

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

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Abstract

Background: Individual level data

Method: We explored

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^[1] R package following the methods specified by.^[2] Data on S-gene target failure (SGTF) observed in the United Kingdom and made available in the analysis^[3] were used in order to estimate proportion of anticipated B1.1.7 variant circulating.

Statistical analysis

Results

Discussion

References

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