Estimating the Transmission Advantage for B.1.617.2

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Executive Summary

1. We use the standard Warwick model to infer the transmission advantage of the B.1.617.2 variant over the B.1.1.7 variant. The inference scheme is regularly used to generate estimates of the reproductive number (R) and to generate medium term projections. Here we have extended the model and the inference scheme to include an additional variant.
2. Given that B.1.1.7 is S-gene negative and B.1.617.2 is S-gene positive, we can use the proportion of S-gene positive samples from the TaqPath system to infer the relative amount of the B.1.617.2 in each of the NHS regions. Similar data is now available for Scotland and will be incorporated into future versions of the modelling framework.
3. The transmission advantage of B.1.617.2 over the B.1.1.7 is estimated based on a set of vaccine efficacy and cross immunity assumptions. Essentially we assume that: one dose of vaccine leads to slightly weaker protection against B.1.617.2 compared to B.1.1.7; two doses of vaccine provides equal protection against both variants; and both variants confer complete cross immunity post infection.
4. **We estimate that the B.1.617.2 variant has a 42% (CI 13-57%) transmission advantage over the B.1.1.7 variant, although ignoring the anomalous results for the North East and Yorkshire our estimate rises to 45% (CI 33-57%).**

This work uses the model that has been developed in Warwick over the past year [1, 2] and is matched to a variety of epidemiological data [3]. The model operates and is fitted to data from the seven NHS regions in England and is matched to daily data on proportion of symptomatic Pillar 2 cases that are positive, the number of hospital admissions, the number of hospital beds occupied, the number of ICU beds occupied and the proportion of samples from the TaqPath system that are S-gene positive (as a proxy for B.1.617.2). The results of this model have been presented to SPI-M and SAGE on a number of occasions, and the model has been used to examine short-term and medium-term projections as well as reasonable worst-case scenarios. The model has previously been extended to include vaccination, initially to investigate priority ordering and has subsequently increased in complexity to include two-dose schedules and multiple actions of vaccine protection [2]. It also used the ratio of S-gene positive to S-gene negative PCR results to infer the spread of the B.1.1.7 variant (which is S-gene negative on TaqPath system) at the end of 2020. This approach has since been expanded to assess the spread of B.1.617.2 (which is S-gene positive).

Vaccine uptake within the model to date mirrors the recorded data in terms of dose and age of those vaccinated. Projecting forwards, we follow the strict JCVI priority ordering for both Phase 1 and

Phase 2. The uptake of vaccines so far has been far higher than initially anticipated, exceeding 95% in many areas and age-groups. Here we assume that uptake in those 40 and over is determined by historical uptake, while for those 18-39 the uptake level is set at 80%. Vaccine efficacy assumptions against B.1.1.7 and B.1.617.2 are given in Appendix 1; other assumptions do not substantially change our estimates of the transmission advantage.

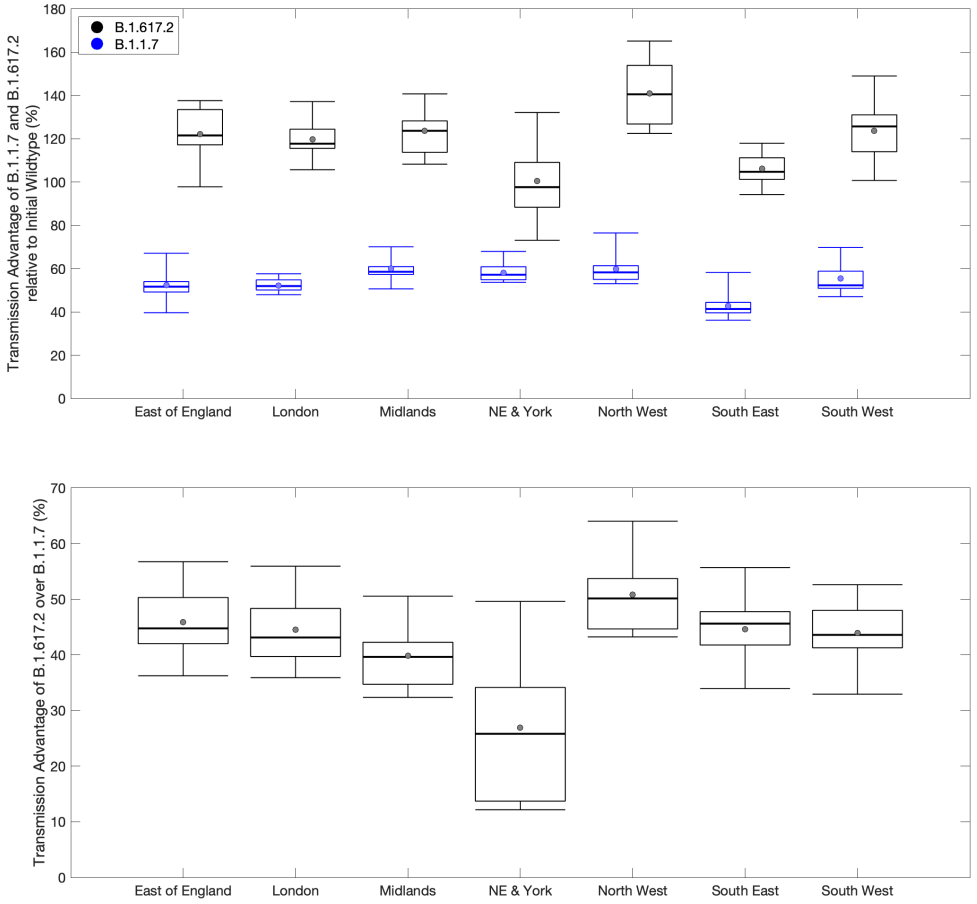

Fig. 1: Upper panel: The estimated transmission advantage of B.1.1.7 (blue) and B.1.617.2 (black) compared to the original wildtype, as inferred from the Warwick MCMC model, accounting for the dynamics in symptomatic Pillar 2 cases, hospital admissions and deaths, in addition to the proportion of symptomatic Pillar 2 cases that are S-gene positive. Lower panels: The estimated transmission advantage of B.1.617.2 compared to B.1.1.7.

We estimate that B.1.617.2 has a 42% (CI 13-57%) transmission advantage over B.1.1.7, which itself had a substantial transmission advantage over the original wildtype (Fig. 1). This advantage is inferred at a regional scale, although there are hyperpriors that constrain the advantages to be similar. We observe that B.1.617.2 consistently has an advantage over B.1.1.7 (non-overlapping confidence intervals) and generally transmits at twice the rate of the wildtype.

We can consider how these advantages (together with any vaccine escape) translate into the proportion of B.1.617.2 in comparison to total infections within the model (Fig. 2), which takes a sigmoidal form. Here the model projections are shown in black (together with the associated 95% prediction intervals); the pink dots are the proportion of S-gene positive samples relative to the total number of COVID positive samples in the TaqPath system (with CT value < 30), which is a reasonable approximation to the required quantity.

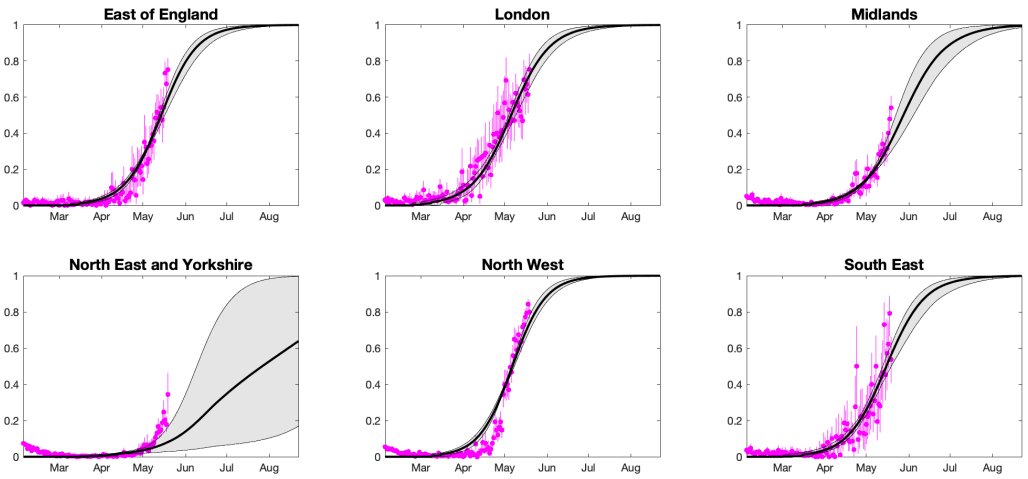

Fig. 2: The predicted proportion of infections that are attributable to B.1.617.2 (black line together with 95% prediction intervals) together with data on the proportion of S-gene positive samples with CT values below 30 (pink, and associated confidence intervals based on the number of samples.) Data and plots from the South West are excluded due to sparsity of samples.

In all regions except the North East and Yorkshire, we have consistent and broad agreement on the transmission advantage over B1.1.7 at 45% (CI 33-57%). The inferred value for the North East and Yorkshire is generally lower and more uncertain at 27% (CI 12-50%). This is also reflected in the poorer fit to S-gene data in this region where we fail to capture the most recent increase in S-gene positive samples. We postulate that this may be due to recent delays in the TaqPath system for this region.

Appendix 1

	Pfizer/Moderna				**AstraZeneca**			
Efficacy	**1st Dose**		**2nd Dose**		**1st Dose**		**2nd Dose**	
against	B.1.1.7	B.1.617.2	B.1.1.7	B.1.617.2	B.1.1.7	B.1.617.2	B.1.1.7	B.1.617.2
Infection	63%	44%	80%	80%	63%	44%	80%	80%
Symptoms	63%	44%	87%	87%	63%	44%	87%	87%
Hosp Adm	80%	70%	93%	93%	80%	70%	93%	93%
Mortality	78%	67%	97%	97%	78%	67%	97%	97%
Transmission	45%	45%	45%	45%	45%	45%	45%	45%

References

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[3] Keeling MJ, Dyson L, Guyver-Fletcher G, Holmes A, Semple MG, *et al.* Fitting to the UK COVID-19 outbreak, short-term forecasts and estimating the reproductive number. *medRxiv* page 2020.08.04.20163782 (2020). doi:10.1101/2020.08.04.20163782.