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.

This paper also includes estimates of the proportion of infections that are hospital associated. Please note that this was preliminary analysis, and has been subsequently revised.

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

SIGNED OFF BY CHAIRS ON BEHALF OF SPI-M-O

Date: 3rd June 2020

Summary

1. There is evidence from other countries that a high proportion of cases may come from clearly defined transmission clusters. Rapid identification of these may be disproportionately important for control.

2. SPI-M-O's best estimate is that the overall reproduction number, R_t, in the UK is between 0.7 and 0.9.

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_t.

4. There is evidence that in some regions or nations R_t is tending towards 1 as the declines in hospital admissions, deaths and calls to NHS 111 are slowing and may be plateauing. There is greater uncertainty in R_t where populations are smaller, and as the numbers of cases declines, so it is not possible to state with confidence in which places or regions of the UK R_t may be greater than one. If the overall R for the UK is close to one, then it is possible that R will be above one in some places or regions.

Clustering

5. There is growing evidence from other countries that a large proportion of cases may come from clearly defined transmission clusters ("superspreading events").

6. The identification of such clusters, through tracing based on locations or events, is likely to be an efficient way to identify transmission chains.

7. Backwards contact tracing (that is, identifying where and by whom a positive case was infected) is an effective way of identifying clusters of transmission, and potentially more efficient than forward-tracing if most index cases transmit to very few people, or if transmission chains of asymptomatic cases are common.

8. The Joint Biosecurity Centre should investigate the role of cluster identification / investigation and backward-tracing in terms of the design of the most efficient means of controlling transmission.

Reproduction number

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

10. Estimates of R_t are dependent on differences in modelling methodology (particularly around the assumed values of the generation time, 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_t independently to reflect this inherent uncertainty, then combine them using a random / mixed effects model with equal proportion weights, and to agree a consensus.

11. 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_t.

12. Uncertainty in R_t increases as numbers of infections drop, or when it is evaluated for a smaller population, such as for the devolved administrations. SPI-M-O agreed estimates of R_t are summarised in Figures 1 and 2.

13. SPI-M-O's consensus view is that the overall **R_t in the UK is between 0.7 and 0.9**.

14. SPI-M-O's consensus view is that the overall **R_t in England is between 0.7 and 1.0**

15. SPI-M-O's consensus view is that the overall **R_t in Scotland is between 0.6 and 0.8**.

16. SPI-M-O's consensus view is that the overall **R_t in Wales is between 0.7 and 0.9**.

17. SPI-M-O's consensus view is that the overall **R_t in Northern Ireland is between 0.7 and 1.0**.

18. Estimates of the growth rate based on ONS's swabbing survey are in line with SPI-M's estimate of R in England. It is not possible to use this to estimate R_t on a comparable basis to the transmission models, as it does not capture all infections in hospitals or care homes.

19. CoMix, London School of Hygiene and Tropical Medicine's longitudinal study of contacts, provides supporting evidence that R remains below 1, although the average number of contacts per person has increased slightly since social distancing measures have been relaxed.

20. SPI-M-O's previous advice concerning the loosening of social distancing measures at the start of June was predicated on there being a highly effective system of contact tracing in place. So effective that 80% of contacts of index cases are identified and quarantined within 48 hours. While SPI-M-O have not yet had access to data on the current performance of the track and trace system, we are concerned that if these criteria are not yet being met, there is a risk that R_t will rise above 1 in many areas of UK with a return to exponential growth of the epidemic.

Incidence

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

22. Imperial, Warwick and LSHTM's estimates of incidence have converged to around 35,000 new infections per day in the UK. Part of the reason for this convergence is that they fit to the same data, including serology.

23. Public Health England's models are fitted on different data streams. Their estimates of incidence in England are lower, at around 12,000.

24. As none of the transmission models explicitly include healthcare-acquired or care home cases in the model structure, they may be overestimating incidence in the general population. However, as models fit well to data on hospital usage and deaths, they capture

the overall patterns of risk and transmission and adequately predict the impact of relaxing social distancing measures.

25. There is no consensus on why ONS's estimates of incidence are lower than those estimated by transmission models, but it is noted that they are based on a very small number of positive tests, and the relationships between test positivity, infection and symptoms remain uncertain.

26. Analysis based on CO-CIN data indicated that as of 1st May, 30% of positive tests in hospital were linked to hospital acquired infection, including those in up to the fourth generation of transmission following discharge. Since then, as the number of cases in hospital have decreased, the proportion of infections that are hospital associated has increased, and was approximately 80% as of the 1st June. These estimates are preliminary and dependent on modelling assumptions used.

Figure 1: SPI-M groups' estimates of median R_t by nation, including 90% confidence intervals. Bars represent different modelling groups. Black bars are combined estimates.

Note added for publication: *Please note that the midpoint of the combined estimate is the mean of the distribution from the meta-analysis, not SPI-M-O's assessment of the most likely value.*

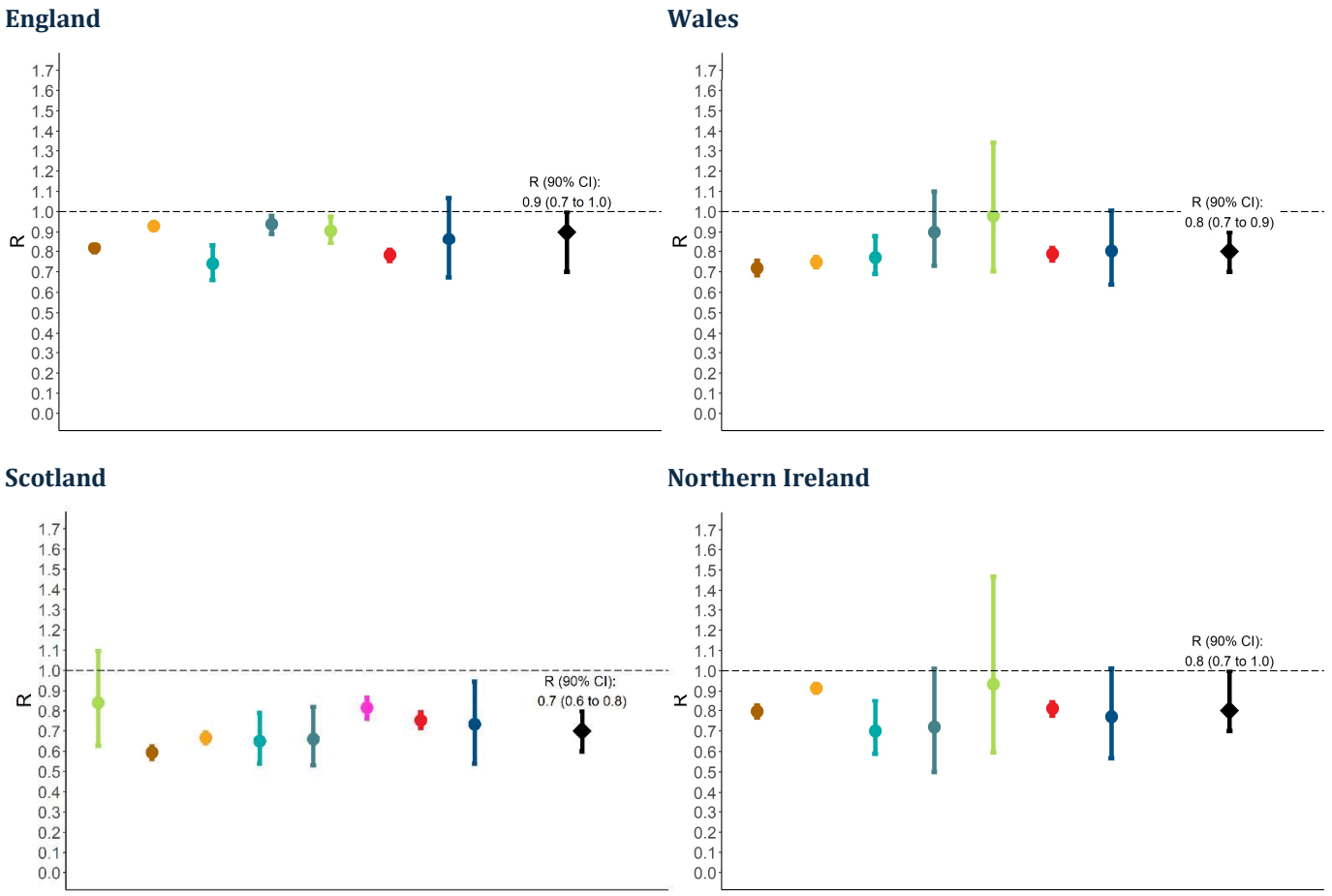

Figure 2: SPI-M groups estimates of median R_t in the UK, including 90% confidence intervals. Bars represent different modelling groups. Black bars are combined estimates.

Note added for publication: *Please note that the midpoint of the combined estimate is the mean of the distribution from the meta-analysis, not SPI-M-O's assessment of the most likely value.*