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Modelling the Current Welsh TTP (Test, Trace, Protect) System

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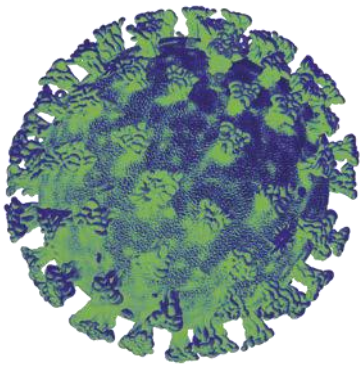

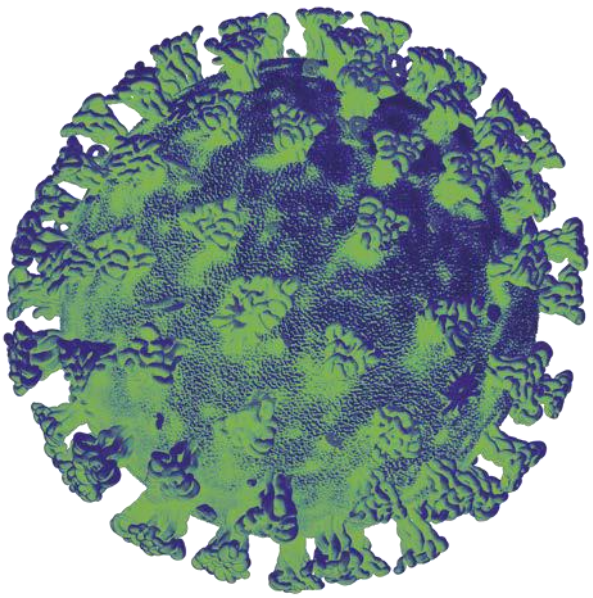

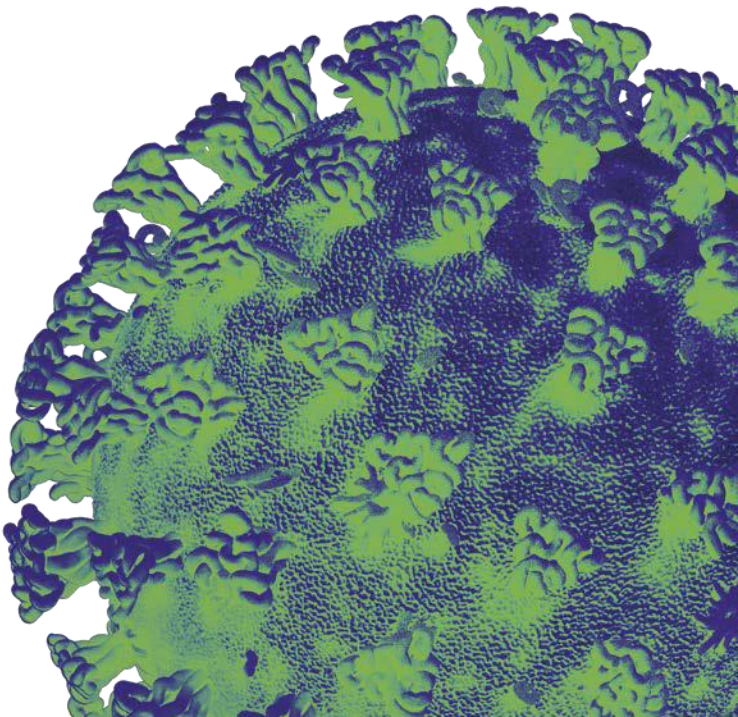

Modelling the Current Welsh TTP (Test, Trace, Protect) System

COVID-19 Technical Advisory Group – TAC Modelling Subgroup

Summary:

- Data from the Welsh TTP system on the observed delays and efficiency of each component was used to estimate the percentage transmissions that may have occurred from an index case or their contacts before they were traced and entered isolation. This was then used to estimate an approximate effect on the reproduction number, R.
- Given that the observed R value in Wales, the characteristics of TTP at the time can be used to try and infer the value in R in its absence. During winter high transmission and prevalence (outside of firebreak), we estimated TTP reduced R from approximately 1.7 to 1.3. Using recent R values and improvements to case ascertainment and test and trace times, the effect may be a reduction from approximately 1.3 to 0.8.
- The largest effect was due to the rapid isolation of the index case. This is due largely to the small observed delay between symptoms, and reporting in to the TTP. On top of this, the effect of subsequent contact tracing can be relatively small, in particular if ascertainment is low. One consequence of this, is that if improvements in index case volume result in longer testing and tracing delays, there can still be an overall improvement in R. Nevertheless, contact tracing remained a significant component in most of our scenarios, especially at high ascertainment of index cases and under the assumed high ascertainment of contacts, and short tracing delays.
- The recent introduction of bi-directional contact tracing in Wales has the potential to further reduce R, comparable in magnitude to the forward tracing. In particular, under scenarios in which case ascertainment is high. However, there are a number of practical challenges encountered and costs introduced by backwards tracing.
- Adherence with isolation policies is not currently considered in this model. We are currently developing this into the model and seeking appropriate data to support this analysis. We hope to include this in future iterations of this model.

Introduction

The aim of this exercise was to investigate the efficiency of the TTP (Test Trace and Protect) System in Wales. This paper considers the how we can start to evaluate the impact of the TTP system in reducing the effective reproduction number, R, using a simple model. The scenarios should be considered approximate, as there are a number of complexities in the system that have not yet been included in the modelling.

In our model we first consider the number of people that enter the system as reported and confirmed index cases. The more people that engage with the TTP system the better its impact on the circulation of COVID-19 in Wales. ONS/ SPI-M estimates suggest that the number of cases represents approximated 25% of the total number of infections in the population [1]. Those infections that are not identified may be due to fully asymptomatic individuals (i.e. never symptoms of COVID-19), mild symptoms, as well as individuals failing to report symptoms. Recent triangulating between hospital admissions, deaths, ONS survey results in Wales, and the incidence estimates from SPI-M, suggest that this % has increased to approximately 40%, and we consider these ranges in our analyses.

The second element is the length of time that it takes to get through (or the efficiency of) the TTP system. We are able to define and measure these lengths of time (time periods one to five defined below), the shorter these lengths of time the more effective the TTP system will be.

The analysis below can be used to estimate the overall impact of TTP on R, and compare the benefits of reducing delays in TTP under different ascertainment scenarios, and conversely, the benefits of bringing more individuals through the existing TTP system by increased ascertainment.

The Model

We considered a simple branching process model, in which individuals spread infection to R individuals in the next generation. Individuals are isolated, and hence cannot pass on the infection further, after specific delays that represent the identification of the index case and the tracing of contacts.

We considered the impact of 5 delays in the TTP system:

- Time period 1: Symptoms to Reporting and isolation (for the index case)
- Time period 2: Reporting to Testing (index case)
- Time period 3: Testing to Test Results (index case)
- Time period 4: Test results to Tracing of contacts
- Time period 5: Tracing to Advising of contacts to isolate

In order to estimate the % transmissions that occur from an index and contact we assumed:

- The incubation period (time of infection until symptoms appear) is a Weibull distribution with mean 5.8 days and standard deviation 2.6 days.
- The serial distribution for an infector is generated by a skewed normal distribution, with mean (xi) 6 days, omega = 2, and k = 0. In this distribution

(based on [2], it is therefore assumed that 50% of transmissions occur before symptoms appear.

- Setting an infection time for index cases (t=0). We then calculated by sampling from the relevant delay distributions:
  - The time at which symptoms appear in the index (sample at random from incubation period distribution)
  - The time at which a secondary case would become infected, by sampling at random from the serial distribution
  - The time at which symptoms would appear in the secondary case (sample at random from incubation period distribution)
  - The time at which the primary case is registered in the contact tracing system, by adding 'time period 1' to the incubation time. *The index case enters isolation on this day.*
  - The time at which all contacts are traced, by adding 'time period 2+3+4+5'. Secondary cases enter isolation at the earliest time point: either through contact tracing, or through appearance of their symptoms (plus time period 1, ie by becoming an index case themselves).
  - For both primary and secondary cases we calculated the % of transmissions that were expected to have already occurred before they were isolated. This is calculated from the percentile of the serial distribution, calculated using the value obtained from the difference between the infection day, and the isolation day.

The final step was to link the reduction in transmission potential of traced cases (identified in the above process) to the overall population effect on *R*. For this, we include untraced individuals. These may be fully asymptomatic, or very mild unreported cases, or cases unreported for other reasons. The current assumption is that this represents a significant proportion of overall infections. As a baseline we assume 25% of infections enter the tracing system in winter 2020, increasing to 40% by March 2021. The PHW reported number of contacts successfully traced has been consistently high during the pandemic, and is approximately 85% (winter) to 90% (current).

We considered three types of individual, and the proportion of transmissions from the index cases (*x*) and from the secondary cases (*y*) obtained from the above analysis.

- Type 0: untraced individual. Causes *R* infections
- Type 1: primary individual entering tracing. Causes *xR* infections
- Type 2: secondary infection of a traced individual. Causes *yR* infections
- *p* = probability of an infected entering tracing system (unknown, assume ascertainment ~ 25% winter 2020)
- *q* = probability of secondary infection of someone in tracing being traced (PHW data ~ 90%)
- we allow a missed secondary infection of someone in tracing to be picked up to enter tracing ["second bite of the cherry"]

- Traced secondary infections of type 2 individuals are also type 2.

Given these assumptions, the next generation matrix is:

		"From" (infecting type)		
		0	1	2
"To" (secondary infections)	0	(1-*p*)*R*	(1-*q*)(1-*p*)*xR*	(1-*q*)(1-*p*)*yR*
	1	*pR*	*p*(1-*q*)*xR*	*p*(1-*q*)*yR*
	2	0	*xqR*	*yqR*

The effective overall *R* value, R_{eff}, is the dominant eigenvalue of the next generation matrix. *Baseline Wales values: p = 25%-40%, q = 90%, x and y obtained from the serial distributions of the model*

Scenario Results

We considered 3 scenarios, broadly reflecting: (1) the performance of TTP in November, where prevalence/R was high and capacity was stretched, resulting in longer delays; (2) current scenario with short delays, improved ascertainment (due in part to testing) and low prevalence/R; and (3) a potential future scenario of high prevalence/R but with the current short delays maintained.

Scenario 1: High R, high prevalence, low ascertainment and long delays

If we assumed that the delays for testing and tracing were on average 5 days (after 1 day delay from symptoms to reporting), and 25% of infections reported as index cases, the TTP was estimated to reduce R from 1.68 to 1.3, and absolute reduction of 0.38. This approximates the situation in November 2020.

Scenario 2: Low R, low prevalence, high ascertainment and short delays

If we assumed that the delays for testing and tracing were on average only 1 day (after 1 day delay from symptoms to reporting), and 40% of infections report as index cases, the TTP was estimated to reduce R from 1.28 to 0.8, and absolute reduction of 0.48. This approximates the current situation in February 2021.

Scenario 3: High R, high prevalence, high ascertainment and short delays

If we assumed that the delays for testing and tracing were on average only 1 day (after 1 day delay from symptoms to reporting), and 40% of infections reported as index cases, the TTP is estimated to reduce R from 2.0 to 1.25, an absolute reduction of 0.75. This approximates a future scenario in which R and prevalence increase, but there is confidence that good ascertainment and short delays can be maintained.

Impact of the different components of the system:

Contact Tracing: Under most scenarios, the greatest reduction in R is due to the early isolation of the index case. For example, in scenario 1 approximately 10% of the reduction in R is due to contact tracing. This effect increases notably with greater ascertainment of index cases. In scenario 2, the contact tracing accounts for

approximately 22% of the reduction in R. One implication of this, is that if greater ascertainment comes at a cost of longer test and tracing delays, there can still be an overall benefit (Figure 1). We note that the strong effect of the index case is due to the observed short delay between the day of symptoms and the day of reporting into the TTP, and hence start of isolation, currently assumed to be 1 day (and often observed to be less). If the delay to case isolation is assumed to be longer then the relative contribution of index case and contact isolation would be different. For example, if the delay was 2 days, in the above scenarios, the contribution of contact tracing would be approximately 20% (scenario 1) and 35% (scenario 2).

We note however, that in our model estimates should be considered a lower bound, and the effect of contact tracing is likely to be higher. We have used a simple branching process for infection, which only considers infected individuals as independent events. We do not consider the complex social structure of *all* contacts in a population, and how they are linked across individuals. It is very likely that making use of a detailed social structure would reveal the contact tracing component more effective, for example by including the ability to exploit overlapping contact structures, whereby the process of tracing for one index case can yield an early capture for another index.

Bi-directional contact tracing

For most of the epidemic in Wales, tracing has been initiated if a contact occurred from any point 48-hours prior to the appearance and symptoms in the index case. Hence the system is largely forward looking. Recently, capacity has allowed backward contact tracing, which has the aim of potentially picking up the source of infection for the index case, and hence their other subsequent infectees at an earlier stage. A more detailed branching process model [3] has suggested that bidirectional contact tracing can significantly improve outbreak control. We applied the approximate Wales TTP parameters which is currently using a ‘look-back’ period of 14 days prior to symptoms, to this model to explore the effects.

The bi-directional model generates similar results to our branching process model described above for forward contact tracing. We found that the impact of bi-directional was roughly equivalent to the impact of forward tracing. Hence there could be a significant additive benefit, in particular at the higher ascertainment of index cases.

We add some important caveats from the early experience of bi-directional tracing:

- The backwards tracing is a much longer process. Experience so far suggests an additional 30-60 minutes per interview.
- Recall accuracy is less, and hence the ascertainment of contacts is expected to be lower
- Currently, backward traced contacts are not required to isolate. Rather, they are made aware of the contact and encouraged to be extra vigilant for the appearance of symptoms, and importance of a test. One the one hand this may reduce the effectiveness, but also reduces unnecessary isolation.

Nevertheless, there is now a good opportunity to monitor the progress of the Welsh TTP system looking forwards and backwards, in particular when there is clear capacity at low R / low prevalence scenarios. Another priority would be for index cases with no clear known source of infection.

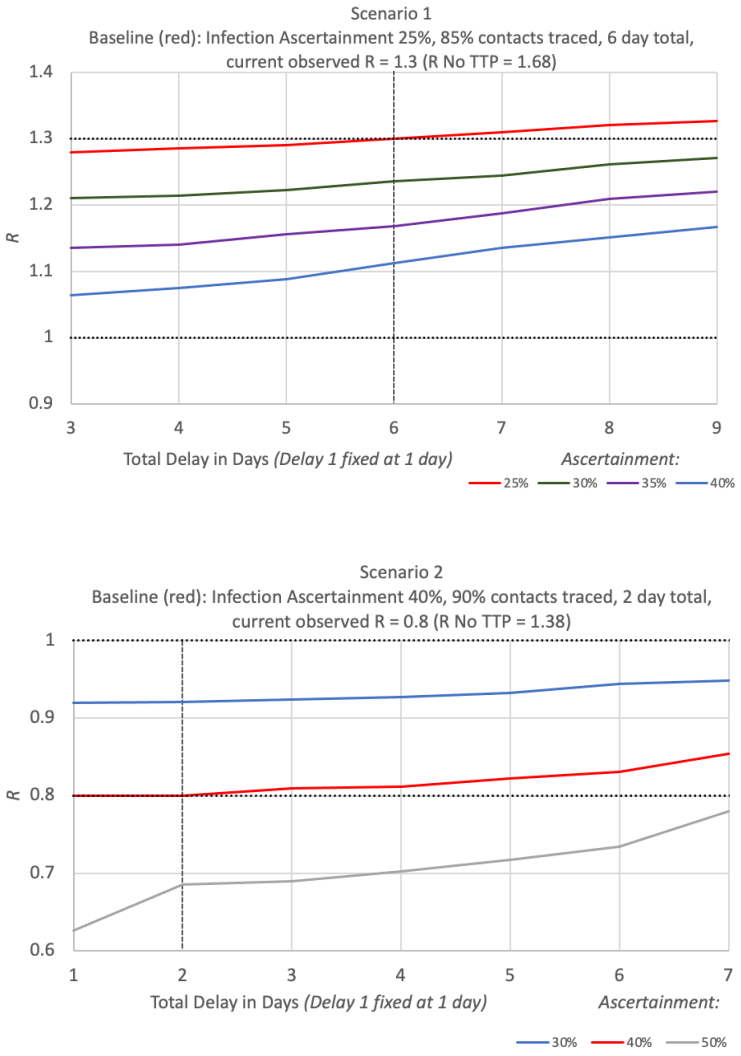

Figure 1. *Effect of improving test and trace delays on R. Baseline scenarios are given in red for scenario 1 (high prevalence, high R, long delays, low ascertainment) and scenario 2 (low prevalence, low R, short delays, high ascertainment). In both cases it can be seen that improved ascertainment has a large effect on R, even at some cost to tracing time.*

References

[1] Colman E, Enright J, Puspitarani GA, Kao RR. (2021). Estimating the proportion of SARS-CoV-2 infections reported through diagnostic testing. medcin doi:10.1101/2021.02.09.21251411

[2] J Hellewell et al. (2020). Feasibility of controlling COVID19 outbreaks by isolation of cases and controls. *The Lancet*. https://doi.org/10.1016/S2214-109X(20)30074-7

[3] Bradshaw WJ, Alley EC, Huggins JH, Lloyd AL, Esvelt KM. (2021). Bidirectional contact tracing could dramatically improve COVID-19 control. *Nature Communications* 12, 232.