Using digital disease surveillance tools for near real-time epidemic forecasting

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Project Partners

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Published Date: 2014-03-22 23:02:06
Subject: PRO/AH/EDR> Ebola virus disease - West Africa: Guinea, Zaire ebolavirus suspected
Archive Number: 20140322.2349865

EBOLA VIRUS DISEASE - WEST AFRICA: GUINEA, ZAIRE EBOLAVIRUS SUSPECTED
****
A ProMED-mail post
http://www.promedmail.org
ProMED-mail is a program of the
International Society for Infectious Diseases
http://www.isid.org

Date: 22 Mar 2014
From: Sylvain Baize & Delphine Pannetier
<sylvain.baize@inserm.fr>

We have investigated 12 samples (7 clinical cases and 5 contacts) from Guinea for suspected viral hemorrhagic fever. We have detected Ebola virus among 6 samples (from clinical cases) using RT-PCR assays and viral isolation is in progress. We are currently analyzing the sequences of different amplified viral fragments to further characterize the strain involved. Sequencing of a part of the L gene has already showed strong homology to Zaire Ebolavirus, suggesting that this species is responsible for the outbreak. This is consistent with the dramatic mortality observed.

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Sylvain Baize & Delphine Pannetier
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<sylvain.baize@inserm.fr>

[ProMED is grateful to Drs. Baize and Pannetier for this prompt firsthand report of the detection of Ebola virus from Guinea in 6 of 7 clinical cases (and apparently in none of 5 contacts) from the Guinea hemorrhagic fever outbreak that began in early

HealthMap

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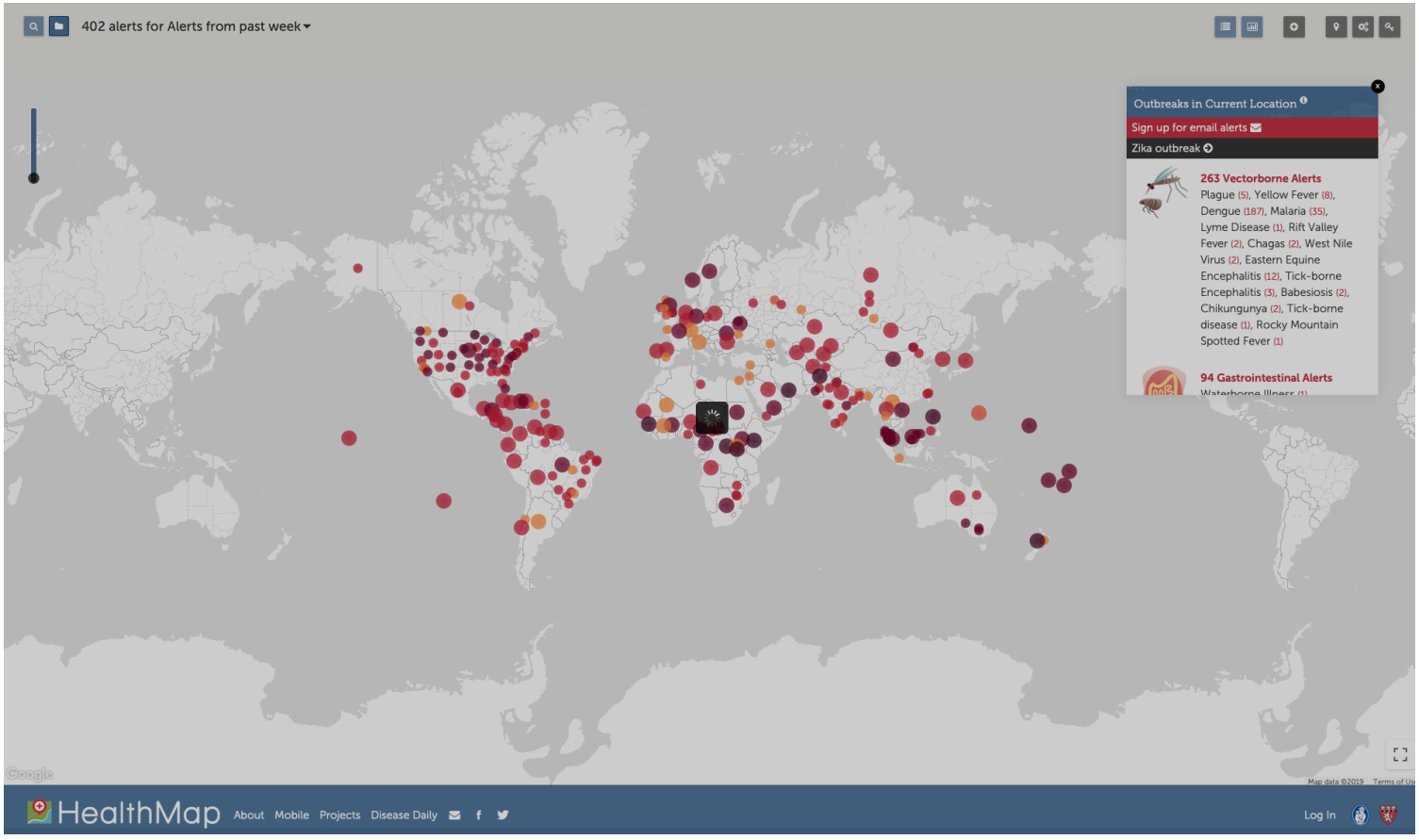
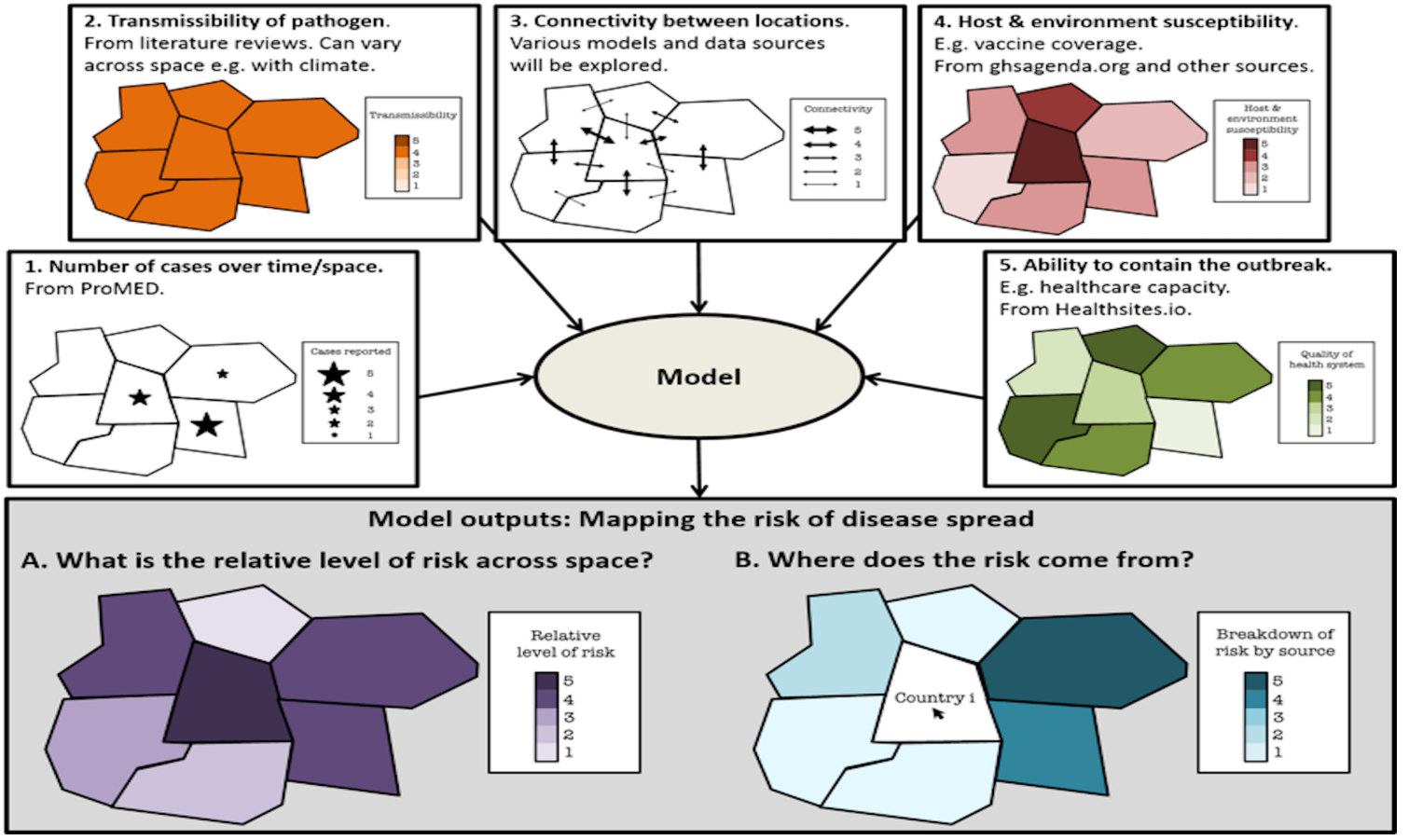


Theoretical Framework



Raw Data

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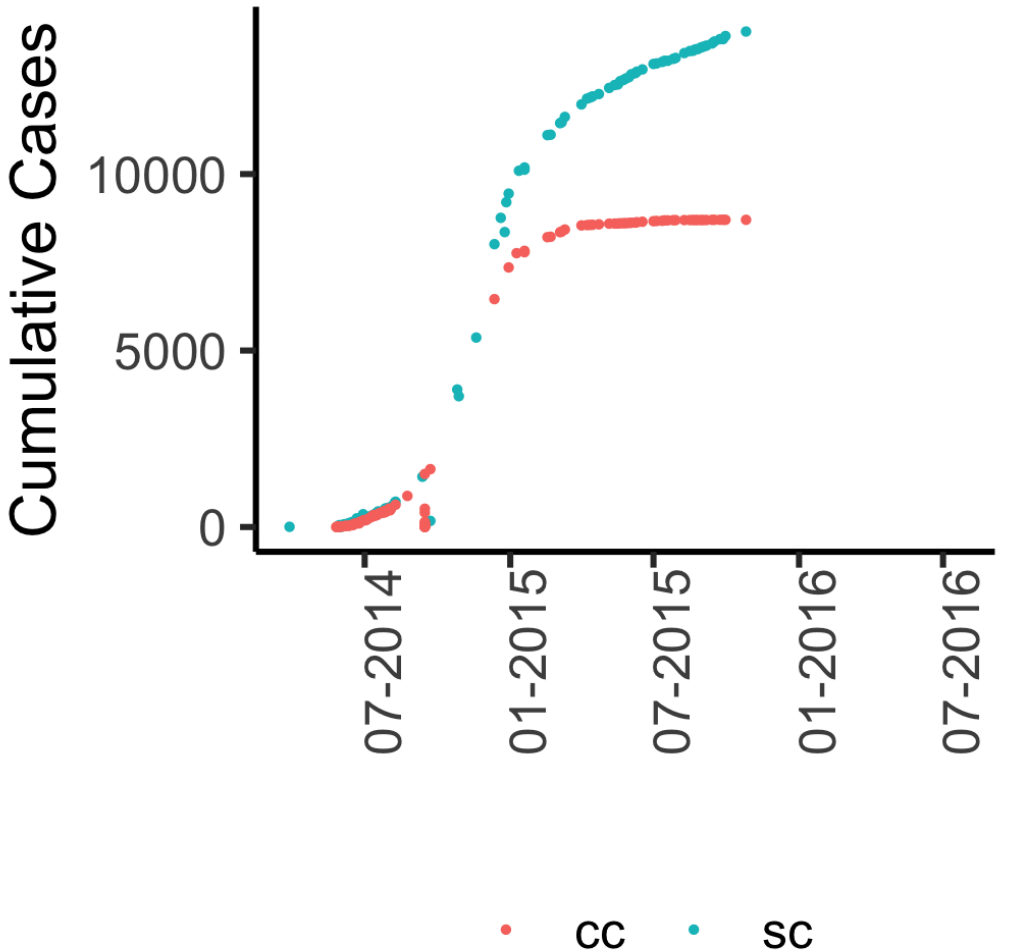
Raw Data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01-2015
07-2015
01-2016
07-2016
cc
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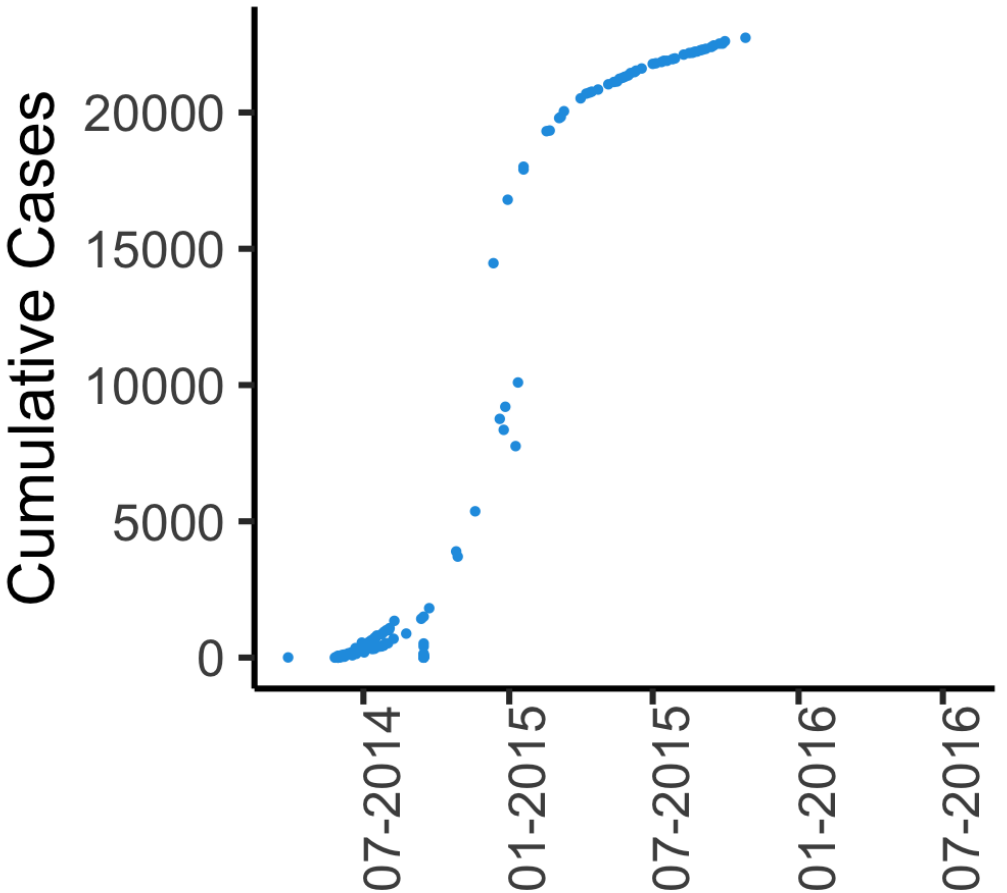
Total Cases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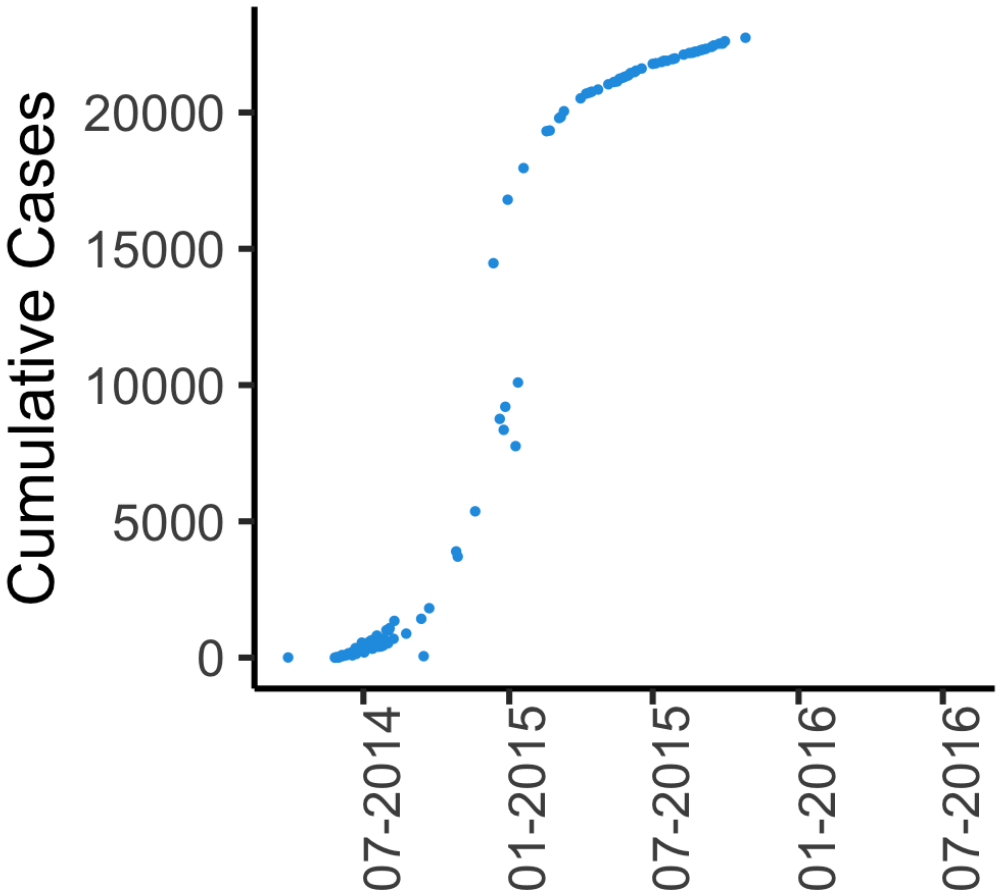
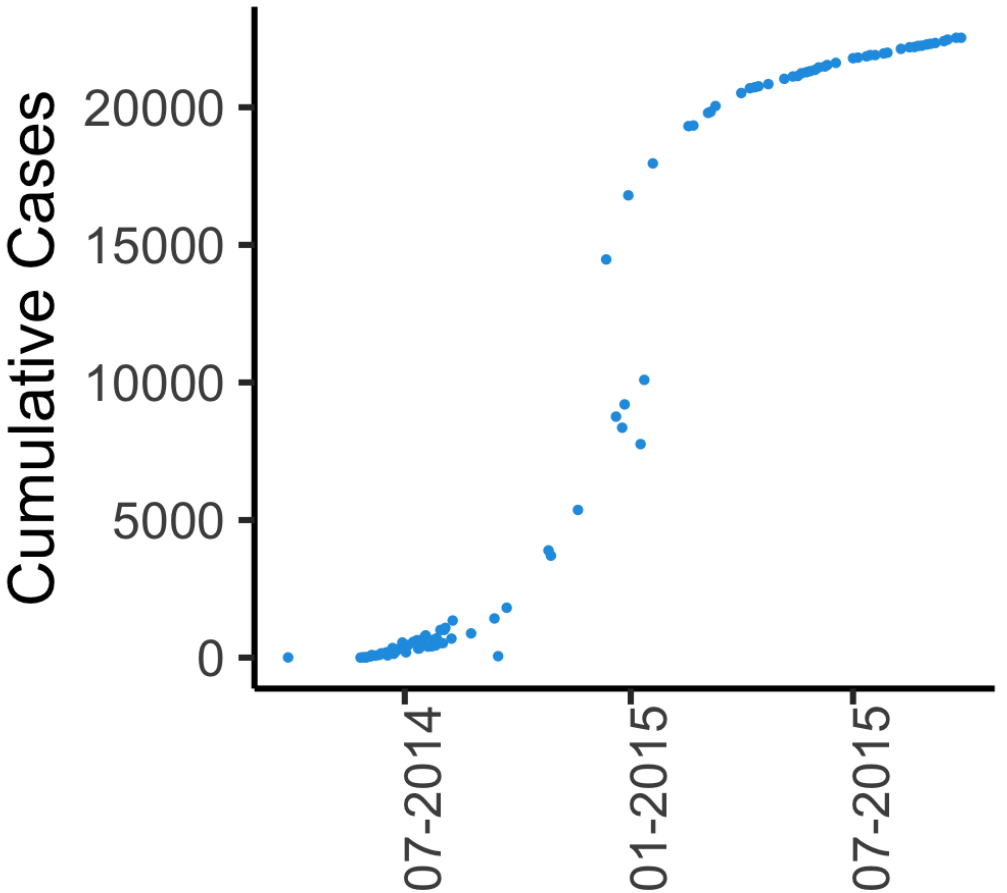
07-2016

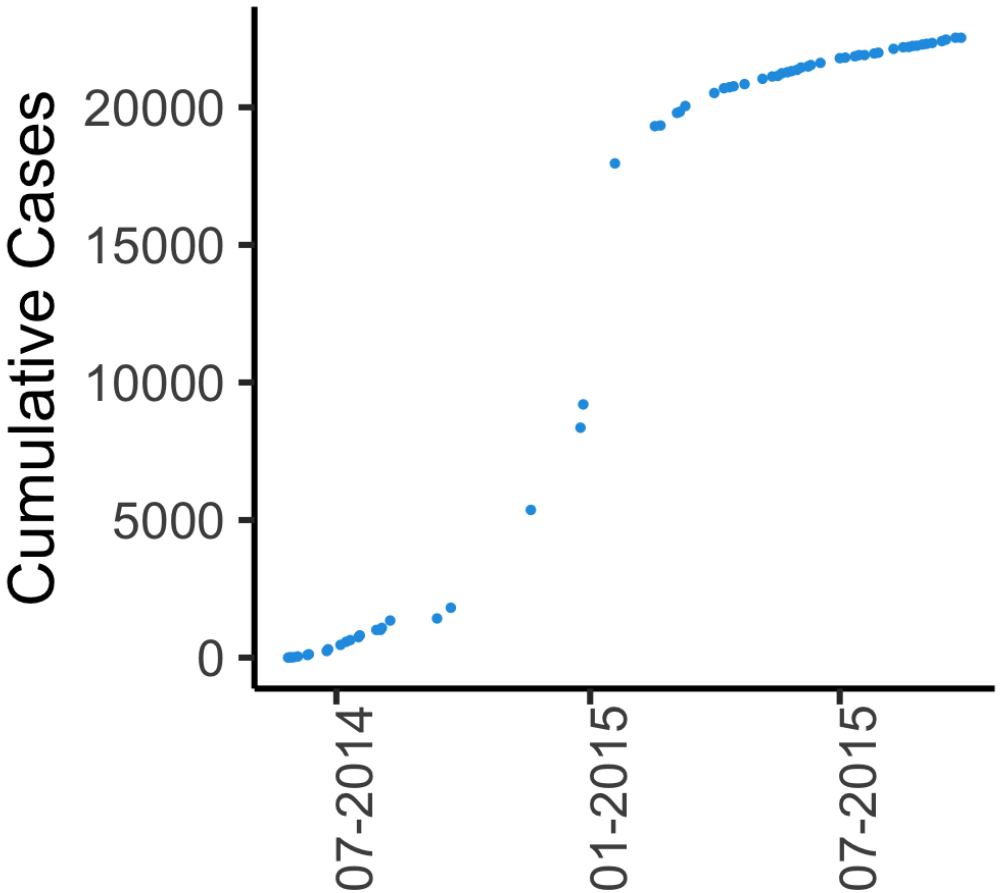
Remove Duplicates



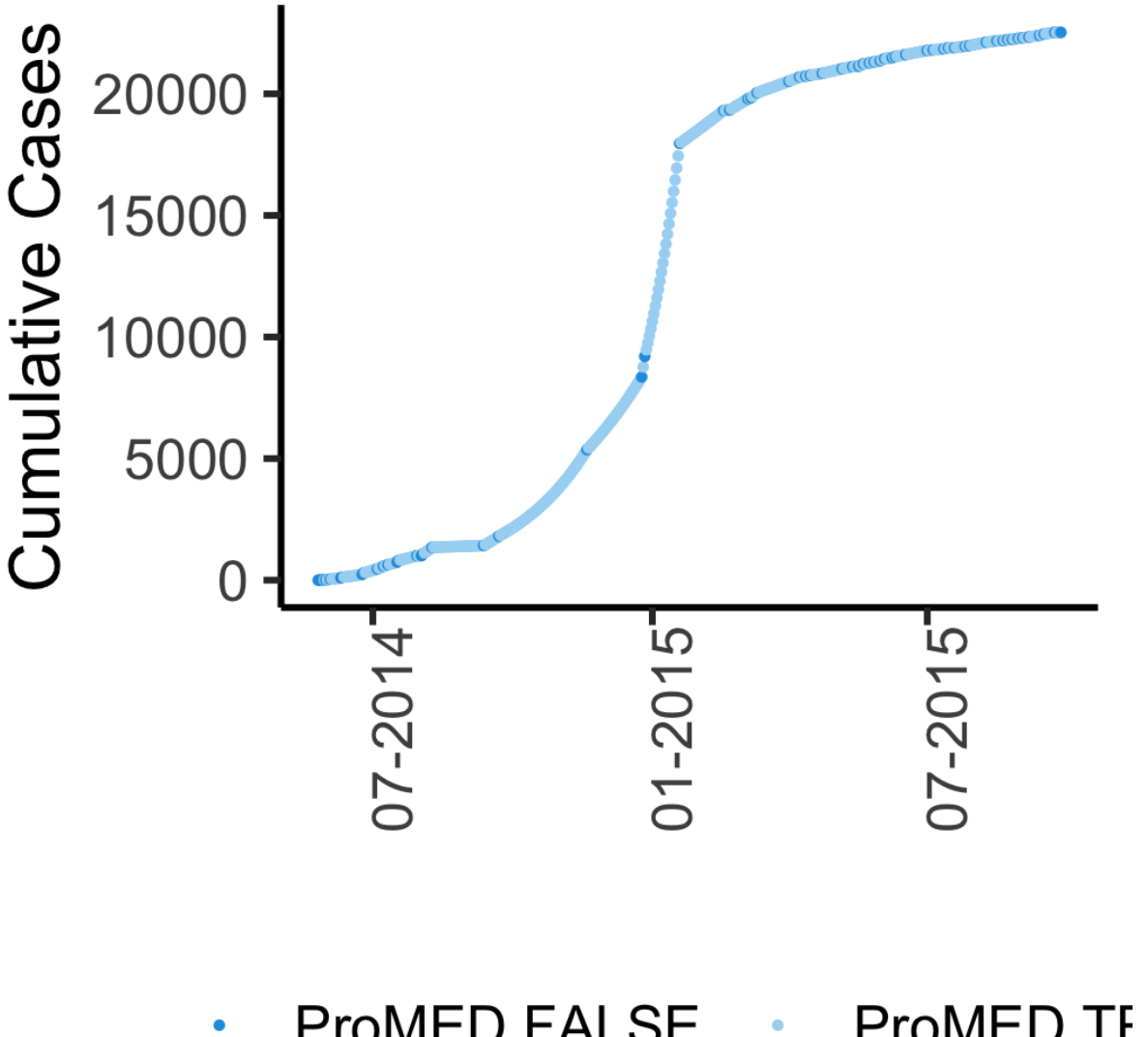
Remove Outliers



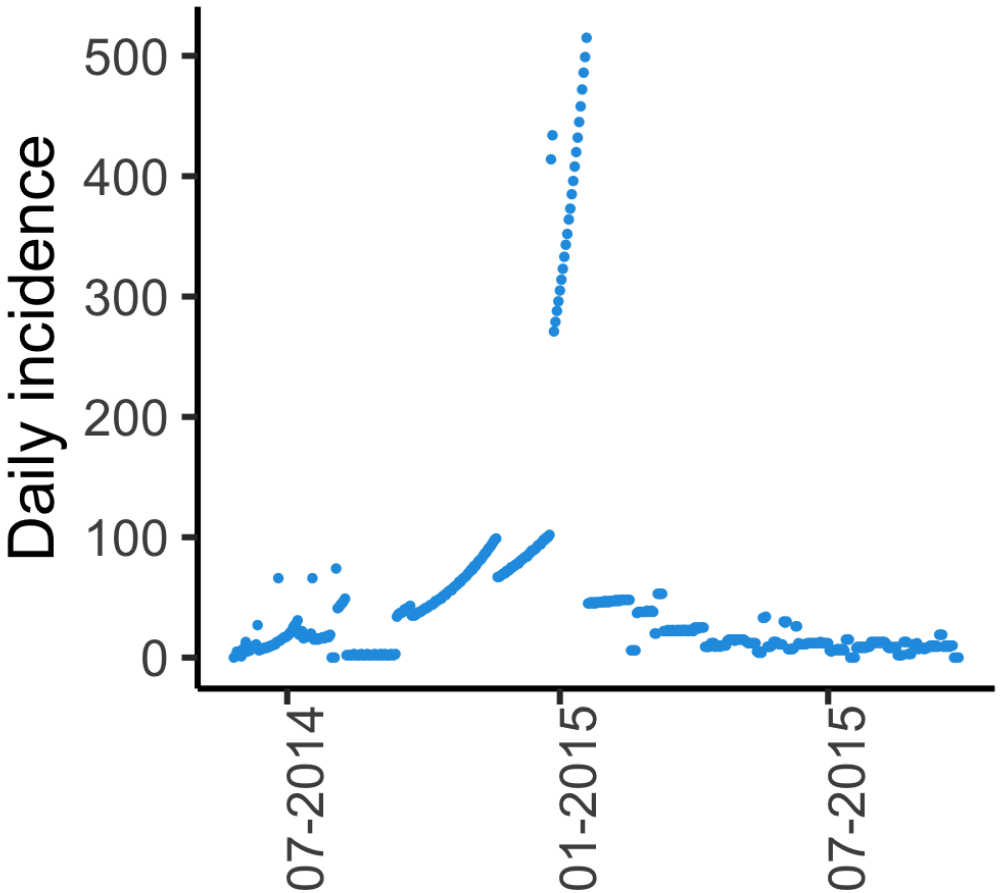
Monotonically Increasing



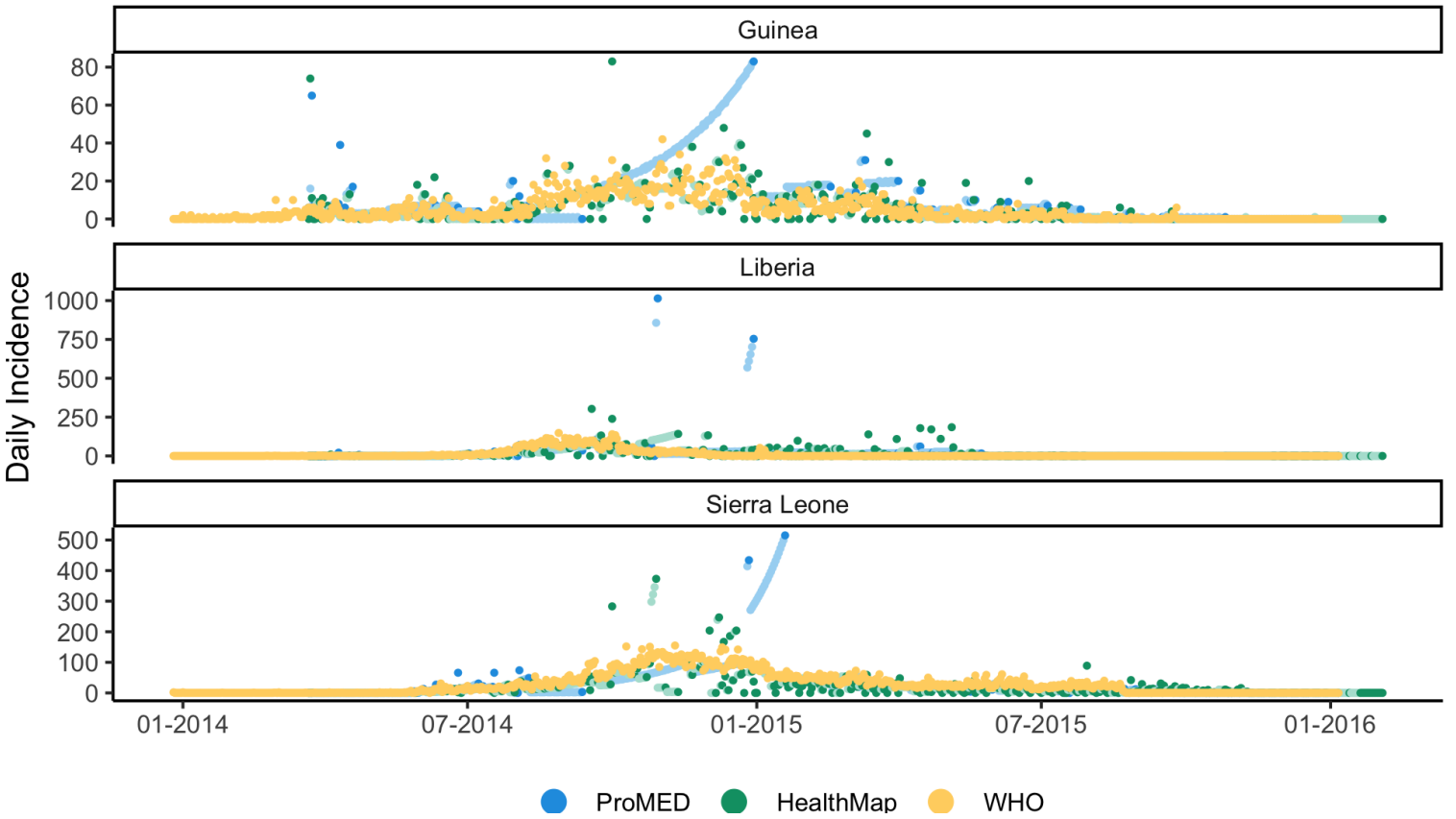
Impute Missing Data



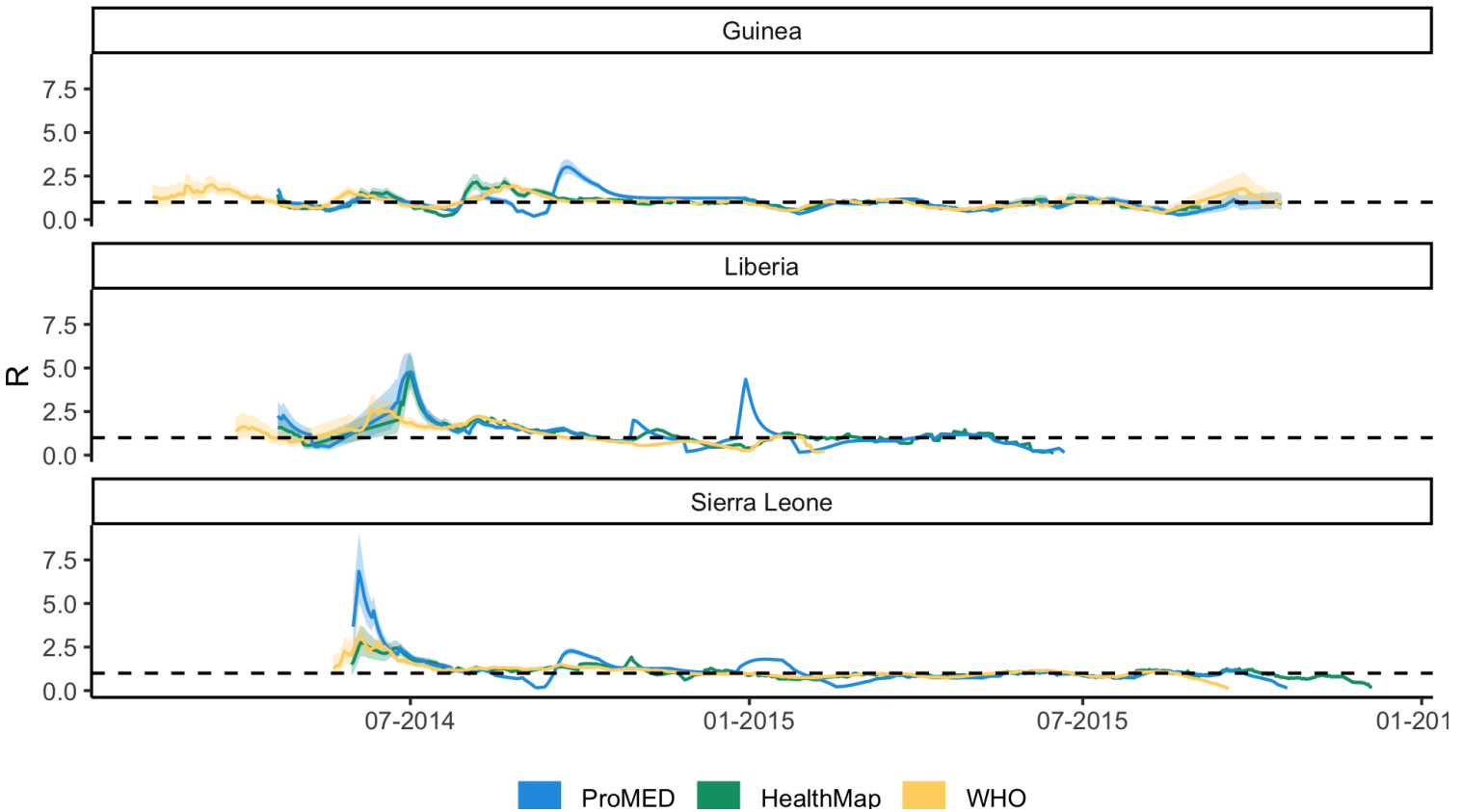
Daily Incidence Trends



ProMED, HealthMap, and WHO: Incidence



Comparing R Estimates



Statistical Model

Movement between spatial units

Approximated by a phenomenological model (e.g. gravity[1] or radiation model[2]), or informed by other sources such as air or road traffic data.

$$\phi_{i \to j} = \frac{N_i N_j}{d_{i,j}^{\gamma}}.$$

$$p_{i \to j} = (1 - p_{stay}^{i}) \frac{\phi_{i \to j}}{\sum_x \phi_{i \to x}}$$

[1] Grosche, T., Rothlauf, F., & Heinzl, A. (2007). Gravity models for airline passenger volume estimation. Journal of Air Transport Management, 13(4), 175-183.

[2] Simini, F., González, M. C., Maritan, A., & Barabási, A. L. (2012). A universal model for mobility and migration patterns. Nature, 484(7392), 96.

Model Fitting & Forecasts

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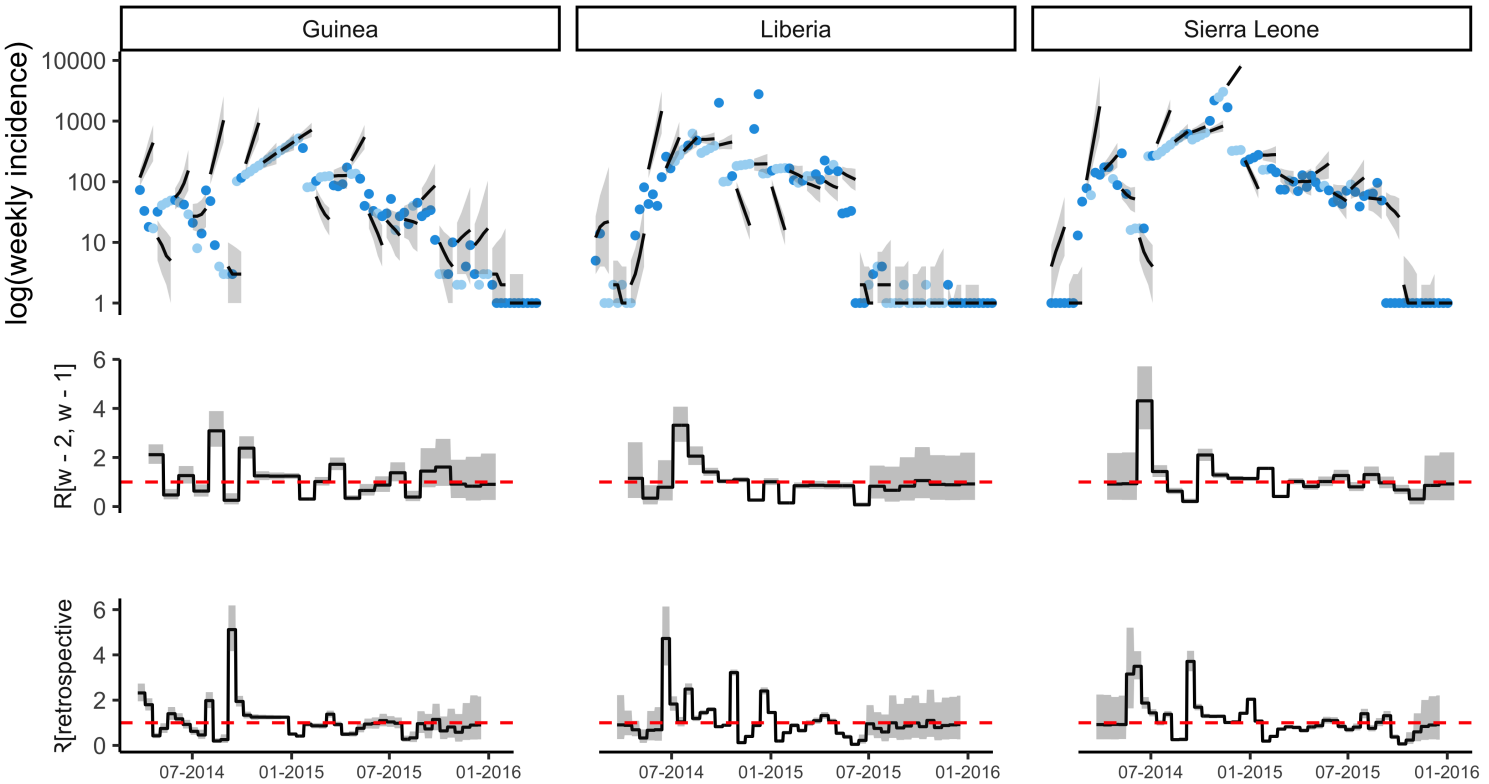
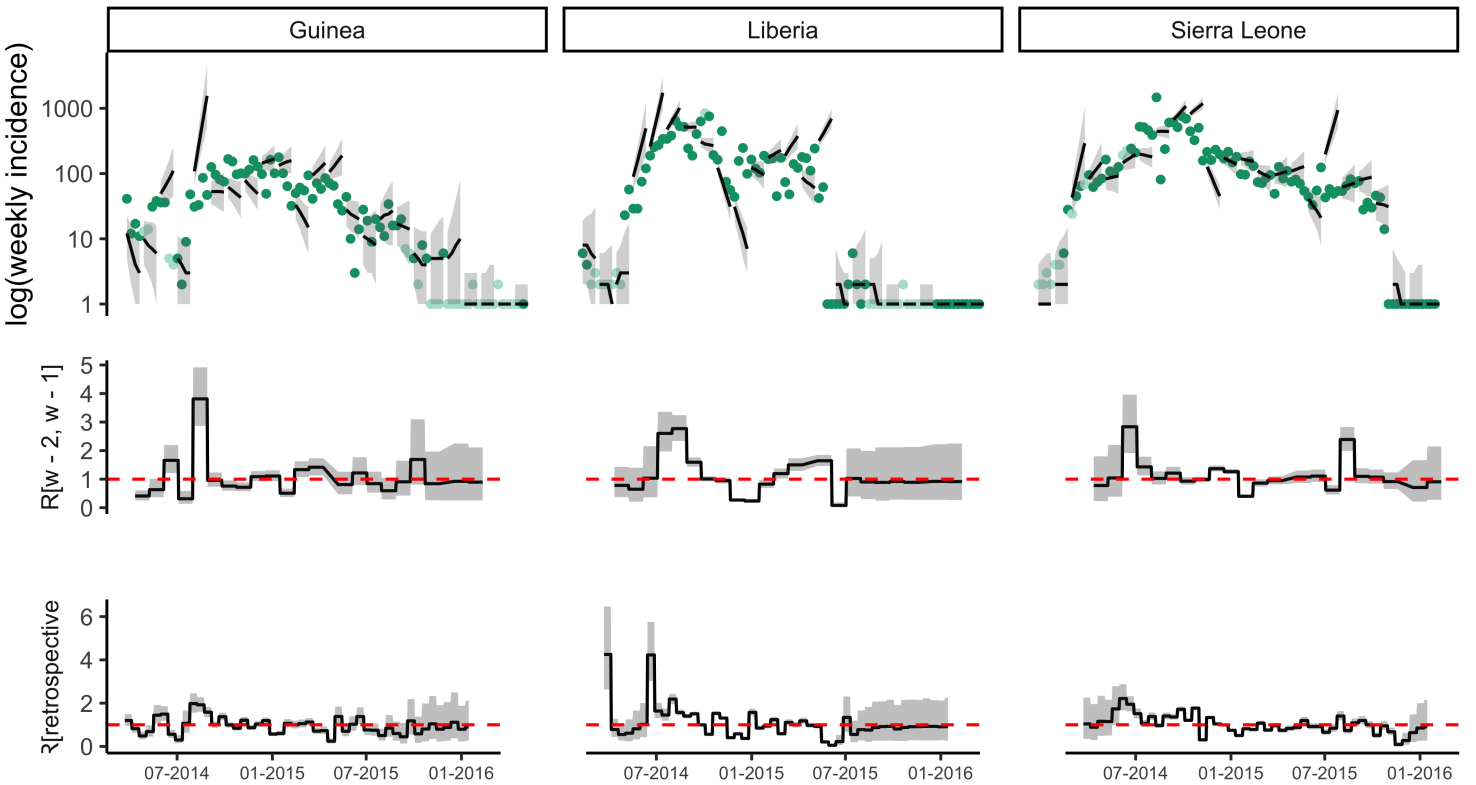
- Model fitted to incidence data from all countries in Africa.
- Model parameters - reproduction numbers for each country, distance exponent, and probability of staying - estimated using MCMC in R.
- For forward simulations, transmissibility assumed to be constant over the forecast horizon.
- Forecasts produce every 7th day, to simulate analysis carried out in an ongoing epidemic.

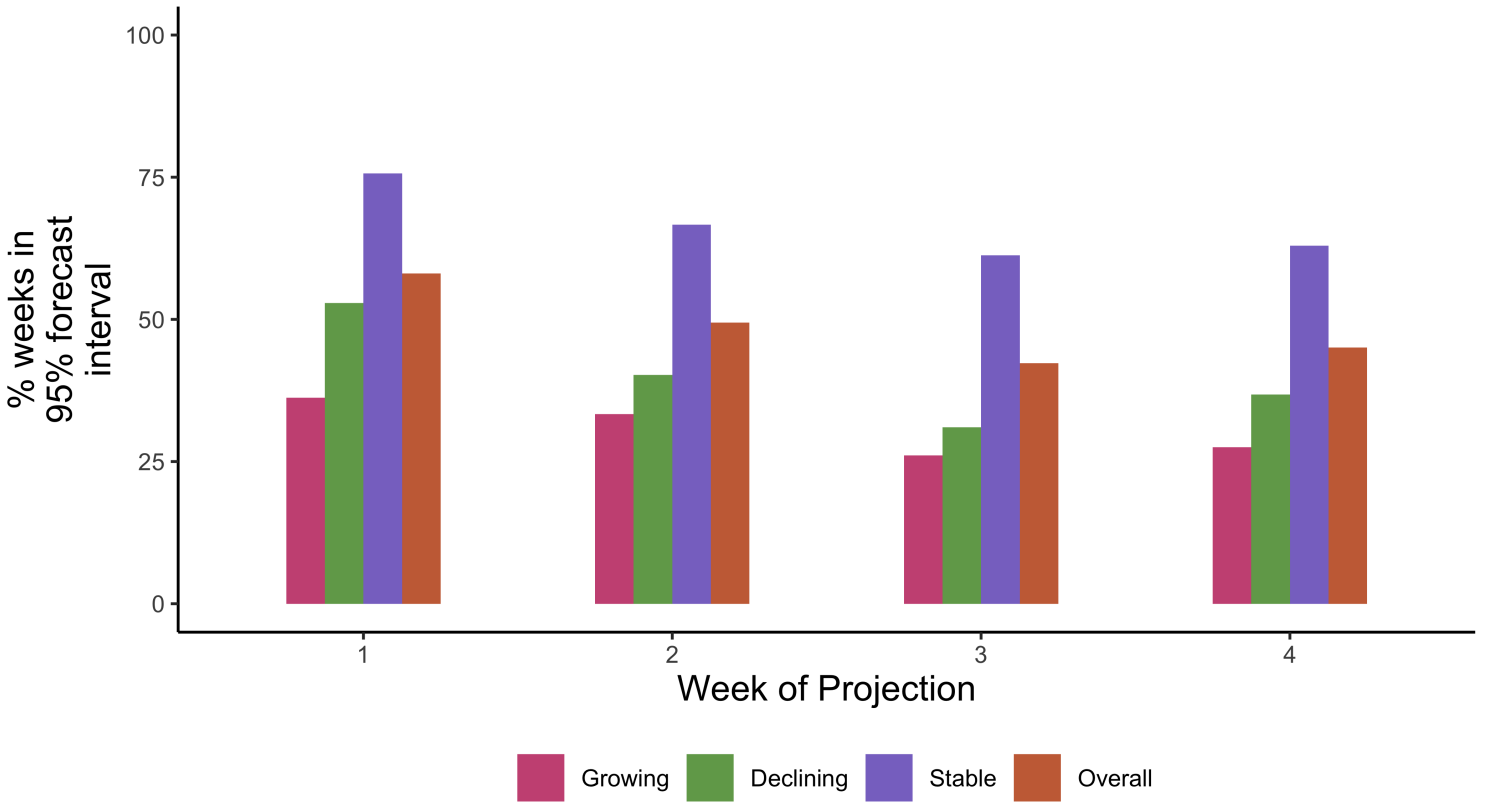
Forecasts using ProMED Data



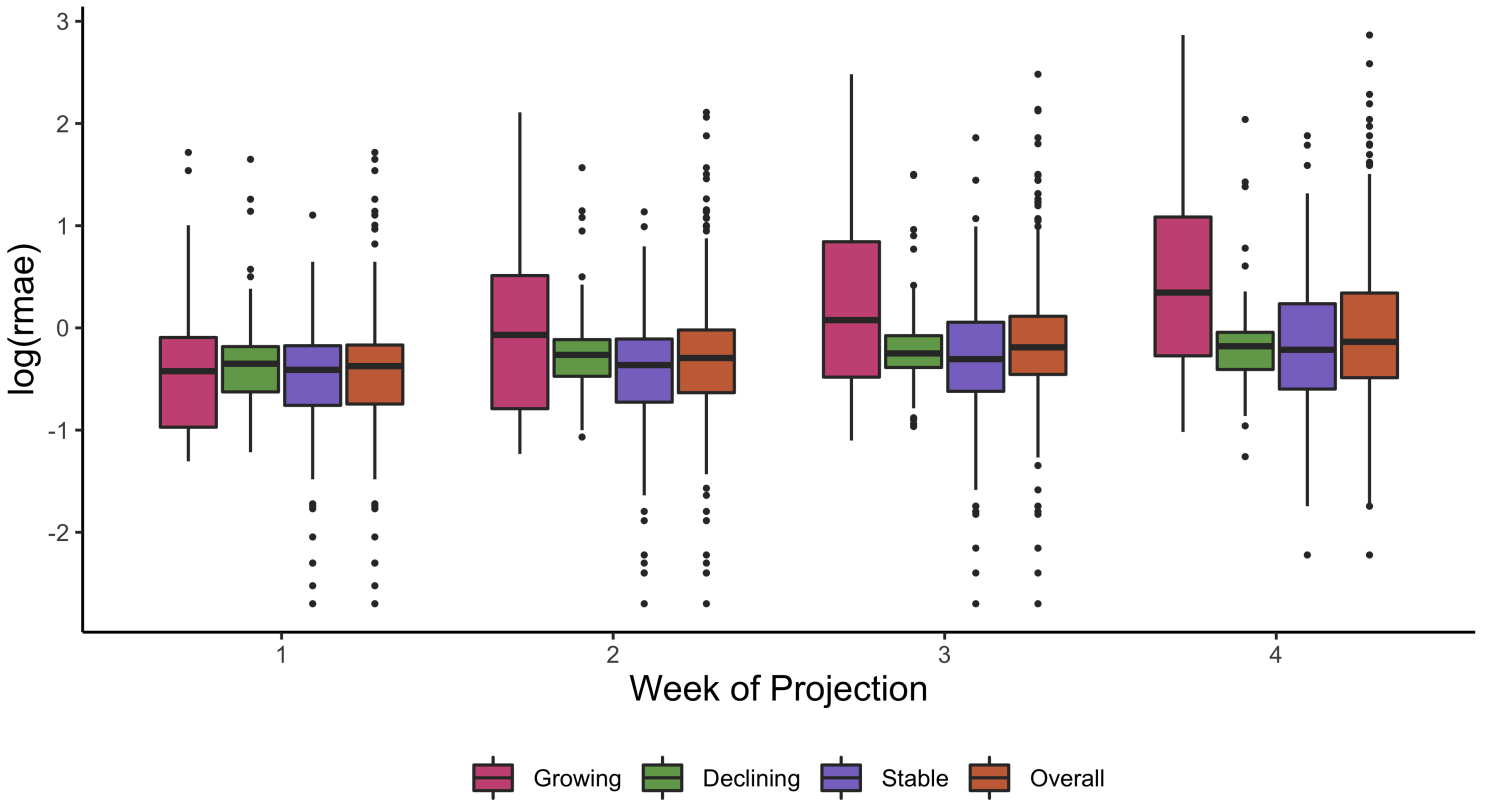
Forecasts using HealthMap Data



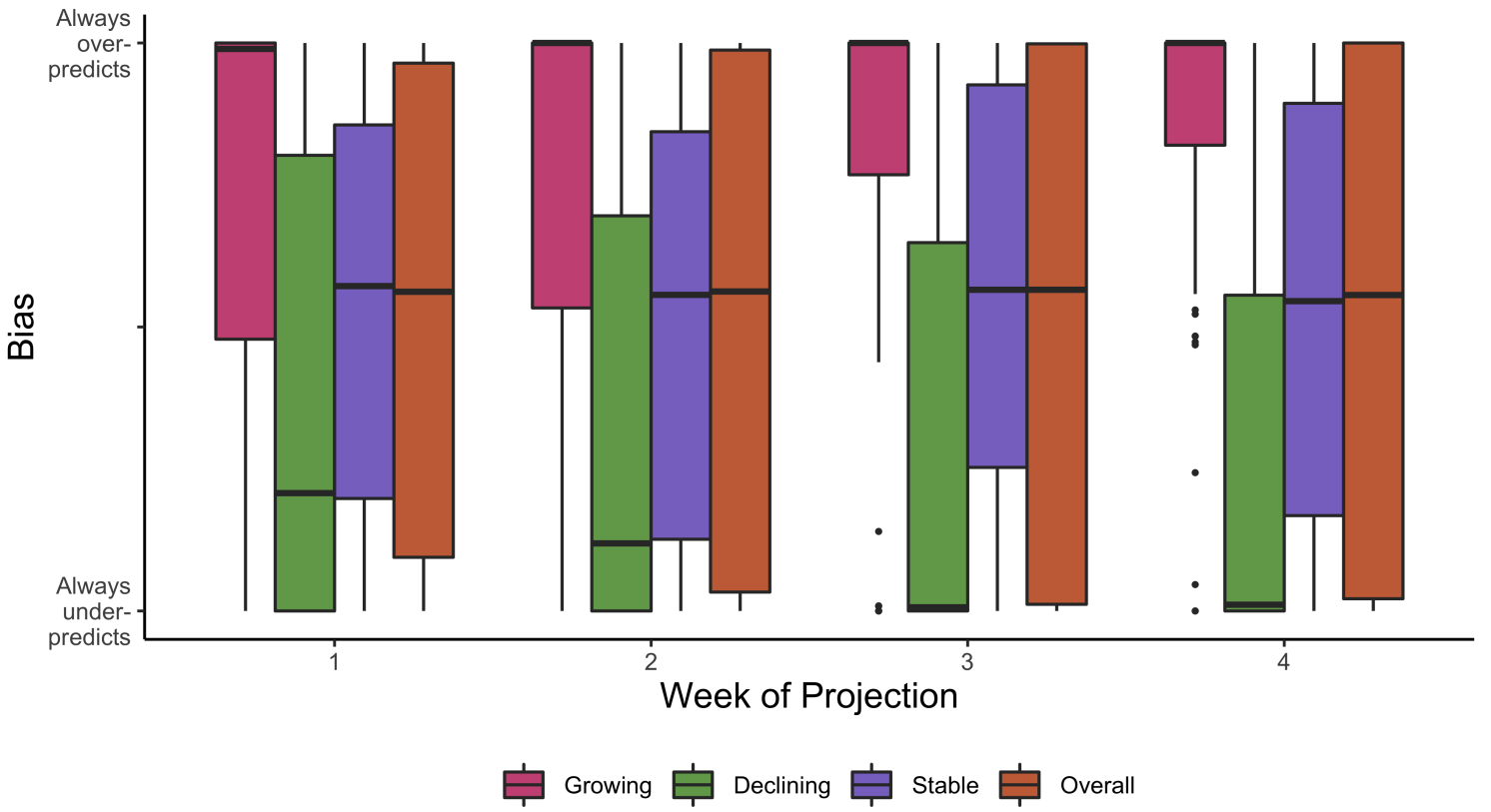
Model Performance: Accuracy



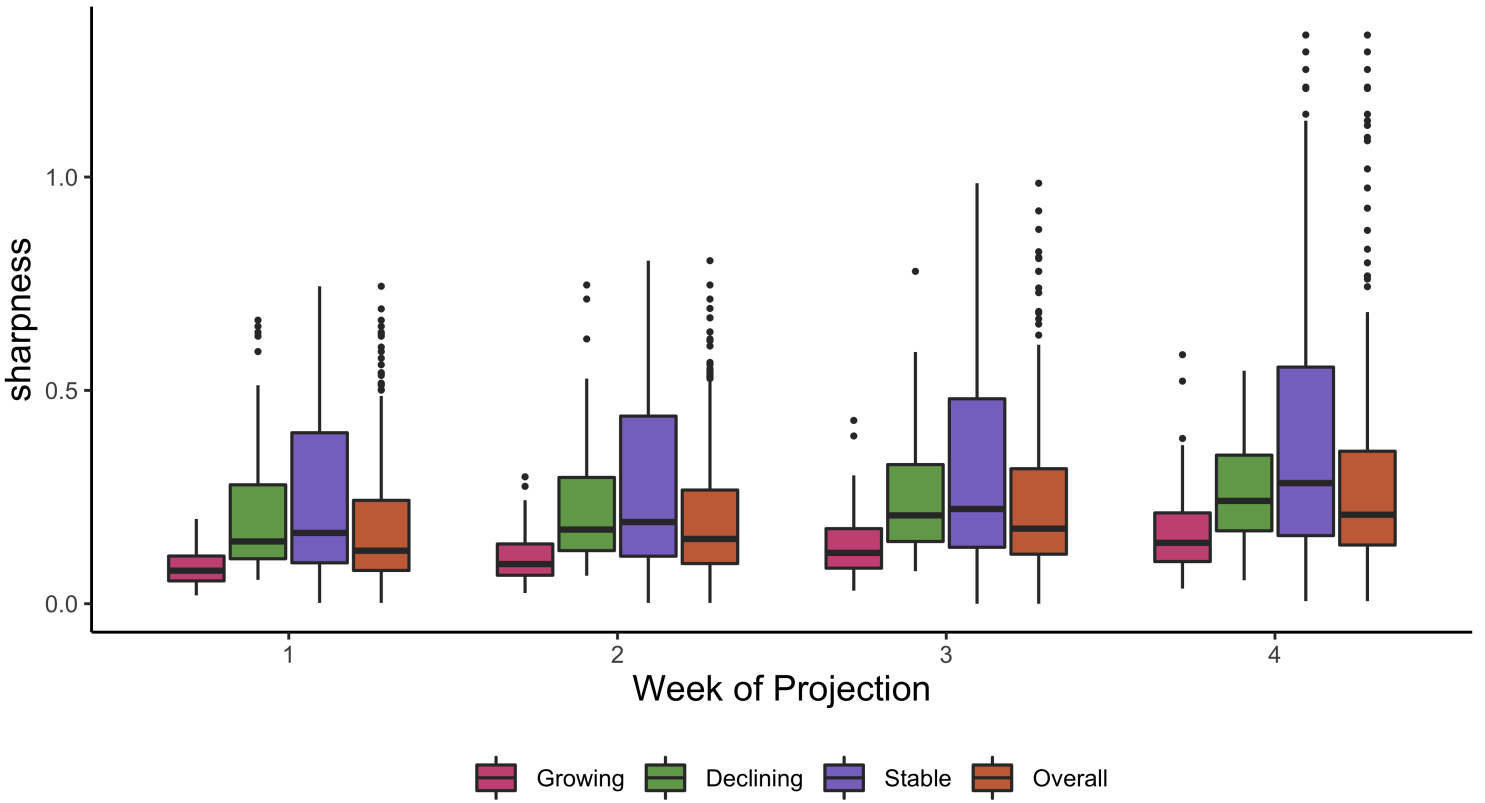
Model Performance: Relative Error



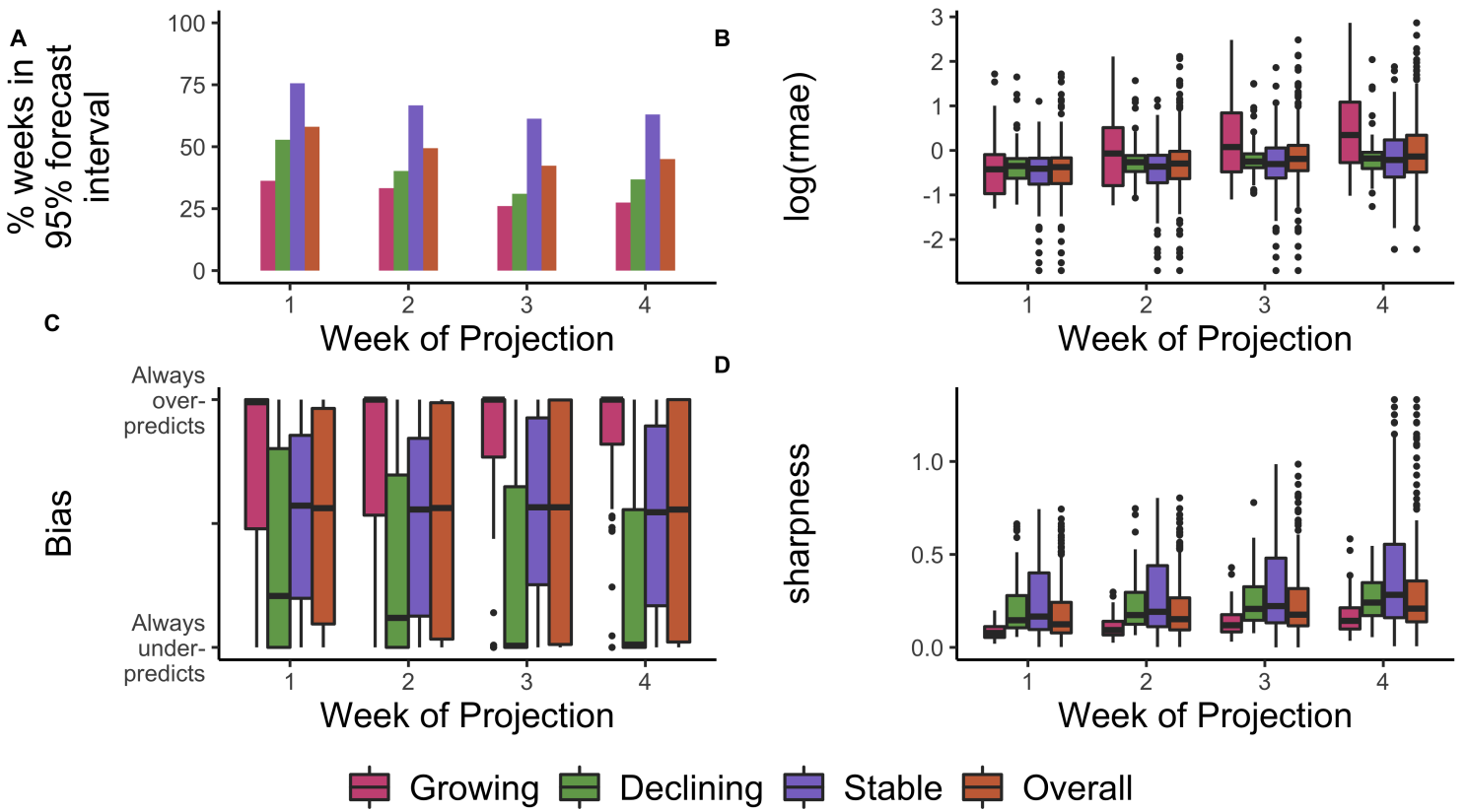
Model Performance: Bias



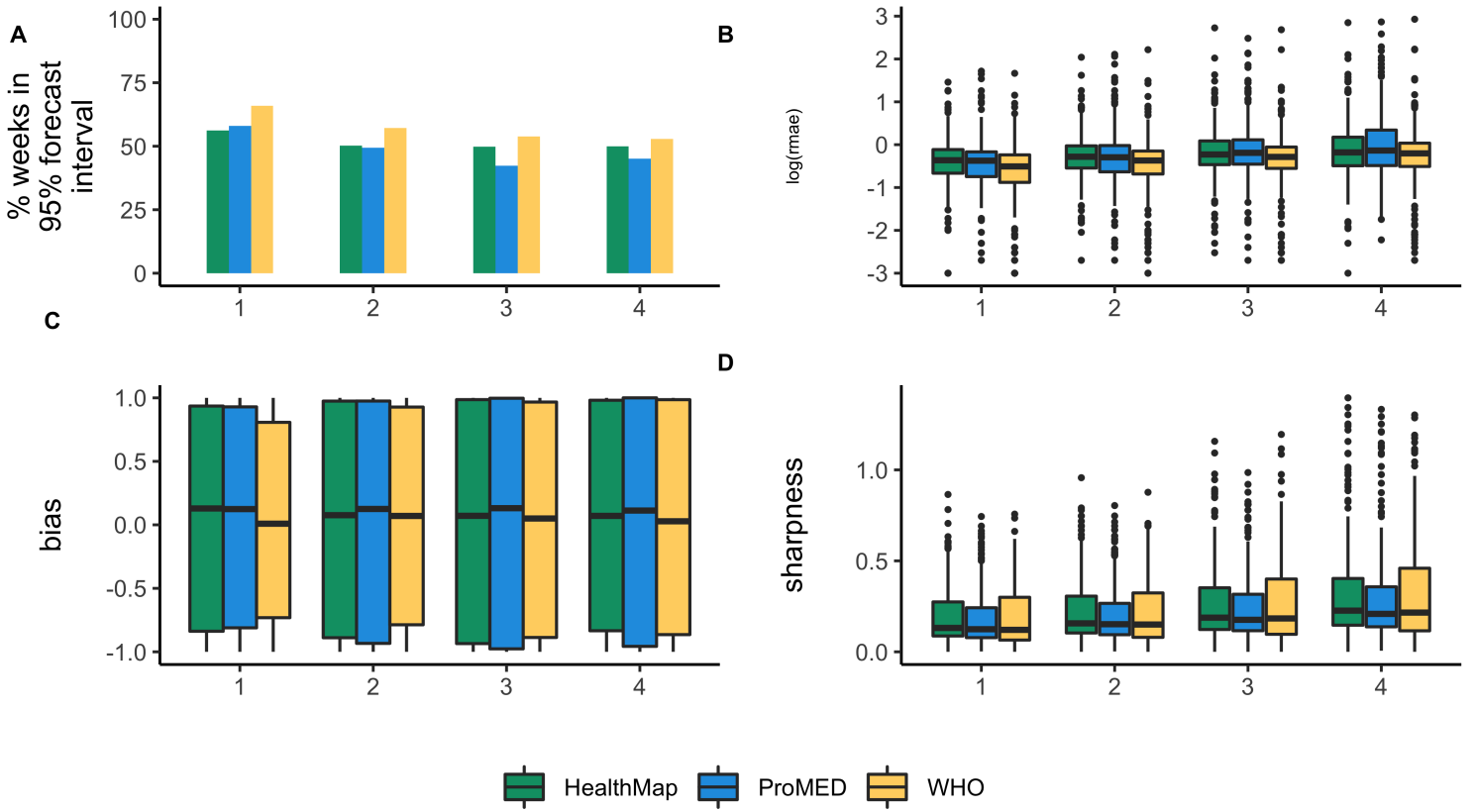
Model Performance: Sharpness



Model Performance



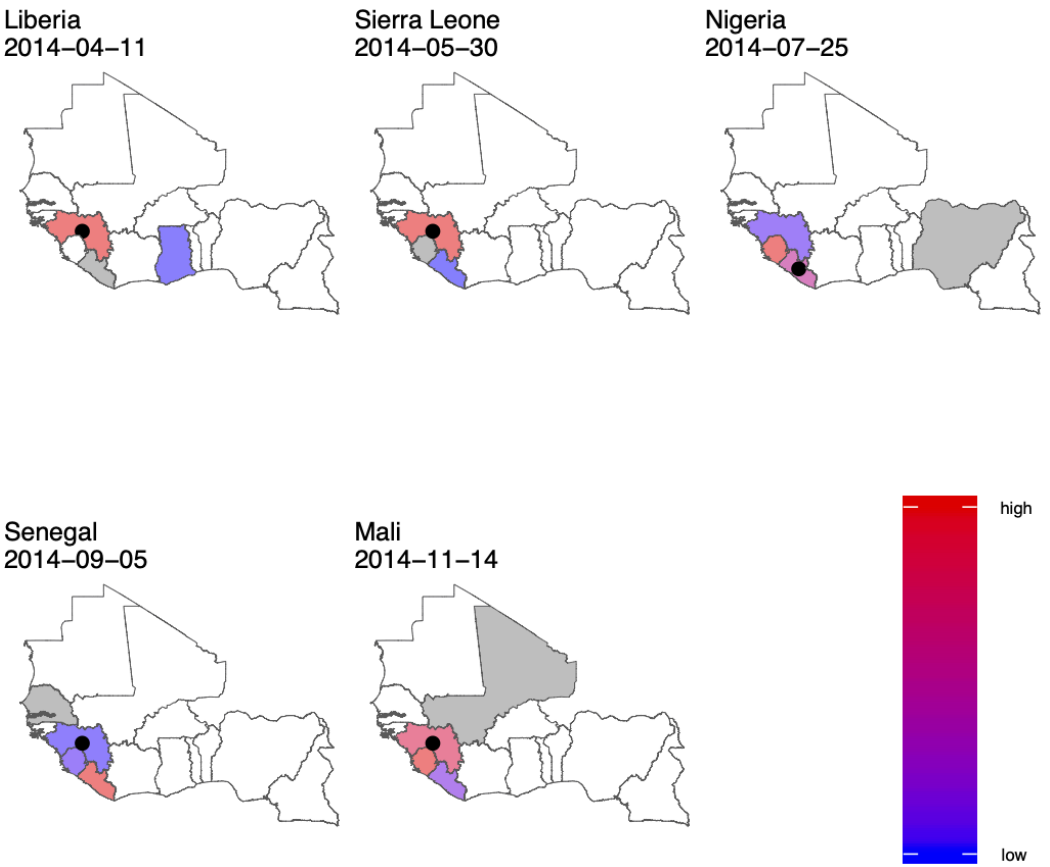
Model Performance: ProMED, HealthMap and WHO



Risk of Spatial Spread: ROC Curve

Risk of Spatial Spread

Risk of Importation



Conclusion

- Variable performance in predicting number of cases.
- Scope for model improvement - different mobility models, increase model complexity, more data on human movement.
- Model performed very well in predicting risk of spatial spread.
- First demonstration of using data from two widely used digital surveillance tools for epidemic forecasting.

Conclusion

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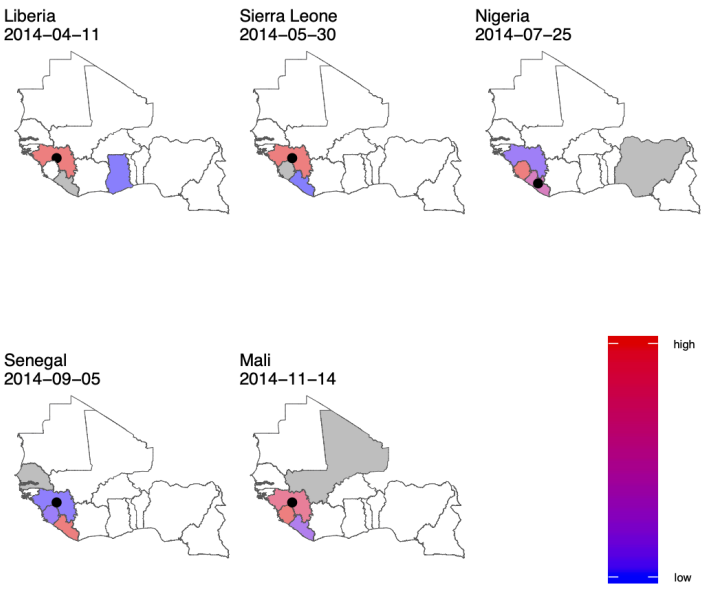

Pre-print and more information

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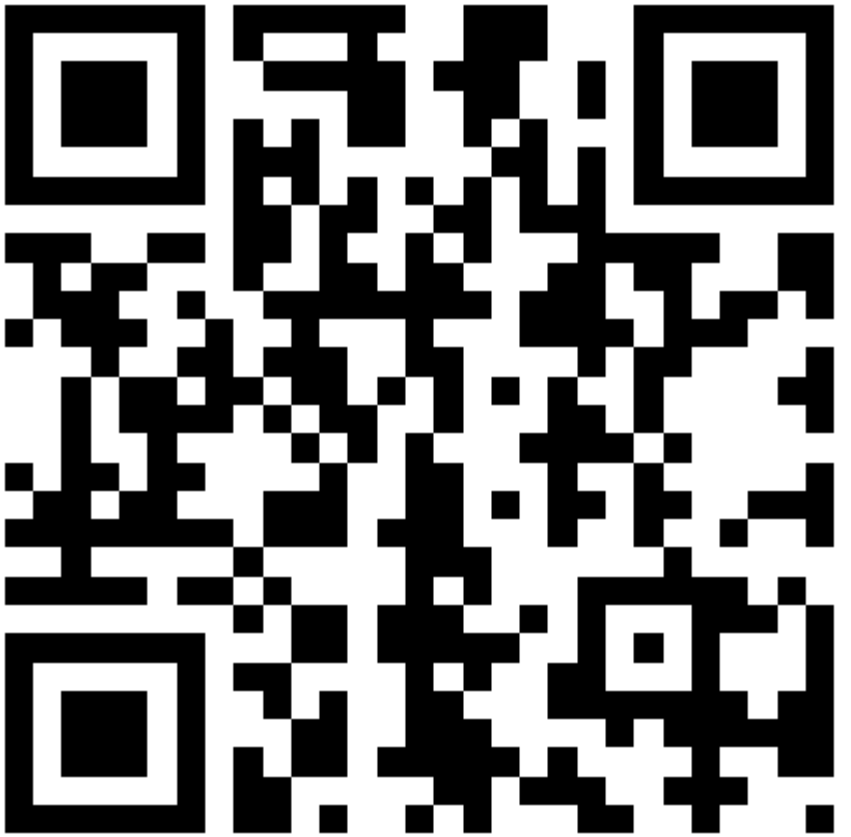

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sangeeta0312