CASL - Lab16 - Epidemic processes

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Code developed in collaboration with Gensale Aurora (s303535).

1 Introduction

The aim of this lab is to simulate an epidemic process by means of Hawkes processes, firtsly in a regular manner, secondly considering the introduction of non pharmaceutical interventions.

2 First part

Each Hawkes process needs a root node to start, called ancestor. In order to simulate an epidemic scenario, we need more ancestors that start the infection at different times. In our case the arrival time of the ancestors is bounded from day $t = 0$ to $t = 10$, while the total simulation days are $t = 100$. Their arrival can be simulated according to a Poisson process of intensity $\sigma(t) = 20 * \mathbf{1}_{(t\in[0,10])}$. To increment the time when generating them, there is used the fertility function $h(t)$ to create τ that is a sort of "inter-arrival" time between two ancestors. Note that $h(t)$ can be generated according two different probability distribution: $\tau \sim U((0, 20))$ or $\tau \sim Exp(\lambda)$ with $\lambda = 1/10$. Also, at the time of the generation, a specific number of children, calculated as $children \sim Poisson(m)$ with $m = 2$, is associated to each ancestor.

For both the cases of $h(t)$ the number of ancestors generated is about 200.

Now that we have all the ancestors, we can start an Hawkes process for each of them. At the beginning of each step of the Hawkes process, we make the ancestor die with probability 2%, generating $u \sim U(0, 1)$ and if $u < death\_rate = 0.02$ than the ancestor is declared dead and cannot infect anyone anymore (no children generation). If it is still alive, we cycle over the number of children extracted from the Poisson at the generation time of the ancestor and, for each of them, we generate a new node object with number of children generated from the Poisson and the time τ of distance at which these children will be infected: $time\_infection\_children = time\_infection\_ancestor + \tau$. If $time\_infection\_children$ is larger that tne *time horizon* of the simulation, then we stop here, we return the ancestor and we start analyzing the further node. Otherwise, we start an Hawkes process for each of the child generated, in order to have a recursive logic in which every node can be considered as an ancestor with its tree of infections.

In figure 1 and 2 there are represented the evolution over time of the number of infected and dead nodes according to the specific distribution of $h(t)$, with their relative 95% confidence interval calculated over 10 runs. In the graphs can be seen that the number of infected generated from the exponential distribution is greater than the ones generated from the uniform, of about one order of magnitude in compliance with the nature of the two distinct $h(t)$. Note that in both cases, the line indicating dead nodes with its confidence interval can be barly seen because the number of dead nodes is much smaller than the number of infected ones.

3 Second Part

In the second part of the lab, our aim is to simulate the behaviour of the system when an epidemic process, modeled with Hawkes processes, is perturbated with the introduction of non pharmaceutical intervention after $t = 20$ days on a time horizon of $t = 365$ days.

The whole simulation, in general, remains the same, with the ancestor generation and the recursive recall of the hawkes process in order to treat each node infected as an ancestor that has its own tree of infections. The difference can be found inside the Hawkes process itself: after checking for the node to be alive, for each children of the ancestor, we check if the time of action (current time) is in the non pharmaceutical intervention stage (current time > 20). If so, we

calculate the strengthness of restrictions as:

$$\rho(t) = \sqrt{\frac{\#dead\_nodes}{\#infected\_nodes}}$$

Consequently, the costs will be calculated as:

$$cost(t) = \sum_{T<t} \rho(T)^2$$

The $\rho(t) \in (0, 1)$ parameter is used, then, to limit the number of infected:

- $\tau \sim Exp(\lambda)$ with $\lambda = \rho(t) * 1/10$ in order to generate new infected nodes more sparse over time;
- $children \sim Poisson(m * \rho(t))$ to generate less infected node in general.

The introduction of the $\rho(t)$ parameter, significantly change the behaviour of the infected/dead curve: in figure 3 there can be notice the, till time $t = 20$, the number of infected is growing exponentially because of the behaviour of $h(t)$. After that, the curve change concavity and starts to grow slower and the number of infected just double from $t = 20$ till $t = 365$, that means that the non pharmaceutical interventions actually help the population to avoid the infection, like keeping people in lockdown will impede them to meet (τ behaviour) and consequently the number of infections will be less (Poisson parameter behaviour).

In figure 4 there are represented the costs of the restrictions introduced by means of $rho(t)$: till time $t = 20$ they are zero, after that moment, they start not from zero because we already have some dead node, so $\rho(t) \neq 0$. The costs tends to grow because they are the cumulative sum of all the precedent days also because, logically, the more a store stay close because of the epidemic, the bigger are the damage for the finances of that store.

Notice that both figures 3 and 4 have a 95% confidence intervals calculated over 10 runs.

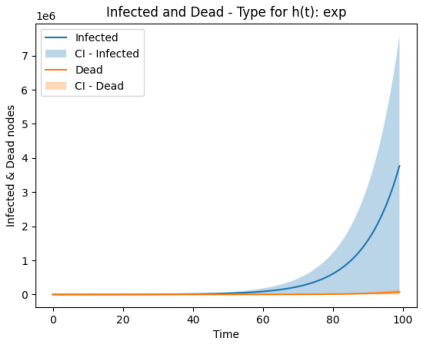

Figure 1: Evolution over time - 95% C.I.

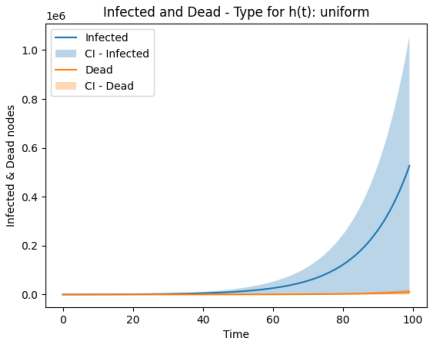

Figure 2: Evolution over time - 95% C.I.

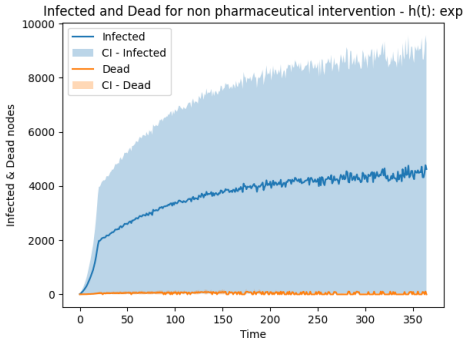

Figure 3: Evolution over time with non pharmaceutical intervention - 95% C.I.

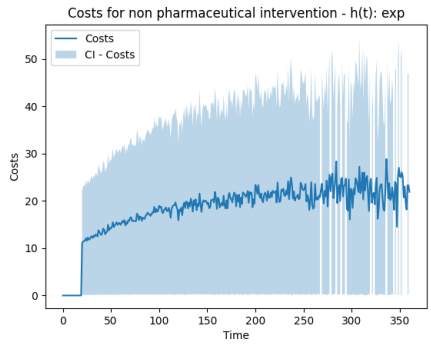

Figure 4: Costs Evolution over time - 95% C.I.