Rapid Impact Analysis of B 1.1.7 Variant on the Spread of SARS-CoV-2 in North Carolina

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31 January, 2021

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Abstract

Background: Several cases of the B1.1.7 variant of the SARS-CoV-2 were identified in North Carolina first on January 23, 2021 in Mecklenburg county and later in Guilford county on January 28, 2021.[1,2] This strain has been associated with higher levels of transmissibility.[3–5] This study examines the potential impact of increased transmissibility as the B1.1.7 strain becomes more predominant given current vaccine distribution plans and the impact

Method: We explored the anticipated impact on the effective reproduction number for North Carolina given the date of import. The approximate growth rate of B1.1.7 observed in the United Kingdom was fit and used to establish the estimate share of B1.1.7 in North Carolina. Using the nowcasted reproduction number, a stochastic discrete compartment model was fit with the current vaccination rates and B1.1.7 transmissibility to estimate the impact on the effective reproduction number.

Results: We found

Conclusions: Population level surveillance data supports

Method

Data

This analysis considered effective reproduction number data generated for the state of North Carolina using the[6] R package following the methods specified by.[7] Data on S-gene target failure (SGTF) observed in the United Kingdom and made available in the analysis[5] were used in order to estimate proportion of anticipated B1.1.7 variant circulating.

Statistical analysis

In order to estimate the growth of B1.1.7, a hierarchical beta regression model was fit to data available from the analysis of.[5]
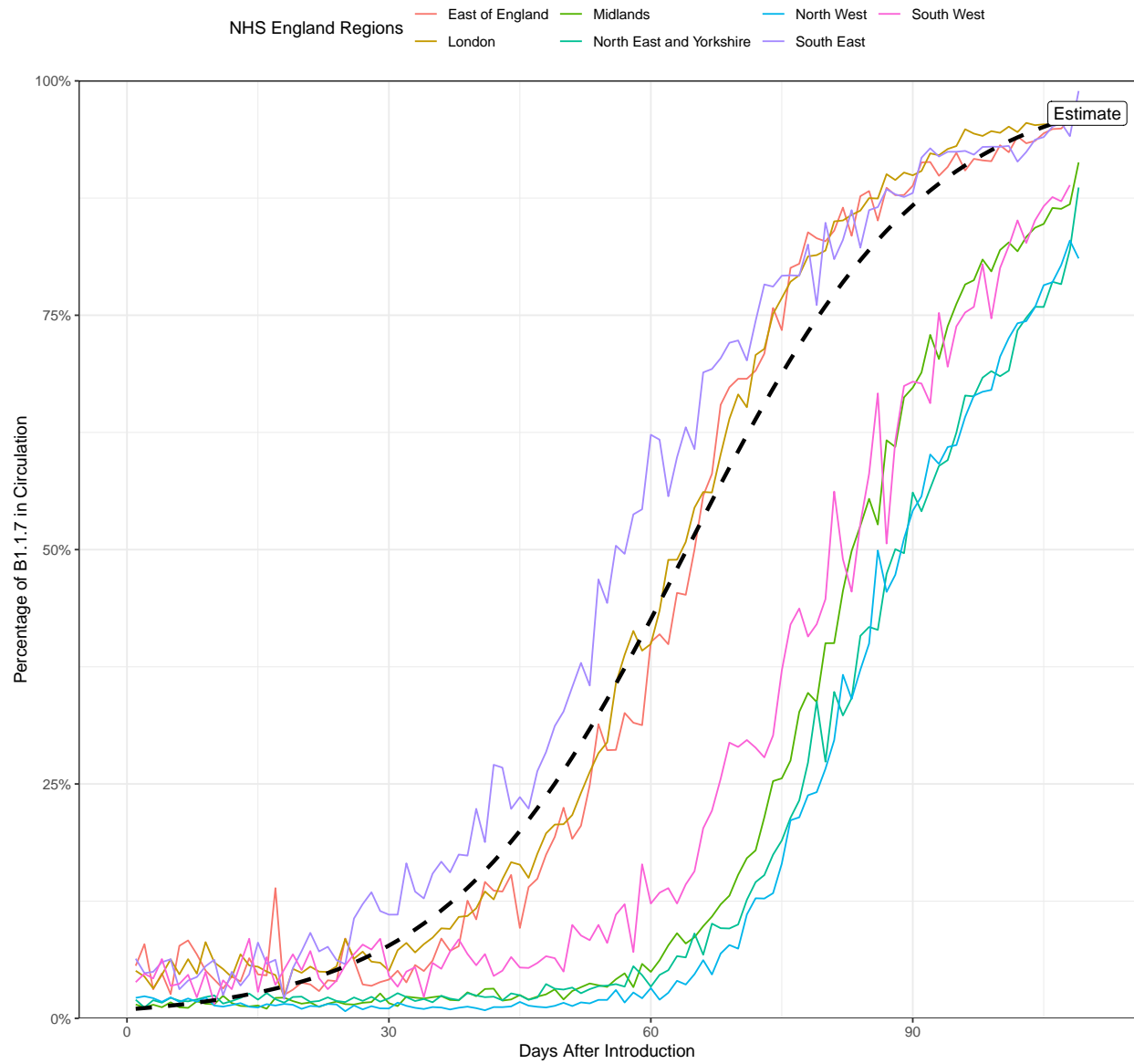
Figure 1: Estimates of SGTF Evolution Used as Proxy for B1.1.7 Share of SARS-CoV-2 Variants in Circulation
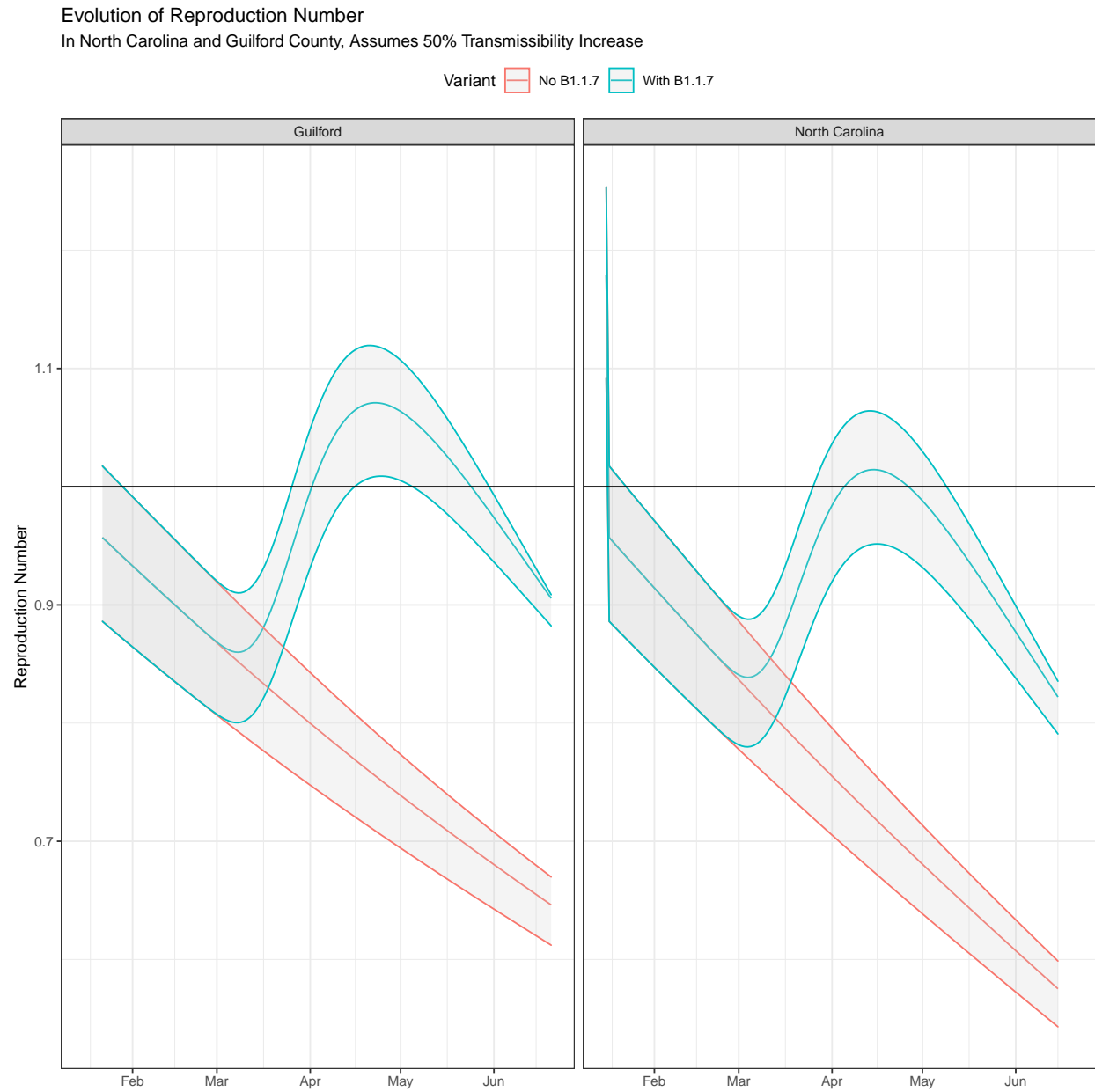
Figure 2: Estimates of Reproduction Number Evolution in North Carolina and Guilford County Shows Heteogenity

Results

Discussion

References

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