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The number of infections at the time of first detection in a SIR epidemic model for large populations.

Bachelor's Project Mathematics

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1 Introduction

The study of epidemic dynamics has long been a critical area of research, with significant implications for public health, policy-making, and disease control strategies. Originally, deterministic models were used to analyse how a disease would develop like in [1]. These models can provide insights into the average behavior of epidemics in large populations with a high level of disease incidence. However, real-world epidemics often exhibit randomness and uncertainties that deterministic models cannot properly predict. This is where stochastic models come into play, offering a more nuanced and realistic representation of epidemic processes and providing more accurate insights at early stages of an epidemic [2].

Stochastic models account for the inherent randomness in disease transmission, the length of recovery, and other epidemiological parameters. By accounting for random fluctuations, stochastic models provide a more accurate analysis of epidemic dynamics, especially in early stages of an outbreak or in small, isolated communities. As an example, [3] employed a heterogeneous transmission model based on a branching process to estimate the reproductive number. Stochastic models are also used for exploring possible epidemic scenarios which is useful for risk assessment and disease control strategies, among other things.

In 1906, compartmental models were suggested by Hamer [4] in his Milroy lectures. He proposed that the spread of a disease should be dependent on the number of individuals that are susceptible and the number of individuals that are infective, effectively dividing the population into different classes dependent on whether they are infectious or not.

After detection intervention measures can affect the spread of a disease as quantified by [5]. Because of this it is valuable to give results about an epidemic at the moment it is first detected because the spread of the disease is not influenced by policy and control strategies. This allows for studying the uninhibited spread and can give a better estimation of the spreading capacity of the disease.

To give a concrete example of this, it is possible to measure the amount of animals with antibodies to a disease in a farm where all the animals are culled when the disease gets detected. If the distribution of this number is known, it is possible to calculate an estimate for the infectivity of the disease. If the distribution is not known, however no such results can be given.

The goal of this paper is to provide an insight to epidemiology for bachelor students of mathematics. To this extent, we will elaborate on the mathematical tools used to stochastically model epidemics. Section 2 will introduce the notation and concepts of mathematical processes and models that are used for analysing and predicting epidemics. After that, we attempt to expand on the results by Trapman and Bootsma [6]. They proved that the distribution of infectives in a SIR epidemic model in large populations is geometric at the time of first detection. By providing a proof that this geometric distribution also holds for the total number of infections, which includes individuals that have since recovered, before the moment of first detection, we attempt to further increase the applicability of their work. Moreover, the paper will introduce submodels, originally introduced by Diekmann et al.[7], for the contact and detection processes in SIR epidemic models. These submodels can be used to more accurately model certain diseases like HIV/AIDS where the infectivity of an individual is very strongly dependent on the time since their infection [8]. We demonstrate that the SIR epidemic model with submodels for the contact process in large populations can be related to a M/G/1-queue with a waiting time based service discipline. Finally, we conjecture that, under the assumption that the infectivity and detectivity of the disease are proportional to each other, this model will also be geometrically distributed. This conjecture will be supported by an intuitive argument and statistical analysis of simulations of SIR epidemics.

2 Definitions and notation

In this section we define the relevant processes and give most of the definitions. We start by defining the little-o notation we use. For a function f(h) we say that f(h) = o(h) if $\lim_{h \searrow 0} \frac{f(h)}{h} = 0$. Furthermore, we define the indicator function $\mathbb{1}(A)$ to be the function that takes the value 1 when A occurs and the value 0 when A does not occur. Most of the notation and definitions that are given closely follow the notations and definitions from [6].

2.1 The Poisson process

In what follows, we often refer to a Poisson process. This is a continuous-time, discrete stochastic process that consists of points on the positive real line $[0, \infty]$. It has the Markovian property meaning that what happens on $(t, \infty]$ is independent of what happened on $[0, t]$. To define a Poisson process we first define a counting process which is a stochastic process $\{N(t), t \geq 0\}$ that represents the total number of events that occur before time t [9, Ch. 5.3]. We can then define a homogeneous Poisson process $N(t)$ with parameter, or rate, λ to be a counting process that satisfies the following properties for small h [10, Thm. 2.7].

(i) $N(0) = 0$

(ii) $N(t)$ has independent increments, i.e. let $I_1, I_2 \subset [0, \infty]$, $I_1 \cap I_2 = \emptyset$, then $N(I_1)$ and $N(I_2)$ are independent.

(iii) $\mathbb{P}(N(t+h) - N(t) \geq 2) = o(h)$

(iv) $\mathbb{P}(N(t+h) - N(t) = 1) = \lambda \cdot h + o(h)$.

Moreover, For the homogeneous Poisson process we have that the amount of events in $[t, t+s]$ is only dependent on the length s of the increment and not on t. Because of this the homogeneous Poisson process is said to have stationary increments.

When the process does not have a constant rate λ the process no longer has stationary increments. Let us therefore define the nonhomogeneous Poisson process to be a random process with parameter $\lambda(t)$ that satisfies the following for small h [9, Ch. 5.4].

(I) $N(0) = 0$

(II) $N(t)$ has independent increments

(III) $\mathbb{P}(N(t+h) - N(t) \geq 2) = o(h)$

(IV) $\mathbb{P}(N(t+h) - N(t) = 1) = \lambda(t) \cdot h + o(h)$.

2.2 SIR epidemic model

An SIR (Susceptible→Infective→Removed) epidemic model is a compartmental model in epidemiology that splits a population into three groups. A compartmental model splits the population into a number of categories where individuals can flow from one compartment to another. The direction of this flow is usually denoted in the name of the model. Initially the entire population is **S**usceptible until an **I**nfective is introduced. This first Infective can spread the disease by contact to the susceptible population (Susceptible→Infective) during its sickness until the infective becomes **R**emoved (Infective→Removed) by, for example, recovery or death [1]. Once a susceptible individual comes into contact with an Infective individual, it will itself become infective and possibly spread the disease to other susceptible individuals. The disease can no longer spread when either all infectives are removed or all susceptibles have become infected. In the SIR model a member of the population can become infected only once because a removed individual is no longer susceptible to that disease. Examples of models where individuals can become infected multiple times are SIRS

(Susceptible→Infective→Removed→Susceptible) and SIS (Susceptible→Infective→Susceptible), also known as SI (Susciptible ↔ Infective) [11].

Assume that every individual in the population comes into contact with other individuals at an equal rate and that the contact pairs are randomly mixing. This is called a homogeneous and randomly mixing population.

Assume also that there is no demographic turnover in the population. Demographic turnover is a change in the total size of the population and can be caused by immigration, emigration, birth, or death in the susceptible population. Although an infective can die from the disease it will be considered removed. Therefore, the total population does not change.

For our model we consider a population size of n and a contact rate for each individual of λ. Because the population is randomly mixing contacts between any pair in the population are made according to a homogeneous Poisson process with parameter $\frac{\lambda}{n-1}$. If a contact is made between an infectious and susceptible individual the susceptible individual immediately becomes infectious. Once an individual, including the first infective, becomes infected it stays infectious for a random infectious period, which is distributed as the random variable L. L is almost surely (a.s.) positive, $\mathbb{P}(0 < L \leq \infty) = 1$. The infectious periods are identically and independently distributed (i.i.d.). After the infectious period an individual will be considered as part of the removed population and cannot leave that compartment.

We let $S^{(n)}(t)$ be the number of susceptible individuals at time t, $I^{(n)}(t)$ the number of infectious individuals at time t, and $R^{(n)}(t)$ be the number of removed individuals at time t. We set the moment of the first infection to be $t = 0$ such that

$$S^{(n)}(0) = n - 1, \quad I^{(n)}(0) = 1, \quad R^{(n)}(0) = 0.$$

To this model we add a detection process. In this process every infectious individual is detected according to a Poisson process with rate δ. This detection process is defined per capita. Therefore, the probability of detection is larger when there are more infective individuals. Let $D_i^{(n)}$ denote the random time of the i'th detection in the population. If the number of infective individuals is 0 before the i'th detection takes place we say that $D_i^{(n)} = \infty$. Note that the individual that is first detected is not necessarily the person that is infectied at T_1.

2.3 Branching process

A branching process is a stochastic process where individuals reproduce and die according to random variables. Generally speaking, branching processes are stochastic models where each entity behaves according to a random variable. One of the most commonly used branching processes is the Galton-Watson process. This was originally used by Francis Galton and Henry Watson to study the extinction of family names [12]. We will use a branching process known as a birth-death process to study the SIR epidemic model in large populations.

Let $Z(t)$ be a continuous branching process where individuals give birth according to a Poisson process with parameter λ. Individual i is born at time T_i and at the start of its life, the i'th individual is assigned a life length L_i which is distributed as a random variable L. The life length of individual i is i.i.d. with respect to other individuals. $A_i(t)$ is defined as the age of the individual i at time t and is defined to be ∞ when the individual has died.

$$A_i(t) = \begin{cases} 0 & \text{for } t \leq T_i \\ t - T_i & \text{for } T_i < t < T_i + L_i \\ \infty & \text{for } t \geq T_i + L_i \end{cases}$$

To give the total number of individuals alive at time t we count the number of births that have happened up to that time and substract the amount of deaths that have happened. This leads to the following definition

$$Z(t) = \sum_{i=0}^{\infty} \mathbb{1}(T_i \leq t) - \mathbb{1}(A_i(t) = \infty). \tag{1}$$

There is only one individual at the start of the branching process and their age A_1 is 0 at $t = 0$. Because each individual that is alive at time t gives birth at a rate λ we have that the probability that another individual is born is given by

$$\mathbb{P}\left(T_i \in (t, t+h) | Z(t) = k, \sum_{j=1}^{\infty} \mathbb{1}(T_j \leq t) = i - 1\right) = \lambda \cdot k \cdot h + o(h).$$

Besides reproducing each individual can also be detected according to a Poisson process with parameter δ. The first time an individual gets detected will be denoted by D_1 and the i'th detection by D_i. Like in the SIR epidemic model, the individual detected at D_1 is not necessarily the individual that was infected at T_1.

2.4 Queueing theory

Queueing theory is the study of queueing models. These models are often used to predict waiting times and the length of the queue. The model considers the arrival of customers at one or more service stations. The customers are assigned a workload upon entering the queue and leave when a service station has provided this workload for the customer [6, p. 377]. In a M(arkovian)/G(eneral)/1 queue, the arrival of customers can be described by a process with the Markovian property. The distribution of the workload of each customer follows a General distribution and the 1 implies that there is only one service station.

How customers in line get serviced is dependent on the model. As an example, take a FIFO model where new customers enter the back of the queue and are only served when all customers that were in the queue when they arrived have been fully serviced. A LIFO model on the other hand will serve the newest customer at all times. If a customer is receiving service while a new customer arrives, it will stop being served and the server will start serving the new customer. The workload that a customer needs when a server stops servicing them does not change while the server is away.

Another way to service the customers is through a round-robin schedule. This has the server working for a fixed time h at each customer before moving on the next customer in line. If the remaining workload of the customer is less than h when the server starts, the customer will be finished servicing early and the server will immediately move on to the next customer when the service is complete.

Because the server can instantaneously change customers, there is no limit to how small h can get. As such the processor sharing service discipline is defined as a round robin schedule with $\lim h \searrow 0$. With processor sharing (PS), all customers get serviced at the same rate. However, the rate is dependent on the amount of customers in the queue. An increase in customers in the queue implies a decrease in service rate per customer.

Define the M/G/1-PS queue with catastrophes, $Q^{PS}(t)$, as follows. Customers arrive according to a Poisson process with rate λ and enter the queue immediately. Each customer is assigned a workload upon entering the queue. The workloads are distributed as the random variable L which has a general distribution. Customers are numbered based on their arrival times $\tilde{T}_i$ such that $\tilde{T}_{i-1} \leq \tilde{T}_i \leq \tilde{T}_{i+1}$ for all i. Because the probability of two arrivals happening in the interval $[t, t+h]$ is $o(h)$, we have that for $i < j$, $\tilde{T}_i < \tilde{T}_j$ a.s.

The workload each customer brings in is denoted L_i and The service each customer receives at time t is based on the amount of customers in the queue and is defined as

$$\frac{d}{dt}\tilde{A}_i(t) := \mathbb{1}(0 < \tilde{A}_i(t) < \infty)/Q(t).$$

The amount of work customer i has had at time t is denoted by $\tilde{A}_i(t)$ and the customer starts being serviced when they enter the queue at $\tilde{T}_i$. The customer leaves the queue at the moment that they have received enough service for their workload i.e. at $\sup_t\{\tilde{A}_i < L_i\}$. After they leave the queue their workload is defined to be ∞ which gives us the following for $\tilde{A}_i(t)$.

$$\tilde{A}_i(t) := \begin{cases} 0 & \text{for } t \leq \tilde{T}_i \\ \int_{\tilde{T}_i}^{t} \frac{1}{Q(s)} ds & \text{for } T_i < t < \sup_t\{\tilde{A}_i < L_i\} \\ \infty & \text{for } t \geq T_i + L_i \end{cases}$$

Catastrophes occur independently of the queue according to a Poisson process with parameter $\tilde{\delta}$. The time of the i'th catastrophe is denoted as $\tilde{D}_i$. We will mostly be interested in the queue at the time of the first catastrophe $\tilde{D}_1$.

Because the arrivals and catastrophes occur according to a Poisson process we have the following probabilities:

$$\mathbb{P}\left(\tilde{T}_i \in (t, t+h) | Q(t), \sum_{j=1}^{\infty} \mathbb{1}(\tilde{T}_j \leq t) = i-1\right) = \tilde{\lambda} \cdot h + o(h).$$

$$\mathbb{P}\left(\tilde{D}_i \in (t, t+h) | Q(t), \sum_{j=1}^{\infty} \mathbb{1}(\tilde{D}_j \leq t) = i-1\right) = \tilde{\delta} \cdot h + o(h).$$

3 The distribution of the total number of infections

In this section we show that for the SIR epidemic in large populations, the number of individuals that has been infected at the time of first detection is distributed geometrically. To show this we will use the work by Trapman and Bootsma [6] which shows that the branching process $Z(t)$ can be related to a M/G/1-PS queue by using a random time change. Using their results we illustrate that $I^{(n)}(t) + R^{(n)}(t)$ can be approximated by a Poisson process. When combining this with a proof of the Poisson superposition theorem we can give the parameter p for the geometric distribution of $I^{(n)}(D_1) + R^{(n)}(D_1)$.

3.1 The total number of births and arrivals in the M/G/1-PS queue

To define the total number of infected individuals we want to define the number of individuals that have died for the branching process. Let

$$R(t) := \sum_{i=1}^{\infty} \mathbb{1}(A_i = \infty)$$

be the number of individuals that have died in the branching process. We want to show that the distribution of $B(t) := Z(t) + R(t)$ is geometric at the moment of first detection. Combining the above definition of $R(t)$ with (1) we see that

$$\begin{aligned} B(t) &= \sum_{i=1}^{\infty} \mathbb{1}(T_i \leq t) - \mathbb{1}(A_i(t) = \infty) + \sum_{j=1}^{\infty} \mathbb{1}(A_j = \infty) \\ &= \sum_{i=1}^{\infty} \mathbb{1}(T_i \leq t). \end{aligned}$$

Define for the queue $Q^{PS}(t)$ the total number of arrivals at time t to be

$$A(t) = \sum_{i=1}^{\infty} \mathbb{1}(\tilde{T}_i < t)$$

From Trapman and Bootsma [6] we know that for large populations the SIR epidemic model can be considered as the branching process $Z(t)$. Furthermore, they showed that the branching process can be transformed to a M/G/1-PS queue through a random time change. From their results we can conclude that

$$\lim_{\mathrm{n}\to\infty} \mathbb{P}\left(R^{(n)}(t) = k | D_1^{(n)} < \infty\right) = \mathbb{P}\left(R(t) = k | D_1 < \infty\right)$$

and that

$$\begin{aligned} \mathbb{P}\left(B(\tau(t)) = k | T_1 = 0, D_1 < \infty\right) &= \mathbb{P}\left(Z(\tau(t)) + R(\tau(t)) = k | T_1 = 0, D_1 < \infty\right) \\ &= \mathbb{P}\left(\sum_{i=1}^{\infty} \mathbb{1}(T_i \leq \tau(t)) = k | T_1 = 0, D_1 < \infty\right) \\ &= \mathbb{P}\left(\sum_{i=1}^{\infty} \mathbb{1}(\tilde{T}_i \leq t) = k | T_1 = 0, D_1 < \infty\right) \\ &= \mathbb{P}\left(\sum_{i=1}^{\infty} A(t) = k | Q^{PS}(0) = 0, A(\tilde{D}_1) > 0\right) \end{aligned}$$

The final equation skips a few details that [6] covers and a similar reasoning is given in section 4.2.2. This leads to the conclusion that analysing the total number of births in the branching process can be done by studying the arrivals in the M/G/1 queue with processor sharing.

3.2 Superposition of Poisson processes

For the M/G/1-PS queue, let $N_A(t)$ denote the number of arrivals in the interval $[0,t]$ and let $N_C(s)$ denote the number of catastrophes in the interval $[0,s]$. We have by the definition of the queue that N_A and N_C are independent Poisson processes. We combine these processes to a counting process $E(t)$ where points of E are either arrivals or catastrophes. We want to show that $E(t) := N_A(t) + N_C(t)$ also satisfies the properties of a homogeneous Poisson process with parameter $\lambda + \delta$. Furthermore, we will show that when an event of E occurs at time t then it belongs to N_C with probability $\frac{\delta}{\lambda+\delta}$.

We start by showing that $E(t)$ satisfies all the properties of a homogeneous Poisson process. First observe that (i) $E(0) = N_A(0) + N_C(0) = 0 + 0 = 0$.

For (ii) we let I_1, I_2 be two independent increments. To show that $E(I_1)$ and $E(I_2)$ are independent we use that $N_A(I_1)$ and $N_A(I_2)$ as well as $N_C(I_1)$ and $N_C(I_2)$ are independent. Because the processes $N_A(t)$ and $N_C(t)$ are independent from each other it follows that $N_A(I_1)+N_C(I_1)$ and $N_A(I_2)+N_C(I_2)$ are independent.

Thirdly we show that the probability of two events happening in $[t, t+h]$ is $o(h)$. For this, observe that two events of any kind can only happen when there are either at least two arrivals, at least two catastrophes, or one of both. For the first case we see that

$$\mathbb{P}\left(N_A(t+h) - N_A(t) \geq 2 | N_C(t)\right) = o(h)$$

because N_A and N_C are independent processes.

The second case is identical and for the third case we have

$$\begin{aligned}\mathbb{P}\left(N_A(t+h) - N_A(t) = 1, N_C(t+h) - N_C(t) = 1\right) &= \mathbb{P}(N_A(t+h) - N_A(t) = 1) \cdot \mathbb{P}(N_C(t+h) - N_C(t) = 1) \\ &= (\lambda \cdot h + o(h)) \cdot (\delta \cdot h + o(h)) \\ &= \lambda \cdot \delta \cdot h^2 + o(h) \\ &= o(h).\end{aligned}$$

Adding these three mutually exclusive cases, we conclude that

$$\text{(iii)}\ \ \mathbb{P}(E(t+h) - E(t) \geq 2) = o(h)$$

For (iv) observe that there being one event in $[t, t+h]$ implies that there is either one arrival and no catastrophe or no arrival and one catastrophe. We first calculate the probability that there is exactly one arrival in the queue and zero catastrophes in the interval $[t, t+h]$

$$\begin{aligned}\mathbb{P}\left(N_A(t+h) - N(t) = 1, N_C(t+h) - N_C(t) = 0\right) &= \mathbb{P}(N_A(t+h) - N(t) = 1) \cdot \mathbb{P}(N_C(t+h) - N_C(t) = 0) \\ &= (\lambda \cdot h + o(h)) \cdot (1 - \delta \cdot h + o(h)) \\ &= \lambda \cdot h - \lambda \cdot \delta \cdot h^2 + o(h) \\ &= \lambda \cdot h + o(h)\end{aligned}$$

Similarly we calculate the probability that there is exactly one catastrophe and zero arrivals.

$$\mathbb{P}\left(N_A(t+h) - N(t) = 0, N_C(t+h) - N_C(t) = 1\right) = \delta \cdot h + o(h)$$

Because these events are mutually exclusive and the arrivals and catastrophes are independent,

$$\mathbb{P}(E(t+h) - E(t) = 1) = (\lambda + \delta) \cdot h + o(h).$$

Lastly, observe that $N_A(t)$ and $N_C(t)$ having stationary increments results in $E(t)$ having stationary increments because

$$\begin{aligned} E(t+s) - E(t) &= \big(N_A(t+s) + N_C(t+s)\big) - \big(N_A(t) + N_C(t)\big) \\ &= \big(N_A(t+s) - N_A(t)\big) + \big(N_C(t+s) - N_C(t)\big). \end{aligned}$$

What remains to show is that the probability of an event occurring in $E(t)$ at time t belongs to $N_C(t)$ with a probability of $\frac{\delta}{\lambda+\delta}$. For this we calculate the probability than an event occurs in N_C conditioned on an event occurring in E.

$$\begin{aligned} \mathbb{P}\left(N_C(t+h) - N_C(t) = 1 | E(t+h) - E(t) = 1\right) &= \frac{\mathbb{P}\left(N_C(t+h) - N_C(t) = 1, N_A(t+h) - N_A(t) = 0\right)}{\mathbb{P}(E(t+h) - E(t) = 1)} \\ &= \frac{\mathbb{P}(N_C(t+h) - N_C(t) = 1)}{\mathbb{P}(E(t+h) - E(t) = 1)} \\ &= \frac{\delta \cdot h + o(h)}{(\lambda+\delta)\cdot h + o(h)} \\ &= \frac{\delta + \frac{o(h)}{h}}{\lambda + \delta + \frac{o(h)}{h}} \\ &= \frac{\delta}{\lambda+\delta} \text{ as } h \searrow 0 \end{aligned}$$

Where the second equivalency follows from N_A and N_C being independent processes. Now we calculate the probability of an event not belonging to N_C, thus belonging to N_A, as

$$1 - \frac{\delta}{\lambda+\delta} = \frac{\lambda}{\lambda+\delta}.$$

We have shown the probability that an occurring event belongs to $N_C(t)$. This allows us to view all events of E as independent trials where the chance of success is the probability that an event belongs to $N_C(t)$. Such Bernoulli trials have been heavily studied in many works, among which [13, p. 256]. It is known that if p is the probability of success and X is the number of trials before the first success, then

$$\mathbb{P}(X = k) = p \cdot (1-p)^{k-1}.$$

Therefore, the probability that the total number of people that have been infected by an outbreak is distributed geometrically and given by

$$\begin{aligned} \mathbb{P}\left(B(D_1) = k | B(0) = 1, B(D_1) > 0\right) &= \mathbb{P}\left(A(\tilde{D}_1) = k | A(0) = 0, A(\tilde{D}_1) > 0\right) \\ &= \frac{\delta}{\lambda+\delta} \cdot (1 - \frac{\delta}{\lambda+\delta})^{k-1} \\ &= \frac{\delta}{\lambda+\delta} \cdot \left(\frac{\lambda}{\lambda+\delta}\right)^{k-1}. \end{aligned}$$

4 A SIR epidemic model with submodels for the infectivity

In this section we discuss what happens when the infectivity or detectivity of an individual changes during its infective period under the assumption that the infectivity and detectivity stay proportional over time. We will define a SIR epidemic model that factors in this change in infectivity. We also define a branching process that models this phenomenon and a M/G/1-queue where the service discipline is based on the waiting time of the customers. We show that these three models can be related through a result by Ball and Donnelly [14] and a random time change. The section ends with a conjecture that states that the distribution of the number of infectives at the time of first detection is geometric.

4.1 Revising models to account for a change in infectivity

We start by defining the infectivity and detectivity of an individual as a function of the time since their infection. To this extent, let $\lambda(t) : \mathbb{R}_{\geq 0} \to \mathbb{R}_{\geq 0}$ and $\delta(t) : \mathbb{R}_{\geq 0} \to \mathbb{R}_{\geq 0}$ be functions satisfying

$$\frac{\delta(t)}{\lambda(t)} = c$$

for some $c \in (0, \infty)$.

In order to let the infection rate for any infective be dependent on the time since their infection, define for the individual infected at T_i

$$\lambda_i(t) := \mathbb{1}(T_i < t < T_i + L_i) \cdot \lambda(t - T_i).$$

Contacts between the i'th infective and another individual are now made according to a nonhomogeneous Poisson process with parameter $\frac{\lambda_i(t)}{n-1}$ where the other individual gets infected if they are susceptible at the time of contact.

One final assumption that is made is that

$$\int_0^t \sum_{i=1}^{\infty} \delta_i(s) ds \to \infty \text{ a.s. for } t \to \infty. \tag{2}$$

This model will be related to a branching process where individual i gives birth according to $\lambda_i(t)$ and is detected at rate $\delta_i(t)$. This gives the following probabilities for the branching process:

$$\mathbb{P}\left(T_i \in (t, t+h) | Z(t), \sum_{j=1}^{\infty} \mathbb{1}(T_j \leq t) = i - 1 \right) = h \cdot \sum_{j=1}^{\infty} \lambda_j(t) + o(h),$$
$$\mathbb{P}\left(D_i \in (t, t+h) | Z(t), \sum_{j=1}^{\infty} \mathbb{1}(D_j \leq t) = i - 1 \right) = h \cdot \sum_{j=1}^{\infty} \delta_j(t) + o(h).$$

An important distinction between this branching process and the one described in section 2.3 is that we scale the life length and change the rate at which an individual ages such that

$$\frac{d}{dt} \hat{A}_i(t) = \lambda_i(t) \cdot \mathbb{1}(T_i < t < T_i + \hat{L}_i).$$

Here $\hat{L}_i$ is the scaled life length and is determined by the random variable

$$\hat{L} := \left(\int_0^L \lambda(t) dt \right)^{-1} \cdot L.$$

$\hat{L}$ has a general distribution, is a.s. positive, and is i.i.d. because L is. Note that

$$\hat{A}_i(t) = \begin{cases} 0 & \text{for } t \leq T_i \\ \int_0^{t-T_i} \lambda(s)ds & \text{for } T_i < t < T_i + L_i \\ \infty & \text{for } t \geq T_i + L_i. \end{cases}$$

We define a queue $Q^{WT}(t)$ with service based on the waiting time of the customer and the total waiting time of customers currently in the queue. This queue will be linked to the newly defined branching process. Let $\tilde{T}_i$ be the time at which the i'th customer enters the queue and define $\tilde{\lambda}(t) := \lambda(t)$ and $\tilde{\delta}(t) := \delta(t)$. We can then define

$$\tilde{\lambda}_i(t) := \mathbb{1}(0 < \tilde{A}_i < \infty) \cdot \tilde{\lambda}(t - \tilde{T}_i)$$
$$\tilde{\delta}_i(t) := \mathbb{1}(0 < \tilde{A}_i < \infty) \cdot \tilde{\delta}(t - \tilde{T}_i).$$

The service customer i gets at time t is given by

$$\frac{d}{dt}\tilde{A}_i(t) := \frac{\tilde{\lambda}_i(t)}{\sum_{j=1}^{\infty} \tilde{\lambda}_j(t)}$$

and the total service provided is 1 when there are customers waiting because

$$\sum_{i=1}^{\infty} \frac{d}{dt}\tilde{A}_i(t) = \sum_{i=1}^{\infty} \frac{\tilde{\lambda}_i(t)}{\sum_{j=1}^{\infty} \tilde{\lambda}_j(t)} = \frac{\sum_{i=1}^{\infty} \tilde{\lambda}_i(t)}{\sum_{j=1}^{\infty} \tilde{\lambda}_j(t)} = 1.$$

The catastrophe process occurs according to a Poisson process with parameter $c = \frac{\tilde{\delta}(t)}{\tilde{\lambda}(t)}$ which is constant.

4.2 Relating the SIR epidemic with changing infectivity to a M/G/1-WT queue

To show the relationship between SIR epidemic for large populations and the M/G/1-WT queue we want to first show that we can study the branching process for results about the SIR epidemic model. For this we will show that

$$\lim_{n\to\infty} \mathbb{P}(I^{(n)}(D_1^{(n)}) = k | D_1 < \infty) = \mathbb{P}(Z(D_1) = k | T_1 = 0, D_1 < \infty) \tag{3}$$

After that, we show that the branching process $Z(t)$ can be related to the queue $Q^{WT}(t)$ through a random time change. We do this by proving that

$$\mathbb{P}\left(Z(D_1) = k | T_1 = 0, D_1 < \infty\right) = \mathbb{P}\left(Q^{WT}(\tilde{D}_1) = k | Q^{WT}(0) = 0, Q^{WT}(\tilde{D}_1) > 0\right). \tag{4}$$

4.2.1 The SIR epidemic model as a branching process

From the work by Ball and Donnelly [14] we know that a coupling between the epidemic process $I^{(n)}(t)$ and the branching process $Z(t)$ can be constructed such that there exists a constant $a > 0$ for which

$$\sup_{0 \leq t \leq a \log n} |I^{(n)}(t) - Z(t)| \to 0$$

almost surely for $n \to \infty$. Note that if at any time t_0 there are no more infective individuals, then there will never be any more infective individuals after that time which implies that there will be no more detections because detections only happen in infective individuals. Therefore, the condition that $D_1 < \infty$ also implies that $I^{(n)}(t) > 0$ for $0 \leq t \leq D_1$.

The probability that D_1 is larger than some t is given by

$$\begin{aligned}\mathbb{P}\left(D_1^{(n)} \geq t | D_1^{(n)} < \infty\right) &= \exp\left(-\int_0^t \sum_{i=1}^{\infty} \delta_i(s) ds\right) \\ &= 1 - \mathbb{P}\left(D_1^{(n)} < t | D_1^{(n)} < \infty\right).\end{aligned}$$

Because of (2) we can say that

$$\begin{aligned}\lim_{\mathrm{n}\to\infty} \mathbb{P}\left(D_1^{(n)} < a \cdot \log n | D_1^{(n)} < \infty\right) &= 1 - \lim_{\mathrm{n}\to\infty} \exp\left(-\int_0^{a\cdot\log n} \sum_{i=1}^{\infty} \delta_i(s) ds\right) \\ &= 1\end{aligned} \tag{5}$$

for $a > 0$. Combining this with the result by Ball and Donnelly we get that for $k \in \mathbb{N}$

$$\begin{aligned}\lim_{\mathrm{n}\to\infty} \mathbb{P}\left(I^{(n)}(D_1^{(n)}) = k | D_1^{(n)} < \infty\right) &= \lim_{\mathrm{n}\to\infty} \mathbb{P}\left(I^{(n)}(D_1^{(n)}) = k | D_1^{(n)} \geq c\log n\right) \cdot \mathbb{P}\left(D_1^{(n)} \geq c\log n | D_1^{(n)} < \infty\right) \\ &\quad + \lim_{\mathrm{n}\to\infty} \mathbb{P}\left(I^{(n)}(D_1^{(n)}) = k | D_1^{(n)} < c\log n\right) \cdot \mathbb{P}\left(D_1^{(n)} < c\log n | D_1^{(n)} < \infty\right) \\ &= 0 + \lim_{\mathrm{n}\to\infty} \mathbb{P}\left(I^{(n)}(D_1^{(n)}) = k | D_1^{(n)} < c\log n\right) \cdot \mathbb{P}\left(D_1^{(n)} < c\log n | D_1^{(n)} < \infty\right) \\ &\overset{(5)}{=} \lim_{\mathrm{n}\to\infty} \mathbb{P}\left(I^{(n)}(D_1^{(n)}) = k | D_1^{(n)} < c\log n\right) \cdot 1 \\ &= \lim_{\mathrm{n}\to\infty} \mathbb{P}\left(Z(D_1) = k | D_1^{(n)} < c\log n\right) \\ &= \lim_{\mathrm{n}\to\infty} \mathbb{P}\left(Z(D_1) = k | D_1 < \infty\right)\end{aligned}$$

This proves (3) and shows that the SIR epidemic in large populations can be studied by analysing the branching process $Z(t)$, and hence we will consider $Z(t)$ rather than $I^{(n)}(t)$.

4.2.2 Transforming the branching process Z(t) to a M/G/1 queue with a waiting-time based service discipline.

In the following part we use a random time change. A random time is a mapping that scales the time in a process and can be used to transform one stochastic process into another. We use this mapping to 'change the time' according to how the process develops. In the random time change we use, for example, time gets scaled according to the total infective pressure $\sum_{i=1}^{\infty} \lambda_i(t)$. We show that with the correct random time change $\tau(t)$ the description of the branching process $Z(\tau(t))$ is equivalent to the description of the queue $Q^{WT}(t)$.

Let us use the following random time change:

$$\tau(t) = \int_0^t \frac{1}{\sum_{i=1}^{\infty} \lambda_i(s)} ds.$$

Let us make a few observations about the process that comes from this random time change. Firstly we have that for all $i \in \mathbb{N}$, $A_i(\tau(t)) = 0$ when $\tau(t) \leq T_i$ and $A_i(\tau(t)) = \infty$ when $\tau(t) \geq T_i + \hat{L}_i$. This implies that $Z(\tau(t))$ is given by

$$Z(\tau(t)) = \sum_{i=1}^{\infty} \mathbb{1}(T_i \leq \tau(t)) - \mathbb{1}(A_i(\tau(t)) = \infty).$$

To find the probability of a new birth we calculate

$$\begin{aligned}\mathbb{P}\left(T_i \in (\tau(t),\tau(t+h))|Z(\tau(t)),\sum_{j=1}^{\infty}\mathbb{1}(T_j\leq t)=i-1\right)&=\sum_{i=1}^{\infty}\lambda_i(t)\cdot(\tau(t+h)-\tau(t))+o(h)\\&=\sum_{i=1}^{\infty}\lambda_i(t)\cdot(\frac{h}{\sum_{j=1}^{\infty}\lambda_j(t)}+o(h))+o(h)\text{ as }h\searrow 0\\&=\frac{\sum_{i=1}^{\infty}\lambda_i(t)}{\sum_{j=1}^{\infty}\lambda_j(t)}\cdot h+2\cdot o(h)\\&=h+o(h)\end{aligned}$$

and for the probability of detection we can similarly calculate

$$\begin{aligned}\mathbb{P}\left(D_i \in (\tau(t),\tau(t+h))|Z(\tau(t)),\sum_{j=1}^{\infty}\mathbb{1}(T_j\leq t)=i-1\right)&=\sum_{j=1}^{\infty}\delta_j(t)\cdot(\tau(t+h)-\tau(t))+o(h)\\&=\sum_{j=1}^{\infty}\delta_j(t)\cdot(\frac{h}{\sum_{j=1}^{\infty}\lambda_j(t)}+o(h))+o(h)\text{ as }h\searrow 0\\&=\frac{\sum_{i=1}^{\infty}\delta_i(t)}{\sum_{j=1}^{\infty}\lambda_j(t)}\cdot h+2\cdot o(h)\\&=\frac{\sum_{i=1}^{\infty}c\cdot\lambda_i(t)}{\sum_{j=1}^{\infty}\lambda_j(t)}\cdot h+o(h)\\&=c\cdot h+o(h).\end{aligned}$$

After the random time change we still have that the random variables $\hat{L}_i$ are i.i.d., distributed as $\hat{L}$, and independent of what happens before T_i. We also see that

$$\frac{d}{dt}A_i(\tau(t))=\mathbb{1}(0<A_i<\infty)\cdot\lambda_i(t)\cdot\frac{d\tau(t)}{dt}=\mathbb{1}(0<A_i<\infty)\cdot\frac{\lambda_i(t)}{\sum_{i=1}^{\infty}\lambda_i(t)}.$$

This shows that $A_i(\tau(t))=\tilde{A}_i(t)$ and that the probabilities of $Z(\tau(t))$ are the same as those of the queue with $\tilde{T}_i$ replaced with T_i and $\tilde{D}_i$ replaced with D_i as long as $Z(\tau(t))>0$. This condition is necessary because when $Z(t)=0$, $\sum_{i=1}^{\infty}\lambda_i(t)=0$ and the random time change is no longer defined. To ensure good behaviour of the random time change until the moment of first detection we will condition our probabilities on $Z(D_1)>0$ which is equivalent to $\inf_{0\leq t\leq D_1}Z(t)>0$ because similar to the SIR epidemic, when $Z(t)=0$ no more births will happen. Because of the aforementioned relation between $Z(\tau(t))$ and $Q^{WT}(t)$ we can say that

$$\mathbb{P}\left(Z(D_1)=k|T_1=0,Z(D_1)>0\right)=\mathbb{P}\left(Q^{WT}(\tilde{D}_1)=k|\tilde{T}_1=0,\min_{0\leq t\leq\tilde{D}_1}Q^{WT}(t)>0\right).$$

This is, however, not yet the result we wanted to show because this probability relies on the first customer arriving at $t=0$ and the queue never having fewer than 1 person waiting. Because of this we want to show that the conditions that the first customer arrives and that the queue is never empty give the same distribution at $\tilde{D}_1$ as the conditions that the queue is empty at $t=0$ and that the queue is not empty at $\tilde{D}_1$. Therefore, we will demonstrate that

$$\mathbb{P}\left(Q^{WT}(\tilde{D}_1)=k|\tilde{T}_1=0,\min_{0\leq t\leq\tilde{D}_1}Q^{WT}(t)>0\right)=\mathbb{P}\left(Q^{WT}(\tilde{D}_1)=k|Q^{WT}(0)=0,Q^{WT}(\tilde{D}_1)>0\right).\quad(6)$$

Let us introduce the notion of busy times for the queue. We say that the queue is busy when there is at least one individual being serviced. The queue is not busy at $t = 0$ and only becomes busy at the first starting time. Someone is being serviced whenever the queue is not empty therefore we can say that the first starting time of the queue is the same as the time of the first arrival. More precisely we say that $\sigma_1 := \min\{t \geq 0, Q^{WT}(t) > 0\}$. We also want to define the stopping time, denoted as ρ, as the moment that queue stops being busy. This is when the server has finished servicing all customers in the queue up to that point. We can therefore define the first stopping time as $\rho_1 = \min\{t \geq \sigma_1, Q^{WT}(t) = 0\}$. We want to define the n'th starting time as the first moment after ρ_{n-1} where the queue is busy. This leads to the following definition.

$$\begin{aligned}
\sigma_1 &:= \min\{t \geq 0, Q^{WT}(t) > 0\} \\
\rho_n &:= \min\{t \geq \sigma_n, Q^{WT}(t) = 0\}, \quad \text{for all } n \in \mathbb{N} \\
\sigma_n &:= \min\{t \geq \rho_{n-1}, Q^{WT}(t) > 0\}, \quad \text{for all } n \in \mathbb{N}\backslash\{1\}.
\end{aligned}$$

Note that a queue, with Markovian arrival times, that is currently not busy can be translated to a queue that is not busy at $t = 0$. In effect,

$$\mathbb{P}\left(Q^{WT}(t+s) = k | \rho_{n-1} < s < \sigma_n\right) = \mathbb{P}\left(Q^{WT}(t) = k | Q^{WT}(0) = 0\right).$$

Similarly it holds that when s is a starting time. Studying a queue at time $t + s$ is the same as studying a queue with $\tilde{T}_1 = 0$ at time t.

$$\mathbb{P}\left(Q^{WT}(t+s) = k | s = \sigma_n\right) = \mathbb{P}\left(Q^{WT}(t) = k | \tilde{T}_1 = 0\right) \tag{7}$$

Define $S(t)$ to be the number of times the queue has become empty before time t. We can find this number by counting the amount of stopping times in the interval $[0, t]$.

$$S(t) := \sum_{i=1}^{\infty} \mathbb{1}(\rho_i \leq t).$$

Now to show (6) we use conditional probabilities to show that

$$\begin{aligned}
\mathbb{P}\left(Q^{WT}(\tilde{D}_1) = k | Q^{WT}(0) = 0, Q^{WT}(\tilde{D}_1) > 0\right) &= \sum_{n=0}^{\infty} \mathbb{P}\left(Q^{WT}(\tilde{D}_1) = k | S(\tilde{D}_1) = n, Q^{WT}(0) = 0, Q^{WT}(\tilde{D}_1) > 0\right) \\
&\quad \cdot \mathbb{P}\left(S(\tilde{D}_1) = n | Q^{WT}(0) = 0, Q^{WT}(\tilde{D}_1) > 0\right) \\
&= \sum_{n=0}^{\infty} \mathbb{P}\left(Q^{WT}(\tilde{D}_1) = k | S(\tilde{D}_1) = n, 0 < \sigma_n < \tilde{D}_1, Q^{WT}(\tilde{D}_1) > 0\right) \\
&\quad \cdot \mathbb{P}\left(S(\tilde{D}_1) = n | Q^{WT}(0) = 0, Q^{WT}(\tilde{D}_1) > 0\right).
\end{aligned}$$

The latter equality holds because having n stopping times before $\tilde{D}_1$ and $Q^{WT}(\tilde{D}_1) > 0$ implies that there are $n + 1$ starting times before $\tilde{D}_1$.

The next steps follow from (7) and the fact that the queue at t is independent of what happened before

its previous stopping times. The latter point is true because the arrival times are Markovian.

$$\begin{aligned}
&\sum_{n=0}^{\infty} \mathbb{P}\left(Q^{WT}(\tilde{D}_1) = k | S(\tilde{D}_1) = n, 0 < \sigma_n < \tilde{D}_1, Q^{WT}(\tilde{D}_1) > 0\right) \cdot \mathbb{P}\left(S(\tilde{D}_1) = n | Q^{WT}(0) = 0, Q^{WT}(\tilde{D}_1) > 0\right) \\
&= \sum_{n=0}^{\infty} \mathbb{P}\left(Q^{WT}(\tilde{D}_1 - \sigma_{n+1} + \sigma_{n+1}) = k | S(\tilde{D}_1) = n, 0 = \tilde{T}_1 < \sigma_n < \tilde{D}_1, Q^{WT}(\tilde{D}_1) > 0\right) \\
&\quad \cdot \mathbb{P}\left(S(\tilde{D}_1) = n | Q^{WT}(0) = 0, Q^{WT}(\tilde{D}_1) > 0\right) \\
&= \sum_{n=0}^{\infty} \mathbb{P}\left(Q^{WT}(\tilde{D}_1) = k | S(\tilde{D}_1) = 0, \tilde{T}_1 = 0, Q^{WT}(\tilde{D}_1) > 0\right) \\
&\quad \cdot \mathbb{P}\left(S(\tilde{D}_1) = n | Q^{WT}(0) = 0, Q^{WT}(\tilde{D}_1) > 0\right).
\end{aligned}$$

Observe that the distribution of $Q^{WT}(\tilde{D}_1)$ is now no longer dependent on n, therefore it can be removed from the summation giving that

$$\begin{aligned}
&\sum_{n=0}^{\infty} \mathbb{P}\left(Q^{WT}(\tilde{D}_1) = k | S(\tilde{D}_1) = 0, \tilde{T}_1 = 0, Q^{WT}(\tilde{D}_1) > 0\right) \cdot \mathbb{P}\left(S(\tilde{D}_1) = n | Q^{WT}(0) = 0, Q^{WT}(\tilde{D}_1) > 0\right) \\
&\quad = \mathbb{P}\left(Q^{WT}(\tilde{D}_1) = k | S(\tilde{D}_1) = 0, \tilde{T}_1 = 0, Q^{WT}(\tilde{D}_1) > 0\right) \cdot \sum_{n=0}^{\infty} \mathbb{P}\left(S(\tilde{D}_1) = n | Q^{WT}(0) = 0, Q^{WT}(\tilde{D}_1) > 0\right) \\
&\quad = \mathbb{P}\left(Q^{WT}(\tilde{D}_1) = k | S(\tilde{D}_1) = 0, \tilde{T}_1 = 0, Q^{WT}(\tilde{D}_1) > 0\right).
\end{aligned}$$

Saying that the $S(\tilde{D}_1) = 0$ is equivalent to saying that the moment of first detection happens before the first stopping time, i.e. that $\tilde{D}_1 < \rho_1$. Combining this with the condition that the first customer arrives at $\tilde{T}_1 = 0$ lets us condition on $\min_{0 \le t \le \tilde{D}_1} Q^{WT}(t) > 0$.

$$\mathbb{P}\left(Q^{WT}(\tilde{D}_1) = k | S(\tilde{D}_1) = 0, \tilde{T}_1 = 0, Q^{WT}(\tilde{D}_1) > 0\right) = \mathbb{P}\left(Q^{WT}(\tilde{D}_1) = k | \tilde{T}_1 = 0, \min_{0 \le t \le \tilde{D}_1} Q^{WT}(t) > 0\right)$$

We have shown (6) and conclude that (4) also holds.

4.3 A geometric distribution for the queue with waiting time based service

After showing that the SIR epidemic model can be related to a M/G/1-PS queue, Trapman and Bootsma continue by using a result from Kitaev [15] that shows that the queue has a geometric distribution at the time of first detection. Kitaev showed this for a queue with a processor sharing discipline while we have only shown the relation between the branching process and a queue with a waiting time based service discipline. Therefore, the result is not usable at this point. Proving a generalisation of the result for this queue is far too technical for this project if it even exists. Because of this we will state the geometric distribution of the queue as a conjecture and argue that it is true.

Let $Q^{WT}(t)$ be a queue with a processor sharing discipline based on the waiting time of each customer and catastrophes as defined above. Given that the queue is empty at $t = 0$ and that it is not empty at the time of the first catastrophe, the distribution of customers in the queue is geometrical.

$$\mathbb{P}\left(Q^{WT}(\tilde{D}_1) = k | Q^{WT}(0) = 0, Q^{WT}(\tilde{D}_1) > 0\right) = p \cdot (1-p)^{k-1} \text{ for some } p \in (0,1)$$

To support this conjecture we will give an intuitive argument and simulate outbreaks of a SIR epidemic to test if their distribution is geometric. Proving this conjecture would generalize earlier results to SIR epidimic models with submodels for the infectivity and allow it to be more broadly applicable when studying epidemics.

If the conjecture holds, proving it can be done by relating the M/G/1-WT queue to another queue for which it is easier to show that the distribution will be geometric. Another way to show it is by generalizing the result from Kitaev [15] to the queue with a waiting time based service discipline. It is, perhaps, also possible to show that the distribution at D_1 of the branching process is geometrical. This would forego the need to relate the branching process to $Q^{WT}(t)$.

4.3.1 An intuitive argument

While the following is not mathematically rigorous, it does give an idea of why the above could be true. Currently the queue uses a waiting time based service discipline which uses the submodel for infectivity to distribute service. The workload each customer brings is i.i.d. and has a general distribution. The workload should therefore be scalable by a function of the workload similar to what was used to obtain $\hat{L}$. This would transform the M/G/1-WT queue to a queue with processor sharing which was already shown to have a geometric distribution at $\tilde{D}_1$.

5 Simulating outbreaks of SIR epidemics

In this section we simulate outbreaks in an SIR epidemic in an effort to support our conjecture that the number of infectives at the time of first detection is geometrically distributed when $\frac{\delta(t)}{\lambda(t)}$ is constant. Moreover, we simulate outbreaks where $\frac{\delta(t)}{\lambda(t)}$ is not constant. The data received from these simulations will be analysed by applying statistical tools supported by literature.

5.1 Method of simulating

Firstly, we explain the simulation process and secondly, we discuss the statistical tools that were used.

The program is written in python for its flexible class structure. This structure allows us to easily create a place to store information about the infected individuals. As an example, we store the time of infection T_i in `infective.timeofinfection`. Furthermore, we can define $\lambda(t)$ and $\delta(t)$ as class functions which makes the program more reusable. The `infective` structure also contains a function to calculate the infectivity and detectivity of that infective. These functions will be modified between different tests to obtain results for, for example, an increasing infectivity and decreasing detectivity.

The `simulateOutbreak` function simulates one instance of an outbreak in the SIR epidemic model. It increments the time t by the timestep that is given as an input until either all infectives have recovered or an infective is detected. It returns an array containing 0 and the amount of people that have recovered if there are no more infectives at some time t. If the outbreak is detected at some point t it returns an array containing the number of infectives at that point and the number of individuals that have recovered before that time.

The chance of a new infection happening is given by

$$\mathbb{P}\left(T_i \in (t, t+h) | Z(t), \sum_{j=1}^{\infty} \mathbb{1}(T_j \leq t) = i-1\right) = h \cdot \sum_{j=1}^{\infty} \lambda_j(t) + o(h).$$

The `simulateOutbreak` function calculates whether a new infection happens by running through the list of infectives and adding their infective pressures. It then uniformly generates a variable `randinfect` in $[0, 1]$. After checking if the infective pressure is greater than the generated variable it will add an infective to the list. It does a similar thing to check if there is a detection in $[t, t+h]$. This program does not account for the $o(h)$ terms in the probability. The error this creates can be reduced by decreasing the time step h.

The `testObservations` function calculates the average of the observations and uses this to obtain a parameter p for the geometric distribution using that the average $X = \frac{1}{p}$. It then calculates the number of expected observations for each value and uses the `SciPy.stats.kstest` function to calculate the test statistic D_n and the power value P.

Finally, the main function declares a value n for the number of successful trials to simulate and uses a loop to run the simulations and store them in an array of observations.

Let I_{D_1} be the random variable that determines the number of infectives and R_{D_1} the random variable that determines the number of removed individuals at the time of first detection. We will perform experiments for two hypotheses.

The first hypothesis H_0^1 states that $I_{D_1} + R_{D_1}$ is geometrically distributed for large populations with parameter $\frac{\delta}{\lambda+\delta}$ as per the result in section 3. We will perform a two-sided test on H_0^1 with a significance level of $\alpha = 0.05$.

The second null hypothesis H_0^2 states that I_{D_1} is geometrically distributed for large populations when $\lambda(t)$ and $\delta(t)$ are not constant. The parameter for the geometric distribution of this second null hypothesis is calculated using the maximum-likelihood estimator (MLE) for geometric distributions $\hat{p} = \frac{1}{\mathbb{E}(I_{D_1})}$ [16, Ch. 7.5]. H_0^2 will also be tested using a two-sided test with significance level $\alpha = 0.05$

We use a two-sided Kolmogorov-Smirnov test which is built into the `SciPy.stats` package. It is a goodnes of fit test which is a category of statistical tests that calculates a test statistic by comparing the observed data to the expected data. This test statistic can be looked up in a Kolmogorov table [17] to see if the null hypothesis should be rejected given the desired significance level [18, p. 283]. The performance of this test for geometrically distributed data has been researched by Özonur et al. [19].

`SciPy` calculates the p-value associated with the Kolmogorov-Smirnov test. This p-value P is the probability that when resampling under the null hypothesis, you obtain a result that differs at least as much from the expected results as the observed result [18, p. 434]. We reject the null hypothesis if $P \leq \alpha$.

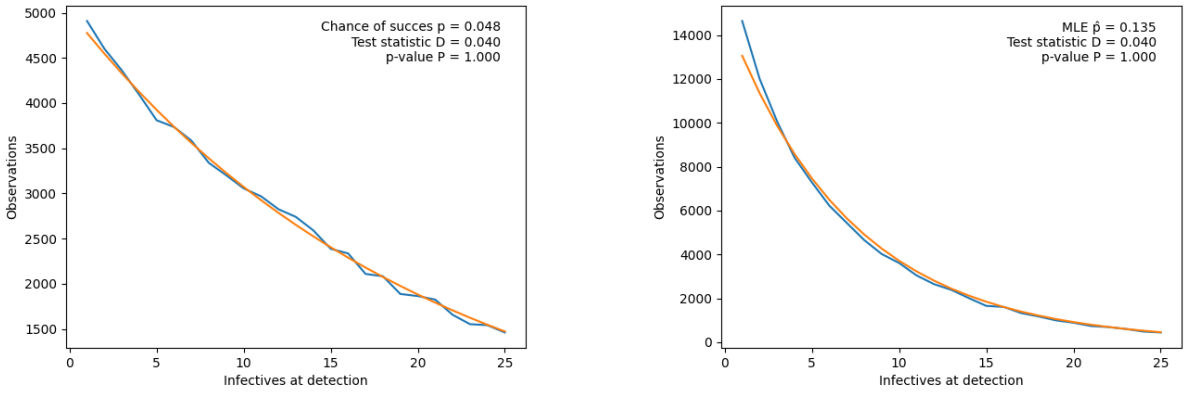
The number of samples is $n = 10^5$ and the time-step used is $h = 0.01$. The Kolmogorov-Smirnov test uses all observations where $I_{D_1} \leq 25$. Unless stated otherwise, the functions used in simulations are

$$\lambda(t) = 0.5 \cdot e^{\frac{t}{10}}, \, \delta(t) = 0.025 \cdot e^{\frac{t}{10}}. \tag{8}$$

We present the results using figures where the observed frequencies are given in blue and the expected frequencies based on the calculated parameter p or the MLE $\hat{p}$ in orange. The estimated parameter p, the Kolmogorov-Smirnov test statistic D, and the p-value P are also given, up to four significant digits, in the figure. The results will be summarized below and all the remaining figures can be found in the appendix.

5.2 Results

Firstly, we plotted the total number of infections at the time of first detection to demonstrate that this is geometrically distributed as was proven in section 3. Here we used $\lambda = 0.5$, $\delta = 0.025$ and tested H_0^1 with a parameter of $p = \frac{0.05}{0.5+0.025} = \frac{1}{21} = 0.048$. Afterwards, we repeated the experiment for a uniformly distributed $L \sim \mathcal{U}(5, 10)$ using $\lambda = 0.1$ and $\delta = 0.03$, testing the results against H_0^1 with a parameter $p = \frac{0.03}{0.23} = 0.130$. The $\hat{p}$ that is shown in the figure is the MLE calculated from the observations.



$L \sim \mathcal{N}(5, 2)$, $\lambda = 0.5$, $\delta = 0.025$ $L \sim \mathcal{U}(5, 10)$, $\lambda = 0.1$, $\delta = 0.03$

Figure 1: The distribution of the number of infections $I^{(n)}(D_1) + R^{(n)}(D_1)$.

Running tests on the $\lambda(t)$ specified above and a $\delta(t)$ that was varied slightly, to obtain different values of c, gave the following estimations for parameters. All of which had a p-value $P = 1.000$. We also calculated $\frac{p}{c}$ to test whether the parameter is directly proportional to c.

c	$\frac{1}{20}$	$\frac{2}{20}$	$\frac{3}{20}$	$\frac{4}{20}$
p	0.053	0.099	0.143	0.178
p/c	1.06	0.99	0.95	0.89

Table 1: Computed p for varying c. See figure 4 in the appendix

The tests were also performed on the $\lambda(t)$ and $\delta(t)$ specified in (8) but with varying distributions for L. All the tested distributions gave a power value of $P = 1.000$. This has been documented in figure 5 in the appendix.

Moreover, we tested the distribution for $\delta(t) = 0.025$ a constant and for $\delta(t) = 0.025 \cdot e^{-\frac{t}{10}}$ a decreasing function.

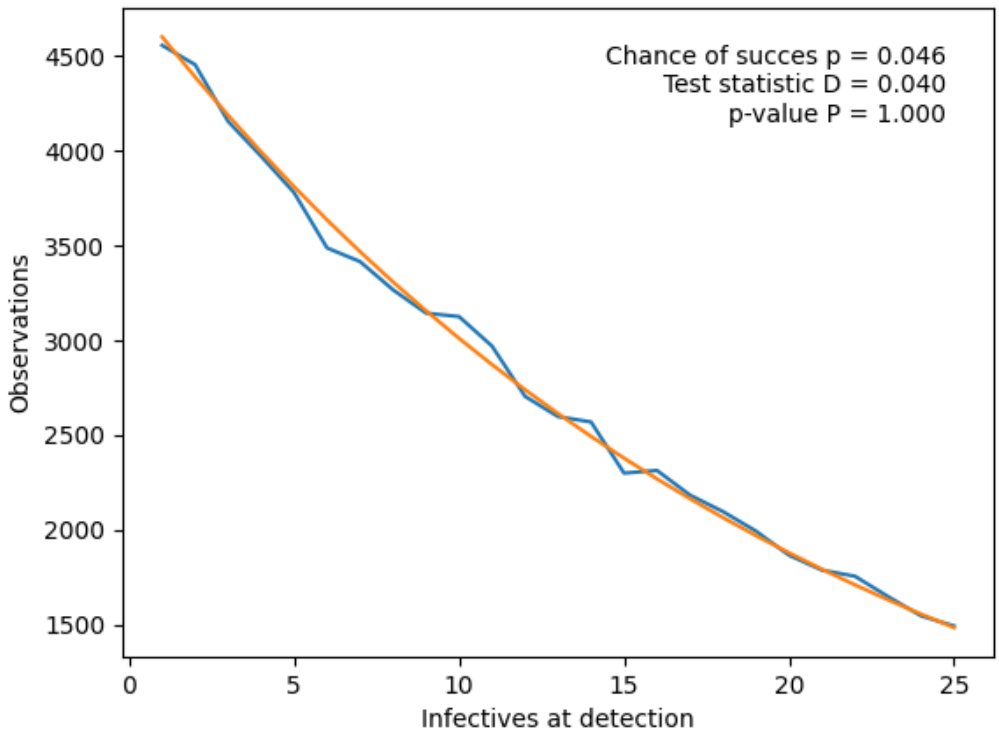


Figure 2: The distribution of $I^{(n)}(D_1)$ with a constant detectivity $\delta(t) = 0.025$, $L \sim \mathcal{N}(5, 2)$

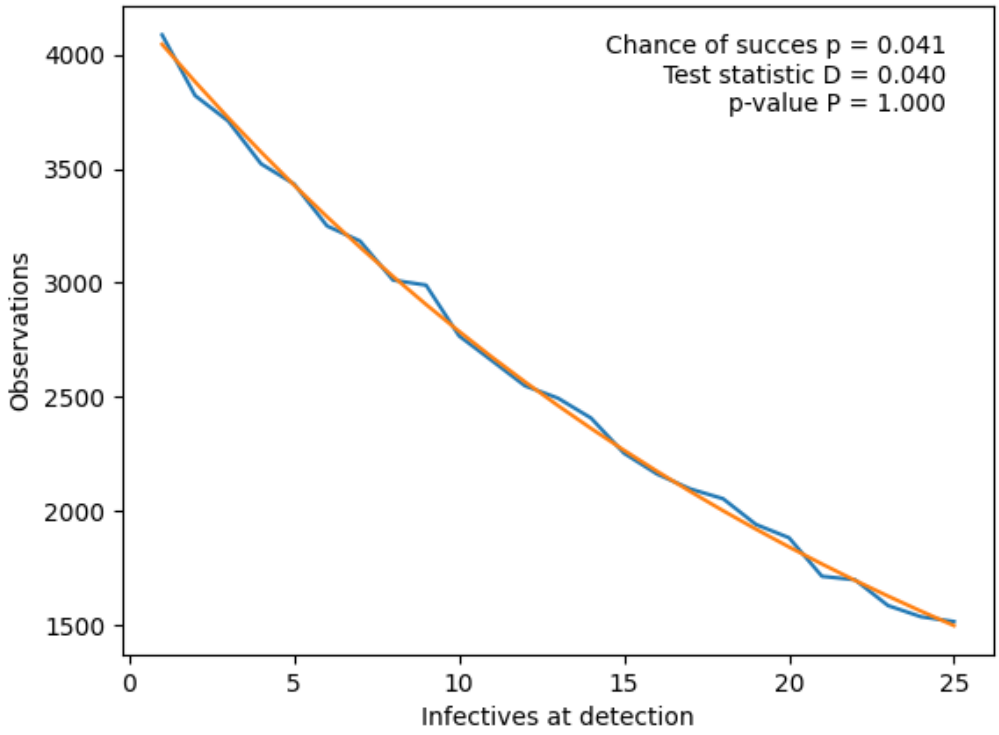


Figure 3: The distribution of $I^{(n)}(D_1)$ with a detectivity that decreases over time. $\delta(t) = 0.025 \cdot e^{-\frac{t}{10}}$, $L \sim \mathcal{N}(5, 2)$

6 Conclusion

We were able to relate the number of births in a branching process with detections to the number of arrivals in a M/G/1-queue with catastrophes. This allowed us to use the Poisson superposition theorem to show that the number of arrivals in the queue at the time of the first catastrophe is geometrically distributed with parameter $p = \frac{\delta}{\lambda+\delta}$. We tested this result by simulating outbreaks of diseases and testing the observations with a Kolmogorov-Smirnov test. These tests showed that the observations do not provide a reason to reject the assumption of a geometric distribution.

After that, we defined a SIR epidemic model with submodels for the infectivity and detectivity of an individual. These models allow for more accurate modelling of diseases that vary over time in their infective pressure. We showed that such models can be described as a branching process when the population size is large. We constructed a random time change for this branching process that related it to the M/G/1-WT queue. This allows for obtaining results about the distribution of the branching process at the time of first detection by analysing the M/G/1-WT queue at the moment of the first catastrophe.

Although we used a lot of the work from [6] to obtain this result, we were not able to complete the proof that the distribution at the time of first detection is geometric. Because of this we stated a conjecture about this distribution and provided a reason to believe that the conjecture is true which was not mathematically rigorous. We also tested the hypothesis that the distribution is geometric by simulating SIR epidemics. The results of these simulations give no reason to discard this hypothesis. We showed that the null hypothesis should not be discarded for several different values of $c = \lambda(t)$ and $\delta(t)$. Moreover, there was no evidence to reject the null hypothesis for different distributions of L. We also calculated p/c in an attempt to find

a constant that relates them but could not find such an answer. It seems unlikely that this constant exists especially because in figure 5 c stays the same between simulations but $\hat{p}$ varies significantly.

Finally, we also tested if the null hypothesis should be rejected for $\lambda(t) = 0.5 \cdot e^{\frac{t}{10}}$, $\delta(t) = 0.025$ and $\lambda(t) = 0.5 \cdot e^{\frac{t}{10}}$, $\delta(t) = 0.025e^{-\frac{t}{10}}$ when $L \sim \mathcal{N}(5, 2)$. Again, there was no evidence that the null hypothesis should be discarded in favour of the alternative hypothesis for these models. This shows that the distribution might be geometric even when $\frac{\delta(t)}{\lambda(t)} = c(t)$ is not constant. Showing that the distribution of $I^{(n)}(D_1)$ is geometric when $c(t)$ is not constant would be an even more powerful result.

All the obtained results gave a very high p-value P. [20] showed that this can be expected for large sample sizes. The test statistic $D = 0.04$ is found for all simulations. This appears to be a result of the `scipy.stats.kstest` function. While this was not included in the results, lowering the number of trials to $n = 10^4$ in the first experiment resulted in a test statistic that was still a multiple of 0.04. However, under the assumption that `kstest` does not contain errors, $D = 0.06$ would be the highest true test statistic. This would still give a p-value close to 1 for our sample size. Therefore, the null hypothesis should still not be rejected.

As discussed, the conjecture still lacks a rigorous proof. If this proof has been found it could also be worth looking into whether there is a stricter requirement than (2) for which the conjecture still holds. The null hypothesis holding when $\frac{\delta(t)}{\lambda(t)}$ is not constant, is reason the question whether the condition $\frac{\delta(t)}{\lambda(t)} = c$ is stronger than strictly necessary. Answering these questions will likely require more research on the distribution of queues with arrival times given by nonhomogeneous Poisson processes.

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A Code for simulation

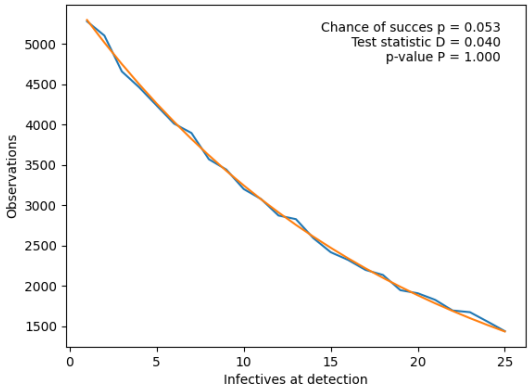
```
import random
import numpy as np
import matplotlib.pyplot as plt
from scipy import stats


class infective:
    def __init__(self, timeOfInfection):
        self.timeofinfection = timeOfInfection
        self.age = 0

        self.lifelength = random.gauss(5, 2)

        # Check if lifelength is nonnegative.
        while self.lifelength < 0:
            self.lifelength = random.gauss(5, 2)

    def infectivity(self):
        """This class function returns the infectivity of the individual."""
        return 0.5 * np.exp(0.1 * self.age)

    def detectivity(self):
        """This class function returns the detectivity of an individual."""
        return 0.025 * np.exp(0.1 * self.age)

    def updateAge(self, time):
        """Adjusts the age of the infective to the specified time."""
        self.age = time - self.timeofinfection
        if self.age >= self.lifelength:
            # If an individuals age surpasses their lifelength
            # the age is set to -1.
            self.age = -1
        return


def simulateOutbreak(h):
    """This simulates an outbreak in the SIR epidemic model
    up to the first detection.

    The function takes the timestep to use as an input.

    Returns the number of infectives at the time of detection
    and the number of removed individuals.

    If there are no more infectives at some time t
    it returns [0, 0].
    """
    t = 0
    listofinfectives = []
    listofremoved = []
```

```
    listofinfectives.append(infective(0))

    while listofinfectives != []:
        t += h

        infectivepressure = 0
        detectivepressure = 0

        # Run through the list of infectives to add their
        # infectivity/detectivity to the total infective/detective pressure.
        for inf in listofinfectives:

            inf.updateAge(t)

            if inf.age == -1:
                # Removes individuals that surpass their lifelength.
                listofinfectives.remove(inf)
                listofremoved.append(inf)

            else:
                infectivepressure += inf.infectivity()
                detectivepressure += inf.detectivity()

        # Two variables are uniformly generated to see if there is
        # an infection or detection.
        randinfect = random.uniform(0, 1)
        randdetect = random.uniform(0, 1)

        # Adds an infective if the infective pressure is subceeded.
        if infectivepressure * h >= randinfect:
            listofinfectives.append(infective(t))

        # If the detective pressure is subceeded the number of infectives is
        # added to the list of results and a new simulation will be started.
        if detectivepressure * h >= randdetect:
            return np.array(
                [len(listofinfectives), len(listofremoved)],
                dtype=int)

    # If at some point the list of infectives is empty the simulation ends and
    # the function returns (0,0)
    return np.array([0, len(listofremoved)], dtype=int)


def testObservations(observations, testsize):
    """Calculates the p-value of a two-sided Kolmogorov-Smirnov test against
    the null hypothesis that the observations are generated by a geometrically
    distributed random variable. The MLE is calculated by
    1/(average of observations).
    It plots the expected frequencies against the observed frequencies and
    displays the relevant values in the plot
```

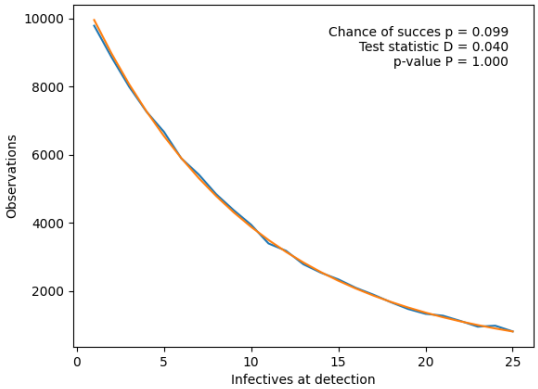
```
    The input is an array of the observed values, which the function translates
    to an array of frequencies of these values, and the highest observation
    that is to be tested.
    """

    highestvalue = np.max(observations)

    # plotter will count the observations stored in results.
    plotter = np.zeros(highestvalue)

    for i in observations:
        plotter[i - 1] += 1

    # Calculate the average number of infectives at time of first detection.
    runningtotal = np.sum(observations)
    averageinfectives = runningtotal/n

    # Calculate the chance of succes from the average.
    p = 1/averageinfectives

    # Total number of observations made where
    # the amount of infectives is smaller than the 'testsize'.
    observationstested = np.sum(plotter[:testsize])

    # Create an array with expected observations based on
    # the succeschance and the number of observations.
    expected = np.zeros(testsize, dtype=float)
    expected[0] = p * observationstested
    for i in range(1, testsize):
        expected[i] = expected[i - 1] * (1 - p)

    # Ensure that the expected observations match
    # the number of actual observations.
    expected = expected * (observationstested/np.sum(expected))

    # Kolmogorov-Smirnov test from the scipy package.
    ks_test = stats.kstest(plotter[0:testsize], expected)

    # Finish by creating the plot figure.
    plt.plot(np.arange(1, testsize + 1), plotter[0:testsize])
    plt.plot(np.arange(1, testsize + 1), expected)
    plt.xlabel('Infectives at detection')
    plt.ylabel('Observations')
    title = "Chance of succes p = {:.3f} \n \
            Test statistic D = {:.3f} \n \
            p-value P = {:.3f} ".format(
            p, ks_test[0], ks_test[1])
    plt.text(
            testsize, plotter[0], title,
            verticalalignment='top', horizontalalignment='right'
```

```
            )
    plt.show()


if __name__ == "__main__":

    # The results array will store the number of infectives
    # at time of detection.
    simulationresults = np.array([], dtype=int)

    # The number of succesful trials to execute.
    n = 100000
    succesfultrials = 0

    while succesfultrials < n:

        simulation = simulateOutbreak(0.01)

        if simulation[0]:
            simulationresults = np.append(simulationresults, simulation[0])
            succesfultrials += 1

    testObservations(simulationresults, 25)
```

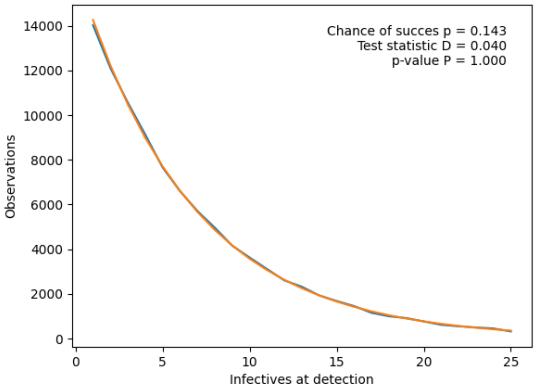
B. Figures



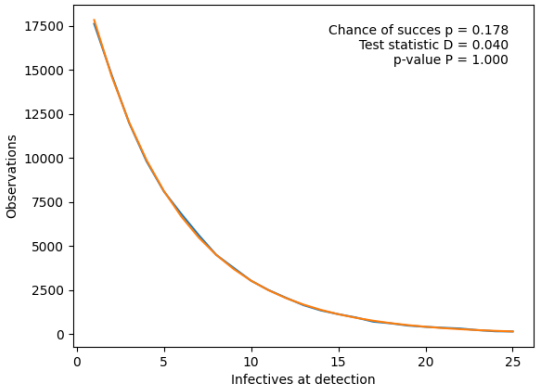
$\delta(t) = 0.025 \cdot e^{\frac{t}{10}}$, $c = \frac{1}{20}$



$\delta(t) = 0.05 \cdot e^{\frac{t}{10}}$, $c = \frac{2}{20}$

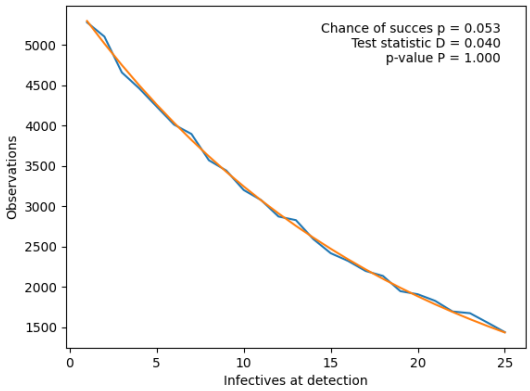


$\delta(t) = 0.075 \cdot e^{\frac{t}{10}}$, $c = \frac{3}{20}$

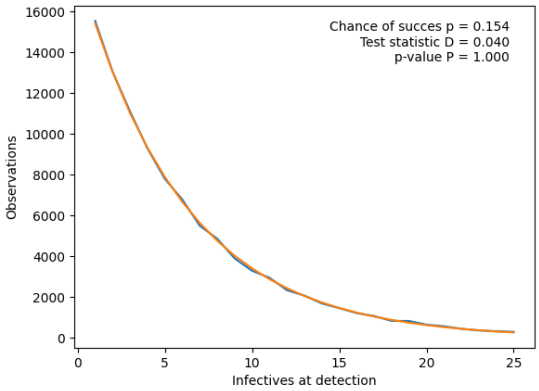


$\delta(t) = 0.1 \cdot e^{\frac{t}{10}}$, $c = \frac{4}{20}$

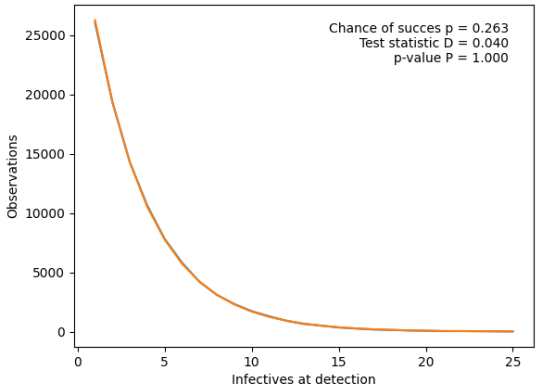
Figure 4: The distribution at D_1 for varying $c = \frac{\delta(t)}{\lambda(t)}$
$\lambda(t) = 0.5 \cdot e^{\frac{t}{10}}$
$L \sim \mathcal{N}(5, 2)$



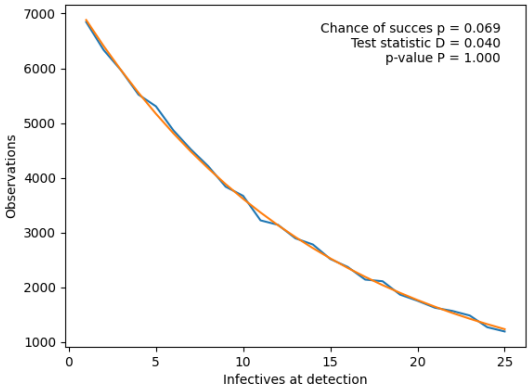
$L \sim \mathcal{N}(5, 2)$



$L \sim \text{Exp}(\frac{1}{2})$



$L \sim \mathcal{U}(0, 3)$



$L \sim \mathcal{U}\{1, 10\}$

Figure 5: The distribution at D_1 for varying distributions of life lengths
$\lambda(t) = 0.5 \cdot e^{\frac{t}{10}}$
$\delta(t) = 0.025 \cdot e^{\frac{t}{10}}$