

Exploring the transmission advantage of Omicron in England

Epiforecasts

17 December 2021

Aims

- We aimed to assess competing explanations of the transmission advantage of Omicron, compared to the existing dominant strain, Delta, in England.
- We explored the likelihood of increased transmissibility compared to immune escape, using S-gene target failure as a proxy for infection with Omicron.
- We use a model framework where we vary only the relationship between variants while holding all other parameters constant.

Methods

- Data are all test-positive cases for England and by PHE region. We used raw data by specimen date (figure 5). Models are based on data between 2021-11-22 and 2021-12-12, which excludes the latest 1 reported dates. Omicron is modelled from those cases reporting an S-gene target result (failure or not)¹.
- We modelled at a 1 day resolution with a 14 day forecast. We used a weakly informative prior for a transmission advantage for the VoC vs non-VoC cases of mean 0.2 (standard deviation 0.2), based on early work from South Africa². We defined the relationship between variants as either scaled or correlated. We used the `forecast.vocs` package³ with a two-strain branching process model.

Results

Transmission advantage is shown where 100% is equivalent to the current dominant strain, Delta (figure 1). Both models indicated a stronger transmission advantage for Omicron. For England as a whole:

- In a fixed relationship estimated Omicron advantage is 1.36 (95% credible interval 1.34 - 1.38).
- In an correlated relationship Omicron advantage is 1.38 (95% CrI 1.1 - 1.58).

We also estimated the growth rate (figure 2), the proportion of cases attributable to Omicron (figure 3) and case counts (figure 4).

Model comparison We compared PSIS-LOO by region (table 1). Using data for all England, comparing the models on PSIS-LOO indicated an estimated difference in expected log pointwise predictive density of -3.4 (with a standard error of 0.8) for the correlated model compared to the scaled model.

¹SGTF data from UKHSA: <https://www.gov.uk/government/publications/covid-19-omicron-daily-overview>

²Carl Pearson et al. (2021). "Omicron spread in South Africa", *Epidemics*8

³Sam Abbott (2021). `forecast.vocs`: Forecast case and sequence notifications using variant of concern strain dynamics, DOI:10.5281/zenodo.5559016

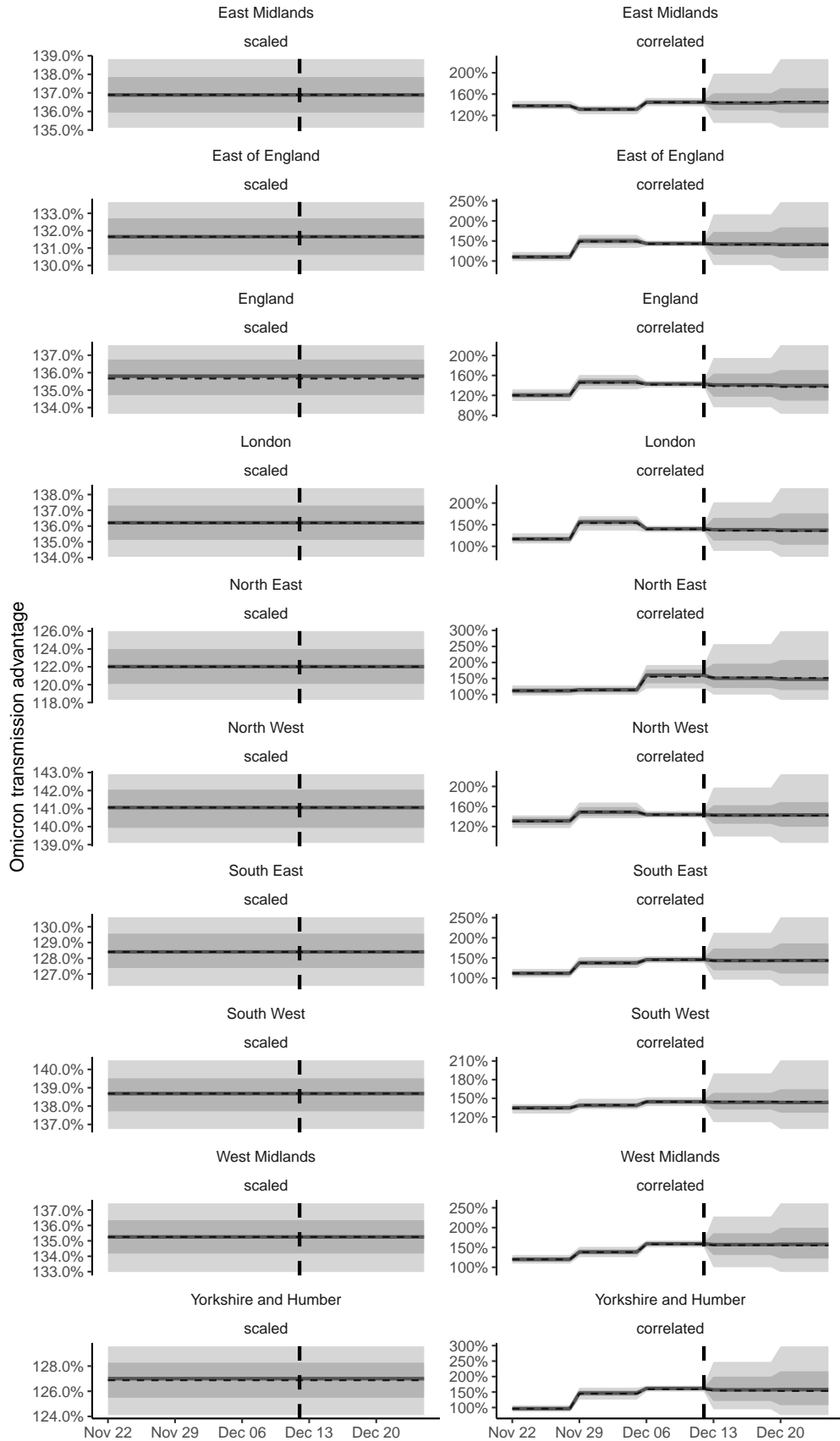


Figure 1: The transmission advantage of Omicron, modelled by NHS region in a fixed relationship to Delta (left) and a time-varying correlated relationship (right).

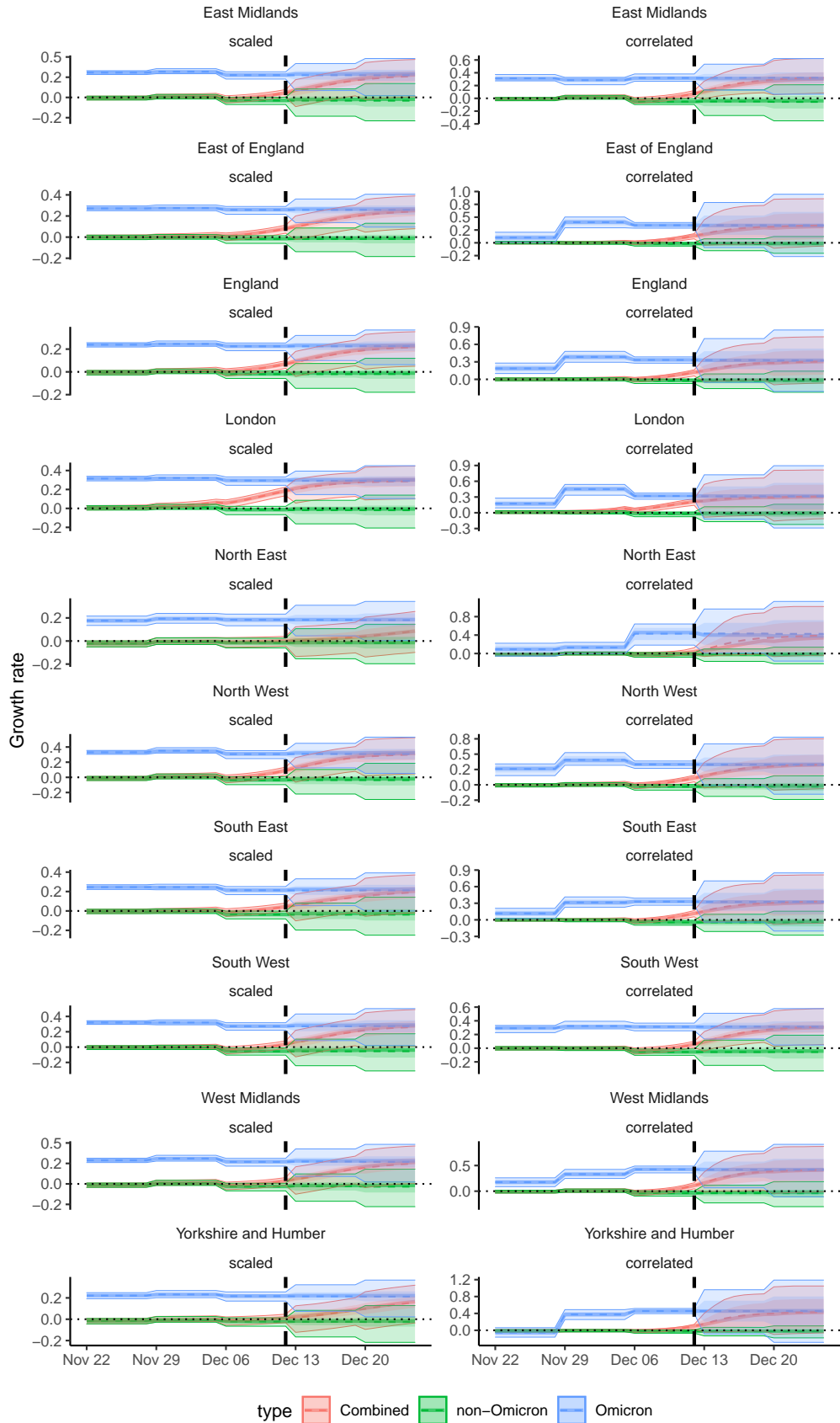


Figure 2: The growth rate of Omicron, modelled by NHS region in a fixed relationship to Delta (left) and a time-varying correlated relationship (right).

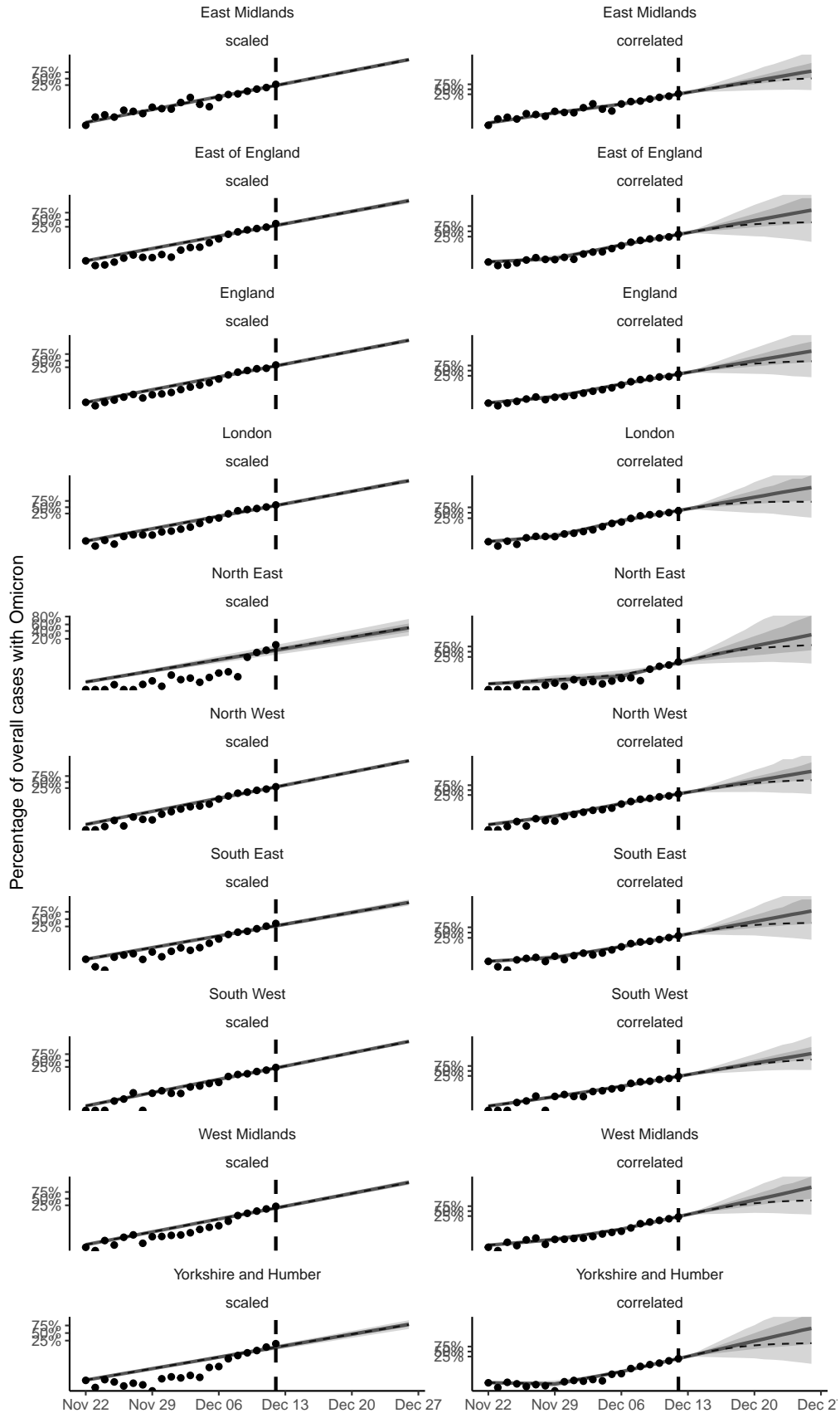


Figure 3: Fraction of cases attributable to Omicron, modelled by NHS region in a fixed relationship to Delta (left) and a time-varying correlated relationship (right).

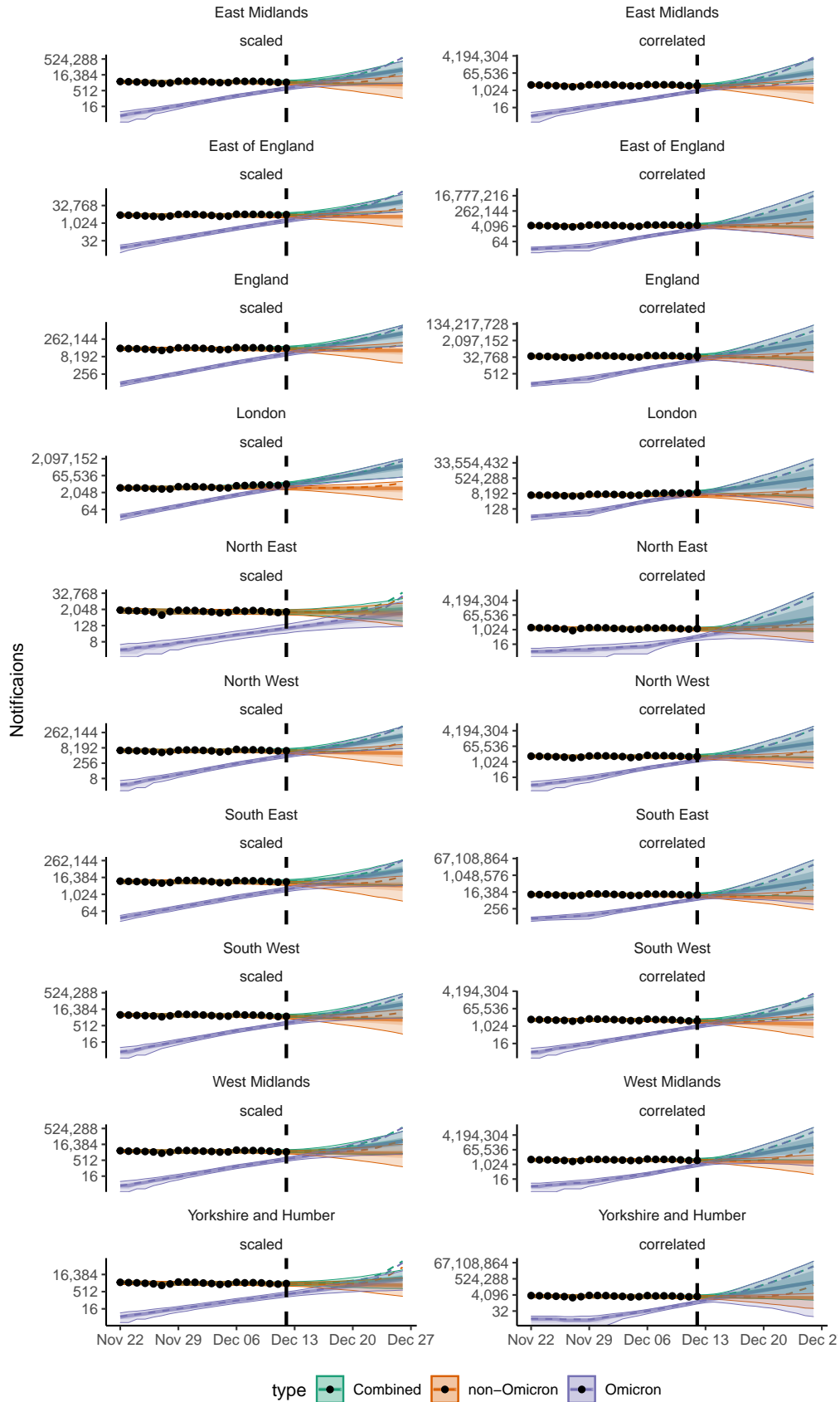
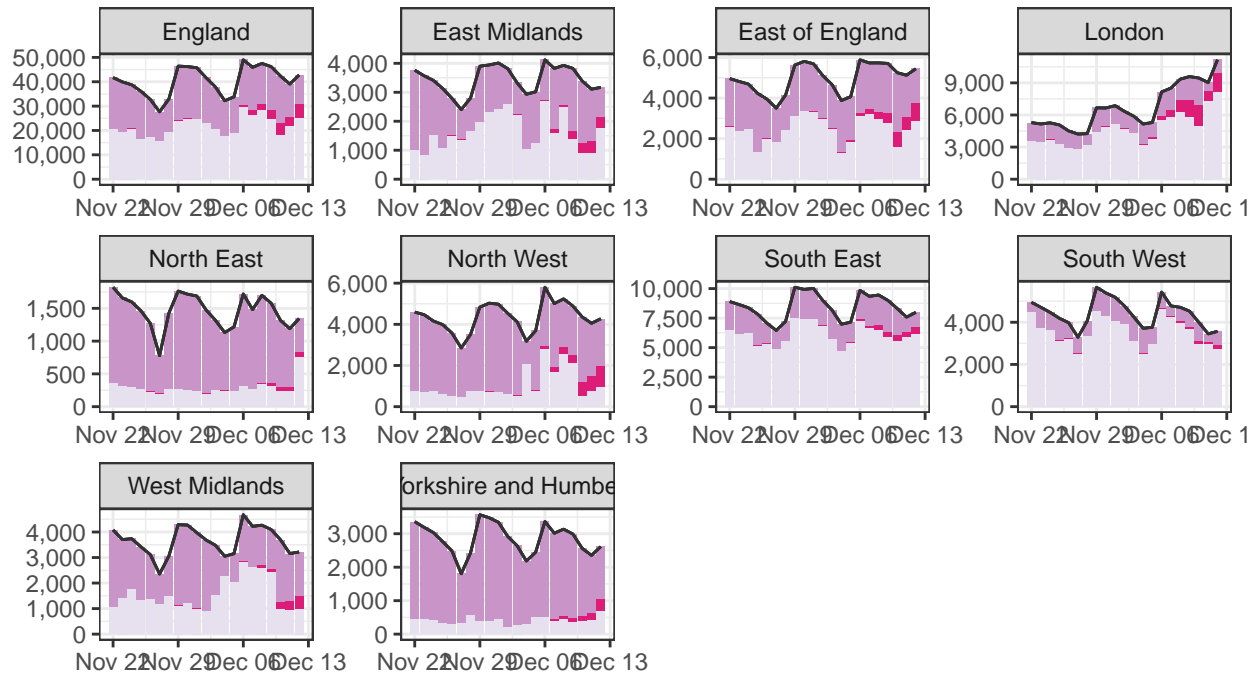


Figure 4: Weekly cases shown on a log scale, modelled by NHS region in a fixed relationship to Delta (left) and a time-varying correlated relationship (right). ⁵

Table 1: PSIS-LOO cross validation by NHS region comparing models with fixed and correlated over time relationships between variants

region	best_model	elpd_diff	se_diff
England	correlated	-3.4	0.8
East Midlands	scaled	-0.7	0.4
East of England	correlated	-4.8	1.4
London	correlated	-2.0	1.1
North East	correlated	-5.2	1.8
North West	correlated	-3.4	0.7
South East	correlated	-2.9	1.5
South West	correlated	-1.1	0.2
West Midlands	correlated	-7.0	1.1
Yorkshire and Humber	correlated	-9.8	2.8



S-gene result non_sgtf sgtf sgtf_unknown

data are public from UKHSA, by specimen date
excludes most recent 1 days

Figure 5: Raw data