Sampling bias in S-gene target data

Epiforecasts

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Background

Among all cases that are test-positive, some are tested for the S-gene target (SGT). A successful test for the S-gene target can give either a failure or a positive result. The proportion of SGT cases that result in SGT-Failure is a useful proxy for the proportion of the Omicron variant in comparison to the Delta variant.

The ability to provide an SGT result is not uniform across all test-positive cases. If cases with an SGT result differ from cases which cannot be tested for SGT, this would create a bias in comparisons of Omicron compared to Delta. For example, test-positive cases with an SGT result may be a result of sampling contacts of a known case with Omicron variant, which are also sent in a batch to a lab which is able to process SGT results.

We can compare these two groups in a two-strain branching process model. If the transmissibility advantage for cases with an SGT result is not centred on 100% then this might indicate sampling bias.

Methods

Data

- We used data for all England test-positive cases (pillar 1 and 2 of the UK testing strategy).
- We used only the most recent three weeks of data, between 2021-11-21 and 2021-12-10.

Model

- We built a two-strain model to compare sampling of all test-positive cases compared to test-positive cases with any confirmed S-gene target (SGT) result.
- We allowed a weekly piecewise constant variation in growth rate.
- We used a uniform prior for the growth rate advantage of SGT-result cases compared to no-SGT-result cases.

Results

- Transmission advantage
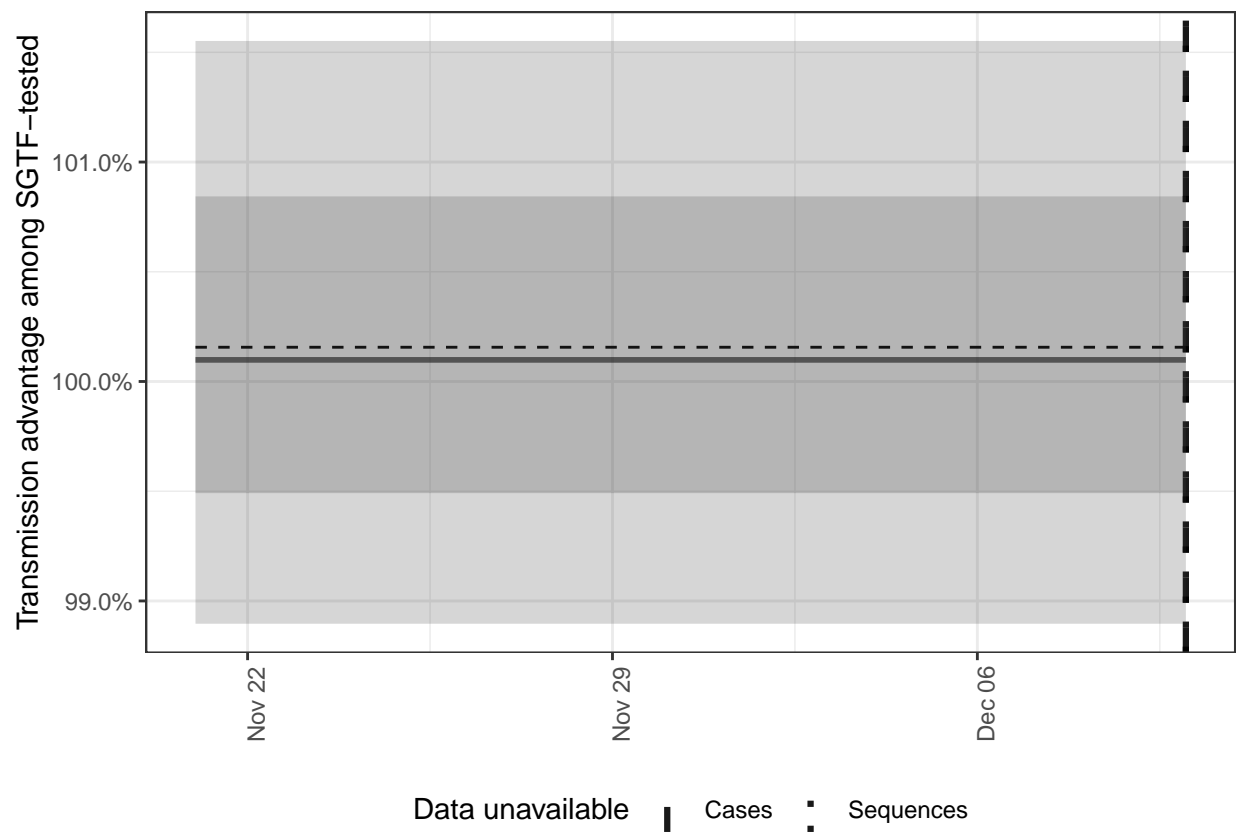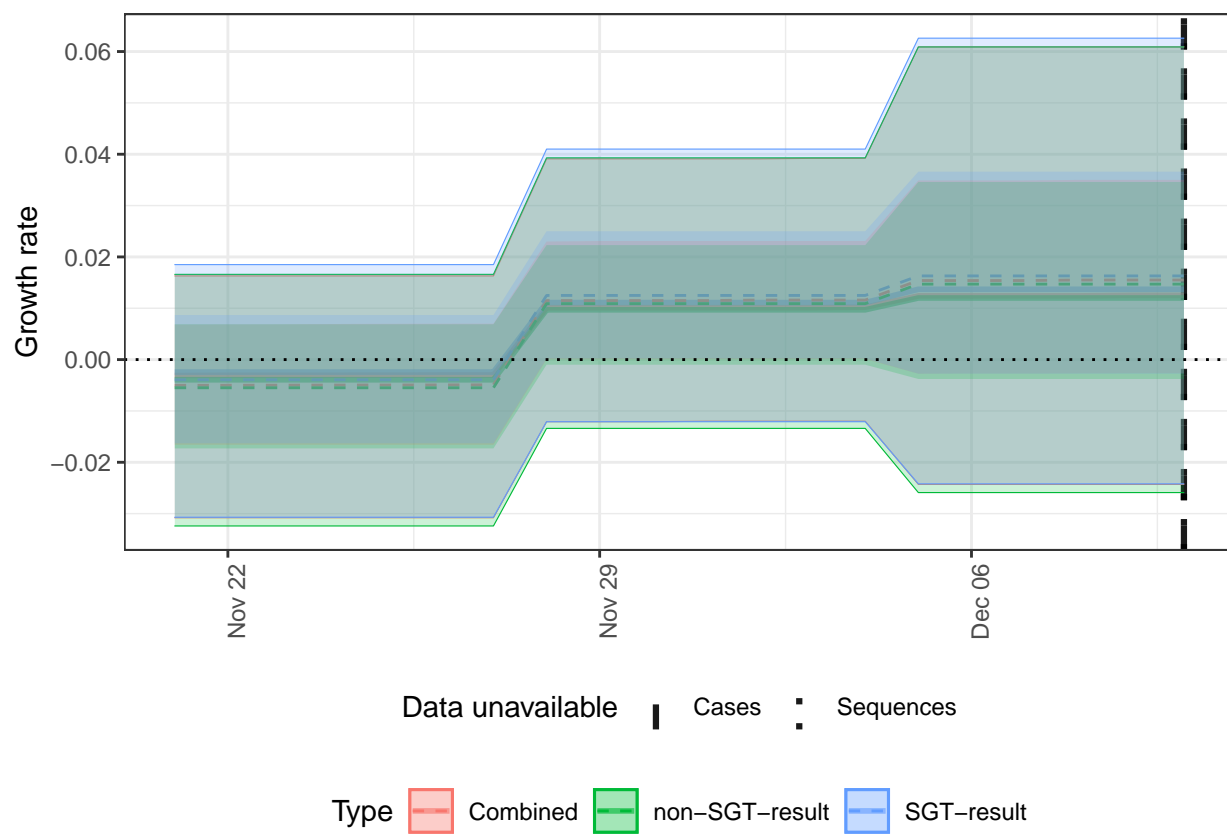

- Growth rate

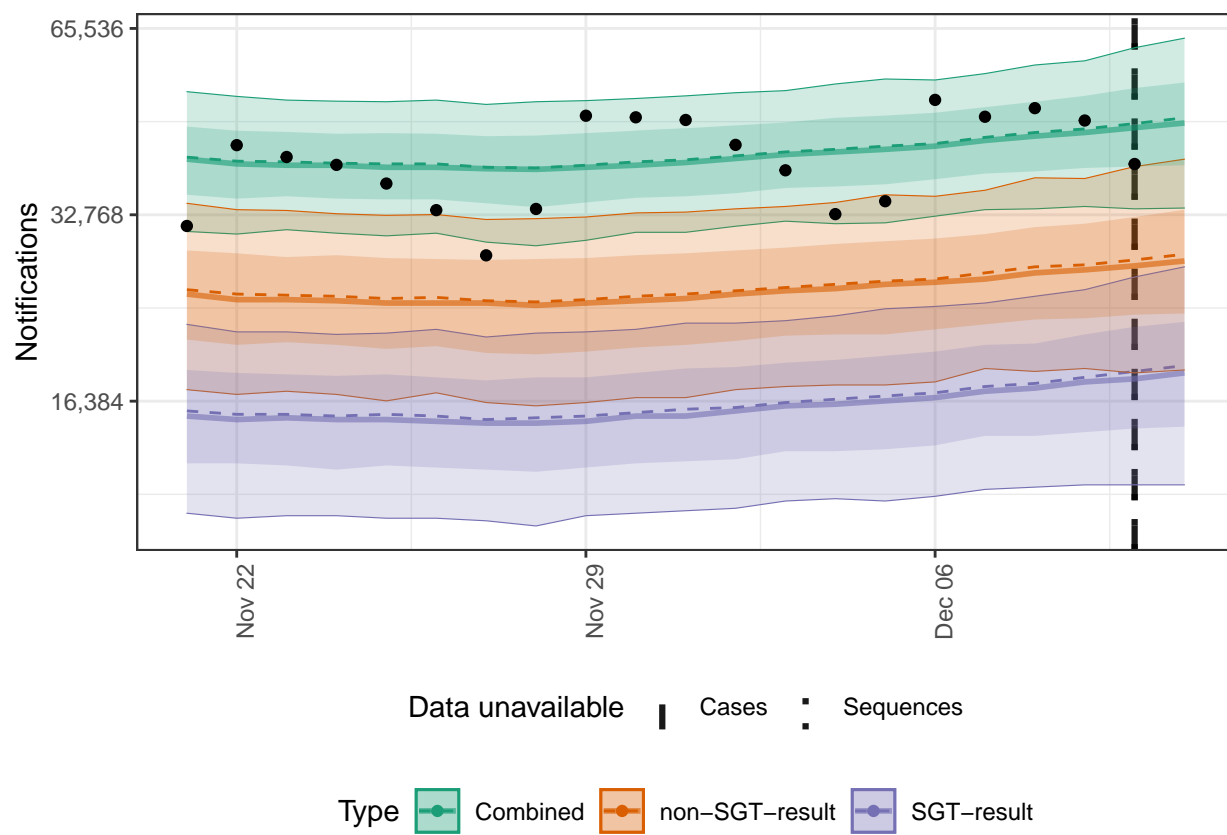- Cases (log)

Figure 1: The transmission advantage

Figure 2: The growth rate

Figure 3: Cases

Discussion

adapt 2-strain model to look for sampling bias: use tested or not instead of strain

growth in non-tested should be same as in tested growth rate always biased up since testing contacts output Rt

transmission adv = simple diff in growth rate * scaling (5.1d)