Glossary

Acronyms and abbreviations

Abbreviation	Meaning
CGI	COVID-19 Genomics Insights
ESR	Environmental Science and Research
GISAID	Global Initiative on Sharing Avian Influenza Data
IP	Inpatient Admission
NCTS	National Contact Tracing Service
NMDS	National Minimum Dataset
PCR	Polymerase Chain Reaction
WGS	Whole Genome Sequencing

Acknowledgements and Data Sources

Community Cases

Data on community cases are sourced from a combination of the National Contact Tracing Service (NCTS) and EpiSurv (New Zealand's public health surveillance platform).

Whole Genome Sequencing (WGS)

All information on WGS is sourced from the ESR COVID-19 Genomics Insights (CGI) Report, a weekly overview of SARS-CoV-2 genomic surveillance across the country.

Modelling

The baseline model has been updated to include a fit to more recent data, especially to capture the impact of changes to public health measures on 12th September 2022 and the impact of new variants. The baseline model uses 22nd November 2022 as the transition date where the previous variant BA.5, loses its dominance in the variant profile in the community. It is replaced by a new VoC with an increased ability to evade immunity from both vaccination and prior infection. The increase in immunity evasion is assumed to be similar to in magnitude to what was observed in June and July 2022 with the change in variant from BA.1/BA.2 to BA.4/BA.5.

Modelling uses many assumptions that are important to keep in mind:

- **The model assumes no new variants occurring in the future.** Beyond November, simulations do not account for new variants of concern or their potential impact on cases, hospitalisations and deaths.
- **Peaks and troughs assumptions.** Because this is a single national model, it may not capture the different size, shape and timing of peaks at a district or regional level. Therefore, the model may overestimate peaks and underestimate troughs, if outbreaks in different population groups are not aligned.
- **Uncertainty around modelled estimates.** The provides credible intervals around estimates of cases, hospitalisations and deaths. This range reflects unknowns such as the share of infections detected and the speed of waning immunity. The model is fit to data up to 15th November 2022, which reduces some of this uncertainty.
- **4th Booster and antivirals**. The model assumes no fourth dose rollout to those aged under 50. And does not include the impact of antivirals on hospitalisation and mortality rates.

Wastewater quantification

Wastewater quantitation is a measure of the levels of virus circulating in the community. Because infectious individuals tend to shed vastly more viral particles than non-infectious individuals (particularly later on in the infection), the wastewater quantitation results are driven largely by infectious individuals, in the first 5-6 days of their infection. Although people can shed detectable virus for some weeks that can be detected by PCR testing, these individuals are unlikely to have a large impact on the quantitation curves.

Wastewater is analysed by ESR's Kenepuru and Christchurch Laboratories.

Data limitations

Prevalence estimates based on routinely tested populations

- The groups of routine testers that have been identified (healthcare, border and emergency workers, and hospital inpatients) are not a representative sample of New Zealanders, overall, they are higher risk of COVID-19 infection than the general population.
- The identification of these groups at a national level is based on surveillance codes, which may not be completed accurately, particularly since the introduction of RAT testing.
- The national estimate is for people who have uploaded at least one test result in the week, so will be an over-estimate if negative test results are not being recorded for these groups.
- National level estimates will be masking differing trends by region.
- Tertiary hospital inpatient data, while likely to be more accurate than the national level data, still reflect a higher-risk group, and neither the estimates nor the trends are generalisable to the rest of the population.
- The identification of these groups is based on surveillance codes, which may not be completed accurately, particularly since the introduction of RAT testing.
- The population has been identified based on ever having a surveillance code related to the respective workforce and having at least 2 tests (at least one of which was negative) in 2022. A sensitivity check was run using at least 3 tests and while these numbers reduced, the incidence estimates remained very similar.

Wastewater quantification

- Approximately 1 million people in New Zealand are not connected to reticulated wastewater systems.
- Samples may be either grab or 24-hour composite samples. Greater variability is expected with grab samples.
- While a standard method is being used, virus recovery can vary from sample to sample.
- SARS-CoV-2 RNA concentrations should not be compared between wastewater catchments.
- Day-to-day variability in SARS-CoV-2 RNA concentrations especially in smaller catchment is to be expected.
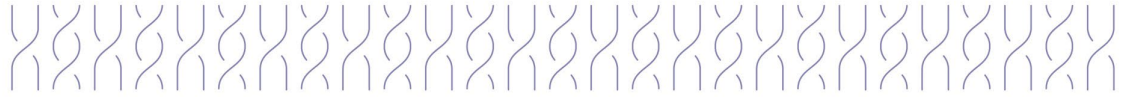
Hospital admissions data

- The Ministry will begin reporting COVID-19 hospitalisations using two datasets: the inpatient admission (IP) dataset – that only includes data from hospitals in certain regions – and the National Minimum Dataset (NMDS). Both of these datasets are patient-level, so they allow demographic and vaccination breakdowns to be calculated.

- Of the two databases, the IP is the more up-to-date data source for admissions. The data provided include a preliminary assessment of hospitalisations where COVID-19 may potentially play a role in the hospitalisation, based on the health specialty associated with the hospitalisation. The IP dataset does not have national coverage; it only covers hospitals in Auckland, Canterbury, Southern, Counties Manukau, Waikato, Capital and Coast, Waitematā and Northland. The IP dataset can be incomplete and provisional; it is subject to revision as the more comprehensive and more accurate NMDS data become available. One caveat is that the IP dataset does not have a reliable discharge date field. As such, it should only be used to report on admissions, not occupancy.

- The NMDS has several advantages: It provides national coverage and is a rich source of data, including data on demographics and an evaluation of the disease conditions associated with the hospital stay (including whether the admission was incidental, i.e., not related to COVID-19). However, the NMDS is only available after a significant data lag. The time lag for hospitalisation data can vary but can be approximately 60 days or more.

- Therefore, we are using a combination of these two databases for hospitalisation: the IP records are included as a provisional tally of more recent COVID-19 hospitalisations for a collection of hospitals, and then these records are overwritten by NMDS records, as soon as the NMDS records are available

- Note that the definition used for 'hospitalisation for COVID-19' in both the IP and NMDS tends to be inclusive. For the IP provisional data, the health specialty associated with the hospitalisation is used to estimate whether the hospital stay might be related COVID-19; hospitalisations that are highly unlikely to be related to COVID-19 are ruled out, as opposed to identifying hospitalisations that are likely to be COVID-related. As NMDS data become available, the clinical codes that retrospectively evaluate the reasons for the hospital stay are used to estimate if the stay was potentially related to COVID-19. The NMDS data are more robust estimation of hospitalisations 'for' COVID-19.

- This new method of data collection for COVID-19 has several advantages over the previous method, as it provides more robust data in a timely manner, using an automated method that is less burdensome and more reliable, and provides access to more detailed data. Most importantly, the new data method provides a timely and reliable way to estimate the number of hospitalisations where COVID-19 could be the reason for the hospital stay (admissions 'for' COVID-19, with some caveats). Moving forward, the majority of the reporting on hospitalisation will use the 'for COVID' definition as described above from the new databases.Nonetheless, we are also still able to estimate the number of hospitalisations 'with' COVID-19, i.e., an estimate of the number of hospitalisations that are associated with a positive test within 28 days of admission. Hence, in conjunction with the new hospitalisation data, we can also estimate the proportion of the total COVID-19 hospitalisations that are 'for' versus 'with'. Previous analysis has shown that the proportion of the total COVID-19 hospitalisations that are 'for' COVID-19 is about 68%.

- In addition, the new system also allows us to estimate the rate of COVID-19 hospital admissions per case or per capita.
- However, the new data feed cannot be used to estimate the proportion of all hospitalisations nationally that are associated with COVID-19. This is because we do not know the total number of patients that currently are in hospital in New Zealand for any reason at any given time (this information exists in NMDS, but only with a lag of a couple of months). Without this denominator data, we cannot calculate the proportion of all hospitalisations are associated with COVID-19.

Mortality data

Mortality data is lagged as to account for death coding delays and recent trends should be interpreted with caution.

Trends by ethnicity & deprivation

Up until 09 December, data has been standardised to Māori population age structure. From the report released 16 December, we'll now be adjusting data to the WHO international standard for age standardisation (WHO 2000-2025).[12]

[1] **https://seer.cancer.gov/stdpopulations/world.who.html**

[2] **https://cdn.who.int/media/docs/default-source/gho-documents/global-health-estimates/gpe_discussion_paper_series_paper31_2001_age_standardization_rates.pdf**