Notes on the new variant

For SAGE, 22nd December
Juniper consortium
http://maths.org/juniper/

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1. **Patterns and growth rates by geography**
2. Patterns and growth rates by geography and age
3. Households analysis of NV
4. Recent hospitalisations data streams
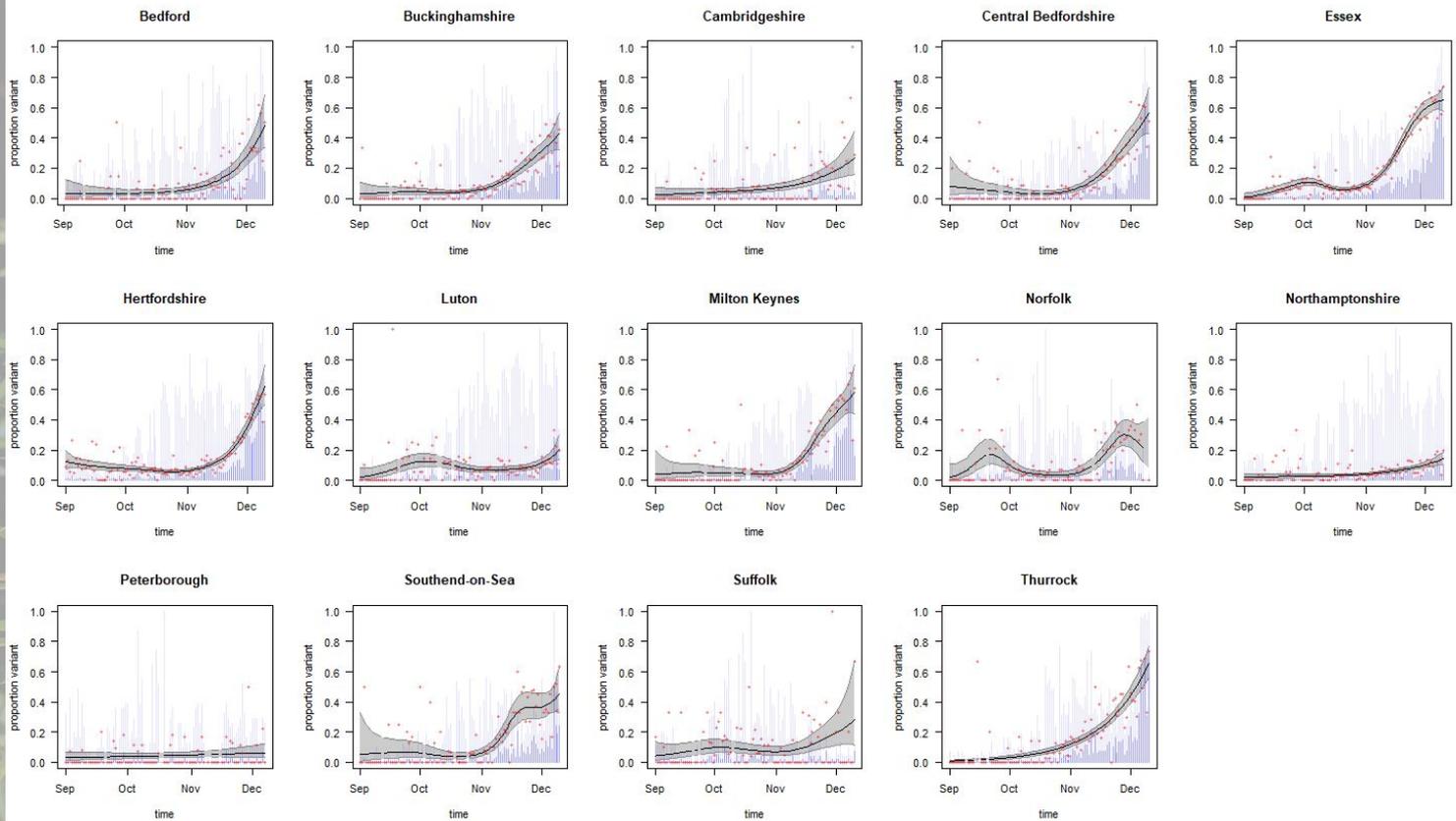5. R, growth rates and generation time

Secular trend in prevalence of S-gene deletion, by NHS region
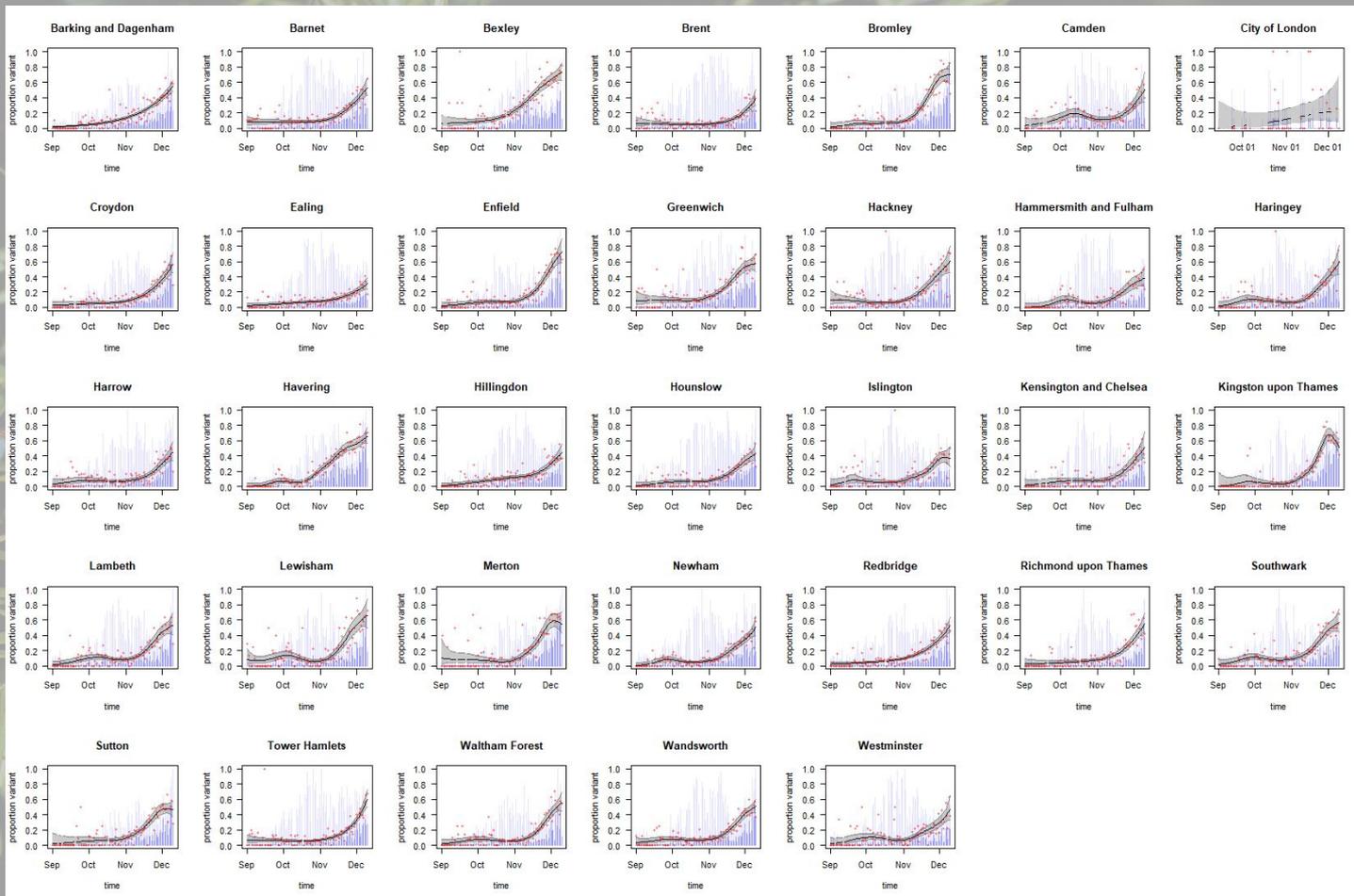## (Non-parametric GAMs, accounting for variation in sampling effort)
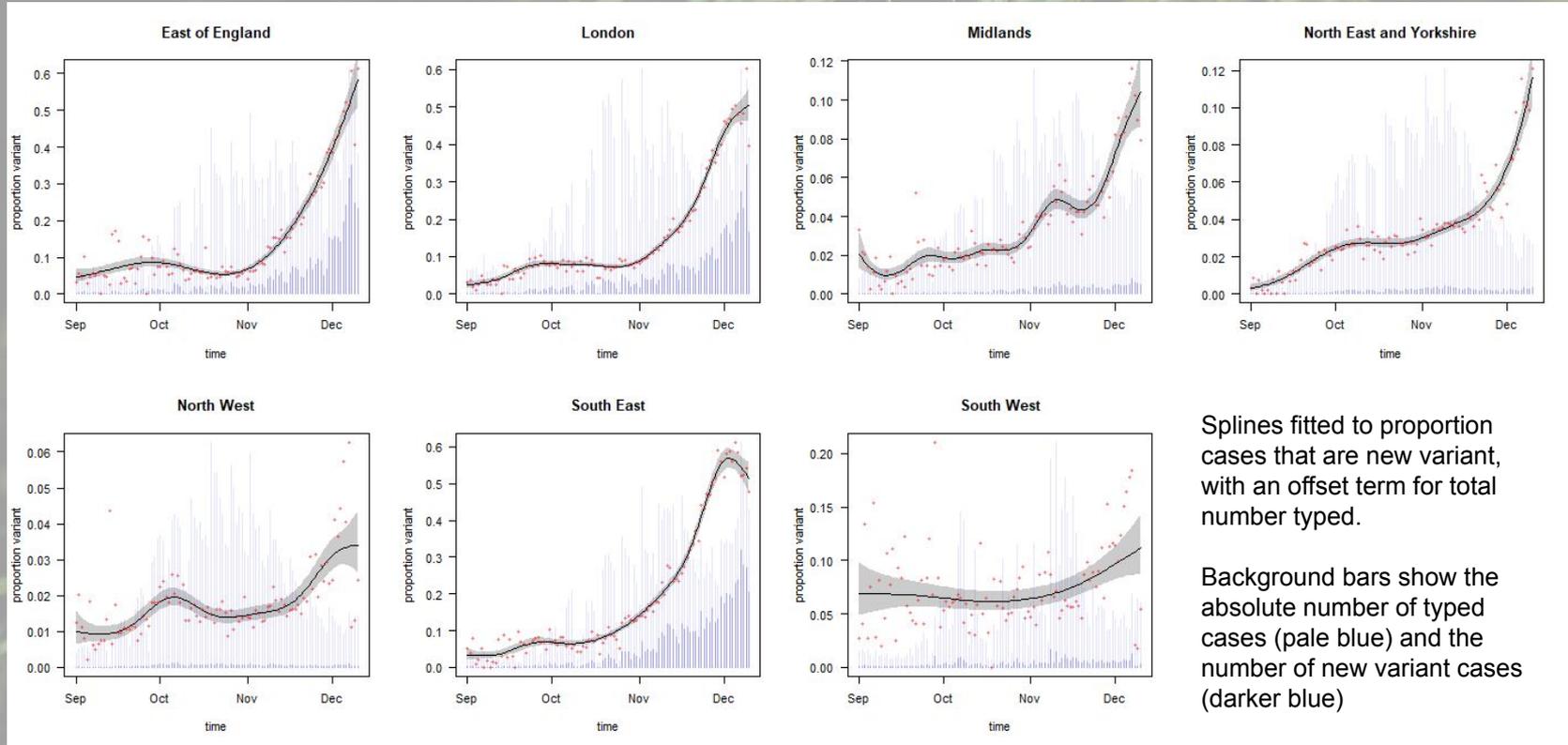
Splines fitted to proportion cases that are new variant, with an offset term for total number typed.

Background bars show the absolute number of typed cases (pale blue) and the number of new variant cases (darker blue)
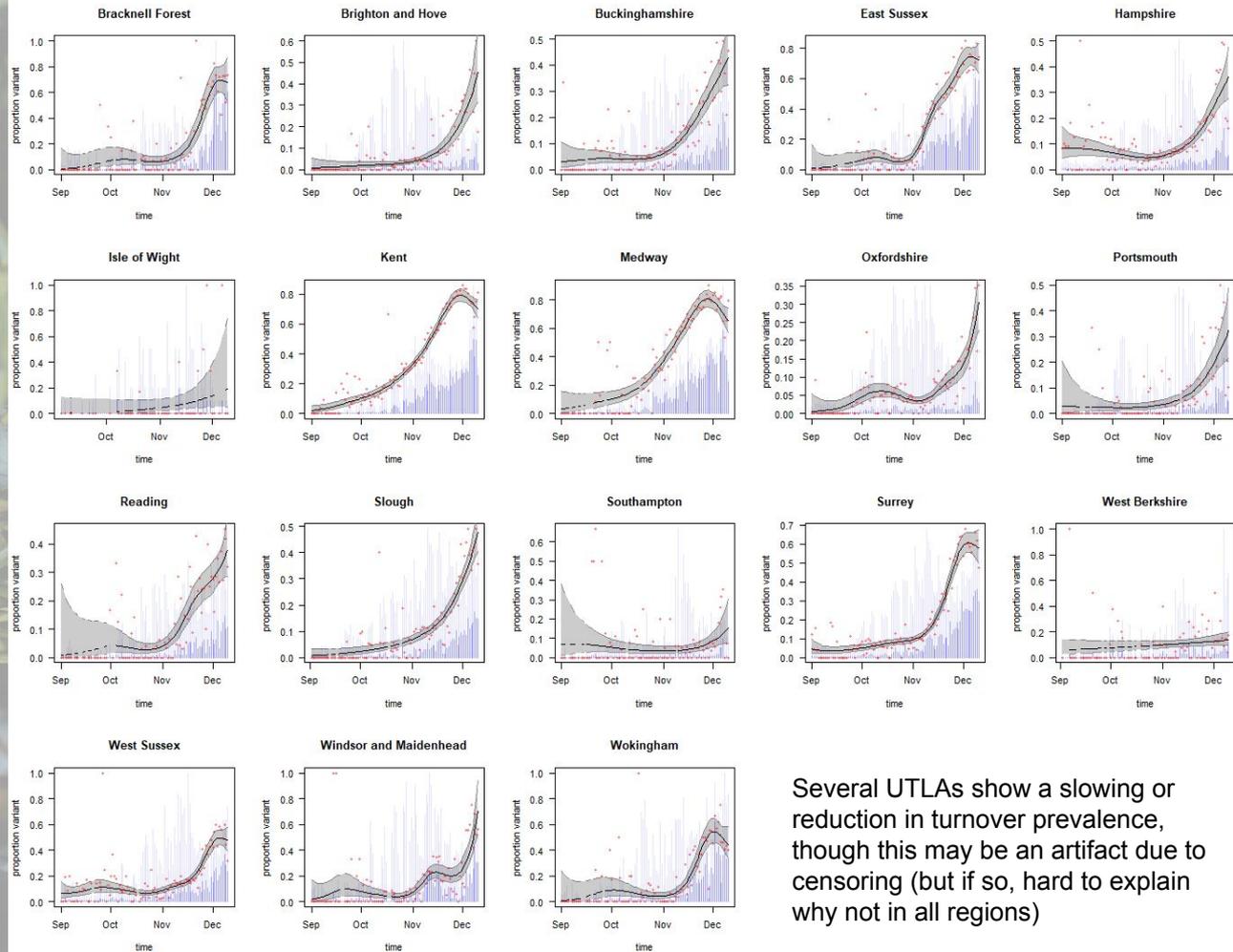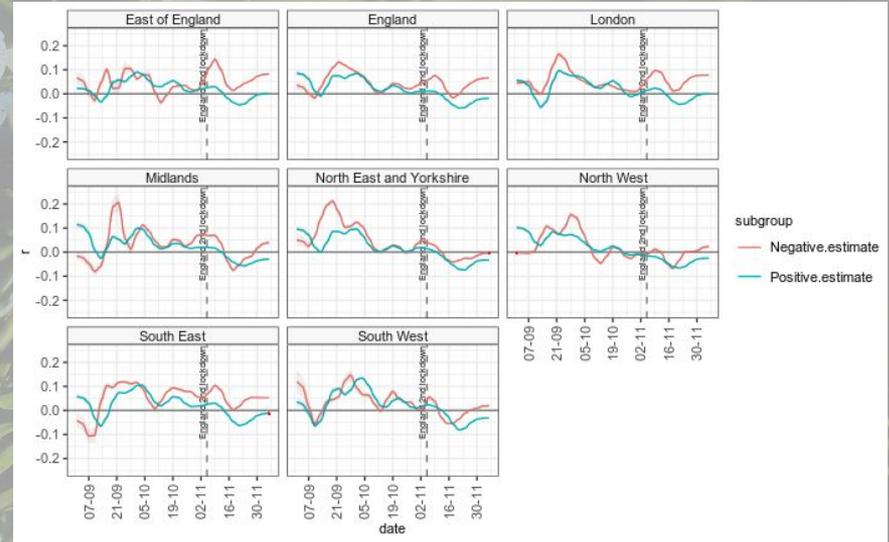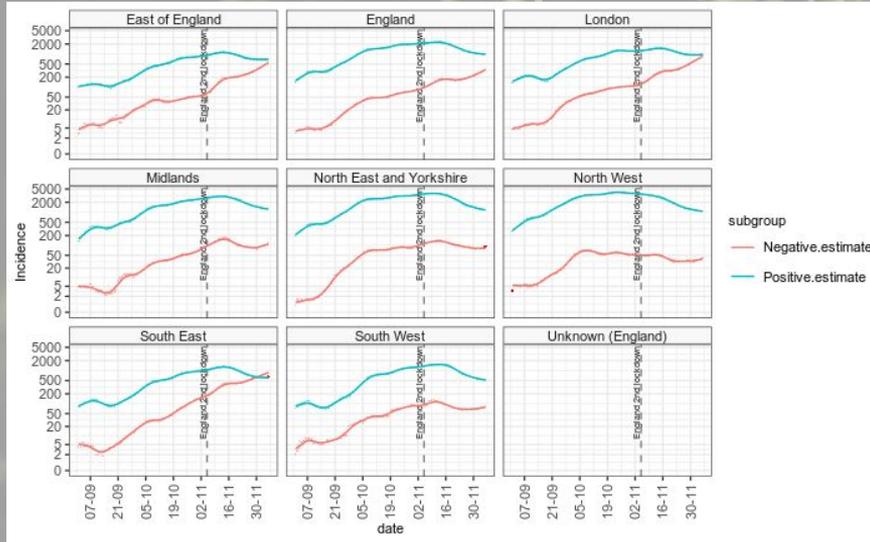
Non-parametric analysis of the relative growth of the new variant (compared to all other existing variants). Highlights the strong growth in East/SE/London, also in other regions (esp NE/Yorks, though starting at a lower %). Suggestion of downturn/turnover in SE and London, could be a censoring effect (though only appears in a few UTLAs within those regions).. S-gene deletion data from Lighthouse Labs (Pillar 2) cross-referenced with PHE anonymous case data.

East of England

London

South East

Several UTLAs show a slowing or reduction in turnover prevalence, though this may be an artifact due to censoring (but if so, hard to explain why not in all regions)

DRAFT - Inferred P2 S+/S- breakdown by region

Differential incidence and growth rates estimated for S-Neg and S-Pos by region

Growth advantage not seen yet in all regions. S-Neg is mixture of strains, and proportion new variant will vary by time, location (and age, see below).

Parametric estimation of relative growth rate of S-gene deletion cases compared to (combined) all other types

$$y_{it} \sim \text{Poisson}(\lambda_{it})$$

$$\log(\lambda_{it}) = \alpha + \beta_1 \mathbf{1}v_i + \beta_2 t + \beta_3 v_i t$$

v_i variant indicator, t time.

- Poisson regression model of Lighthouse lab case data, by NHS region
- **Significant growth advantage in all regions**
- Does not account for potential biases in observed incidence of variant and sampling effort
- Growth relative to all other types, not type specific (data limitation)

Region	Relative growth advantage, % (95%CI)
East of England	73.3 (72.4, 74.1)
London	73.7 (73.1, 74.2)
Midlands	51.9 (50.2, 53.3)
NE & Yorkshire	56.3 (54.2, 58.2)
North West	55.6 (48.3, 61.5)
South East	67.3 (66.6, 67.9)
South West	23.8 (14.3, 31.1)

Model-based case exceedance pattern

- Lancaster stochastic spatial SEIR model
- Fitted 2020-12-15
- Exceedance probability previous 7 days relative to model-predicted incidence.
- **Pillar 2 positive tests** higher than expected in SE/London.
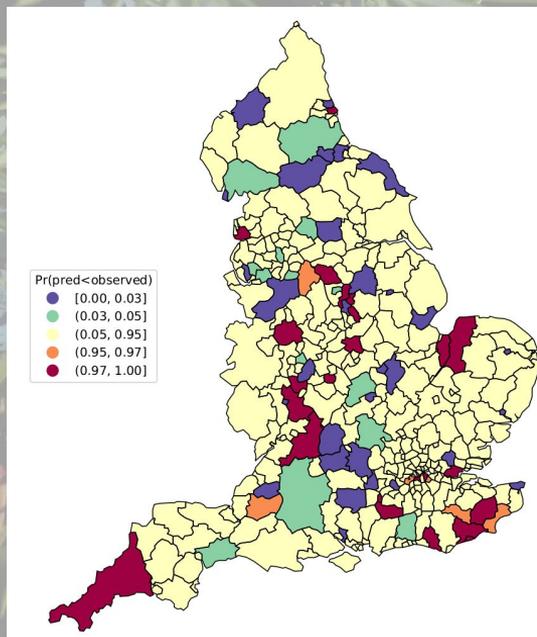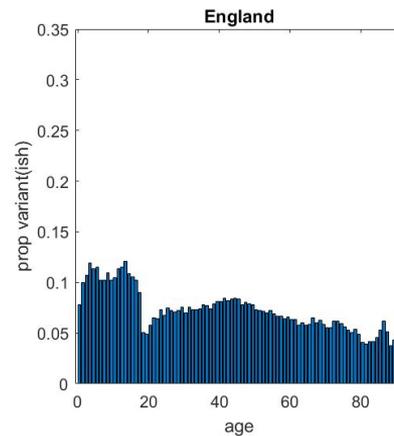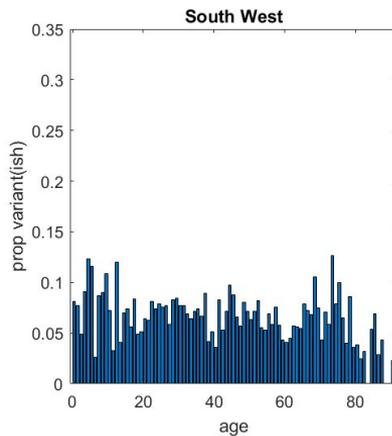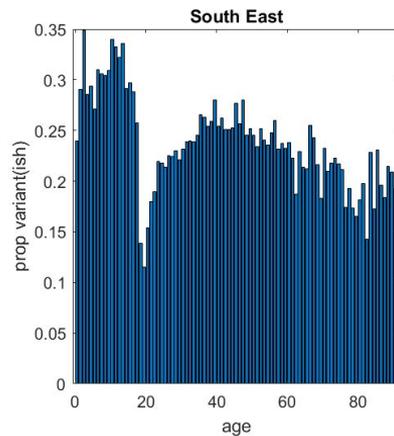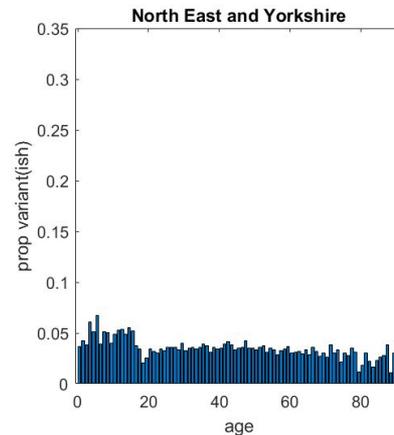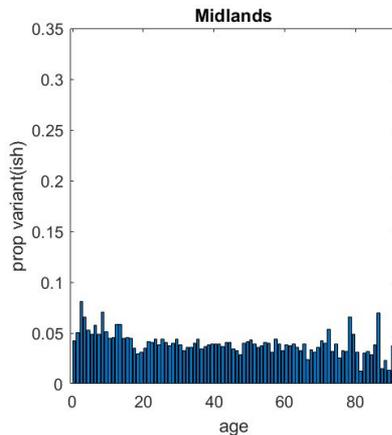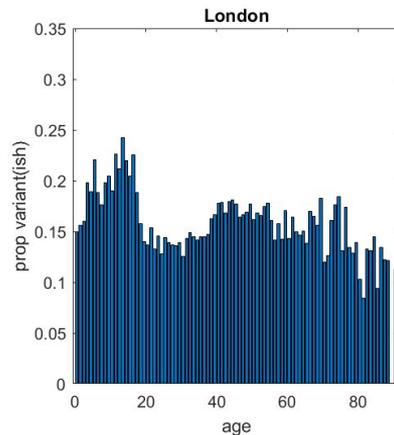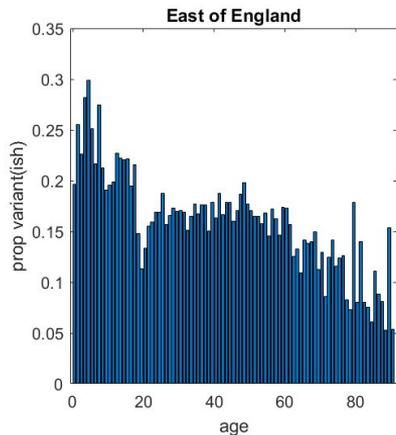

Pillar 1
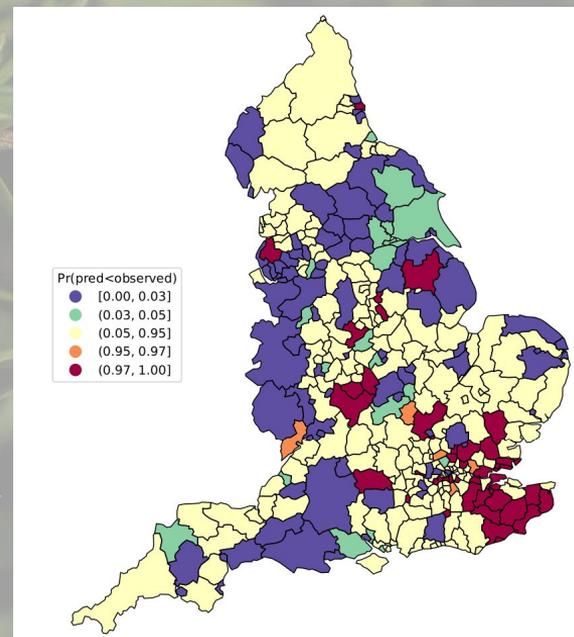
Pillar 2

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2. **Patterns and growth rates by geography and age**
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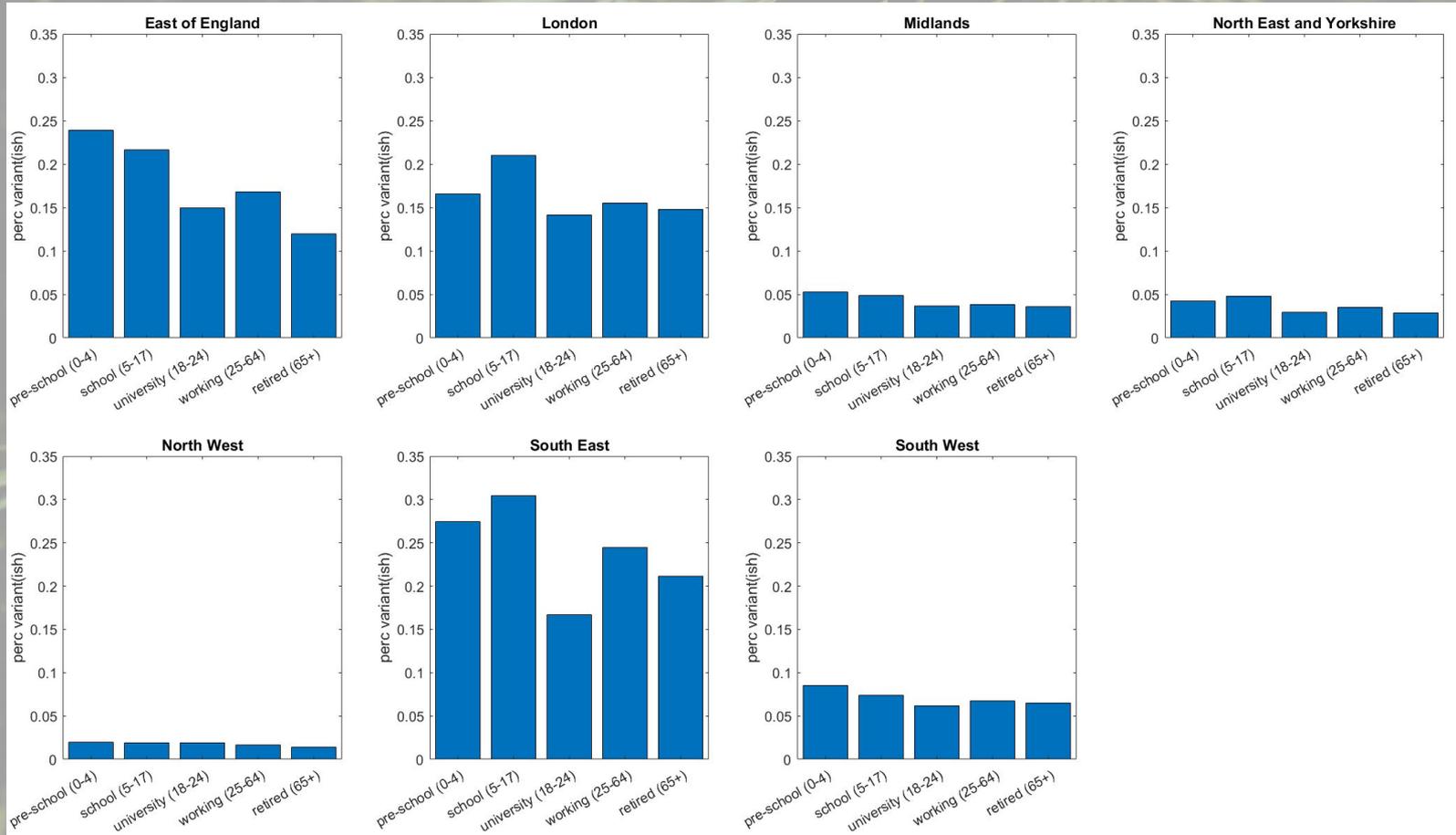5. R, growth rates and generation time

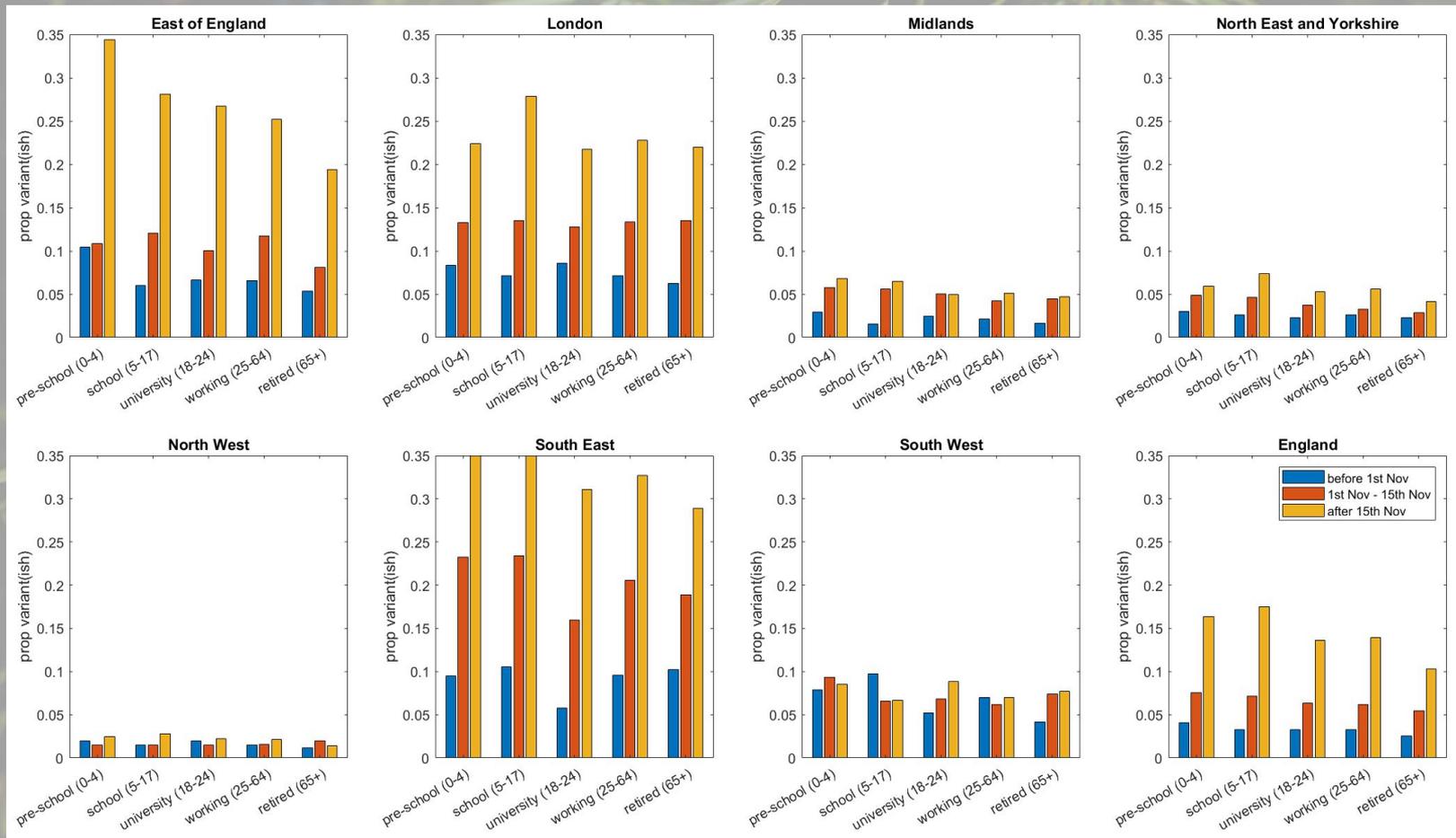# Percentage of new positive tests that are the new variant by age (but CAUTION: see temporal split below)
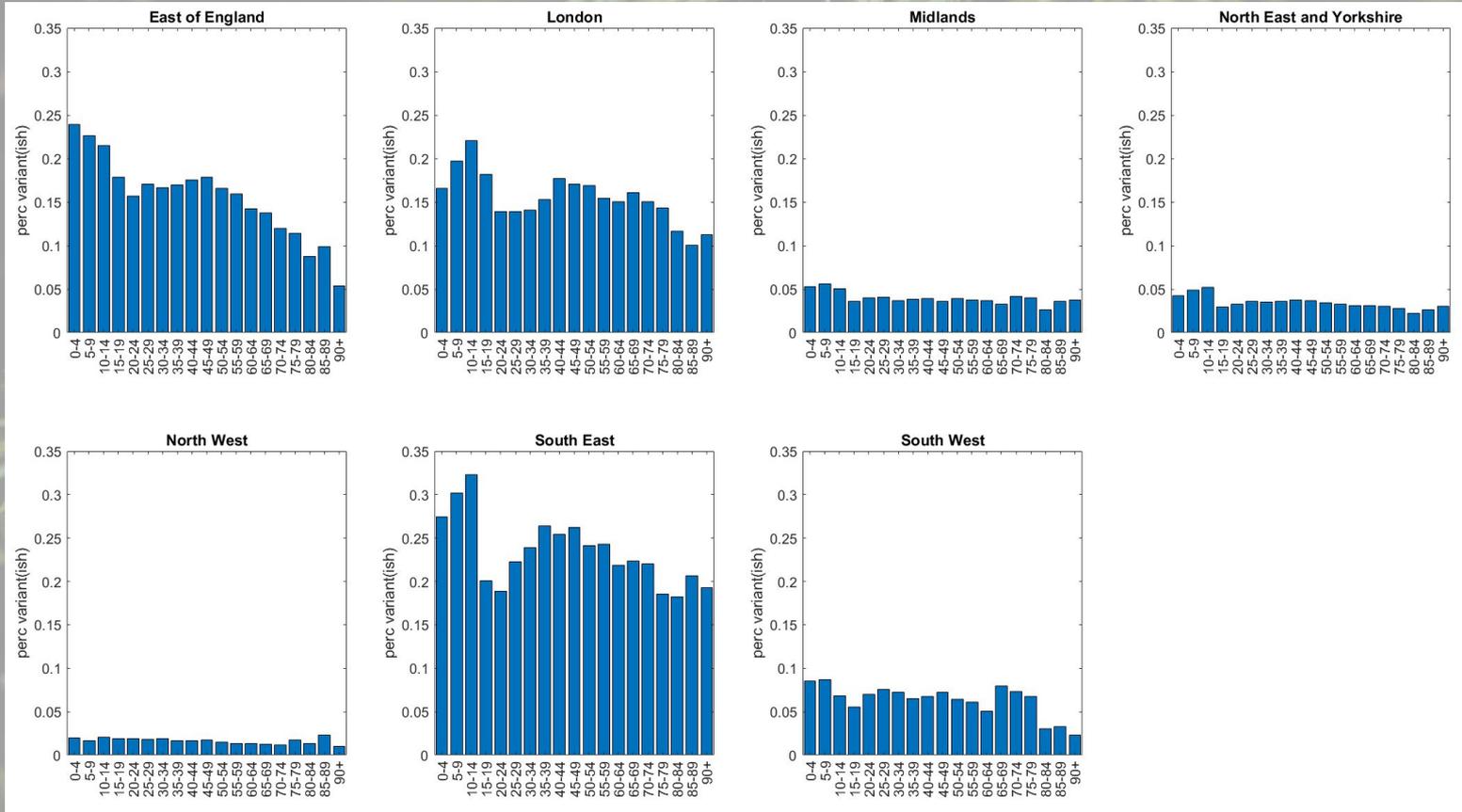
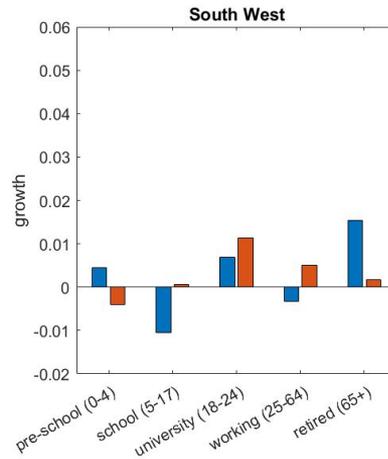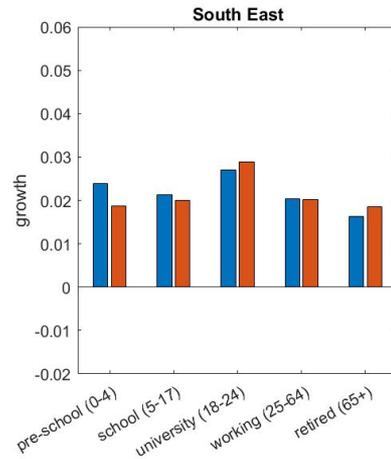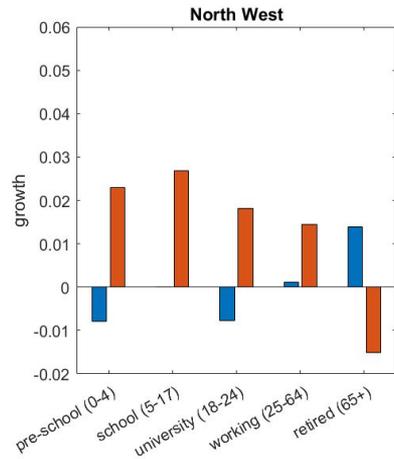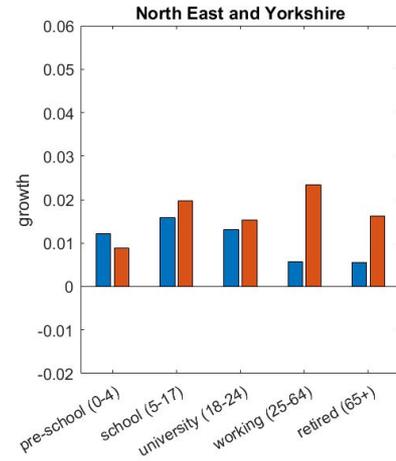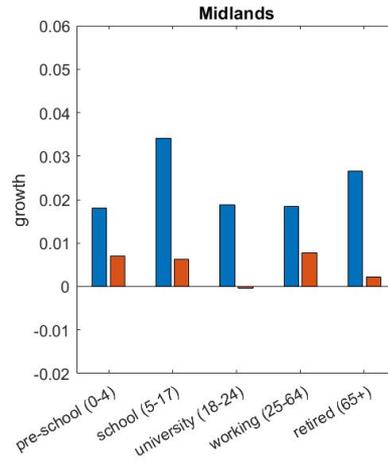# Same as previous, in 1 year age bands
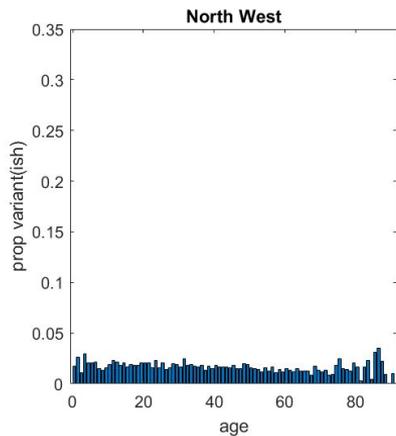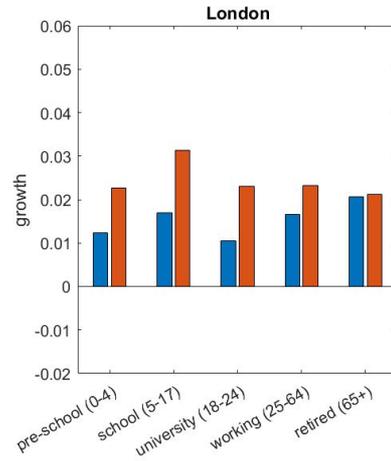
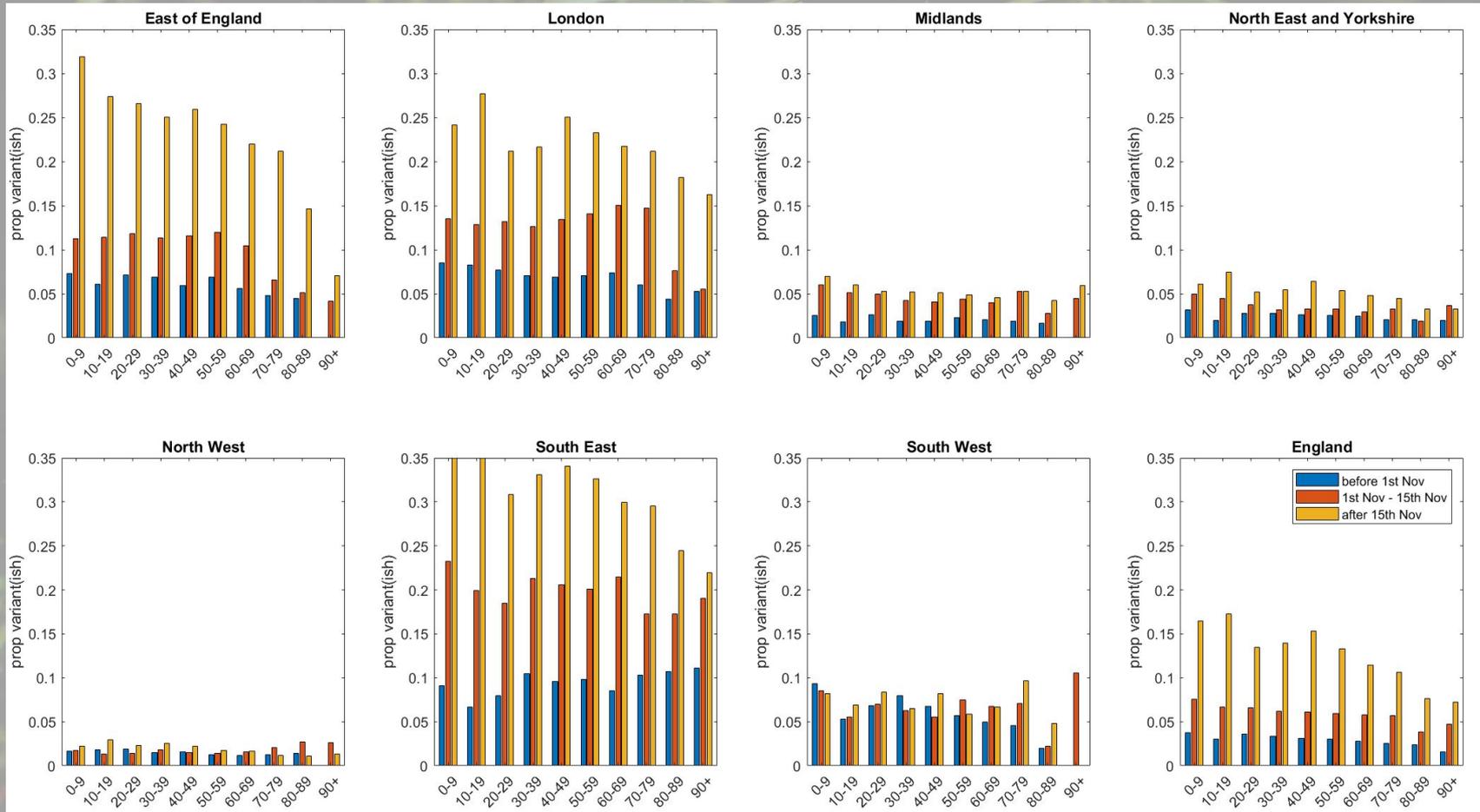# Using more informative age groupings

Age groupings over time bands
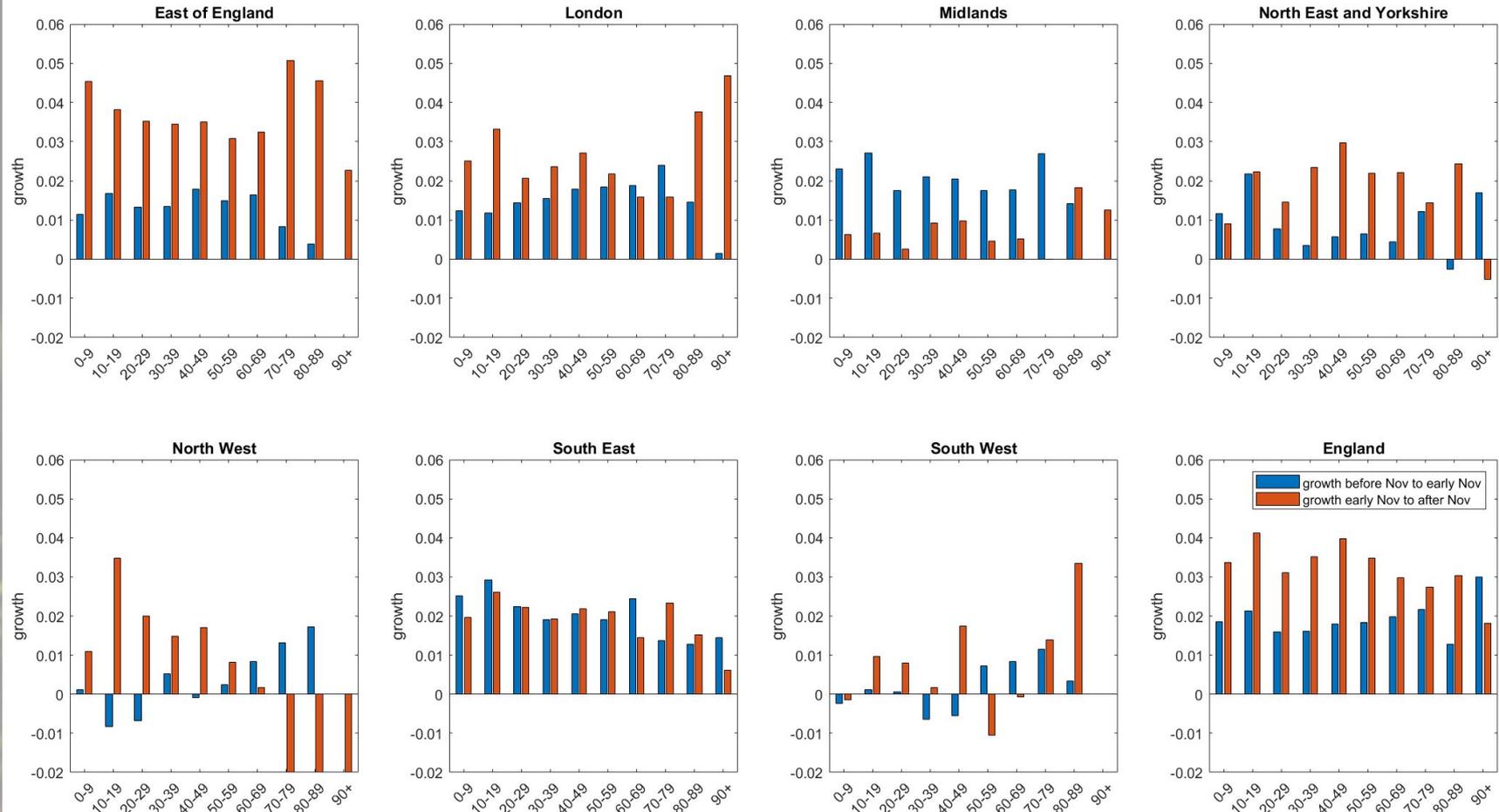
Associated growth rates
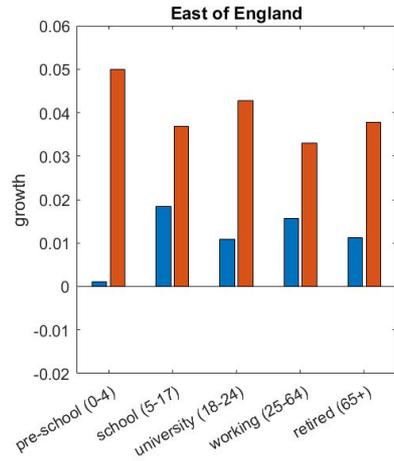
Growth rates are calculated as: (log(y1)-log(y2))/(t1-t2) Where yi is the percentage new variant, and ti is the midpoint of the time window used

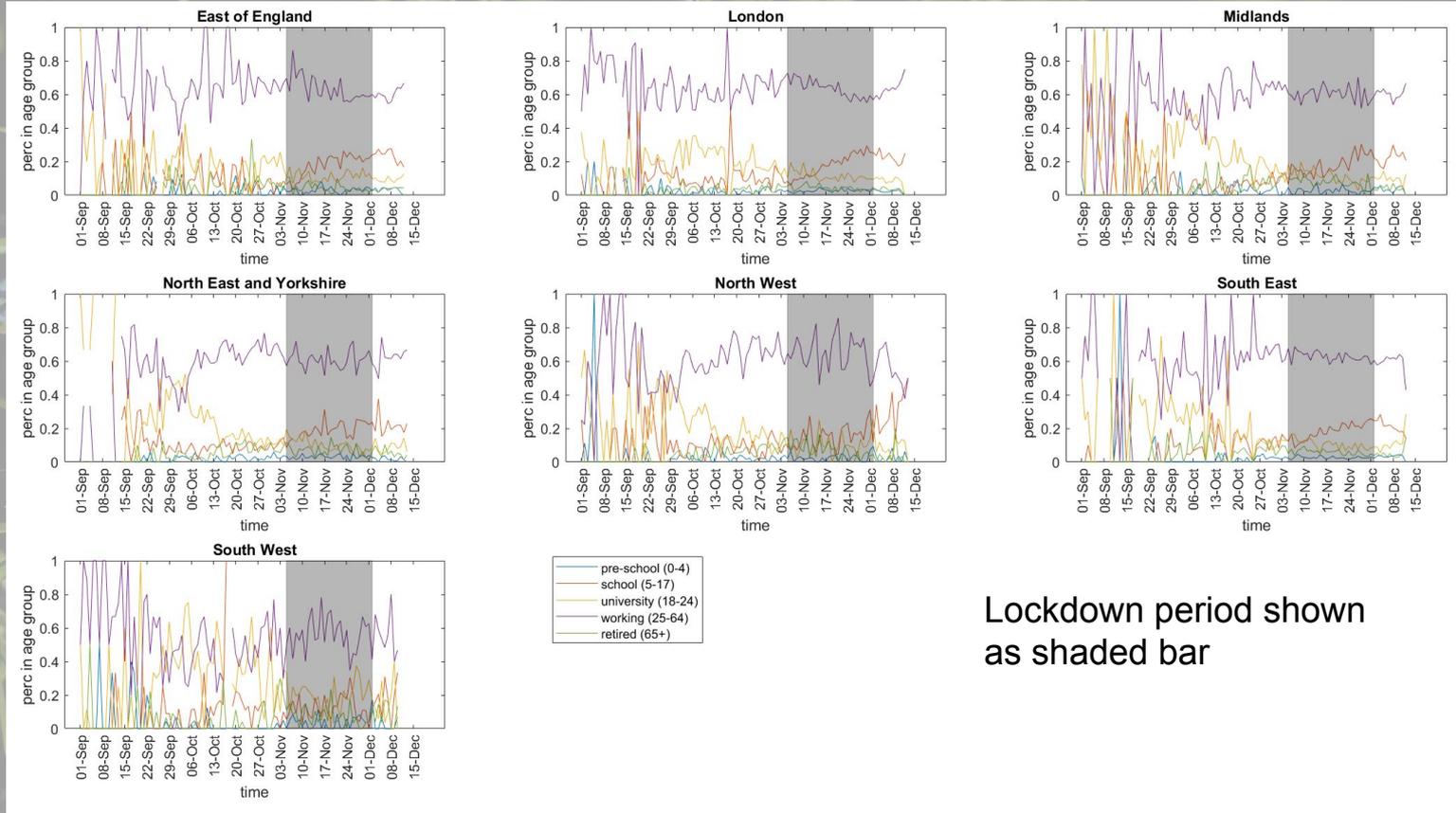# Age groupings over time bands (10y bands)

Associated growth rates (10y bands)

Detail over time, panel per region (percentage of new variant by age bands as lines)

This gives the proportion of S-negative tests on a given day that are in each of the age groups.
Since the groups are different sizes this should be used only to see how the proportions change over time
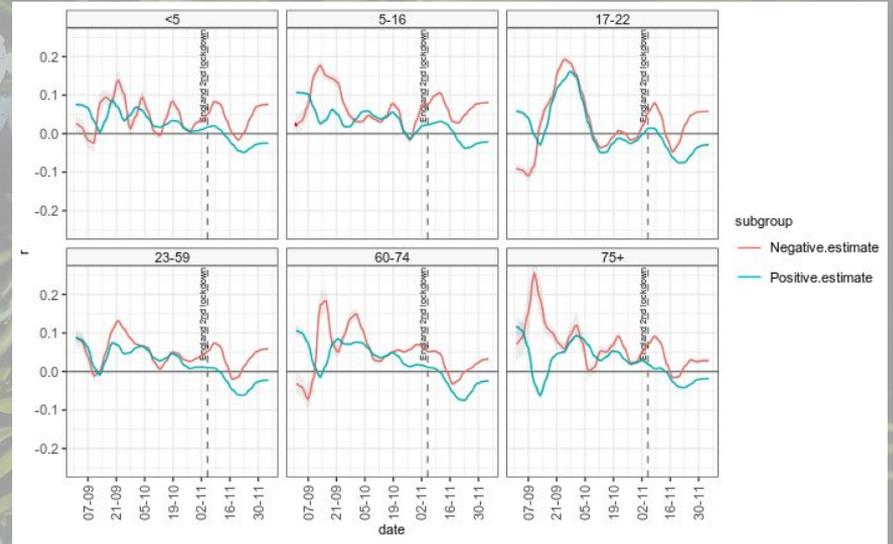

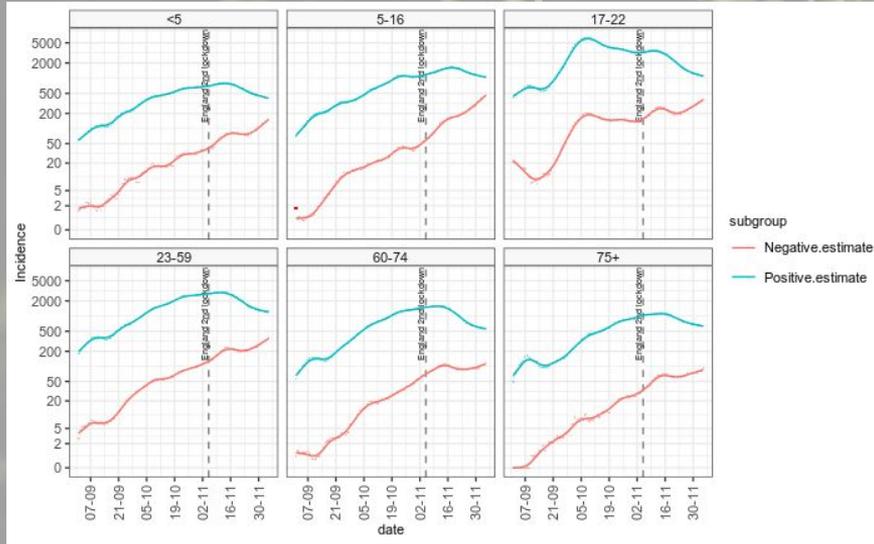Lockdown period shown as shaded bar

Percentage of cases that are new variant, panel per age band, lines are regions
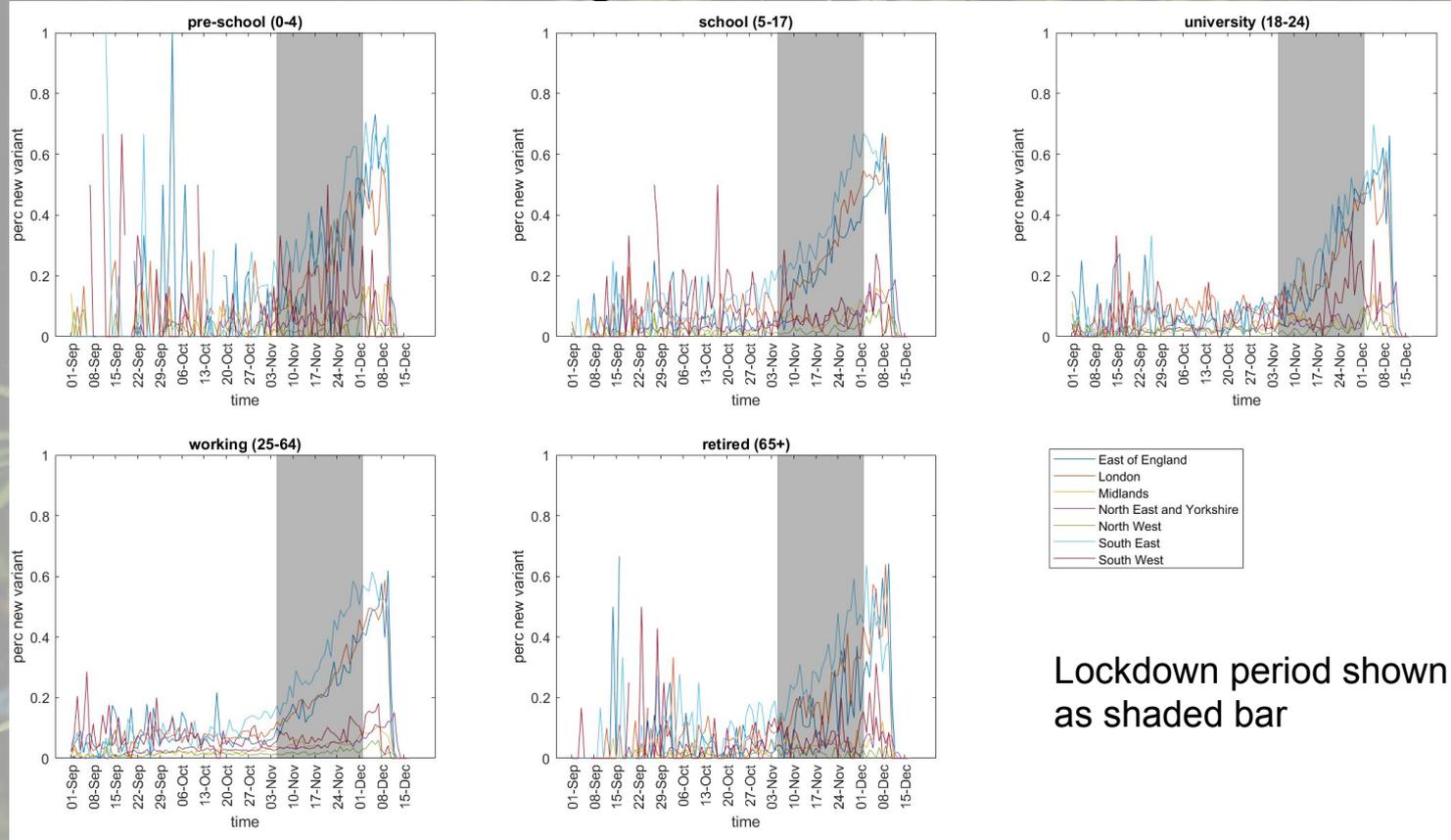
Lockdown period shown as shaded bar

DRAFT - Inferred P2 S+/S- breakdown by age

Differential incidence and growth rates estimated for S-Neg and S-Pos by age

Suggests growth rate advantage larger for younger age groups, but this may reflect different S-Neg strain composition in elderly.

Proportion P2 cases where S gene result available
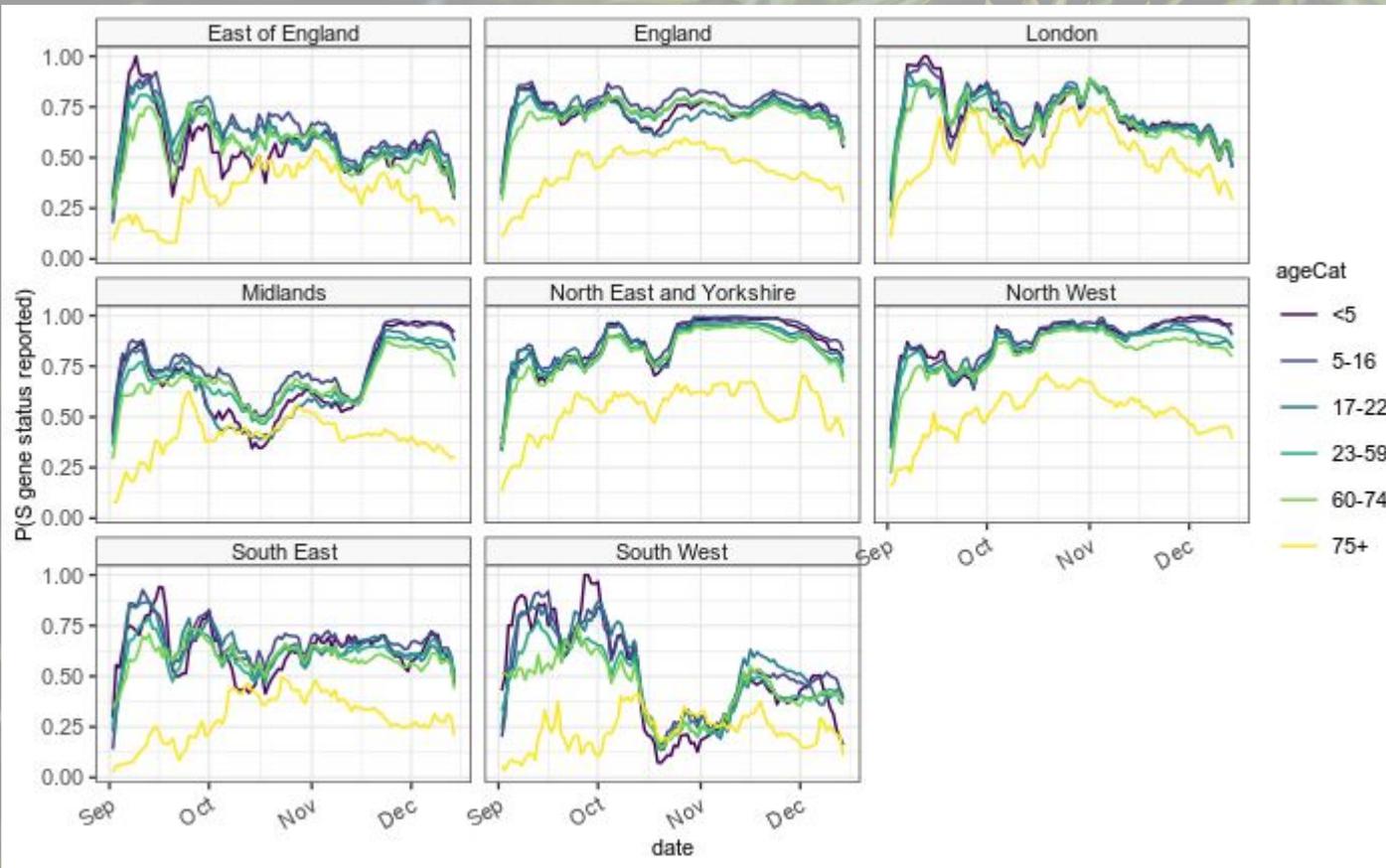
S gene testing not entirely random sample of tests.

Elderly slightly under-represented

Presumed capacity issues in SW in mid Oct

Biases in the data set need further characterisation

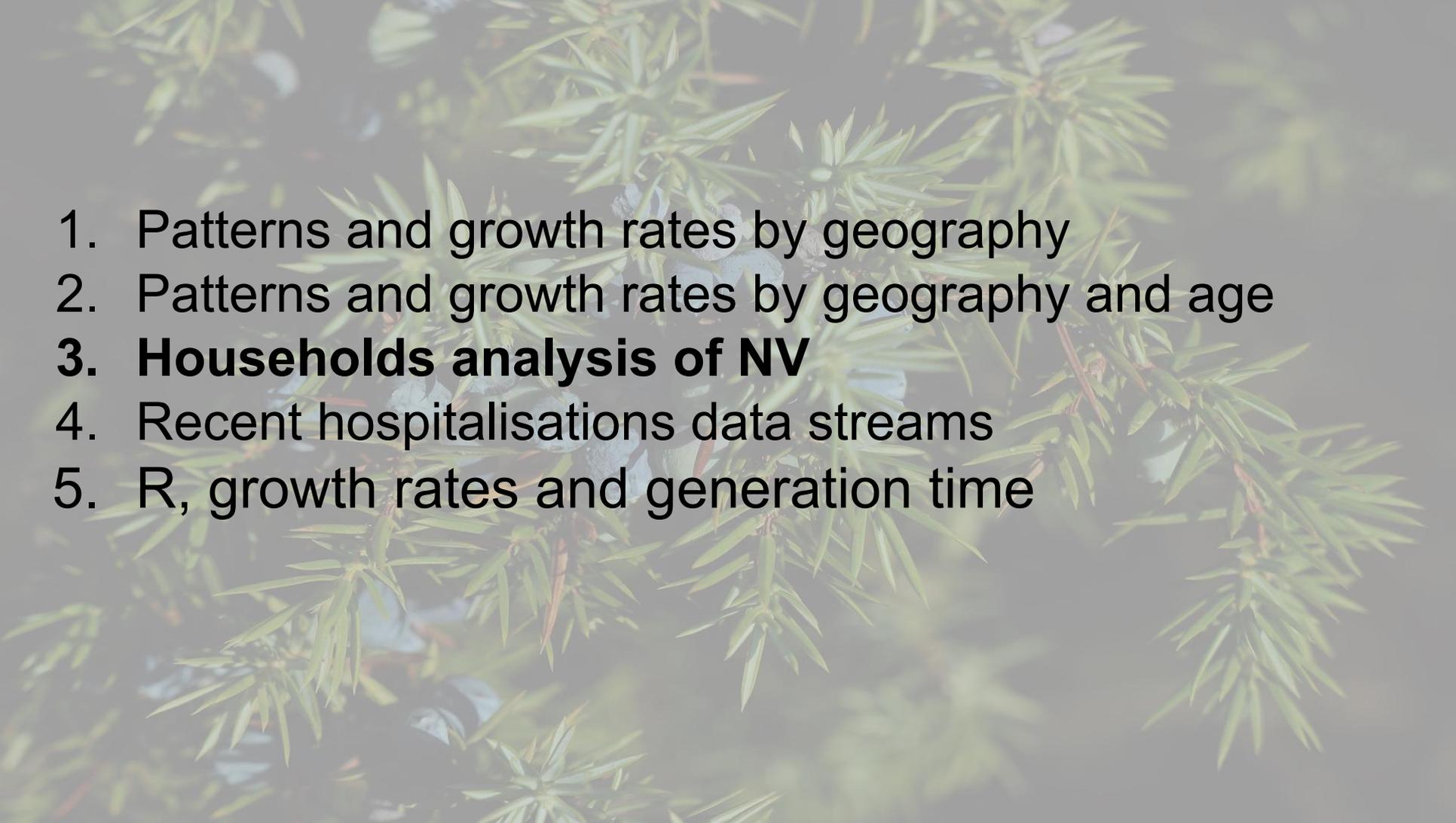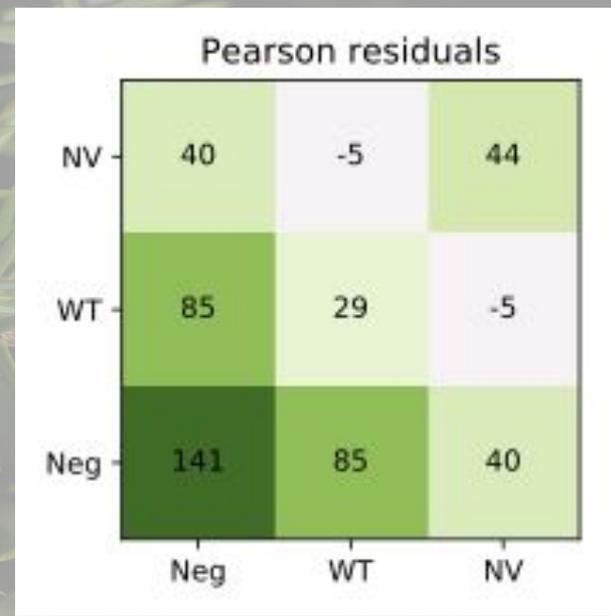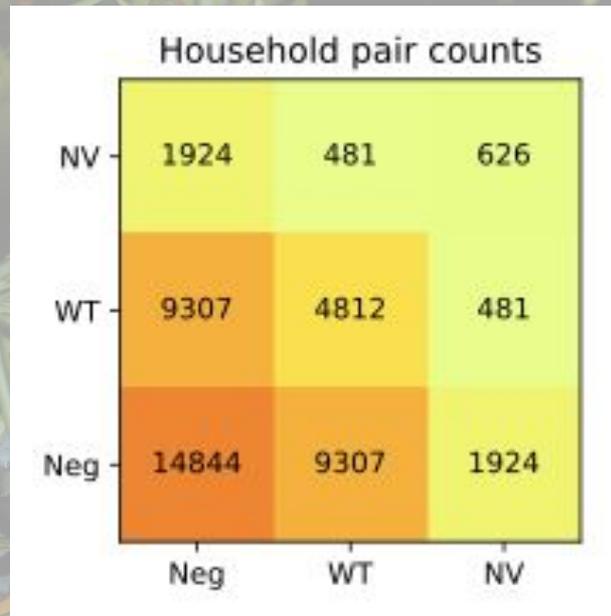1. Patterns and growth rates by geography
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ONS Households

Left shows the counts of pairs of different PCR pattern types in households with at least one positive. Right shows the Pearson residuals versus the null of unclustered types.

These are consistent with the hypothesis that the new variant is more transmissible within households, but can't be interpreted as a causal effect size.

(NB "NV" stands for "OR+N" PCR+ and "WT" for all other PCR+ patterns. These outputs are provided for operational purposes and should not be forwarded until the ONS publishes them.)

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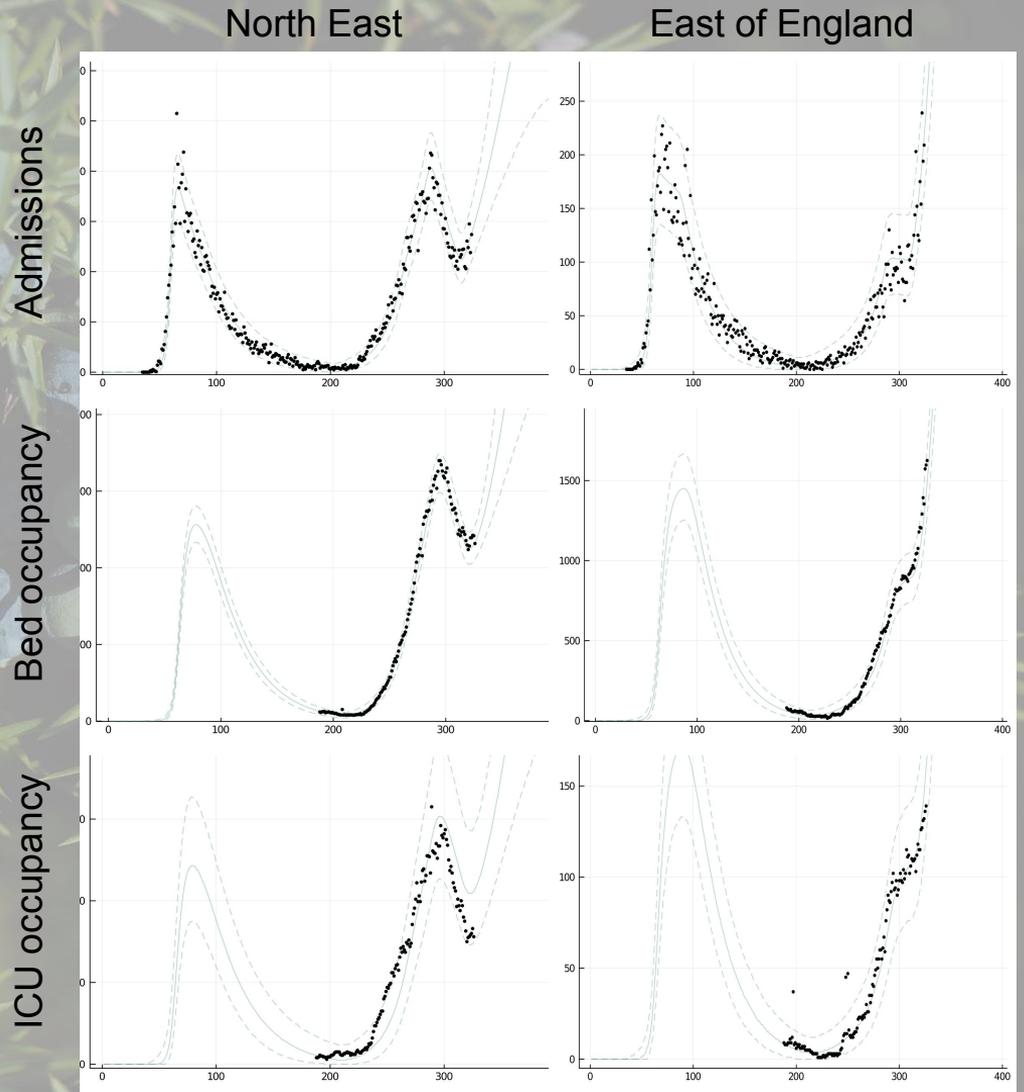
Hospital streams

In LO, EE and SE

- No decline in hospital data during lockdown
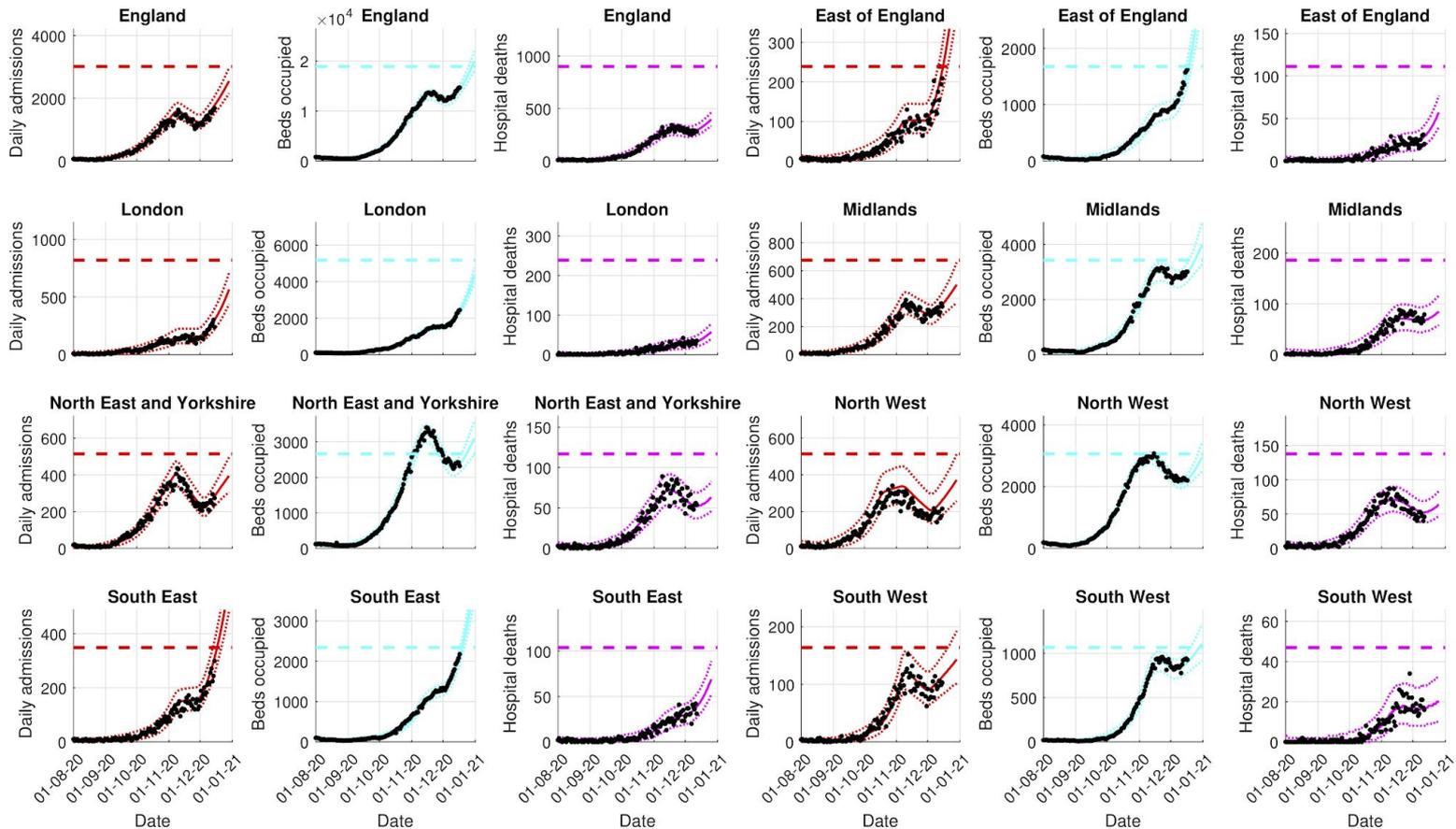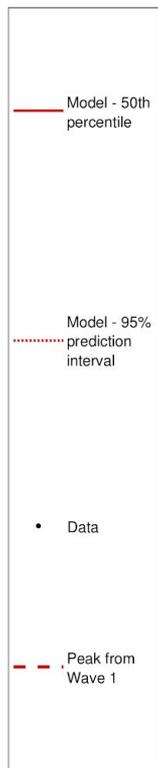- Fast rise after reopening

In NE, NW, SW (a bit MI):

- Decline during lockdown
- Less/slower growth after

England average: in 2 weeks we lost all benefit of a 4-week lockdown

Hospital data streams in all regions

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Inferred R is sensitive to a change in generation time

Given a fixed growth rate (contours on plot), the inferred R (y-axis) depends on assumed generation time distribution (x-axis). If true generation time is lower than assumed, the R estimate will be exaggerated away from 1.

Small print: assuming gamma distributed generation times, kappa=0.446.

Contours are fixed growth rate