The feasibility of targeted test-trace-isolate for the control of B.1.1.7

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Abstract

The SARS-CoV-2 variant B.1.1.7 reportedly exhibits substantially higher transmission than the ancestral strain and may generate a major surge of cases before vaccines become widely available. As B.1.1.7 can be sensitively detected using the Thermo Fisher TaqPath S-gene RT-PCR test, contact tracing and isolation programs appear well-suited to slowing the spread of the new variant, which is still rare in most of the dozens of countries in which it has been identified. However, key determinants of outcomes such as data-sharing, trace success, and isolation compliance vary widely between regions, which may discourage public health agencies from explicitly redirecting existing contact tracers to contain B.1.1.7. Here we apply a branching-process model to estimate the effectiveness of implementing a B.1.1.7-focused testing, contact tracing, and isolation strategy with realistic levels of performance. Our model indicates that bidirectional contact tracing can substantially slow the spread of B.1.1.7 even in regions where a large fraction of the population refuses to cooperate with contact tracers or to abide by quarantine and isolation requests.

The frequency of the B.1.1.7 variant of SARS-CoV-2 has grown rapidly from its initial detection in October 2020 to become the dominant strain in southeastern England by 2021. Studies have estimated the new strain is between 40% and 80% more contagious1,2. The rapid exponential growth of B.1.1.7, which is now found in dozens of countries, risks another and potentially higher wave of COVID-19 cases prior to widespread vaccination.

Due to the B.1.1.7 variant’s characteristic ΔE69-70 mutation in the spike protein, cases of the new variant can be sensitively detected and distinguished from the ancestral SARS-CoV-2 via a Thermo Fisher TaqPath RT-PCR diagnostic test for COVID-191. Twenty million such kits are manufactured weekly4. As such, existing COVID-19 testing infrastructure can be used to track the transmission of the new variant. Samples testing positive by other kits can be re-screened5 without an emergency use authorization.

Test-trace-isolate (TTI) strategies have been widely used to mitigate the spread of SARS-CoV-2. Models by the present authors* and others8 have found that incorporating backwards tracing to identify infecto individuals could dramatically increase the efficacy of tracing programs. However, testing delays, mistrust, and low compliance in some communities have undermined the confidence of health authorities in the benefits of TTI9,10. Moreover, efficacy sharply decreases when caseloads are high11, as is true for SARS-CoV-2 – but not yet B.1.1.712,13 – in many regions.

Given the current low prevalence of B.1.1.7 in most jurisdictions and the ability to identify cases of the new variant using existing testing infrastructure, we hypothesised that TTI programs dedicated to controlling B.1.1.7 could substantially reduce the harm inflicted by the new variant prior to widespread vaccination of populations later in 2021. Such programs could be enhanced through incorporation of bidirectional tracing.

However, the effectiveness of TTI strategies varies widely from region to region due to programmatic and population-level differences in variables such as the proportion of cases who share their contact history with contact tracers; the proportion who comply with quarantine and isolation requests; and the overall rate of tracing success. Given this variation, it is unclear whether tracing programs exhibiting realistic levels of performance could feasibly dampen the spread of B.1.1.7.

To evaluate the potential benefits of applying targeted test-trace-isolate to control B.1.1.7, we applied a previously published branching-process model of COVID-19 contact tracing1 to estimate the change in the effective reproduction number achievable across a wide range of parameters.

NOTE: This preprint reports new research that has not been certified by peer review and should not be used to guide clinical practice.
Methods
In our model, each case generates a number of new cases drawn from a negative binomial distribution, according to some pre-specified incubation- and generation-time distributions (Table 1). Cases could be identified and isolated based on symptoms alone or through contact tracing. Cases were assumed to either comply with quarantine and isolation requests, or ignore them completely, according to some fixed probability of compliance; cases that comply with quarantine & isolation were assumed to generate no further cases.

Successful tracing depended on the identified case sharing their contact history with tracers, and on the contact in question taking place within the time window (measured in days pre-symptom onset for symptomatic cases, and days pre-identification for asymptomatic cases). Environmental transmission was assumed to be untraceable. Symptomatic cases required a positive test before initiating contact tracing, as in the EU\cite{14} and most US jurisdictions.

Each outbreak was initialized with 20 index cases to minimize stochastic extinction and designated as “controlled” if it reached extinction (zero new cases) before reaching 10,000 cumulative cases. Effective reproduction numbers ($R_{\text{eff}}$) were computed as the mean number of child cases produced per case.

Results
To investigate the potential for TTI to mitigate the spread of B.1.1.7, we investigated the effective reproduction number achieved across a range of data-sharing and trace-success rates (Figure 1). To account for uncertainty in the transmissibility of B.1.1.7, we explored outcomes for reproduction numbers between 1.2 and 2.0; these values assume that non-tracing interventions are already in place.

In the absence of contact tracing, identification and isolation of symptomatic cases alone reduced $R_{\text{eff}}$ by 0.2 to 0.3 even when quarantine and isolation compliance was low (Figure 1, top rows). When identification and isolation left $R_{\text{eff}}$ substantially greater than 1 (when base $R \geq 1.4$), moderate levels of tracing could have substantial effects.

When contacts were traced up to 2 days prior to symptom onset, roughly 60-70% data sharing and trace success was required to achieve an $R_{\text{eff}}$ reduction of at least 0.1, relative to isolation alone. If the window was extended to 6 days pre-onset to enable more effective bidirectional tracing, roughly 45-55% data sharing and trace success was sufficient. Higher levels of data sharing and trace success could achieve substantially larger reductions: in many scenarios, 85% data sharing and trace success reduced $R_{\text{eff}}$ by >0.2 in the 2-day case and >0.35 in the 6-day case.

Due to the exponential growth of uncontrolled epidemics, small reductions in $R_{\text{eff}}$ can have a large impact on the total number of downstream cases arising from a given index case over a given timespan. For example, under a simple geometric series approach, reducing $R_{\text{eff}}$ by 0.1 from a starting value between 1.2 and 2.0 reduces the total number of child cases after 10 generations by 37-43%; an $R_{\text{eff}}$ reduction of 0.2 results in a reduction in child cases of 61-66%. Given an average generation time of 6 days, 10 generations equates to roughly 2 months – enough time, given sufficient delay in the spread of the new variant, to vaccinate a substantial fraction of the population.

Discussion
Our results suggest that regions with even moderately functional contact tracing programs focused on B.1.1.7 could substantially slow the spread of the variant. Given a 2-day window for bidirectionally tracing contacts pre-symptom onset, our model predicts that a program with 70% trace success, 70% data sharing, and 70% compliance with isolation could achieve an $R_{\text{eff}}$ reduction of at least 0.1 relative to the no-tracing case. Given a 6-day window for efficient bidirectional tracing, regions with just 50% data-sharing, trace success, and isolation compliance could achieve a reduction of 0.1.

Under simple assumptions, such a reduction would reduce the number of child cases produced in two months by roughly 40%, buying time for vaccination to immunise many more people. More effective tracing programs can achieve larger reductions. Higher rates of cooperation might be achieved through home visits by contact tracers\cite{15}; exoneration for anything discovered in the course of B.1.1.7 contact tracing\cite{16}; and financial and other support of people in quarantine and isolation\cite{17}. In principle, concentrating vaccination in communities with clusters of uncontrollable B.1.1.7 transmission could further impair viral spread and increase the sustainability of testing, tracing, and isolation for the control of COVID-19.

These results assume a high availability of suitable tests for B.1.1.7, and a rapid and consistent testing turnaround. They also take no account of any medical, demographic, geospatial or behavioural variation between cases which could influence the spread of the new variant.

Our results suggest that TTI programs could help slow the spread of B.1.1.7 in regions where it is currently rare, providing vital time for vaccination to end the COVID-19 pandemic. As TTI efficacy is limited at high caseloads\cite{18}, these findings indicate that tracing programs should immediately prioritise controlling B.1.1.7 over less transmissible – but currently more widespread – strains.
Figure 1. Evaluating the efficacy of bidirectional contact tracing for controlling B.1.1.7. Neighbour-averaged contour plots, showing $R_{\text{eff}}$ achieved by bidirectional manual contact tracing with a tracing window of (a) 2 or (b) 6 days pre-symptom onset, under different combinations of trace success probability (x-axis), rate of data sharing with manual contact tracers (y-axis), rate of compliance with isolation and quarantine (row) and base reproduction number (columns). Other disease parameters are specified in Table 1. Isolation of symptomatic cases is sufficient to reduce $R$ even when no traces succeed and/or no cases share their data with contact tracers. “Trace success probability” refers to trace attempts that are not otherwise blocked by environmental transmission or refusal to share data.
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Data Availability: The data supporting the findings of this study are in the main manuscript and the Supplementary Information, and are available at https://github.com/willbradshaw/covid-bidirectional-tracing.

Code Availability: Code for configuring and running the model is publicly available at https://github.com/willbradshaw/covid-bidirectional-tracing.

Competing Interests: The authors declare no competing interests.

Table 1: Parameters of the branching-process model.

| Parameter                              | Value                          | Sources and Notes                                           |
|----------------------------------------|--------------------------------|-------------------------------------------------------------|
| % asymptomatic carriers                | 40%                            | 17–21                                                       |
| Relative infectiousness of asymptomatic carriers | 45%                            | Informed by viral loads and tracing results described in 17,21–25 |
| % environmental transmission          | 5%                             | 26,27                                                       |
| Proportion of pre-symptomatic transmission | 38%                            | Informed by 21,22,24,25,28–33                               |
| Generation time skew parameter (α)    | 0.397                          | Corresponds to pre-symptomatic transmission rate specified above. |
| % of symptomatic cases identified without tracing | 50%                            | 34                                                          |
| % of cases who comply with isolation  | 50%, 70%, 90%                  | Assumed                                                     |
| Test sensitivity                       | 70%                            | 35,36                                                       |
| $R_{base}$ (before test/trace/isolate) | 1.0 to 2.0                     | Assumes a pre-B.1.1.7 $R$ of ~1.0^{12}.                     |
| Overdispersion                         | 0.11                           | 37                                                          |
| Number of initial cases               | 20                             | Assumed                                                     |
| Incubation period                      | 6.0 ± 2.1 days (lognormal distribution) | 1,38,39                                                    |
| Delay from onset to isolation         | 3.8 ± 2.4 days (Weibull distribution) | 40                                                          |
| Delay for testing                     | 1 ± 0.3 days (gamma distribution) | Assumed                                                     |
| Delay for manual tracing              | 1.5 ± 4.8 days (lognormal distribution); median 0.5 days | Previous reports suggest most contacts can be traced within one day, but some take longer 41 |