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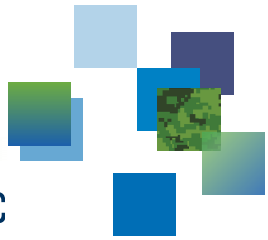

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Title

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IMPORTANT INFORMATIVE STATEMENTS

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Abstract

This is the abstract.

Significance for defence and security

This is the significance.

Résumé

Ceci est le résumé.

Importance pour la défense et la sécurité

Ceci est la signification.

Table of contents

List of figures

List of tables

1 Introduction

Quick background on COVID.

Background on branching model.

Limitations of branching model.

[Motivation:] This work presents an epidemiological model inspired by a branching model[**?**]. The presented model addresses some of the limitations listed above; it not only predicts the number of infected, but it also predicts the number of positive tests, and the number of contacts. It also enables impact assessment of different mitigation strategies such as self-isolation, testing, contact tracing, non-pharmaceutical interventions (NPI), and lockdown.

The goal of this work is to evaluate the use of the proposed model for the CAF. The following objectives are to be met:

1. Show different applications of the model;
2. Determine how the model could be useful to the CAF; and,
3. Evaluate the model and its limitations.

[Overview:] Section 2 presents some terminology used throughout this work, Section 3 presents the model, Section 4 describes the assumptions and model parameters of the disease used in the scenarios that are presented in Sections 5 to 6. These sections illustrate various applications of the model. Section 8 discusses some of the models limitations, and the final section, prior to concluding, discusses the model's usefulness to the CAF. Finally, the conclusion lists future work and recommendation for the model.

2 Definitions

The terminology and definitions used in this work are listed in Table 1.

3 Towards the proposed interrupted branching model

Overview of section here...

3.1 General branching model

This is a subsection.

we need to put R_0, R_{eff}, branching R_{eff} somewhere in this section...

Table 1: *Terminology and definition used in this work.*

Terminology	Definition
Basic reproduction number (R_0)	The average number of secondary infections (known or unknown) caused by a single infectious individual (known or unknown) in a population where all, but one individual, are susceptible, and where no mitigation measures, including self-isolation, are in place.
Effective reproduction number (R_{eff})	The average number of secondary infections (known or unknown) caused by a single infectious individual (known or unknown) in a population where some individuals are susceptible and others are non-susceptible due to mitigation measures that may be in place.
Latent phase	Begins when an individual is exposed, and ends when the individual is infectious.
Incubation period	Begins when an individual is exposed and ends when the individual self-isolates or are is no longer infectious.
Infected individual	Someone that has contracted the COVID-19 virus.
Infectious individual	Someone that has contracted the COVID-19 virus and that can infect others.
Infectious non-spreading individual	Someone that has contracted the COVID-19 virus, but does not infect anyone.
Infectious phase	Begins at the end of the latent phase, and ends when the individual is no longer infectious or self-isolates.
Non-self-isolating individuals	Infected individuals that do not self-isolate either because they are asymptomatic, mildly symptomatic, or ignore symptoms.
Observable path	An outbreak is observable if an individual tests positive to COVID-19, and the outbreak is non-extinct or not yet extinct.
Observable reproduction number (R_{obs})	The average number of secondary infections that reported positive caused by a single infectious individual that reported positive in a population where some individuals are susceptible and others are non-susceptible due to mitigation measures that may be in place.
Outbreak	Begins as soon as a single individual is infected. The outbreak path can become extinct, if the number of infectious individuals reaches zero, otherwise it is defined as a growing outbreak because the number of individuals infected increase perpetually.
Pre-symptomatic phase	Begins when a symptomatic individual is exposed, and ends when a symptomatic individual becomes symptomatic.
Probability of extinction	The probability that an outbreak will reach extinction.
Probability of infection	The probability that a susceptible individual, present at an infectious event, gets infected.
Self-isolating individual	Infected individuals that self-isolate when symptoms occur.
Symptomatic individual	An infected invidual that shows symptoms.

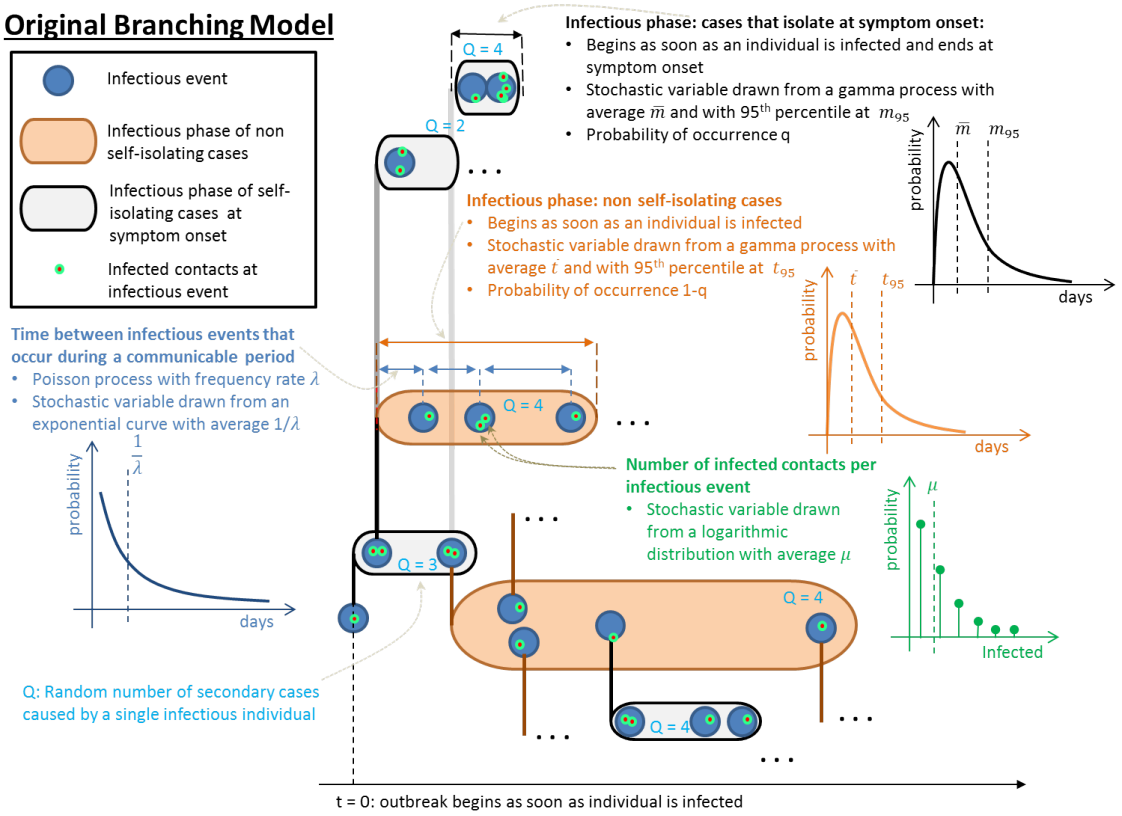

Figure 1: *Figure Title.*

blabla...

In this work, the main period designates non-self-isolating individuals, whereas the alternate period designates the self-isolating individuals.

3.2 Modified branching model

We added latent phase, the probability of infection, contacts, and testing.

we need to put modified R_0, R_{eff}, branching R_{eff} somewhere in this section...

The default parameters for the contacts and testing are listed in in Table 2. Although these must always be set, they are not relevant when only interested in the number of infected.

3.3 Interrupted branching model

This is a subsection.

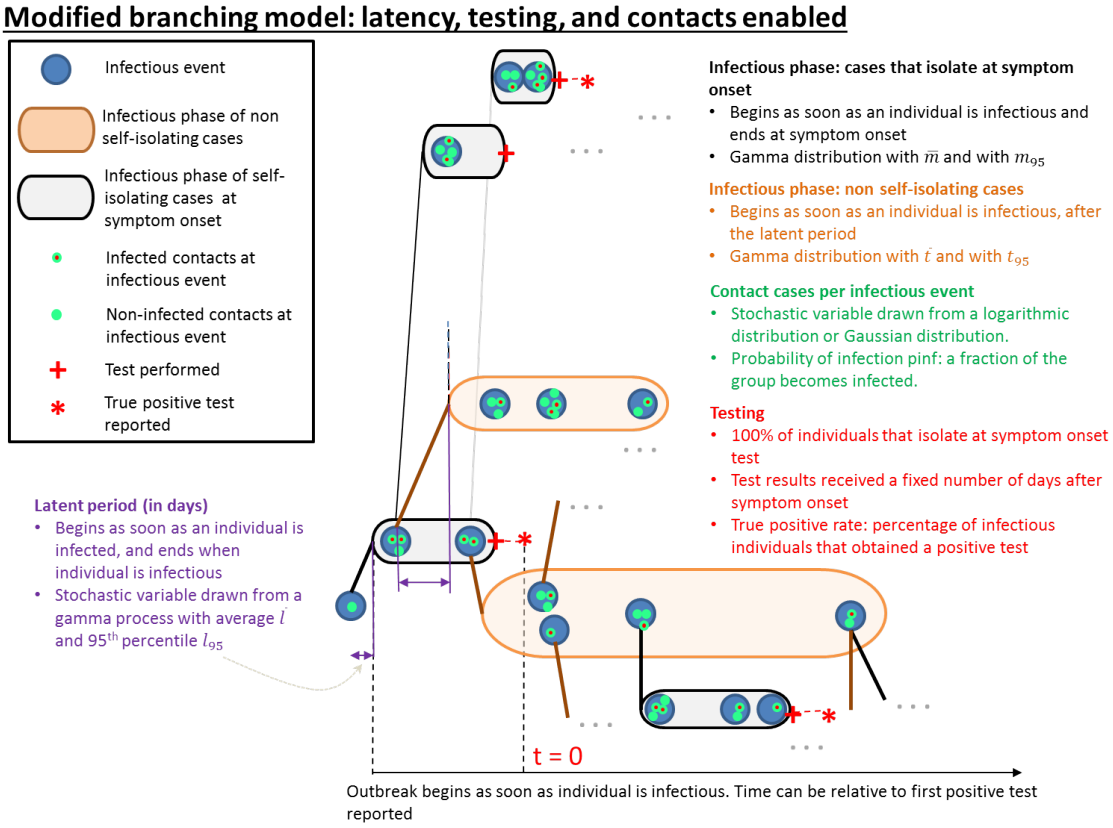

Figure 2: *Figure Title.*

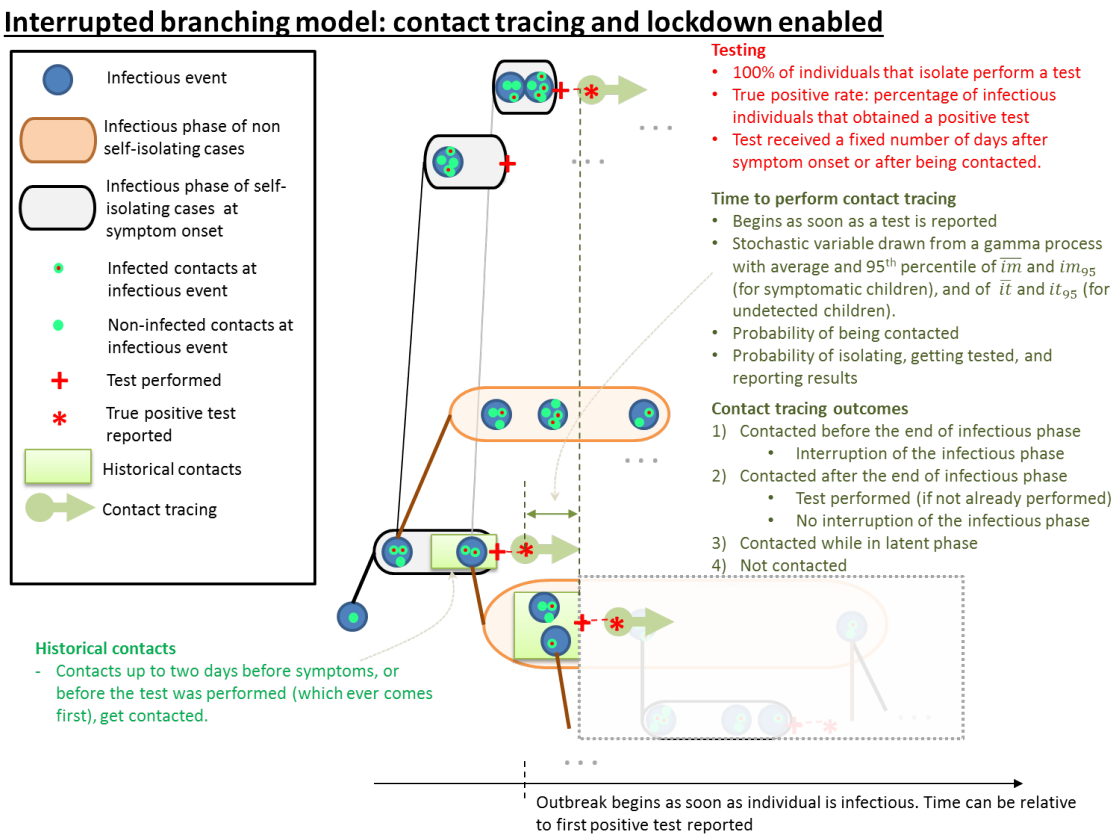

Figure 3: *Figure Title.*

Lockdown is an effective method at controlling the spread of the virus [REF]. The model was modified to support, and evaluate the impacts of, full lockdown...

Lockdown is a drastic measure that has a negative impact on the economie and... [REF]. It has been shown that reducing the infectious phase helps control the spread of the virus [REF]. It is reported that contact tracing has for objective to shorten the infectious phase window by encouraging non-self-isolating individuals to self-isolate [REF].

Support for contact tracing and lockdown were added.

3.4 Summary of the interrupted branching model and its parameters

This is a subsection.

From P-L email to Melanie... The original model is a continuous time branching process of COVID-19 propagation based on a compound Poisson process of transmission event.

Table 2: *List of parameters and their default values (when applicable).*

Parameter	Designation	Default value
Branching parameters		
Probability of infection	P_{inf}	1%
Probability of self-isolating	q	0%
Testing parameters		
Test true positive rate for non-self-isolating individuals	$t_{\text{t.p.r.}}$	70%
Test true positive rate for self-isolating individuals	$m_{\text{t.p.r.}}$	70%
Testing delay	$T_{\Delta t}$	2 days
Contact tracing parameters		
Probability of being contacted	P_{t}	80%
Historical contact window	`ctwindow`	2 days

The number of infections that occur at each event follows a logarithmic distribution. The Poisson process is subordinated by a random infectious period. The distribution for the random period can be itself randomly selected between two cases, each one represented by a different gamma distribution. There is no support for a latent period in the original model. There is no support for the generation of contacts and testing either, which are required to estimate contact tracing resources. The infectious periods cannot be truly interrupted through isolation in the original model, or at least in a way that is representative of how contact tracing is applied.

In the modified model, a latent period is introduced, which delays the start of the infectious period, post contamination. The propagation components required to estimate CT resources and to more correctly apply CT in the simulation have been added. The concept of probability of infections has been introduced, which is necessary to generate contacts, but that also allows to decouple interactions from contaminations, which produces a parameterisation that can be interpreted, but also be input much more easily. For scenarios where transmission occur through events where the number of interactions is not logarithmically distributed, other types of distributions can be used with the modified model. With the modified model it is also possible to look at observed infections (through positive test results), and to change the time reference when generating output distributions (e.g., time since the first positive test). In the modified model, there are options to select characteristics for the primary infectious individuals, and also to apply filters and cuts when generating results.

The model is different, but the implementation is also completely independent from the original model. The code of the modified model is about 1,000 faster than the one of the original model, and it supports parallel processing, which allows to generate far more statistics in the same amount of time.

Table 3: *Disease time period for self-isolating and non-self-isolating infected individuals used in this work.*

	Gamma distribution -	Estimate (95^{th} percentile)
Infected type	**Latent phase**	**infectious phase**
Self-isolating	3.3 (3.3)	2.2 (6.8)
Non-self-isolating	3.3 (3.3)	6.79 (12.2)

4 Assumptions and parameters about the infectious disease

The following assumptions about the infectious disease, summarized in Table 4, were considered:

- The incubation period of self isolating infectious individuals is drawn from a gamma distribution with a mean of 5.5 days and a 95^{th} percentile of 9.72 days [Lauer et al...find ref].
- The infectious phase of self-isolating infectious individuals is drawn from a gamma distribution with mean of 2.2 days and a 95^{th} percentile of 6.8 days [Zhao... find ref].
- The latent phase was set as the difference between the self isolating individuals' incubation phase (5.5 days) and infectious phase (2.2 days); therefore, the mean was 3.3 days. To match the 95^{th} percentile of the combined latent and infectious phases of self-isolating individuals with the 95^{th} percentile of the non-self-isolating individuals' incubation phase as closely as possible, the 95^{th} percentile of the latent phase was also set to 3.3 days. Thus, the duration of the latent phase is assumed fixed.
- The infectious phase for non-self-isolating infectious individuals was based on assumptions in [REF to Steve and Ramzi's calculator].

The parameters listed in this section were used throughout this work, unless specified otherwise.

5 Simulations I - Modified branching model: General evaluation of the impact of self-isolating, of group size, of frequency of event, and of probability of infection on the spread of the virus

It is common for epidemiologist to use the basic or effective reproduction number (R_0 and R_{eff}, respectively) to measure the spread of a virus [REF]. It is well known that if the R_0

of a virus is bellow 1, outbreaks will go extinct. If $R_0 > 1$, measures to contain the spread of a virus need to be put in place. R_{eff} measures the spread of the virus once measures are in place, and if $R_{\text{eff}} < 1$ than the control measures are effective at preventing the spread of the outbreak.

But what happens to outbreaks if R_0 and R_{eff} are greater than 1? Although the exact value of the COVID-19 R_0 is debatable [REF,REF...], it is consensus that its value is well above 1; therefore, measures need to be put in place to prevent the spread of the virus.

According to branching theory, the average R_{eff} can be computed as in Equation (add link here). It is well known that self-isolating when infected with the COVID-19 virus limits the infectious phase, which helps control the spread of the virus [REF]. It is also known that the group size (represented by the average of the distribution μ, in Equation (addl link)), frequency of infectious events (λ), and probability of infections (P_{inf}) all impact the spread of the virus [REF]. Figure 4 shows the value of R_{eff} for different values of probability of self-isolating (q) and of $\mu\lambda P_{\text{inf}}$. From this figure, it is noticeable that as the probability of self-isolating (q) increases, $\mu\lambda P_{\text{inf}}$ can be relaxed (i.e., increased) for a given R_{eff} value.

As mentioned, for all outbreaks to become extinct the R_{eff} must be smaller than 1, but for larger values of R_{eff}, some outbreaks may also become extinct. The probability of extinction, defined as the number of outbreaks that are extinct overall outbreaks, captures the chances that outbreaks go extinct for $R_{\text{eff}} > 1$. As R_{eff} increases, the probability of extinction may, or may not decrease, as it is dependent on the various factors previously mentioned (μ, λ, P_{inf} etc.). To help make decisions, it is important for health officials to understand the impact that these various factors have on the probability of extinction when $R_{\text{eff}} > 1$.

Using the branching model, this section shows the impact of varying μ, λ, and P_{inf} on the probability for extinction for specific values of R_{eff}, q, and $\mu\lambda P_{\text{inf}}$. These specific values are illustrated by a star marker in Figure 4, where $R_{\text{eff}} = 2.018$ and $R_{\text{eff}} = 1.009$. These were selected as the literature reports that 60% of individuals self-isolate when symptomatic [REF], and several have reported that, on average, one individual infected with COVID-19 will infect 2 others [REF]. The $R_{\text{eff}} = 1.009$ was evaluated for comparison purposes.

5.1 Methodology, assumptions, and parameters

The simulations in this section had disease parameters listed in Table 4, and had a q = 0.6.

Two categories of simulations, with different $\mu\lambda P_{\text{inf}}$ value, were performed. The values of $\mu\lambda P_{\text{inf}}$ evaluated were 0.25 and 0.5, each of which having an R_{eff} of 1.009 and 2.018, as illustrated in Figure 4. For each of the values evaluated, the P_{inf} was either 0.125 or 1, and the μ value was 1, 2, 4, 8, 16, or 32. The λ value was selected to satisfy the $\mu\lambda P_{\text{inf}}$ as illustrated in Figure 8. This resulted in a total of 24 different simulations listed in Table . For all, the group was assumed to be drawn for a log plus 1 distribution with μ.

Each simulation were ran for 60 days on 10,000 outbreaks. The following performance metrics

Table 4: *Disease time period for self-isolating and non-self-isolating infected individuals used in this work.*

	Gamma distribution -	Estimate (95^{th} percentile)
Infected type	**Latent phase**	**infectious phase**
Self-isolating	3.3 (3.3)	2.2 (6.8)
Non-self-isolating	3.3 (3.3)	6.79 (12.2)

were evaluated:

1. The total number of infected over the 60 days averaged across the 10,000 outbreaks;
2. The probability of extinction, which is defined as the number of outbreaks that go extinct overall the outbreaks; and,
3. The average time of extinction, across all paths that went extinct.

Since the the beginning of an outbreak in real-time is unknown, the concept of time relative to the beginning of the outbreak is abstract; therefore, the time of extinction was computed relative to the first positive test reported. Testing parameters were set to the default values listed in Table 2. The simulations were also performed on observable paths only as those that are unobserved go extinct without any positive test reported.

5.2 Results

Results for the probability of extinction, time of extinction, and total number of infected as μ and λ increase for the simulations listed in Table 5 are illustrated in Figure 5, Figure 6, and Figure 7 respectively.

Figure 5 shows that simulations with $R_{\text{eff}} = 1.009$ (the orange and blue markers) obtained highest probability of extinction on 10,000 observable outbreaks. The figure also shows that for increasing μ and decreasing λ, the probability of extinction increases. For a given R_{eff}, the simulations with highest P_{inf} also obtained better p-ext.

Figure 6 shows that simulations with smaller $R_{\text{eff}} = 1.009$ (the orange and blue marker) take, extinct outbreaks took more time to reach extinction, this is especially true for increasing λ and smaller μ. With the exception of $R_{\text{eff}} = 2.018$ and $P_{\text{inf}} = 0.125$ (green markers), increasing μ while reducing λ reduced the time to extinction. Some simulations obtained negative extinction time, meaning that the extinct outbreaks occurred, on average, before the first positive test was received.

Figure 7 shows that simulations with $R_{\text{eff}} = 1.009$ had fewer infected individuals averaged overall 10,000 observable outbreaks after 60 days. Simulations with larger μ and P_{inf} also had a higher number of infected individuals average across 10,000 observable outbreaks.

Table 5: *Parameter values used in simulations I.*

Sim Num.	R_{eff}	P_{inf}	μ	λ	$\mu\lambda P_{\text{inf}}$	P-ext
1	2.018	0.1250	1	4	0.50	0.3854
2	2.018	0.1250	2	2	0.50	0.4088
3	2.018	0.1250	4	1	0.50	0.4726
4	2.018	0.1250	8	0.5	0.50	0.5831
5	2.018	0.1250	16	0.25	0.50	0.7068
6	2.018	0.1250	32	0.125	0.50	0.8219
7	2.018	1.0000	1	0.5	0.50	0.3805
8	2.018	1.0000	2	0.25	0.50	0.5523
9	2.018	1.0000	4	0.125	0.50	0.7172
10	2.018	1.0000	8	0.0625	0.50	0.8488
11	2.018	1.0000	16	0.03125	0.50	0.9281
12	2.018	1.0000	32	0.015625	0.50	0.964
13	1.009	0.1250	1	2	0.25	0.8672
14	1.009	0.1250	2	1	0.25	0.8756
15	1.009	0.1250	4	0.5	0.25	0.9076
16	1.009	0.1250	8	0.25	0.25	0.9325
17	1.009	0.1250	16	0.125	0.25	0.9559
18	1.009	0.1250	32	0.0625	0.25	0.9772
19	1.009	1.0000	1	0.25	0.25	0.8679
20	1.009	1.0000	2	0.125	0.25	0.9256
21	1.009	1.0000	4	0.0625	0.25	0.962
22	1.009	1.0000	8	0.03125	0.25	0.9825
23	1.009	1.0000	16	0.015625	0.25	0.9902
24	1.009	1.0000	32	0.00781250	0.25	0.9964

5.3 Discussion of results

The results from Figure 5 show that reducing R_{eff} improves the probability of extinction, this is due to the fact that each infectious individual infect fewer people. For a given R_{eff}, the probability of extinction can be improved by reducing the frequency of infectious events. Reducing the frequency of events allows for larger group gatherings (for constant R_{eff} values) without negatively impacting the p-ext, however this could results in a larger number of infected individuals, as illustrated in Figure 7. The average number of infected individual overall 10,000 observable outbreaks is high due to the the number of infected individual from non-extinct paths. This is illustrated in Figure 9 and Figure 10 where the average number of infected individual after 60 days are averaged across extinct, and non-extinct outbreaks, respectively.

Figure 5 also shows that, reducing the frequency of infectious events allows for larger P_{inf}, explaining why the curves with highest P_{inf} obtained better p-ext. In fact, for a given average group size and R_{eff}, reducing the frequency of events while increasing P_{inf} improved p-ext. This was especially true for $R_{\text{eff}} = 2.018$. But, larger P_{inf} could also have disastrous consequences: a population with a larger proportion of infected individuals as illustrated in Figure 7.

Reducing the frequency of events increase the time to reach extinction as illustrated in Figure 6. This is explained by the fact that infectious events are spread out in time, meaning that the last event will occur later in time. Events with large μ reduce the time of extinction as infections are likely to occur at the same moment; and, hence also end at the same moment. In some cases, outbreaks will go extinct before the first positive test case is received. Unless $R_{\text{eff}} < 1$, this is undesirable as it does not allow health authorities enough time to react to the outbreak; by the time a test results is received, the outcome of the outbreak has already past, and if the outbreak is not extinct, it has already gone out of control. High values of μ and P_{inf} drive the extinction time down. This can be explained by the fact that a larger number of people are getting infected in any single infectious event, rather than infections occurring more spread out in time. This can be undesirable as it does not allow health official enough time to react to non-extinct paths.

5.4 Conclusions

The probability of extinction (for $R_{\text{eff}} > 1$) is not linearly proportional to R_{eff} as it depends on μ, λ and P_{inf}. Therefore, R_{eff} alone (if above 1) is an insufficient metric to describe the spread of a virus. Several factors not only impact R_{eff} and p-ext, but also the time of extinction, and the total number of infected individuals. There are all important measures to help describe the spread of the virus.

The results suggest that having a low frequency of infectious events prevents the spread of the disease and, in the context of the disease parameters selected (Table 4), is the most effective course of action to control an outbreak. Although it may increase the time for outbreaks to

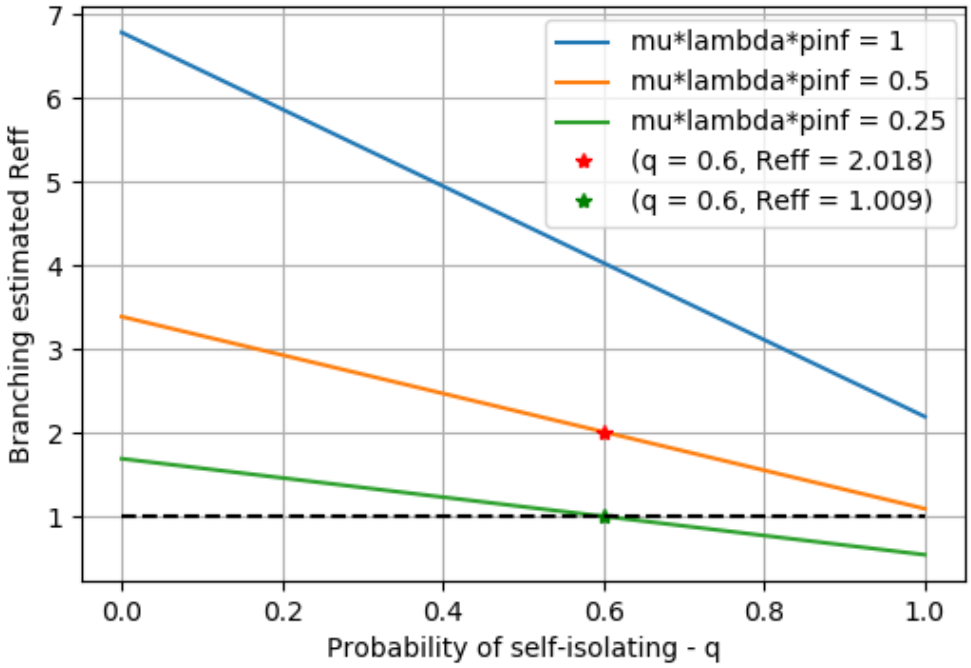

Figure 4: *Figure Title.*

reach extinction, it also allows official more time to react and control the outbreak. If the reduction in the rate of infectious events is compensated by large groups, or by an increase in P_{inf}(relaxing social distancing measure or not using NPIs, for example), the probability of extinction may not be impacted, but the high number of infected individuals in non-extinct outbreaks could have disastrous consequences. Reducing the group size and the probability of extinction not only reduces the total number of infected individuals, but it also allows authorities more time to observe outbreaks (via positive test reports of COVID-19) before it is too late.

The best way to improve the probability of extinction is by reducing R_{eff}. This can be achieved various ways, and most importantly by increasing the percentage of infected people that self-isolate, as illustrated in Figure 4. When people self-isolate, they reduce their chances of infected others by reducing their infectious time window. Unfortunately, as reported in the literature [REF], not all infectious individuals that contract the COVID-19 virus have symptoms indicating to them that they should self-isolate. It is anticipated that other measures, such as contact tracing and isolating individuals that are contacted could help control the spread of the virus.

The next Section evaluates the impact of different mitigation strategies in the context of the Diamond Princess outbreak.

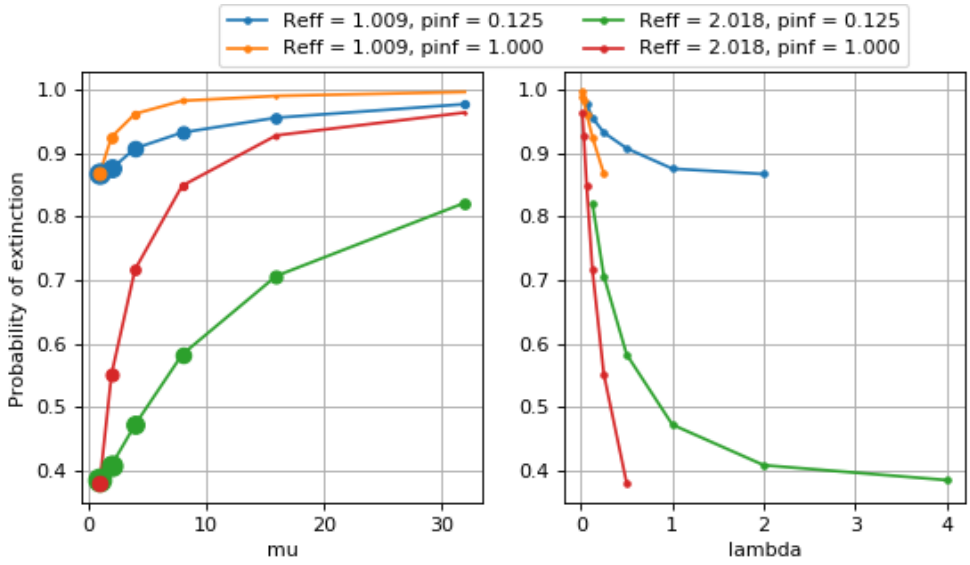

Figure 5: *Probability of extinction as a function of mu (left plot) and lambda (right plot). Increasing marker size indicates larger lambda (left plot).*

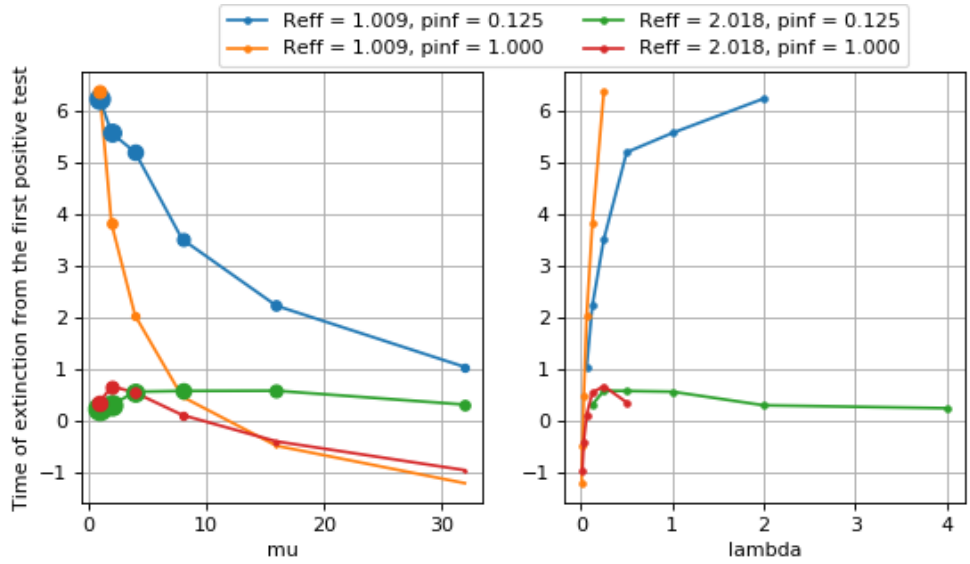

Figure 6: *Figure Title.*

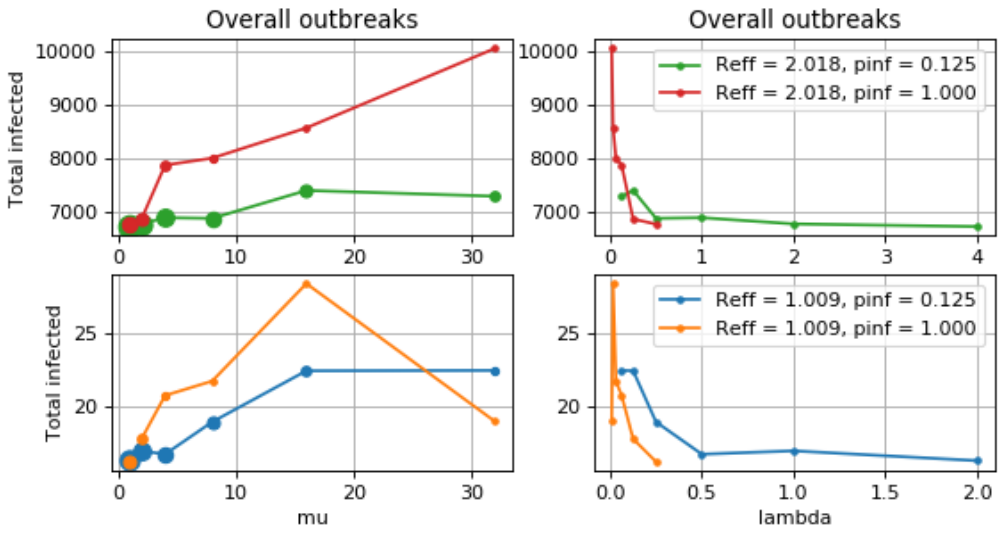

Figure 7: *Figure Title.*

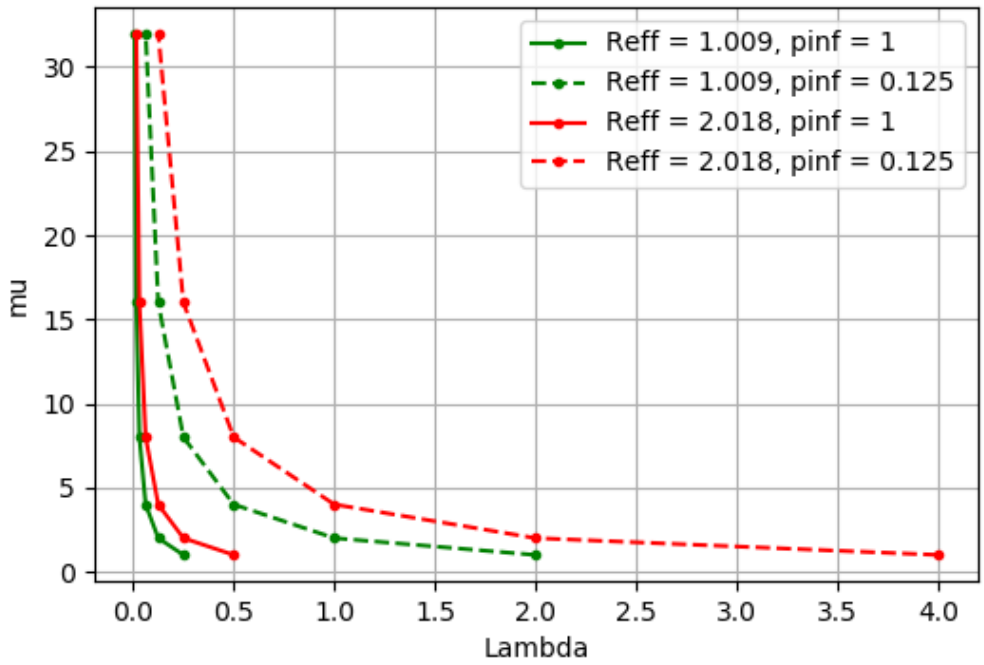

Figure 8: *Corresponding λ values satisfying $\mu\lambda P_{\text{inf}}$ for given μ, P_{inf}, and R_{eff}.*

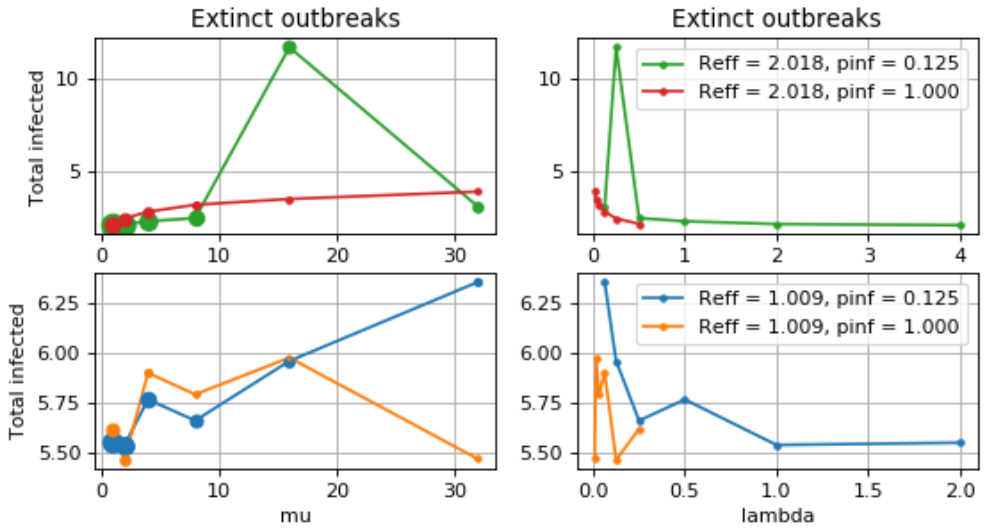

Figure 9: *Figure Title.*

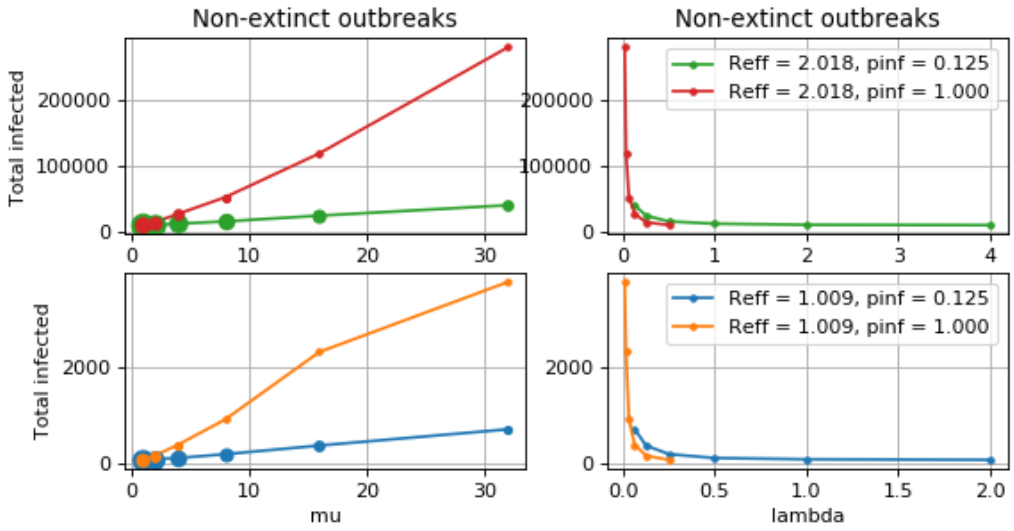

Figure 10: *Figure Title.*

6 Simulations II - Interrupted branching model: Scenario specific evaluation of the impact of different mitigation strategies

This is a section.

6.1 The Diamond Princess outbreak

The Diamond Princess cruise ship departed Japan on January 20th 2020 [1]. On January 25th, the presumed primary infected individual left the ship. Some report that this individual was coughing before onboarding the ship [2] while others report that coughing did not being till the 23rd of January [3]. This individual tested positive on February 1st, while on February 3rd the ship was quarantined, and passengers were isolated from each other starting February 5th. Crew members continued working, even if they had been in direct contact with a confirmed case. On February 4th, 10 COVID-19 cases were confirmed on-board the Diamond Princess. Initial testing was performed on individuals with symptoms and their close contacts.

Figure 11 (from [1]) illustrates the outbreaks chronology of events as well as the number of reported cases to the WHO. By definition, a reported case is a "person with laboratory confirmation of COVID-19 infection, irrespective of clinical signs and symptoms" [4].

There were a total of 2666 passengers and 1045 crew members (for a total of 3711 people) onboard the Diamond Princess [1]. A total of 706 were confirmed cases.

There are reports that mitigation strategies to control the spread of COVID-19 on the Diamond princess were not properly executed [5]. Although the ship was quarantined 3 days after the primary individual reported positive to COVID-19, and contact tracing was executed on the ship to help control the outbreak among those on-board, it has been reported that the following may have contributed to the spread of the virus:

- The suspected primary individual did not self-isolated on board of the Diamond princess, even if he/she may have had symptoms while on the ship [3][2];
- Crew members that were in direct contact with a confirmed case did not self-isolate [5] [1]; and,
- A red-zone with proper decontamination was not set into place [5].

This section illustrates the use of the interrupted branching model to evaluate the impact of different mitigation strategies on the outbreak that occurred on the Diamond princess. The following are to be met:

1. Model the outbreak that occurred on the Diamond princess using a modified branching model;
2. Demonstrate the impact of isolating the primary individual, of isolating all passengers and crew members that were in contact with an infected individual, and of minimizing the risk (or probability) of infection; and,
3. Demonstrate the impact of the outbreak if no meausues (i.e., no contact tracing) would have been in place.

6.1.1 Methodology, assumptions, and parameters

The simulations in this section had disease parameters listed in Table 4, and had a q = 0.6.

Although mitigation strategies were applied to the Diamond Princess, the outbreak had already begun once the first positive test case was reported. Therefore, the parameters that represent the social dynamics of the individuals on the ship were set to represent normal interaction before mitigation strategies were set in place.

The average number of passengers per cabin was reported to be 1.98, whereas the average number of crew member was reported to be 1.73 [1]. Therefore, it was assumed that people traveled as couples (i.e., in pairs of 2). However, the average group size at infectious events was 5 (therefore mu = 4), as it was assumed that couples congregated, and that at meal times congregated couples were served by at least one crew member. It was assumed that there were 4 infectious events per day (breakfast, lunch, diner, and one other event that could either be when an infected individual goes to bed, attends the gym, or attends a social event). Since there is a possibility to attend various events on the Diamond Princess, and that there are several dining rooms, and exercise rooms, the group distribution was assumed log to allow for large group gatherings.

The probability of infection at each infectious event was set to be 7% (i.e., $P_{\text{inf}} = 0.07$). This value was selected, because on February 4th, 10 days from when the primary individual left the diamond princess, 10 people were confirmed positive. These ten cases were assumed to have resulted from the same outbreak, therefore it can be assumed that during 9 days prior, an average of 1.11 individuals were infected per day. At 4 events per day, this results in 0.27 infected individuals per event (i.e., 10 infected / 9 days / 4 events per day = 0.27 infected per event). Since the distribution mu = 4, it was assumed that at each infectious event, 0.07 of the population was infected (i.e., 0.27 infected / 4 = 0.0675).

Since testing was performed in a controlled environment, it was assumed 0 days in testing delay, and 1.0 true positive test rate for all those who tested (symptomatic and their contacts tested, symptoms or not). Since health authorities began isolating individuals after they received the first confirmed test, but that the primary individual had already left the ship, the time was set relative to the end of the primary individuals communicable period, which in this case is analogous to when the primary individual got off the ship (since some report that the primary individual had symptoms while on the ship).

It was also assumed that on a ship, the probability of successful contact tracing was 1.0, and that the contact tracing window was short (0.5 days). The historic window of contacts was set to 5 days, meaning that on such a controlled setting, it was anticipated that those who tested positive were able to recall who they had been in contact with over the last 5 days. Asymptomatic crew members were not self-isolating even if they had been in contact with a positive case; therefore, the probability that non-self-isolating individual get contact traced and isolates was set to the ratio of passengers to total number of people on board (i.e., $P_{i_t} = 2666/3711 = 0.72$). All individuals that were symptomatic and that were in contact with a positive case self-isolated, either once contacted, or once symptoms appears (which ever occurred first). Since there is no mention of the primary individual self-isolating while on the Diamond Princess, if was assumed that the primary individual was non-self isolating.

The parameters of the Diamond Princess outbreak are summarized in Table 6, and are referred to as the baseline simulation.

From this baseline simulation, referred to as Sim0, some parameters were modified to simulate the following 5 scenarios and/or mitigation strategies:

1. Isolating all individuals (not just passengers) that were in direct contact with a confirmed cases. That is the probability that non-self-isolating individual get contact traced and isolate was set to 100% (i.e., $P_{i_t} = 1.0$). This simulation is referred to as Sim1;

2. Minimizing the probability of infection. Although it is unclear how masks, decontamination, or social distancing impacts the probability of infection, it was assumed that having a red-zone with proper decontamination would reduce the probability of infection by half, that is $P_{\text{inf}} = 0.035$. This simulation is referred to as Sim2;

3. Self-isolation of the primary individual as soon as he/she had symptoms.This simulation is referred to as Sim3;

4. No contact tracing at the beginning of, and throughout the outbreak.This simulation is referred to as Sim4;

5. No contact tracing at the beginning of, and throughout the outbreak, but the primary individual self-isolated as soon as he/she had symptoms. This simulation is referred to as Sim5.

All simulations were performed on 10,000 outbreaks over 30 days. The parameters for all the above simulations are summarized in Table 6 and their appellation are summarized in Table 7. The parameters that differ from the baseline are in bold font.

For each simulations, the average number of confirmed cases (i.e., positively reported tests) across all outbreaks was computed over time as well as the average number of infections over time. The probability of extinction, the time of extinction, and the distribution of the average number of infected was also computed.

Since the statistics in the branching model cannot be changed over time, the model assumes that symptomatic individuals self-isolated from the beginning, and that contact tracing was initiated as soon as the outbreak began. Since this may not be the case, the model cannot be used as an absolute estimate, but rather as a relative study to evaluate the impacts of the various mitigation strategies.

6.1.2 Results

The probability of extinction as well as the time of extinction for each simulation are listed in Table 8. These results show that Sim3 obtained highest probability of extinction followed by Sim5 and then Sim2. Sim4 obtained lowest probability of extinction. Extinct outbreaks reached extinctions within 0.456 and 5.389 days on average from the end of the primary's individual infectious phase.

The total number of confirmed cases overtime is illustrated in Figure 12. These results show that the baseline simulation follows the real number of confirmed cases obtained from the WHO. It is also worth mentioning that the R_{eff} for the baseline simulation is 3.57, which closely matches R_0 values estimated at the beginning of the outbreak in China [REF]. Sim2 has the slowest rate of reported cases, however Sim3 have fewer reported cases up to 18 days where the number of reported cases start growing exponentially. Sim0, Sim1, and Sim4 have a comparable number of reported case, however Sim4 has fewer reported cases in the first 15 days.

The total number of infected overtime is illustrate in Figure 13. The results show that Sim4 obtained the highest numbers of infected individuals and the fastest rate of infected. Sim5 is shifted from Sim4 in time. Sim3 and Sim0 are also shifted in time. The results also show that Sim2 obtained the slowest rate of infected, but Sim3 had the least number of infected in the first 15 days.

The total number of infected overtime for non-extinct path is illustrate in Figure 14. The results show Sim4 obtained the highest numbers of infected individuals and the fastest rate of infected for non-extinct path. Sim5 is shifted from Sim4 in time. Sim3 and Sim0 are also shifted in time. The results also show that Sim2 obtained the slowest rate of infected.

Figure 15 shows the distribution of the number of secondary infections. Since some simulations obtained a noticeably larger amount of infected individuals, the distribution is relative to the total number of infected overall outbreaks for a given simulation. For clarity, relative counts bellow 0.1% aren't shown. The results show a peak in infected with 0 secondary infections; that is, between 47% (Sim0, Sim12 and Sim3) and 54% (Sim1) of infected individuals did not infect others. For Sim4 and Sim5, 20% of infected did not infect others. The cumulative sum of this distribution (shown in Figure 16) illustrates that for Sim2 $\tilde{0}$% of the infected individuals infected more than 15 other people, whereas for the other simulations between 5% and 8% of the infected individuals infected more than 15 other people.

6.1.3 Discussion of results

The results from Table 8 demonstrate that the probability of the outbreak going extinct within 30 days would have increased by 70% if the primary individual infected that boarded the Diamond Princess would have self-isolated once symptoms appeared. Self-isolation alone (Sim5) without the measures taken on the Diamond Princess during the outbreak would have also improved the probability of extinction. These results suggest that, in this scenario, the infectious phase of the primary individual had a dramatic impact on the probability of extinction. It is interesting to note that extinction, if it were to occur, would have occurred rapidly or would have been unnoticeable (i.e., before a positive test was received) as extinction on averaged occurred in half a day from the end of the primary individuals infectious phase.

Although self-isolation of the primary individual increases the likelihood of extinction, this control measure does not necessarily suppress the total number of infected in non-extinct outbreaks. This will only shift the outbreak in time as it reduced the number of infections at the beginning of an outbreak, explaining the shift in time between Sim0 (baseline without primary individual self-isolating) and Sim3 (baseline with primary individual self-isolating), and between Sim4 (no control measure) and Sim5 (primary individual self-isolating only) in Figure 13 and Figure 14. This measure will have very little impact on the outbreak overtime. In fact, self-isolating the primary individual will have no impact on the number of secondary infections as shown in 15 and Figure 16 where Sim0 and Sim3, and Sim4 and Sim5 have the same distribution in the secondary number of infected. These results suggest that the outbreaks are the same, but shifted in time. Such a time shift could have given authorities more time to better respond to the outbreak, but additional measures would have been required to mitigate the number of infected.

Proper contact tracing of passengers and crew members, as in Sim1, increases the number of individuals that don't infect others, as demonstrated in Figure 16 where Sim1 obtained 54% of individuals with 0 secondary infections, compared to 20% for simulations without contact tracing (i.e., Sim4 and Sim5). Contact tracing will start to reduce the number of infected in non-extinct outbreaks 5 days after the end of the primary's individual communicable period, as illustrated in Figure 14 when comparing Sim1 to Sim4. However, it has little impact on the initial stages of the outbreak, and by the time the benefits of contact tracing are observed, there are already several infected individuals. In reality, contrary to the modeling that assumed that the contact tracing efforts are constant throughout the outbreak, contact tracing efforts may become less productive as more resources are required when the number of infected increases. This suggests that contact tracing alone was not a successful mitigation strategy for the outbreak that occurred on the Diamond Princess. Additionally, when comparing Sim1 to Sim5 in Figure 14, it is noticeable that, at the initial stages of the outbreak self-isolation of the primary individual will help minimize the number of infected more efficiently than proper contact tracing.

Reducing the probability of infection, as in Sim2, noticeably reduces the number of infected in non-extinct outbreaks (Figure 14). This can be explained by the fact that there are fewer

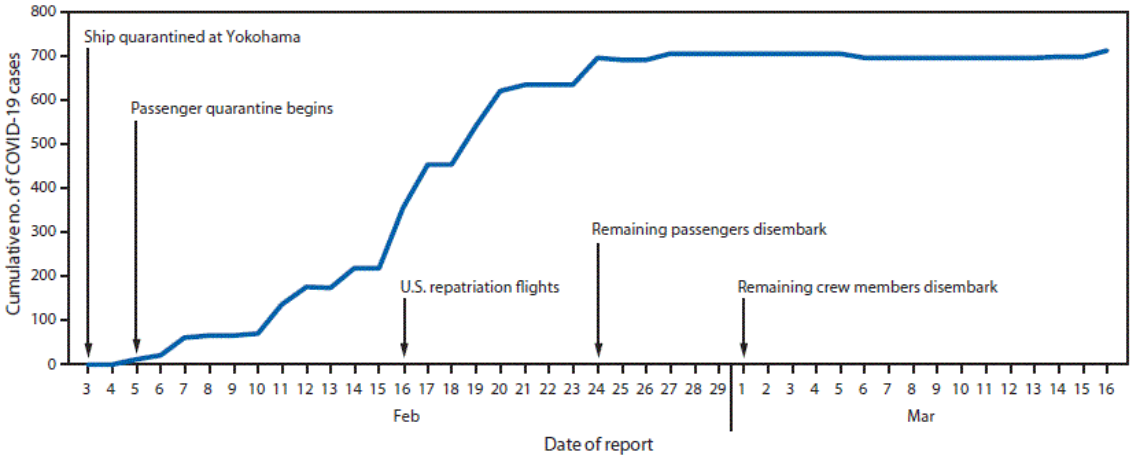

Figure 11: *Figure Title.*

infected individuals that infect more than 15 others, as noticed in Figure 15 and Figure 16. From these Figures, it is interesting to note that reducing the probability of infection (Sim2) had no noticeable impact on the number of individuals with 0 secondary infections. This suggest that reducing the number of super spreaders on the Diamond Princess outbreak could have helped mitigate the number of infected. Although reducing the probability of infection only provided 18% probability of extinction (Table 8) after 30 days, the average number of days to extinction had a large variation, suggesting that increasing the simulation time would increase both the probability of extinction, and the time of extinction. This is illustrated in Figure 17 and Figure 18. These results suggest that, reducing the probability of infection effectively improves the probability of extinction, but that it just takes longer to reach extinction because the outbreaks occur at a slower rate when to the simulations where the primary individual self isolated (Sim3 which had highest probability of extinction 8).

6.2 Tent scenario

See BranchingForCT-20200929

Table 6: *List of parameters for the Diamond princess simulations listed in Table 7.*

Parameter	Baseline	Sim1	Sim2	Sim3	Sim4	Sim5
μ	4	4	4	4	4	4
λ	4	4	4	4	4	4
P_{inf}	0.07	0.07	**0.035**	0.07	0.07	0.07
$T_{\Delta t}$	0	0	0	0	0	0
$t_{\text{t.p.r.}}$	1	1	1	1	1	1
$m_{\text{t.p.r.}}$	1	1	1	1	1	1
P_{t}	1	1	1	1	1	1
`ctwindow`	5	5	5	5	5	5
$P_{\text{i}t}$	0.72	**1**	0.72	0.72	**0**	**0**
$P_{\text{i}m}$	1	1	1	1	**0**	**0**
${}^{\text{i}}\bar{m}$, ${}^{\text{i}}\bar{t}$	0.5	0.5	0.5	0.5	**n-a**	**n-a**
n_{paths}	10000	10000	10000	10000	10000	10000
t_{max}	30	30	30	30	30	30
`group_log`	✓	✓	✓	✓	✓	✓
`time_rel_pri_end_comm`	✓	✓	✓	✓	✓	✓
`observable_paths_only`	✓	✓	✓	✓	✓	✓
`pri_no_alt_period`	✓	✓	✓		✓	
`pri_no_main_period`				✓		✓

Table 7: *Appellation of the simulations.*

	Simulation
Sim0	Baseline
Sim1	Contact tracing of both passengers and crew members in direct contact with a confirmed positive case
Sim2	Lowered probability of infection
Sim3	Primary self-isolated as symptoms appeared
Sim4	No contact tracing was performed at the beginning of the outbreak
Sim5	No contact tracing was performed at the begging of the outbreak, but the primary individual self-isolated

Table 8: *Probability of extinction (after 30 days) and average time to extinction across all extinct outbreaks, for each simulation.*

Metric	Sim0	Sim1	Sim2	Sim3	Sim4	Sim5
Simulated R_{eff}	3.575	3.101	2.000	3.567	5.527	5.525
Probability of extinction	0.032	0.0664	0.1822	0.7278	0.0079	0.3695
Average days to extinction (+/-)*	3.048 (3.407)	4.653 (4.177)	5.389 (5.996)	0.573 (1.280)	1.400 (2.254)	0.456 (1.456)

*Time is relative to the end of the primary individual's communicable period

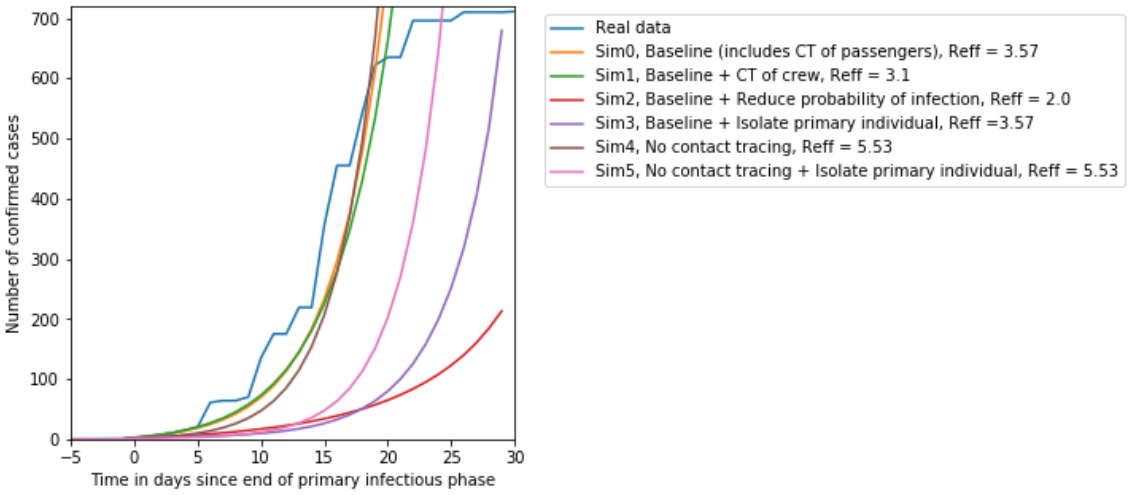

Figure 12: *Total number of confirmed cases over time averaged across all 10,000 observable outbreaks.*

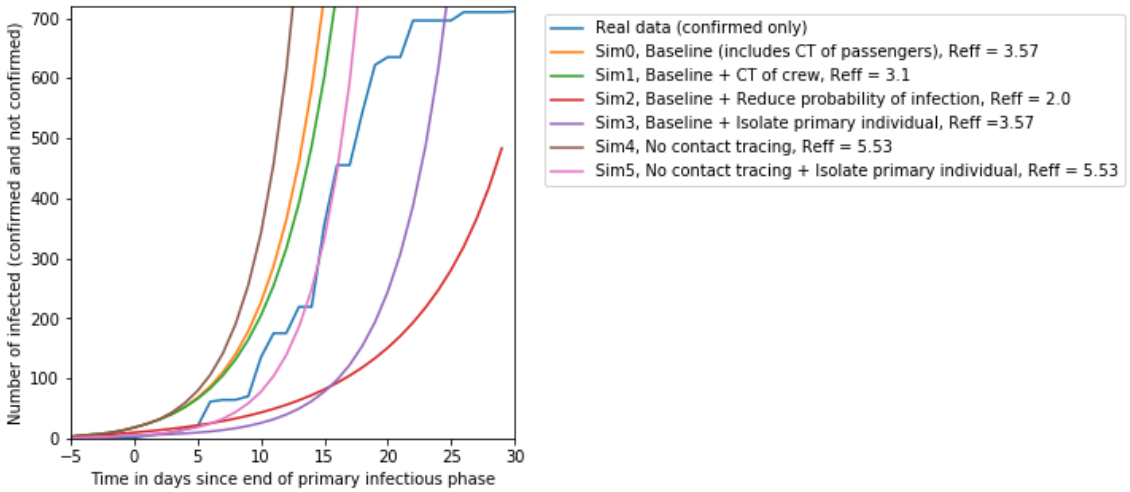

Figure 13: *Total number of infected over time averaged across all 10,000 observable outbreaks.*

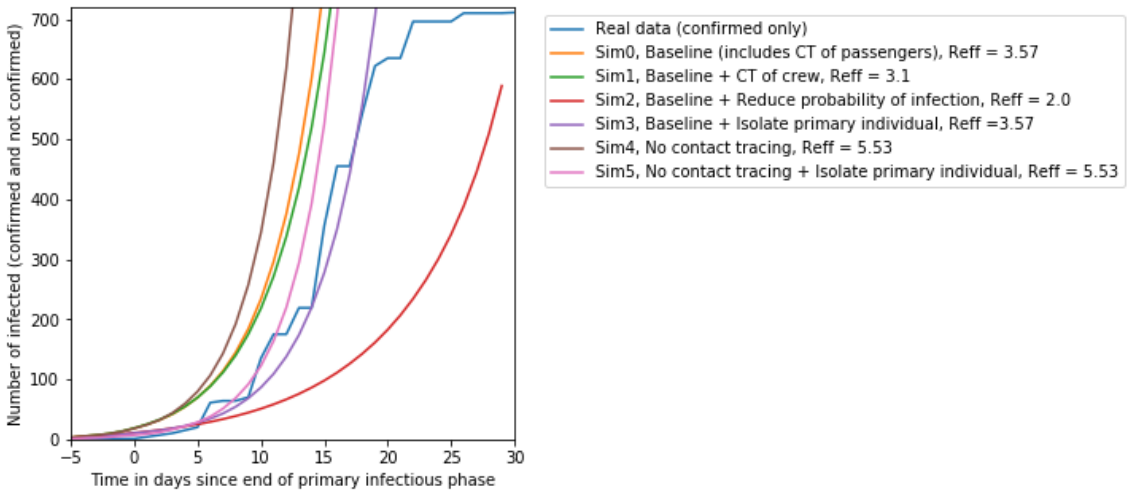

Figure 14: *Total number of infected over time averaged across all non-extinct and observable outbreaks.*

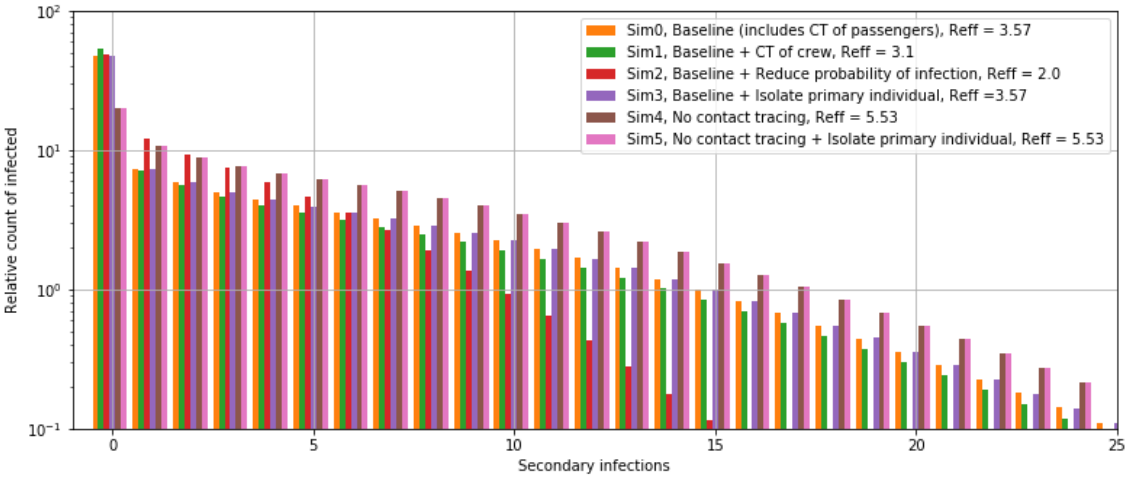

Figure 15: *The distribution of the number of the number of secondary infections caused by an infected person. The y-axis shows the log of the percentage of primary infected individuals between 0.1% and 100% across all the 10,000 outbreaks. The x-axis bins the number of secondary infected by integers from 0 to 25.*

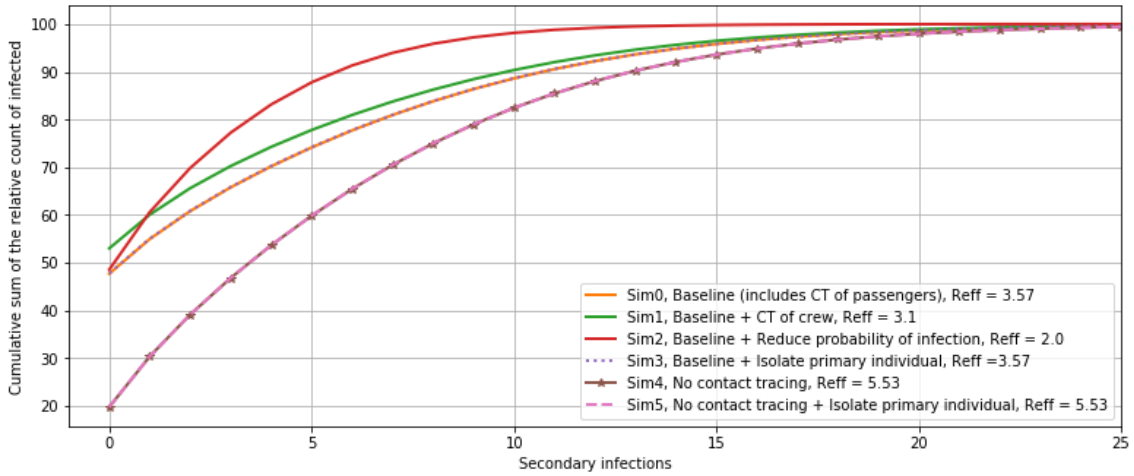

Figure 16: *The cumulative sum of the number of infected causing secondary infections. The y-axis shows the log of the cumulative sum of infected individuals between across all the 10,000 outbreaks. The x-axis bins the number of secondary infected by integers from 0 to 25.*

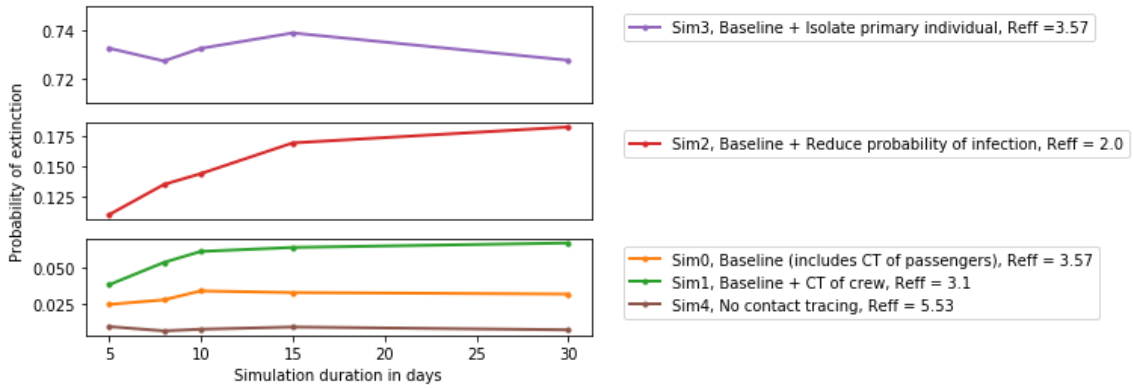

Figure 17: *Probability of extinction for Sim2 as the simulation duration increases.*

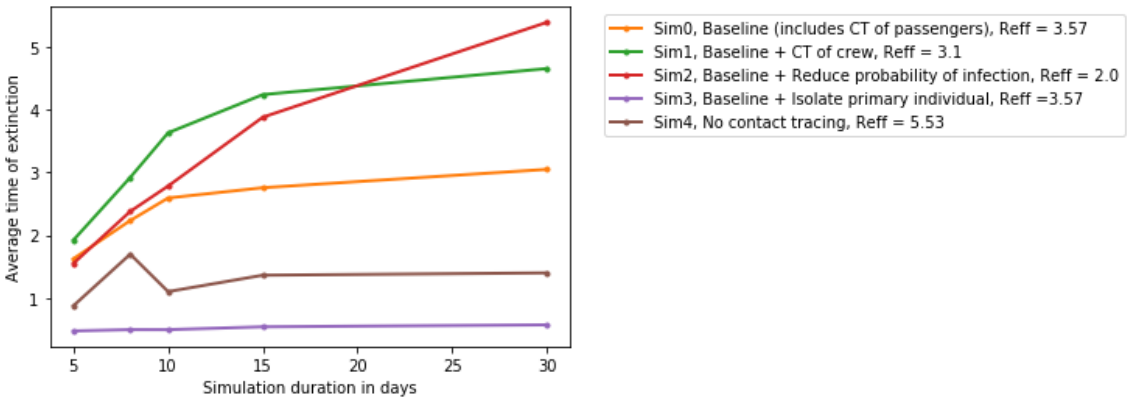

Figure 18: *Time of extinction for Sim2 as the simulation duration increases.*

6.2.1 Assumptions and parameters
6.2.2 Methodology
6.2.3 Results
6.2.4 Discussion of results
6.3 Conclusions and discussion
7 Simulations III - Comparison to other models: CAF Ship Scenario
7.0.1 Assumptions and parameters
7.0.2 Methodology
7.0.3 Results
7.0.4 Discussion of results
8 Limitations of the interrupted branching model

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9 This model's application to the CAF

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As shown in Section ?? on Page ??. According to [6], . . .

In Figure 19 and in Table ??.

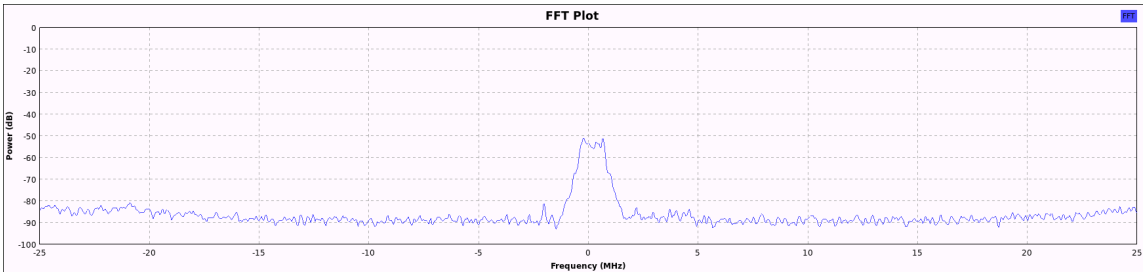

Figure 19: *Figure Title.*

Table 9: *My table.*

Name	Value 1
Name1	0
Name2	8

10 Conclusions

Given the average social dynamics of the CAF scenario, what would be the chances of an outbreak not going extinct?

References

[1] Moriarty, L. F., Plucinski, M. M., Marston, B. J., and al., e. (2020), Public Health Responses to COVID-19 Outbreaks on Cruise Ships — Worldwide, February–March 2020, *Morbidity and Mortality Weekly Report, Volume 69, Issue 12, pp. 347-352*, 69, 347–352.

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[6] Agashe, A., Rooyakers, L., Salmaninan, M., and Drouin, P.-L. (2019), A physical layer frame detector – The design and implementation guide, (DRDC-RDDC-2019-R???) Defence Research and Development Canada – Ottawa Research Centre.

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