Note added for publication

This paper contains estimates of the reproduction number (R) for the UK and four nations.

R is an average value that can vary in different parts of the country, communities, and subsections of the population. It cannot be measured directly so there is always some uncertainty around its exact value. Estimates for Scotland, Wales, and Northern Ireland are subject to greater uncertainty given the lower number of cases and increased variation.

Different modelling groups use different data sources to estimate R using complex mathematical models that simulate the spread of infections. Some may even use all these sources of information to adjust their models to better reflect the real-world situation. There is uncertainty in all these data sources, which is why R estimates can vary between different models, and why we do not rely on one model; evidence is considered, discussed and R is presented as a range.

Given wide uncertainty ranges, it should not be concluded from estimates in this paper that R is higher or lower in different nations.

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

FINAL: REISSUED 12TH JUNE FOLLOWING FEEDBACK FROM COMMITTEE

Date: 10th June 2020

Summary

1. It is highly likely that the overall reproduction number, R, in all four nations of the UK is below 1. SPI-M-O's best estimate for the UK is that it remains between 0.7 and 0.9.

2. Regional estimates of R are less reliable and less useful in determining the state of the epidemic at smaller spatial scales. R is an average measure and will smooth over outbreaks at very small spatial scales. There is no strong evidence of systematic regional variation in how the epidemic is growing or shrinking.

3. Any changes in transmission that may have occurred in the past two to three weeks will not yet be reflected in health system data, nor therefore in SPI-M-O's estimates of R or growth rates.

4. Backwards contact tracing is an important part of a control programme given its potential to identify clusters of infections and, in particular, places where such clusters occurred. It is likely to be more effective in terms of proportion of cases found, but should be carefully designed to take account of the evidence of the effective and practical depth of searches that can be achieved.

Reproduction number

5. The reproduction number is the average number of secondary infections produced by a single infected individual. R is an average over time, geographies and communities. Whilst it varies in different geographies and settings of the population, separating transmission within and between these sub-populations increases uncertainty.

6. Estimates of R are dependent on differences in modelling methodology (particularly around the assumed distribution of the generation interval, the data sources used, the time frame considered, and the estimation framework) and will always carry some level of uncertainty. SPI-M-O's approach is for different modelling groups to estimate R independently to reflect this inherent uncertainty, then combine them using a random / mixed effects model with equal proportion weights, and to agree a consensus. The methodology for this combination is continuously scrutinised and developed.

7. Any changes in transmission patterns that may have occurred in the last two to three weeks will not yet be reflected in the healthcare data, nor therefore in SPI-M-O's estimates of R. Other studies, however, provide more timely indications of changes in transmission, such as the ONS swabbing survey and the Comix behavioural survey that studies how contact patterns are changing over time.

8. Uncertainty in R increases as the number of infections decrease, or when it is evaluated for a smaller population, such as for the devolved administrations and regions. SPI-M-O agreed estimates of R are summarised in Figures 1 and 2.

9. SPI-M-O's consensus view is that the overall **R in the UK is highly likely to be between 0.7 and 0.9**.

10. SPI-M-O's consensus view is that the overall **R in England is highly likely to be between 0.8 and 1.0**.

11. SPI-M-O's consensus view is that the overall **R in Scotland is highly likely to be between 0.6 and 0.9**.

12. SPI-M-O's consensus view is that the overall **R in Wales is highly likely to be between 0.7 and 1.0**.

13. SPI-M-O's consensus view is that the overall **R in Northern Ireland is highly likely to be between 0.6 and 1.0**.

Incidence

14. The relationship between infection, symptoms, swab positivity, hospitalisation and death is becoming clearer, but uncertainties remain in estimating the number of new daily infections.

15. Modelled estimates of incidence are generally higher than those from the ONS swabbing surveys. The reason for this is not yet clear. It is likely to be partly explained by the fact that the ONS survey does not include care homes or hospitals, where infection rates are higher than the general population.

16. Data from the ONS swabbing survey between 25th May and 7th June estimate that an average of 33,000 people in the community in England (confidence interval 14,000 to 68,000) who would have swabbed positive for SARS-CoV-2 during this time period. The study estimates that between 26th April and 7th June there were an average of 31,600 new infections per week in the community (including asymptomatic individuals), but with a wide confidence interval from 22,200 to 43,500.

Regional variation

17. Estimates of R are less reliable and less useful in determining the state of the epidemic as cases decrease. There are three main reasons for this:

18. Firstly, when there are few cases, R is impossible to estimate with accuracy and will have wide confidence intervals that are likely to include 1. This does not necessarily mean that the epidemic is increasing but could be the result of greater uncertainty.

19. Secondly, as incidence decreases, R will tend towards 1, and has to be evaluated in conjunction with incidence. The policy implications of R = 1 when there are 1,000 new infections per day are very different to when there are 100,000 per day.

20. Finally, R is an average measure. When incidence is low, an outbreak in one place could result in estimates of R for the entire region to become higher than 1. Conversely, small, local outbreaks will not be detected. Estimates of R based on small numbers may also not capture change in the area fast enough to inform policy in a useful way.

21. Estimates of R at regional levels are subject to the same difficulties in interpretation of national estimates, but amplified because of the smaller numbers of cases. Publishing large numbers of estimates increases the statistical chance that one of them is artificially high. SPI-M-O does not have confidence that regional R estimates are sufficiently robust

to inform regional policy decisions. This is true even after we have combined estimates from several groups to produce a consensus value.

22. Estimates of the growth rate of the epidemic require fewer assumptions and are inherently more statistically stable. SPI-M-O will produce consensus values of growth rates in order to provide an alternative measure of changes in transmission.

23. For small daily changes, the growth rate is approximately the proportion by which the number of infections increases or decreases each day, i.e. the rate at which an epidemic is growing or shrinking[1].

24. As with the reproduction number, SPI-M-O's consensus estimates of the regional growth rate are based on a statistical combination of estimates from several modelling groups.

25. SPI-M-O's consensus estimate is that the epidemic is slowly shrinking in the UK, with a growth rate which can be interpreted as -2% to -4% per day. In England the growth rate is estimated to be -1% to -3%; in Scotland -8% to 0%; in Wales -5% to +2%; and in Northern Ireland -8% to +4%.

26. Consensus estimates for the regional growth rates are given in **Figure 3**. They show that **there is little regional variation in growth rates**. It is highly likely that the epidemic is shrinking in all regions, apart from the South West region where the growth rate is possibly zero or slightly positive. The number of deaths and hospital occupancy in the South West, however, is very low. This should be monitored carefully.

27. For completeness, consensus regional estimates of R are given in **Figure 4.** Some of these ranges include R = 1. This is not to be interpreted that we are confident that transmission rates of COVID are increasing, but that *some* of the data streams are showing increases that could be explained by increased uncertainty at low case counts.

28. Neither measure, growth rate or R, is inherently better. Growth rate relates to both data and projections more clearly whereas the reproduction rate relates more directly to strength of intervention required.

Care home testing

29. Given current capacity of around 40,000-50,000 tests in care homes, several strategies were considered to determine which was most likely to detect an outbreak. Strategies were

[1] The growth rate, λ, is the slope of the exponential curve $y = e^{\lambda t}$, where *y* is the number of new infections, and *t* is time, given in days

modelled for residents only and not staff, and were only applied to those homes not under outbreak investigation or management.

30. A strategy of testing care home residents entirely at random performed poorly. Two further strategies – i) modifying this strategy to test at least one person in each home, then using the rest of the testing capacity at random, and ii) testing all residents in a random selection of care homes – were better and were roughly as successful as one another.

31. An alternative strategy was considered where up to 10 randomly sampled residents in each home are tested and their pooled samples is tested. **This strategy was considerably more effective at detecting outbreaks**, despite needing fewer tests to be carried out.

32. Further work is required to refine testing strategies to maximise the effectiveness and efficiency of testing to reduce transmission in care and nursing home settings.

Contact tracing

33. Backwards contact tracing is an important part of infectious disease control. It is likely to increase the proportion of cases found can support identifying clusters of infections and, in particular, the places and settings where such clusters occurred. This can allow for isolation of infected individuals that would otherwise not be detected and provide additional information on relative risk of different settings.

34. Backwards contact tracing in combination with forward tracing is likely to be more effective in terms of proportion of cases found than forward tracing alone, and may be more efficient in terms of the reduction in transmission achieved in return for the additional effort required per case detected.

35. From the analyses presented to SPI-M, there was a consensus that contacts from 5–8 days pre-symptom onset is a suitable cut-off to maximise transmission impact. Any backwards contact tracing programme, however, needs to be carefully designed to take account of the evidence of the effective and practical depth of searches that are achievable.

Annex: PHIA framework of language for discussing probabilities

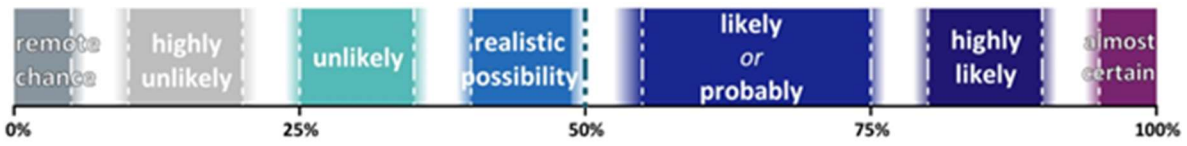

Figure 1: SPI-M groups' estimates of median R in the UK, including 90% confidence intervals. Bars represent different modelling groups. Black bars are combined estimates and the midpoint is the mean of the distribution from the meta-analysis, not SPI-M's assessment of the most likely value.

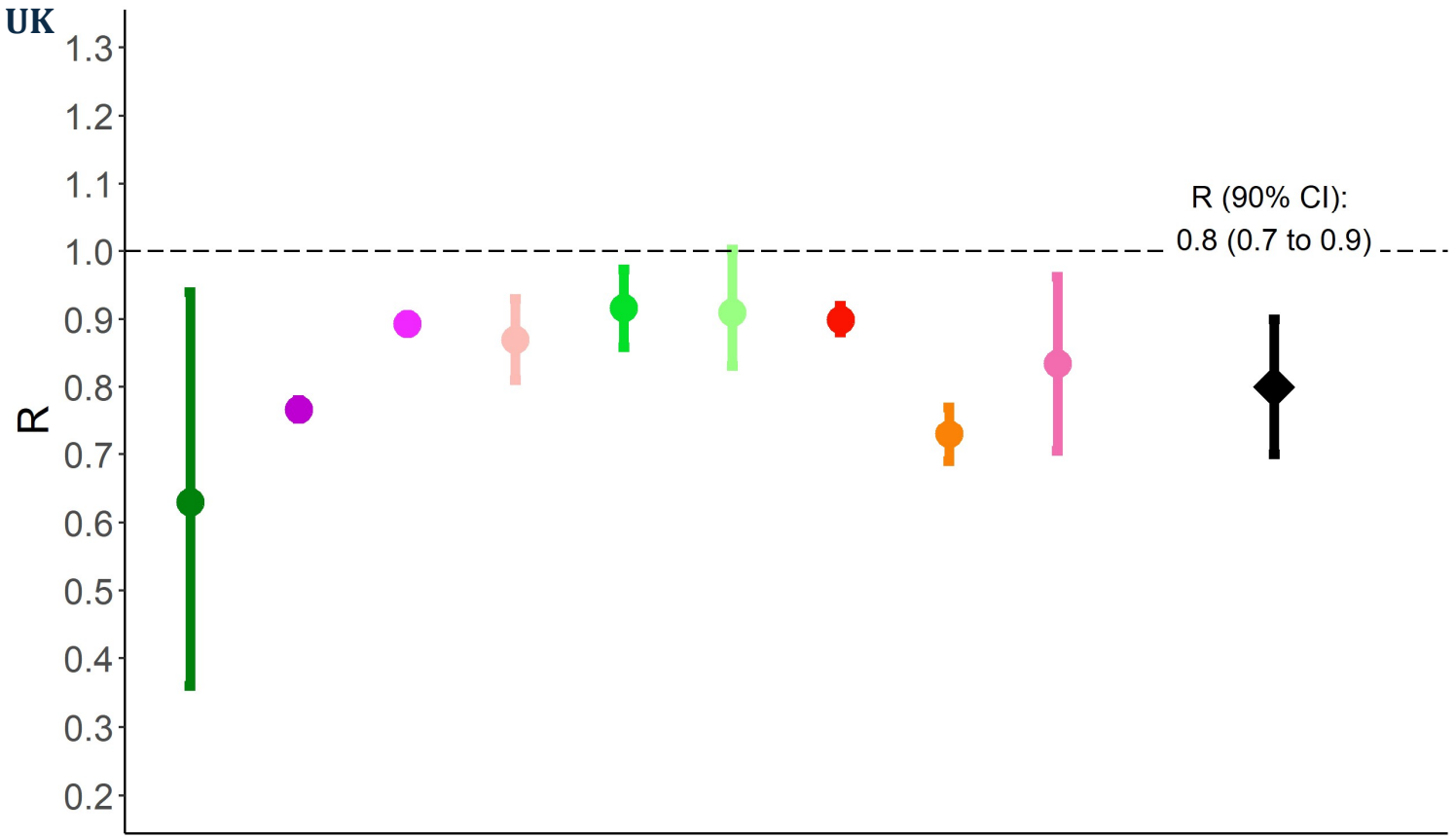

Figure 2: SPI-M groups estimates of median R in the four nations of the UK, including 90% confidence intervals. Bars represent different modelling groups. Black bars are combined estimates and the midpoint is the mean of the distribution from the meta-analysis, not SPI-M's assessment of the most likely value.

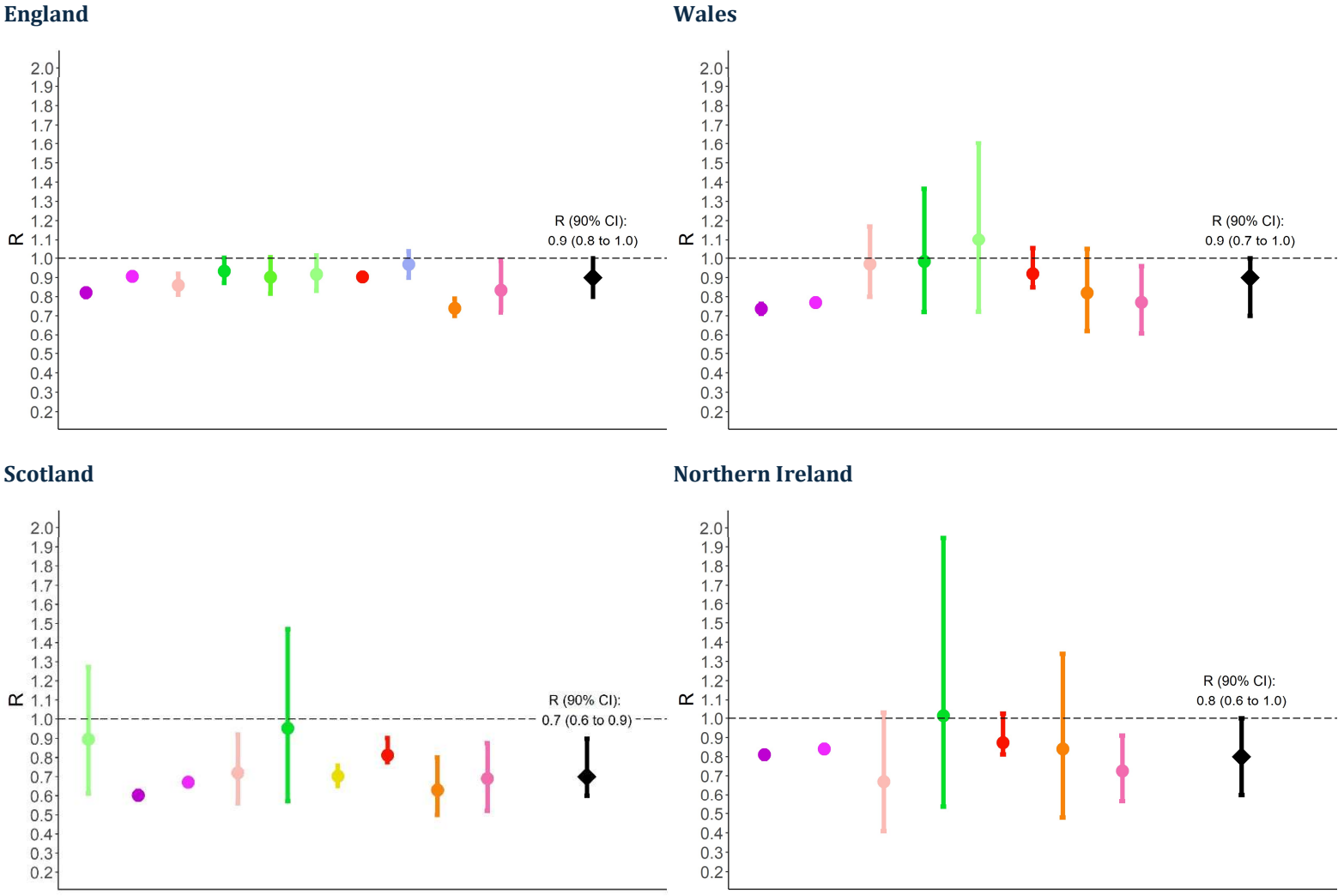

Figure 3: SPI-M groups estimates of the growth rate in English NHS regions, including 90% confidence intervals. Black bars are combined estimates and the midpoint is the mean of the distribution from the meta-analysis, not SPI-M's assessment of the most likely value.

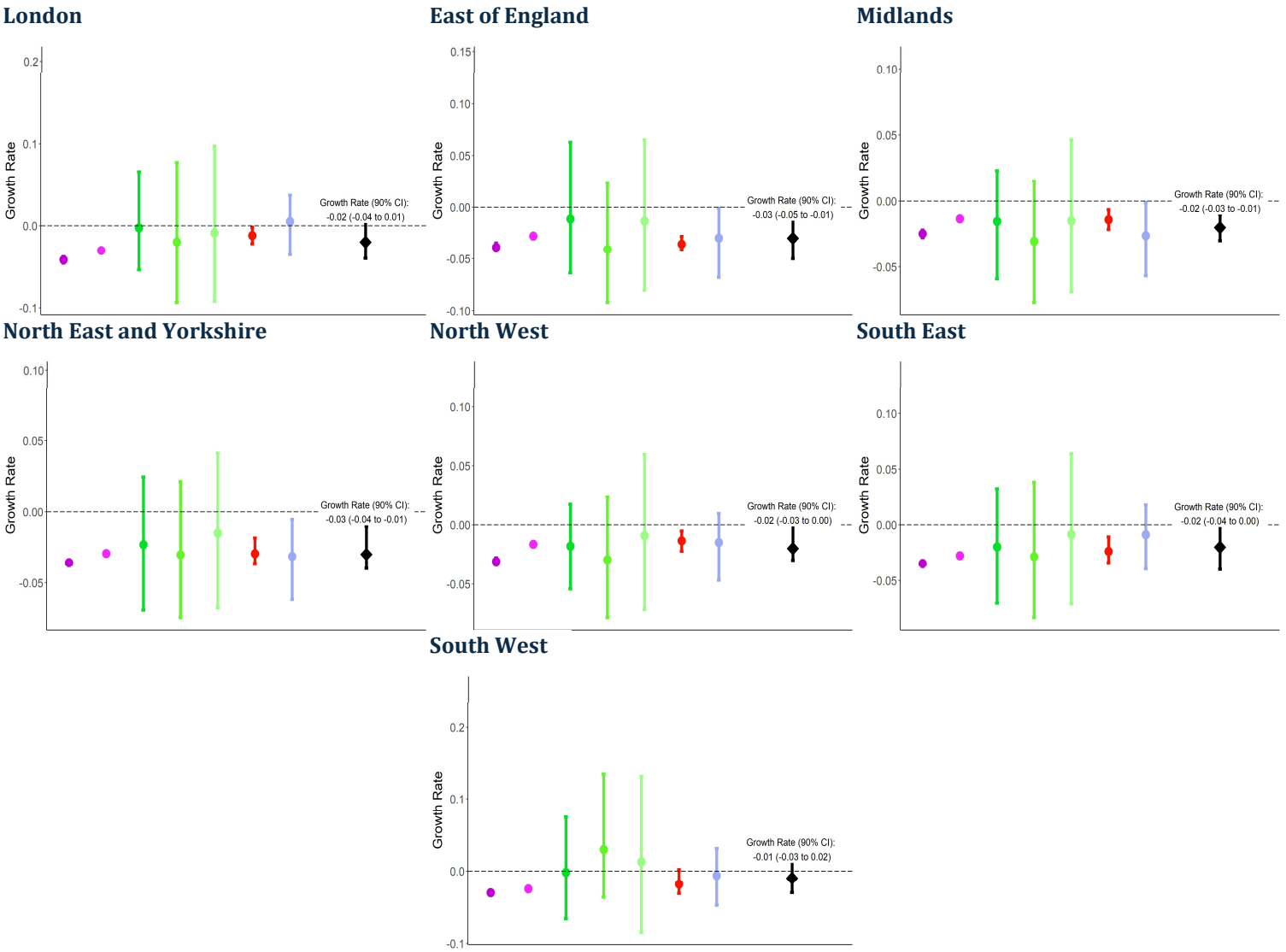

Figure 3: SPI-M groups estimates of median R in the English NHS regions, including 90% confidence intervals. Black bars are combined estimates and the midpoint is the mean of the distribution from the meta-analysis, not SPI-M's assessment of the most likely value.