

# SPI-M-O: Consensus Statement on COVID-19

*Date: 12<sup>th</sup> May 2021*

All probability statements are in line with the framework given in the Annex.

## Summary

1. SPI-M-O's best estimate for **R in England is between 0.8 and 1.1. R is estimated to be between 0.8 and 1.0 for Scotland, 0.7 and 1.0 for Wales, and 0.8 and 1.1 for Northern Ireland.** These estimates are based on the data available up to 10<sup>th</sup> May, including hospitalisations and deaths as well as symptomatic testing and prevalence studies.
2. Overall, the epidemic in England could be either flat, shrinking slowly, or growing slightly. There are local areas in all nations where the epidemic is increasing and some localities, such as parts of the North West and Bedford, have fast growth of S-gene positive variants that is concerning. This includes the B.1.617.2 variant.
3. Clusters of such new variants mean it is becoming more difficult to interpret R estimates as they are averages over populations, viral variants and areas. Situations could change quickly, especially as restrictions are relaxed further from 17<sup>th</sup> May.
4. SPI-M-O estimates that there are between **1,000 and 7,000 new infections per day in England.**
5. The number and proportion of cases that are S-gene positive continues to increase and this is highly heterogeneous across regions and ethnicities. SPI-M-O is confident that B.1.617.2 is more transmissible than B.1.1.7, and it is a realistic possibility that this new variant of concern could be 50% more transmissible. If B.1.617.2 does have such a large transmission advantage, it is a realistic possibility that progressing with all Roadmap steps would lead to a substantial resurgence of hospitalisations.
6. SPI-M-O has also considered the merits of surge vaccination. While the impact of such a programme is uncertain, from a non-operational epidemiological perspective alone, it has a large potential upside and relatively small potential drawbacks with regard to transmission.

## Incidence and prevalence

7. Combined estimates from four SPI-M-O models, using data available up to 10<sup>th</sup> May, suggest there are between **1,000 and 7,000 new infections per day in England.**
8. During the most recent week of the ONS community infection survey (2<sup>nd</sup> to 8<sup>th</sup> May), the study estimates that an average of **40,800 people had COVID-19** in the community in

England (credible interval **31,900 to 50,900**). The survey does not include people in care homes, hospitals, or prisons. Estimates from across the four nations of the UK are:

England	40,800 (credible interval 31,900 to 50,900)
Scotland	4,200 (credible interval 1,900 to 7,700)
Wales	700 (credible interval 100 to 1,900)
Northern Ireland	1,300 (credible interval 300 to 3,000)

### Growth rate and reproduction number

9. For small daily changes, the growth rate is approximately the proportion by which the number of infections increases or decreases per day, i.e. the speed at which an epidemic is growing or shrinking<sup>1</sup>.

10. SPI-M-O's consensus estimates for the **growth rates in the four nations are:**

**England** is between **-3% and +1% per day**,

**Scotland** is between **-3% and 0% per day**,

**Wales** is between **-5% and -1% per day**, and

**Northern Ireland** is between **-3% and +1% per day**.

SPI-M-O's national and regional estimates of growth rates are summarised in Table 1 and Figure 4.

11. The reproduction number (R) is the average number of secondary infections produced by a single infected individual; it is an average over time, geographies, viral variants and communities. This should be considered when interpreting the R estimate for England, given the current local heterogeneity in epidemiological situations.

12. SPI-M-O's best estimates for **R in England is between 0.8 and 1.1. R is estimated to be between 0.8 and 1.0 for Scotland, 0.7 and 1.0 for Wales, and 0.8 and 1.1 for Northern Ireland**. SPI-M-O's agreed national estimates are summarised in Table 1 and Figure 3, and these are based on the latest data available up to 10<sup>th</sup> May. R is an indicator that lags by two to three weeks and, therefore, does not reflect the full impact of behavioural changes that have happened during this time. Regional estimates can be seen in Table 1 and Figure 5.

13. Overall, the epidemic in England could be either flat, shrinking slowly, or growing slightly. There are local areas in all nations where the epidemic is increasing and some localities, such as the North West and Bedford, have fast growth in cases of S-gene positive variants, including B.1.617.2. These are a cause for concern.

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<sup>1</sup> Further technical information on the growth rate can be found in [Plus magazine](#)

**Table 1:** Combined estimates of R values and growth rates in the four nations of the UK and NHS England regions (90% confidence interval)<sup>2</sup>

<b>Nation</b>	<b>R</b>	<b>Growth rate per day</b>
<b>England</b>	0.8 to 1.1	-3% to +1%
<b>Scotland*</b>	0.8 to 1.0	-3% to 0%
<b>Wales</b>	0.7 to 1.0	-5% to -1%
<b>Northern Ireland*</b>	0.8 to 1.1	-3% to +1%
<b>NHS England region</b>	<b>R</b>	<b>Growth rate per day</b>
<b>East of England</b>	0.8 to 1.1	-5% to +1%
<b>London</b>	0.8 to 1.0	-4% to 0%
<b>Midlands</b>	0.8 to 1.0	-3% to 0%
<b>North East and Yorkshire</b>	0.8 to 1.0	-4% to 0%
<b>North West</b>	0.8 to 1.1	-3% to +2%
<b>South East</b>	0.8 to 1.0	-5% to -1%
<b>South West</b>	0.8 to 1.1	-4% to +1%

14. The rapid growth of clusters of new variants mean it is becoming more difficult to interpret R estimates, as they are averages over populations and areas and reflect recent history, rather than being predictive of the future. Situations could change quickly, especially as restrictions are relaxed.
15. At the moment, many places have slowly decreasing numbers of cases, which are generally of genetic variants that have been present in the UK for some time. This is happening in tandem with a small number of places with exponentially increasing cases that are S-gene positive which are spread over different parts of the country.
16. In particular, as there is a slowly declining prevalence of B.1.1.7 across the country, if another variant is growing rapidly from a low baseline, estimates of overall R and growth rates will not reflect the latter.

### **S-gene positivity and variants of concern**

17. A critical surveillance stream is the association of variants with cases, hospital admissions, and clinical outcomes. Sequencing monitors the genetics of variants, but it is how they present clinically that determines their impact. SPI-M-O strongly advise that there is timely

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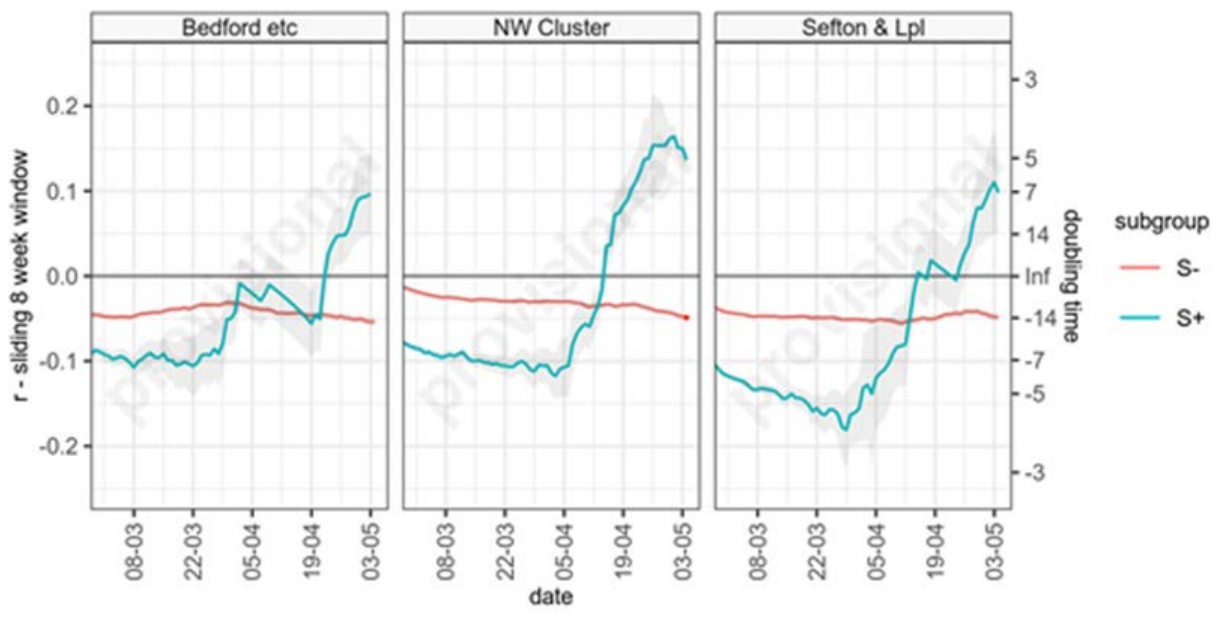
<sup>2</sup> The estimated intervals for R and growth rate may not exactly correspond to each other due to the submission of different independent estimates and rounding in presentation.

\* Particular care should be taken when interpreting these estimates as they are based on low numbers of cases, hospitalisations, or deaths and / or dominated by clustered outbreaks and so should not be treated as robust enough to inform policy decisions alone.

linkage between vaccination, hospitalisation, and sequencing data sets to quickly reveal outbreaks of more pathogenic variants.

18. SPI-M-O are particularly concerned about the increase in cases of the B.1.617.2 variant in some localities of England, for which S-gene positivity can now be used as a reasonable proxy. One modelling group's assessment estimates that R for B.1.617.2 is approximately 1.64 (95% CI: 1.61 to 1.67). This analysis accounts for the importation of this variant from India in estimating R for onward community transmission. The model assumes that non-B.1.617.2 cases continue to decline at the same rate (3% per day) as they did in late April 2021, that the generation time for B.1.617.2 is the same as B.1.1.7, and there is no leakage of cases out of hotel quarantine.
19. This estimate is sensitive to the assumed number of imported cases; for example, if there were fewer importations, more local community transmission would be needed to give the outturn data seen or less community transmission if importations were higher. Timely data on traveller information, however, is limited, reflecting some of the uncertainty behind these estimates. Nonetheless, the principal result, that B.1.617.2 is growing more quickly than B.1.1.7, is robust to these sensitivities.
20. S-gene positivity and sequenced B.1.617.2 cases are regionally heterogeneous with clusters in Bolton, Blackburn and Hyndburn (North West cluster) as well as Sefton, Bedford, and London. Observed doubling times are short and getting shorter even under Step 2 restrictions (Figure 1). The diversity of locations and the difference between S-gene positive (such as B.1.617.2) and S-gene negative (such as B.1.1.7) variant growth rates suggests this apparent increase in transmissibility is unlikely to be wholly due to inherently higher transmission in the communities within which B.1.617.2 is currently circulating.

**Figure 1:** Daily growth rate by S-gene status (red – negative; blue – positive) in areas known to have clusters of B.1.617.2 (an S-gene positive variant). S-gene positive cases have had steadily increasing growth rates (y-axis) since mid-April 2021, and now have doubling times or around a week or faster. S-gene negative cases remain in steady decline (i.e. have a constant negative growth rate).



21. **SPI-M-O is therefore confident that B.1.617.2 has a significant growth advantage over the UK's currently dominant strain, B.1.1.7.** The difference in growth rates between B.1.617.2 and B.1.1.7 is consistent with the former having a transmission advantage of more than 50%; this is based on observed growth that has already happened and it is unclear whether this same growth advantage would apply to sustained wider community transmission regionally or nationally. Resolving this question of the applicability of this growth advantage to the wider population will be difficult while the number of cases are small and relatively focussed.
22. Considering this, it is a realistic possibility that this scale of B.1.617.2 growth could lead to a very large increase in transmission. At this point in the vaccine roll out, there are still too few adults vaccinated to prevent a significant resurgence that ultimately could put unsustainable pressure on the NHS, without non-pharmaceutical interventions.

23. SPI-M-O would become more confident in this assessment of increased transmissibility advantage if any of these four possible situations were to arise. Any of these could happen extremely quickly, potentially even within days:

- Any emerging evidence of vaccine escape, such as more S-gene positive cases than expected in vaccinated people.
- More rapid increase in hospitalisations in areas with high or rising S-gene positivity compared to elsewhere, or higher than expected levels of B.1.617.2 cases in hospital.
- Other parts of the country reflecting similar situations to the North West cluster that cannot be easily identified as being linked to either that cluster or travel.
- If the North West cluster has another consistent doubling at the same speed (i.e. less than 1 week).

24. There is currently insufficient evidence to indicate that any of the variants recently detected in India cause more severe disease or render the vaccines currently deployed any less effective<sup>3</sup>. It is also too early to comment on the impact of B.1.617.2 on hospital admissions or deaths; reported COVID-19 hospitalisations in Bolton are concerning. Only accumulating more data on B.1.617.2 will provide this much needed clarity. If there were a time series of the total number of hospitalised B.1.617.2 cases according to their vaccination status, SPI-M-O would be much better placed to assess the threat that the variant poses.

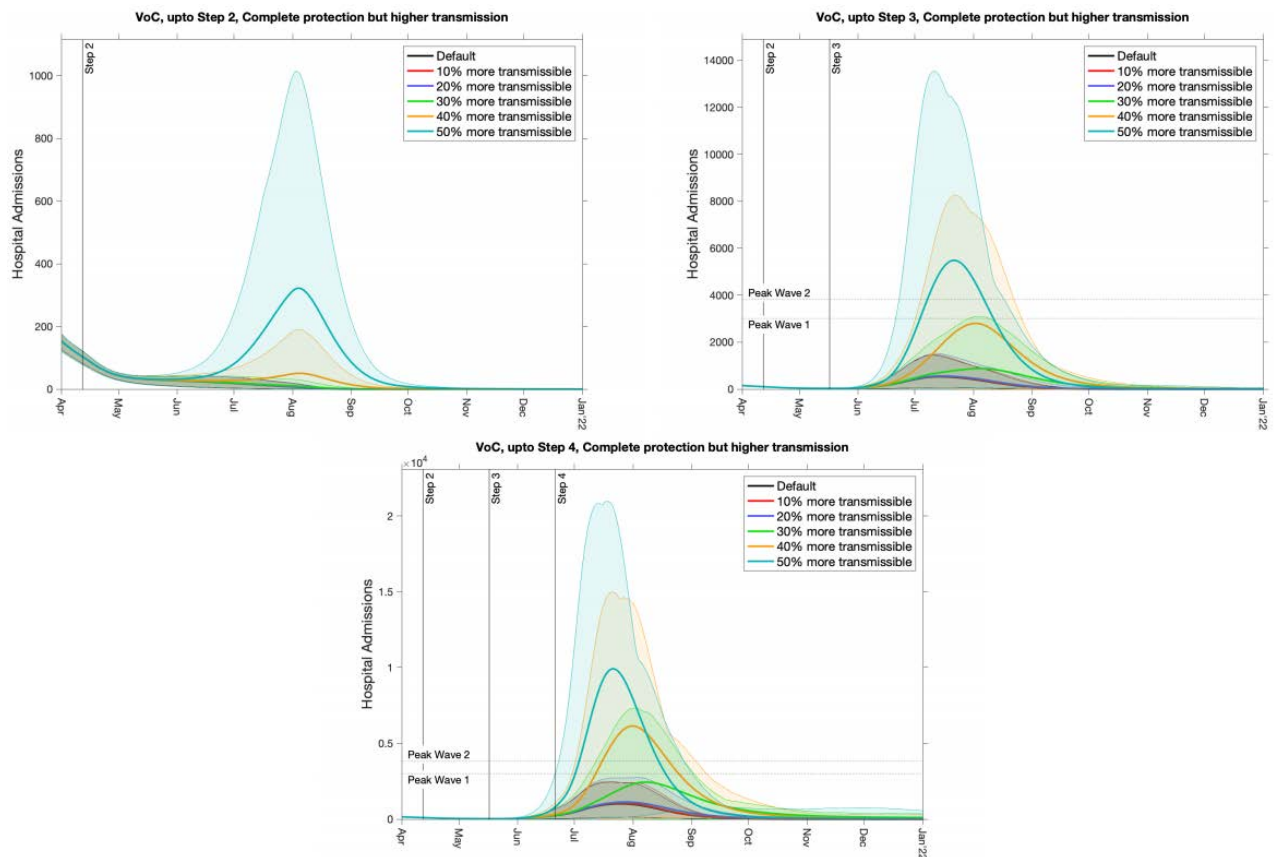
25. SPI-M-O considered the implications of different characteristics of variants of concern in modelling to support Roadmap Step 3 decision making<sup>4</sup>. Both Warwick and London School of Hygiene and Tropical Medicine (LSHTM) performed sensitivity analyses for a variant of concern that was more transmissible than B.1.1.7, but without escape from immunity, in their modelling. If Step 3 alone were taken with a variant circulating in the population that is more than 40% more transmissible than B.1.1.7 with no increase in severity, a further resurgence in hospitalisations similar in size or larger than those seen in spring 2020 and January 2021 is likely (Figure 2, top right plot). If Steps 3 and 4 are taken (Figure 2, bottom plot) with such a variant, peaks could be double that seen in January 2021 if no interventions were taken.

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<sup>3</sup> [Confirmed cases of COVID-19 variants identified in the UK](#); Public Health England

<sup>4</sup> [SPI-M-O: Summary of further modelling of easing restrictions – Roadmap Step 3](#); [University of Warwick: Roadmap scenarios and sensitivity – Steps 3 and 4](#); [LSHTM: Interim roadmap assessment – prior to Steps 3 and 4](#); SAGE 88 5<sup>th</sup> May 2021

**Figure 2:** Comparative potential epidemic trajectories for an undefined variant of concern with different levels of increased transmissibility (same as B.1.1.7 – black; 10% more – red; 20% more – blue; 30% more – green; 40% more – yellow; 50% more – light blue) but no immune escape, assuming Step 3 is not taken (top left), Step 3 alone is taken (top right), and Steps 3 and 4 are taken. From [modelling conducted by Warwick University](#) to support Roadmap Step 3 decisions.



26. Until more data accumulates it will be difficult for SPI-M-O to give a confident plausible range for the transmissibility of B.1.617.2 in the wider population beyond that it is more transmissible than B.1.1.7 and that 50% more transmissible cannot be ruled out. Whilst there are clear observations that B.1.617.2 is currently spreading very fast in some places, numbers are still low and SPI-M-O cannot yet tell if that pattern will pertain across the whole population.

27. Testing of S-gene status by TaqPath assays is regionally heterogeneous with good coverage in those places that have clusters of concern now. There is a need, however, for better coverage with these assays, for example in South West England, to ensure any new hotspots are found early. Such capability allows the use of S-gene positivity as a leading indicator for B.1.617.2 cases.

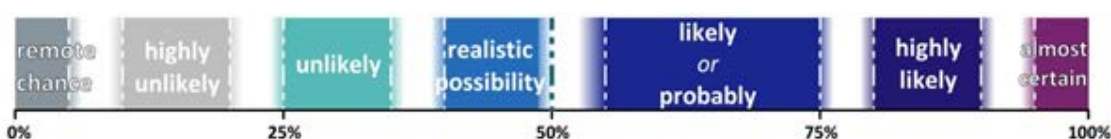
28. B.1.617.2 is an urgent concerning issue due to its high levels of transmissibility. By contrast, B.1.351 continues to grow in the UK albeit much more slowly. There has been good localised control and extinguishing of clusters of B.1.351 and this will have contributed to its slower growth. **As restrictions are eased further from 17<sup>th</sup> May, cases of both these variants of concern will increase.**



## Surge vaccination

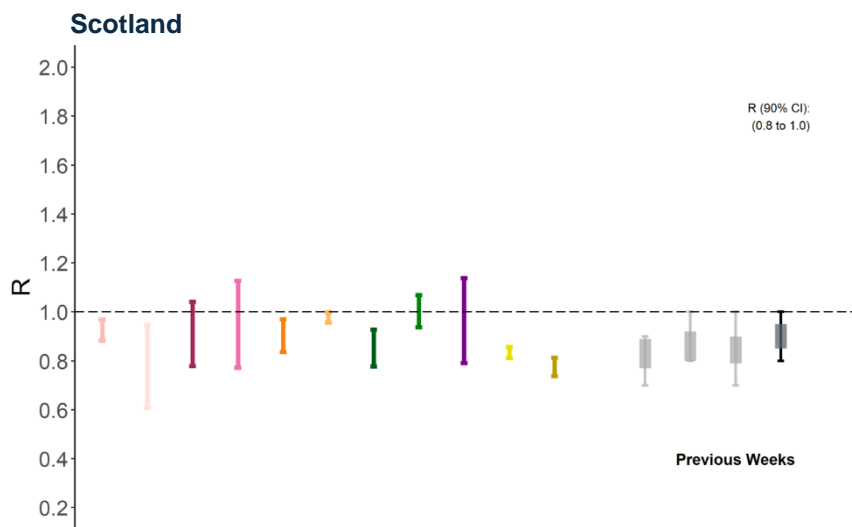
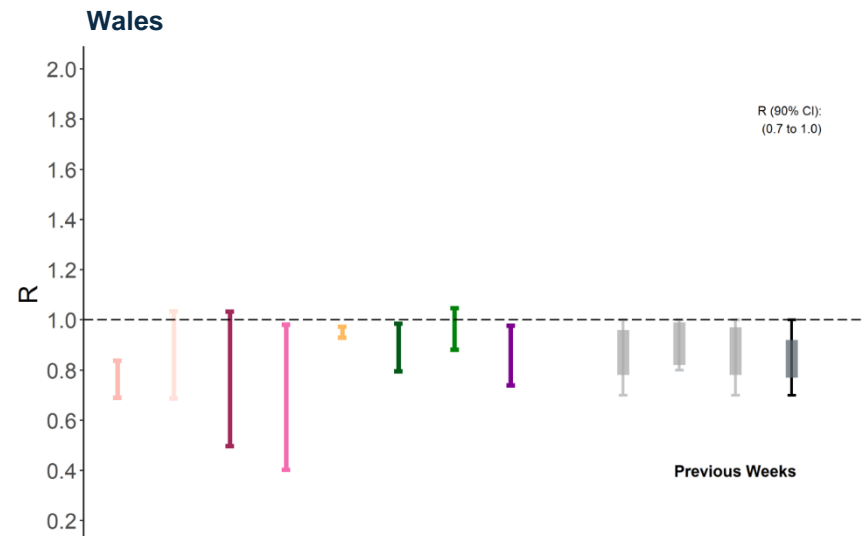
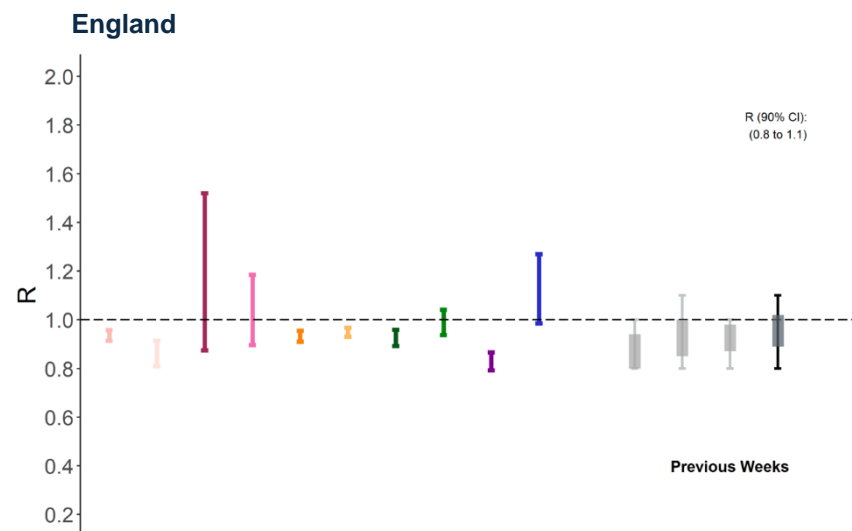
29. SPI-M-O have considered the merits of surge vaccination. This refers to preferentially targeting vaccination (both of younger age groups and previously unvaccinated people already eligible for a dose) towards areas with either sustained high prevalence or with rapidly growing outbreaks of the B.1.617.2 variant, with the aim of dampening transmission rather than stopping it completely.
30. Such a strategy is consistent with JCVI prioritisation of vaccinating those with highest risk. It would be operationally challenging and has an opportunity cost of slowing the rollout of vaccines to other parts of the country. The marginal benefit of vaccines at present in areas of high variants of concern growth, however, is many times higher than it is in lower prevalence parts of the country.
31. The extent to which surge vaccination would curb outbreaks of B.1.617.2 is unknown until evidence for the effectiveness of existing vaccines against it has been established. That does not preclude there being a strong case for prioritising delivering doses in areas where the variant is widespread. If a variant of concern did escape vaccine protection, then slowing delivery in some parts of the country while attempting surge vaccination elsewhere would not be detrimental.
32. There is an inherent lag between vaccination and the establishment of protection of the vaccinated individual, and B.1.617.2 has the potential to spread very rapidly out of areas where it is currently present. It will take some time before surge vaccination starts to break chains of transmission, and thus the variant could spread beyond the targeted area. For that reason, for surge vaccination to be successful it would need to be:
- Started as soon as possible, while the absolute number of cases B.1.617.2 remains relatively low
  - Targeted at a wider geographical area than that where the variant is prevalent
  - Combined with short term non-pharmaceutical interventions covering the area in question, to allow for the surge vaccination to have time to take effect.
33. In summary, while the success of a surge vaccination programme is not guaranteed, from a non-operational epidemiological perspective alone, it has a large potential upside with relatively small potential drawbacks with regard to transmission.

## Annex: PHIA framework of language for discussing probabilities

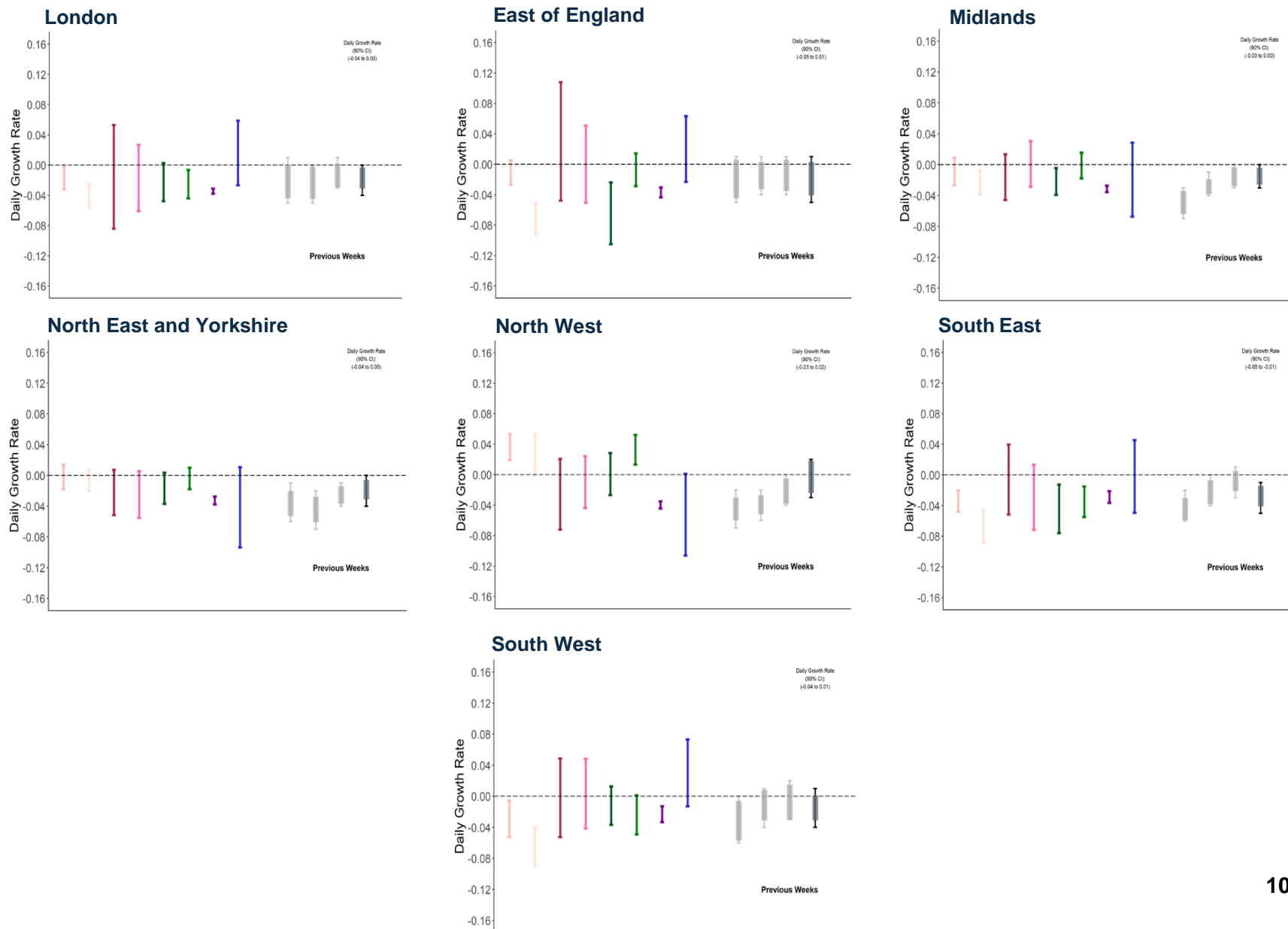




**Figure 3:** SPI-M-O groups estimates of median R in the four nations of the UK, including 90% confidence intervals. Bars represent different independent estimates. The grey shaded areas represent the combined numerical range and the black bars are the combined range after rounding to 1 decimal place.



**Figure 4:** SPI-M-O groups' estimates of the growth rate in NHS England regions, including 90% confidence intervals. Bars represent different modelling groups. The grey shaded areas represent the combined numerical range and the black bars are the combined range after rounding to 2 decimal places.



**Figure 5:** SPI-M-O groups' estimates of median R in the NHS England regions, including 90% confidence intervals. Bars represent different independent estimates. The grey shaded areas represent the combined numerical range and the black bars are the combined range after rounding to 1 decimal place.

