R explainer

What is R?

The reproduction number (R) is the average number of secondary infections produced by one infected person. An R number of 1 means that on average every person who is infected will infect 1 other person. If R is 2, on average, each infected person infects 2 more people. If R is 0.5 then on average for each 2 infected people, there will be only 1 new infection. If R is greater than 1 the epidemic is growing, if R is less than 1 the epidemic is shrinking.

R can change over time. For example, it falls when there is a reduction in the number of contacts between people, which reduces transmission.

R is not the only important measure of the epidemic. R indicates whether the epidemic is getting bigger or smaller but not how large it is. The number of people currently infected with COVID-19 very important. This is estimated by ONS and available on this [website](). R should always be considered alongside the number of people currently infected. If R equals 1 with 100,000 people currently infected, it is a very different situation to R equals 1 with 1000 people currently infected.

Limitations of R

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.

How is R estimated?

Individual modelling groups use a range of data to estimate R including:

- **Epidemiological data** such as hospital admissions, ICU admissions and deaths. It generally takes 2-3 weeks for changes in R to be reflected in these data sources, due to the time between infection and needing hospital care.
- **Contact pattern surveys** that gather information on behaviour. These can be quicker (with a lag of around a week) but can be open to bias as they often rely on self-reported behaviour.
- **Household infection surveys** where blood samples and swabs are performed on individuals which can provide estimates of how many people are infected. Longitudinal surveys (which sample the same people repeatedly) allow a direct estimate of the infection rates.

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.

Who estimates R?

R is estimated by a range of independent modelling groups based in universities and Public Health England (PHE). The modelling groups present their individual R estimates to the Science Pandemic Influenza Modelling group (SPI-M) - a subgroup of SAGE - for discussion. Attendees compare the different estimates of R and SPI- M collectively agrees a range which R is very likely to be within.