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Modelling and analysis of dynamical systems

LINMA2370
Project Part 1
30th October 2020

1 A simple model

Question 1

Following the assumptions, here is the resulting model :

$$\begin{cases} \dfrac{\mathrm{d}S}{\mathrm{d}t}(t) &= \mu N - \mu S(t) - \dfrac{\beta}{N} S(t) I(t) \\ \dfrac{\mathrm{d}I}{\mathrm{d}t}(t) &= -\mu I(t) + \dfrac{\beta}{N} S(t) I(t) - \gamma I(t) \\ \dfrac{\mathrm{d}R}{\mathrm{d}t}(t) &= -\mu R(t) + +\gamma I(t) \end{cases} \tag{1}$$

It results from different phenomenon to take into account :

- Births are denoted by μN and each new individual is considered as susceptible.
- Deaths are denoted by $\mu S(t)$, $\mu I(t)$, $\mu R(t)$ because the death rate is the same for each group. These individuals are removed from the corresponding group.
- Infected individuals who recover from the disease are denoted by $\gamma I(t)$. These individuals are removed from the infected group and added to the recovered group.
- Susceptible individuals who are infected by the disease by infected individuals are denoted by $\frac{1}{N}\beta S(t) I(t)$. Indeed, the population is mixed homogeneously thus $S(t)/N$ is the rate of contact of an infected individual with susceptible individuals and the transmission rate is β. Each infected individual will infect $\beta S(t)/N$ susceptible individuals at time t. These individuals are removed from the susceptible group and added to the infected group.

Question 2

We can express the system (1) using functions $f_i : \mathbb{R}^2 \to \mathbb{R}$ for $i \in \{1, 2, 3\}$:

$$\begin{cases} \dfrac{\mathrm{d}S}{\mathrm{d}t}(t) &= f_1(S(t), I(t)) \\ \dfrac{\mathrm{d}I}{\mathrm{d}t}(t) &= f_2(S(t), I(t)) \\ \dfrac{\mathrm{d}R}{\mathrm{d}t}(t) &= f_3(R(t), I(t)) \end{cases} \tag{2}$$

First, since one variable can be expressed as a function of the others ($S(t) + I(t) + R(t) = N$), we only need two ODE's.

Then, since the two first derivative $\dfrac{\mathrm{d}S}{\mathrm{d}t}(t)$ and $\dfrac{\mathrm{d}I}{\mathrm{d}t}(t)$ do not depend on the value of $R(t)$ and only depend on $S(t)$ and $I(t)$ (see equation (2)), the third ODE is the easiest to remove (with $R(t) = N - S(t) - I(t)$) :

$$\begin{cases} \dfrac{\mathrm{d}S}{\mathrm{d}t}(t) &= \mu N - \mu S(t) - \dfrac{\beta}{N} S(t) I(t) \\ \dfrac{\mathrm{d}I}{\mathrm{d}t}(t) &= -\mu I(t) + \dfrac{\beta}{N} S(t) I(t) - \gamma I(t) \end{cases} \tag{3}$$

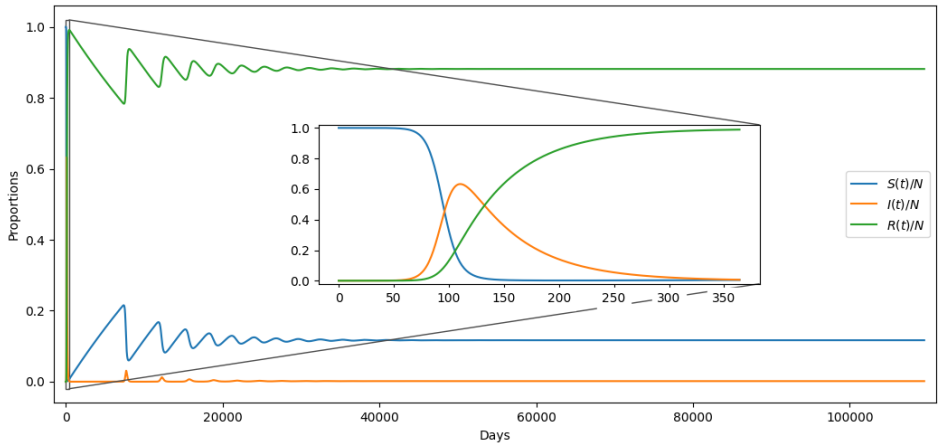
In fact, it is not needed to consider $R(t)$ as a state variable since we do not need it to simulate the behavior of the system.

Question 3

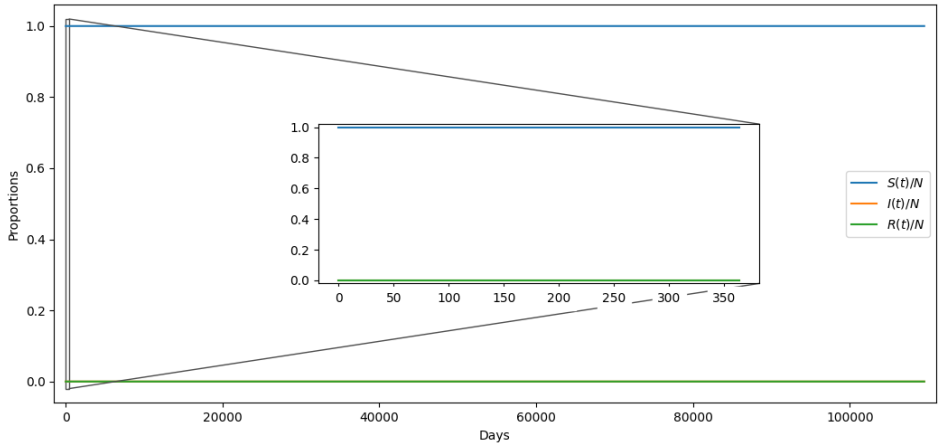
	N	μ [years^{-1}]	β [years^{-1}]	γ [years^{-1}]	T_{end} [years]	$[S_0, I_0, R_0]$
Simulation 1	10^{-7}	1/80	60	7	300	$[N - 10, 10, 0]$
Simulation 2	10^{-7}	1/80	21	23	300	$[N - 10, 10, 0]$

Table 1: Parameters of simulations

We simulate our system (1) with parameters in Table 1. The code for this question (and Question 8) is in the python file `project.py`.

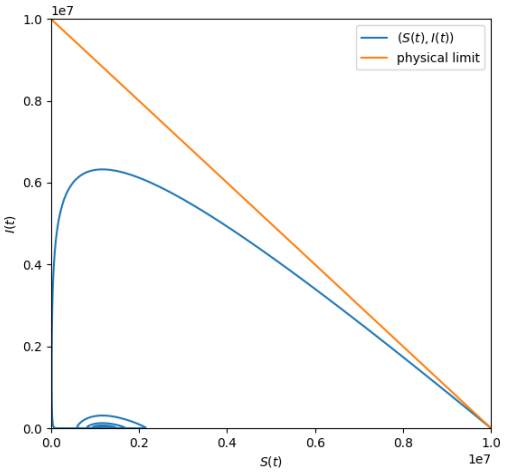


(a) Simulation 1

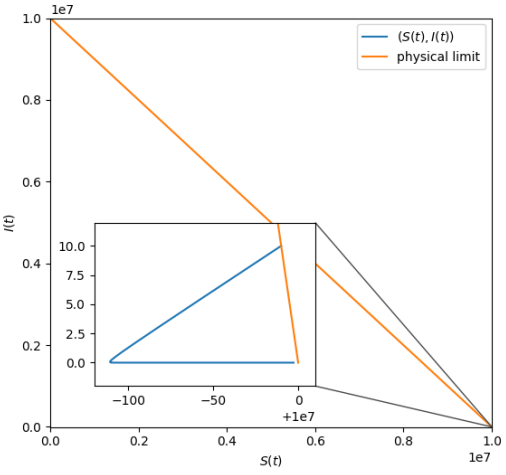


(b) Simulation 2

Figure 1: Evolution of the percentile of susceptible, infected and recovered individuals in the population



(a) Simulation 1



(b) Simulation 2

Figure 2: Phase plane of susceptible and infected individuals

Figure 1a is the result of the simulation for parameters at row "Simulation 1" in Table 1 and represents the

situation of an endemic equilibrium after many years.

Figure 1b is the result of the simulation for parameters at row "Simulation 2" in Table 1 and represents the situation when the disease disappears, i.e. variables $S(t)$, $I(t)$ and $R(t)$ reaches an equilibrium where no one is infected and the entire population becomes susceptible again.

In each figure, we zoom on the first year since a different behavior is visible, and we keep simulating for 300 years in order to visualize different equilibria of the system. We can also observe two very different behaviors for each scenario : we see that systems converge to a different equilibrium. We will cover this topic in questions 4 and 5.

Figures 2a and 2b represent phase plane for each scenario in Table 1. The orange line is the "physical limit", i.e. the physical condition that says that $S(t) + I(t) \leq N$ for any time t.

Question 4

We want to find values of $S^*, I^* \in \mathbb{R}$ such that, in equation (2) :

$$\begin{aligned} f_1(S^*, I^*) &= 0 \\ f_2(S^*, I^*) &= 0 \end{aligned} \tag{4}$$

There are two solutions to these equations. The first one is easy to find, assuming that $N \geq 0$ is constant, we have :

$$\begin{aligned} S^* &= N \\ I^* &= 0 \end{aligned} \tag{5}$$

Then, a less obvious solution (the *endemic equilibrium*) is given as follows, recalling that $R_0 = \dfrac{\beta}{\gamma + \mu}$:

$$\begin{aligned} S^* &= \frac{(\gamma + \mu)N}{\beta} = \frac{N}{R_0} \\ I^* &= \frac{\mu N}{\beta}\left(\frac{\beta}{\gamma + \mu} - 1\right) = \frac{\mu N}{\beta}(R_0 - 1) \end{aligned} \tag{6}$$

In order to discuss the physical existence of the endemic equilibrium (equation (6)), we can start from different physical conditions on the values of S^* and I^*. We will then derive some conditions related to R_0 which excludes this equilibrium. Indeed, we know that $0 \leq S^* \leq N$ and $0 \leq I^* \leq N$. Since then we have four physical conditions (using expressions in equation (6)) :

$$S^* \geq 0 \iff R_0 \geq 0 \tag{7}$$

$$S^* \leq N \iff R_0 \geq 1 \tag{8}$$

$$I^* \geq 0 \iff R_0 \geq 1 \tag{9}$$

$$I^* \leq N \iff R_0 \geq 1 + \frac{\beta}{\mu} \tag{10}$$

Conditions (7) and (10) are useless. Indeed R_0 is always positive and $R_0 \geq 1 + \dfrac{\beta}{\mu} \iff \mu^2 + \mu\gamma + \beta\gamma \leq 0$, which is impossible since $\mu, \gamma, \beta > 0$. However, we know from equivalences (8) and (9) :

$$R_0 < 1 \iff S^* > N \text{ and } I^* < 0 \tag{11}$$

Relation (11) tells us that, if $R_0 < 1$, it is impossible that we reach the endemic equilibrium, we will then reach the other equilibrium (equation (5)). Otherwise, if $R_0 \geq 1$, then the endemic equilibrium does not contradict any physical property.

In fact, we can prove that, if $R_0 \geq 1$, the first equilibrium is unstable.

Let us linearize the system (3) in order to check at the stability of each equilibrium. We define $\mathbf{x}(t) = (S(t)\ I(t))^T$, $\mathbf{x}^* = (S^*\ I^*)^T$, $\tilde{\mathbf{x}}(t) = \mathbf{x}(t) - \mathbf{x}^*$, $\mathbf{f}(\mathbf{x}(t)) = (f_1(\mathbf{x}(t))\ f_2(\mathbf{x}(t)))^T$ and the system becomes :

$$\begin{aligned}\frac{\mathrm{d}}{\mathrm{d}t}\tilde{\mathbf{x}}(t) &= \mathbf{A}\tilde{\mathbf{x}}(t) \\ &= \left.\frac{\partial \mathbf{f}}{\partial \mathbf{x}(t)}\right|_{\mathbf{x}^*} \tilde{\mathbf{x}}(t) \\ &= \begin{pmatrix} -\mu - \frac{\beta}{N}I^* & -\frac{\beta}{N}S^* \\ \frac{\beta}{N}I^* & \frac{\beta}{N}S^* - (\mu+\gamma) \end{pmatrix} \tilde{\mathbf{x}}(t)\end{aligned} \tag{12}$$

We look at the eigenvalues of $\mathbf{A}$ when we reach the equilibrium with no disease left. Matrix $\mathbf{A}$ becomes :

$$\mathbf{A} = \begin{pmatrix} -\mu & -\beta \\ 0 & \beta - (\mu+\gamma) \end{pmatrix} \tag{13}$$

an upper diagonal matrix with eigenvalues $\lambda_1 = -\mu < 0$ and $\lambda_2 = \beta - (\mu+\gamma)$. We see that $\lambda_2 < 0 \iff \beta - (\mu+\gamma) < 0 \iff R_0 < 1$. In other words, the equilibrium $(S^*, I^*) = (N, 0)$ is unstable if and only if R_0 is greater or equal than 1, i.e. when the endemic equilibrium can be reached.

We can also prove that the endemic equilibrium is stable in this case. The matrix $\mathbf{A}$ in equation (12) becomes :

$$\mathbf{A} = \begin{pmatrix} -\mu R_0 & -\beta R_0 \\ \mu(R_0 - 1) & 0 \end{pmatrix} \tag{14}$$

The characteristic polynomial of $\mathbf{A}$ is $p(\lambda) = \lambda^2 + \mu R_0 \lambda + \mu\beta R_0(R_0 - 1)$. Following Routh-Hurwitz criterion, this polynomial has only negative roots since coefficients are positive when $R_0 \geq 1$: the endemic equilibrium is always stable when we can reach it (i.e. when $R_0 \geq 1$), as we expected regarding Figures 1a and 1b.

Question 5

First, we can affirm that the equivalence (11) tells us that an epidemic occurs only when R_0 is greater or equal than 1. We could then suppose that, if an epidemic is well modeled by the system (1), then we would want to have a value of R_0 less than 1 in order to avoid an epidemic equilibrium, and thus make the number of infected people decreasing. In fact, we would be guaranteed to be in this scenario. Thus we can think that value of R_0 is crucial in epidemics management.

Then, let us focus on an interpretation of R_0. The value R_0 is called the basic reproduction number, it's the expected secondary infected individuals caused by one single infected people in a entire susceptible population.

In our model $R_0 = \frac{\beta}{\mu+\gamma}$ and, in order to interpret these value, we need to remember that μ is the rate of death which means that the average lifetime of individuals is $1/\mu$ (for example an average lifetime of 80 years in Table 1 in Question 3). Similarly, γ is the rate of recovery and $1/\gamma$ is the average time of contamination (for example approximately 6 and 17 days in in Table 1 in Question 3). The rate of individuals who are not anymore infected (because they are dead or recovered from the disease) is equal to $\mu + \gamma$ and thus the average time of being infected is equal to $\frac{1}{\mu+\gamma}$.

We also know that β is the rate of contamination a susceptible individual when a contact occurs. By equation 1, We had that there are $\frac{1}{N}\beta S(t)I(t)$ susceptible individuals who become infected a each time t. If the whole population is susceptible and there is only one infected individual, these one will infected approximately β individuals at each time t.

Thus, if a single infected individual is infected during on average $\frac{1}{\mu+\gamma}$ years and infects approximately β individuals each year, he will infect on average $\frac{\beta}{\mu+\gamma}$ individuals in total (which correspond to the value R_0).

We can actually observe the equilibrium with no diseases left (equation (5)) in Figure 1a with $(S^*/N, I^*/N) = (1, 0)$ and the endemic equilibrium (equation (6)) in Figure 1b with $(S^*/N, I^*/N) \approx (0.117, 0.001)$.

Since we proved in Question 4 that we have an endemic equilibrium if and only if $R_0 \geq 1$, we can verify that, in the scenario represented in Figure 1a $R_0 \geq 1$ and, in the scenario represented in Figure 1b, $R_0 < 1$. And, indeed, in the first case $R_0 \approx 8.556$, and in the second case $R_0 \approx 0.913$.

2 Stratified Age Groups

Question 6

First, we can express our system (3) with 3 stratified age groups as a *compartmental* system. In order to lighten the indices in the equations, we define our nine variables to model the system (with $S_i(t)$ the number of susceptible people in group i at time t, $I_i(t)$ the number of infected people in group i at time t and $R_i(t)$ the number of recovered people in group i at time t) :

$$\begin{aligned} x_1(t) &= S_1(t) \quad x_4(t) = I_1(t) \quad x_7(t) = R_1(t) \\ x_2(t) &= S_2(t) \quad x_5(t) = I_2(t) \quad x_8(t) = R_2(t) \\ x_3(t) &= S_3(t) \quad x_6(t) = I_3(t) \quad x_9(t) = R_3(t) \end{aligned} \tag{15}$$

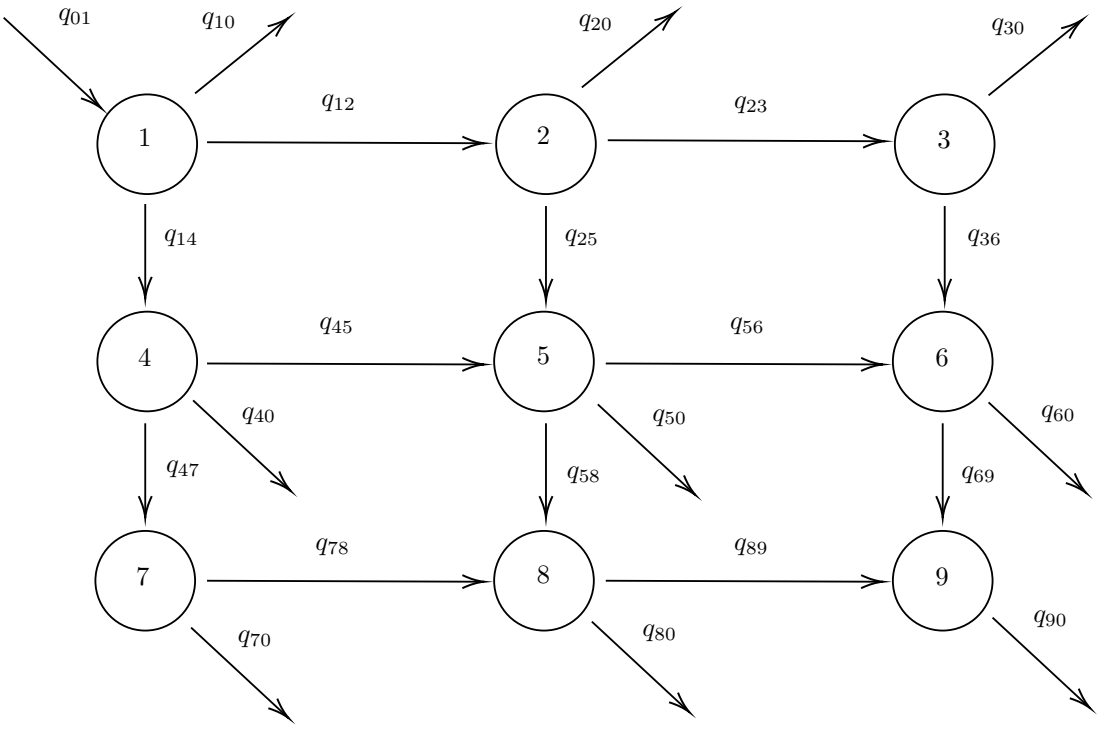


Figure 3: Compartmental system graph

Since then, we can express our system in the following way :

$$\frac{\mathrm{d}x_i}{\mathrm{d}t}(t) = \sum_{j=0}^{9} q_{ji}(t) - \sum_{j=0}^{9} q_{ij}(t) \tag{16}$$

with $q_{ij}(t)$ the flow from compartment i to compartment j with $i, j \in \{1, \ldots, 9\}$, and q_{i0}, q_{0i} respectively the output flow from compartment i and the input flow into the compartment i.

Hence we precise the flow q_{ij} for $i, j \in \{0, \ldots, 9\}$ as follows.

The input :

$$q_{01}(t) = \mu N \tag{17}$$

From susceptible people :

$$\begin{aligned} &q_{10}(t) = \mu x_1(t) && q_{20}(t) = \mu x_2(t) && q_{30}(t) = \mu x_3(t) \\ &q_{13}(t) = \frac{x_1(t)}{13} && q_{23}(t) = \frac{x_2(t)}{48} && \\ &q_{14}(t) = \frac{x_1(t)}{N} \sum_{i=1}^{3} \beta_{i1} x_{3+i}(t) && q_{25}(t) = \frac{x_2(t)}{N} \sum_{i=1}^{3} \beta_{i2} x_{3+i}(t) && q_{36}(t) = \frac{x_3(t)}{N} \sum_{i=1}^{3} \beta_{i3} x_{3+i}(t) \end{aligned} \tag{18}$$

From infected people :

$$\begin{aligned} &q_{40}(t) = \mu x_4(t) \qquad q_{50}(t) = \mu x_5(t) \qquad q_{60}(t) = \mu x_6(t) \\ &q_{45}(t) = \frac{x_4(t)}{13} \qquad q_{56}(t) = \frac{x_5(t)}{48} \\ &q_{47}(t) = \gamma x_4(t) \qquad q_{58}(t) = \gamma x_5(t) \qquad q_{69}(t) = \gamma x_6(t) \end{aligned} \tag{19}$$

From recovered people :

$$\begin{aligned} &q_{70}(t) = \mu x_7(t) \qquad q_{80}(t) = \mu x_8(t) \qquad q_{90}(t) = \mu x_9(t) \\ &q_{78}(t) = \frac{x_7(t)}{13} \qquad q_{89}(t) = \frac{x_8(t)}{48} \end{aligned} \tag{20}$$

Formulas of those flows will be explained in Question 7. We can represent the compartmental system as the diagram represented in Figure 3.

Question 7

The following state space model (equation (21)) is the direct consequence of equation (16) with flows in equations (17), (18), (19) and (20) :

$$\begin{cases} \frac{\mathrm{d}S_1}{\mathrm{d}t}(t) = \mu N - \mu S_1(t) - \frac{S_1(t)}{N}\sum_{j=1}^{3}\beta_{j1}I_j(t) - \frac{1}{13}S_1(t) \\ \frac{\mathrm{d}S_2}{\mathrm{d}t}(t) = -\mu S_2(t) - \frac{S_2(t)}{N}\sum_{j=1}^{3}\beta_{j2}I_j(t) + \frac{1}{13}S_1(t) - \frac{1}{48}S_2(t) \\ \frac{\mathrm{d}S_3}{\mathrm{d}t}(t) = -\mu S_3(t) - \frac{S_3(t)}{N}\sum_{j=1}^{3}\beta_{j3}I_j(t) + \frac{1}{48}S_2(t) \\ \frac{\mathrm{d}I_1}{\mathrm{d}t}(t) = -\mu I_1(t) + \frac{S_1(t)}{N}\sum_{i=1}^{3}\beta_{j1}I_j(t) - \gamma I_1(t) - \frac{1}{13}I_1(t) \\ \frac{\mathrm{d}I_2}{\mathrm{d}t}(t) = -\mu I_2(t) + \frac{S_2(t)}{N}\sum_{i=1}^{3}\beta_{j2}I_j(t) - \gamma I_2(t) + \frac{1}{13}I_1(t) - \frac{1}{48}I_2(t) \\ \frac{\mathrm{d}I_3}{\mathrm{d}t}(t) = -\mu I_3(t) + \frac{S_3(t)}{N}\sum_{i=1}^{3}\beta_{j3}I_j(t) - \gamma I_3(t) + \frac{1}{48}I_2(t) \\ \frac{\mathrm{d}R_1}{\mathrm{d}t}(t) = -\mu R_1(t) + \gamma I_1(t) + \frac{1}{13}R_1(t) \\ \frac{\mathrm{d}R_2}{\mathrm{d}t}(t) = -\mu R_2(t) + \gamma I_2(t) + \frac{1}{13}R_1(t) - \frac{1}{48}R_2(t) \\ \frac{\mathrm{d}R_3}{\mathrm{d}t}(t) = -\mu R_3(t) + \gamma I_3(t) + \frac{1}{48}R_2(t) \end{cases} \tag{21}$$

We can verify in equation (21) that $\sum_{i=1}^{3}\frac{\mathrm{d}S_i}{\mathrm{d}t}(t) + \frac{\mathrm{d}I_i}{\mathrm{d}t}(t) + \frac{\mathrm{d}R_i}{\mathrm{d}t}(t) = 0$, i.e. the population remains constant.

Obviously, SIR model equations for each group look very similar to equations of our first model (equation 1) with some differences :

- Births are added in the susceptible group 1 given that babies are in the first stratified age group.
- We consider a homogeneous population regarding ages thus there is 1/13 (resp. 1/48) of the group of individuals between 0 and 12 years old (resp. 13 and 60 years old), who go to the next group due to ageing each year.
- There are different transmission rates between the different groups. The transmission rate for a infected individual for group j to a susceptible individual for group i is denoted by β_{ji}. With the same reasoning with each group as in Question 1, there are now $(1/N)S_i(t)\sum_{j=1}^{3}\beta_{ji}I_j(t)$ individuals of group i who become infected at each time by infected individuals of the 3 groups.

The point here is to model the whole population with these nine state variables but if we are only interested by the susceptible and infected individual it could be possible to model these groups with only six state variables in a similar way as in Question 2.

Question 8

We will simulate equations 21 with similar parameters than in the Question 3 :

- Size population N : 10^7
- Initial situation of the population $P(0) = (S(0), I(0), R(0) : (N - 10, 10, 0)$
- Initial partition between stratified age groups $P_1(0) = \frac{13}{80}P(0)$, $P_2(0) = \frac{48}{80}P(0)$, $P_3(0) = \frac{20}{80}P(0)$ (initial homogeneous aged population between 0 and 80 years)
- Time interval $[0, T_{end}]$ with T_{end} : 100 [years^{-1}]
- Birth rate μ : $\frac{1}{80}$ [years^{-1}]
- Death rate μ : $\frac{1}{80}$ [years^{-1}] (no matter if they are susceptible, infected, recovered, young, old)
- Recovery rate γ : 7 [years^{-1}]
- Transmission rates β_{ij} [years^{-1}] from a group i to a group j :

$$\begin{pmatrix} \beta_{11} & \beta_{12} & \beta_{13} \\ \beta_{21} & \beta_{22} & \beta_{23} \\ \beta_{31} & \beta_{32} & \beta_{33} \end{pmatrix} : \quad \underbrace{\begin{pmatrix} 60 & 60 & 60 \\ 60 & 60 & 60 \\ 60 & 60 & 60 \end{pmatrix}}_{\text{(simulation 1)}} \qquad \underbrace{\begin{pmatrix} 60 & 0 & 0 \\ 0 & 60 & 0 \\ 0 & 0 & 60 \end{pmatrix}}_{\text{(simulation 2)}}$$

  where 60 [years^{-1}] was the transmission rate of the first simulation in Question 3.

The code for this question (and Question 3) is in the python file `project.py`.

Figures 4, 5, 6 show five subplots : on the first row, the cumulative percentage of susceptible, infected and recovered individuals from each group in the population and on the second row, the evolution of the percentage of susceptible, infected and recovered individuals in the whole population and the evolution of the percentage of infected individuals in each group.

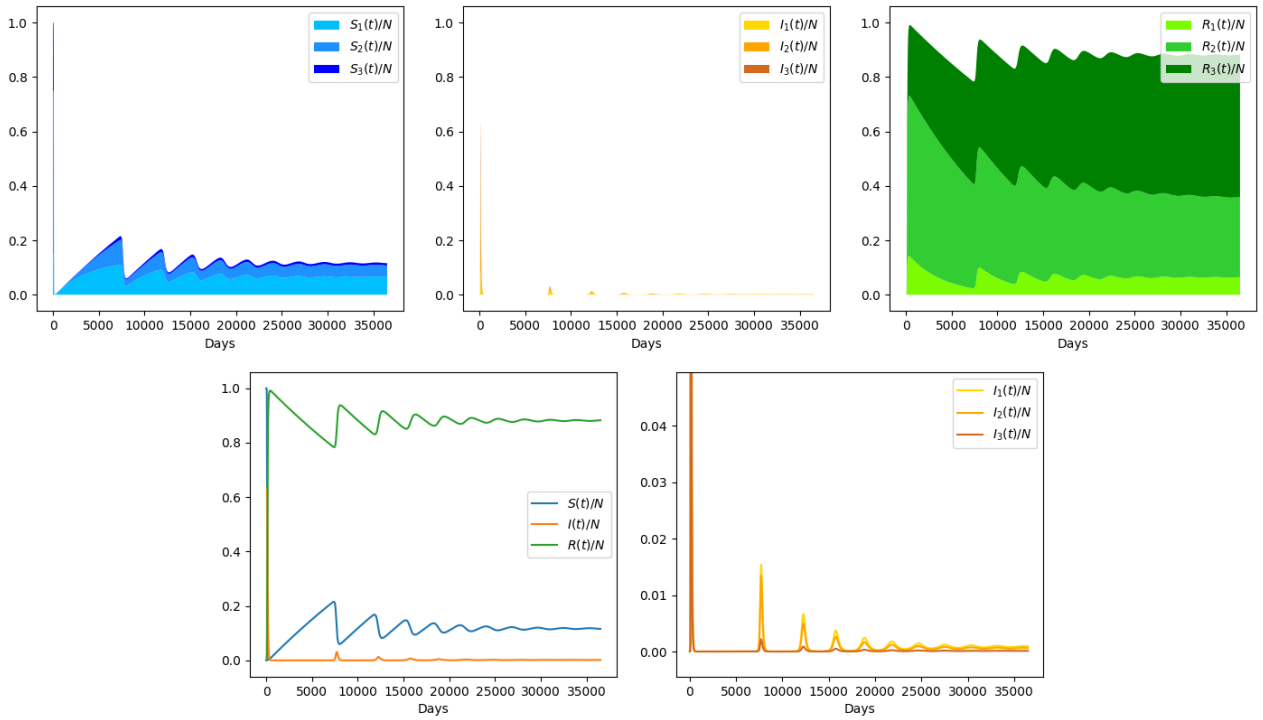


Figure 4: Simulation 1

Figure 4 shows the first simulation where individuals can infect individual from each same stratified age group with the same transmission rate. It actually corresponds to the first simulation in Question 3 because there is no difference between individuals from different groups and they are mixed.

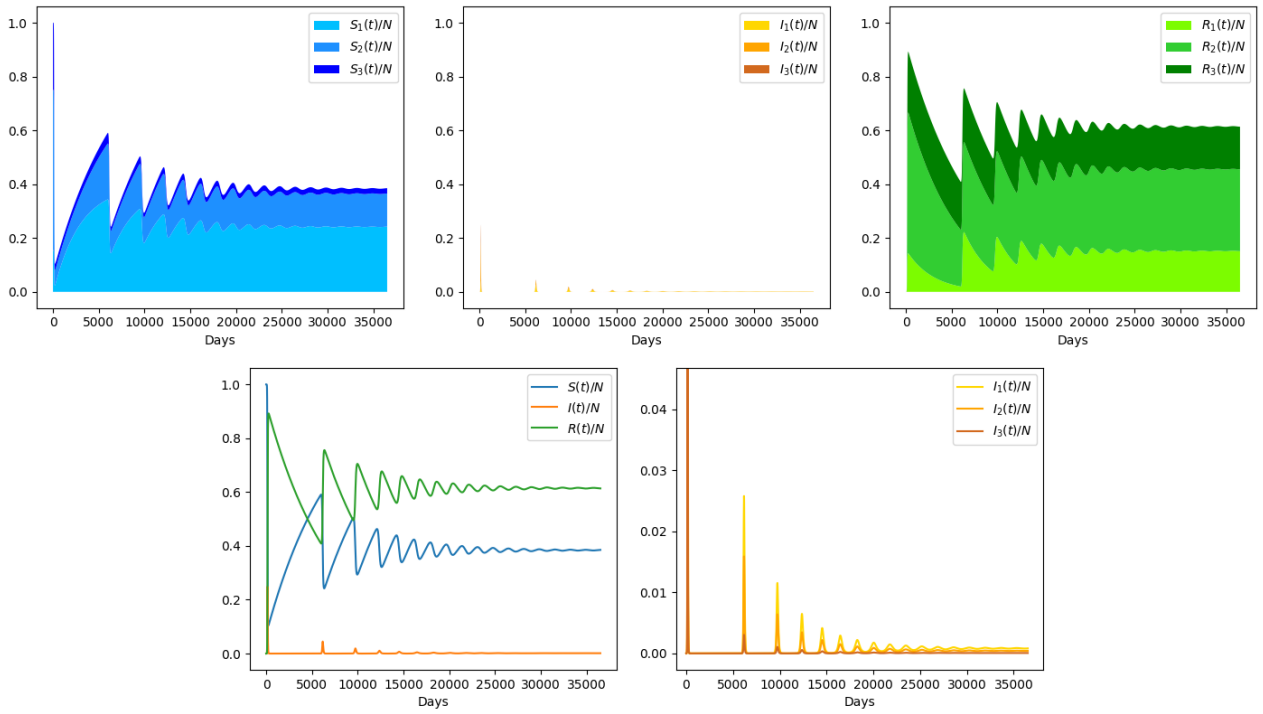


Figure 5: Simulation 2

Figure 5 shows the second simulation where the lifetime $(1/\mu)$ is divided by four.

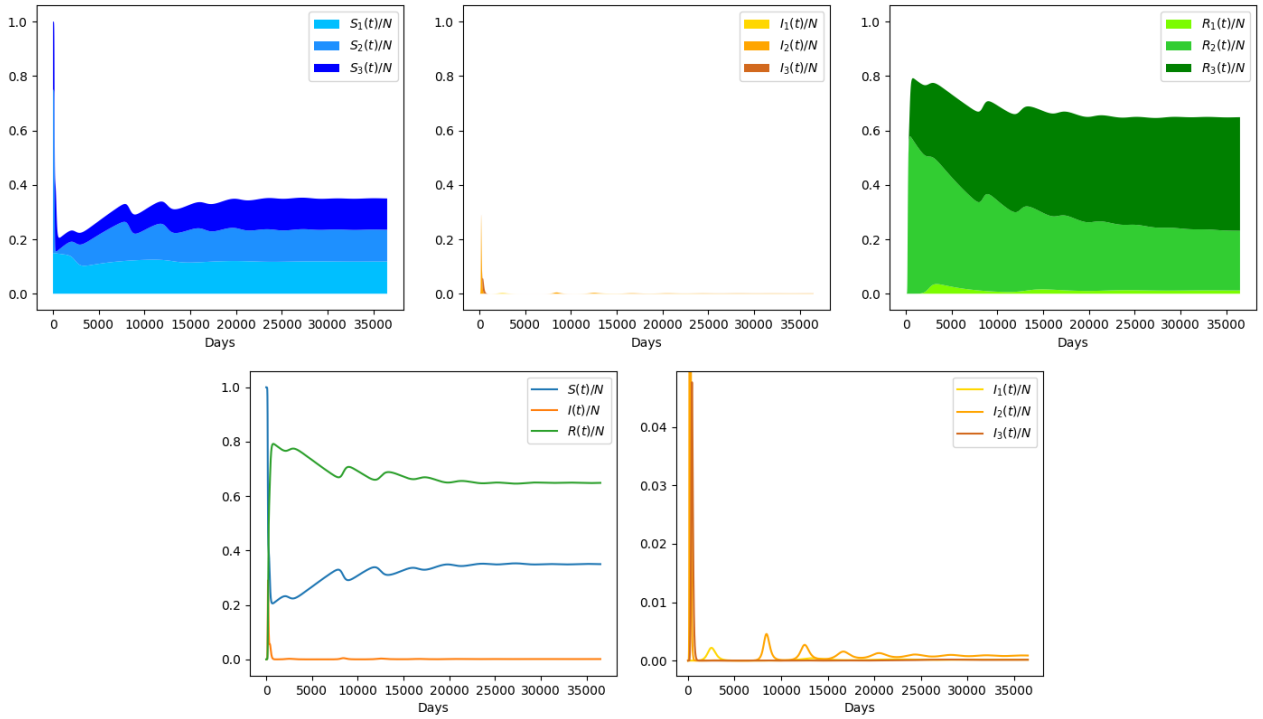


Figure 6: Simulation 3

Figure 6 shows the third simulations with the initial parameters but infected individuals can only infect indi-

viduals from their group (i.e. $\beta_{ij} = 0$ if $i \neq j$).

Obviously, it is very restrictive to make these 3 simulations, there are a lot of parameters which can vary. We will limit us to not too complex situations that we can handle.

Speaking about differences between the first simulation and the second, since rates of "group changing" (i.e. 1/13 and 1/48) remain constant, then, if we choose μ such that it is greater than these rates, we will observe than people get old slower than they die. The result is that, for recovered group, the subgroup of old people will tend to a smaller subgroup than the other ones. It's more complex for susceptible and infected groups : even if individuals died later, there are less old individuals in susceptible and infected groups. Indeed, there are more younger susceptible individuals because births are added in these group and a old susceptible individual corresponds to a individual who succeeds to not be infected during more than 60 years. The partition of infected individuals is a direct consequence of the observation : if the transmission rate is the same for each individual regardless of their age and if their are more young susceptible individuals, there will be more young infected individuals. We can observe that on figures 4 and 5.

Then, we can focus on differences in behaviors for different transmission rates β_{ij}. The result is that curves of infections on Figure 6 are more wider since the disease is less spreaded than in the first case. We also observe less oscillations on the fourth plot of Figure 6 than on the fourth plot of Figure 4 : the epidemic is less intense.

We also observed that, for some set of parameters, the `numpy` function `odeint` does not achieve to solve the system, probably due to numerical issues.

3 Epidemics on networks

Question 9

First, let us interpret the networks provided in the statement. What rule is it ?

The first network represents the fact that every person is allowed to have some contacts with a transmission risk with 5 other people.

The second network represents the rule according to which the population must group in bubbles of 20 people. Here, we make the assumption that each person in each bubble strictly respects the rule. Hence, the network consists in 50 disconnected K_{20} graphs.

The third network is similar to the second (bubbles of 20 people), except from the fact that each bubble is linked since two people in each bubble has a contact with transmission risk with one another bubble, the graph is thus a cycle of K_{20} graphs.

The fourth network is a more realistic model. There still bubbles (of 15 people), and the respect of this rule is randomly distributed : close contacts vary from 5 close contacts to 19 close contacts.

Then, we will analyse and discuss the results of the stochastic simulations. In order to do that, we will focus on some key results :

- $\overline{I_{\max}}$: the empirical mean of maximum number of infected people during the epidemic,
- $\overline{t_{10}}$: the empirical mean of time from which the number of infected people becomes again less than 10 % of the whole population,
- The spreading of the stochastic simulations.

The aim of the two first key of analysis is obvious : we want to measure the intensity of the epidemic. The last key result, the spreading of the stochastic simulations, mainly, is analysed for two reasons. First, a less spread simulation will lead to more revealing values of $\overline{I_{\max}}$ and $\overline{t_{10}}$ since we do the same number of simulations for all networks. Moreover, it may be important to know whether the epidemic situation can be reliably simulated. In crisis management circumstances, we could assume that it would be important to know what comes next. Note that, in the following tables (tables 2 and 3), + and − respectively means that there are a lot and not a lot of spreading.

Our results for 50 simulations for our networks are presented in Table 2, with 0.5 % of the population initially infected. Note that these results are highly related to the shape of curves simulated (especially the spreading that we see on the plots). Since they are provided in the statement, we decided not to directly analyse them.

	$\overline{I_{\max}}$	$\overline{t_{10}}$	Spreading
Network 1	753.600	285.523	−−
Network 2	89.260	154.112	−
Network 3	250.680	262.292	++
Network 4	326.920	276.387	++

Table 2: Analysis of the four networks for 0.5% of initially infected people

We see that different measures lead to very different results.

Speaking of the value of $\overline{I_{\max}}$, the measure represented in the second network is by far the better measure against an hospital congestion for example, but it is sufficient to make some links between bubbles, even one unique link in network 3, to increase dramatically the value of $\overline{I_{\max}}$. More links (network 4) leads to an even greater value of $\overline{I_{\max}}$. Finally, with measures that leads to a very interconnected graph (network 1), the situation would be tragic since more or less than 75 % of the population would be infected at the peak of the epidemic.

If we focus on the value of $\overline{t_{10}}$, we observe some values that contradict the fact that the more intense the epidemic, the sooner it ends. Indeed the greater the value of $\overline{I_{\max}}$, the greater the value of $\overline{t_{10}}$. We also observe that this value does less vary than $\overline{I_{\max}}$. The strict bubble strategy remains the best measure by far.

The spreading of the simulations is also really different from one measure to another. We could explain results in Table 2 by the fact that, the more there are links, the more random events there are, and thus the more possible realisations there are.

	$\overline{I_{\max}}$	$\overline{t_{10}}$	Spreading
Network 1	766.780	285.040	$--$
Network 2	587.040	275.73	$-$
Network 3	703.700	284.457	$++$
Network 4	644.740	282.685	$++$

Table 3: Analysis of the four networks for 5% of initially infected people

We will know check whether these values are really different if we multiply by 10 the number of infected people : 5 % is initially infected. Results are shown in Table 3.

The spreading does not change. The worst situation remains the same. However, we observe that situations with "bubble" strategy, even with a strict respect of measures (network 2), are really bad. In fact, since there are a high probability that the whole bubble become infected if one infected people is in it, it is logical that this strategy does not work anymore if there are a lot of initially infected people.

Question 10

The aim is to imagine an heterogeneous measure adapted to the age of the individuals. In order to do that, we want to consider different measures for each age group.

We considered a population with 1000 nodes, composed of 4 groups :

- Childrens : 200 people aged from 0 to 12 years,
- Young people : 200 people aged from 13 to 25 years,
- Adults : 400 people aged from 26 to 60 years,
- Old people : 200 people aged from 61 years to natural death.

The measures are described as following :

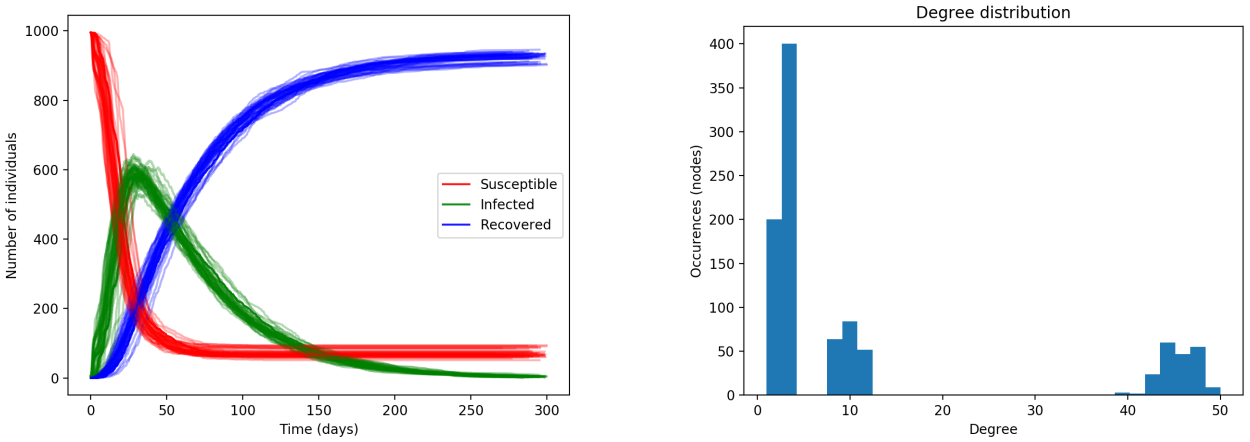
- The childrens have to go to school and it is too complicated to consider that they respect any sanitary measure. We consider 4 schools of 50 childrens, with more or less than 35 links per child with childrens in his school,
- We consider that young people need a bigger "bubble" in order to keep a healthy state of mind. We consider thus 20 bubbles of 10 people. However, some young people do not strictly respect this rule, and we added 50 links between random people in this age group,
- The adults must respect bubbles of 4 persons, we have therefore 100 bubbles of 4 people. Adults strictly respect rules but they need to see their kids. Since then, in each bubble, two different people sees two different childrens, and a third person sees an young adult,
- Old people are very limited since the epidemic is more dangerous for them. If they are in a relationship, they stay together, and if they are alone they can see one another old people. Thus each old people is in a 2-people bubble. Also, they are allowed to keep contact with one adult : each 2-people bubble of old people is linked with one 4-people adults bubble.

We consider that only the topology of the graph change (parameters remain the same, except for the initial number of infected people which is equal either to 0.5% or 5%), since then it has some sense to compare values of $\overline{I_{\max}}$ and $\overline{t_{10}}$ for our network with values in tables 2 and 3.

We constructed such a network in the file `network.py`, and the adjacency list is in `network_pers.dat`. We can use the file `epidemics_networks.py` provided in the statement to analyse the results.

We have $\overline{I_{\max}} = 599.720$ infected people and $\overline{t_{10}} = 284.398$ days for 0.5% of the population initially infected. And we have $\overline{I_{\max}} = 629.280$ infected people and $\overline{t_{10}} = 284.052$ days for 5% of the population initially infected. The information is never scattered. In comparison with values in tables 2 and 3, we see that this kind of measure is not really efficient : the epidemic is more intense than network 2, network 3 and network 4 but still better than network 1.

We can see on Figure 7a the 50 simulations for 5% of the population initially infected : it corroborates values found for $\overline{I_{\max}}$ and $\overline{t_{10}}$. Also, figures 7b and 8 provide information about the graph described above. We particularly see on Figure 8 that the network is heterogeneous, as we wanted heterogeneous measures.



(a) Stochastic simulations

(b) Degree distribution

Figure 7: Result of `epidemics_networks.py` for network described in `network_pers.dat`

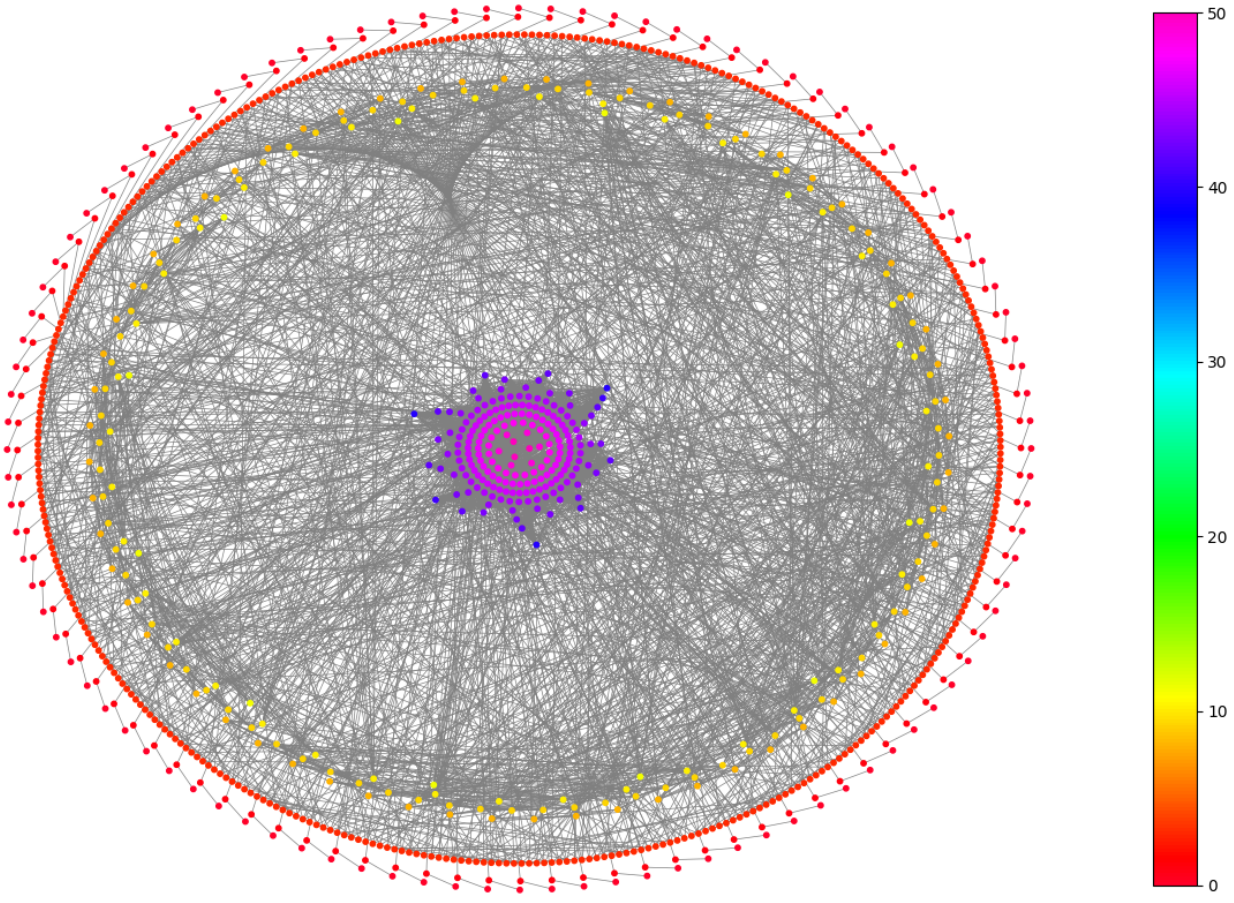


Figure 8: Representation of the heterogeneous network, colored by degree