

Weekly Report: Nowcasts and forecasts for measles in South Africa, 2023 (Week 25)

For Public Release

SACEMA's Modelling and Analytics Response Team

2023-06-30

Overview

This report provides transmission estimates, nowcasts, and short-term forecasts for measles cases, in order to improve situational awareness and inform resource planning. The report is intended for use by national and provincial departments of health, the National Institute for Communicable Diseases (NICD), and district-level managers. Current and previous versions of this report are available at <https://www.sacema.org/sacema-nicd-measles-forecast>.

This report is based on line list data with sample collection dates through 2023-06-14 reported to NICD as of 2023-06-20. The data are provided by NICD for the purpose of these analyses and are the same data used in the NICD Situation Report dated 2023-06-23 (<https://www.nicd.ac.za/south-african-measles-outbreak-update-2023-23-june-2023>).

The time-varying reproduction number is a metric that indicates whether infections are increasing ($R > 1$), decreasing ($R < 1$), or stable ($R = 1$).

Important note: Due to the decline in the measles epidemic, for which cases are now largely restricted to a single district, this will be the final Weekly Report on Nowcasts and forecasts for measles in South Africa, 2023. We may restart the report in future if the epidemic situation changes.

Highlights

- Given the small number of districts reporting cases in the most recent data, we are no longer presenting national and provincial level reproduction number estimates. Twelve of the eighteen cases since the last report were reported from one district in Limpopo.
- At the district level, the reproduction number as of 2023-06-14 was estimated to be 1.1 (0.69 – 1.4) in Waterberg, suggesting that infection incidence may be increasing, and 1 (0.6 – 1.6) in Greater Sekhukhune, suggesting that infection incidence is stable; however, the small number of cases overall leads to substantial uncertainty in these estimates. Greater Sekhukhune has reported only one case since the last report.

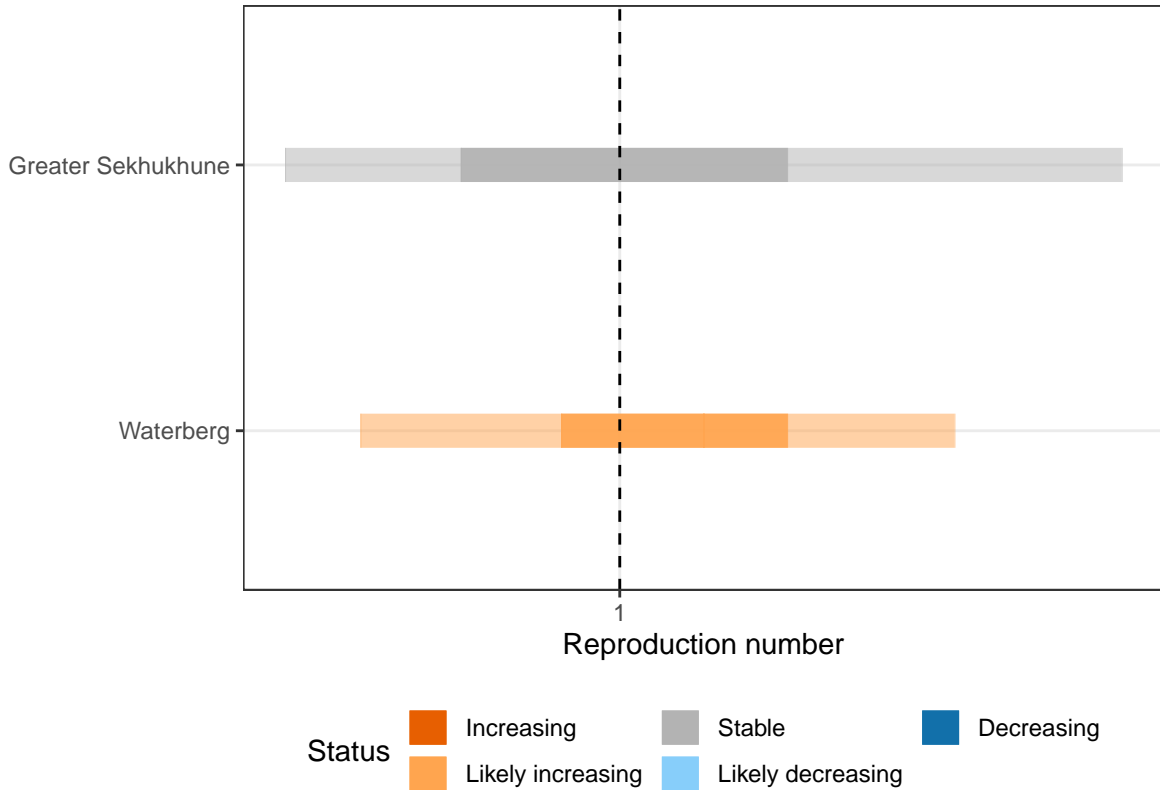
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Reproduction number

Latest estimates

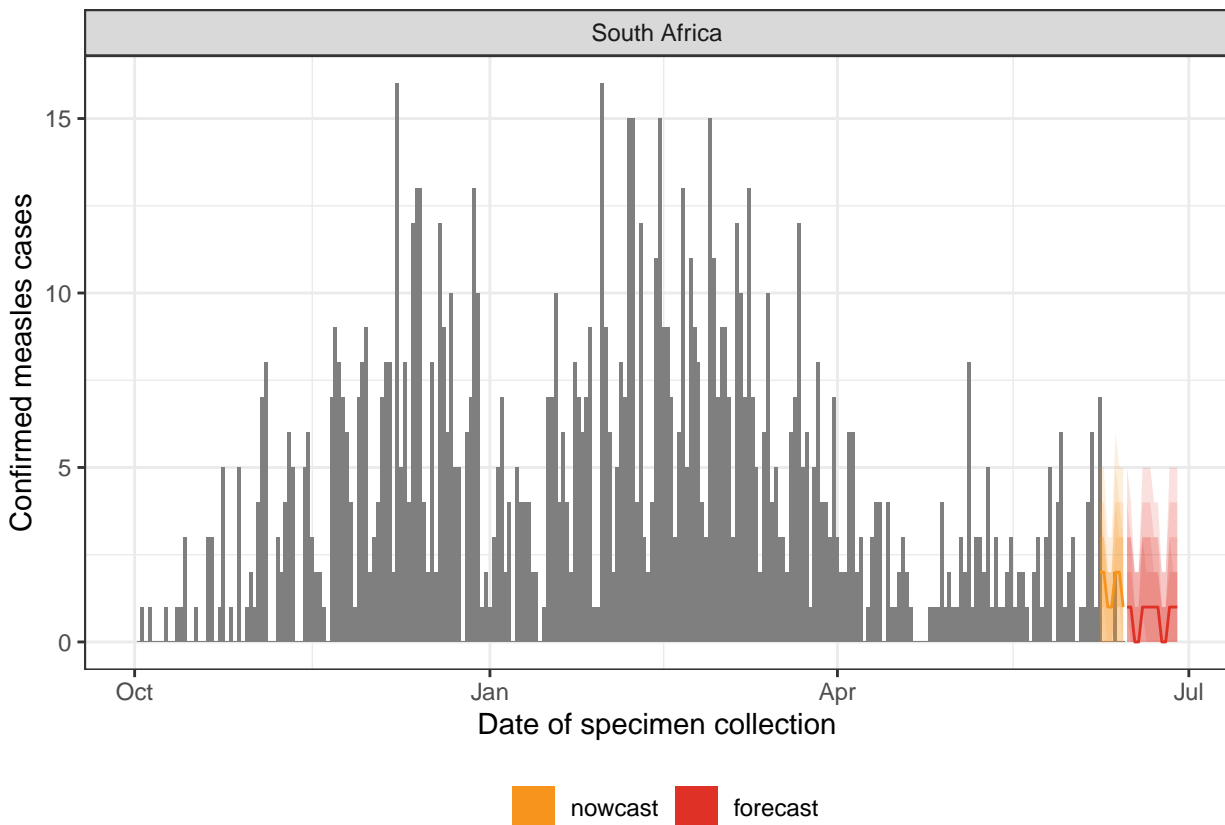
The figure below shows the latest reproduction number estimates, for districts with a minimum of 40 detected cases since week 40 of 2022 and at least 7 days with cases in the past 60 days.

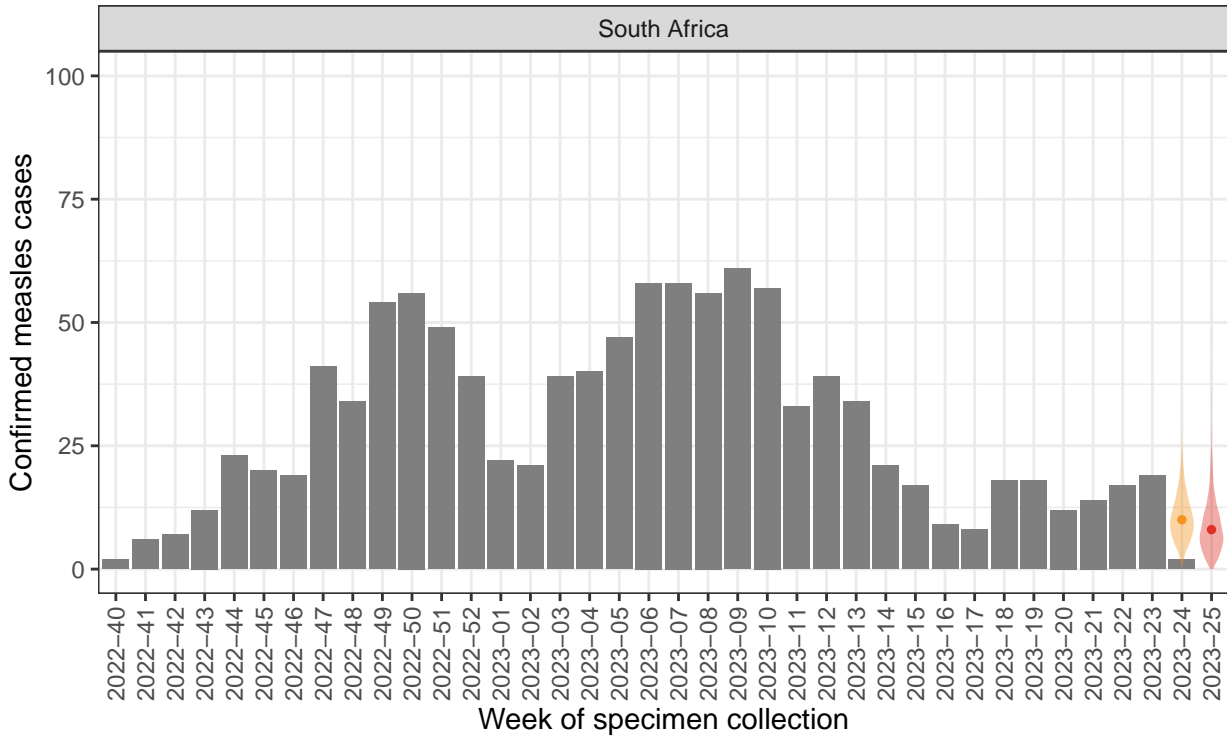


Nowcasts and Forecasts

The following plots present nowcasts and forecasts for each region that has a minimum of 40 detected cases since week 40 of 2022 and at least two days with cases in the past 60 days. Nowcasts are estimates of the number of cases that will be detected in a time period for which reporting may be incomplete, accounting for reporting delays. Forecasts are projections of the epidemic trajectory that take into account uncertainty in the reproduction number and relevant delays. See the Methods section for additional details.

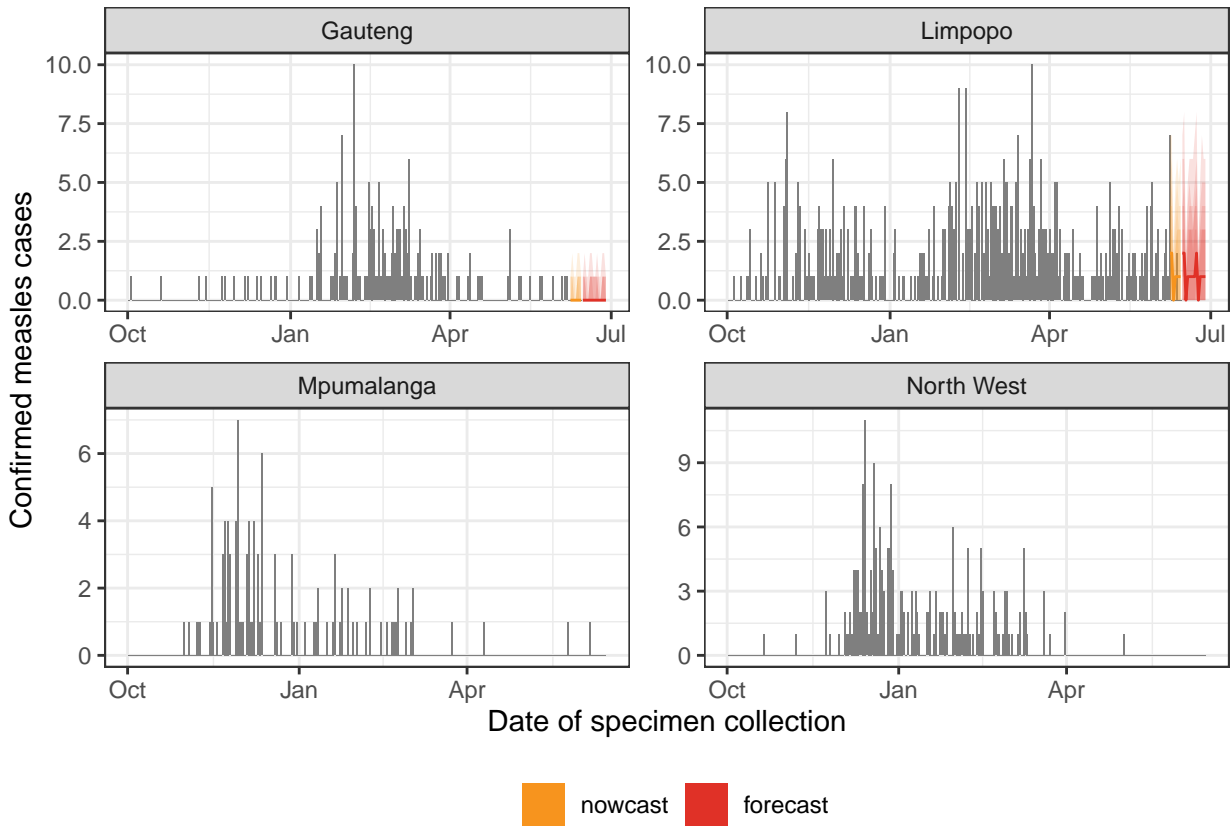
National level

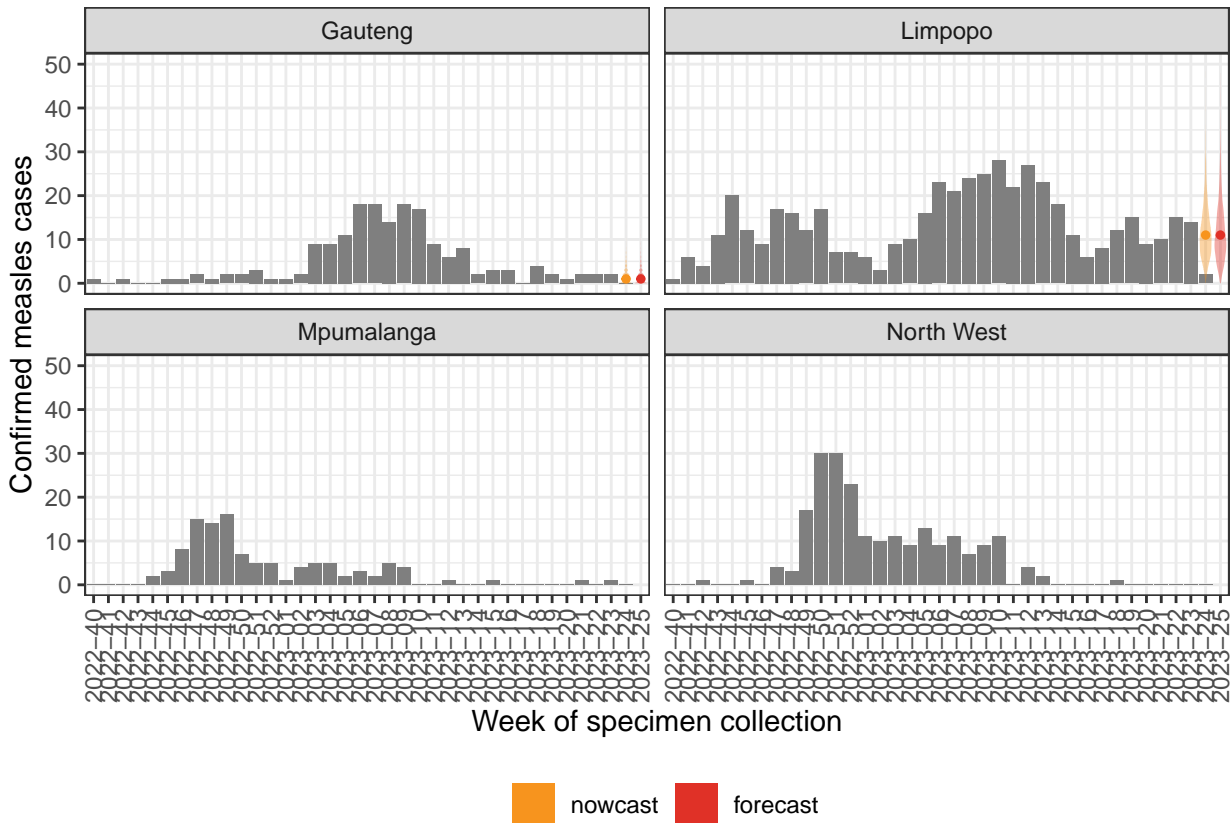




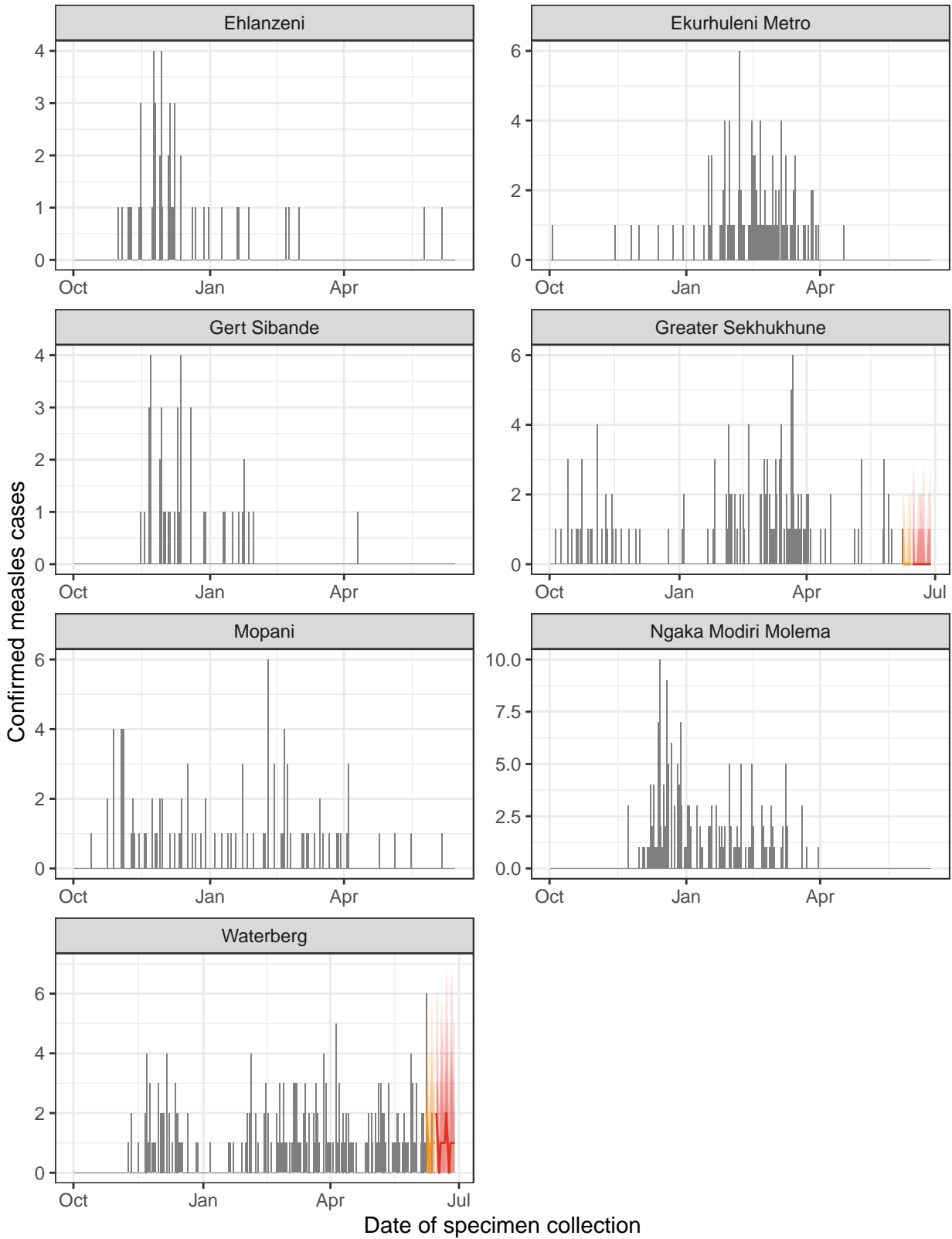
■ nowcast
 ■ forecast

Province level

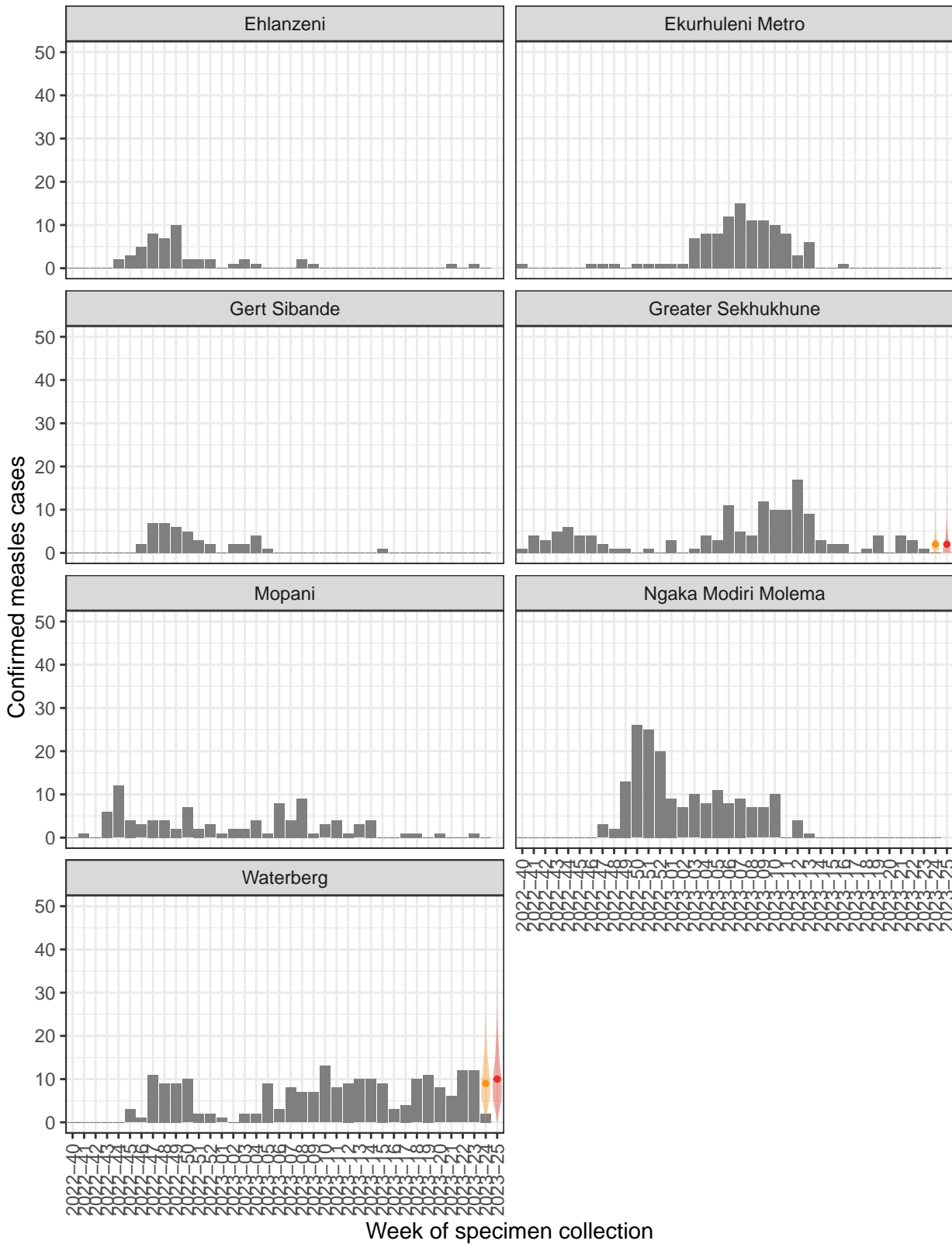




District level



 nowcast  forecast



■ nowcast
 ■ forecast

Methods

Data source

This report is based on line list data with sample collection dates through 2023-06-14 reported to NICD as of 2023-06-20. The sample collection date of the most recent case included in this analysis was 2023-06-12.

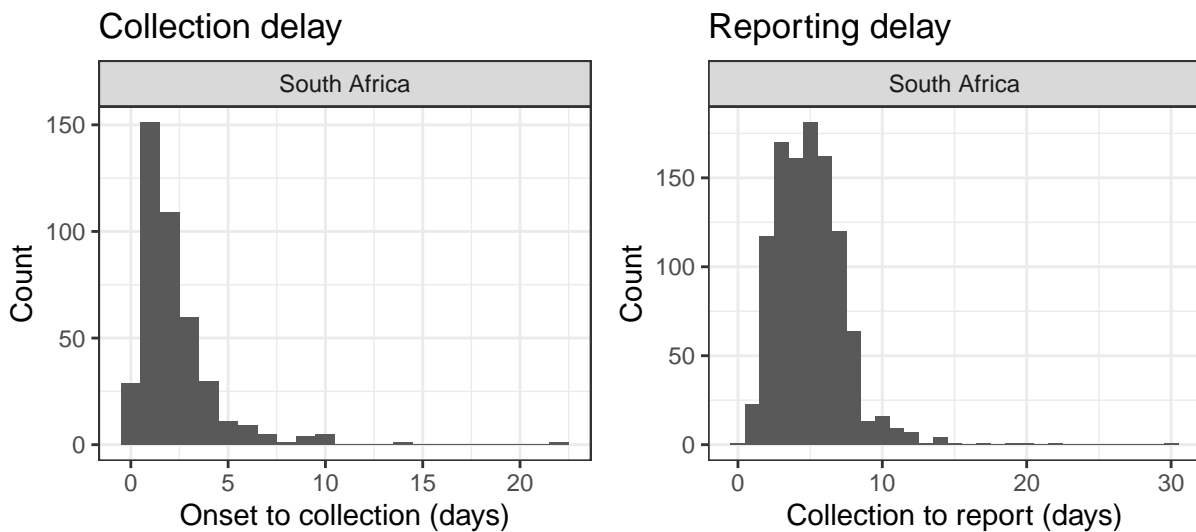
Estimation procedure

Case forecasts are simulated using the `EpiNow2` package in the R statistical programming language, as described in Abbott *et al.* (2020). Briefly, the method estimates an instantaneous time-varying reproduction number (R_t) based on the reported case time series, a specified generation interval distribution, and specified reporting delays and then simulates infection trajectories based on 4,000 draws from the posterior distribution of R_t . Simulated case trajectories are then generated based on these infection trajectories and the specified delay distributions.

Each simulated case trajectory can be analyzed in the same manner as actual reported case data. This allows us to, for example, examine weekly aggregates of simulated cases.

Delay distributions

The nowcasts and forecasts presented here are produced using generation interval and incubation period distributions estimated by Klinkenberg *et al.* (2011). The delays from onset to specimen collection and from specimen collection to report are estimated directly from line list data using the `bootstrapped_dist_fit` function in `EpiNow2`. The delay distributions are estimated at the national level and used for nowcasts and forecasts at all scales.



Limitations

The main limitation of the approach used is that case forecasts can substantially overshoot when close to the epidemic peak.

A further limitation is that the reporting date used for the estimation of the delay from specimen collection to report is the date on which the district was notified of the lab result, which may occur substantially before the case is added to the national line list. As a result of this limitation, reproduction number estimates, nowcasts, and forecasts may all be biased downward. This approach is taken because the date a case is added to the line list is not currently recorded.

Finally, because the methods employed depend on the numbers of reported cases, changes in reporting (e.g., as may occur over holiday periods) have the potential to bias estimates and the resulting nowcasts and forecasts. Typically, these biases appear as an artificial drop in the reproduction number estimates approximately one generation interval prior to the holiday period, followed by an artificial increase in the estimates as reporting returns to baseline levels.

References

- Abbott *et al.* (2020) Estimating the time-varying reproduction number of SARS-CoV-2 using national and subnational case counts [version 2]. *Wellcome Open Research* 5: 112. <https://doi.org/10.12688/wellcomeopenres.16006.2>
- Klinkenberg and Nishiura. (2011) The correlation between infectivity and incubation period of measles, estimated from households with two cases. *Journal of Theoretical Biology* 248(1): 52-60. <https://www.sciencedirect.com/science/article/pii/S0022519311003146>

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About SACEMA

The South African Centre for Epidemiological Modelling and Analysis (SACEMA, www.sacema.org) is a national DSI-NRF Centre of Excellence founded in 2006 and hosted at Stellenbosch University. SACEMA aims to improve health in South Africa, and across the continent, through modelling and analysis.

About SMART

SACEMA's Modelling and Analytics Response Team (SMART) provides training in outbreak response analytics and tackles real-world outbreak response projects as they arise. Current SMART members include: Jeremy Bingham (convener), Lauren Brown, Zinhle Mthombothi, Prof Juliet Pulliam, Tumelo Sereo, and Dr Cari van Schalkwyk.

Contact

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