

Real-time estimation of the difference in the test seeking distribution of Omicron compared to Delta in England using S-Gene Target Status as a Proxy

Summary report

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Introduction

Methods

Data

We use S-gene status by specimen date sourced from UKHSA as a direct proxy for the Omicron variant with a target failure indicating a case has the Omicron variant. Data was available by UKHSA region.

Models

Statistical Inference

Implementation

All models were implemented using the `forecast.vocs` R package^[1,2] and fit using `stan`^[3] and `cmdstanr`^[4]. Each model was fit using 2 chains with each chain having 1000 warmup steps and 2000 sampling steps. Convergence was assessed using the Rhat diagnostic^[3]. Models were compared using approximate leave-one-out (LOO) cross-validation^[5,6] where negative values indicate an improved fit for the correlated model.

Limitations

Results

Summary

Data description

Daily

Fraction of those tested for the S gene with target failure by UKHSA region

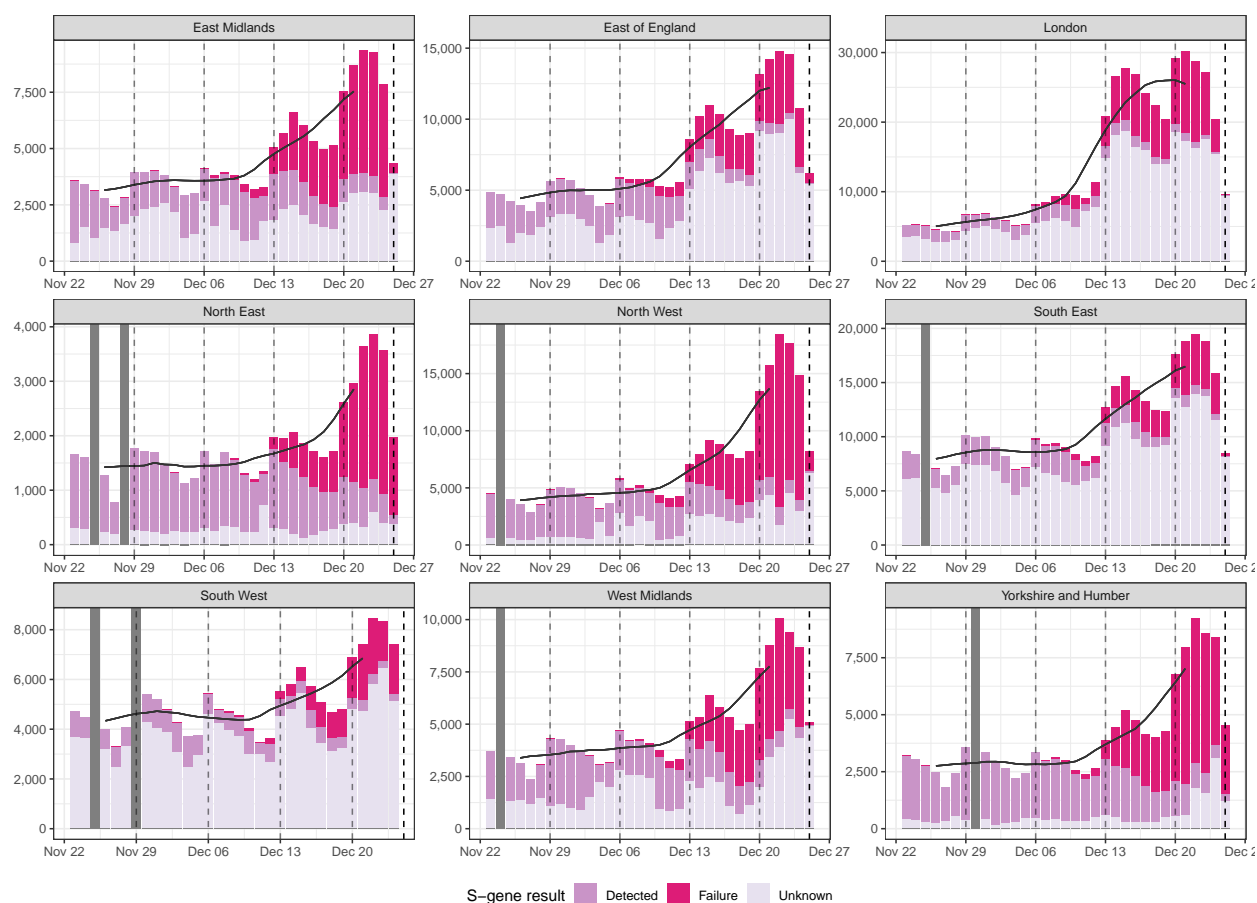


Figure 1: Daily cases in England and by UKHSA region, with S-gene target result (failed, confirmed detected, or unknown), and centred 7-day moving average up to date of data truncation (dotted line). Source: UKHSA and coronavirus.gov.uk; data by specimen date.

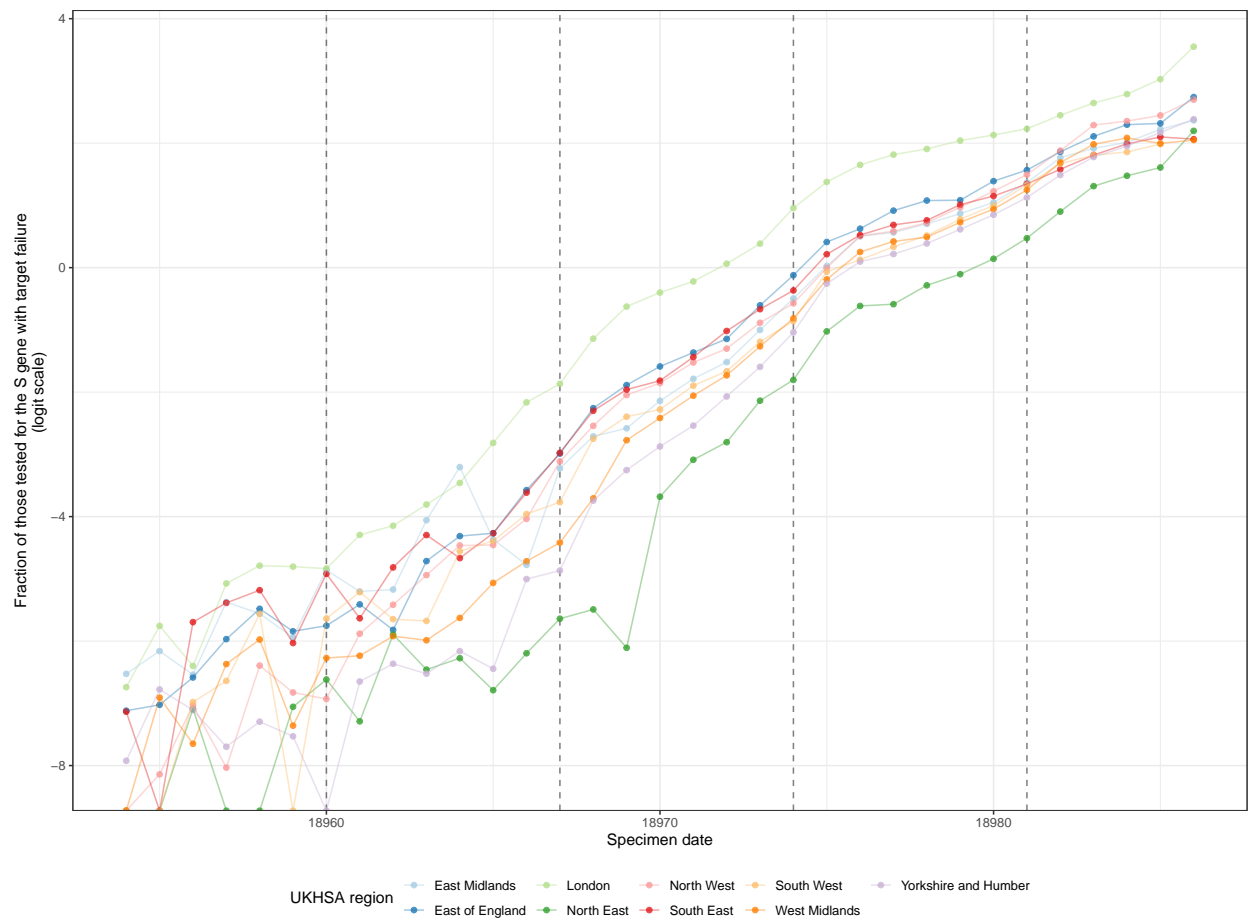


Figure 2: Daily fraction of those tested for S gene status with SGTF by UKHSA region on the logit scale. The dashed vertical lines indicate Mondays. Note that the data is by specimen date and more recent dates may be from an incomplete sample. Source: UKHSA

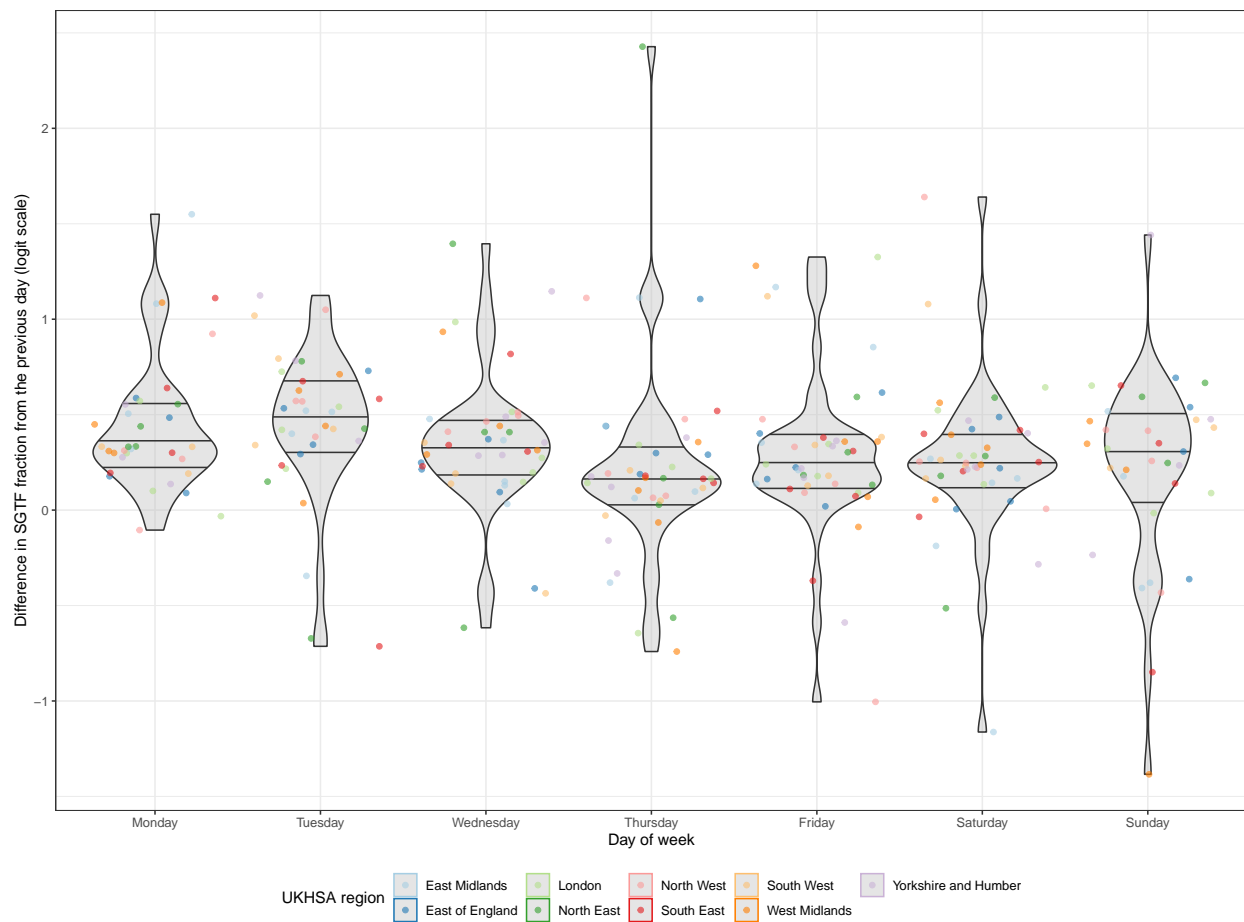


Figure 3: Daily fraction of those tested for S gene status with SGTF by UKHSA region on the logit scale. The dashed vertical lines indicate Mondays. Note that the data is by specimen date and more recent dates may be from an incomplete sample. Source: UKHSA

Growth in those with SGTF by day on the week for each UKHSA region

References

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5. Vehtari, A., Gabry, J., Magnusson, M., Yao, Y., Bürkner, P.-C., Paananen, T., & Gelman, A. (2020). *Loo: Efficient leave-one-out cross-validation and WAIC for bayesian models*. <https://mc-stan.org/loo/>
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