and the smartphone's geolocation are paving the way for contact tracing. For this reason, the field of epidemic models on dynamic network is now under the interest of many scientists, even though we are still far from having standard approaches and formal mathematical theories. In this chapter we present one simple and original dynamic model for the description of an epidemic and then we show the results of some simulations on those models, trying to investigate relationships and behaviours of key epidemiological quantities, even looking to their variations to varying of parameters and choices on the construction of the model. A particular attention is given to the *generation time* which is one of the conceptual corner-stones of mathematical epidemiology: by its classical definition, it is the time interval between the infection of a secondary case and the infection of its infector. Along with the already mentioned basic reproduction number, the generation time allows for the characterization of the dynamics of an epidemic.

4.1 Theoretical formulation

We have already presented the *SIR* model without demography: while referring the reader to Sec. 1.1 for its formal mathematical description, we now want to do a short summary of the main aspects of this model.

We consider a closed population of N individuals divided in three time-dependent subgroups: susceptibles, infectious and recovered. The key property of this model is that only two possible transitions can occur:

1. $S \rightarrow I$: After an “infectious contact” with an infectious individual, a susceptible one contracts the disease and becomes infectious himself.
2. $I \rightarrow R$: An individual who has been infected for a while recovers and gets immunity against the disease.

We want to recall that the population size N is constant due to the fact that we are not considering birth or death in our population.

The main simplification of this model is that it is assumed that every person is moving and has equal chance of contact with each and every person among the population (*homogeneous mixing*).

To make more realistic our study we also saw that compartmental model can be considered in network, however again a strong limitation arises: in those models it is often assumed that the contact that we have with our neighbours doesn't change in time.

To give a further generalization of *SIR* model, we embed it in a dynamical random network in which the nodes represent the individuals of the population and each edge (i, j) stands for a (potential) contact between the nodes i and j . Let us now be more precise.

We assume that at time $t = 0$ only one node i_0 of our starting graph becomes infected from external individuals. Then, we assume that each edge of the graph starts activating/deactivating according to a Poisson process HPP: when the contact between an infected individual i and a susceptible one j is activated, the virus can spread through this link with a probability that is proportional both to the duration of the contact and to the transmissibility of the virus, whereas i can't infect j when the edge which link them is deactivated. Moreover, we consider that each infectious recovers with a constant recovery rate: when recovered, an individual gains immunity from the virus so he stops influencing the spreading.

While the following pictures (Fig. 4.1-4.2-4.3-4.4) give a visual representation of model's functioning, the rest of the section is devoted to the mathematical description of its main ingredients: the network and the spreading's process.

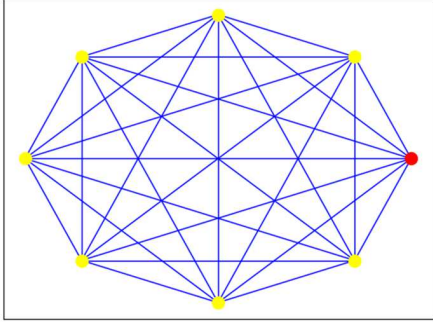


Figure 4.1: Beginning of the model. All the edges are deactivated (**blue**), the only infectious is in **red** whereas the others (suceptibles) are in **yellow**.

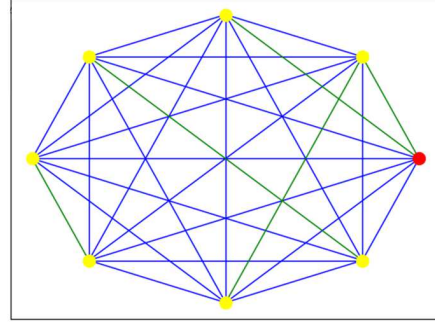


Figure 4.2: The contacts' dynamics. Some edges (the **green** ones) activate: from on now the virus can spread through them.

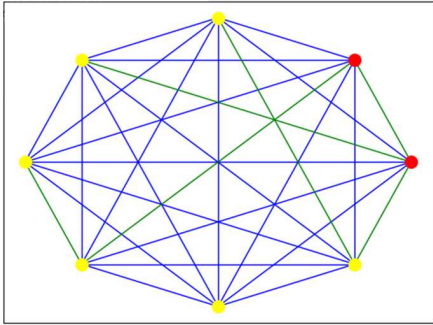


Figure 4.3: The spreading starts. Edges keep activating/deactivating and the virus spreads, so that a new infectious (**red** node) appears.

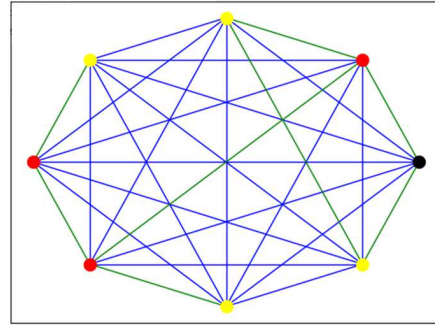


Figure 4.4: Spreading and recovers. The number of infectious grows, but some of them recover becoming **black**: now they stop influencing the spreading.

We want to be allowed to describe in a more realistic way the human's interaction, taking into account several significative facts:

1. Every individual i of the population has a different network of acquaintances, which is the set of people with which i *could* enter into contact.
2. The real contact between i and any node belonging to the network of acquaintances of i starts and stops randomly in time with a rate λ_{ij} .

To develop a structure with these properties, we start from a simple random network $G = (V, E)$, where $V = \{1, \dots, N\}$ is the set of nodes of G (individuals of the population) and $E \subseteq \{(i, j) \mid i, j \in V, i \neq j\}$ is the set of edges of G (mutual knowledge between two nodes, i.e. *possibility* to have an effective contact between those two individuals of the population). In order to integrate our model with a dynamical random process whose purpose is to emulate human's contacts, we use a Poisson process which can activate/deactivate in time any edge (real contact) between two nodes (individuals) of the existing graph (population) G . To be more precise, we proceed in this way: for all $(i, j) \in E$ we introduce the edge's value:

$$\sigma^{i,j}(t) \in \{-1, 1\} \quad (4.1)$$

where -1 stands for “deactivate” and 1 stands for “activate”. At the same time, we call μ the deactivation rate between any couple of in-contact nodes whereas for each contact $(i, j) \in E$ we indicate with λ_{ij} its activation rate.

We are now able to define a random process $H^{i,j} = \{H_n^{i,j}\}_{n \in \mathbb{N}}$ suitable to describe the time-dynamics of each edge of the graph G . The definition is the following:

$$H_n^{i,j} := S_n(\alpha_{ij}(t)) \quad \forall n \in \mathbb{N} \quad (4.2)$$

where: $\{S_n(\star)\}_{n \in \mathbb{N}}$ indicates the homogeneous Poisson process (HPP) of intensity \star and α_{ij} is defined as:

$$\alpha_{ij}(t) = \frac{1 - \sigma^{i,j}(t)}{2} \lambda_{ij} + \frac{1 + \sigma^{i,j}(t)}{2} \mu \quad (4.3)$$

It should be noted that the above equation simply means that the parameter α_{ij} , which determines the dynamic of the edge (i, j) , is equal to λ_{ij} when the edge (i, j) is not activated, and it is equal to μ when (i, j) is activated.

Assuming that the family $\{H^{i,j}\}_{(i,j) \in E}$ is made of independent HPP, we can make use of Th. A.1.17 to build up a new HPP $H = \{H_n\}_{n \in \mathbb{N}}$ which describes the whole interactions' system:

$$H_n = H_n(t) = \sum_{(i,j) \in E} H_n^{i,j} = \sum_{(i,j) \in E} S_n(a_{ij}(t)) \quad (4.4)$$

Every time that the process H rings, one has to know which one of the competing processes $H^{i,j}$ has caused the ring. The answer to this question is provided by Th. A.1.18: denoting with J the index of the HPP responsible for the first event, the following holds:

$$\mathbb{P}(J = ij) = \mathbb{P}(J = ij)(t) = \frac{\alpha_{ij}(t)}{\sum_{(i,j) \in E} \alpha_{ij}(t)} \quad (4.5)$$

We finally need to embed the SIR model in our setting-up.

To this end, we assign to each node i a time-dependent function representing the state of the node i at the time t :

$$\omega^i(t) \in \{-1, 0, +1\} \quad (4.6)$$

where -1, 0 and 1 stands respectively for “Susceptible”, “Recovered” and “Infectious”. Just before starting the simulation, we select randomly one node $\bar{i} \in V = \{1, \dots, N\}$ and we initialize

$$\begin{cases} \omega^{\bar{i}}(0) = 1 \\ \omega^i(0) = -1 \quad \forall i \neq \bar{i} \end{cases} \quad (4.7)$$

which means that the spread of a virus starts due to a single infectious individual in a fully susceptible population.

When the simulation starts running, those nodes' values change according to the contacts' dynamics we introduced in the last paragraph: we will now explain it in more details.

Firstly, we let run the process H defined above, and we indicate with t_0 the time of the first ring, which from now on will be considered the *origin*. Thank to Th. A.1.18 we establish randomly which one of the edge $(i, j) \in E$ has been activated with this ring (the ring could not corresponds to a deactivation because, before t_0 , no edge is activated). Now that we know which contact (i, j) is taking place, we update the edges' values $\sigma^{i,j}$ and, as a consequence, the parameters α_{ij} of H ; then, we wait for the second ring which will happen at time $t_1 = t_0 + \Delta_0$: before checking again which event has been responsible of the ring, we decide randomly (with probabilities which are valid less than ϵ) if some of the following has happened:

1. $S \rightarrow I$: During the time Δ_0 a susceptible individual i has been infected, i.e. $\omega^i(t_0) = -1 \xrightarrow{\Delta_0} \omega^i(t_1) = 1$. The probability of this event is equal to:

$$\mathbb{P}(I_i^{\Delta_0}) = \alpha \cdot \phi(i, \Delta_0) \cdot \Delta_0 \quad (4.8)$$

where $\alpha \in \mathbb{R}_+$ is the disease's infection rate and $\phi(i, \Delta_0)$ indicates the number of neighbors of the node i at the beginning of the time-period Δ_0 .

2. $I \rightarrow R$: During the time Δ_0 an infectious individual j has recovered, i.e. $\omega^j(t_0) = 1 \xrightarrow{\Delta_0} \omega^j(t_1) = 0$. The probability of this event is equal to:

$$\mathbb{P}(R_j^{\Delta_0}) = \beta \Delta_0 \quad (4.9)$$

where $\beta \in \mathbb{R}_+$ is the disease's recovery rate.

After we eventually modify some nodes's values, we then establish which edge $(i, j) \in E$ has been activated/deactivated during Δ_0 (and we update the parameters α_{ij} just in the same way as before). We conclude the procedure iterating this procedure step by step until we reach the results we expected.

It is important to stress again that in this model we are assuming that there are no births and there is no possibility that a recovered individual is infected another time so that each simulations will end with the disease's disappearance (no possibility of an endemic disease).

Until now we described a procedure which is valid for any choice of the underlying graph G ; however, in order to do our simulation, we focus on two possible topologies. Firstly, we take $G = G(N, p)$ as a random Erdős-Renyi graph (see App. A.2.2) where we choose $p \gg \frac{\log N}{N}$ so that the graph $G = G(N, p)$ is almost surely connected, i.e. that there is a path between every pair of nodes (thinking about human relationships in a closed population, it seems quite reasonable).

Secondly, we take G as a scale-free network, i.e. a network characterized by the presence of hubs, which are nodes with a number of links that greatly exceeds the average. From an epidemiological point of view, those hubs represent the presence of super-spreaders of the virus, which only a scale-free network can allow to consider. Precisely, we considered $G = G(N, m)$ as a Barabási-Albert graph where we start with m isolated nodes and then, the network develops following the steps illustrated in App A.2.3. The following pictures (Fig. 4.5-4.6) show an example on how much those graph can differ one from the other, even when they both have the same number of nodes (10^4) and approximatively the same average degree $\langle k \rangle \simeq 14$.

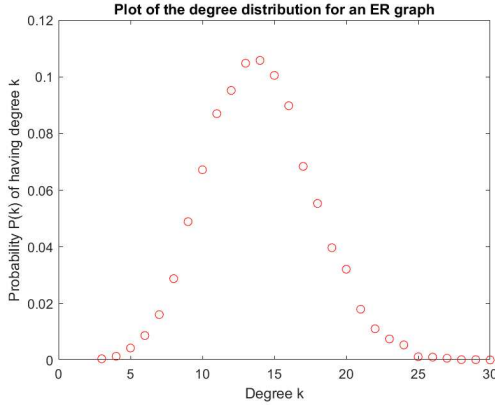


Figure 4.5: The degree distribution of an Erdős-Renyi graph presents a bell-shape (truncated in zero) with typical values very close the average.

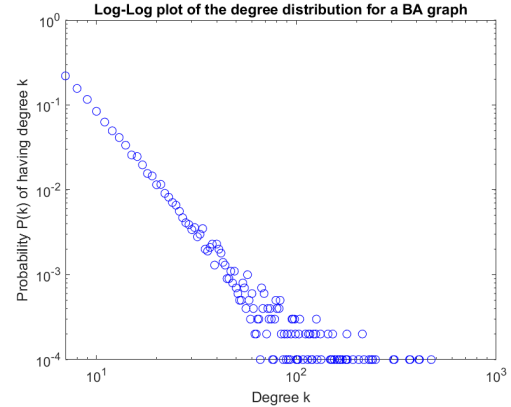


Figure 4.6: The degree distribution of a Barabási-Albert graph (in log-log) is a line, with many values below and few that greatly exceed the average.

4.2 Implementation

We implement our model with Python using “NetworkX”, which is a package for the creation, manipulation and study of the structure, dynamics and functions of complex networks. As the reader can see in the App. B, the code is quite long and it is splitted in several functions that we piece together at the end of the code in the so-called “main”. In this section we report a pseudo-code of our algorithm, which purpose is to illustrate in a plain and simple way the functioning of it. For the sake of brevity we omitt the parts of the code that describe precisely how we calculate GT and R_0 or other quantities that we will investigate in the next section such as the final size of the epidemic and the probability of a real outbreak: for these parts of the code we refer to App. B, whereas we present here only the mathematical idea behind them.

Taking into account all the events (infections and recovers) we create a matrix $A = (a_{ij})_{i,j \in E}$ where:

$$a_{ii} = \text{Time in which } i \text{ gets infected} \quad (4.10)$$

$$a_{ij} = \text{Time in which } i \text{ infects } j \quad (4.11)$$

and $a_{ij} = \text{“None”}$ if i hasn’t infected j Now, if i_0 is the first infectors, i.e. $a_{i_0, i_0} = 0$, one can compute the number of individuals infected by i_0 simply counting how many numbers appear in the i_0 -th raw of the matrix, and R_0 is the mean value of this number, obtained by simulating the model many times. In order to get GT , we can compute, for each node i , the times between when it is infected a_{ii} and when it infects any other individuals:

$$a_{ij} - a_{ii}, \quad \forall j : a_{ij} \neq \text{None} \quad (4.12)$$

Putting together all those values over all nodes i and taking the mean value one get (one relization of) GT . With similar arguments one can compute also the final size and the probability of an outbreak. The computing of the time-evolution of generation time and basic reproduction number can be obtained by a discretization of the results in entire days, so that GT_j and R_j with $j \in \mathbb{N}$ are respectively the reproduction number and the generation time at day j , i.e. computed only from individuals who get infected at day j .

We underline that in the pseudocode we will use a notation that is consistent with the one we introduced in the previous section.

Algorithm 1 Simulate the spreading of an infection in our model.

Require: $G, \lambda_{ij}, \mu, \alpha, \beta,$

Ensure: $\omega^i, \sigma^{i,j}, t, GT, R_0$

Choose randomly $\bar{i} \in V$

$\omega^{\bar{i}} \leftarrow 1$

$\omega^i \leftarrow -1 \quad \forall i \neq \bar{i}$

$\sigma^{i,j} \leftarrow -1 \quad \forall (i, j) \in E$

$\alpha_{ij} \leftarrow \frac{1-EV^{i,j}(t)}{2} \lambda_{ij} + \frac{1+EV^{i,j}(t)}{2} \mu \quad \forall (i, j) \in E$

$\Lambda \leftarrow \sum_{(i,j) \in E} \alpha_{ij}$

Let us wait the first time in which an HPP H with intensity Λ rings, and choose r randomly in $(0, 1)$.

Initialize an auxiliary index: $j \leftarrow 0$

while $r > 0$ **do**

$r \leftarrow r - \mathbb{P}\{\text{The } j\text{-th element of } E \text{ has caused the ring}\}$

$j \leftarrow j + 1$

end while

The j -th element of E , let us call it (\bar{i}, \bar{j}) , has caused the ring, so $\sigma^{\bar{i}, \bar{j}} \leftarrow 1$

Update Λ taking into account the change of $\sigma^{\bar{i}, \bar{j}}$

$t \leftarrow 0$

Initialize the counter of events: $i \leftarrow 0$

Compute i the current number of infectious

while Number of infectious individuals > 0 **do**

$\Delta_t \leftarrow H(\Lambda)$

for Node n in V **do**

if n is infected, i.e. $\omega^n = +1$ **then**

 With probability $\beta \Delta_t$ make it recovered: $\omega^n \leftarrow 0$

else if n is susceptible, i.e. $NV^n = -1$ **then**

 Count $\phi(n)$ the number of neighbors of n that are actually infected

 Make n infected with probability $\alpha \cdot \phi(n) \cdot \Delta_t$

else

 Do nothing

end if

end for

With the same procedure between ***, establish which element of E has caused the ring. Let us suppose that this element is (\tilde{i}, \tilde{j})

if the edge (\tilde{i}, \tilde{j}) is activated, i.e. $\sigma^{\tilde{i}, \tilde{j}} = 1$ **then**

 Deactivate the edge: $\sigma^{\tilde{i}, \tilde{j}} \leftarrow -1$

else

 Activate the edge: $\sigma^{\tilde{i}, \tilde{j}} \leftarrow +1$

end if

Update Λ

$t \leftarrow t + \Delta_t$

$i \leftarrow i + 1$

end while

Compute GT and compute R_0 as the number of nodes have been infected from the first infectors

return $\omega^i, \sigma^{i,j}, t, GT, R_0$

4.3 Simulations

Since we are interested in the mean behaviour of the model, we let run the algorithm several times: for each choice we want to look for key quantities of the model, as the reproduction number R_0 , the generation time GT but also the expected duration of the epidemic $\mathbb{E}(T)$, the correspondent final size of epidemic $FS := \frac{N-S(T)}{N}$ and the probability of a real outbreak $\mathbb{P}(O)$. First of all, we establish that the unit time correspond to 1 day. Finally, we choose the main parameters as it follows:

- $\mu = 24$: this means that the average number of deactivation of an activated edge per day is equal to 24 whereas the corresponding average interevent time is equal to $\frac{1}{24}d = 1h$. In words, what we are saying is that the average duration of a contact is of 1h.
- $\alpha = 1$: if an individual has only one infected neighbour and the contact between them lasts for a time Δt , the transmission of the virus occurs with probability $\alpha\Delta t$ which is equal to Δt under this hypothesis. This means that a one-day-long contact is enough for the virus to being transmitted.
- $\beta = 0.06 \sim \frac{1}{15}$: with the same reasoning as the one we used for α , this choice implies that 15 days are enough for the removal of the virus.

The choice of the contacts' rates λ_{ij} have to be treated separately, as it is the most difficult choice. Indeed, contrary to the above parameters, it still lacks an easy method to describe effectively humans' interactions. Moreover, such a method should depend not only on the structure of the population, but also on the infections itself: for instance, the contacts' rates in a network used for describing an airborne transmission need to be very different from those of a network describing sexual transmission.

In our case we are thinking about a non-lethal airborne disease, so relevant contacts are both casual and frequent contacts. For this reason, we will consider contacts' rates in $[0, 10]$ which means that a contact between two linked nodes could occur a number of times per day between 0 (no contact) or 10 (a number of contact which is so high to be unrealistic, but useful in order to analyze the behaviour of some quantities).

4.3.1 Erdős-Renyi graph

We start our discussion by considering an Erdős-Renyi graph $G = G(100, 0.14)$ where the parameter p has been chosen in order to give a realistic average degree $\langle k \rangle = 14$, whereas the clustering coefficient (see App. A.2.1) C is equal to 0.137. We start from the simplest case to analyze, which is the *homogeneous* one, in which each edge (i, j) has the same contact rate, i.e. $\lambda_{ij} \equiv c$. We want to see the main differences with different choices of $c \in [0, 10]$. The behaviour of R_0 and

GT w.r.t. c are represented in Fig. (4.7-4.8-4.9).

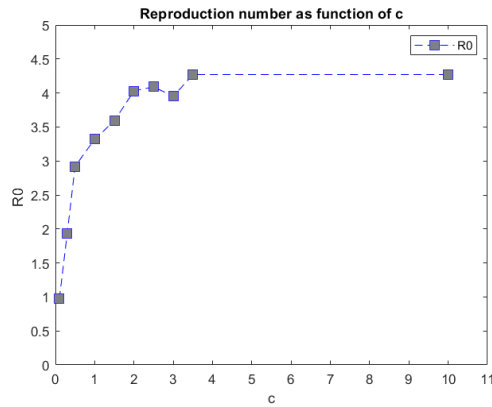


Figure 4.7: Reproduction number as function of the contacts rate on Erdős-Renyi graph: after a first growing, it reaches a steady-state approximatively at $c \simeq 3$.

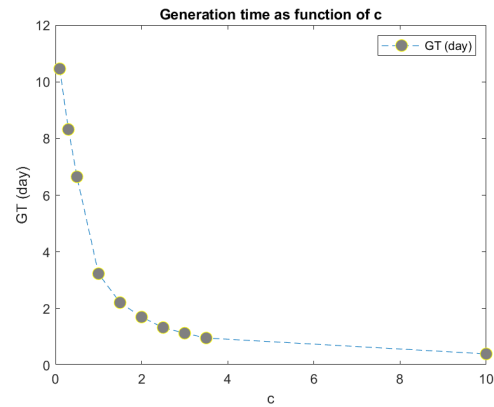


Figure 4.8: Generation time as function of the contacts rate on Erdős-Renyi graph: it decreases exponentially approaching the 0 as the contacts get very frequent.

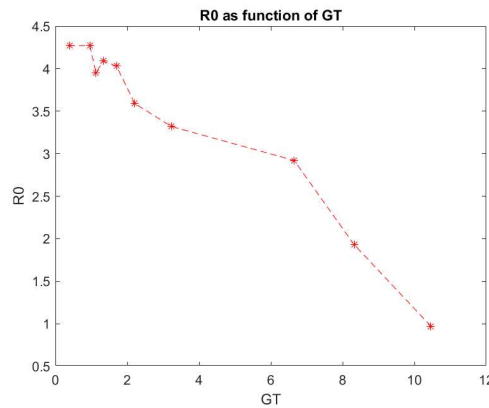


Figure 4.9: Reproduction number as function of the generation time on Erdős-Renyi graph: for low values of R_0 it seems a linear relation, but when R_0 gets high a precise relation is hard to be found.

We can see that, when the constant rate gets higher, it is easiest and fastest to spread the virus since R_0 increases whereas GT decreases. What is most interesting about those quantities is the way in which they change w.r.t. c . As we

can see for R_0 the growth seems to be logarithmic and a steady-state is reached approximatively in $c \simeq 3$: here R_0 stops growing and keep itself constant around the value of $R_0 \simeq 4$. On the contrary, generation time presents an exponential decreasing behaviour, and a steady-state doesn't appear whereas it seems that GT would approach to 0 as c gets higher. This fact may suggest that, especially for spreading in small population, GT could be a better descriptor than R_0 since it isn't affected from the competition-effect which boxes R_0 quite far from $< k >$. An univocal relation between R_0 and GT is hard to be found: when $R_0 \leq 3$ a good fitting between the reproduction number and the generation time could be given by a linear relation between, whereas when R_0 reaches its steady-state a precise relation can't be argued anymore.

In order to have a more precise view of what happens to the (beginning of a) spreading when reaching the steady-state of R_0 , we can see how it evolves differently with $c = 1.5, 3.5$ and $c = 10$.

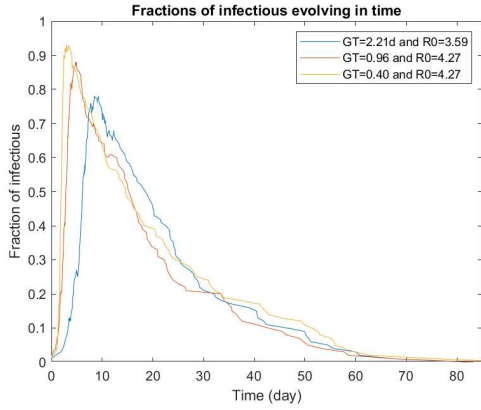


Figure 4.10: Realizations of the spreading (in terms of the fraction of infectious at time t) with different generation times and basic reproduction number on Erdős-Renyi graph.

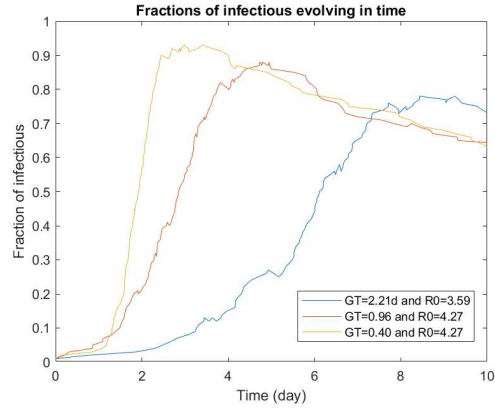


Figure 4.11: Zoom of the spreading on the early stage. Both the exponential rate and the peak's height gets higher as the generation time decreases, even when the basic reproduction number reaches the steady state.

What we see from Fig. 4.11 is that, even when R_0 is kept constant, if GT continues decreasing the exponential rate r of the fraction of infectious grows, i.e. the spreading gets faster. Moreover, higher contacts' rates correspond also to higher peak height, which means an higher number of contemporary infectious. This fact seems to confirm the above hypothesis: in small populations, when the strenght of the spreading grows too much, R_0 loses its effectiveness as descriptor of the epidemic, since it stops catching some fundamental properties of the spreading. On other hand, generation time isn't affected from those limitations, and it seems to

be a preferable descriptor. It is also important to underline that those limitations make very difficult to establish a mathematical relation between GT and R_0 .

Other interesting facts arise when looking at the final size fractions of the epidemic and at the probability of outbreaks $\mathbb{P}(O)$. In Fig. 4.12 we compare those quantities between them and between the theoretical probability for stochastic models given by Eq. (2.56) which we shall denote $\mathbb{Q}(O)$ to avoid confusion.

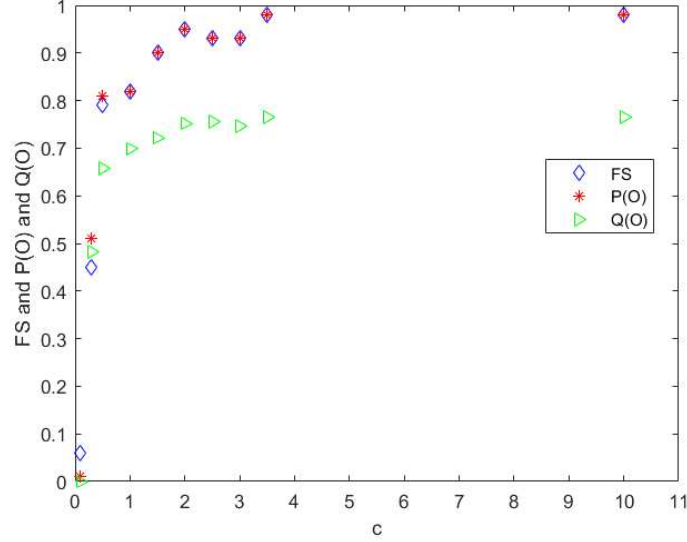


Figure 4.12: Comparison between FS , $\mathbb{P}(O)$ and $\mathbb{Q}(O)$ on Erdős-Renyi graph. The theoretical probability always underestimates the computed one, which overlaps with the final size when the contacts' rate is high enough ($c \geq 1$).

First, we can observe that generally all those quantities are increasing w.r.t. the contacts' rates c , which is epidemiologically reasonable. Secondly, we see that the theoretical probability for stochastic models, doesn't apply for network models since it is much smaller than the computed probability $\mathbb{P}(O)$. In our opinion the reason again besides in the behaviour of R_0 in our model (and more in general, in network models): since it has an upper bound that stochastic models doesn't take into account, the value that we compute for R_0 is so much lower then its theoretical value in stochastic models that a breakdown Eq. (2.56) occurs.

The most interesting thing is that the fraction of individuals who have taken the virus during the epidemic (FS), from $c = 1.5$ perfectly overlaps with the probability of an outbreak $\mathbb{P}(O)$. Since from $c = 1.5$ outbreak occur most of the times, one could argue that the probability of an outbreak coincides with the final size of the epidemic conditioned to the fact of having a real outbreak. This fact suggests that point 3 in Th. 3.1.12 might be true even for more sophisticated networks as the

one we introduced. It is also important to underline that the results of our model is quite consistent with common network model, and not with simpler model, since if $R_0 < 1$ ($c = 0.1$) an outbreak (almost surely) doesn't occur, but when $R_0 > 1$ there is also a positive probability of not having an outbreak. Another important quantity that we want to investigate is the average time that the virus needs to complete its spreading, i.e. the average time before that either all individuals are being infected or there are no more infected in the population. Let $\mathbb{E}(T)$ be this quantity. Then $\mathbb{E}(T)$ behave according to Fig. 4.13

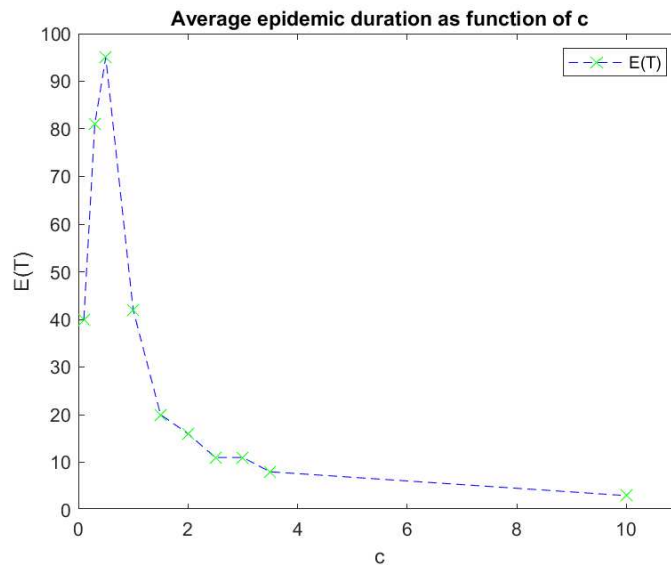


Figure 4.13: $\mathbb{E}(T)$ as function of c on Erdős-Renyi graph. The peak is reached when the contacts' rate is high enough to cause real epidemic, but is sufficiently small that the speed's of the spreading doesn't grow too much.

Here we can see that there is a non-monotonic behaviour with a critical point reached by $c = 0.5$. Particularly we see that for very low values of c ($c \simeq 0.1$) the spreading have a short life since most of the times a real outbreak doesn't occur; then, when c increases the final size gets higher, many outbreak occur and the epidemic begins to have a quite long course. When c exceeds 0.5, even if the final size keep growing, the generation time becomes so small that the epidemic gets faster and faster. Even when R_0 reaches its steady-state, the increasing of contacts' rates with the corresponding decreasing of GT , brings $\mathbb{E}(T)$ to every lower levels.

The last property that we want to investigate is the time-evolution of the basic reproduction number and the generation time. In Chapter 1 we have already mentioned the concept of R_t which is the average number of susceptibles that would

be infected by an individual who gets the infection at time t . We have also already observed that in simplest deterministic model $R_t \leq R_0$. On other hand we denote GT_t as the generation time which computations is restricted to individuals which gets infection at time t . In order to do this analysis we are considering $c = 0.5$.

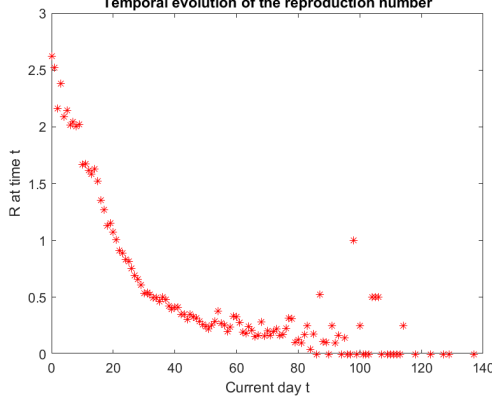


Figure 4.14: R_t to varying of t on Erdős-Renyi graph. The behaviour is basically decreasing: from $t \simeq 70$ strong fluctuations occur.

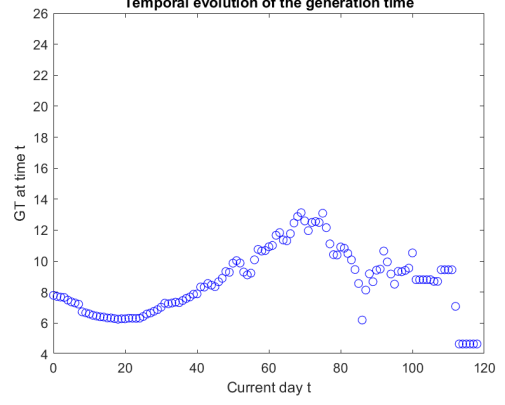


Figure 4.15: GT_t to varying of t on Erdős-Renyi graph. There is a first contraction around the peak, and then an increasing occurs.

Apart from the physiological noise, that is given by the high randomness of the model and the limited number of the simulations, we can see an interesting different behaviour in the evolution of those quantities. The reproduction number basically decrease monotonically in time, and the reason is that, as time goes on, the number of susceptible decreases so that the average number of infections that a node can cause decrease too. Particularly, R_t is always below the basic reproduction number R_0 as it happens in classical epidemiological theories. Generation times presents a totally different behaviour, since it presents a non-monotonic behaviour: from day 0 to approximatively day 25 (which is typically around the epidemic's peak) it slightly decreases, thus it starts growing until a maximum of approximatively 14 days. The first decreasing behaviour could be explained by the contraction of susceptibles and the competition among infectors: infectors are induced to more likely infect an individual i in a short time frame since the probability of contacting a susceptible later on is lower and since they are in competition with all others potential infectors of i (see [5]). After the peak, some infectors recovers, the competition loosens and infecting starts requiring more time. The U-turn around $t \simeq 70$ is much more counterintuitive and difficult to explain: indeed, it is probably due to the statistical fluctuations that occur when t becomes large, because most of the individuals get the infection in the first days of the spreading and only few of them spread the virus when t is around 70.

4.3.2 Barabási-Albert graph

We now want to make the same analysis with a different choice in the topology of the graph. From now on, we will consider $G = G(100, 7)$ as a Barabási-Albert graph, in which the parameter $m = 7$ has been chosen in order to obtain an average degree almost equal to the one of the Erdős-Rényi graph that we have considered in the previous section; the clustering coefficient is here significantly higher: $C \simeq 0.23$. The behaviour of R_0 and GT w.r.t. to c are presented in the following figures.

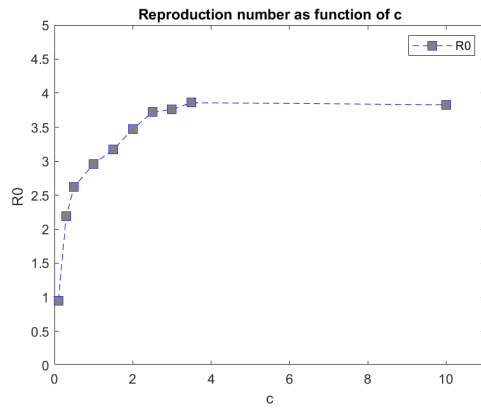


Figure 4.16: Reproduction number as function of the contact rate on Barabási-Albert graph. Again, after a first growing, it reaches a steady state.

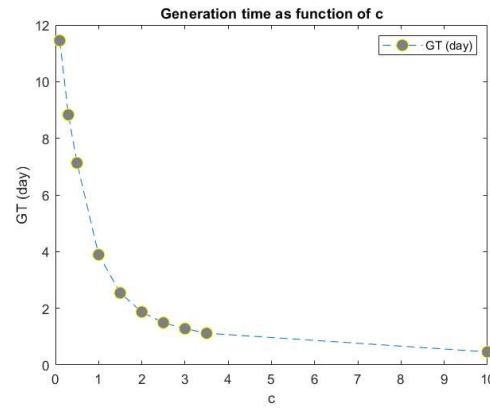


Figure 4.17: Generation time as function of the contact rate on Barabási-Albert graph. Again it decreases exponentially approaching the 0 as the contacts get more and more frequent.

Here the same considerations as the ones we did in the previous section hold: R_0 reaches a steady-state whereas GT decreases exponentially approaching to zero as the contacts' rates get higher and higher. Moreover, we can see that here R_0 remains below the level of 4, whereas in the random network it exceeded this level. More in general we can see that, for each choice of the constant c , the generation time and the basic reproduction number are respectively higher and lower in the scale-free network than in the Erdős-Rényi graph. The reason is that, even if the two graphs are built in such a way that they have the same average degree, the median degree in the scale-free network is lower than the one in the random one. Indeed, in the first case we have few nodes with high degree while the remaining have a degree smaller than $\langle k \rangle$, in the second case we have a kind of symmetry in which each node has basically the same degree that is close to the average one. Speaking of the relation between the reproduction number and the generation time, also with the Barabási-Albert graph it seems linear for low values of R_0 .

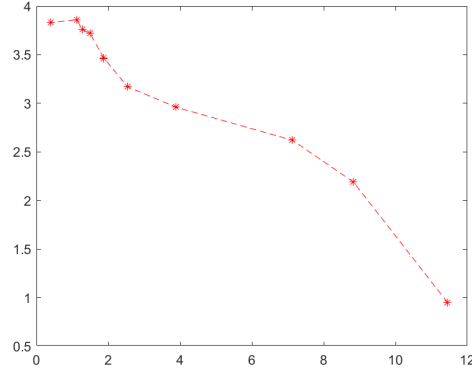


Figure 4.18: Reproduction number as function of the generation time on Barabási-Albert graph: for low values of R_0 it seems a linear relation, but when R_0 gets high a precise relation is hard to be found.

On the contrary, it is difficult to determine a precise relation between these quantities when R_0 reaches the steady state while GT keeps decreasing.

Again it is interesting to investigate the speed of the spreading, i.e. the growth of the number of infectious individuals until the reaching of the peak. We take three indicative cases which are the ones determined by $c = 1.5, 3.5, 10$. As we can see in Fig. 4.20, higher values of c correspond both to higher exponential rate and to higher height of the peak in the fraction of infectious. However, differently from Fig. 4.11, here the growth seems to be less regular, especially for small values of c , in the sense that at the beginning the number of infectious keep it self very plain, and then at a certain point it starts growing very fast. Epidemiologically this means that in the first days (i.e. in the days in which most probably the virus hasn't reached any hubs) the spreading is very slow, whereas, when the virus inevitably reaches a super-spreader ($t \simeq 10$ for the blue line and $t \simeq 4$ for the orange one), the growth becomes faster and faster, reaching a peak in very small time-intervals.

Pictures (Fig. 4.21-4.22) give a more precise idea of how different can be the spreading with different choices on the first infectors. We investigate for two contacts' rates value ($c = 1.5$ and $c = 10$) the two most extreme cases, in which i_0 is either the node with highest or minimum degree. As we can see, the difference is very clear when c is small and, in terms of prevention measures, this fact suggests that clusters and super-spreaders are the factors which overall must be controlled while they are the most dangerous factors in the spreading.

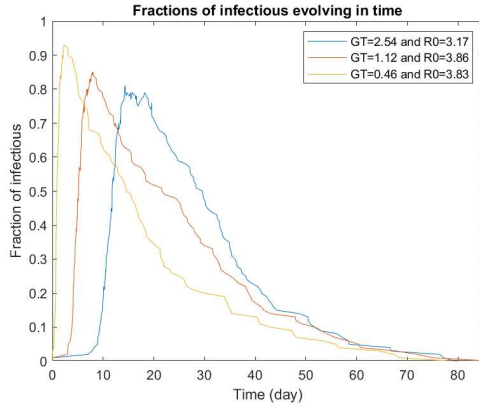


Figure 4.19: Realizations of the spreading (in terms of the fraction of infectious at time t) with different generation times and basic reproduction number on Barabási-Albert graph.

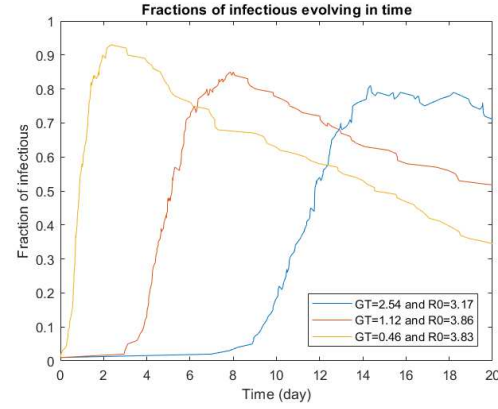


Figure 4.20: Zoom of the spreading on the early stage. Both the exponential rate and the peak's height gets higher as the generation time decreases, even when the basic reproduction number reaches the steady state.

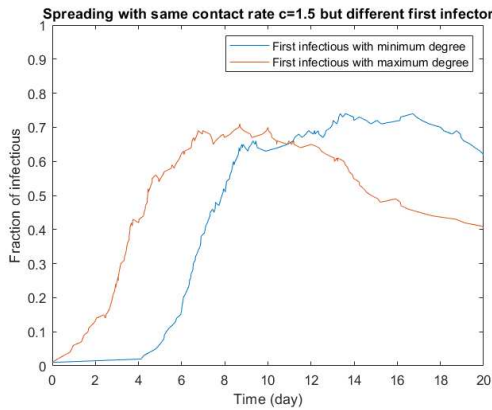


Figure 4.21: Spreading with $c = 1.5$ and different first infector i_0 . When the degree of i_0 is minimum the spreading is significantly slower than when it is maximum.

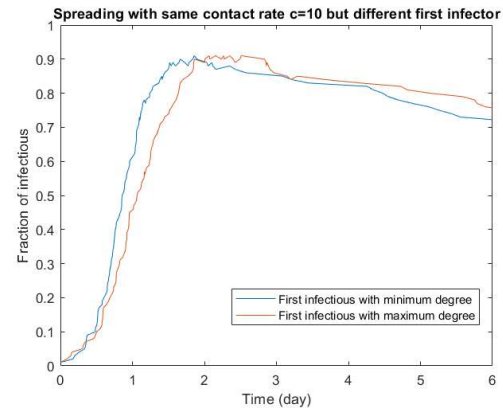


Figure 4.22: Spreading with $c = 10$ and different first infector i_0 . The difference of the spreading when i_0 has maximum or minimum degree totally vanishes.

The difference in the spreading caused by different choices of the first infector becomes increasingly blurred, until it is completely lost when the contacts' rates get sufficiently higher. In our opinion this blurring-effect is simply caused to the fact that, when the contacts are very frequent, the virus spreads very fast and with

an high probability it reaches hubs in small time intervals, even if it starts from a node with low degree. Speaking of the probability of an outbreak and the final size, we give here a representation of the realizations of those quantities in the Barabási graph (Fig. 4.23).

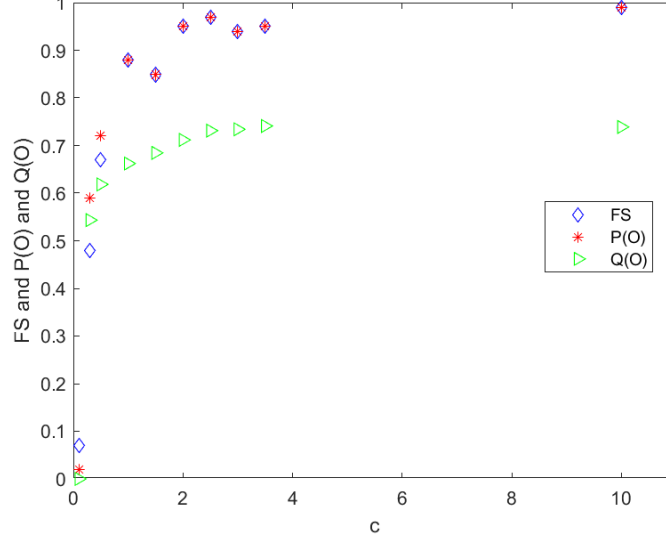


Figure 4.23: Comparison between FS , $\mathbb{P}(O)$ and $Q(O)$. As in Erdős-Renyi graph the theoretical probability always underestimates the computed one, which again overlaps with the final size when the contacts' rate is high enough ($c \geq 1$)

Also in this case we have very-similar behaviours with both the topologies, even if it is important to underline that for small values of c the probability of an outbreak is significantly greater in the Erdős-Renyi graph. In our opinion the explanation of this fact is the same of the blurring-effect on the first infectors choice caused by the increasing of the contacts' rates, and it besides in the intrinsic property of the scale-free network of having most of the nodes with a degree lower than the average one. What we mean is that, in scale-free network, there is an high probability to have a first infector which has a low-degree, and this fact jointly with a low contact rate makes difficult the spreading of a virus. This behaviour is less evident in the random-network because there the typical degree of the first infectors is very close to the average degree, and in particular it is in general higher than the degree of a first infectors in a scale-free network. As we have seen for the fraction of infectious, even for the probabilities of outbreak a blurring-effect occurs: in the two different topologies those probabilities get closer and closer as the contact rates increases.

The duration of the epidemic also maintains its properties in scale-free network,

and another time it confirms the suggestion that (in general) the virus spreads slower in the scale-free network, as we can see from Fig. 4.24.

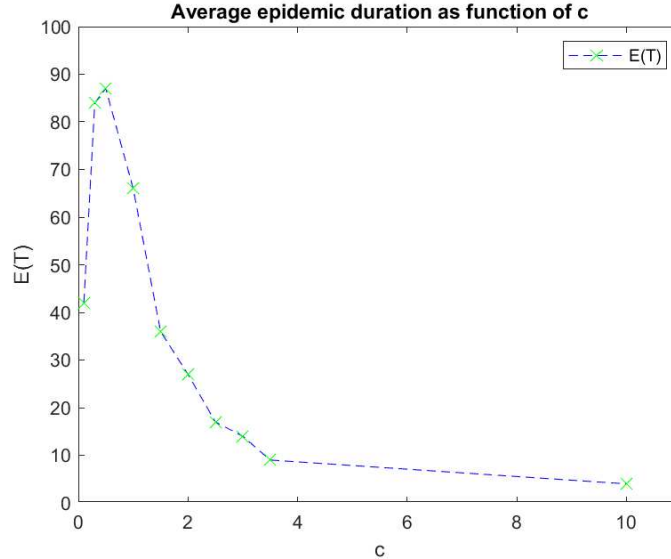


Figure 4.24: $\mathbb{E}(T)$ as function of c on Barabási-Albert graph. The peak is reached when the contacts' rate is high enough to cause real epidemic, but is sufficiently small that the speed's of the spreading doesn't grow too much.

However, it seems that the height of the peak (the highest mean duration of epidemic) is higher in the random-network, in correspondence to $c = 0.5$. This is probably due to the fact that for Barabási-Albert graph the peak isn't actually reached with our choices of contacts' rates. Indeed the peak is reasonably reached with another value of $c \in]0.5, 1[$, because, as we have already noted, with the scale-free topology the spreading is slower, so that the contact rates correspondent to the peak in the random-network doesn't suffices for the reaching of the peak in a Barabási-Albert graph.

We want now end this section by analyzing the time evolution of GT and R , as we did in the previous case, and to achieve this goal we present the pictures of R_t and GT_t to varying of t (Fig. 4.25-4.26). While the behaviour of R_t doesn't present so much difference between the random and the scale-free network, since in both the case it has a general decreasing behaviour, the evolution of GT_t is more interesting. As in the Erdős-Renyi graph, also in this case GT first contracts and then restarts growing, however the speed of contraction is significantly greater for scale-free network (local minimum reached for $t \simeq 15$ on Barabási-Albert graph, for $t \simeq 20$ on Erdős-Renyi graph) whereas the contraction is stronger on the Erdős-Renyi graph (local minimum close to 6.5 on Barabási-Albert graph, close to 6.2 on Erdős-Renyi

graph). This fact could be explained by the differences in the competition among infectors that are caused by the topology: in the scale-free network the competition occurs basically at the beginning of the spreading, when the hubs get infected and compete among themselves; when the epidemic's peak is going to be reached, hubs start recovering and the competition effect vanishes because the remaining infectors are the ones with very low degrees. On the contrary, in Erdős-Renyi graphs, the degrees' symmetry makes the competition last longer, so that the contraction is much more evident. When t gets around 70, fluctuations occur and the generation time reaches an huge value of 26 day: again we think that the explanation besides on the unreliability of the GT (and R) values when t increases too much.

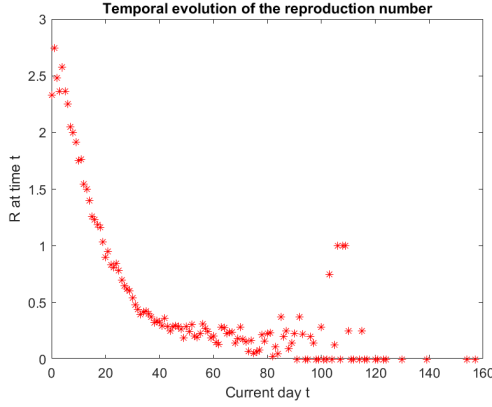


Figure 4.25: R_t to varying of t on Barabási-Albert graph. The behaviour is basically decreasing consistently with what happened on Erdős-Renyi graph.

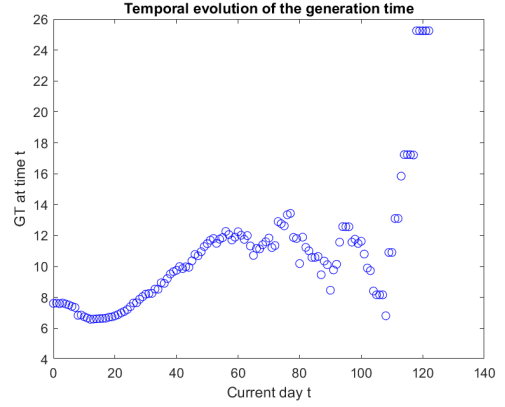


Figure 4.26: GT_t to varying of t on Barabási-Albert graph. There is a first contraction around the peak, and then an increasing occurs. The last period is dominated by fluctuations.

4.3.3 Other simulations with heterogeneous contacts' rates

Another interesting analysis to do in our model, is to investigate how it behaves in the *heterogeneous* case, where the word heterogeneous means that the parameters λ_{ij} are no more constant but they are sampled by a probability distribution.

We will focus on the differences between the average epidemiological quantities in the homogeneous case and in the heterogeneous ones. In order to get a consistent comparison, we have to fix the mean number of contact between two linked nodes. We decide to consider this mean, namely $\langle \lambda_{ij} \rangle$, in $\{0.1, 1, 3, 10\}$. We think real contacts as divided in three categories:

1. Many frequent contacts
2. Many sporadic contacts
3. A few of average contacts

and we construct explicitly a distribution in order to fit this tripartition. Particularly, given a mean $\langle \lambda_{ij} \rangle$ we consider the S distribution which is obtained by composing an s -shape function with an uniform r.v. in order to have

$$\mathbb{E}(S) = \langle \lambda_{ij} \rangle \quad (4.13)$$

Let then f be defined as

$$f(x) = \frac{2 \langle \lambda_{ij} \rangle}{1 + e^{-2x}} \quad (4.14)$$

and consider $U([-10, 10])$ as the uniform random variable which takes values in the close interval $[-10, 10]$, so that its mean is 0. Let us define the r.v. S as

$$S := f(U([-10, 10])) \quad (4.15)$$

and let us compute explicitly mean and variance of S .

$$\begin{aligned} \mathbb{E}(S) &= \int_{-10}^{10} \frac{f(x)}{20} dx = \frac{1}{10} \int_{-10}^{10} \frac{\langle \lambda_{ij} \rangle}{1 + e^{-2x}} dx = \\ &= \frac{\langle \lambda_{ij} \rangle}{10} \left[\frac{1}{2} \ln(e^{2x} + 1) \right]_{x=-10}^{x=10} = \langle \lambda_{ij} \rangle \end{aligned} \quad (4.16)$$

$$\begin{aligned} Var(\lambda_{ij}) &= \int_{-10}^{10} \frac{(f(x))^2}{20} dx - (\mathbb{E}(S))^2 \\ &= \frac{\langle \lambda_{ij} \rangle^2}{20} \int_{-10}^{10} \frac{4}{1 + 2e^{-2x} + e^{-4x}} dx - 1 \end{aligned} \quad (4.17)$$

$$\begin{aligned} &= \frac{\langle \lambda_{ij} \rangle^2}{20} \left[2 \left(\frac{1}{e^{2x} + 1} + \ln(e^{2x} + 1) \right) \right]_{x=-10}^{x=+10} - 1 \\ &\simeq \frac{9}{10} \langle \lambda_{ij} \rangle^2 \end{aligned} \quad (4.18)$$

Which allows to calculate also the variance of S to varying of $\langle \lambda_{ij} \rangle$:

$$Var(S) = \begin{cases} 0.009, & \langle \lambda_{ij} \rangle = 0.1 \\ 0.9, & \langle \lambda_{ij} \rangle = 1 \\ 8.1, & \langle \lambda_{ij} \rangle = 3 \\ 90, & \langle \lambda_{ij} \rangle = 10 \end{cases} \quad (4.19)$$

As we see from the above computations, even when S and the homogeneous choice $\lambda_{ij} \equiv \langle \lambda_{ij} \rangle$ shares the same mean value, they are not at all equal, since the variance is significantly different from one case to each other. The pictures Fig. (4.27-4.28-4.29-4.30) represent a typical sampling from the S distribution with different choice on the mean $\langle \lambda_{ij} \rangle$.

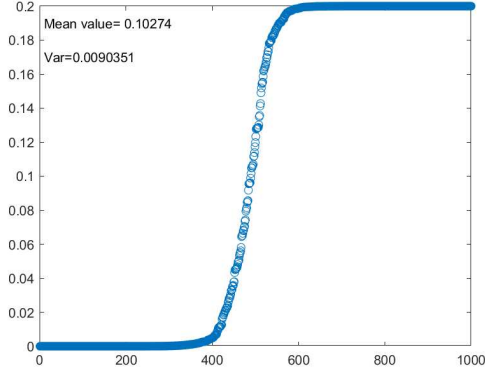


Figure 4.27: Sigmoid distribution centered in $\langle \lambda_{ij} \rangle = 0.1$: most of the values belong either to the plateau in 0 or to the one in 0.2.

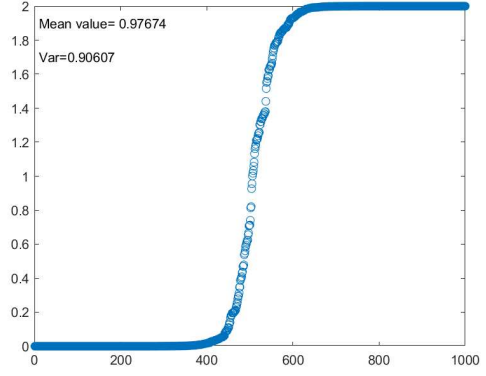


Figure 4.28: Sigmoid distribution centered in $\langle \lambda_{ij} \rangle = 1$: most of the values belong either to the plateau in 0 or to the one in 2

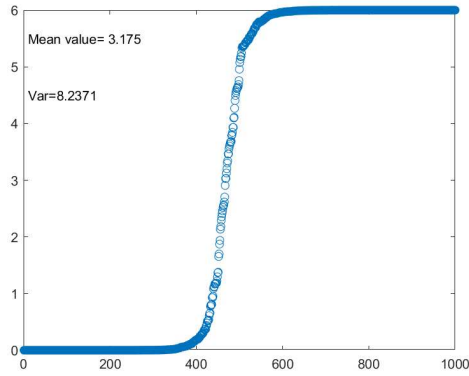


Figure 4.29: Sigmoid distribution centered in $\langle \lambda_{ij} \rangle = 3$: most of the values belong either to the plateau in 0 or to the one in 6

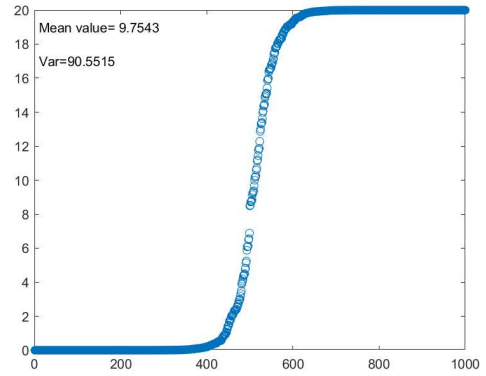


Figure 4.30: Sigmoid distribution centered in $\langle \lambda_{ij} \rangle = 10$: most of the values belong either to the plateau in 0 or to the one in 20

As we can see, mean values and variances are consistent with the ones that we have just computed. Moreover, the shape of each of this samples is exactly the one that we were looking for: most of the contacts' rates belong to the two plates of the sigmoid around 0 and $2 < \lambda_{ij} >$. We start investigating the behaviour of the main epidemiological quantities to varying of the mean contact rate $< \lambda_{ij} >$, and with values taken from the S distribution. The following pictures (Fig. 4.33-4.34) represent the growing (decreasing) of R_0 (GT) w.r.t. $< \lambda_{ij} >$ and in comparison with the homogeneous case.

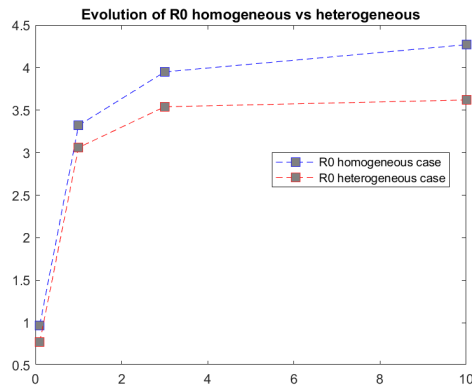


Figure 4.31: R_0 as function of $< \lambda_{ij} >$ on Erdős-Renyi graph. In the homogeneous case the spreading is stronger than in the heterogeneous.

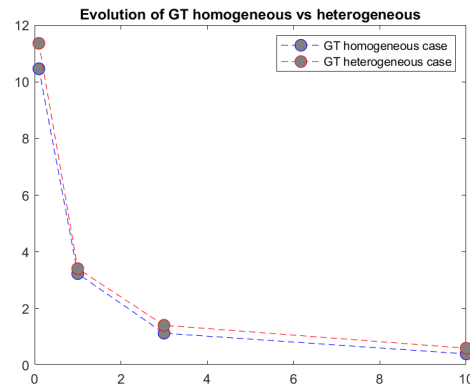


Figure 4.32: GT as function of $< \lambda_{ij} >$ on Erdős-Renyi graph. In the homogeneous case the spreading is (generally) faster than in the heterogeneous.

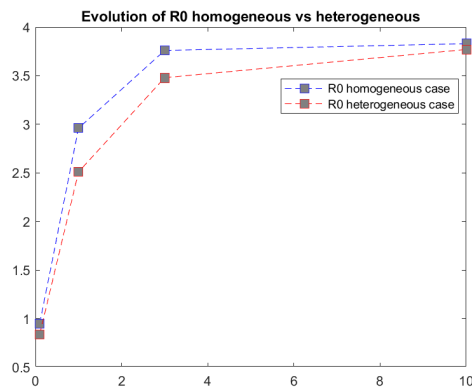


Figure 4.33: R_0 as function of $< \lambda_{ij} >$ on Barabási-Albert graph.

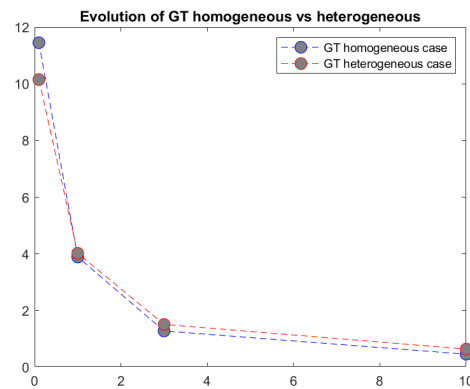


Figure 4.34: GT as function of $< \lambda_{ij} >$ on Barabási-Albert graph.

As we can see, even in the non-homogeneous case R_0 and GT keep evolving in

the same way: R_0 grows until it reaches a steady-state which it doesn't exceed, whereas GT decreases exponentially approaching the 0 (instantaneous diffusion) when the average contacts' rates goes to ∞ . Under the same average $\langle \lambda_{ij} \rangle$, both the strenght and the speed of the spreading are lower in the heterogeneous case. Roughly speaking, this suggests that it is worse to have a population where each individual enters in contact a moderate number of times with all his contacts than have a population where each individual have mainly very frequent and very sporadic contacts.

In the same way, simulations suggest that also other quantities behave in a very similar way than in the homogeneous case, and the only difference is quantitative: fixed the mean contact rate, probabilities of outbreak and final sizes are greater in the homogeneous case, whereas the persistence time is longer when the contact rates are sampled from a distribution. Also the distribution of GT isn't so much different in the two cases, even if it is observed that in the heterogeneous case it present more outliers (and consequently, the variance is higher) and it is more right-skewed, suggesting that a Gamma-distribution is preferable under this hypothesis.

Conclusions

We have presented four possible ways to model an epidemic, highlighting how much each one of these approaches differs from the others.

We formally presented deterministic and stochastic models, which can be deeply studied with mathematical rigor. The main pro of these models is their simplicity, which allows to take into account highly detailed features such as demography, latent period and preventive measures; on the contrary, the main con is that they are oversimplified since, for example, they assume homogeneous mixing of the population, which in the real life typically doesn't occur.

We also discussed the more recent epidemic models on static networks, underlying that they have both advantages and disadvantages too: on the one hand they reflect more closely the mixing of the population, on the other hand they can be mathematically investigated only through approximations or strong assumptions, and from a practical perspective they are mainly useful only for the early stage of an epidemic.

We presented our simple in-vitro epidemic model on dynamic network, which aim is both to consider a non-homogeneous mixing of the population and a time-evolution of the human contacts. We first gave a formalization of the model, which is mainly a Markovian epidemic process on a network in which edges activate/deactivate according to the competition among a family of independent Poisson processes. Then, we reported some results that we found during simulations of our model. We showed that the basic reproduction number has an upper bound which is fairly below the average degree of the graph. When it reaches this bound, it stops growing even if the average of the contacts keeps increasing so as the exponential rate and the peak's height of the number of infectious. On the contrary, generation time presents an exponential decreasing behaviour w.r.t. the mean contacts rate, and it seems to approach zero as the contacts get more and more frequent. We saw that, when epidemic's parameters are such that the probability of an outbreak is high enough, it coincides with the fraction of individuals who have been affected from the virus during the whole duration of the epidemic: this fact suggests that a result which applies for static networks (Th. 3.1.12) could be generalized in a more general framework. We investigated the temporal evolution of the basic reproduc-

tion number and of the generation time: if the first is monotonically decreasing regardless of the graph's topology, the second one present a non-monotonic behaviour, with a contraction around the peak that is stronger and longer-lasting in the Erdős-Renyi graph, suggesting that the competition effect could be biased by the graph's topology. In any case, both generation time and reproduction number are always far to have constant phases and, as suggested by [1] and [5], this fact needs to be considered especially from those studies whose aim is to infer the replacement number from the generation time.

Appendix A

Mathematical Tools

During the thesis we have silently used several mathematical notions. The aim of Appendix A is to justify those notions or, at least, frame them in their specific mathematics' areas. Particularly, we will give a brief introduction to Markov Chains and graph theory, with emphasis to the instruments that we used during our work such as Poisson Process, Erdős-Renyi graph and so on. In the last chapter of Appendix A, we will mention also other tools we used, especially from Linear Algebra. Appendix B is dedicated to the Python Code which is completely reported. We refer to [9], [15] for App. A.1, whereas we will follow [10] for App. A.2. The first part for App. A.3 is take from [18], [24] and [25], whereas for the algorithm for the resolution of tridiagonal system we refer to [21].

A.1 Markov chains

A.1.1 Markov chains in discrete time

Let us denote with E a finite or countable set.

Definition A.1.1. A sequence $\{X_n\}_{n \in \mathbb{N}}$ of E -valued random variables is a *Markov chain* if for each $n \geq 1$ and $x_0, x_1, \dots, x_{n+1} \in E$ the following holds:

$$\mathbb{P}(X_{n+1} = x_{n+1} | X_n = x_n, \dots, X_0 = x_0) = \mathbb{P}(X_{n+1} = x_{n+1} | X_n = x_n) \quad (\text{A.1})$$

In words, a Markov chain is a stochastic process in which, given the present, the future is independent to the past. In some case the quantity $\mathbb{P}(X_{n+1} = j | X_n = i)$ is independent from n , and then we say that the chain is *homogeneous*. The most important notion for an homogeneous markov chain is the one of *transition matrix*, which is the matrix $M = (\alpha_{ij})_{i,j \in E} \in M_{|E|}(\mathbb{R})$ where:

$$\alpha_{ij} := \mathbb{P}(X_{n+1} = j | X_n = i) \quad (\text{A.2})$$

The reason of the importance of the transition matrix besides in the fact that jointly with the initial distribution of the process, it determines the law of the whole process:

$$\mathbb{P}(X_n = x_n, \dots, X_0 = x_0) = \mathbb{P}(X_0 = x_0) \alpha_{x_0 x_1} \cdots \alpha_{x_{n-1}, x_n} \quad (\text{A.3})$$

A.1.2 Markov chains in continuous time

The concept of Markov chain can be generalized in a continuous time framework. From now on we consider $X = \{X_t\}_{t \in \mathbb{R}_+}$ an E -valued continuous time stochastic process and we denote $\mathcal{F} = \{\mathcal{F}_t\}_{t \in \mathbb{R}_+}$ the sigma-algebra generated by X , i.e.

$$\mathcal{F}_t = \sigma(X_s : s \leq t), \quad \forall t \in \mathbb{R}_+ \quad (\text{A.4})$$

We remember the \mathcal{F} is the smallest sigma algebra (with respect to the insemistic inclusion \subseteq) which makes *measurable* the process X .

Definition A.1.2. The process X is a *Markov chain* if for every $x \in E$ and $0 \leq s \leq t$ the following holds:

$$\mathbb{P}(X_t = x | \mathcal{F}_s) = \mathbb{P}(X_t = x | X_s) \quad (\text{A.5})$$

A continuous time Markov chain is said to be *time-homogeneous* when the quantity $\mathbb{P}(X_t = j | X_s = i)$ depends on s, t only through the distance between them $t - s$. For a time-homogeneous markov chain we can define for all $t \in \mathbb{R}_+$ a linear operator S_t from \mathbb{R}^E to itself as follows:

$$S_t f(i) := \mathbb{E}(f(X_t) | X_0 = i) = \sum_{j \in E} f(j) \mathbb{P}(X_t = j | X_0 = i) \quad (\text{A.6})$$

where $f \in \mathbb{R}^E$ and $t \geq 0$. It is quite easy to show that $\{S_t\}_{t \in \mathbb{R}_+}$ is a *semigroup* because:

$$S_0 = \mathbb{1} \quad (\text{A.7})$$

$$S_{t+s} = S_t \circ S_s \quad (\text{A.8})$$

Since it is a linear operator, S_t can be expressed in matrix form as $S_t = ((S_t)_{ij})_{i,j \in E}$ with

$$(S_t)_{ij} = \mathbb{P}(X_t = j | X_0 = i) \quad (\text{A.9})$$

From now on, we will indicate with S the operator which sends t to S_t , so that $S(t)$ and S_t are equivalent. This further notation is useful to avoid ambiguity and to underline that the semigroup is actually a function of t . When S is continuous it can be shown that

$$\lim_{t \rightarrow 0^+} \frac{S(t) - S(0)}{t} = \frac{S(t) - \mathbb{1}}{t} := Q \quad (\text{A.10})$$

exists. The left hand-side of this expression is a derivative of $S(t)$ in $t = 0$, however for a markov chain one can show that S is differentiable for all $t \geq 0$ and that it holds:

$$S'(t) = S(t)Q = QS(t) \quad (\text{A.11})$$

Consistently with this observation it can be proved that

$$S_t = e^{tQ} \quad (\text{A.12})$$

The right hand-side in Eq. (A.10) is actually a matrix $Q = (q_{ij})_{i,j \in E}$ and it is commonly called *infinitesimal generator* of the process X . Since S_t is a stochastic matrix, it clearly holds:

$$\sum_{j \in E \setminus \{i\}} (S_t)_{ij} = 1 - (S_t)_{ii} \quad (\text{A.13})$$

from which dividing both side for t and letting t approach to zero we deduce

$$\sum_{j \in E \setminus \{i\}} q_{ij} = -q_{ii} \geq 0 \quad (\text{A.14})$$

hence Q isn't a stochastic matrix since the sum of the rows is zero and the elements on the diagonal are negative. Since the elements q_{ij} are effectively derivatives of probabilities they are usually called *rates* of the transition from state i towards state j . The name rates reflects also the fact that for $i \neq j$ it holds:

$$0 \leq \mathbb{P}(X_t = j | X_0 = i) = (S_t)_{ij} = tq_{ij} + o(t) \quad (\text{A.15})$$

whereas

$$\mathbb{P}(X_t = i | X_0 = i) = 1 - q_{ii}t + o(t) \quad (\text{A.16})$$

where $q_i = -q_{ii}$. Similarly to what we have seen before, the law of a continuous time markov chain $X = \{X(t)\}_{t \in \mathbb{R}_+}$ is fully determined by its initial distribution jointly with the semigroup $\{S_t\}_{t \in \mathbb{R}_+}$, in the sense that for $0 < t_1 < t_2 < \dots < t_n$ and $x_0, x_1, \dots, x_n \in E$ it holds:

$$\mathbb{P}(X_{t_n} = x_n, \dots, X_0 = x_0) = \mathbb{P}(X_0 = x_0)(S_{t_1})_{x_0 x_1} \cdots (S_{t_n - t_{n-1}})_{x_{n-1} x_n} \quad (\text{A.17})$$

In particular if we define π_t the distribution at time t , i.e. $\pi_t(j) = \mathbb{P}(X_t = j)$ it easily follows

$$\pi_t(j) = \sum_{i \in E} \mathbb{P}(X_t = i | X_0 = j) = \sum_{i \in E} (S_t)_{ij} \pi_0(i) \quad (\text{A.18})$$

which turn implies

$$\pi_t = \pi_0 S_t \Leftrightarrow \begin{cases} \pi'(t) = \pi(t)Q \\ \pi(0) = \pi_0 \end{cases} \quad (\text{A.19})$$

where we have denoted $\pi(t)$ as the function which sends t to π_t . Eq. (A.19) allows to introduce the following, fundamental, notion.

Definition A.1.3. A probability π on E is called a *stationary distribution* if for every $t \geq 0$ one of the two following equations holds:

$$\pi S_t = \pi \Leftrightarrow \pi Q = 0 \quad (\text{A.20})$$

The importance of this concept is that, starting from a stationary distribution, the probability distribution of the process remains unchanged as time progresses, so it describes the limiting behavior of the markov chain. In general a stationary distribution could not exists, however certain hypothesis guarantee positive results in this direction.

Proposition A.1.4. *If the states' space E is finite then at least one stationary distribution exists.*

It is important to underline that this proposition it is no more true for infinite countable sets. In order to give another positive results, we need some other notions.

Definition A.1.5. A markov chain X is said to be *irreducible* if every couple of different states $i, j \in E$ is linked through a path with a strictly positive probability: when this fact happens, it is common to say that states i, j *communicate*. In formula, this means that exists an integer n and a path of lenght n $i = x_0, x_1, \dots, x_n = j$ such that $x_k \neq x_{k+1}$ for evert $k = 0, \dots, n - 1$ and with $q_{x_k x_{k+1}} > 0$

Theorem A.1.6. *An irreducible markov chain has at most one stationary distribution π . When such π exists $\pi(i) > 0$ for evert $i \in E$ and for every initial distribution π_0 the distribution of the process approach π , i.e.*

$$\pi = \lim_{t \rightarrow \infty} \pi_0 S_t \quad (\text{A.21})$$

We end this section with the concept of embedded markov chain. Before giving the formal definition, we need to define and investigate the notions of sojourn time.

Definition A.1.7. We call *sojourn time* in the state $i \in E$ the quantity:

$$\tau_i = \inf\{t > 0 : X(t) \neq i\} \quad (\text{A.22})$$

under the hypothesis that $X_0 = i$. It is the time spent in the state i before jumping to another state

The following result provides an interesting fact about the distribution of the soujorn times for a markov chain.

Theorem A.1.8. *The sojourn times τ_i of a continuous time markov chain in a state $i \in E$ are independent, exponential random variables with mean $\frac{1}{q_i}$*

Let us now denote

$$V_{ij}(t) = \mathbb{P}(X_t = j | X_t \neq i, X_0 = i) \quad (\text{A.23})$$

Thus $V_{ij}(t)$ describes the probability that, if a transition occurs in a time interval of length t , the process *jumps*, i.e. moves from a state i to a different state j . Using the definition of conditional probability, we have

$$V_{ij}(t) = \frac{\mathbb{P}(X_t = j, X_t \neq i | X_0 = i)}{\mathbb{P}(X_t \neq i | X_0 = i)} = \frac{(S_t)_{ij}}{1 - (S_t)_{ii}} \quad (\text{A.24})$$

In the limit $h \rightarrow 0^+$ it holds

$$V_{ij} := \lim_{t \rightarrow 0^+} V_{ij}(t) = \frac{q_{ij}}{q_i} \quad (\text{A.25})$$

which by the above mentioned properties of q_{ij}, q_i implies that

$$\sum_{j=1, j \neq i} V_{ij} = 1 \quad (\text{A.26})$$

i.e. that the matrix $V = (V_{ij})_{i,j \in E}$ is a stochastic matrix provided that $V_{ii} = 0$ for all $i \in E$. Under this further hypothesis the matrix V is the transition matrix for the *embedded Markov chain* which is ultimately the chain derived from the initial process X under the assumption that every transition coincides with a jump.

A.1.3 Transience and recurrence of the states

In many applications it is very important to classify the nature of the states of a markov chain. In this section, unless otherwise noted, X is a continuous time markov chain as defined in the previous section.

Definition A.1.9. Given a state $i \in E$ we define the *return time to state i* as

$$T_i = \inf\{t > 0 : X_t = i\} \quad (\text{A.27})$$

where by convention $T_i = \infty$ if $X_t \neq i$ for all $t \in \mathbb{R}_+$. It is easy to prove that it is actually a stopping time.

Definition A.1.10. A state $i \in E$ is *recurrent* if:

$$\mathbb{P}_i(T_i < \infty) := \mathbb{P}(T_i < \infty | X_0 = i) = 1 \quad (\text{A.28})$$

otherwise i is called *transient*. A recurrent state is called *positive recurrent* if

$$\mathbb{E}_i(T_i) < \infty \quad (\text{A.29})$$

and otherwise it is called *null recurrent*.

The property of transience and recurrence are both class property, in the following sense.

Theorem A.1.11. *If i, j communicate, they are either both recurrent or both transient.*

For discrete time markov chains there exists a very useful tool to prove the recurrence of a state, which is the following theorem

Theorem A.1.12. *Let $X = \{X_n\}_{n \in \mathbb{N}}$ a discrete time markov chain and let us define the potential matrix G associated to its transition matrix M as:*

$$G = \sum_{n \geq 0} M^n \quad (\text{A.30})$$

which general term is given by

$$g_{ij} = \sum_{n=0}^{\infty} p_{ij}(n) := \sum_{n=0}^{\infty} P_i(X_n = j) \quad (\text{A.31})$$

Then a state $i \in E$ is recurrent if and only if $g_{ii} = \infty$.

A.1.4 Poisson processes

In the definition of our original model in Chapter 4, we made a massive use of Poisson processes and their properties, so we end this section by doing a short review of this arguments.

Definition A.1.13. A random point process on \mathbb{R}_+ is a sequence $\{T_n\}_{n \in \mathbb{N}}$ of nonnegative random variables such that, almost surely,

1. $T_0 \equiv 0$
2. $0 < T_1 < T_2 \dots$
3. $\lim_{n \rightarrow \infty} T_n = +\infty$

Random point processes are often used to describe the happening of events. For instance, in our model the points of the Poisson process indicated the activation (or deactivation) of a contact between two individuals. This empirical meaning motivates the need of introducing the following two quantities.

Definition A.1.14. The sequence $\{S_n\}_{n \geq 1}$ defined by

$$S_n = T_n - T_{n-1} \quad (\text{A.32})$$

is called the *interevent sequence*. Those elements represent the time interval between two consecutive events of the process.

For any interval $(a, b] \subseteq \mathbb{R}_+$ we define the number of events occurring in the time interval $(a, b]$ as

$$N((a, b]) := \sum_{n \geq 1} \mathbb{1}_{(a, b]}(T_n) \quad (\text{A.33})$$

The process $\{N_t\}_{t \in \mathbb{R}_+}$ defined by

$$N_t = N((0, t]) \quad (\text{A.34})$$

is called the *counting process* of the point process $\{T_n\}_{n \in \mathbb{N}}$.

The above mentioned Poisson process is nothing but a particular case of random point processes, in which the interevent times are exponentially distributed, as we now see.

Definition A.1.15. A point process N on \mathbb{R}_+ is called *homogeneous Poisson process* (HPP) with intensity $\lambda > 0$ if

1. For all $t_i \in \mathbb{R}_+, i \in \{1, 2, \dots, k\}$, such that $0 \leq t_1 \leq t_2 \leq \dots \leq t_k$ the random variables $N(t_i, t_{i+1}]$ are independent.
2. For any interval $(a, b] \subset \mathbb{R}_+$ the random variable $N(a, b]$ is a Poisson random variable with mean $\lambda(b - a)$.

Directly from the definition one can deduce the following

Theorem A.1.16. Let N be an HPP with intensity $\lambda > 0$. Then the interevent sequence $\{S_n\}_{n \geq 1}$ is i.i.d, with exponential distribution of parameter λ . This turn imply that:

$$\mathbb{P}(S_n \geq t) = 1 - e^{-\lambda t}, \quad \mathbb{E}(S_n) = \frac{1}{\lambda} \quad (\text{A.35})$$

In many applications there are several different poisson processes which compete for the same singular process. For instance, in our model, we have that all activations and deactivations of the edges contribute to the overall dynamic of the network. The following result states that, under certain hypothesis, the superposition of poisson processes is again a poisson process.

Theorem A.1.17. Let $\{N_i\}_{i \geq 1}$ be a family of independent HPP's with respective positive rates $\{\lambda_i\}_{i \geq 1}$. Then:

1. Almost surely, two distinct HPP's of this family have not point in common
2. If $\sum_{i=1}^{\infty} \lambda_i := \lambda < \infty$ then

$$N(t) := \sum_{i=1}^{\infty} N_i(t) \quad (\text{A.36})$$

defines the counting process of an HPP with intensity λ

When considering a process N made by the competition of a family of HPP's $\{N_i\}_{i \geq 1}$, one central question arises: given a ring (point) generated by N , how can one establish which is the index i such that the process N_i is the one that has actually caused the ring? The following theorem, usually known as *Competition Theorem* provides an answer for that question.

Theorem A.1.18. *Under the same hypothesis of the previous Theorem and assuming $\lambda < \infty$, let us denote by Z the first event time of N and by J the index of the HPP responsible for it, so that Z is the first event of the process N_J . Then:*

$$\mathbb{P}(J = i, Z \geq a) = \mathbb{P}(J = i)\mathbb{P}(Z \geq a) = \frac{\lambda_i}{\lambda} e^{-\lambda a} \quad (\text{A.37})$$

In particular, J and Z are independent, Z is an exponential random variable with mean $\frac{1}{\lambda}$ and the distribution of J is given by:

$$\mathbb{P}(J = i) = \frac{\lambda_i}{\lambda}, \quad \forall i \geq 1 \quad (\text{A.38})$$

We end this section by considering the so-called *graphical construction* of a chain that is the procedure to associate to a generator Q a continuous-time homogeneous Markov chain which admits Q as infinitesimal generator. This procedure involves Poisson processes.

Let E be a countable space, and let $Q = \{q_{ij}\}_{i,j \in E}$ be such that for all $i, j \in E$ with $i \neq j$,

$$q_i \in [0, \infty], \quad q_{ij} \in [0, \infty) \quad (\text{A.39})$$

and

$$q_i < \infty, \quad q_i = \sum_{k \in E \setminus \{j\}} q_{ik} \quad (\text{A.40})$$

where $q_i = -q_{ii}$. It is important to observe that for a general infinitesimal generator of a continuous semigroup, only Cond. (A.39) are guaranteed. Let now $\{N_{ij}\}_{i,j \in E, i \neq j}$ be a family of independent HPPs with respective rates $\{q_{ij}\}_{i,j \in E, i \neq j}$.

Moreover let X_0 be a given E -valued initial state independent of the above family of Poisson processes. We construct explicitly a process as a jump process:

$$\tilde{X}_t = X_n \quad \forall t \in [\tau_n, \tau_{n+1}), \quad (\text{A.41})$$

where $\{\tau_n, X_n\}_{n \in \mathbb{N}}$ is defined recursively as it follows:

1. X_0 is already given and $\tau_0 \equiv 0$
2. If $\tau_n < \infty$ and $X_n = \tilde{X}_{\tau_n} = i \in E$, then $\tau_{n+1} - \tau_n$ is the first event of the competing HPPs $\{S_{\tau_n} N_{ij}\}_{j \in E, j \neq i}$ where

$$S_{\tau} N_l(a, b] := N_l(\tau + a, \tau + b] \quad (\text{A.42})$$

- If $q_i = 0 \Leftrightarrow \tau_{n+1} - \tau_n = \infty$, then the construction ends by setting $X_{n+m} = \Delta$ and $\tau_{n+m} = \infty$ for all $m \geq 1$ and for an arbitrary element $\Delta \notin E$
- If $\tau_{n+1} - \tau_n < \infty$, X_{n+1} is the index $k \neq i$ such that $S_{\tau_n} N_{ik}$ is the first among the competing HPPs to produce an event.

The process is defined by reiterating this procedure up to $\tau_\infty = \lim_{n \rightarrow \infty} \tau_n$. What is important is the following result.

Theorem A.1.19. *If $\tau_\infty = \infty$ almost surely, the process \tilde{X} is a continuous time markov chain with infinitesimal generator Q .*

A.2 Graph theory

The various networks presented in the previous chapters are different realizations of the same mathematical object commonly known as a graph.

A.2.1 First definitions

Definition A.2.1. A *graph* G is assigned by giving a set V of vertices (or nodes) and a set E of edges (or links) between them. The mathematical symbol to indicate a graph is then the following:

$$G = G(V, E) \quad (\text{A.43})$$

whereas a vertex is simply denoted by an index i and the edge between two vertices i, j by the tuple (i, j) . Edges may have arrows, and in this case the graph is said to be a *directed graph*. On other hand, if edges have not direction, G is said to be an *undirected graph*. One could assign to each edge a value: in this case, the graph is said to be a *weighted graph*.

From now on, unless we specify otherwise, the graphs that we will consider will be undirected and unweighted graphs. The following definition is an useful notion which allows to fully describe a graph with a particular matrix.

Definition A.2.2. Let $G = G(V, E)$ be a graph and let us suppose that $|V| = n$ where $n \in \mathbb{N}$, so that V can be seen as the discrete set: $V = \{1, \dots, n\}$. The matrix $A = (a_{ij})_{i,j \in V} \in M_n(\mathbb{R})$ defined by:

$$a_{ij} = \begin{cases} 1, & \text{if } (i, j) \in E \\ 0, & \text{otherwise} \end{cases} \quad (\text{A.44})$$

is called the *adjacency matrix* of the graph G .

The diagonal elements of the adjacency matrix represent the presence of *loops* which are edges between a vertex and it self. It is important to underline that an adjacency matrix A is symmetric only in the case of undirected graph, because in this case $(i, j) \in E$ is equivalent to $(j, i) \in E$ so that $a_{ij} = a_{ji}$ for all $i, j \in V$. The natural generalization of adjancecey matrix for weighted graph is the following one.

Definition A.2.3. Let $G = G(V, E)$ be a weighted graph, i.e. a graph in which every edge (i, j) is associated to a quantity λ_{ij} . Then the *weighted adjacency matrix* of G is the matrix $A^w = (a_{ij}^w)_{i,j \in V}$ given by:

$$a_{ij}^w = \lambda_{ij} \quad (\text{A.45})$$

The same observation for loops and symmetry of the matrix holds. We now provide some basic definitions for undirected and unweighted graph.

- The graph *order* is the number n of its nodes
- The graph *size* is the number m of its edges

In a graph of order n and with no loops the maximum number of edges is given by $m_{max} = \frac{n(n-1)}{2}$. If we allow loops, we have to add a term n in the expression of m_{max} which then becomes $\frac{n(n+1)}{2}$. If no edge is drawn, the graph is said to be *empty* whereas if all edges are drawn it is said to be *complete*: those are the two extreme cases for a graph.

- Given a vertex i its *degree* k_i is the number of its edges. Any edge contributes both to the degree of the vertex origin and to the degree of vertex destination, so it holds:

$$\sum_{i \in V} k_i = 2m \quad (\text{A.46})$$

where $m = |E|$ is the size of the graph.

The degree can be computed from the adjacency matrix as it follows:

$$k_i = \sum_{j=1}^n a_{ij} \quad (\text{A.47})$$

By replacing a_{ij} with a_{ij}^w in the previous formula one gets the *strenght* of degree i in a weighted graph.

- In an undirected graph two vertices $i, j \in V$ are *connected* if there exists a path from i to j . A graph $G = G(V, E)$ is said to be connected if every pairs of nodes in V are connected. Sometimes a graph isn't connected but can be splitted in a finite number of connected subgraphs which are usually called *connected component* of G . A connected component $C = (\tilde{V}, \tilde{E})$ which order is near to the order of the starting graph G , i.e. $|\tilde{V}| = \mathcal{O}(|V|)$, is usually called a *giant component*.
- If two nodes i, j of a graph G are connected, we can define the *distance* between them d_{ij} as the shortest number of edges one needs to travel to get from i to j .
- The *diameter* D of a graph G is defined as the largest distance that one can find between two nodes of the graph.
- The *clustering coefficient* C_i of a vertex i in an undirected graph G is given by the average fraction of pairs of neighbours of i that are also neighbours of each other. C_i can be explicitly computed from the adjacency matrix A :

$$C_i = \frac{2}{k_i(k_i - 1)} \sum_{j,k} a_{ij} a_{ik} a_{jk} \quad (\text{A.48})$$

- The *clustering coefficient* C of a graph G is simply the average clustering coefficient over the various vertices i of the graph.

A.2.2 Erdős-Rényi model

Graph theory is a powerful instrument because graphs naturally appears in several applications. However, it is often impossible to deduce from real-word phenomena the specific structure of a graph. For this reason mathematicians have introduced the so-called *random graph models* which are tools to generate graph randomly by following certain schemes. The simplest random graph model is due to Paul Erdős and Alfred Rényi and it follows a similar idea of the percolation.

Let us suppose to have a set V of n vertices, which corresponds to $\frac{n(n-1)}{2}$ possible edges. Given a probability $p \in [0, 1]$ we establish that each of those potential edges is drawn with probability p . Then the size of the graph G is a stochastic random

variable, and we can only find an average size of the graph $\mathbb{E}(n)$ which is given by:

$$\mathbb{E}(n) = p \frac{n(n-1)}{2} \quad (\text{A.49})$$

One could be interested in computing what is the probability $\mathbb{P}(G(n, m))$ of generating a graph with exactly m edges. A straightforward computation gives the following result

$$\mathbb{P}(G(n, m)) = p^m (1-p)^{\frac{n(n-1)}{2}-m} \quad (\text{A.50})$$

The degree of each node is a random variable too, which has an average $\langle k \rangle$ given by:

$$\langle k \rangle = \frac{2\mathbb{E}(n)}{n} = p(n-1) \simeq pn, \quad n \gg 0 \quad (\text{A.51})$$

What is most interesting is the *degree distribution*. In order to compute it, we need to avoid considering the correlation between the various degree in the graph, so we assume that n is very large. To obtain a vertex of degree k we must have exactly k links (whose probability is p) and, consequently, $(n-1-k)$ unsuccessful events (whose probability is $1-p$). Since it is not important what are the links, we can choose them in $\binom{n-1}{k}$ combinations, thus it follows that the probability p_k that a random chosen node has degree k is given by:

$$p_k = \binom{n-1}{k} p^k (1-p)^{n-1-k} = \frac{(n-1)!}{(n-1-k)!k!} p^k (1-p)^{n-1-k} \quad (\text{A.52})$$

which is actually a distribution since, from the binomial theorem we have

$$\sum_{i=1}^{n-1} p_i = (p + (1-p))^{n-1} = 1 \quad (\text{A.53})$$

This discrete distribution is called a *binomial distribution* and it is usually approximated by the continuous *Poisson distribution* in the two limits $n \rightarrow \infty$ and $p = p(n) \rightarrow 0$ so that np is kept constant:

$$p_k = \frac{n!}{(n-k)!k!} p^k (1-p)^{n-k} \simeq \frac{(np)^k e^{-np}}{k!} \quad (\text{A.54})$$

The mean value $\langle k \rangle$ of the above distribution is given by np so we can write

$$p_k = \frac{\langle k \rangle^k e^{-\langle k \rangle}}{k!} \quad (\text{A.55})$$

It is easy to observe that, depending on p , the configuration of an Erdős-Renyi graph can be very different. For instance, if $p \equiv 0$, the graph is almost surely made

of n isolated nodes whereas if $p \equiv 1$ the graph is almost surely a complete graph. The most interesting thing is that, in the case in which $n \rightarrow \infty$ and $p = p(n) \rightarrow 0$, there are threshold quantities for $p(n)$ that determine phase transitions on the configuration of the graph. Let us discuss it into more detail.

Definition A.2.4. Let $G = G(V, E)$ be a graph of order n and P any graph property. P is said to be a *monotone property* if the fact that G satisfies P implies that every \tilde{G} of order n which has G as subgraph satisfies P too.

From now on we denote $G = G(n, p)$ the Erdős-Renyi graph with n nodes and probability of drawing an edge equal to p .

Definition A.2.5. Let $G = G(n, p)$ and P be respectively an Erdős-Renyi graph with $p = p(n)$ and a monotone property. A *threshold function* for P is a function $t : \mathbb{N} \rightarrow \mathbb{R}$ such that

$$\begin{cases} p(n) = o(t(n)) \Rightarrow \mathbb{P}(P) = 0 \\ p(n) = \omega(t(n)) \Rightarrow \mathbb{P}(P) = 1 \end{cases} \quad (\text{A.56})$$

as $n \rightarrow \infty$.

The following theorem provides three threshold functions for key properties of a random graph $G = G(n, p)$.

Theorem A.2.6. Let $G = G(n, p)$ and let us define P_1, P_2 and P_3 respectively as the property for G of having at least one edge, the property of having a giant component and the property of being connected. Then each property P_i has t_i as threshold function, where

$$t_i(n) = \begin{cases} n^{-2}, & i = 1 \\ n^{-1}, & i = 2 \\ \frac{\log(n)}{n}, & i = 3 \end{cases} \quad (\text{A.57})$$

A.2.3 Barabási-Albert model

Many real networks presents the characteristic of having few nodes with a number of links that greatly exceeds the average whereas the remaining ones are slightly connected. The Barabási-Albert graph $G = G(n, m)$ is specifically suited to reproduce this property and it is generated by following three steps:

1. **Initialization:** The graph G is initialized by simply taking a subset of $n_0 \geq m$ nodes of G and keeping them isolated.
2. **Growth:** At each timestep a new node is added, and it is connected randomly to m nodes already in the network.

3. **Preferential attachment:** The probability that a link of the new node connects to node i depends on the degree of the node i , namely k_i :

$$p(k_i) := p(\{\text{A link of the new node connects to node } i\}) = \frac{k_i}{\sum_j k_j} \quad (\text{A.58})$$

The already mentioned hubs are the result of a rich-gets-richer phenomenon: due to preferential attachment new nodes are more likely to connect to the more connected nodes than to the smaller nodes. Hence, the larger nodes will acquire links at the expense of the smaller ones, eventually becoming hubs. Since we started with n_0 nodes, and at each time step we added only one vertex linking it with m_0 other vertices, after t time steps we have the following expression for the order and the size of the graph:

$$n = n_0 + t \quad (\text{A.59})$$

$$m = \frac{\sum_{i=1}^n k_i}{2} = m_0 t \quad (\text{A.60})$$

We now present the original derivation of the fact that those rules produce naturally a scale-free network, i.e. a network in which the degree distribution is power-law distributed: $p_k \propto k^{-\gamma}$. Let us assume that the degrees k_i are continuous functions of the time and that new vertices enter the network at constant rate. Since the change of connectivity in one time step is equal to m_0 , the variation in time of the i -th degree is given by:

$$\frac{\partial k_i}{\partial t} = m_0 p(k_i) = \frac{k_i}{2t} \quad (\text{A.61})$$

whih together with the initial condition $k(t_i) = m_0$ implies:

$$k_i(t) = m_0 \left(\frac{t}{t_i} \right)^{\frac{1}{2}} \quad (\text{A.62})$$

Directly from Eq. (A.62) one deduces that the probability $\mathbb{P}(k_i < k)$ that a vertex has degree lower than a fixed value k satisfies

$$\mathbb{P}(k_i < k) = \mathbb{P}\left(t_i > \frac{m_0^2 t}{k^2}\right) \quad (\text{A.63})$$

Since new vertices enter the network at constant rate, the distribution of the times t is uniform so the density $f_t \equiv \text{const}$ and the constant is determined by the normalization:

$$\int_0^n f_t(i) d_i = 1 \quad (\text{A.64})$$

which implies $f_t \equiv \frac{1}{n} = \frac{1}{n_0+t}$. Thus we can compute:

$$\mathbb{P}\left(t_i > \frac{m_0^2 t}{k_2}\right) = 1 - \mathbb{P}\left(t_i < \frac{m_0^2 t}{k_2}\right) = 1 - \frac{m_0^2 t}{k_2} \frac{1}{n_0 + t} \quad (\text{A.65})$$

From which

$$p_k = \frac{\partial \mathbb{P}(k_i > k)}{\partial k} = \frac{2m_0^2 t}{n_0 + t} \frac{1}{k_3} \propto k^{-3} \quad (\text{A.66})$$

i.e. the degree distribution is a power law with exponent $\gamma = 3$.

A.2.4 Configuration model

In Sec. 3.1 we have used another graph model in which the degree of each vertex is fixed beforehand, i.e. the degrees' vector $\vec{k} := (k_1, \dots, k_n)$ is a constant vector belonging to \mathbb{R}^n . This model is usually called *configuration model* and aim of this section is just to introduce this kind of model, since several computations have already been made in Sec. 3.1.

Despite of its simplicity, the configuration model is more flexible compared to many random models such the Erdős-Renyi one. For instance, a particularly unrealistic feature of the random graph $G = G(n, p)$ is that its degree distribution doesn't have the heavy-tail that many real networks exhibit, and this problem can be definitely avoided by generating a graph with pre-determined degrees. To be more precise, one could think to configuration models as proper generalizations of Erdős-Renyi graphs, since one can create the vector \vec{k} by taking its entries k_i from a Poisson distribution.

The fact that the degrees are pre-determined doesn't implies that a graph generated with a configuration model is a deterministic model: given a set of nodes $V = \{1, \dots, n\}$ and a degrees' vector \vec{k} , we only know that a vertex i has k_i neighbours, but those neighbours are chosen randomly respecting other degrees k_j . From an algorithmic point of view, the generation of a configuration graph proceeds as it follows:

1. **Initialization** The n nodes are drawn and, for all i , k_i half-edges (stubs) are attached to vertex i .
2. **Drawing of the links** Iteratively the stubs of each node are linked to other stubs in order to create usual edges. The procedure finish when there are no more stubs.

Specific properties of configuration models can be investigated with the generating functions, as we did in Sec. 3.1, however we here present some basic computations on such a model.

Let $i, j \in V$ be two vertex and let k_i, k_j denote their degrees. We are interested in compute the probability p_{ij} that the two vertices are connected. A first easy observation is that $p_{ij} = 0$ whenever $k_i k_j = 0$, so we assume $k_i k_j > 0$. Now, if we start from one of the k_i stubs of i , we have $2m - 1 = \sum_{i=1}^n k_i - 1$ remaining hubs in which we can arrive, and exactly k_j of them are attached to the vertex j . So

$$p_{ij} = \frac{k_i k_j}{2m - 1} \simeq \frac{k_i k_j}{2m} \quad (\text{A.67})$$

under the assumption that $m \gg 0$. It follows that the higher the degrees are of i and j , the greater is the probability that they connect under the configuration model. Unless specified otherwise, configuration models allows both multiedges and loops, which probabilities can be explicitly computed. For instance, given an edge (i, j) the probability that a second edge between those two nodes appears is given by:

$$\frac{(k_i - 1)(k_j - 1)}{2m} \quad (\text{A.68})$$

so the probability that both the first and the second edge between i, j appears is given by

$$\frac{k_i k_j}{2m} \frac{(k_i - 1)(k_j - 1)}{2m} = \frac{k_i k_j (k_i - 1)(k_j - 1)}{4m^2} \quad (\text{A.69})$$

The expected value of multi-edges in the entire network can then be computed:

$$\begin{aligned} \sum_{i \neq j} \frac{k_i k_j (k_i - 1)(k_j - 1)}{4m^2} &= \frac{1}{2} \frac{1}{4m^2} \left(\sum_{i=1}^n k_i (k_i - 1) \sum_{j=1}^n k_j (k_j - 1) \right) \\ &= \frac{1}{2 < k >^2 n^2} \left(\sum_{i=1}^n k_i^2 - k_i \right) \left(\sum_{j=1}^n k_j^2 - k_j \right) \\ &= \frac{(< k^2 > - < k >)^2}{2 < k >^2} \\ &= \frac{1}{2} \left(\frac{< k^2 > - < k >}{< k >} \right)^2 \end{aligned} \quad (\text{A.70})$$

where we used the fact that $2m = < k > n$ and that $< k^m > = \frac{1}{n} \sum_{i=1}^n k_i^m$. With same arguments one can compute also the probability of self loops:

$$p_{ii} = \frac{k_i(k_i - 1)}{4m} \quad (\text{A.71})$$

and the expected number of self loops which turns to be

$$\frac{< k^2 > - < k >}{2 < k >} \quad (\text{A.72})$$

A.3 Some results from Linear Algebra

A.3.1 Gershgorin's Theorem

Let $A = (a_{ij}) \in M_n(\mathbb{C})$ a \mathbb{C} -valued n -square matrix.

Definition A.3.1. Given an index i , the following region of the complex plane is called the i -Gershgorin's circle

$$C_i(A) = \{z \in \mathbb{C} : |z - a_{ii}| \leq R_i\} \quad (\text{A.73})$$

where the radius R_i is given by

$$R_i = \sum_{j \neq i} |a_{ij}| \quad (\text{A.74})$$

The importance of the Gershgorin's circles besides in the following theorem, which is commonly known as *Gershgorin's Theorem*.

Theorem A.3.2. Let $A \in M_n(\mathbb{C})$ be a \mathbb{C} -valued n -square matrix, and let us denote with $\sigma(A)$ the spectrum of A , i.e. the set of eigenvalues of A . Then

1. For every $\lambda \in \sigma(A)$ there exists an index i such that $\lambda \in C_i(A)$
2. If there exist an integer $k \leq n$ and k Gershgorin's circles $C_{i_1}(A), \dots, C_{i_k}(A)$ such that their union D is a connected region disjoint from the union of the remaining $n - k$ Gershgorin's circles, then D contains exactly k elements of $\sigma(A)$ (with their algebraic multiplicity).

The importance of this theorem is that it gives bounds for the eigenvalues of a matrix, and those bounds turn have several consequences. Since we have used it in Sec. 2.2, we now present one of those consequences, which is the fact that particular species of matrix are always non singular. We need three preliminar definitions.

Definition A.3.3. A matrix $A \in M_n(\mathbb{C})$ is said to be *diagonally dominant* if

$$|a_{ii}| \geq \sum_{j \neq i} |a_{ij}|, \quad \forall i \quad (\text{A.75})$$

If the same property holds when replacing \geq with the stric inequality $>$, then A is said to be a *strictly diagonally dominant* matrix.

Definition A.3.4. A matrix $A \in M_n(\mathbb{C})$ is said to be *reducible* when there exists a permutation matrix P such that the matrix $P^T A P$ is block upper triangular. If such a matrix doesn't exist, A is said to be *irreducible*.

Definition A.3.5. A matrix $A \in M_n(\mathbb{C})$ is said to be *irreducibly diagonally dominant* if it is irreducible, diagonally dominant and there is at least one index i such that

$$|a_{ii}| > \sum_{j \neq i} |a_{ij}| \quad (\text{A.76})$$

The above mentioned consequence of the Gershgorin's Theorem is the following result.

Theorem A.3.6. *If $A \in M_n(\mathbb{C})$ is either a strictly diagonally dominant matrix or an irreducibly diagonally dominant matrix, then A is non-singular.*

A.3.2 Tridiagonal systems

Let us end this section by presenting the so-called *Thomas Algorithm* which is an efficient way of solving particular matrix systems which are the tridiagonal system.

Definition A.3.7. Let $A \in M_n(\mathbb{C})$. A is *tridiagonal* if the only non-zero elements are on the main diagonal, the first diagonal below this, and the first diagonal above the main diagonal only, i.e.

$$a_{ij} = 0 \quad \forall i, j \text{ s.t. } i - j \notin \{-1, 0, 1\} \quad (\text{A.77})$$

Definition A.3.8. A tridiagonal system is given by the equation

$$Ax = b \quad (\text{A.78})$$

where $A \in M_n(\mathbb{C})$ is a tridiagonal matrix, $x \in \mathbb{C}^n$ is a column vector which entries are unknown and $b \in \mathbb{C}^n$ is another column vector.

The Thomas algorithm is based on LU decomposition, in which the matrix system is rewritten as $LUx = b$ where $L, U \in M_n(\mathbb{C})$ are respectively a lower triangular and an upper triangular matrix. The idea is to set $Ux = \rho$, then solving first $L\rho = b$ for ρ and then $Ux = \rho$ for x . The key instrument in order to do that is the *Gaussian elimination*. We present the whole procedure step by step.

Thomas Algorithm We will denote r_i the i -th row of the initial matrix A , and we will indicate operations on the rows as usual algebraic operations. Let us

write the system A.78 in an explicit form:

$$\begin{bmatrix} b_1 & c_1 & 0 & 0 & 0 & \cdots & 0 & 0 \\ a_2 & b_2 & c_2 & 0 & 0 & \cdots & 0 & 0 \\ 0 & a_3 & b_3 & c_3 & 0 & \cdots & 0 & 0 \\ 0 & 0 & a_4 & b_4 & c_4 & \cdots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \ddots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \cdots & a_{n-2} & b_{n-2} & c_{n-2} & 0 \\ 0 & 0 & 0 & \cdots & 0 & a_{n-1} & b_{n-1} & c_{n-1} \\ 0 & 0 & 0 & \cdots & 0 & 0 & a_n & b_n \end{bmatrix} \begin{bmatrix} x_1 \\ x_2 \\ x_3 \\ x_4 \\ \vdots \\ x_{n-2} \\ x_{n-1} \\ x_n \end{bmatrix} = \begin{bmatrix} r_1 \\ r_2 \\ r_3 \\ r_4 \\ \vdots \\ r_{n-2} \\ r_{n-1} \\ r_n \end{bmatrix}$$

Now, we first divide r_1 by b_1 , i.e. $r_1 \leftarrow \frac{r_1}{b_1}$ so that the first equation of the system becomes:

$$x_1 + \gamma_1 x_2 = \rho_1 \quad (\text{A.79})$$

where $\gamma_1 := \frac{c_1}{b_1}$ and $\rho_1 := \frac{r_1}{b_1}$. We now substitute r_2 with a linear combination of itself and (the new) r_1 :

$$r_2 \leftarrow \frac{r_2 + a_2 r_1}{b_2 - a_2 \gamma_1} \quad (\text{A.80})$$

so that the second equation becomes:

$$x_2 + \gamma_2 x_3 = \rho_2 \quad (\text{A.81})$$

where $\gamma_2 = \frac{c_2}{b_2 - a_2 \gamma_1}$ and $\rho_2 = \frac{r_2 - a_2 \rho_1}{b_2 - a_2 \gamma_1}$. We adopt the same procedure for the third row:

$$r_3 \leftarrow \frac{r_3 + a_3}{b_3 - a_3 \gamma_2} \quad (\text{A.82})$$

which allows us to rewrite the third equation as

$$x_3 + \gamma_3 x_4 = \rho_3 \quad (\text{A.83})$$

where $\gamma_3 = \frac{c_3}{b_3 - a_3 \gamma_2}$ and $\rho_3 = \frac{r_3 - a_3 \rho_2}{b_3 - a_3 \gamma_2}$.

We can then reiterate this procedure again and again until we have reduced the initial system in the following, equivalent, system

$$\begin{bmatrix} 1 & \gamma_1 & 0 & 0 & \cdots & 0 \\ 0 & 1 & \gamma_2 & 0 & \cdots & 0 \\ 0 & 0 & 1 & \gamma_3 & \cdots & 0 \\ \vdots & \vdots & \ddots & \ddots & \ddots & \vdots \\ 0 & 0 & \cdots & \ddots & 1 & \gamma_{n-1} \\ 0 & 0 & \cdots & \cdots & 0 & 1 \end{bmatrix} \begin{bmatrix} x_1 \\ x_2 \\ x_3 \\ \vdots \\ x_{n-1} \\ x_n \end{bmatrix} = \begin{bmatrix} \rho_1 \\ \rho_2 \\ \rho_3 \\ \vdots \\ \rho_{n-1} \\ \rho_n \end{bmatrix} \quad (\text{A.84})$$

where

$$\gamma_i = \begin{cases} \frac{c_1}{b_1}, & i = 1, \\ \frac{c_i}{b_i - a_i \gamma_{i-1}}, & i = 2, \dots, N \end{cases} \quad \rho_i = \begin{cases} \frac{r_1}{b_1} & i = 1 \\ \frac{r_i - a_i \rho_{i-1}}{b_i - a_i \gamma_{i-1}}, & i = 2, \dots, N \end{cases} \quad (\text{A.85})$$

It is now elementary found with a backward recursion the explicit solution of x , which is given by:

$$x_i = \begin{cases} \rho_n, & i = n \\ \rho_i - \gamma_i \rho_{i+1}, & i = n-1, n-2, \dots, 1 \end{cases} \quad (\text{A.86})$$

Appendix B

Python Code

```
#Import all the packages and the functions that we need
import multiprocessing
from multiprocessing import Pool
import numpy as np
import scipy
from scipy.stats import truncnorm
import matplotlib.pyplot as plt
import random
import networkx as nx
from nxviz import CircosPlot
import math
import statistics as st

#Generate the first time of an HPP of intensity _lambda
def Activation(_lambda):
    n=random.random()
    event_time=-math.log(1.0-n) / _lambda
    return event_time

#Given a dictionary and a value, return the key correspondent to that value
def get_key(dict,val):
    for key, value in dict.items():
        if val == value:
            return key

#Given the states and the activation/deactivation' rates of the edges,
#compute the parameter of the competing process. If either the states or the
#rates of edges aren't given, initialize them as all deactivated edges and
#all equal to 1 rates.
def parcompetition(G,edstates,edrates,mu):
    if edstates=={}
        for ed in G.edges():
            edstates[ed]=-1
```

```

    if edrates=={}:
        for ed in G.edges():
            edrates[arco]=1
    l=0
    for ed in G.edges():
        l=l+edrates[ed]*((1-edstates[ed])/2+ +mu*((edstates[ed]+1)/2)
    return [l,edstates,edrates]

#Establish which activation/deactivation has caused the first ring
def firstevent(G,edstates,edrates,mu):
    l=parcompetition(G,edstates,edrates,mu)[0]
    effrates={}
    effprob=[]
    j=0
    r=random.random()
    for ed in G.edges():
        if edstates[ed]==1:
            effrates[ed]=[j,mu/l]
        else:
            effrates[ed]=[j,edrates[arco]/l]
        j=j+1
    effprob=list(effrates.values())
    prob=[]
    for el in effprob:
        prob.append(el[1])
    j=0
    while r>0:
        r=r-prob[j]
        j=j+1
    el=[j-1,prob[j-1]]
    edstates[get_key(effrates,el)]=edstates[get_key(effrates,el)]
    return get_key(effrates,el)

#Given a node n, the states of the nodes and the activated edges,
#return the list of n's infected contacts
def infneigh(G,nodestates,acted,node):
    listin=[]
    for n in G.neighbors(node):
        if nodestates[n]==1 and ((n,node) in acted or (node,n) in acted):
            listin.append(n)

```

```

    else:
        pass
    return listin

#Given the states of the nodes, the list of activated edges,
#the transmissibility and the recovery rate of the virus,
#the current time and the time-interval from the last event,
#establish which events happen and keep track of those events
def modnodestates(G,nodestates,nodestory,acted,Dt,alpha,beta,t):
    for n in G.nodes():
        if nodestates[n]==1:
            r=random.random()
            if r<Dt*beta:
                nodestates[n]=0
                nodestory[n].extend(['Recovered',t])
            else:
                pass
        elif nodestates[n]==-1:
            l=infneigh(G,nodestates,acted,n)
            m=len(l)
            r=random.random()
            if r<alpha*m*Dt:
                nodestates[n]=1
                i=random.choice(l)
                nodestory[n].extend(['Infected',t])
                nodestory[i].extend(['Infect',t])
            else:
                pass
    return

#Compute the generation time from the nodes' story
def compgentime(nodestory):
    listgtimes=[]
    for n in nodestory.keys():
        l=len(nodestory[n])
        if l <=2:
            pass
        else:
            gentimes=[]
            for t in range(3,l+1,2):
                gentimes.append(nodestory[n][t]-nodestory[n][1])

```

```

        listgtimes.append(st.mean(gentimes))
    if listgtimes==[]:
        pass
    else:
        print(st.mean(listgtimes))
        return(st.mean(listgtimes))

#Compute the number of infectious caused by the first infector i
def comprn(nodestory,i):
    n=((len(nodestory.get(i)))/2)-1
    print(n)
    return n

#Given all the parameters, simulate an epidemic starting from a single
infected and until the end of the spreading
def epidemic(G,pos,i0,edrates,mu,alpha,beta):
    nodestates=
    edstates=
    t=0
    intert=0
    acted=[]
    nodestory=
    n=len(G.nodes())
    I=[1]
    T=[0]
    S=[n-1]
    s=99
    i=1
    R=[0]
    l=parcompetition(G,estates,edrates,mu)[0]
    edstates=parocompetition(G,edstates,edrates,mu)[1]
    edrates=parcompetition(G,edstates,edrates,mu)[2]
    for node in G.nodes:
        if node==i0:
            nodestates[node]=1
            nodestory[node]=['Infected',t]
        else:
            nodestates[node]=-1
            nodestory[node]=[]
    while s*i>0:

```

```

modnodstates(G,nodstates,nodestory,edacted,intert,alpha,beta,t)
intert=Activation(1)
t=t+intert
edactive=firstevent(G,edstates,edrates,mu)
if edactive in acted:
    acted.remove(edactive)
else:
    acted.append(edactive)
l=parcompetition(G,edstates,edrates,mu)[0]
i=list(nodstates.values()).count(1)
s=list(nodstates.values()).count(-1)
I.append(i)
S.append(s)
T.append(t)
R.append(n-s-i)
GT=compgentime(nodestory)
RN=comprn(nodestory,i0)
plt.plot(T, S, color='r', label='S')
plt.plot(T, I, color='g', label='I')
plt.plot(T, R,color='b',label='R')
plt.xlabel("Time in unit time")
plt.ylabel("Number of individual in each compartment")
plt.title("Susceptibles,Infectious and Recovered")
plt.legend()
plt.grid()
plt.show()

return [nodstates,edstates,acted,t, GT, RN, s, nodestory]

#Choose which graph we will use
G=nx.erdos_renyi(100,0.14)
#G=nx.barabasi_albert(100,7)

#Collect all in one function
def main():
    i0=random.randint(0,99)
    edrates={} #Here we establish which rates we want
    mu=24
    alpha=1
    beta=0.06

```

```

h=epidemic(G,pos,i0,edrates,mu,alpha,beta)
t=h[3]
GT=h[4]
RN=h[5]
s=h[6]
return [t,GT,RN,s]

#In the following we present the code which allows to compute the
(mean) RN(t), GT(t) to vary of t from a list of nodes' stories liststories
liststories=[{},...,{},...]

#Compute RN averaging only in a specified list of nodes
def comprrnlist(list,nodestory):
    r=[]
    for i in list:
        if len(nodestory[i])<2:
            pass
        else:
            h=(len(nodestory[i])/2)-1
            r.append(h)
    return st.mean(r)

#Compute GT only in (a neighbour of) a specified day d
def gtime(d,nodestory):
    excl=[]
    dict={}
    if d==0:
        output=compgentime(nodestory)
    else:
        for i in nodestory.keys():
            if len(nodestory[i])<4 or d-7<nodestory[i][1]<d+7:
                excl.append(i)
        list=list(set(list(nodestory.keys()))-set(excl))
        for el in list:
            dict[el]=nodestory[el]
        output=compgentime(nodestory)
    return output

```

```

#Consider together all the stories and compute the average values
of GT(t)'s to varying of tpop=[]
for nodestory in liststories:
    l1=[]
    d={}
    for i in range (100):
        if len(nodestory[i])<2:
            pass
        else:
            l1.append(nodestory[i][1])
    b=int(max(l1))
    for i in range(b+1):
        d[i]=gtime(i,nodestory)
    pop.append(d)

super_dict=
listvalues=[]
for d in pop:
    listvalues.extend(list(d.keys()))
reallistvalues=list(set(listvalues))
for i in reallistvalues:
    gt=[]
    for d in pop:
        if i in d.keys():
            gt.append(d[i])
        else:
            pass
    for el in gt:
        if el==None:
            gt.remove(el)
    if gt==[]:
        pass
    else:
        super_dict[i]=st.mean(gt)
print(list(super_dict.keys()))
print(list(super_dict.values()))

```

```

#Consider together all the stories and compute the average values
of RT(t)'s to varying of t
pop=[]
for nodestory in listadizionariV:
    l1=[]
    a=[]
    for i in range(100):
        if len(nodestory[i])<2:
            pass
        else:
            a.append(nodestory[i][1])
            l1.append(i)
    b=int(max(a))
    d={}
    for num in range(b+1):
        s=[]
        for i in l1:
            if num<=nodestory[i][1] and nodestory[i][1]<num+1:
                s.append(i)
            else:
                pass
        d[num]=s
    p=
    for el in d.keys():
        if d[el]==[]:
            pass
        else:
            p[el]=comprrrnlist(d[el],dict)
    pop.append(p)
listvalues=[]
super_dict=
for d in pop:
    listvalues.extend(list(d.keys()))
reallistvalues=list(set(listvalues))
for i in reallistvalues:
    ri=[]
    for d in pop:
        if i in d.keys():
            ri.append(d[i])
        else:

```

```
        pass
    super_dict[i]=st.mean(ri)
print(list(super_dict.keys()))
print(list(super_dict.values()))
```


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