

## Practice 4 – Epidemics

Instructor: *Augustin Chaintreau***N.B. :** Exercise levels are indicated as follows

( $\rightarrow$ ) “elementary”: the answer is not strictly speaking obvious, but it fits in a single sentence, and it is an immediate application of results covered in the lectures.

*Use them as a checkpoint: it is strongly advised to go back if the answer to one of these questions does not come to you in a few minutes.*

( $\curvearrowright$ ) “intermediary”: The answer to this question is not a simple application of results covered in class, it can be deduced from them with a reasonable effort.

*Use them as a practice: how far are you from the answer? Do you still feel uncomfortable with some of the notions? which part could you complete quickly?*

( $\curvearrowleft$ ) “tortuous”: this question requires either to manipulate an advanced notion or to follow a demonstration that is either long or inventive.

*Use them as an inspiration: can you answer any of them? does it bring you to another problem that you can answer or study further? It is advised not to spend too much time on it unless you have already covered everything else very well.*

**Exercise 1: Continuous epidemics in the  $S \leftrightarrow I$  case**

**Motivation** In this exercise, you will show that the final outcome in a epidemics with recovery to susceptible state depends on the parameter.

We consider a continuous (or fluid flow) model of an epidemic in a population, in the special case where nodes infect susceptible nodes with rate  $\beta$  and recover (*i.e.*, come back to the susceptible state) with rate  $\gamma$ . We denote by  $y(t)$  the fraction of the population of nodes that are infected. Note that the fraction  $x(t)$  of susceptible nodes satisfies  $x(t) = 1 - y(t)$ . According to our fluid flow assumption, both are real valued variables which increase and decrease continuously with time  $t$ .

Starting at time  $t = 0$  with a fraction  $y_0$ , the evolution of this epidemic may be modeled as the solution of the following differential equation:

$$\frac{dy}{dt} = \beta x \cdot y - \gamma y = \beta(1 - y) \cdot y - \gamma y .$$

1 ( $\rightarrow$ ) Find the solution of this differential equation for the initial condition  $y(t) = y_0$  at time  $t = 0$ .

2 ( $\rightarrow$ ) What is the limit behavior of the epidemics after a long time (*i.e.*, characterized by  $\lim_{t \rightarrow \infty} y(t)$ ) ? What is the role of  $y_0$ ?

**Exercise 2: Discrete Epidemics in the  $S \rightarrow I \rightarrow R$  case**

**Motivation** When a discrete epidemic spread on a graph with symmetric structure, we can relate its span using known properties of random graph. Here is an example for a model of  $S \rightarrow I \rightarrow R$  infection.

Discrete epidemics spread from one node to another following the edge of a graph. In a simple model of a  $S \rightarrow I \rightarrow R$  a node spends only one time slot in infectious state, in which the node may infect each of its neighbor independently with probability  $\beta$ . It is then entering the removed state where it does not interact any more with others.

For any finite graph  $G$  and probability  $\beta$ , it is clear that, starting from a single node  $u \in V$  infected, the network eventually reach a state where nodes are partitioned between removed nodes (which form a connected component  $C^{(\beta)} \subseteq V$  that contains  $i$ ) and all other nodes (possibly none of them if the epidemics reach everyone) are still susceptible. The main question is how large  $C^{(\beta)}$  can be, in particular in comparison with  $|V|$ . Note that it depends not only on  $\beta$  but also on the topology of the graph.

To make this notion more precise, we consider a family of graph  $G_n$  indexed by  $n = 0, 1, \dots$  with growing sizes (*i.e.*,  $|V_n| \rightarrow \infty$  as  $n$  grows). As an example  $G_n$  may be a graph of  $n$  nodes arranged according to some particular model, as seen below. We denote by  $R_n^{(\beta)}$  the connected component containing all removed node in the epidemic shown above with infection probability  $\beta$ , starting from a point chosen randomly.

We say that the sequence  $(\tilde{\beta}_n)_{n \geq 0}$  is an *epidemic threshold* for this family if we have:

- When  $\beta_n < \tilde{\beta}_n$ , then for the model described above, the epidemic is small (“it reaches a negligible fraction of the nodes”), formally defined as:

$$\frac{|R_n^{(\beta_n)}|}{|V_n|} \rightarrow 0 \text{ in probability (i.e., } \forall \varepsilon > 0, \mathbb{P} \left[ |R_n^{(\beta_n)}|/|V_n| > \varepsilon \right] \rightarrow 0 \text{ as } n \text{ grows large).}$$

- When  $\beta_n > \tilde{\beta}_n$ , then for the model described above, the epidemic is large (“it reaches a positive fraction of the nodes”), formally defined as:

$$\text{There exists } \delta > 0 \text{ such that } \forall n \geq 0, \mathbb{P} \left[ |R_n^{(\beta_n)}|/|V_n| > \delta \right] > \delta.$$

We will admit the following result on the connected component of random graph.

**Theorem 1.** Let  $G_n = (V_n, E_n)$  denote a uniform random graph where  $V_n = \{1, 2, \dots, n\}$  and  $E_n$  is a random subset of  $V_n$  such that, for any pair  $(u, v)$  ( $u, v \in V_n, u \neq v$ ),  $(u, v)$  is included in  $E_n$  independently and with probability  $p_n = \frac{\lambda}{N}$ .

Let  $C_n^{(1)}$  denote the size of the largest connected component in  $G_n$ . We have:

(i) If  $\lambda < 1$ , there exists  $A > 0$  such that  $\mathbb{P} \left[ C_n^{(1)} \geq A \ln(n) \right] \rightarrow 0$  as  $n \rightarrow \infty$ .

(ii) If  $\lambda > 1$ , then  $\forall \varepsilon > 0, \mathbb{P} \left[ \left| \frac{C_n^{(1)}}{n} - f_\lambda \right| \geq \varepsilon \right] \rightarrow 0$  as  $n \rightarrow \infty$ ,

where  $0 < f_\lambda < 1$  is the unique fixed point of the function  $x \mapsto \exp(-\lambda(1-x))$  on  $]0; 1[$

1 ( $\curvearrowright$ ) Let  $G_n$  be a complete graph with  $n$  nodes (*i.e.*, every pairs of nodes in  $G_n$  is connected). Show that if  $\beta_n < \frac{1}{N}$  then the epidemic is small (according to the definition above).

2 ( $\curvearrowright$ ) On the complete graph containing  $n$  nodes, we wish to estimate the probability that an epidemic starting in a random node reaches a positive fraction of nodes. Formally speaking can you provide a general condition on  $(\beta_n)_{n \geq 0}$  such that (for a suitable choice of  $\delta \in ]0; 1[$  independent of  $n$ ),  $\mathbb{P} \left[ |R_n^{(\beta_n)}|/|V_n| > \delta \right]$ ?

(i) 1

(ii) 0 for any  $\delta > 0$

(iii)  $f_\lambda$  (for some choice of  $\lambda$ ).

How does the answer to the above question depends on  $\beta$ ? How does it depend on the choice of  $\delta$ ?

3 ( $\curvearrowright$ ) Let us now consider  $G_n^{(\pi)}$  to be a complete graph with some nodes that cannot be infected. Formally speaking,  $G_n^{(\pi)}$  will be a graph containing  $n$  nodes, where each node is tagged as “removed” with probability  $\pi > 0$  and all pairs of nodes that are not removed are connected, while all removed nodes are isolated.

Can you describe an epidemic threshold for  $G_n^{(\pi)}$ ?

4 ( $\curvearrowright$ ) Imagine now that for any  $n \geq 0$ , the graph  $G_n$  is not a complete graph but a uniform random graph such that each edge is present independently with probability  $p_n = \frac{\lambda}{N}$ . We will denote this sequence of graphs by  $G_n^{(p)}$ .

Can you describe an epidemic threshold for  $G_n^{(p)}$ ?