Queueing System for COVID-19 Testing - A Parameter Study

February 10, 2021

Team Gamma: Sarah Bjärkby, Erik Flodmark, Kevin Olsson, Axel Strömberg,
MSc students, KTH, Royal Institute of Technology, Stockholm, Sweden

***Abstract*—The COVID-19 pandemic has shocked the world and efforts are being made to suppress the spread of the disease. This study contributes to research by performing a parameter study on current COVID-19 testing in Stockholm, Sweden. Interesting questions appear regarding how to model the queueing process in the pursuit of lowering the total expected waiting time, from queueing to receiving test results for COVID-19. In addition, sensitive parameters are identified and the implications are further discussed. The results derive from using a modified SIR-model in combination with an adapted M|M|s queue. Relevant parameter data is obtained from academic and non-academic sources and assumptions. With the parameters and assumptions used, the conclusions drawn is that testing alone is not effective enough to stop the spread. However, testing in combination with contract-tracing, might make the test results beneficial for decreasing the spread of the disease, and not only for analysis purposes.**

I. Introduction

A. Background

Diseases are troubling the world from time to time, where some epidemics develop into pandemics, most recently the rapid spread of the Novel Coronavirus (COVID-19) which first emerged late 2019 in China. When it was publicly known that the virus had spread over the world from its origin, governments worldwide decided to close their borders and announcing nationwide lockdowns in the hope of containing the spread. Yet the virus is still among us and efforts are still being made to lower the stress on the healthcare sector. The COVID-19 virus is a new disease introduced to the human population, which means that the entire world is susceptible of catching the disease since no one has developed antibodies at the point of the outbreak. Conspiracy theories aside, the virus has no purpose of massive destruction on its own, but examining the disease progression can be crucial in order to predict future outcomes of the spread and if or how the dynamics of such could be changed to speed up the containment of the virus. One of the most discussed topics during this ongoing pandemic is the extent of testing.

B. Literature Review

A simple mathematical model useful for modelling epidemics is the SIR-model or the SIS-model, differing in the development of immunity after recovering from the infection, where the former assumes that once infected you cannot be infected again. The SIR-model can be utilized for predicting the consequences of the spread such as infected people over time, total number of people infected simultaneously and expected pandemic duration[1]. Comprehensive research has examined these models in order to understand the probability of when and why an outbreak occurs, especially in the light of the currently ongoing pandemic. Greater focus has been put on determining the basic reproduction number, R_0, which becomes increasingly reliable as more validated data is being gathered. The World Health Organization (WHO) posted a preliminary estimation suggesting that R_0 lays in between 1.4 and 2.5[2], while further research concludes it is much higher. One study published in Elsevier explores the virus spread, taking undetected infectious cases into account, concluding that the basic reproduction number, R_0, in China is closer to 4.27[3]. Another study published in Oxford Academic summarizes different study estimates of the R_0, showing the range from 1.4 to 6.49, with WHO actually being at the lower end of the range[4].

Aside from the R_0, there is a number of additional assumptions that need to be considered in order to build credible models, including incubation time, size of the initial population, number of initially infected, and the actions taken by governments across the world to prevent the spread. Around the world, extensive discussions are underway considering different strategies of tackling the virus and which countries that are testing the most people per citizen[5]. Sweden stands out as controversial in the discussions regarding the efforts being made to stop the spread, since they did not order a strict lockdown or the closure of shops, restaurants, or schools, like most countries. This was at first considered highly risky and coupled with a high death rate as an implication[6]. International criticism and praise have named it "the Swedish model", describing a more relaxed

[1] Allen, *An Introduction to Stochastic Epidemic Models*.

[2] Rahman et al., "Preliminary Estimation of the Basic Reproduction Number of SARS-CoV-2 in the Middle East".

[3] Ivorra et al., "Mathematical modeling of the spread of the coronavirus disease 2019 (COVID-19) taking into account the undetected infections. The case of China".

[4] Liu et al., "The reproductive number of COVID-19 is higher compared to SARS coronavirus".

[5] European Data Portal, *Widespread Testing: Differing Strategies across Europe*.

[6] Cohen, *Sweden's Covid-19 policy is a model for the right. It's also a deadly folly — Coronavirus outbreak*.

strategy in the pursuit of reaching herd immunity, with the focus on offering optimal care rather than stopping the spread since the continuation of the spread was considered inevitable[7]. Today, fears of a second wave is ongoing in many countries across Europe, while the spread in Sweden is at lower levels partly due to developed immunity within the country[8]. Consequently, with the lack of face mask obligation or nationwide lockdown, the importance of testing presents itself in order to slow down the spread. It is thus important to know whom to isolate and when, which makes it interesting to investigate the testing strategy for a country or region.

Previous studies regarding COVID-19 in combination with queueing theory have been pursued using different approaches. One study conducted by American students from Cornell University, Princeton University, and University of Michigan, have analyzed the time evolution of hospitalized COVID-19 patients using queueing theory[9]. Since the infection rate fluctuates over time the study modelled hospitalized patients with an infinite queueing system with arrival rates being non-stationary Poisson distributed, with the aim to discuss how intensively the curve must be flatten in order to prevent overwhelming the hospital capacity. Their findings allowed them to calculate the dependency between the infection duration and peak queue length.

Another study published in the Social Science Research Network (SSRN) analyzes the effect of pooling and balking in combination with COVID-19 testing[10]. In particular, the question is whether centralized testing facilities or decentralized testing sites are preferable in handling the virus, and how expected queue length, waiting time, and balking probability are dependent on the current service rate, i.e. the efficiency of placing potential COVID-19 patients in the same centralized queue to mitigate people not entering a decentralized queue because of the current queue length. The study concludes that the balking behavior decreases if pooling is applied.

A third study within the same theme from The Medical Journal of Australia, investigates queueing theory to model the needs of intensive care unit (ICU) beds in Australia in response to the exponential rise in infected cases in Italy at the time[11]. The aim with this short study was similar to the first mentioned one, to not overwhelm the healthcare system and accordingly predict the ICU demand.

C. Purpose and Aim

Since the virus already is among us and possibly will be for the unforeseeable future, the purpose of this study is to target the actual testing process with the aim of isolating infected people as quickly and efficient as possible. One can model the SIR-model in combination with queueing theory in order to determine how many testing facilities or testing servers that are sufficient to have an impact on the spread, and to identify the implication of the spread depending on the efficacy and quality of the tests as well as the impact of the underlying parameters in the SIR-model. The objective of this study is thus to determine how the testing of potential COVID-19 patients should be performed in order to lower the total queueing time so that infected individuals can self-quarantine, until healthy, as quickly as possible. Subsequently, a sensitivity analysis of included parameters can be performed to simulate interesting scenarios regarding how many people that actually queues to be tested at different time steps as well as the ratio between people susceptible for catching the disease, people infected, and people recovered (or dead). The different scenarios can provide an indication of how the dynamics must change for these to be actualized. Considering that the Swedish model has attracted a lot of attention and also that the authors are resided in Sweden, this study will examine and model the testing in Sweden, in Stockholm, in particular.

The aim is to determine how to test infected individuals efficiently and isolate them in order to eventually flatten the curve. The queueing model will be simulated in combination with a sensitivity analysis in order to identify the parameters most important for the model to properly function. Additionally, predictions or conclusions can perchance be made about the duration of the pandemic for instance, if optimal testing occurs and isolation obedience is assumed.

1) Research Question: Defining total expected waiting time for current COVID-19 infection testing as the time from a person feels symptomatic until a test result - including queuing time, service time and response time.

- What are the implications of total expected waiting time for the spread of the virus in Stockholm?
- Which are the most sensitive underlying parameters and how do they affect the spread of the disease?

D. Scope

The extent of this research can become large quickly, consequently numerous limitations are assumed beforehand. As aforementioned, the study focuses on Stockholm, where a constant population will be considered, meaning that the model will not take entries and exits, or births and deaths, into account. The region Stockholm is chosen to symbolize how the general testing in Sweden looks like. Since it is accessible for a person living in Stockholm to travel anywhere in the region within reasonable time, it is assumed that the entire region counts as one singular testing facility with one associated queue. The phenomenon is known as pooling where numerous servers across the region pull patients from the same single queue. This benefits the service with respect to queueing time, which is a critical factor in the handling of sick patients in line with what previous research

[7]Ramachandran, "COVID-19—a very visible pandemic".

[8]Milne, *Anders Tegnell and the Swedish Covid experiment*.

[9]Palomo et al., *Flattening the Curve: Insights From Queueing Theory*.

[10]Long, Wang, and Zhang, "Pooling and Balking: Decisions on COVID-19 Testing".

[11]Meares and Jones, "When a system breaks: queueing theory model of intensive care bed needs during the COVID-19 pandemic".

published in SSRN confirms. The testing facility can then have servers (individuals performing the tests) spread out evenly over Stockholm. It is considered reasonable that all people in Stockholm wait in the same queue since the time it takes to travel to any testing server within the region is negligible in this case. Within such a delimited region there is no need to implement several parallel queues for different testing facilities. The thought of modelling the queueing system to multiple servers with a single line, also makes sense since delays caused by server failure can be prevented. This way, patients waiting in line are not affected by such bottlenecks which benefits the whole system since waiting times in general are lowered. It will be a shame if one particular server would break down (e.g. testing server is out of COVID-19 tests), leading to that people waiting in this particular queue are disadvantaged and have to be rerouted to another queueing system to receive a test. That would neither be fair nor practical considering that it is crucial to efficiently isolate infected people as soon as they feel symptoms.

Another argument supporting a centralized queueing system with one single line, is the prevention of balking discussed earlier. This study will thus omit the balking risk and instead implement the occurrence of reneging, which is more applicable considering that patients can recover during the queueing time, and that the event of relapse is unlikely with respect to developed antibodies. In general, reneging means that people are leaving the queue based on the lack of patience, but in this case, it exemplifies patients starting to feel healthy and thus decide to leave the queue with some probability. With that said, the results from this study can presumably be applicable for other closed regions as well. Moreover, it is also assumed that all people share the same demographic variables, like age, gender, and underlying diseases, but also all socio-economic data and behavioral patterns. Besides, all people live evenly distributed over Stockholm and every individual therefore faces the same risks of getting infected. Accordingly, the model does not distinguish between people in any way, making the model comparatively flawed considering hypotheses dealing with higher death rate among elderly for instance. Furthermore it is assumed that full testing capacity is ready to be utilised from day one. In addition, there are great limitations in trustworthy data considering the early stages of the pandemic and the knowledge-deficiency about the characteristics of the disease, such that the rate of secondary infections, the existence of immunity development, and the level of severity once infected. Basically, the model just takes the different stages into consideration about where a person stands in the process of getting infected. The stages are that one can be susceptible for catching the disease, infectious, symptomatic, or removed, where the latter means that the once infected patient has been isolated and stay isolated until clinically recovered.

The study utilizes mathematical modelling of infectious diseases as well as queueing theory as a foundation for the analysis. In order to make calculations simplified, a number of specific assumptions will be further described in the Data section. One major initial assumption in the model is that only infected COVID-19 patients are entering the queueing system which will imply that all people in the system eventually will be tested positive and therefore isolate themselves. This event is by all means highly unlikely since it is impossible to decide beforehand which people in the queueing system that are infected and which people that show false symptoms. However, this simplification facilitates the study results which in turn will be used to analytically provide a conclusion to the research question taking false symptoms and negative test results into consideration. Therefore, the events of false positives and false negatives are avoided and neglected. In addition, all people are expected to act as the model suggests, meaning that if the model decides that a person is tested positive, this particular individual will self-quarantine until recovered. Lastly, the study aims to take an unbiased opinion regarding measurements taken in the fight against the virus.

Summary of delimitations

- System of analysis is Stockholm
- Full testing capacity available from day one
- Homogeneous population
- One queue for testing
- Only symptomatic individuals get tested

II. Theoretical Framework

In this section the mathematical theory that provides the basis for the model is presented. The components are described rather briefly only addressing the cores of the theories and are mainly based on *An Introduction to Stochastic Epidemic Models* by Linda Allen[12].

A. The SIR-Model

The SIR model builds upon three separate compartments including; S for *Susceptible*, I for *Infected*, and R for *Removed*. A susceptible person is a person in the examined population who is healthy but can become infected. Once infected, the person has developed the disease and whether or not s/he shows symptoms, s/he is infectious and can spread the disease further to others in the susceptible group. Eventually a person in the infected group either recovers or dies from the disease and therefore is considered to be included in the removed group, since it is assumed that once recovered from the disease the person has developed antibodies against that disease.

The flow between the different states of the model is visualized below and mathematically illustrated by Kermack and McKendrick's differential equations as in (1-3).

[12]Allen, *An Introduction to Stochastic Epidemic Models*.

$$\frac{dS_t}{dt} = -\beta SI \tag{1}$$

$$\frac{dI_t}{dt} = \beta SI - \gamma I \tag{2}$$

$$\frac{dR_t}{dt} = \gamma I \tag{3}$$

B. The M|M|s Model

Customers are entering a queueing system and the queue sequentially. Arrivals to the queue come from a finite or infinite calling population where customer arrivals are often modeled as a statistical pattern, a distribution by how customers are generated into the system. By the queueing discipline one customer is selected to be served and thereafter leave the queue. The choosing factor deciding which customer to serve next can be random, first-come-first-served, or prioritized in some other way.

The M|M|s model is a modified birth-and-death process that irrespective of the current state of the system has both constant mean arrival rate (λ_n) and mean service rate per busy server (μ_n). The first M indicates that the inter-arrival times have the Poisson distribution (Markovian) which are assumed to be independently and identically distributed (i.i.d.). The second M specifies that the service times also are i.i.d. Markovian but with an exponentially distributed time. The "s" is a positive integer denoting how many servers that are in the system. The servers work in parallel and when a server is finished with a customer a new one is immediately picked from queue to be served[13].

C. The Poisson Distribution

A Poisson Process is a model for a series of discrete events where the average time between events is known, but the exact timing of events is random. Events are independent of each other but events per time period is constant. The Poisson Distribution probability mass function gives the probability of observing k events in a given interval of time or space and the average events per time or space according to:

$$f(k, \lambda) = P(X = k) = \frac{\lambda^k \mathrm{e}^{-\lambda}}{k!} \tag{4}$$

D. The Exponential Distribution

The exponential distribution is used to model time between events, in which events occur continuously and independently at a constant average rate:

$$f(x, \lambda) = \begin{cases} \lambda \mathrm{e}^{-\lambda x} & x \geq 0 \\ 0 & x < 0 \end{cases} \tag{5}$$

E. Reneging

Reneging occurs when an individual arriving to a queue have a certain patience for staying in the queue. The patience is exponentially distributed with a known intensity. If the waiting time in the queue is longer than the patience, the customer will leave the system, i.e renegade.

[13]Hillier and Lieberman, *Introduction to Operations Research 9th Edition*.

III. Data

A. Data Preprocessing of Assummptions

1) Susceptible: The investigation regarding the testing process is examined on Stockholm and therefore the initial calling population susceptible of catching the disease is the population of Stockholm, i.e. approximately 2.4 million people registered according to Statistics Sweden[14]. This number of unique customers available for the model is chosen since it is assumed that no one has developed antibodies at the time of the national outbreak. The assumption about a constant population also proves justifiable since Statistics Sweden states that the population growth has been low during the pandemic, actually the lowest since 2005.

2) Initially infected: In order to have trustworthy data, in line with previous spreading of diseases and the current number of infected individuals, it is assumed that initially infected individuals at the time of the outbreak is 1% of the total population, i.e. 24 000 initially infected in a population of 2.4 million. This implies a total population of 2 424 000 individuals used in the model. The additional 24 000 can for example be assumed to have traveled to Stockholm. This since 90 000 people in Sweden currently have been confirmed infected, which is almost 1% of the total population of 10 million[15]. In reality, the number of initially infected depends on several factors. In this model, though, it is assumed that all initially infected people have become infected at the same time step.

3) Incubation time: The time for an individual to show symptoms after getting exposed to the virus is called incubation time. The incubation time ranges within the confidence interval 1-14 days, where the mean is 5-6 days[16]. It is thus assumed that it takes approximately 5 days to develop symptoms of COVID-19 once infected. In addition, it has been noted some cases being contagious during the pre-symptomatic time period leading to the conclusion that all infected patients in this study are indeed infectious during the entire incubation time[17].

4) γ (rateIR): In the *Report of the WHO-China Joint Mission on Coronavirus Disease 2019 (COVID-19)*[18] preliminary data suggested that mild cases of Coronavirus have a median clinical recovery time from onset of symptoms of around two weeks, while the same time for more severe cases is 3-6 weeks, and the death of patients usually occurred 2-8 weeks after onset of symptoms[19]. However, this was early invalidated data, and later research suggests that around 99.9% of infected individuals are fully recovered two weeks

[14]Statistiska Centralbyrån, *Låg folkökning i Sverige under coronapandemin*.

[15]Worldometer, *Sweden Coronavirus: 90,923 Cases and 5,880 Deaths - Worldometer*.

[16]WHO, *Coronavirus disease 2019 (COVID-19) Situation Report-73 HIGHLIGHTS*.

[17]Ibid.

[18]Aylward and Liand, *Report of the WHO-China Joint Mission on Coronavirus Disease 2019 (COVID-19)*.

[19]Ibid.

after onset symptoms[20]. The Public Health Agency of Sweden, Folkhälsomyndigheten, uses a γ with 5 days average infectious time since it is the estimated time of how long an individual can infect others[21]. The γ-value is normally chosen as $1/$(infectious time)[22], where the infectious time in this model is 10 days, i.e. 5 days incubation time plus 5 days to stop being infectious after onset of symptoms. For calculating β (see below), the γ-value of $1/10$ is thereby chosen. For the SIR-model used in this project, all infected individuals are given a randomized time to recovery with a mean of 10 days, including 5 days incubation time. This means that the normal flow from the infected to recovered stages in the SIR-model, is replaced.

5) R_0: The basic reproduction number, R_0, is unknown and therefore hard to take into account. However, estimates of R_0 have been made and according to the article *The reproductive number of COVID-19 is higher compared to SARS coronavirus*, estimates "range from 1.4 and 6.49 with a mean of 3.28, a median of 2.79."[23]. The choice of R_0 in this project came from the mean of the mean and median found in the article study, i.e approximately 3.

6) β (rateSI): Research suggest that β is derived from the other parameters by the formula $\beta = R_0 * \gamma$[24]. Since γ is estimated as $1/10$ and R_0 as 3, the β is calculated to $3/10$.

7) Number of servers: In order to find a reasonable number of initial testing stations for the region, the existing testing capacity in Stockholm was investigated. It appears that there exist over a hundred testing stations in Stockholm[25]. In reality, a fraction of those who get tested, receives a positive test result. The fraction of tested and not infected varies greatly between regions and weeks, leading to a bold assumption that 75% of tested individuals is not infected with COVID-19. Therefore, since this model only considers symptomatic people that are infected with COVID-19, the number of initial testers is chosen as $0.25 \times 100 = 25$ testers. It is assumed that the servers are working seven days a week. If the server is serving someone when a working day ends they will finish the testing of that person and compensate for that time the next day.

8) Testing capacity per server: This data point corresponds to how many tests one server can complete during one day. It is assumed that the time for the test including preparation time is around 15 minutes. If one server is expected to work eight hours per day (assuming no breaks), one server can complete four tests an hour for eight hours, i.e. 32 tests per day per server. It is assumed that the number of tests per day does not differ between workdays and weekdays.

The Public Health Agency of Sweden (Folkhälsomyndigheten, FHM) has a national goal of 100 000 tests a week[26], which simply estimates the goal of Stockholm to be around 25 000 tests since approximately one quarter of the population is registered there. Now, taking into account the fact that 75% of the tested are assumed to be negative, means that 6 250 tests are positive, which is the number this model seeks. A test to evaluate and verify if the data of the number of servers and the tests per day is reasonable is carried out by calculating 25servers$\times$32tests per day$\times$7days per week = 5 600 tests per week which matches the estimated goal of 6 250 tests per week well.

9) Waiting time for test results: The waiting time to receive the test result appears to differ between different regions. For example, in Stockholm it is said that test results should be received within one week, in Skåne the result is received after 1-3 days etc. An arbitrarily median waiting time was thus assumed to be 3 days considering Stockholm expects the waiting time to be within one week, while other regions report it to take up to just a few days[27],[28],[29],[30].

10) Probability of showing symptoms and having COVID-19: Estimations of the probability of a COVID-19 infected individual showing symptoms have been carried out on isolated groups, such as the "Diamond Princess" cruise ship that was hit by COVID-19 early in its spread[31]. The estimations showed that 82.1% of infected individuals were showing symptoms. Other studies have pointed to even lower values. The choice of the probability of showing symptoms was decided to 80%.

11) Probability of showing symptoms but not having COVID-19: It is difficult to estimate the number of people showing symptoms associated with COVID-19 but that is not infected. These individuals might queue for testing and should thereby be considered. Looking at past data a broad assumption that 50%, 75% or 95% of the tested are not infected with COVID-19 is made[32]. In the standard case 75% will be assumed and the other percentages will be analysed. The percentages vary when looking at countries that have succeeded with isolation and contact tracing in an early stage of the outbreak. The assumption of 50%, 75% or 95% not infected will be added analytically to the results in

[20]Ibid.

[21]Folkhälsomyndigheten, *Estimates of the number of infected individuals during the covid-19 outbreak in the Dalarna region, Skåne region Stockholm region, and Västra Götaland region, Sweden*.

[22]Wearing, Rohani, and Keeling, "Appropriate models for the management of infectious diseases".

[23]Liu et al., "The reproductive number of COVID-19 is higher compared to SARS coronavirus".

[24]Ridenhour, Kowalik, and Shay, "Unraveling R0: Considerations for public health applications".

[25]Lindholm, *Alla stockholmare erbjuds gratis coronatester*.

[26]Fjellström, *Hallengren: Vi ska testa 100 000 i veckan — SVT Nyheter*.

[27]Stockholm 1177, *Provtagning för dig som är sjuk - 1177 Vårdguiden*.

[28]Universitetssjukhuset, *Vanliga frågor och svar - Sahlgrenska Universitetssjukhuset*.

[29]Skåne 1177, *Frågor och svar om självtest för covid-19 - 1177 Vårdguiden*.

[30]J. 1177, *Lämna prov för covid-19 - 1177 Vårdguiden*.

[31]Mizumoto et al., "Estimating the asymptomatic proportion of coronavirus disease 2019 (COVID-19) cases on board the Diamond Princess cruise ship, Yokohama, Japan, 2020".

[32]Folkhälsomyndighetenn, *Genomförda tester för covid-19 — Folkhälsomyndigheten*.

the discussion. Additionally a model extension adding that 1%, 2.5% and 4% of susceptible individuals showing false symptoms is made. Furthermore, it is assumed that a false infected susceptible will recover in 5 days.

12) Queueing discipline: It has been discussed how the prioritization of customers queueing to be tested needs to be done. The standard setting is that the first person in the queueing system is the first person out to be served (FIFO), by obvious reasons. However, another discipline examined is that the last person in the queueing system is the first person out to be served (LIFO), by the fact that newly infected patients are more likely to be sick for a longer time period and therefore are crucial to isolate first. Of course, it would improve the model significantly if a prioritization disciplined taking underlying diseases into account (since they are in most need of proper healthcare if infected) was to be deployed, but since this model assumes a homogeneous population this is not implemented.

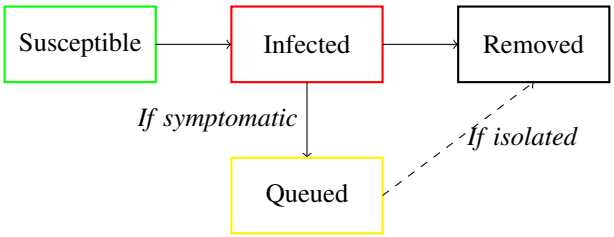
B. Final Data

The final data used for the parameters in the standard case is stated below, which acted as the foundation going forward into the modelling and fine tuning of parameters:

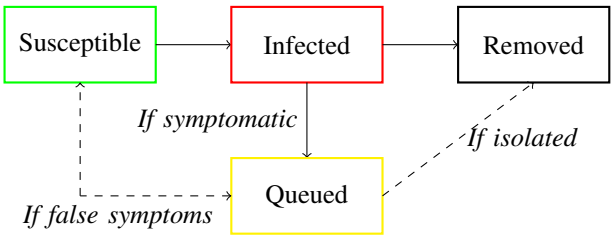
Susceptible	2,400,000
Initially infected	24,000
Incubation time	5 days
γ	1/10
β	3/10
Number of servers	25
Testing capacity per server	32 tests per day per server
Time until test result	3 days
Probability of showing symptoms when COVID-19 infected	80%
Probability of showing symptoms but not having COVID-19	75%

IV. Method and Modelling

The flow between the states in this modified SIR-model is illustrated in the figure below.



The flow between the states in a more realistic scenario handling false testing as well is illustrated in the figure below, which analytically will be presented as well as exemplified with a potential mathematical implementation.



A. Method

The method in this study was at first to approach the question at hand and formulate a problem description focused on the Coronavirus, and then problematize how to go forward modelling the problem with included assumptions. The data for the assumptions is a crucial part in order for the final model to provide reasonable results. A quantitative research method was therefore conducted to collect the most reliable numerical data to include in the model. The data was analyzed thoroughly with the aim to reflect the current situation in Stockholm, where numbers were foremost used as initial data open to change. Some data points were more complicated to determine considering that the literature mostly uses early preliminary data. Accordingly, the study will do a parameter study by doing adjustments to some parameters while keeping others unchanged in order to see how sensitive the model is for the respective changes.

The SIR-model is to be revised and combined with a queueing system, that reminds of a M|M|s queue, to handle the testing process. The adapted M|M|s queue has servers and exponentially distributed service time as the original model. However, it replaces the Poisson distributed arrival rates from the original model, with individuals arriving to the queue according to their incubation time, which is Poisson distributed. The difference is thus that there is no steady arrival rate to the queue as there would be in the original model.

The entire population of Stockholm, i.e. 2.4 million people, are susceptible for catching the disease and are thus included in stage S. Once a susceptible individual becomes infected by COVID-19, the person enters the infectives stage I. However, stage I is in this model divided into two subgroups, which are one group consisting of infectious individuals not showing symptoms while the other group comprises infectious individuals having symptoms as well. The model then assumes that a symptomatic person in I starts to queue for taking a test, meaning that the person still is in stage I but also waiting in line to be tested. Later on, once tested, the person will receive a result from the test and if this result shows positive, the person will self-quarantine until recovered or dead. If a person receives a positive test, the person will stay isolated and be unable to infect others. In the case of a negative test, the person is considered to have shown false symptoms and therefore stays in S, although

never occurring in the main model handling only positive COVID-19 patients.

The ultimate model will in detail be described below. However, the process of constructing the final model have been iterative, where functionality have been added continuously after revision of preliminary results and when new implementation ideas have surfaced. Two things that have subsequently been added are the implementation of different serving priorities from the queue, and the event of reneging, i.e. when infected people in the queue start to feel better and are thus likely to leave the queue before getting served with a test. Since the model intends to analyze the optimal testing for 2.4 million people, the simulation is expected to take extensive time considering that the aim is to do a parameter study that will require the system to run repeatedly. To tackle this problem, the simulation was made on much smaller data sets starting at 2 400 people and was further increased to 24 000 and 240 000. When testing the model with the different data set sizes, a linear relationship pattern was identified so that the model can be used on a much smaller data set. Consequently, the running time of the system can decrease manifold when trying to find the optimal combination of parameters for different purposes. However, smaller data sets are more sensitive to the randomization functions utilized and therefore need to be thoroughly analyzed before being extrapolated in use with larger data sets. Since the scaling worked out well, all simulations were be made on a population of 24 000 people, which can be multiplied by a factor of 100 in order to visualize the true population size.

B. Model

When creating the model, some assumptions were made. Firstly, the initially infected individuals are assumed to become infected on the first day. This can be thought of as if all initially infected got infected on the same flight and simultaneously infected all people at Stockholm Arlanda Airport, which marks the start of the national outbreak. Secondly, every person who feels symptomatic (and have COVID-19) queues and stays in the queue until served or leaves the queue with an exponentially distributed time after feeling asymptomatic, i.e. the occurrence of reneging. Lastly, only individuals infected with COVID-19 queues, this is discussed further in the analysis.

In order to take into account complex details, this model implements an object-oriented, time and person discretized simulation. The objects are shown below.

- Model
  - People
    - Person
      - States
        a. Stage - S/I/R
        b. IsInfective
        c. IsSymptomatic
        d. IsQueued
        e. IsIsolated
      - Methods
        a. Infect()
        b. Queue()
        c. Test()
        d. Isolate()
        e. Recover()
        f. Renegade()
  - Queue
    - List
      - States
        a. Queue
      - Methods
        a. Pop()
        b. Put()
        c. SimulateDay()
        d. Renegade()
    - Server
      - States
        a. μ
        b. EmploymentRate
      - Methods
        a. SimulateDay()

1) SIR Model: The SIR-model used in this project has relations to the original SIR-model. It has the same flow from S to I (rounded to integer) whereas the flow from I to R is replaced so that an infected person recovers after a random, Poisson distributed number of days, with mean 1/ γ.

The time in the model is discretized, where one time step is one day. An individual in the model is discretized and all individuals are placed in a list of person objects. A person/object is thereby not “moved” between S, I and R but rather gets a ”tag” with S, I or R. Furthermore, by preserving the order of the list, indexes can successfully be tracked for optimization purposes. Parts of the model use stochastic values where random numbers are generated from specific distributions.

The flow of an individual in the SIR-model used, is described below.

1) Susceptible
   All individuals start off as susceptible to the virus, except for the initially infected that are needed to start a spread of the virus in the society.

2) Susceptible to Infected
   The same flow equation from susceptible to infected as the default SIR model is used in this project, i.e.

$$\begin{aligned} \frac{dS}{dt} &= -\frac{\beta IS}{N} \\ \frac{dI}{dt} &= \frac{\beta IS}{N} \end{aligned} \tag{6}$$

   and the flow is rounded to the nearest integer. The

differential equations are numerically solved using the Euler method. The susceptible people are randomly selected and infected according to the infectious rate, meaning that no regard is taken to if these people have "met" or not.

Infect() - The function Infect(), "infects" an individual with COVID-19. When this individual is infected, a list of Poisson random numbers are generated to give:

- Time until symptomatic
- Time until recovery

with mean values according to the derived data. Furthermore, a person won't show symptoms at all with probability $1 - p_{\text{symptomatic}}$. A person stays infectious until it is recovered or gets a positive test result and isolates.

3) Infected
When an individual is infected it goes through several steps in the model until it is removed. The steps are described below in the order of the model flow.

Queue() - When an individual feels symptomatic, that individual is queued for a test and eventually receives a test result or renegades. The individual is placed last in the queue. Depending on the length of the queue, an individual can be served from the same day of queueing and forward.

Renegade() - If the queue time is long, an individual can recover while waiting in line. After an individual recovers and no longer shows symptoms, he or she will not stay in the queue forever. The individual will leave the queue after a random, exponentially distributed, time of patience.

Test() - When an individual is tested, the time until the test result is given with a number of days delay, which is defined in the model and is allowed to be zero, i.e. a person can get served (tested) the same day it feels symptoms and queues. The person must still wait to receive the result.

Isolate() - If the result is positive, the individual is isolated until it recovers. That means that this person can no longer infect anyone, i.e. dS/dt only takes into account infectious, non-isolated individuals. The isolation is thereby assumed to be complete.

4) Infectious to Removed
Every individual receives a randomly distributed time to recover with a mean of $1/\gamma$ days at the time of infection.

Recover() When an individual is recovered, according to its distributed time, all infection parameters are deactivated and the individual is tagged as Removed.

5) Removed
A person is recovered when the discretized time goes beyond the randomized time when the person should recover. All individuals recovered (or dead) from the Infectious group ends up being Removed.

2) Queue: **M|M|s queue**
When an individual is infected, it gets a random, Poisson distributed time until it is symptomatic. The arrival rate to the queue depends on when an individual is symptomatic, since it will start to queue when feeling symptoms.

The flow of actions in the queue model is described below.

1) Put in queue
Put() - When an individual is infected and symptomatic, it is put in the queue.

2) Get served
- Each server serves with an exponentially distributed random number.
- The individuals in the queue are served as FIFO - pops the first element in the list (the individual that has been queueing for the longest amount of time).
- Each server serves (tests) as many people as possible during a day (one time step) according to a randomized service length with a mean of 1/maximum number of tests per server per day. If the day is over, a servers is assumed to finish the patient it is currently working with. However, s/he will work less the day after corresponding to the overtime today.
- If `nServers = 1.5` is specified, one server work full time and one server works half time, i.e. serves half as many people per day.

3) Remove from queue
Pop() - When an individual is tested, it is popped out of the queue, i.e removed from the queue.

SimulateDay() - Determines how many individuals from the queue to test in one day. This method calls on `server.SimulateDay` so that each server serves patients according to an exponentially distributed death rate.

Renegade() - When an individual feels asymptomatic, its patience for staying in the queue are randomized to a number of days. If the randomized number of days have passed and the individual have not been tested, it will leave the queue, it renegades.

C. Simulation

The simulation has been made using Python, where all the code can be found in the GitHub-repository[33], linked in references.

[33]Strömberg, Axel, Erik Flodmark, Kevin Olsson, and Sarah Bjärkby, *COVID-19: SIR-model with M|M|s queue for testing*.

V. Results

To obtain an optimal test strategy, an analysis has been made by varying the:

- number of servers
- queue inclusion of symptomatic non COVID-19 infected
- sensitivity analysis of β, γ and R_0
- time to receive test result

Apart from the parameters that are varied in each simulation, all other data is according to section III-B.

A comparative SIR-model analysis with the respective parameter values is run. Secondly, a simulation showing the expected total waiting time in days, the fraction of infected, asymptomatic and isolated individuals every day as well as the respective SIR-model are run. This, together with the peak value of the infectious curve, showing the number of infected per day, the peak of the queue (in days), and the total number of infected will provide the basis for the discussion.

A. Number of servers

As discussed in Section III-A, 25 servers in Stockholm correspond to the testing goal of The Public Health Agency of Sweden. Since using only 24 000 as population size, this corresponds to 0.25 servers. The number of servers analysed will be 0, 0.25 and 4 in order to see what would happen without any testing, with testing goal of The Public Health Agency of Sweden and with a much higher testing strategy.

SIR-model comparison of 0, 0.25 and 4 servers.

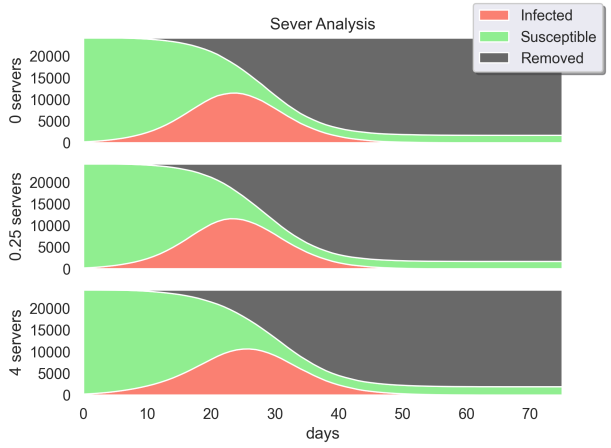


Fig. 1. SIR-model server analysis

0 servers

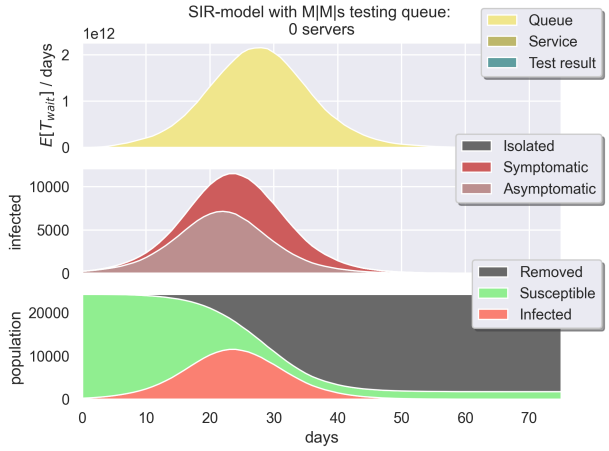


Fig. 2. Simulation showing 0 servers

0.25 servers

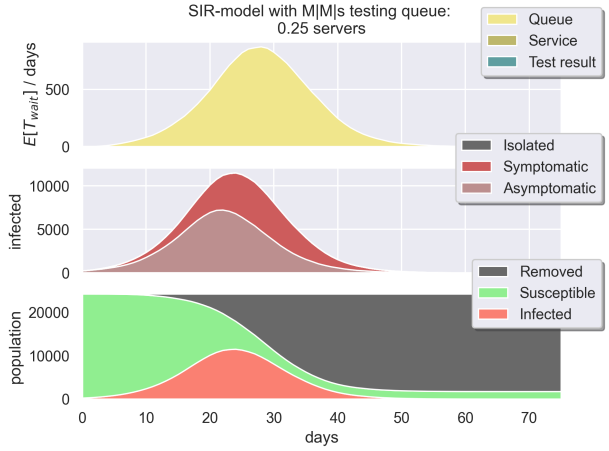


Fig. 3. Simulation showing 0.25 servers

4 servers

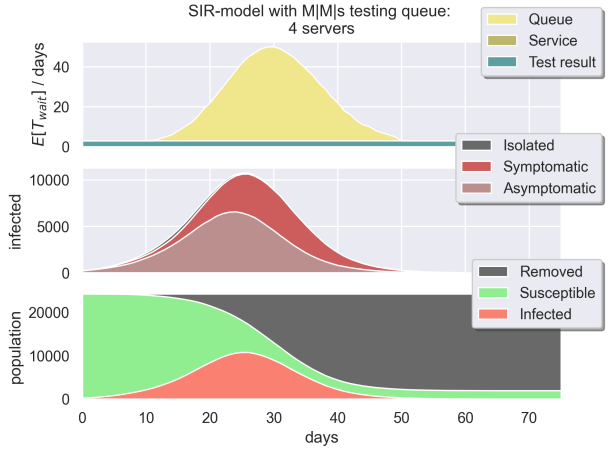


Fig. 4. Simulation showing 4 servers

Number of servers analysis

No. of servers	Peak of queue (days)	Peak of infected	Total number of infected
0	∞	11 673	22 515
0.25	859	11 492	22 496
4	49	10 675	22 314

1) Effect of queue time and spread using other parameters: To show when the testing actually affects the spread, the model is run using different data for γ, β, time for test result and incubation time. This could correspond to the spread of another disease or COVID-19 as the data for this disease is not trustworthy at this point.

Figure showing the queueing time, spread of infected individuals and SIR-model with no servers.

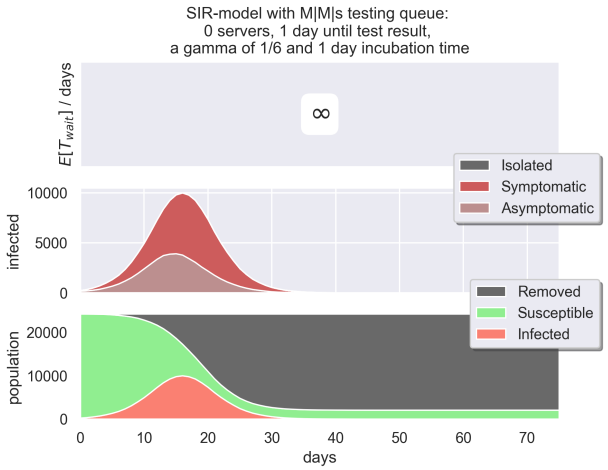


Fig. 5. Simulation showing 0 servers

Figure showing the queueing time, spread of infected individuals and SIR-model with 4 servers.

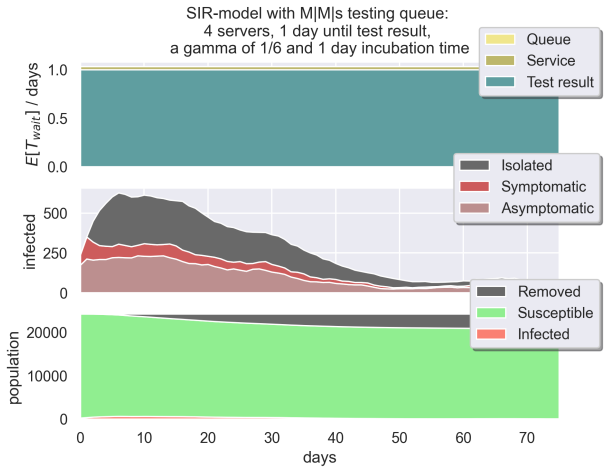


Fig. 6. Simulation showing 4 servers

Effect on queue time and spread using other parameters

No. of servers	Peak of queue (days)	Peak of infected	Total number of infected
0	∞	9 995	22 178
4	1.03	627	3 481

B. Including Symptomatic Susceptibles in Queue

Individuals showing symptoms similar to COVID-19 might queue to rule out possible infection. Therefore, an addition to the model to assess the consequences of this additional queueing is added and analysed.

For the analytical part, the number of servers disregarding symptomatic non COVID-19 infected individuals will be divided by (1 – the chosen fraction), e.g. 25 servers and 75% of those in queue not being infected, leading to 25/(1-0.75) = 100 servers. The probabilities and corresponding server volume is shown in the table below.

Taking negative COVID-19 tests into account

Contact tracing:	Good	Normal	Bad
Probability of showing symptoms	50%	75%	95%
Fraction of positive tests	50%	25%	5%
Total number of servers needed	25*2=50	25*4=100	25*20=500

For visual purposes, model simulations with 1%, 2.5% and 4% of the susceptible population getting false symptoms every day are executed. There are difficulties with implementing a more realistic setting. Therefore, this simulations work as an example on how the qeueuing would behave if including symptomatic susceptibles. Here, the total expected waiting time is replaced by the queue distribution of susceptible, infected, and removed individuals.

SIR-model comparison

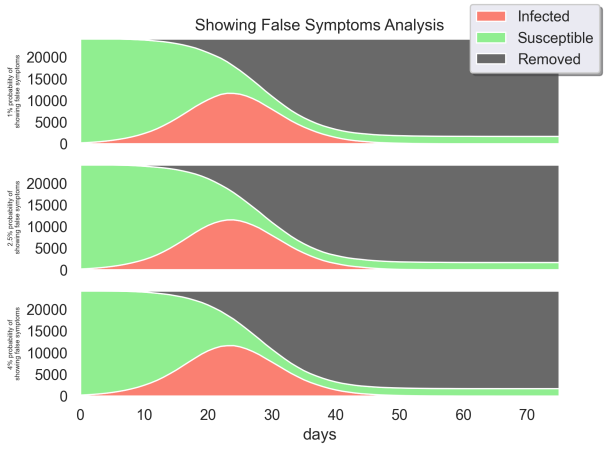


Fig. 7. SIR-model analysis of additional queueing by symptomatic susceptibles

1% probability of showing false symptoms

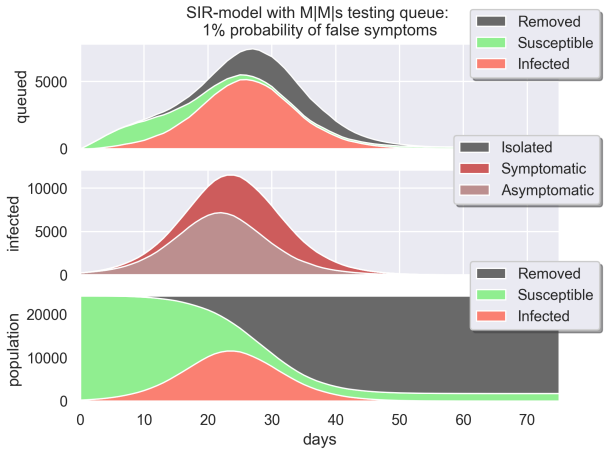


Fig. 8. 1% probability of showing false symptoms

2.5% probability of showing false symptoms

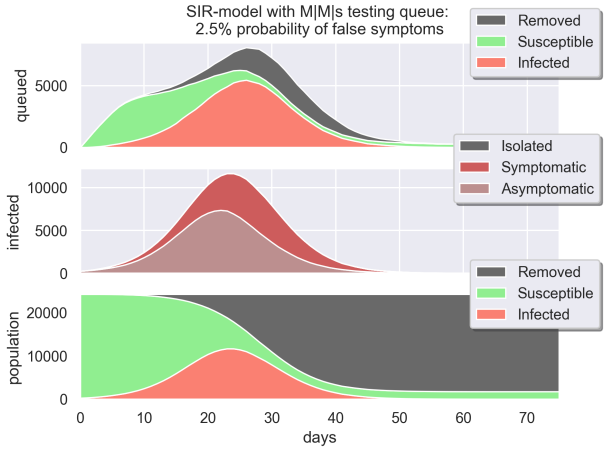


Fig. 9. 2.5% probability of showing false symptoms

4% probability of showing false symptoms

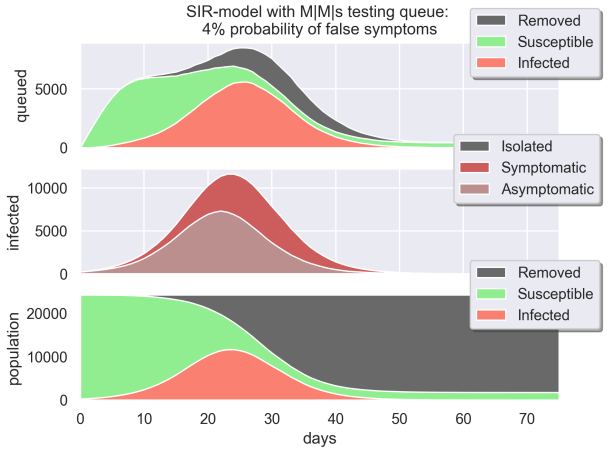


Fig. 10. 4% probability of showing false symptoms

The results from the false COVID-19 symptoms analysis

Probability of showing false symptoms	Peak of queue (days)	Peak of infected	Total number of infected
1%	971	11 594	22 499
2.5%	1 089	11 754	22 521
4%	1 163	11 473	22 467

C. *Sensitivity analysis of β, γ and R_0*

The β-value calculated from R_0 and γ does not have a high certainty since both the R_0 and γ values are estimated from literature. Therefore, an analysis of how small variations in β, γ and R_0 affect the total result is carried out. The implied β's utilized for this sensitivity analysis are derived with respect to R_0 and infectious time which are stated in the table below. The table suggests that γ ranges from 0.05 to 0.167, while β ranges from 0.233 to 0.427.

Beta, gamma and R0 comparison

Description	R_0	Incubation Time (days)	Symptomatic Time (days)	γ	β
Lowest R_0, short recovery	1.4	1	5	0.167	0.233
WHO's highest R_0	2.5	5	5	0.100	0.250
Standard case	3.0	5	5	0.100	0.300
Elsevier's R_0	4.27	5	5	0.100	0.427
Highest R_0, long recovery	6.49	10	10	0.050	0.325

The SIR-model with different values on β, γ and R_0 respectively is depicted below.

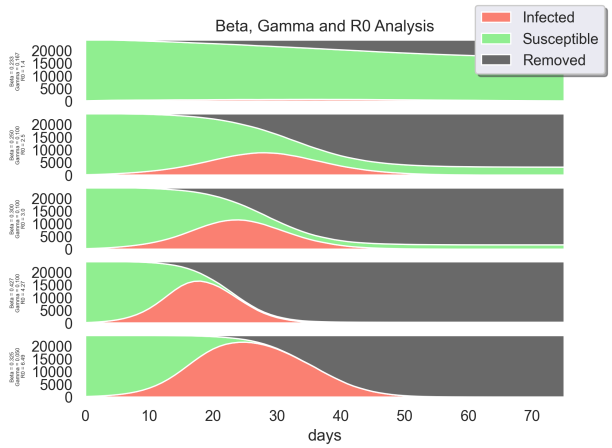


Fig. 11. Analysis of β, γ and R_0 values

Beta = 0.233, Gamma = 0.167, R0 = 1.4

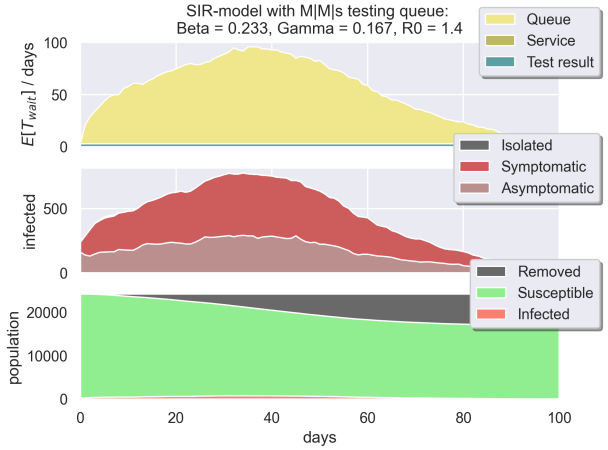


Fig. 12. Simulation of Beta = 0.233, Gamma = 0.167, R0 = 1.4

Beta = 0.250, Gamma = 0.100, R0 = 2.5

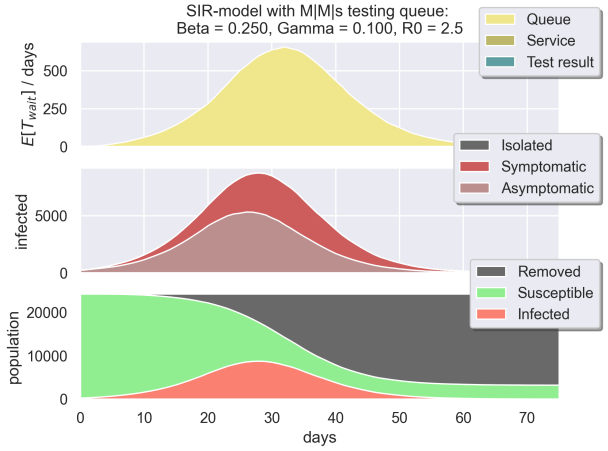


Fig. 13. Simulation of Beta = 0.250, Gamma = 0.100, R0 = 2.5

Beta = 0.300, Gamma = 0.100, R0 = 3.0

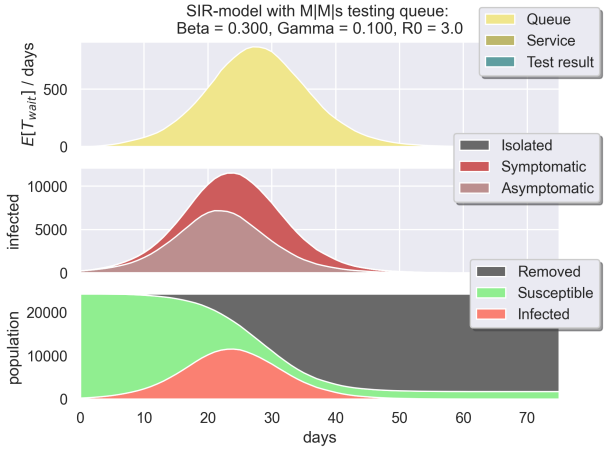


Fig. 14. Simulation of Beta = 0.300, Gamma = 0.100, R0 = 3.0

Beta = 0.427, Gamma = 0.100, R0 = 4.27

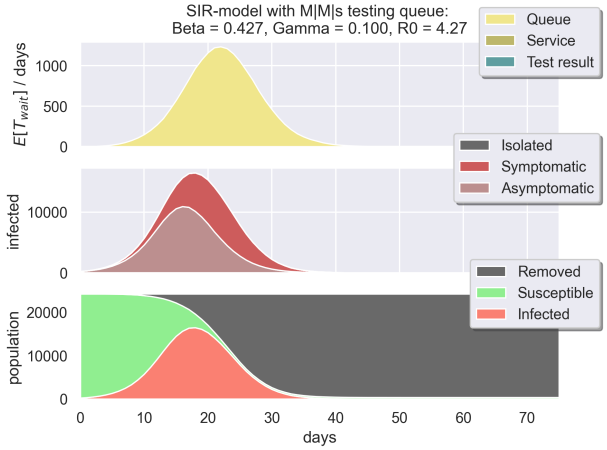


Fig. 15. Simulation of Beta = 0.427, Gamma = 0.100, R0 = 4.27

Beta = 0.325, Gamma = 0.050, R0 = 6.49

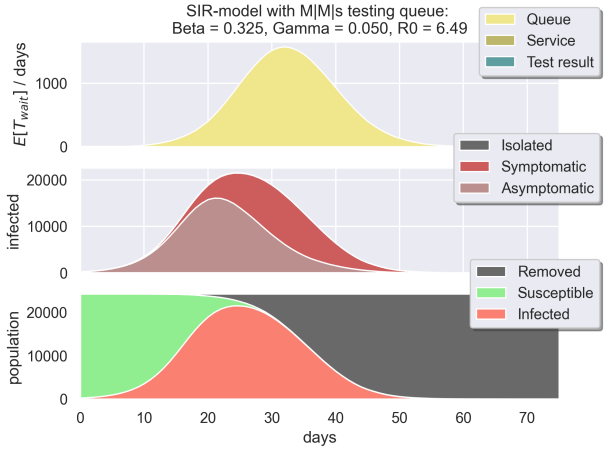


Fig. 16. Simulation of Beta = 0.325, Gamma = 0.050, R0 = 6.49

The results from the sensitivity analysis

β	γ	R_0	Peak of queue (days)	Peak of infected	Total number of infected
0.233	0.167	1.4	97	790	7 224
0.250	0.100	2.5	653	8 653	21 008
0.300	0.100	3.0	878	11 597	22 514
0.427	0.100	4.27	1 231	16 489	23 884
0.325	0.050	6.49	1 575	21 569	24 214

D. Time for test result

The average time for waiting on a test result in Stockholm today is estimated to one week with a total range in Sweden from one to seven days depending on region. Therefore, the choices of test values for the time to test result are 1, 3 and 7 days.

The SIR-model comparison of 1, 3 and 7 day(s) until test result is received counted from the day the test is taken.

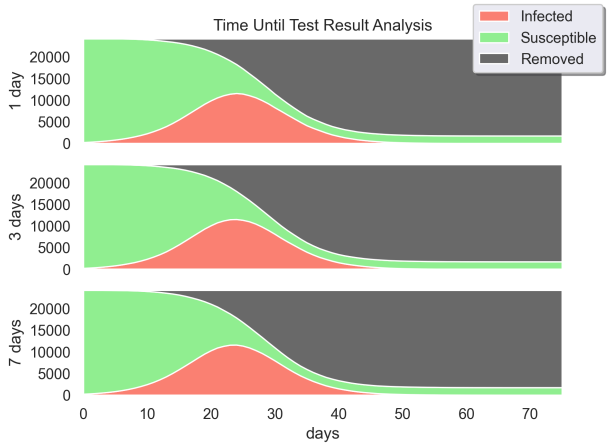


Fig. 17. SIR-model analysis of time to test result

1 day

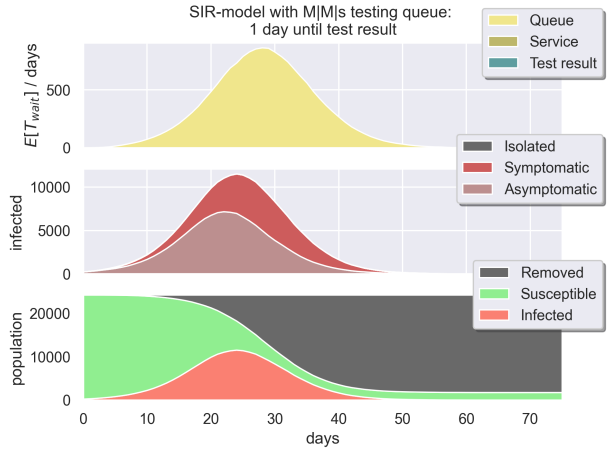


Fig. 18. Simulation of receiving test result after approximately 1 day

3 days

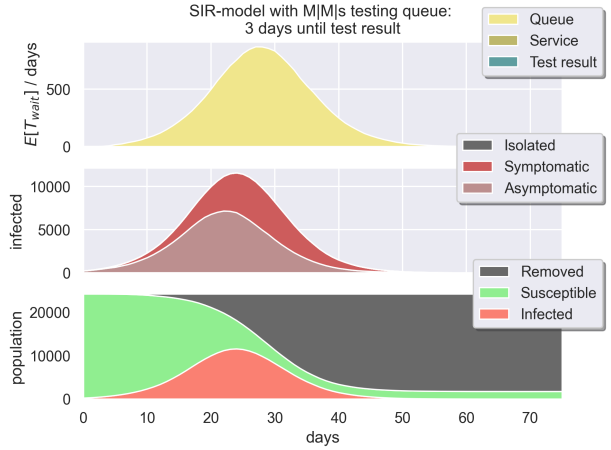


Fig. 19. Simulation of receiving test result after approximately 3 days

7 days

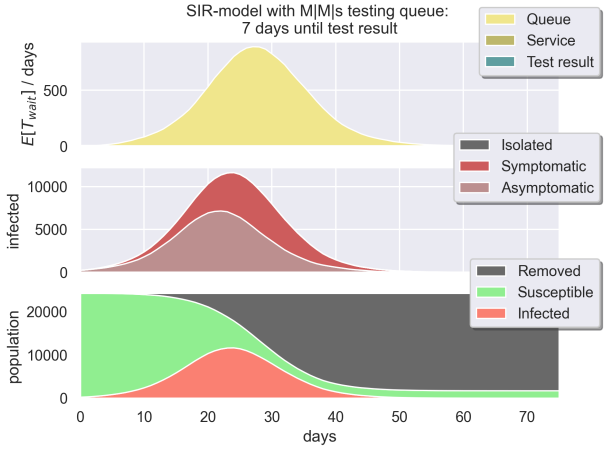


Fig. 20. Simulation of receiving test result after approximately 7 days

Numbers of from time for test result analysis

Days until result	Peak of queue (days)	Peak of infected	Total number of infected
1	858	11 418	22 473
3	869	11 509	22 496
7	871	11 578	22 492

VI. Discussion and Analysis

The obtained results and its implications will be discussed alongside suggestions of model improvements and further research.

A. Server Analysis and Analytical Solution

Examining Figure 1 showing the share of susceptible, infected and removed individuals at any given time point, one can at a first glance realize that increasing the number of servers, from none to 25 in the region of Stockholm, will not at all reduce the spread. To have around 25 testers available is the calculated goal of The Public Health Agency of Sweden, which demonstrably is not enough to slow down the spread. One should however remember that this is in the particular case when no other countermeasures, like awareness of social distancing, are taken into account. Unfortunately, even when the number of testers is increased by a factor of sixteen, i.e. having 400 testers, the peak number of infected simultaneously, is similar as before. Comparing the numbers in Table V-A1 shows that when the number of servers is sixteen times as many as in the standard case, the number of infected only lowers by just over 7%, and still around 93% of the population is getting infected. This major increase in the number of servers thus shows to have minimal effect on the containment of the spread. Surely, a decrease is still a decrease, but with limited resources the testing cannot be increased indefinitely considering that a sixteen-fold of the current testing capacity probably already has its impact on the available testing budget. In addition, as can be derived from Table V-A1, the peak expected waiting time in the queue would be close to 500 days, which clearly is catastrophically bad. The peak queueing time decreases as expected when

more servers are added, but not as much as needed in order to isolate infected people before the disease continues to spread rapidly. It is clear that if the expected queueing time exceeds five days, a person that starts getting symptoms today will not even have the chance to be tested before feeling healthy again.

Besides, this model assumes a 100% positivity rate in the testing, meaning that if non-infected people were to queue for taking a test as well, the number of servers needed would obviously be even more ridiculously high. This means that even if the number of servers would be enough to only test positive COVID-19 patients, the queue would get far too long to test non-infected people as well. Analytically, the number of servers needed, when assuming 5% positivity rate in the testing, is 20 times higher than the number presented to test only COVID-19 patients, i.e. 500 servers. Unfortunately, this would not be enough as presented in the previous paragraphs. However, if efficient contact tracing were to be performed, asymptomatic infected people might be isolated even before showing symptoms in a best-case scenario, i.e. if the queue were shorter than five days and only infected people queued. It can be seen in figures 8, 9 and 10 that, the more non-symptomatic people from the susceptible group and infectives group that queue for a test, the longer the queue. A constant percentage of the susceptible population experiences false symptoms every day. The proportion of susceptibles decreases with time, leading to more people feeling false symptoms at the beginning of the outbreak. However, since people with false symptoms start reneging much faster than infected people, it is seen that the susceptibles do not make up as big part of the total queue later in time. The number of infected people shows to be steady independently of the number of people feeling false symptoms. This aligns with previous discussed results handling the undercapacity of servers, since the queueing time is too long, all people feeling false symptoms will most likely renegade before getting a test which implicitly means that the testing positivity rate still will be close to 100%. The assumptions about that only COVID-19 patients are tested proves to be a reasonable assumption in the end since they are sicker longer and therefore might not renegade before taking the test.

The testing process of people feeling symptoms of COVID-19 shows to be inefficient (and perhaps a waste of resources if not combined with contact tracing or other countermeasures) to hinder the continuation of the spread, since it is already too late if the expected waiting time in the queue exceeds the time it takes to recover from the disease. In order to motivate the continuation of the testing process, contact tracing is truly important to identify asymptomatic people as well. The identification of asymptomatic infected people is similar as thinking of a shorter incubation time, which is illustrated in Figure 6 by an example on how the spread would behave in this case also in combination with a shorter time until received test result. The figure shows that the spread would decrease dramatically with other parameters, adding to the reasoning about sensitive parameters and importance of contact tracing.

Now, the testing more works as a way of counting the number of infected cases to keep statistics instead of providing help to lower the spread. However, concerns arise regarding the reasonability of the results in this part and the robustness of the other parameters creating the situation at hand. Although, it is considered not at all unreasonable assuming that approximately 1% of the population was infected at the commencement of the testing process, as well as that a test server can handle about 32 patients a day. Even is the number of patients handled by a single server were to be doubled, this would not affect the queueing system since this is the same as doubling up on the number of servers needed which did not show to make the desired impact.

In the model it is assumed that a person is infectious during the entire incubation time which makes it increasingly hard to slow down the spread, since a person only starts queueing to take a test when symptoms starts to appear. The long incubation time is evidently an issue since the isolation process from the testing would not make too much of a difference when people are isolated the last day of the disease for instance. However, the assumption that people are infectious when asymptomatic might not hold true but is the assumed standard case here which makes the testing process increasingly hard.

To conclude the discussion about the number of servers and the aim of testing, the authors argues that whether the governments uses testing to flatten the curve or to eliminate the virus, these results show that the testing process in its own have no or limited impact. Nonetheless, it can be useful since it provides an indication of the scale of testing needed. This will of course also depend on other countermeasures and the on the availability of test kits and servers to occupy the test stations. This suggests that the other parameters explaining the disease spread might be very sensitive and will consequently be targeted in the coming paragraphs.

B. Different Values of β, γ and R_0

The sensitivity analysis of the basic parameters in the SIR-model is presented by five different scenarios reasonable from theory. Comparing the figures and numbers, it is clear that small variations in β, γ and R_0 affect the results to a large extent. Varying the β-values implicitly mean varying R_0 and/or γ. Since both these variables are unknown and estimated, varying them will provide an indication of the sensitivity of the model. By looking at the results in Figure 11 one can see that small variations in β and γ lead to big changes in the SIR-model. In Figure 11, it is clearly visualized that there is at least a higher peak of the number of infectives simultaneously as the R_0 increases, while the duration of the disease appears to be quite stable independent of the parameters, i.e. 40-60 days. One exception is however seen in the second graph from the bottom in the same figure, where the peak is among the highest and the disease dies out faster, implying that the β-value also plays a major role in the disease spread, which will be discussed further.

In the first case (Figure 12, where the estimated R_0 is in the lower end of the range, i.e. 1.4, the incubation time is also assumed to be low, indicating that people feel symptoms rather instantly. This means that infected individuals will enter the queueing process early in the course of the disease which gives the testing process a chance to actually isolate people before the spread goes out of hand. The average time people feel symptoms is still around five days, implying that the expected queue length has to be lower than this in order for people not to start recovering during the waiting time and thus start reneging. As can be seen in Figure 12, not at all that many people are infected concurrently. This mean that the spread of the disease is not that harmful or that the testing process works fine in this particular setting. The former can be ruled out by the fact that the R_0 indeed fulfills the assumed requirements of a potential disease outbreak, i.e. a R_0 greater than 1. The latter however cannot be perfectly assumed since the expected queue length at the peak still is quite high, see Table V-C. This number can be a bit misleading at a first glance though since people in front of an arbitrarily chosen person in the line can renegade making room for the person faster than expected. In this scenario the disease spread is determined manageable under the circumstances, since not many people are infected at the same time meaning lower pressure on the healthcare sector at any given point in time. It can be derived from Table V-C that this scenario still would imply that around 30% of the population will get infected over time, but since these people are infected at different time points helped from the testing process, the situation is still manageable from the perspective of the healthcare. Furthermore, thinking of the situation with an almost non-existent incubation time is similar to think that this can be an illustration of a scenario with perfect contact tracing. Contact tracing would in the standard case mean that people can queue for taking a test before showing any symptoms which would speed up the isolation process. In this scenario with short incubation time, the infectives can be queued instantly and hopefully isolated early in the course of the disease. This is of course under the assumption that disease transmission is possible during the incubation time, which might not be the case, but this argumentation goes beyond the scope of this study.

Moving on to scenario 2 (Figure 13), which is similar to scenario 3 (Figure 13), only with a slightly lower R_0. It is clear that an increase of the R_0, from 2.5 (highest WHO estimation) to 3.0 (assumed standard case), results in a higher peak in the number of infected as well as a slightly higher proportion of infected in the end. The increase in R_0 implies a proportional increase in β which actually gives an additional 35% infected during the peak, which can be derived from Table V-C. It shows terrifying that such a relatively minor change in an assumption regarding the spread can have major consequences of the outcome and consequently a greater impact on the healthcare sector. Obviously, the increases in β and R_0 are 20% respectively which sounds like much but comparing with the range of R_0 and β-values presented, this is considered as a relatively minor change. However, in both these cases it can be seen in Figure 13 and Figure 14 that a large share of the population is infected in the end which is sadly considering the removed group consists of both dead and clinically recovered cases.

Examining Figure 15, visualizing a similar setting as in scenario 2 and 3 but with the use of the R_0 of 4.27 estimated by a study published in Elsevier taking undetected infectious cases into account. Undetected cases are undeniably an issue considering the continuation of the spread from asymptomatic infectives, which makes this scenario not too far-fetched considering the unknown spread during the incubation time. Unsurprisingly, an even higher R_0 than in the standard case results in an outrageous expected queueing time and that practically the entire population eventually catches the disease. If the population in general is fragile this would certainly imply major social consequences. Furthermore, in the last scenario presented (Figure 16), the R_0 is increased to the higher end of the range, i.e. R_0 equals to 6.49, in combination with a twice as long incubation period as well as symptomatic period. This scenario shows to be quite similar to the already bad situation previously describe, where the major difference is that the peak queue length is shifted to the right in Figure 16 compared to Figure 15, due to the longer incubation time since people only start queueing once their symptoms start to appear. In this scenario it can also be seen in the lower graph in Figure 16 that the majority of the population will be infected simultaneously for a large part of the duration of the disease. Such a scenario would probably lead to more deaths than clinical recoveries among the removed cases visualized in the graph. This is not something that can be said with certainty but considering previous research regarding overwhelmed hospitals, this is not an illogical hypothesis.

C. Time for Test Results

The waiting time for receiving a test result is included in, and an important part of the total expected waiting time. Regions in Sweden have seen a very varied expected time to get test results. Stockholm is at the lowest end of the range, with seven days as expected time to receive test results (see section III-A).

The results showing different times until the test results conclude that there is no difference in the outcome of the disease depending on the time until receiving the test result, see Table V-D. One could expect that the shorter time until the result, the lower the peak and the total number of infected. However, with the data used in the modeling, the queueing time is too long to have an effect. In turn, it makes the time until test results insignificant. If the queues were shorter, with people becoming isolated in time, the time until test results would be important. This because of the assumption that an individual will not isolate until receiving a positive result. As discussed in the Server Analysis section, Section VI-A, the testing is only efficient if the total expected waiting time

is shorter than the time from symptoms to recovery. The implication is that the time for receiving test results would have to be short, as the recovery time is not long in any tested case, see Section V-C, and one cannot expect the queueing time to be zero.

An easy conclusion of this is that it is very important not only to have wide-spread testing with contact-tracing, but also that the test results need to be delivered quickly. This conclusion might not be true. Realistically, an individual would isolate earlier than at the time of test result. In Sweden, an individual is told to isolate already when feeling symptomatic. Although it is not checked, it is fairly reasonable to assume that the vast majority will isolate earlier than when receiving the result from the test. An earlier isolation process, starting before, or at the time of testing will make the time to receive test results insignificant to the spread of the virus. However, getting results fast can have other benefits. Analysis of the virus and its spread is based on various data including the number of infected, susceptible, and recovered (or dead). If the results from the tests are one week behind, the predictions by the government will also be one week behind and might lead to wrongful decisions about measures to contain the virus spread.

Furthermore, as discussed in this section it is fairly justifiable to assume that people not only isolate while their waiting for the test results, but also stay isolated from the point that they feel symptoms related to COVID-19 to the time they know if they have been infected or not. If this were to be incorporated in the model the simulation would have taken another turn since this would mean that people both start queueing for a test and self-quarantine at the same time step. The infectives would thus move to the removed stage once they become symptomatic. In such a scenario, the disease spread only would depend on the disease spreading caused by asymptomatic people during the incubation time and the length of the queue for taking a test would not have life-threatening consequences to the same extent. Still, it can be critical to know if a person is tested positive considering the adaptation of treatment to these patients. This paragraph raise concerns with the existing model leading to the next couple of paragraphs suggesting model improvements and modifications.

D. Model Improvements and Real-World Application

The problem at hand on how to model the testing process can indeed be applied to reality, especially considering the existing shortage of included substances important for the tests. When there exists a shortage, the question about how to efficiently perform large-scale testing is undeniably paramount considering the need to quickly reduce the spread. Even if there might exist limited number of tests, one can presumably assume that there are even less capacity within the healthcare system if the spread starts to increase again. However, any model can be improved in some way, and the model presented in this study is clearly no exception. There are a lot of assumptions made to even start the simulation of the problem, and with assumptions come insecurity, and too much insecurity unfortunately implies a bad performing model. For example, one potential fallacy is the assumption about the isolation process of sick individuals which might be inaccurate, since sick people of course should isolate as soon as their symptoms appear. Accordingly, it is unknown whether disease transmission is possible during the incubation time, or when being asymptomatic, and if infected people isolate as soon as they become symptomatic. Nonetheless, it is considered a bit naïve to think that all infected people stay completely isolated before getting tested. In other words, if transmission were not possible during the incubation time or when being asymptomatic, in combination with that people isolate immediately when they feel symptomatic, the outbreak would not even have occurred, implying that at least one of the assumptions cannot hold true. In addition, all parameters are preliminary and invalidated, so basically every assumption is up for debate. Consequently, concerns materialize if the model really can be connected to reality. Undoubtedly, there have been some major simplifications, but the main results do still provide some valid analysis points to build conclusions on.

A number of potential model improvements and modifications can be formulated. Firstly, the implementation of different actions taken to lower the spread and its implication. Perhaps analyze the spread in different regions that have been under certain government orders like lockdowns, face mask demands or strict social distancing rules. Such a parameter could have contributed significantly to highlight the connection to reality. Secondly, the assumption that infected patients develop immunity is not set in stone since the virus has not been in circulation for that long. It would have been interesting to implement and analyze a scenario where the immunity only holds for a certain amount of time, meaning that once infected people enter the susceptible stage again. Lastly, the implementation of differentiation between people instead of using a homogeneous population. This would allow the model to target other queueing disciplines as well, for instance a prioritization for elderly or fragile people to proceed with testing first, since they are considered as risk groups and probably need help first. This implementation would demand extensive research and data classification of the population.

E. Further Research

Model improvements and modifications are truly central from the study point of view. However, future study areas to research in more extensively that would increase the presented model's usability, is the hospitalization of patients. The model can be taken one step forward by the implementation of another queueing system for people in the need of proper healthcare. Hospitals can easily be overwhelmed if they decide to hospitalize all people asking for treatment. Hospitals are in need for supplying the right treatment to the right people. People infected by COVID-19 may need different treatment from people being sick in general. A model for whom to treat and whom to prioritize is a large and interesting research area. Furthermore, within hospitals, another queueing system

with prioritized queueing discipline may need to be formulated based on the type of symptoms patients enter the hospital with. In order to identify who are in the most need of hospital beds in the intensive care unit, one needs to focus research in this field of study. In addition, similar queueing methods could be applied to address the upcoming vaccine question. Which people have to be prioritized when the vaccine demand exceeds the first batch of supply, is also a highly interesting topic going forward. Subsequently, a scenario could be created where all the aforementioned study areas are combined (i.e. the interaction of subsystems for testing, hospitalization, ICU, and vaccination) into one complete system. This would probably induce great insights into the entire disease process.

VII. Conclusion

Having the sensitivity analysis of the disease spread parameters from the SIR-model in mind, it can be argued that the β-value in combination with a higher R_0 plays a significant role in the severity of the spread. With lower values of these estimated parameters, the spread could effectively be contained with the means available. However, as the R_0 increases, the spread becomes unmanageable from a pure testing strategy perspective. According to the current situation in Stockholm presented with a assumed R_0 of 3.0, the testing capacity shows not to be enough, mostly due to the long infectious incubation time. It is thus deemed troublesome to slow down the spread by taking a reactive testing strategy approach. The testing must preferably be proactive with the assistance from contact tracing to show effect. However, it can be seen that even in the mildest case presented, the expected queueing time is still cumbersome when the number of cases increases rapidly. The main issue at hand is that once the spread starts to increase exponentially, the queue grows longer quickly and becomes overcrowded since there is such a significant increase in infected cases simultaneously. At first, the testing probably works fine, but as the outbreak evolves, the testing process needs to be scaled up substantially to be able to serve that many people concurrently. With that said, the testing capacity today is not enough on its own, under the assumptions presented in this study. However, if proper contact tracing is performed alongside the testing process, infected cases can be identified early. Such a scenario is similar to that the incubation time approaches zero since these people are already identified as potential infectives.

In this scenario with a perfectly estimated spread, the disease only expects to last for a shorter time period, 40-60 days in this case, which is no doubt not the real-world case suggesting some fallacies in the model. However, under the settings provided, it can still be concluded that a pure testing strategy of people once they start to feel symptoms is not enough. Countermeasures may affect the effective reproduction number at different time steps making the situation in Stockholm perhaps slightly better considering the awareness of social distancing. Nonetheless, the importance of contact tracing and other countermeasures cannot be emphasized enough to be able to isolate people early in their disease course and slow down the spread of the virus.

References

1177, Jämtland/Härjedalen. *Lämna prov för covid-19 - 1177 Vårdguiden*. URL: https://www.1177.se/Jamtland-Harjedalen/sjukdomar--besvar/lungor-och-luftvagar/inflammation-och-infektion-ilungor-och-luftror/om-covid-19--coronavirus/lamna-prov-for-covid-19/.

1177, Skåne. *Frågor och svar om självtest för covid-19 - 1177 Vårdguiden*. URL: https://www.1177.se/Skane/sa-fungerar-varden/varden-i-skane/samlad-information-om-coronaviruset-i-region-skane/provtagning-for-covid-19-i-skane/fragor-och-svar-om-sjalvtest-for-covid-19/.

1177, Stockholm. *Provtagning för dig som är sjuk - 1177 Vårdguiden*. URL: https://www.1177.se/Stockholm/sa-fungerar-varden/varden-i-stockholms-lan/om-corona/allt-om-provtagning-for-covid-19/provtagning-for-dig-som-ar-sjuk/.

Allen, Linda J S. *An Introduction to Stochastic Epidemic Models*. URL: https://www.math.mun.ca/%7B~%7Dzhao/ARRMSschool/StochEpidModels.pdf.

Aylward, Dr Bruce and Dr Wannian Liand. *Report of the WHO-China Joint Mission on Coronavirus Disease 2019 (COVID-19)*. WHO, 2020. URL: https://www.who.int/docs/default-source/coronaviruse/who-china-joint-mission-on-covid-19-final-report.pdf.

Cohen, Nick. *Sweden's Covid-19 policy is a model for the right. It's also a deadly folly — Coronavirus outbreak*. 2020. URL: https://www.theguardian.com/world/commentisfree/2020/may/23/sweden-covid-19-policy-model-for-right-also-a-deadly-folly.

European Data Portal. *Widespread Testing: Differing Strategies across Europe*. 2020. URL: https://www.europeandataportal.eu/en/impact-studies/covid-19/widespread-testing-differing-strategies-across-europe.

Fjellström, Anders. *Hallengren: Vi ska testa 100 000 i veckan — SVT Nyheter*. 2020. URL: https://www.svt.se/nyheter/inrikes/hallengren-vi-ska-testa-100-000-i-veckan.

Folkhälsomyndigheten. *Estimates of the number of infected individuals during the covid-19 outbreak in the Dalarna region, Skåne region Stockholm region, and Västra Götaland region, Sweden*. 2020. URL: www.folkhalsomyndigheten.se/publicerat-material/..

Folkhälsomyndighetenn. *Genomförda tester för covid-19 — Folkhälsomyndigheten*. 2020. URL: https://www.folkhalsomyndigheten.se/smittskydd-beredskap/utbrott/aktuella-utbrott/covid-19/statistik-och-analyser/genomforda-tester-for-covid-19/.

Hillier, Frederick S. and Gerald J. Lieberman. *Introduction to Operations Research 9th Edition*. McGraw-Hill Higher Education., 2010, pp. 760–763, 778. ISBN: 978-0077298340.

Ivorra, B et al. "Mathematical modeling of the spread of the coronavirus disease 2019 (COVID-19) taking into account the undetected infections. The case of China". In: *Communications in Nonlinear Science and Numerical Simulation* 88 (2020). ISSN: 10075704. DOI: 10.1016/j.cnsns.2020.105303. URL: /pmc/articles/PMC7190554/?report=abstract%20https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7190554/.

Lindholm, Amanda. *Alla stockholmare erbjuds gratis coronatester*. 2020. URL: https://www.dn.se/sthlm/sa-ska-covidtestningen-utokas-i-stockholm/.

Liu, Ying et al. "The reproductive number of COVID-19 is higher compared to SARS coronavirus". In: *Journal of Travel Medicine* 27.2 (2020), pp. 1–4. ISSN: 17088305. DOI: 10.1093/jtm/taaa021. URL: https://academic.oup.com/jtm/article/27/2/taaa021/5735319.

Long, Daniel Zhuoyu, Rowan Wang, and Zijin Zhang. "Pooling and Balking: Decisions on COVID-19 Testing". In: *SSRN Electronic Journal* (2020). ISSN: 1556-5068. DOI: 10.2139/ssrn.3628484. URL: https://papers.ssrn.com/abstract=3628484.

Meares, Hamish D D and Michael P Jones. "When a system breaks: queueing theory model of intensive care bed needs during the COVID-19 pandemic". In: *Medical Journal of Australia* 212.10 (2020), pp. 470–471. ISSN: 0025-729X. DOI: 10.5694/mja2.50605. URL: https://onlinelibrary.wiley.com/doi/abs/10.5694/mja2.50605.

Milne, Richard. *Anders Tegnell and the Swedish Covid experiment*. 2020. URL: https://www.ft.com/content/5cc92d45-fbdb-43b7-9c66-26501693a371.

Mizumoto, Kenji et al. "Estimating the asymptomatic proportion of coronavirus disease 2019 (COVID-19) cases on board the Diamond Princess cruise ship, Yokohama, Japan, 2020". In: *Eurosurveillance* 25.10 (2020). ISSN: 15607917. DOI: 10.2807/1560-7917.ES.2020.25.10.2000180. URL: /pmc/articles/PMC7078829/?report=abstract%20https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7078829/.

Palomo, Sergio et al. *Flattening the Curve: Insights From Queueing Theory*. 2020. URL: https://arxiv.org/pdf/2004.09645.pdf.

Rahman, Bootan et al. "Preliminary Estimation of the Basic Reproduction Number of SARS-CoV-2 in the Middle East". In: (2020). DOI: 10.2471/BLT.20.251561. URL: http://dx.doi.org/10.2471/BLT.20.262295.

Ramachandran, Raja. "COVID-19—a very visible pandemic". In: 396.10248 (2020). ISSN: 1474547X. DOI: 10.1016/S0140-6736(20)31673-1. URL: http://ees.elsevier.com/thelancet/www.thelancet.com.

Ridenhour, Benjamin, Jessica M Kowalik, and David K Shay. "Unraveling R0: Considerations for public health applications". In: *American Journal of Public Health* 104.2 (2014). ISSN: 15410048. DOI: 10.2105/AJPH.2013.301704. URL: /pmc/articles/PMC3935673/?report=abstract%20https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3935673/.

Statistiska Centralbyrån. *Låg folkökning i Sverige under coronapandemin*. 2020. URL: https://www.scb.se/hitta-statistik/statistik-efter-amne/befolkning/befolkningens-sammansattning/befolkningsstatistik/pong/statistiknyhet/befolkningsstatistik-forsta-halvaret-2020/.

Strömberg, Axel, Erik Flodmark, Kevin Olsson, and Sarah Bjärkby. *COVID-19: SIR-model with M|M|s queue for testing*. 2020. URL: https://github.com/axelstr/COVID-19_SIR-model_with_testing.

Universitetssjukhuset, Sahlgrenska. *Vanliga frågor och svar - Sahlgrenska Universitetssjukhuset*. URL: https://www.sahlgrenska.se/for-dig-som-ar/patient/covid-19-viruset/vanliga-fragor-och-svar/.

Wearing, Helen J, Pejman Rohani, and Matt J Keeling. "Appropriate models for the management of infectious diseases". In: *PLoS Medicine* 2.7 (2005). ISSN: 15491277. DOI: 10.1371/journal.pmed.0020174. URL: /pmc/articles/PMC1181873/?report=abstract%20https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1181873/.

WHO. *Coronavirus disease 2019 (COVID-19) Situation Report-73 HIGHLIGHTS*. 2020. DOI: 10.3201/eid2606.200239. URL: https://www.who.int/docs/default-source/coronaviruse/who-china-joint-mission-on-covid-19-final-.

Worldometer. *Sweden Coronavirus: 90,923 Cases and 5,880 Deaths - Worldometer*. 2020. URL: https://www.worldometers.info/coronavirus/country/sweden/.