Contact-tracing strategies for SARS-CoV-2 eradication **** UNFINISHED DRAFT ****

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ABSTRACT

As of 27th March a large and increasing proportion of the global population are living under social distancing measures in order to control the spread of COVID-19. If these measures are successful we will, in a few months, be in a situation where prevalence is again low in certain parts of the world, however, it is not clear what the best policy will be at that point. This paper investigates the feasibility of using contact tracing along with a combination of other measures in order to ease the social distancing measures while preventing a resurgence of the disease.
**** THIS IS UNFINISHED RESEARCH WHICH MAY CONTAIN ERRORS AND IS SUBJECT TO CHANGE ****

Keywords COVID-19, SARS-CoV-2

1 Introduction

Many countries in the world are now committed to a surge in incidence of COVID-19 and are practising social distancing in order to suppress its spread. If successful, these countries will soon be in a situation where prevalence is reducing. Once this is achieved there are a number of strategies:

- lift the social distancing measures and allow a second (and subsequent) waves until herd immunity is achieved(Ferguson et al., 2020).
- maintain low levels until a vaccine is available
- eradicate the virus locally and impose strict border controls and containment strategies until the virus is contained globally

Here we investigate the feasibility of the third option by slowly lifting social distancing measures while maintaining self isolation of symptomatic individuals and implementing an extensive testing and contact-tracing capability.

2 Description of the Model

The model we use is an agent-based discrete event simulation. It is based on the stochastic branching model described in (Hellewell et al., 2020) but modified in order to capture enough detail to explore different testing and contact-tracing strategies while capturing the workload on a centralised testing and contact-tracing facility and the increasing delays in this facility as workload increases.[2]

The model consists of infected agents, each of which belongs to a household and a workplace/school. Once infected, an agent goes though an incubation period with duration drawn from a Weibull distribution (with shape parameter 2.322737 and scale parameter 6.492272)(Backer, Klinkenberg, & Wallinga, 2020). The transmission serial interval (i.e.

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[2]Although a discrete-event simulation is slower than a branching model, execution time is not a bottleneck so it is worthwhile in order to capture the dynamics.

time from exposure to transmission) is drawn from a skew normal distribution with location parameter equal to the clinical onset time (i.e. end of the incubation period), scale parameter of 2.0 and skew parameter of 1.95(Hellewell et al., 2020). This results in 15% of infections occurring before clinical onset(Hellewell et al., 2020). In order to avoid unrealistically early transmissions, the serial interval was bounded to a minimum of 1 day. At creation, 17.9% of agents are deemed to be asymptomatic(Mizumoto, Kagaya, Zarebski, & Chowell, 2020)[3]. Asymptomatic carriers are assumed to be $\frac{2}{3}$ as infectious as symptomatic carriers(Ferguson et al., 2020). The number of susceptible agents that an infected agent will infect if not isolated is drawn from a negative binomial distribution with overdispersion parameter 10.0(Zhuang et al., 2020)(Riou & Althaus, 2020) and mean of $\frac{3R_0}{3-\rho}$ for symptomatic agents and $\frac{2R_0}{3-\rho}$ for asymptomatic agents where $\rho = 0.179$ is the probability of being asymptomatic and R_0 is the basic reproductive number. At each transmission event a new infected agent is created, unless the agent is isolated, in which case the event has no effect.

Each transmission event occurs either in the household, at the workplace/school or in the community. This allows us to capture the differences in ease and speed of contact tracing in these three cases, and to capture the effect of different policies for tracing in these contexts. It also allows us to capture the effect of household-wide self-isolation policies such as those implemented in the UK. The relative probability of transmission in the three locations was calibrated in order to obtain equal aggregate numbers of transmission events in each location(Ferguson et al., 2020). The distribution of number of members in a household was calibrated against(Smith, 2014).

In order to account for people who have already been infected during the first wave of infection, a proportion of the population is immune to infection. A transmission event to an immune agent does not cause infection. This immunity is applied only to school/workplace and community under the assumption that, during the peak, under "stay at home" rules during the initial peak of infections, if one member of a household contracts the disease it is highly likely that all other members will also contract it, and so the whole household will become immune. This means that only members of non-immune households can subsequently become infected.

2.1 Contact tracing and isolation policy

It was assumed that a "self-isolate" policy was in place such that anyone who becomes symptomatic must self-isolate and report to authorities. At this point all members of that person's household must also self-isolate. It was assumed that there was a delay between symptom onset and self-isolation/reporting. Once reported, all members of the household are tested and those that test positive are contact-traced. Contact tracing was assumed to identify 90% of contacts in the workplace/school and 10% of contacts in the community. Symptomatic contacts in the workplace must isolate immediately, other contacts are tested and must isolate on positive test result. The time for a test result to be processed was assumed to be 24 hours. It was assumed that 10% of the population do not comply with these rules and never self-isolate or report themselves.

The source code of the model is available at https://github.com/danftang/Covid19

3 Preliminary results

Simulations were carried out to find the probability that an initial population of 100 infected agents could be eradicated under different scenarios. Eradication was deemed to have been achieved if the cumulative number of cases remained below 5000 and there was no untraced infected population at 15 weeks into the simulation. $R0$ was set to 2.4(Ferguson et al., 2020) and it was assumed that 5% of the population was immune. The probability of eradication was estimated by performing a monte-carlo run of 300 simulations and counting the proportion that achieved eradication.

It was found that the probability of eradication was highly sensitive to the delay between symptom onset and self-isolation, and to the time after exposure that an infected person would test positive, so monte-carlo runs were performed for a range of values of these parameters. Figure 1 shows the probability of eradication against the delay between symptom onset and self-isolation while figure 2 shows the probability of eradication against the delay between exposure and positive test result.

4 Discussion

These early results are subject to further calibration of the model and are likely to change as our understanding of the dynamics of SARS-CoV-2 develops. It also remains to do a proper sensitivity analysis of the model, and to properly treat uncertainty, which is large. However, they do indicate that while it is not impossible in theory for contact-tracing to be effective, a very high proportion of the population will have to isolate, or be isolated, within 1 day of symptom onset. This will be difficult to achieve in practice, and so for contact tracing to work, it is likely that it will have to be implemented in combination with some other policy or policies to suppress community transmission. Our ongoing research will investigate these possibilities.

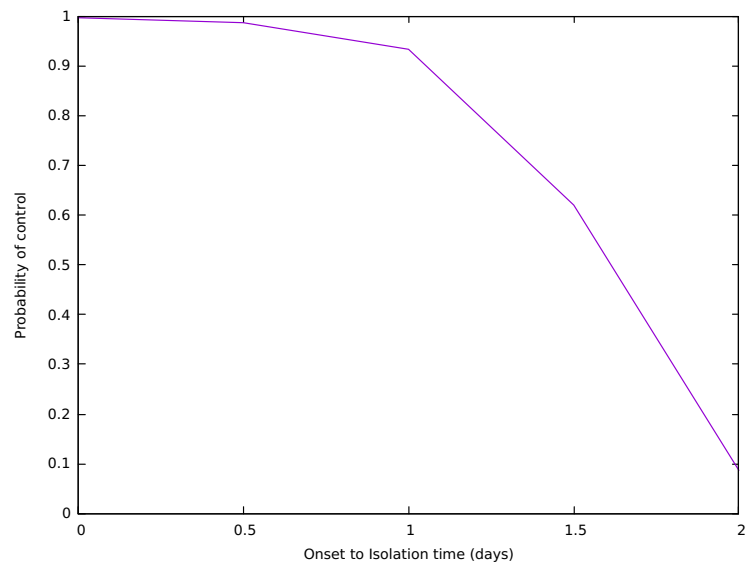
[3][TODO: Age weight this figure]

Figure 1: Probability of eradication for different delays between the onset of symptoms and self-isolation, assuming all infected test positive.
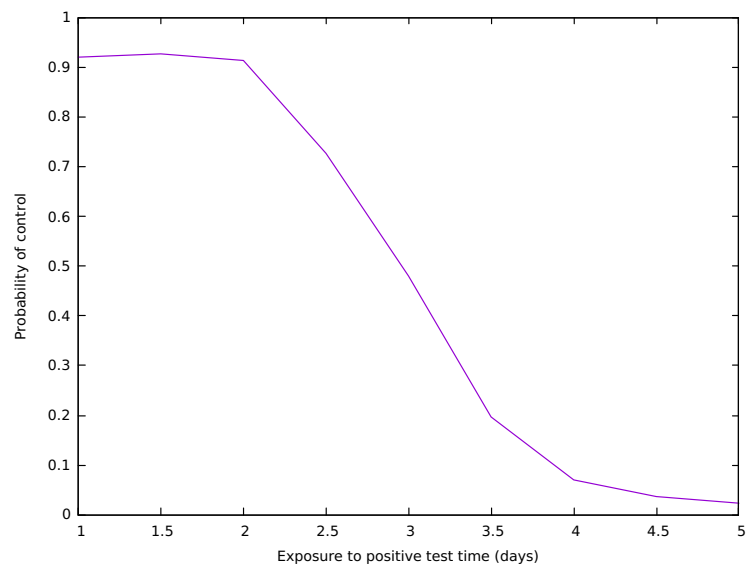

Figure 2: Probability of eradication for different delays between exposure and a test result becoming positive, assuming a delay of 1 day between symptom onset and self-isolation.

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