Government publishes latest R number

R number range for the UK 0.7-1.0 (Up to date as of 22 May 2020)

The reproduction number (R) is the average number of secondary infections produced by 1 infected person.

The Scientific Pandemic Influenza Group on Modelling (SPI-M), a sub-group of the Scientific Advisory Group for Emergencies (SAGE), has built a consensus on the value of R based on expert scientific advice from multiple academic groups. This has been reviewed by SAGE.

The range of 0.7-1.0 is an estimate based on latest data available to determine infection and transmission rates. Data such as contacts, hospital admissions, ICU admissions and deaths generally takes 2 to 3 weeks for changes in R to be reflected in these data sources, due to the time between infection and needing hospital care.

As data on infection is estimated through data on symptomatic cases, hospitalisations, or deaths, there is a delay of around 2 to 3 weeks because as there is a lag between people between people becoming infected, entering hospital, and dying. Consequently, this range applies to data before the recent adjustments to the restrictions the government has put in place earlier this week.

An R number of 1 means that on average every person who is infected will infect 1 other person, meaning the total number of new infections is stable. 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 generally seen to be growing, if R is less than 1 the epidemic is shrinking.

SAGE is confident that overall the R is not above 1. This means that the number of infections is not increasing, and is very likely to be decreasing.

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

In the coming weeks and months, the R number will be updated every week on the $\underline{GO-Science\ website}$.

Sir Patrick Vallance, Government Chief Scientific Adviser said:

R is one of the most important things you can track to understand an epidemic. If you can estimate R, then you have part of a reliable tool for planning how to combat the virus.

If the R is higher than 1 that means this disease is growing exponentially and will keep on spreading to more and more people.

To keep R below one and control the virus, it is vital that people stay alert and continue to follow the latest government guidelines to the letter.

In the coming weeks we will update this estimate regularly.

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 – and so able to pass it on – is very important. It is estimated by ONS and available on their <u>website</u>. ONS will publish this figure regularly, so as to enable tracking of whether it is going up or down.

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 1,000 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 to 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.