Coronavirus (COVID-19): modelling the epidemic in Scotland (Issue No. 34)

Background

This is a report on the Scottish Government modelling of the spread and level of Covid-19. This updates the previous publication on modelling of Covid-19 in Scotland published on 7 January 2021. The estimates in this document help the Scottish Government, the health service and the wider public sector plan and put in place what is needed to keep us safe and treat people who have the virus.

This edition of the research findings focuses on the epidemic as a whole, looking at estimates of R, growth rate and incidence as well as local measures of change in the epidemic.

Key Points

- The reproduction rate R in Scotland is currently estimated as being between 1.0 and 1.4. This is an increase compared to last week.
- The number of new daily infections for Scotland is estimated as being between 89 and 262, per 100,000 people.
- The growth rate for Scotland is estimated as being between 0% and 6%.
- A higher proportion of those thought to have the new variant[1] are in the two least deprived groups and are aged 20-24.
- The risk of being admitted to hospital with the new variant appears the same as for non-new variant cases. Individuals with a weak positive result are at a lower risk of being admitted to hospital.

[1] Based on S gene dropout, which is a proxy for the new variant.

- Modelled rates per 100K indicate that by the week of 24 - 30 January 2021, 30 (up 2 from last week) local authorities have at least a 75% probability of exceeding 50 cases, 29 (up 1) of those have at least a 75% probability of exceeding 100 cases, 22 (up 1) of those have at least a 75% probability of exceeding 300 cases and 13 (down 2) have at least a 75% probability of exceeding 500 cases. This is similar to the position last week. The probability of exceeding will be effected by the lockdown as well as by how much new variant is present in a local authority area. This adds to the uncertainty around this modelling this week.

Overview of Scottish Government Modelling

Epidemiology is the study of how diseases spread within populations. One way we do this is using our best understanding of the way the infection is passed on and how it affects people who catch it to create mathematical simulations. Because people who catch Covid-19 have a relatively long period in which they can pass it on to others before they begin to have symptoms, and the majority of people infected with the virus will experience mild symptoms, this “epidemiological modelling” provides insights into the epidemic that cannot easily be measured through testing e.g. of those with symptoms, as it estimates the total number of new daily infections and infectious people, including those who are asymptomatic or have mild symptoms.

Modelling also allows us to make short-term forecasts of what may happen with a degree of uncertainty. These can be used in health care and other planning. The modelling in this research findings is undertaken using different types of data which going forward aims to both model the progress of the epidemic in Scotland and provide early indications of where any changes are taking place.

Modelling outputs are provided here on the current epidemic in Scotland as a whole, based on a range of methods. Because it takes a little over three weeks on average for a person who catches Covid-19 to show symptoms, become sick, and either die or recover, there is a time lag in what our model can tell us about any re-emergence of the epidemic and where in Scotland this might occur. However modelling of Covid deaths is an important measure of where Scotland lies in its epidemic as a whole. In addition, the modelling groups which feed into the SAGE consensus use a range of other data along with deaths in their estimates of R and the growth rate. These outputs are provided in this research

findings. The type of data used in each model to estimate R is highlighted in Figure 1.

A short term forecast and projection of the number of cases, ICU and hospital bed demand is also provided at this stage of the epidemic in Scotland.

It should be noted that this research findings covers a period of uncertainty with the growth of the new variant in Scotland (SARS-CoV-2 VUI 202012/01). The percentage of cases composed of this new variant is increasing in Scotland, from 49.7% in the 24 hour reporting period from 3 to 4 January to 62% from 10 to 11 January 2021[2]. It is very likely that this strain will further increase in dominance in Scotland.

Although these research findings include the initial effects of the stay-at-home lockdown in Scotland announced on 4 January, changes associated with the restrictions will not be seen fully for another two weeks.

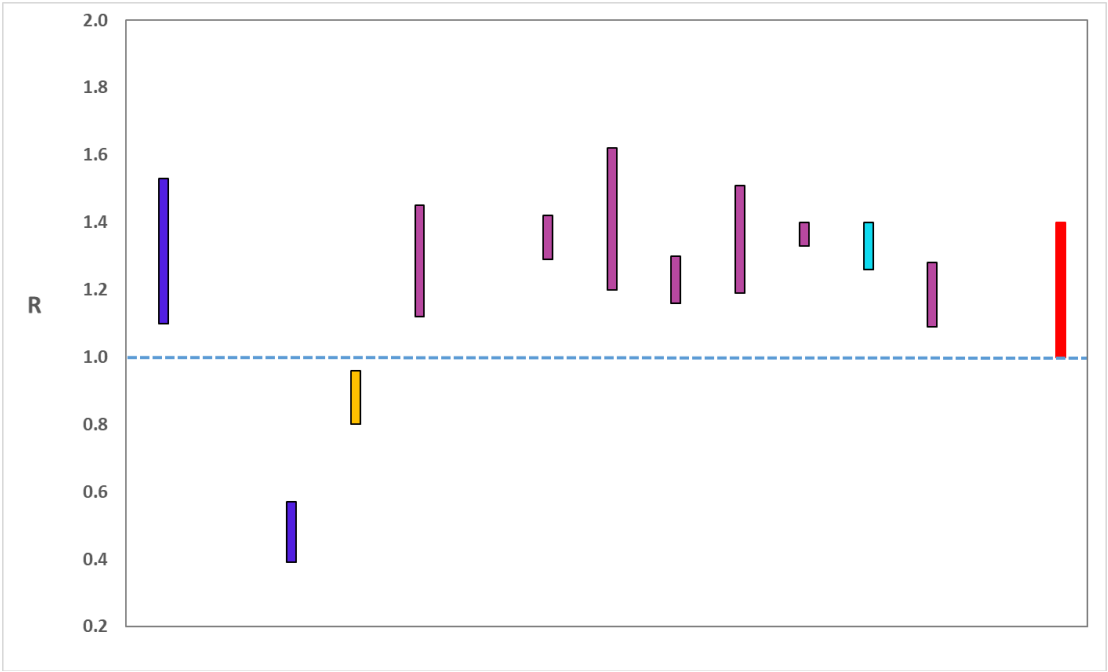
Analysis of risk of hospitalisation for those who have the new variant (testing positive with S gene deletion, which is a proxy for the new variant) has been included.

What the modelling tells us about the epidemic as a whole

The various groups which report to the Scientific Pandemic Influenza Group on Modelling (SPI-M) use different sources of data in their models (i.e. deaths, hospital admissions, cases) so their estimates of R are also based on these different methods. SAGE's consensus view across these methods, as of 13 January, was that the value of R in Scotland was between 1.0 and 1.4 (see Figure 1). The value of R on 6 January was between 0.9 and 1.3.

[2] https://beta.isdscotland.org/find-publications-and-data/population-health/covid-19/covid-19-statistical-report/

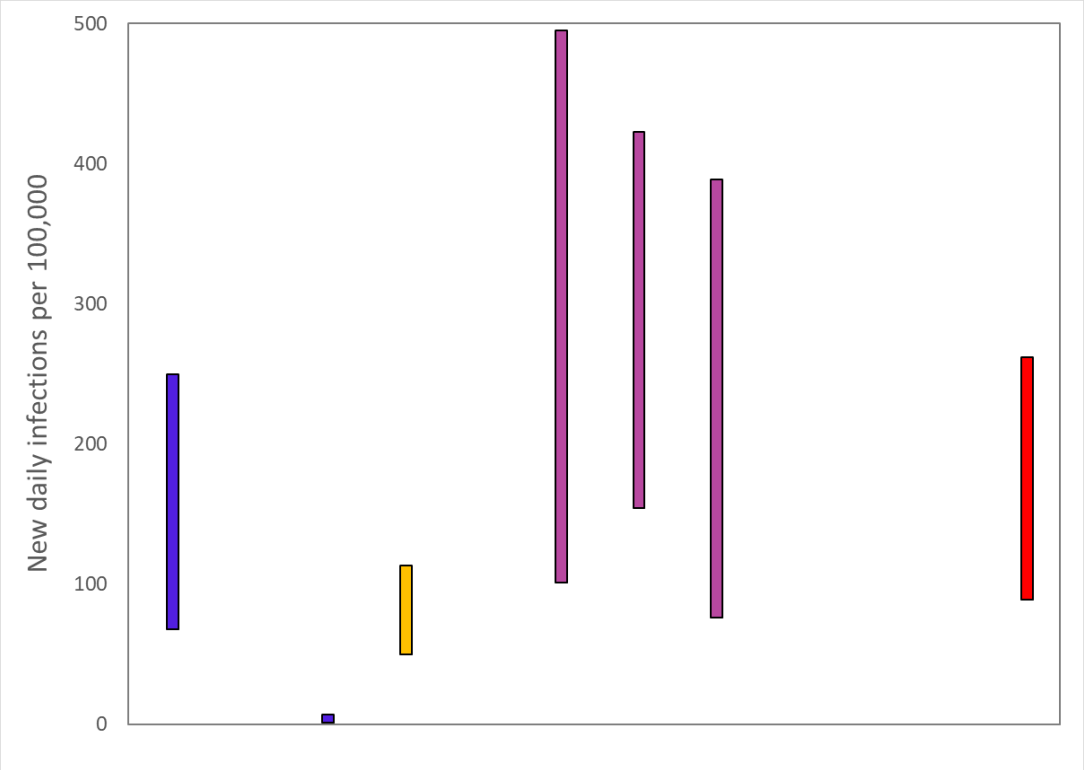
Figure 1. Estimates of R_t for Scotland, as of 13 January, including 90% confidence intervals, produced by SAGE. The blue bars are death-based models, purple use multiple sources of data and cyan use Covid-19 test results. The estimate produced by the Scottish Government (a semi-mechanistic model) is the 3rd from left (yellow), while the SAGE consensus range is the right-most (red). The estimate of R from the Scottish Government this week lies below the consensus.



Source: Scientific Advisory Group for Emergencies (SAGE).

The various groups which report to the Scientific Pandemic Influenza Group on Modelling (SPI-M) use different sources of data in their models to produce estimates of incidence (Figure 2). SPI-M's consensus view across these methods, as of 13 January, was that the incidence of new daily infections in Scotland was between 89 and 262 new infections per 100,000. This equates to between 4,900 and 14,300 people becoming infected each day in Scotland.

Figure 2. Estimates of incidence for Scotland, as of 13 January, including 90% confidence intervals, produced by SPI-M. The blue bars are death-based models and the purple bars represent models which use multiple sources of data. The estimate produced by the Scottish Government (a semi-mechanistic model) is the 3rd from left (yellow), while the SAGE consensus range is the right-most (red). The estimate of incidence from the Scottish Government this week is within the consensus.



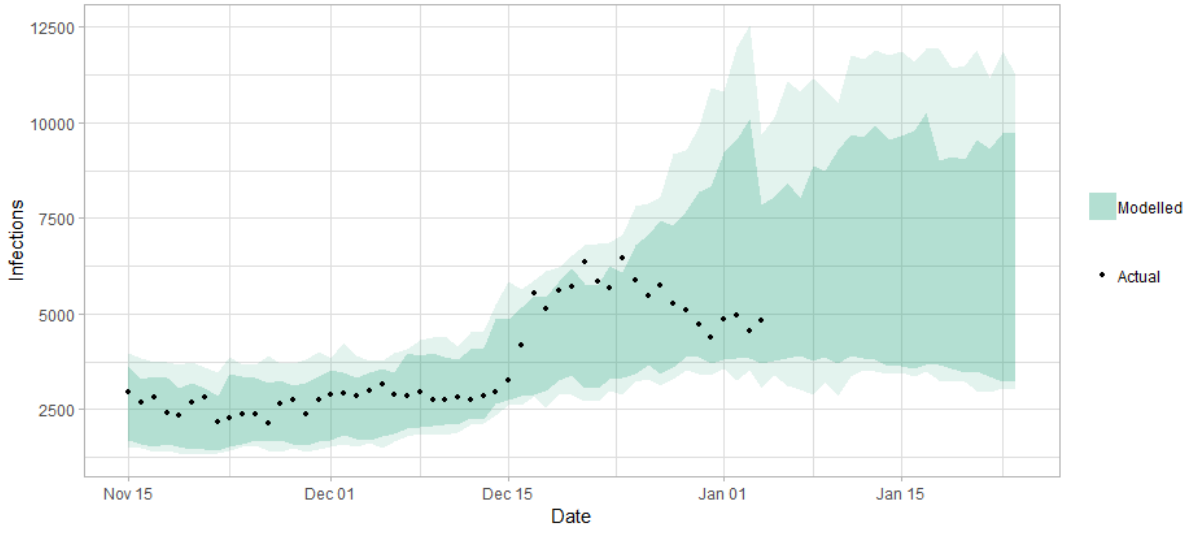
Source: Scientific Pandemic Influenza Group on Modelling (SPI-M).

The consensus from SAGE for this week is that the growth rate in Scotland is between 0 and 6% per day. On 6 January the growth rate was in the range -2% and 5%.

The logistical model developed by Scottish Government to assess implications for health care demand (see previous Research Findings) has been adapted to produce a short/medium-term prediction of infections.

Figure 3 shows a projection that assumes the R value is rising as the new more transmissible variant spreads.

Figure 3. Short term forecast of modelled total new infections, adjusting positive tests to account for asymptomatic and undetected infections, from Scottish Government modelling, positive test data up to 9 January.



What the modelling tells us about Hospital bed and ICU bed demand

Figure 4 shows the impact of the projection on the number of people in hospital.

Figure 4. Short term forecast of modelled hospital bed demand, from Scottish Government modelling.

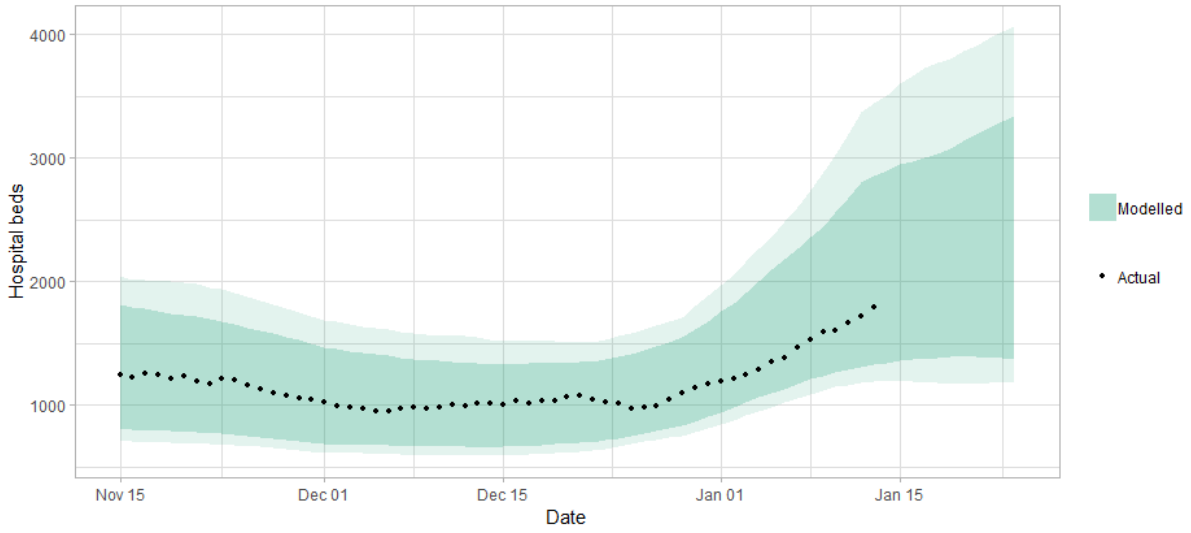
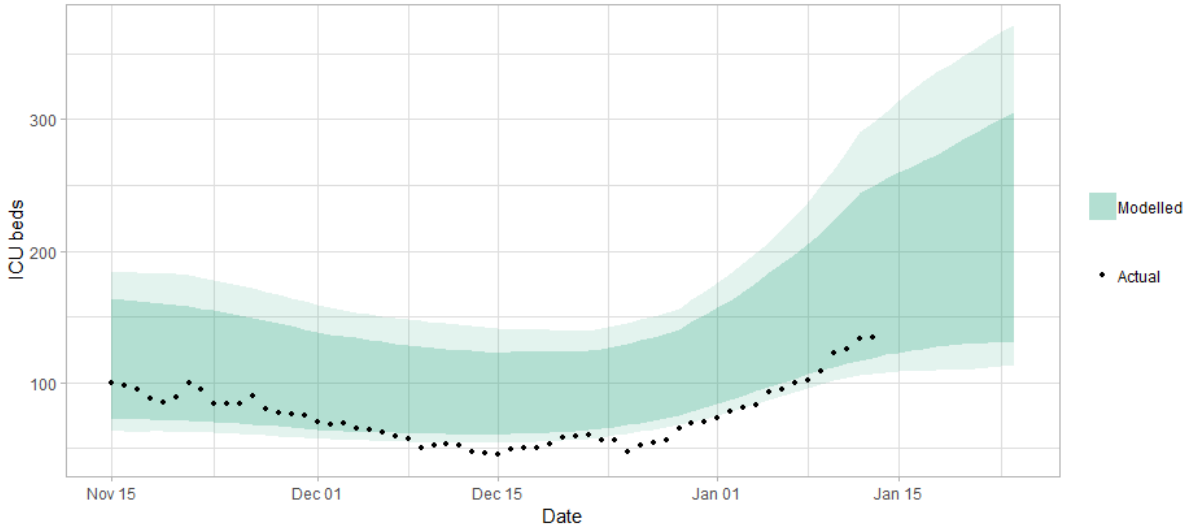


Figure 5 shows the impact of the projection on ICU bed demand.

Figure 5. Short term forecast of modelled ICU bed demand, from Scottish Government modelling[3].



What the modelling tells us about projections of hospitalisations in the medium term

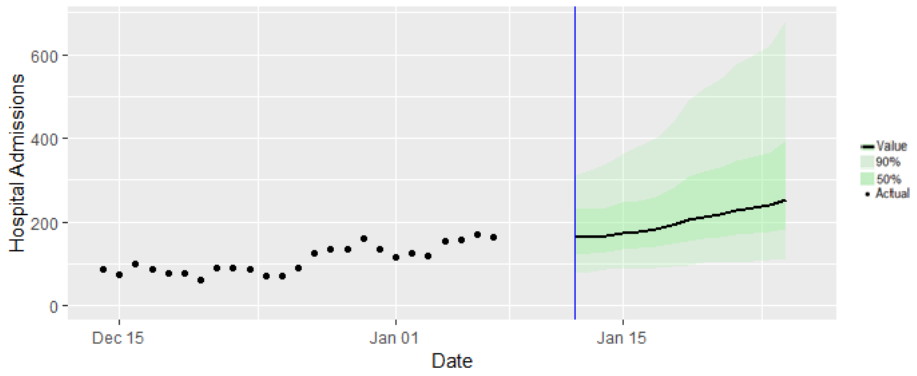
SAGE produce projections of the epidemic[4] (Figure 6), combining estimates from several independent models (including the Scottish Government Government's logistics modelling, as shown in figures 3, 4 and 5). These projections are not forecasts or predictions. **They represent a scenario in which the trajectory of the epidemic continues to follow the trends that were seen in the data up to 11 January and do not account for the impact of future policy or behaviour changes.** Nor do they include seasonal effects that might increase transmission.

The delay between infection, developing symptoms, hospitalisation and death means the projections cannot fully reflect changes in transmission that might have occurred over the past two to three weeks.

Beyond two weeks, the projections become more uncertain with greater variability between individual models. This reflects the large differences that can result from fitting models to different data streams, and the influence of small deviations in estimated growth rates and current incidence.

[3] Actual data does not include full numbers of CPAP or people staying longer than 28 days.
[4] A two week projection is provided here.

Figure 6. SAGE medium-term projection of daily hospitalisations in Scotland, including 50% and 90% credible intervals.



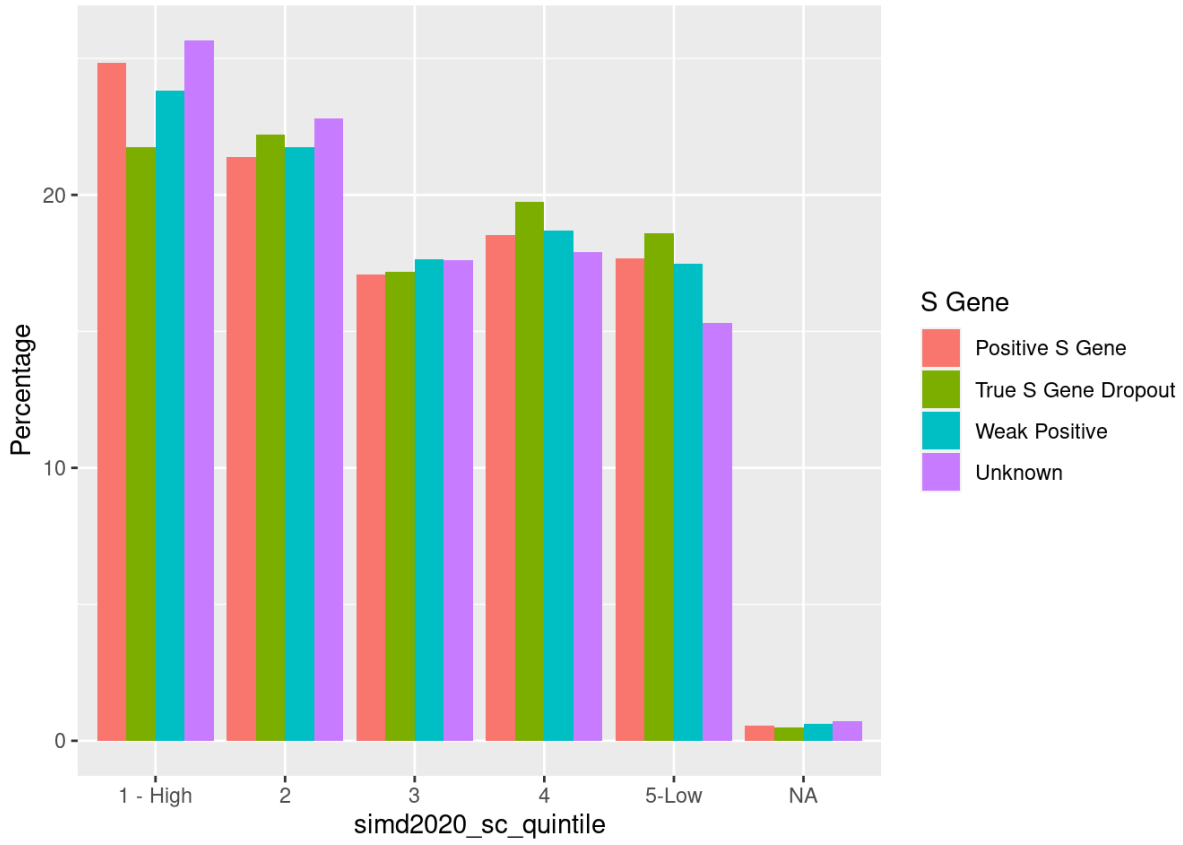
What we know about the risk of hospitalisation from the new variant

The Early Pandemic Evaluation and Enhanced Surveillance of COVID-19 (EAVE) 2 Study Group[5] linked individual patient-level data from all primary, secondary, mortality and virological/serological testing data in Scotland (see Technical Annex). They used this national dataset to investigate the temporal progression of COVID-19 in the Scottish population and the development of COVID-19 morbidity and mortality in individuals.

A higher proportion of those thought to have the new variant[6] are in the two least deprived groups (Figure 7). The age distributions are quite similar (Figure 8) but with a greater proportion of weak positive samples among children aged 0-19, a greater proportion of those thought to have the new variant are aged 20-24.

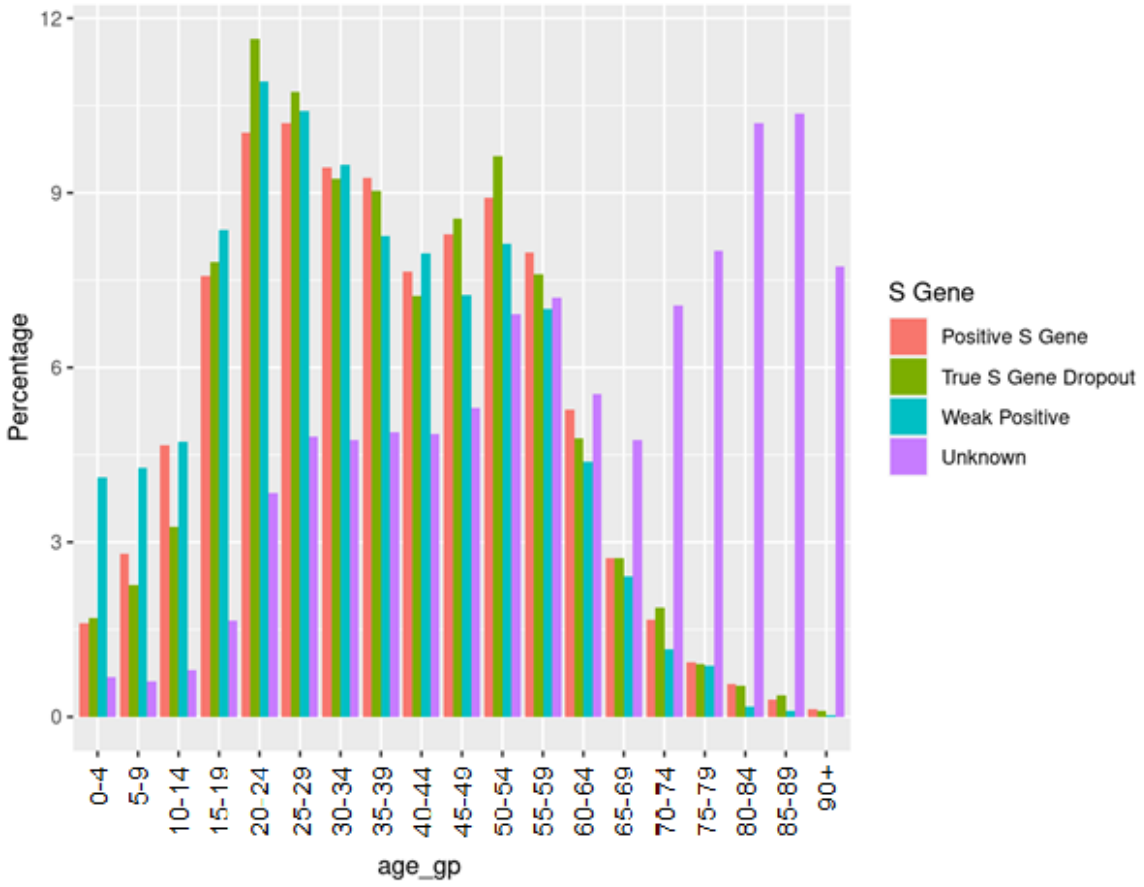
[5] Based at Edinburgh University, Strathclyde University Aberdeen University and Public Health Scotland.
[6] Based on S gene dropout, which is a proxy for the new variant.

Figure 7: The percentage of individuals who are thought to have tested positive with the new variant[7], by SIMD quintile (deprivation group).



[7] The analysis of the S gene drop out data uses Lighthouse samples only and the true drop out corresponds to negative on the S gene and Ct values < 30 for at least one of the OR and N genes. A weak positive is negative for S and Ct >= 30 for both OR and N genes; all other Lighthouse samples are labelled S gene positive. Unknown corresponds to individuals who are tested in the NHS labs attached to the hospitals and S Gene dropout status cannot be determined from these samples. The bar charts show the percentage of individuals within each S gene group who have the characteristic. For example the percentage of S gene positive who are in the lowest deprivation group, the percentage of true S gene dropout who are in the lowest deprivation group and the percentage of weak S gene positive who are in the lowest deprivation group. Differences in these percentages indicate subgroups where S gene deletion may be more (or less) common.

Figure 8: The percentage of individuals who are thought to have tested positive with the new variant[8], by age group.



Within the EAVE-II GP data there is information on the presence of 26 clinical risk groups - such as Asthma, Diabetes, Chronic Respiratory Disease and Dementia. They are summarised in a number of clinical risk groups coded as 0, 1, 2, 3-4 and 5+ as a summary measure of multi morbidity. There is not a large difference in the distribution of these risk groups between those with the new variant and non-new variant cases.

The risk of hospitalisation following a positive test result has been estimated and individuals with the new variant are not at increased risk of hospitalisation compared to those with the non-new variant. Individuals with a weak positive result are much less likely to be admitted to hospital. These are preliminary results and the analyses will be updated in the coming weeks.

[8] Based on S gene dropout, which is a proxy for the new variant.

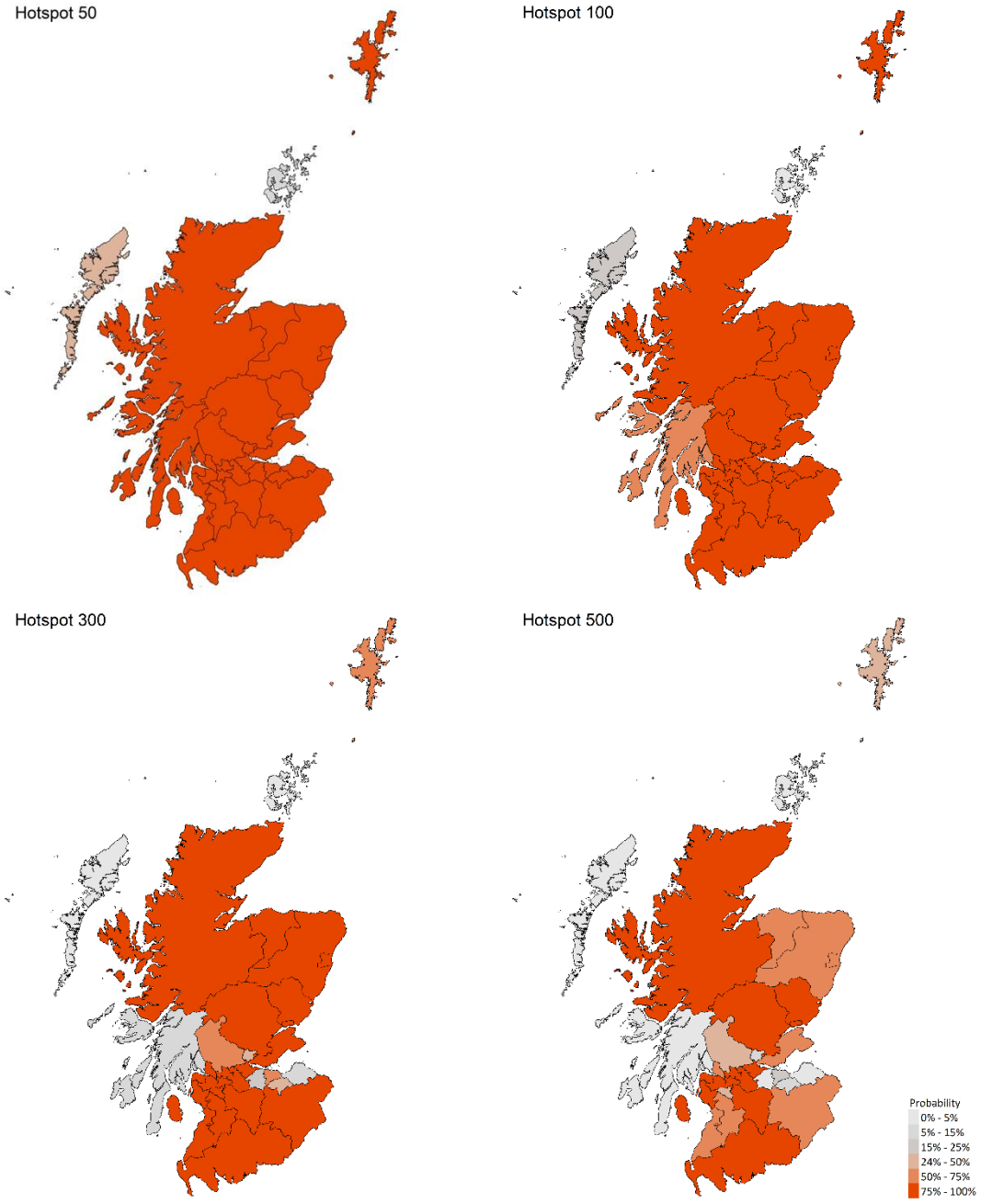
What we know about which local authorities are likely to experience high levels of Covid

We use modelling based on Covid cases and deaths[9], conducted by Imperial College London, to give us an indication of whether a local authority is likely to experience high levels of Covid in the future. An area is defined as a hotspot if the two week prediction of cases (positive tests) per 100K population are predicted to exceed a threshold, e.g. 500 cases. See technical annex in issue 24.

Modelled rates per 100K (Figure 9) indicate that by the week of 24 - 30 January 2021, 30 (up 2 from last week) local authorities have at least a 75% probability of exceeding 50 cases, 29 (up 1) of those have at least a 75% probability of exceeding 100 cases, 22 (up 1) of those have at least a 75% probability of exceeding 300 cases and 13 (down 2) have at least a 75% probability of exceeding 500 cases. The probability of exceeding will be affected by the lockdown as well as by how much new variant is present in a local authority area. This adds to the uncertainty around this modelling this week.

[9] https://www.medrxiv.org/content/10.1101/2020.11.24.20236661v1

Figure 9. Probability of local authority areas having more than 50, 100, 300 or 500 cases per 100K (24 - 30 January 21). Data updated on 12 January[10].



[10] 10.5281/zenodo.4246047

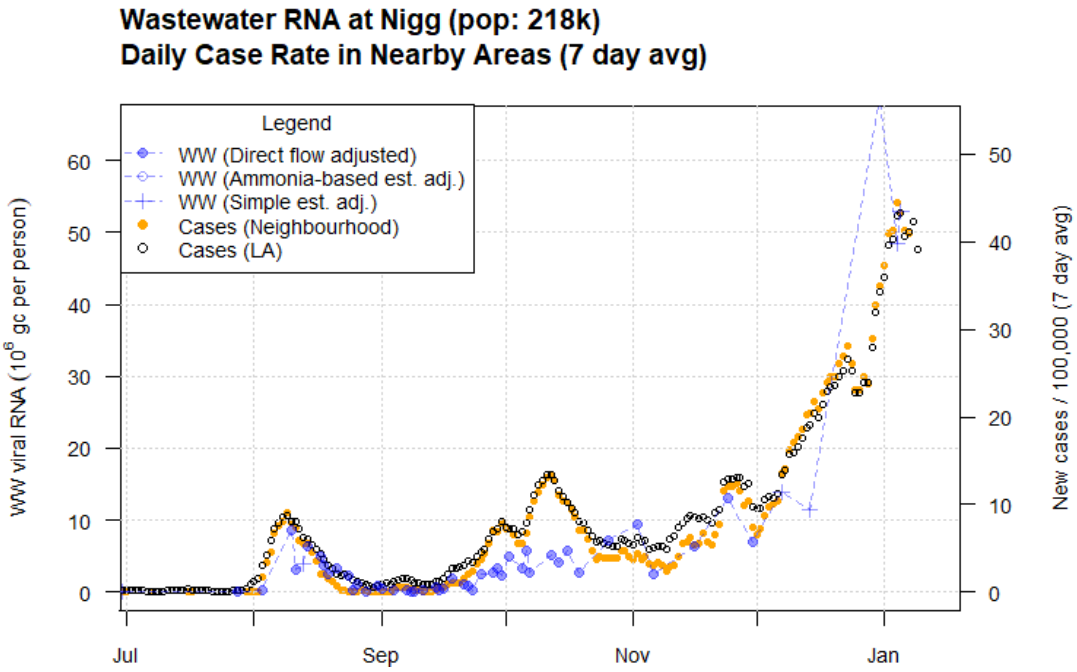
What can analysis of wastewater samples tell us about local outbreaks of Covid-19 infection?

Levels of Wastewater SARS-Cov-2 RNA collected at 28 sites around Scotland are adjusted for population and local changes in intake flow rate and compared to daily 7-day average positive case rates derived from Local Authority and Neighbourhood (Intermediate Zone) level aggregate data. See Technical Annex for the methodology.

Figures 10-12 show some of the larger wastewater catchments, covering Aberdeen, Glasgow and Edinburgh. For these sites, the case data based on neighbourhoods match closely to that based on local authorities. For some of the smaller catchments, the population covered represents a much smaller portion of the local authority. In these cases, there can be larger differences between the case data estimates at the two levels of aggregation.

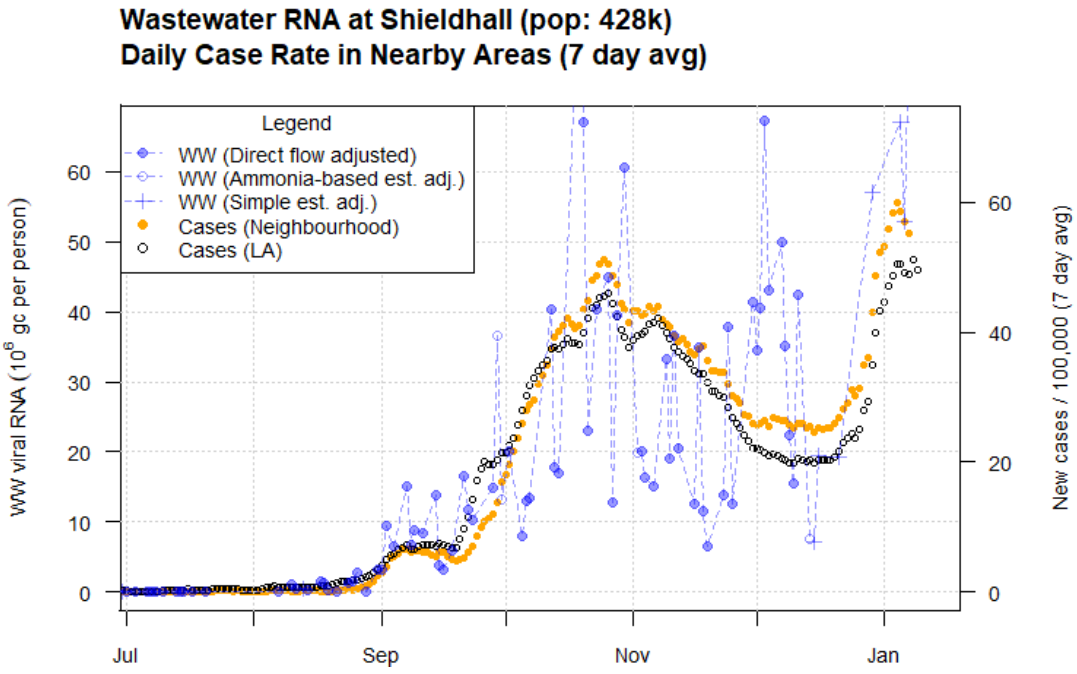
For all three major city WWTWs, the wastewater measurements pick up key changes in COVID-19 levels seen in the case data. In particular, the large increase through December to the latest data is clear. As noted earlier, a contributing factor to recent highs in WW RNA concentrations may be weather conditions – so some of these recent values may be adjusted downwards in future updates. Prior to that, Shieldhall (corresponding to Glasgow City) has the highest wastewater RNA levels, followed by Seafield (City of Edinburgh), with Nigg (Aberdeen City) the lowest of these three.

Figure 10. Graph for Nigg in Aberdeen City.



For Nigg (corresponding to Aberdeen) in Figure 10, a recent (estimated) peak of 69 Mgc/p on 31 December 31 falls outside of the limits of the graph. Overall, while the wastewater captures the recent case rate peak and that in August, the peak in October is less clearly shown.

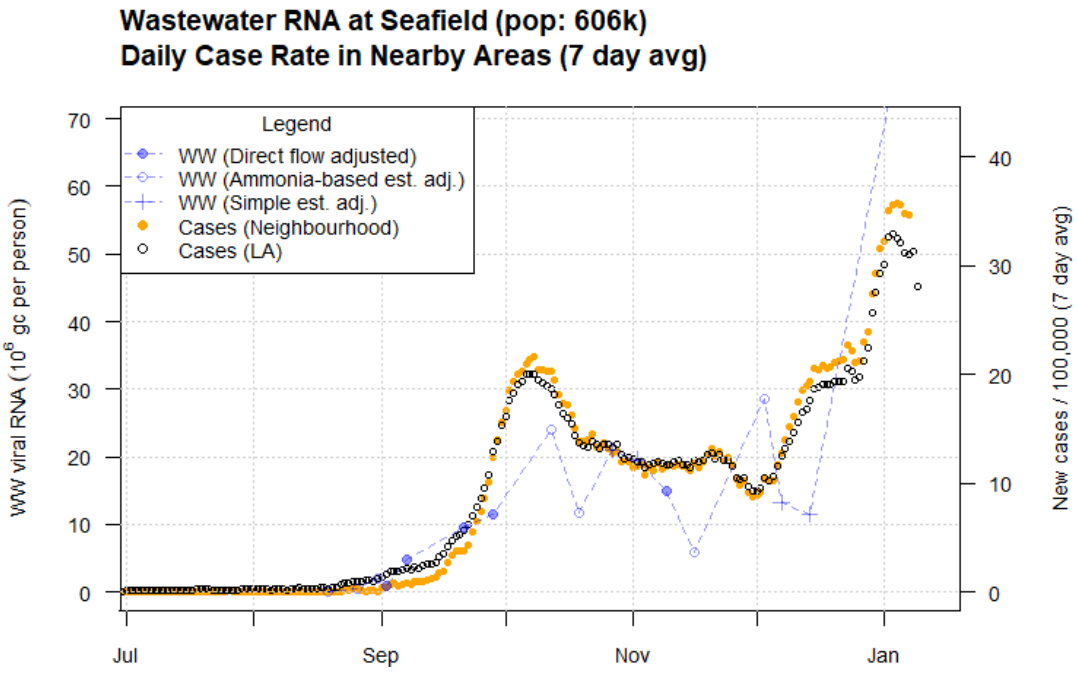
Figure 11. Graph for Shieldhall in Glasgow City.



The most recent measurement is a level of 81 Mgc/p on 7 January, lying outside of the limits of the graph.

Challenges with wastewater data are evident in Figure 11 for Shieldhall (in Glasgow). Here, whilst the measurements overall reflect the changes in COVID-19 levels seen in the case data, there is considerable variability present from day to day, even after normalisation. This noise can potentially hide the underlying signal. Over the coming weeks, methods will be developed to assist interpretation.

Figure 12. Graph for Seafield in City of Edinburgh.



Compared to Shieldhall, Seafield (Figure 12) has in prior months lower levels of both wastewater RNA and case numbers, but in the recent period both have climbed to similar levels, with the most recent wastewater reading at a level of 79 Mgc/p on 4 January.

What next?

The Scottish Government continues to work with a number of academic modelling groups to develop other estimates of the epidemic in Scotland.

The modelled estimates of the numbers of new cases and infectious people will continue to be provided as measures of the epidemic as a whole, along with measures of the current point in the epidemic such as R_t and the growth rate. Further information can be found at https://www.gov.scot/coronavirus-covid-19**.**

Investigations are ongoing by NERVTAG, SPI-M, SAGE and Scottish Government regarding the impact of the new variant, SARS-CoV-2 VUI 202012/01, which will be reflected here as work is undertaken.

In the coming weeks the impact of the lockdown will be reflected in the modelling.

Technical Annex

Table 1. Probability of local authority areas having more than 50, 100, 300 or 500 cases per 100K (24 – 30 January 21). Data updated on 12 January.

LA	P (Cases > 500)	P (Cases > 300)	P (Cases > 100)	P (Cases > 50)
Aberdeen City	50-75%	75-100%	75-100%	75-100%
Aberdeenshire	50-75%	75-100%	75-100%	75-100%
Angus	75-100%	75-100%	75-100%	75-100%
Argyll and Bute	0-5%	5-15%	50-75%	75-100%
City of Edinburgh	15-25%	50-75%	75-100%	75-100%
Clackmannanshire	5-15%	25-50%	75-100%	75-100%
Dumfries and Galloway	75-100%	75-100%	75-100%	75-100%
Dundee City	75-100%	75-100%	75-100%	75-100%
East Ayrshire	50-75%	75-100%	75-100%	75-100%
East Dunbartonshire	75-100%	75-100%	75-100%	75-100%
East Lothian	0-5%	5-15%	75-100%	75-100%
East Renfrewshire	25-50%	75-100%	75-100%	75-100%
Falkirk	75-100%	75-100%	75-100%	75-100%
Fife	50-75%	75-100%	75-100%	75-100%
Glasgow City	75-100%	75-100%	75-100%	75-100%
Highland	75-100%	75-100%	75-100%	75-100%
Inverclyde	75-100%	75-100%	75-100%	75-100%
Midlothian	5-15%	25-50%	75-100%	75-100%
Moray	50-75%	75-100%	75-100%	75-100%
Na h-Eileanan Siar	0-5%	0-5%	15-25%	25-50%
North Ayrshire	75-100%	75-100%	75-100%	75-100%
North Lanarkshire	75-100%	75-100%	75-100%	75-100%
Orkney Islands	0-5%	0-5%	0-5%	5-15%
Perth and Kinross	75-100%	75-100%	75-100%	75-100%
Renfrewshire	75-100%	75-100%	75-100%	75-100%
Scottish Borders	50-75%	75-100%	75-100%	75-100%
Shetland Islands	25-50%	50-75%	75-100%	75-100%
South Ayrshire	50-75%	75-100%	75-100%	75-100%
South Lanarkshire	75-100%	75-100%	75-100%	75-100%
Stirling	25-50%	50-75%	75-100%	75-100%
West Dunbartonshire	50-75%	75-100%	75-100%	75-100%
West Lothian	0-5%	15-25%	75-100%	75-100%

Wastewater Covid-19 report methodology

Samples from Waste Water Treatment Works (WWTW) in Scotland have been analysed by the Scottish Environment Protection Agency (SEPA)

to detect fragments of SARS-Cov-2 virus RNA in wastewater (see section ‘what can analysis of wastewater samples tell us about local outbreaks of Covid-19 infection’). This is reported from lab analysis as gene copies per litre. Raw measurements of this concentration of wastewater RNA are affected by both the size of the catchment area at each waterworks (and hence the population served), as well as the amount of flow into the works (with high volumes of fluid flow diluting RNA values).

Hence, values are normalised by three methods depending on data availability.

- Direct flow: when measurements of flow are available, the raw RNA measurement is multiplied by the daily flow total, and divided by the population served at each site, to produce a daily value of RNA copies per person.
- Ammonia-based estimate: In some cases (especially with the most recent data), flow measurements are unavailable; if however measurements of ammonia concentration are available, they can be used to estimate flow via a statistical model.
- Simple estimate: when both flow and ammonia measurements are unavailable, flow is estimated as the historical average for that site; when a site has no associated flow data at all, a prediction is calculated based on the population characteristics of the site. For all methods, the normalised figures are measured in daily value of RNA copies per person.

Case data are available aggregated at the Local Authority and Neighbourhood (IZ) spatial scales. Case data are associated with each wastewater sampling site by estimating the extent to which Local Authorities or Neighbourhoods (IZs) overlap with the catchment. To do this, census data from 2011 is used to quantify the population of each LA or Neighbourhood that live within each site’s catchment area. These population counts are then used to weigh case data to produce weighted averages for that site. The focus is on the daily case rate (i.e. the daily number of new cases, scaled to population), with the data presented as 7 day moving averages.

The scaling on the double-plotted graphs is automatically chosen at each site to best align the wastewater data to these local case trends. In consequence, especially high daily observations of waste water may exceed the limits of the plots.

EAVE 2 Study Group – clinical characteristics of S Gene dropout cases

The analysis of the S gene drop out data in the section 'what we know about the risk of hospitalisation from the new variant' is based on Lighthouse samples only and the true drop out corresponds to negative on the S gene and Ct[11] values < 30 for at least one of the OR and N genes. A weak positive is negative for S and Ct >= 30 for both OR and N genes; all other Lighthouse samples are labelled S gene positive. Unknown corresponds to individuals who are tested in the NHS labs attached to the hospitals. Those tested in hospital represent a different population from those tested in the Lighthouse laboratory and many of these individuals tested in hospitals are admitted directly to hospital.

Counts of the individuals testing positive are presented from November 16, 2020. The analysis was carried out using all data report to Public Health Scotland by 5 January, 2021.

The testing data are linked to the EAVE study data of GP clinical conditions for a clinical and demographic description of the individuals testing positive with the S gene deletion in comparison to those who do not have this deletion. The laboratory data and GP data are then linked to hospital admissions and deaths.

A hospital admission is defined as an admission to hospital within 14 days of testing positive for Covid 19. Individuals who tested positive within two days following the hospital admission are also counted. The time from test to hospital admission is the number of days from the date of the sample to the date of admission with individuals who tested positive on the two days following admission defined as having a time from test to admission of zero days. Hospital acquired Covid infections are not included in this analysis. Hospital admission data is largely complete up to the 29 December 2020.

[11] Cycle Threshold

This publication will be available in accessible HTML on the gov.scot website

The views expressed in this report are those of the researcher and do not necessarily represent those of the Scottish Government or Scottish Ministers.

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