MAH Q1 Meeting – *A showcase of measles risk mapping tools*

9th March 2026

MEASLES ANALYTICS HUB

Measles risk assessment – an overview of methods, challenges, and future directions

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March 2026 MAH meeting

Gates Foundation

Measles modelers get **questions about risk all the time** – the details of those questions lead to very different outcomes.

Risk of what?

- Cases, infections, susceptibility, outbreaks, morbidity, vaccine hesitancy?

At what spatial scale?

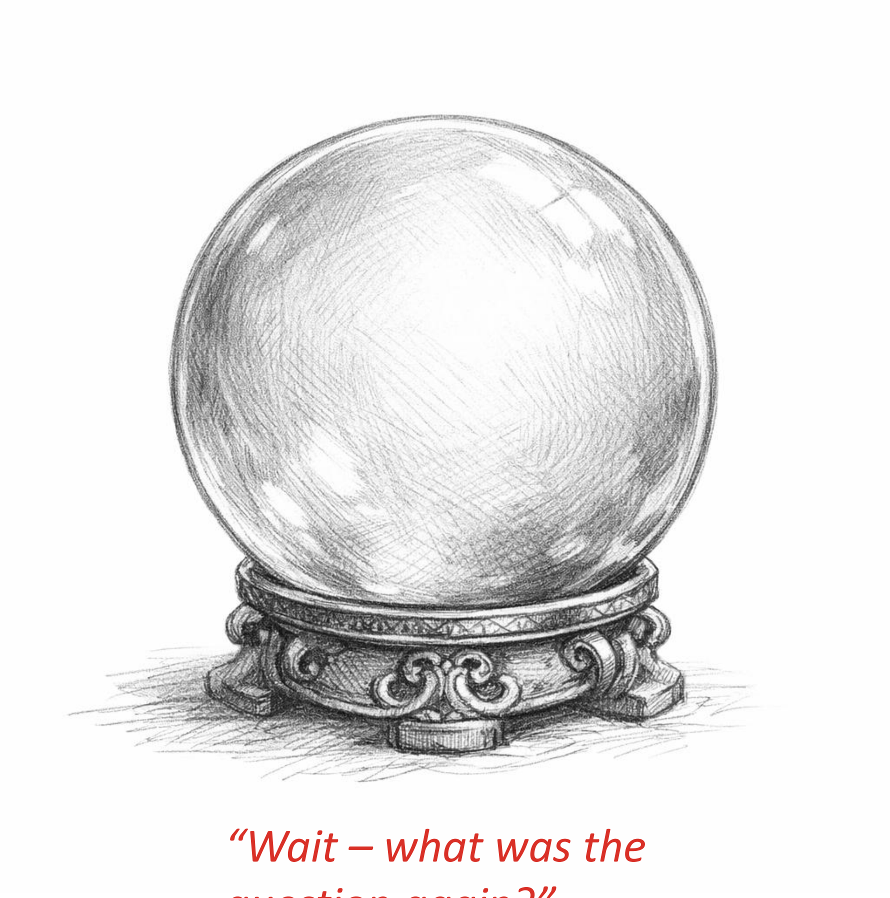
- Can the same approach work for districts and for countries?

On what time horizon?

- Is the best method on a 2-month scale also best on a 2-year scale?

For what decision?

- A preventative campaign, outbreak response, investments in RI systems, outreach?



"Wait – what was the question again?"

Image made using Copilot

Today is a first step towards **a collective picture** of “risk assessment” questions, approaches, challenges, and future directions.

Supporting measles campaign planning with forecasting models	Niket Thakkar
Overview of the Measles Programmatic Risk Assessment Tool	Anna Minta
Predicting Measles Outbreaks & Measles Immunity Profiles	Amy Winter
Endemic Measles Forecasting with EpiFlowML	James Schlitt
Risk Mapping of Measles in Niger – predicting high-burden districts	Anton Camacho
URGEPI: Measles risk and operational prioritization in southeastern DRC	Matt Ferrari
Subnational measles modeling - IHME	Jon Mosser
High level overview of Safinea’s risk mapping tool	Helen Johnson
Wrap-up and upcoming MAH activities	Megan Auzenbergs

Supporting measles campaign planning with forecasting models

Niket Thakkar

March 2026

MAH risk assessment symposium

nthakkar.github.io

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Campaign **planning and advocacy** leads to a set of forecasting problems.

- Measles vaccination campaigns are huge – they have to be **planned roughly 1 year in advance.**
- Decisions include **phasing of subnational areas** (which states go first?), **timing of the campaign overall**[1] (should be plan for March or October?), and **who to target**[2] (what's an appropriate age range?).
- A common pattern is responding to threats of campaign delay – forecasting models help us **translate delay into expected burden** for advocacy.

Table 17. Campaign targets.

Campaign strategy	Proportion of the target population	Target population
Fixed posts	10%	9,722,469
Mobile posts	90%	87,502,221
Total	100%	97,224,690

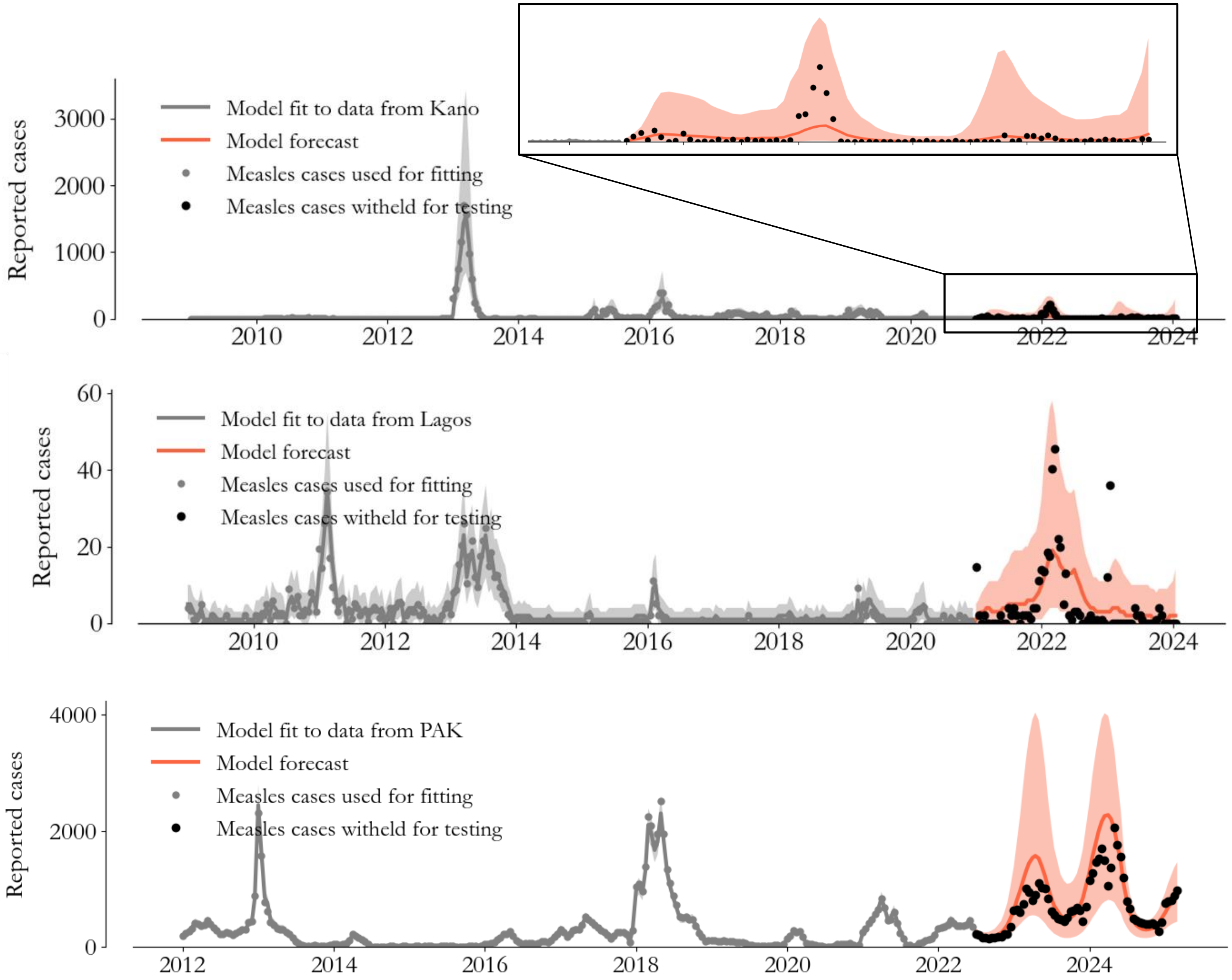
Table 18. Operation of vaccination posts

Campaign strategy	Organisation of vaccination posts and team composition	Number of teams	Number of children vaccinated per vaccinator per day	Number of children vaccinated per day
Fixed Post	1 Supervisor/Vaccinator 1 Health Worker Vaccinator 2 Recorder 1 Town Announcer 1 Community leader/mobiliser	7,300	125 (Senior Supervisor) 150 (Health Worker Vaccinator)	300 (urban) 250 (rural) 275 (average)
Mobile Post	1 Supervisor/Vaccinator 1 Health Worker Vaccinator 2 Recorder 1 Town Announcer 1 Community leader/mobiliser	65,719	125 (Senior Supervisor) 150 (Health Worker Vaccinator)	300 (urban) 250 (rural) 275 (average)
Total		73,019		

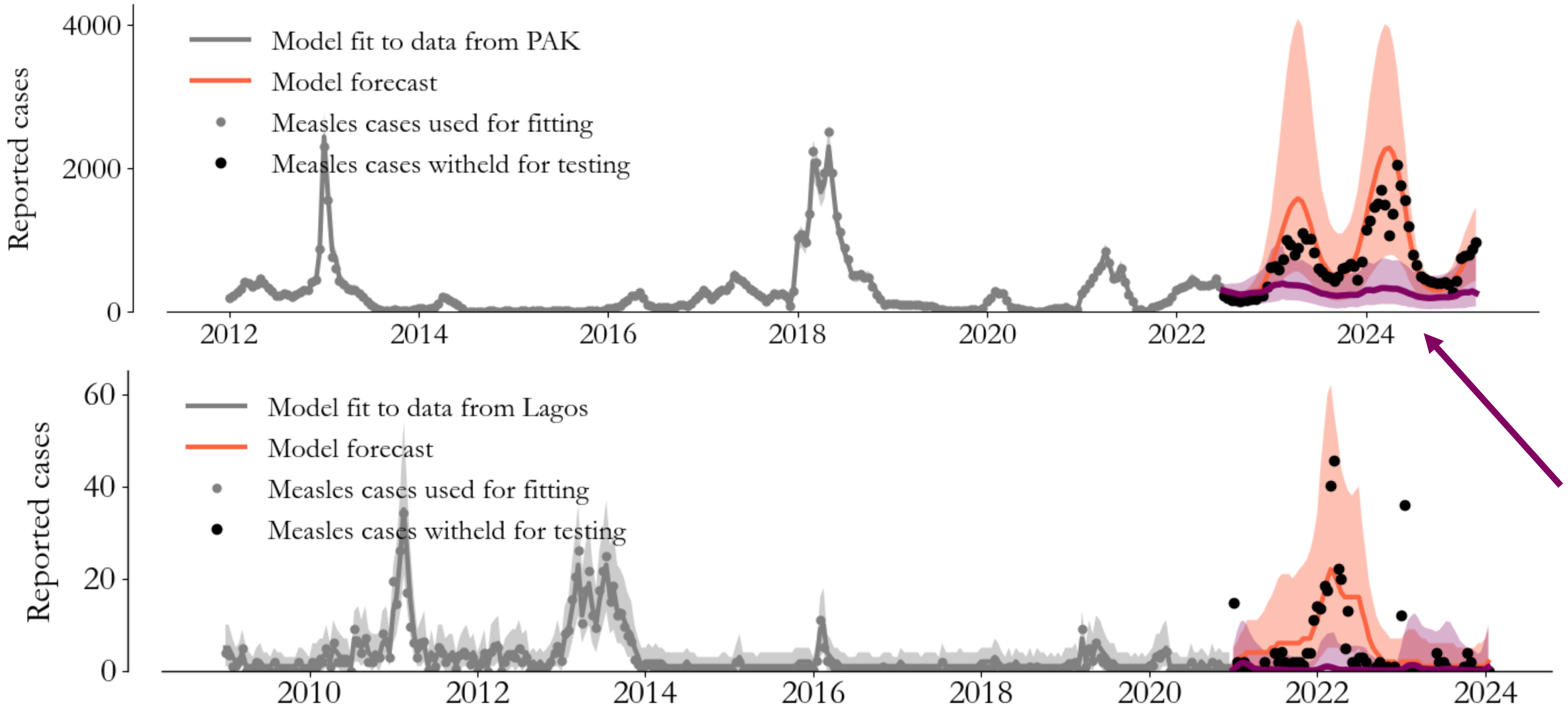
≈ 440 thousand people!

(1) Thakkar et al. *PNAS* 2019. (2) Thakkar et al., *PLoS One* 2026.
Tables via Nigeria's 2025 Gavi application

We've created models with **viable accuracy on operationally relevant time horizons** in key campaign geographies.



We've found that forecasts need epidemiology – **purely empirical models fail**, even with modern AI architectures and much more data.



Amazon's Chronos[1] has up to 700M parameters trained on millions of time series.

[1] Ansari et al., *Trans. on ML*, 2024, this example used v2.0.0

Demographic data, usually surveys

Coverage estimation, past interventions

$$S_{t+1} = S_t + B_t - I_{t+1} - V_t$$

$$I_{t+1} = \beta_t \varepsilon_t S_t I_t^{\alpha}$$

Comparisons to climate, movement, and serological data

$$C_t \sim \text{Binomial}\{I_t, r_t\}$$

Case-based surveillance, including lab rejected cases

Regularization via age distributions of cases

We're continuing to understand, improve, and build upon these models.

Key challenges	Ongoing work
The approach has a large data footprint	Can we make sparse approximations[1]?
It's restricted to endemic scales and settings	Can we better understand transient elimination dynamics?
It's not a "tool"	Can we make certain elements (like underlying immunity profiles) a general tool[2]?
Forecast uncertainty is sometimes unreasonably high	Can we improve uncertainty quantification and other methods elements?

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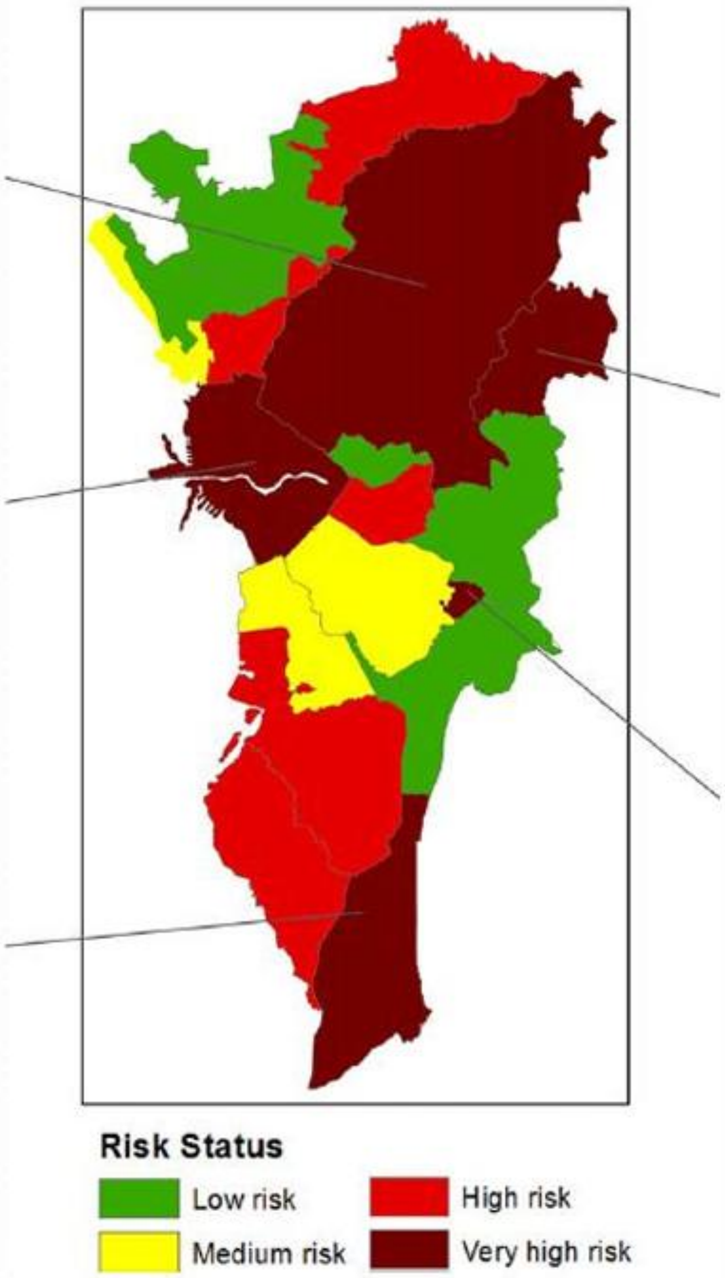
(1) See for example Thakkar et al., *arXiv* 2024. (2) Gates Foundation recently funded a grant for this work.

Overview of the Measles Programmatic Risk Assessment Tool (MRAT)

Anna Minta, MD, MPH
Medical Epidemiologist
Global Immunization Division
Center for Global Health
March 9, 2026



Measles Risk Assessment Tool (MRAT) - Background

- MRAT is an Excel and ArcGIS based program assessment tool developed by US CDC and WHO in 2014
- Purpose: Identify subnational areas failing to meet measles programmatic targets to guide and strengthen elimination activities
- **Not** a measles outbreaks risk prediction tool nor is it designed for SIA planning
- Current uses include annual program planning and country report preparations

MRAT Indicators

- Subnational programmatic risk calculated as sum of indicator scores in 4 categories
  - Population immunity (40 points)
  - Surveillance quality (20 points)
  - Program performance (16 points)
  - Threat assessment (24 points)
  - Total (100 points)
- Each district is assigned a risk category of low, medium, high, or very high risk based on the overall risk score

MRAT Data Inputs

Data	Details
Administrative vaccine coverage data by district	MCV1 and MCV2 for previous 3 years DTP1/Penta1 year 3
Measles Supplementary Immunization Activity (SIA) campaign data	District coverage, target age group, year of SIA
Measles case-based surveillance data	Previous 3 years
Total population, geographic area, shape files by district	Year 3
Completed "Vulnerable groups by district" spreadsheet	Recommended input from immunization, surveillance, cold chain, etc personnel familiar with local communities

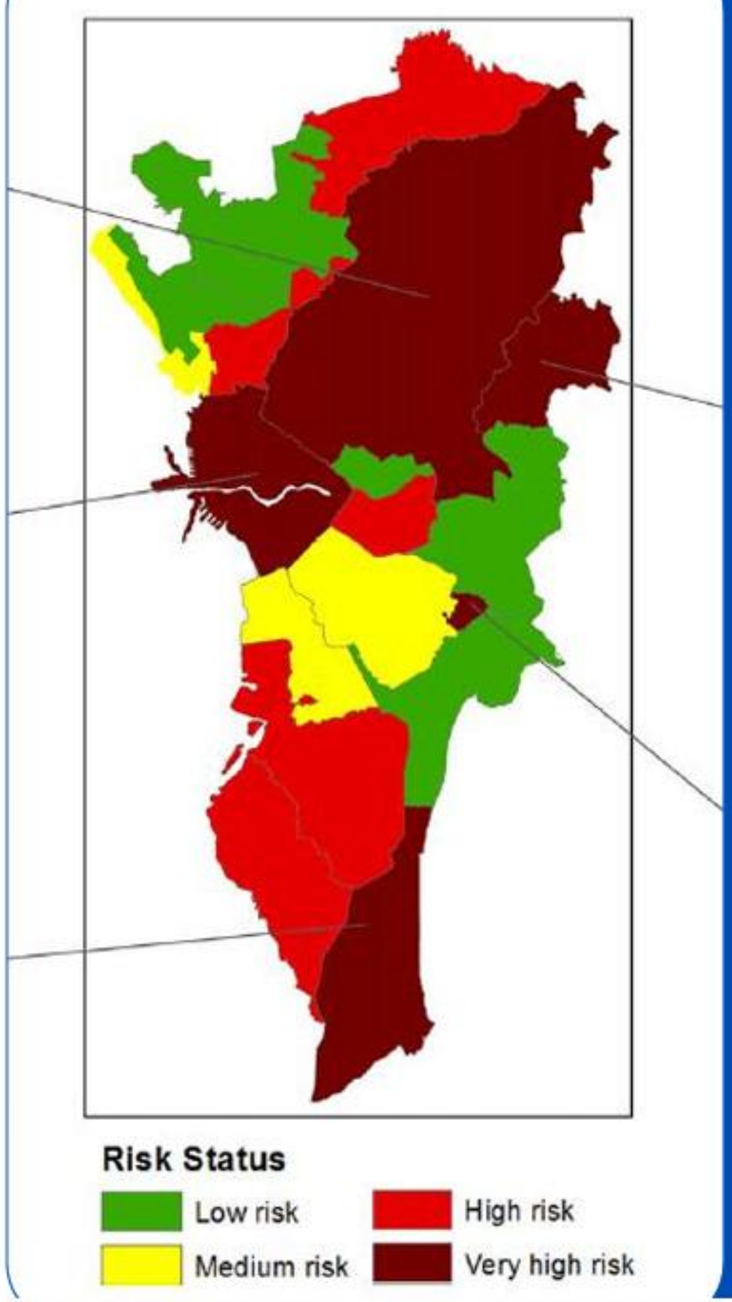
MCV = measles containing vaccine, DTP = diphtheria/tetanus/pertussis vaccine, Penta = pentavalent vaccine

MRAT Key Assessments

Population Immunity	Surveillance Quality	Program Performance	Threat Assessment
Vaccination coverage (MCV1, MCV2)	Non measles discarded case rate	Trends in routine MCV1 and MCV2 coverage	Reported measles cases in specific age groups
SIA coverage	Percent of adequately investigated cases	Dropout rates from MCV1 to MCV2	Recent cases in bordering areas
Proportion of suspected measles cases with known vaccination coverage	Timeliness of specimen collection and laboratory results	Dropout rates from DTP1 to MCV1	Population density and presence of vulnerable groups
Total points = 40	Total points = 20	Total points = 16	Total points = 24

District risk scoring

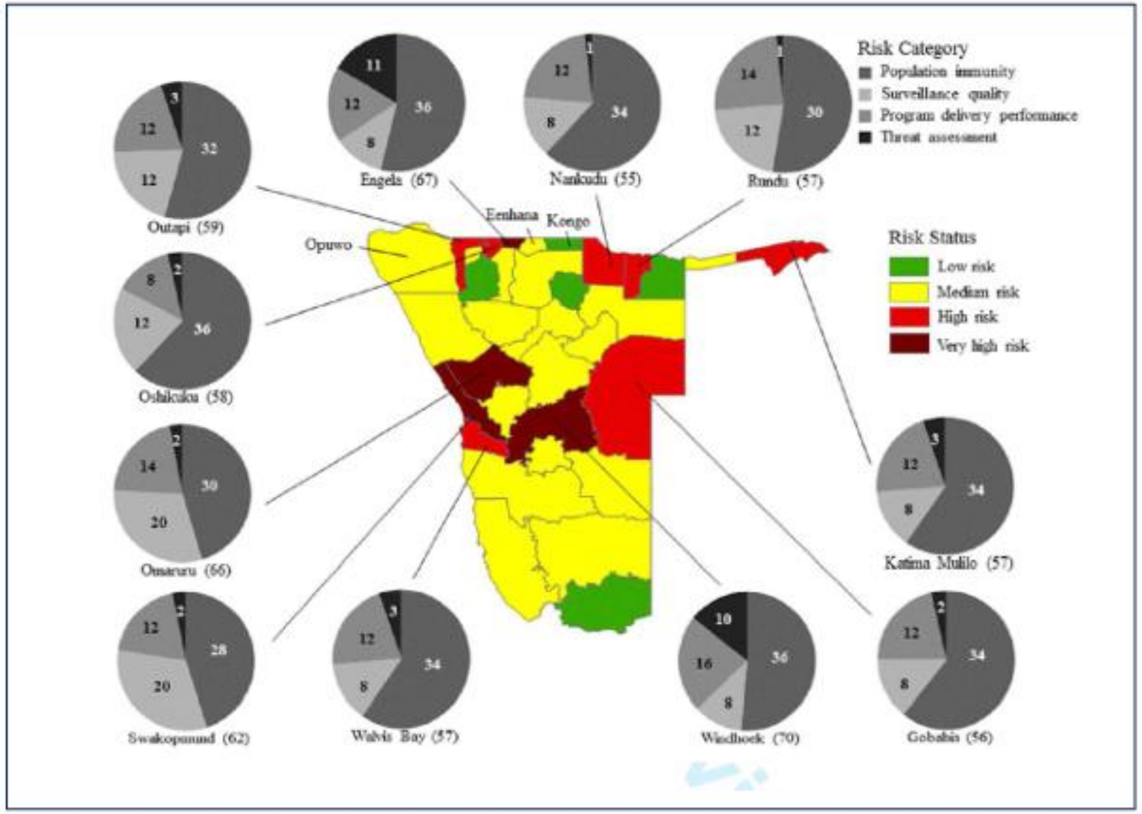
Risk Categories	Total risk points
Low risk	≤ 47
Medium risk	48-54
High risk	55-60
Very high risk	≥ 61



Metro Manila, Philippines, 2010 – 2012

MRAT Outputs

- Subnational risk scored by indicator category
- Tables and maps color-coded by risk category
- Country report directly generated by tool



Overall risk score breakdowns of high- and very-high-risk districts by risk category, Namibia, 2006 - 2008

MRAT Strengths and Limitations

- Strengths
  - Setup guide, technical appendix, and excel files for data entry available online
  - Countries can monitor trends over time
- Limitations
  - Results of any risk assessment depend on quality of data entered into the tool
  - Administrative coverage data ≥100% set to 100%
  - Tool uses previous 3 years of data and trends may have been affected by factors outside of the measles program

MRAT Country Implementation

- MRAT development and initial country use reported in *Risk Analysis* supplement in 2017
    - Senegal, Philippines, India (one state), Namibia, Romania
- MRAT is now used routinely in many countries
- Feedback on the MRAT: develop an electronic version that is more user-friendly, improve the mapping and visualizations
- MRAT is used by countries to assess their measles program for annual planning and for country reports to advance progress towards measles elimination

Resources

- Ducusin MU, de Quiroz-Castro M, Roesel S, Garcia LC, Cecilio-Elfa D, Schluter WW, Goodson JL, Lam E. Using the World Health Organization measles programmatic risk assessment tool for monitoring of supplemental immunization activities in the Philippines. Risk Anal. 2017;37(6):1082-1095. doi:10.1111/risa.12404.
- Goel K, Naithani S, Bhatt D, Khera A, Sharapov UM, Kriss JL, Goodson JL, Lam E. The World Health Organization Measles Programmatic Risk Assessment Tool - Pilot Testing in India, 2014. Risk Anal. 2017;37(6):1063-1071. doi:10.1111/risa.12615.
- Harris, J. B., Badiane, O., Lam, E., Nicholson, J., Ba, I. O., Diallo, A., Fall, A., Masresha, B. G., & Goodson, J. L. (2016). Application of the World Health Organization Programmatic Assessment Tool for Risk of Measles Virus Transmission—Lessons Learned from a Measles Outbreak in Senegal. *Risk Analysis*, 36(9), 1708-1717. https://doi.org/10.1111/risa.12431
- Kriss JL, Stanescu A, Pistol A, Butu C, Goodson JL. The WHO measles programmatic risk assessment tool - Romania, 2015. Risk Anal. 2017;37(6):1096-1107. doi:10.1111/risa.12669.
- Kriss JL, De Wee RJ, Lam E, Kaiser R, Shibeshi ME, Ndevaetela E, Goodson JL. Development of the World Health Organization Measles Programmatic Risk Assessment Tool using experience from the 2009 measles outbreak in Namibia. Risk Anal. 2017;37(6):1072-1081. doi:10.1111/risa.12544.
- Lam E, Schluter WW, Masresha BG, Teleb N, Bravo-Alcántara P, Shefer A, Jankovic D, McFarland J, Elfakki E, Takashima Y, Perry RT, Dabbagh AJ, Banerjee K, Strebel PM, Goodson JL. Development of a district-level programmatic assessment tool for risk of measles virus transmission. Risk Anal. 2017;37(6):1052-1062. doi:10.1111/risa.12409.
- https://www.who.int/teams/immunization-vaccines-and-biologicals/immunization-analysis-and-insights/surveillance/measles-programmatic-risk-assessment-tool

Thank you.

For more information, contact CDC
1-800-CDC-INFO (232-4636)
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Predicting Measles Outbreaks

Gates Foundation project wrapping up now

UNIVERSITY OF GEORGIA

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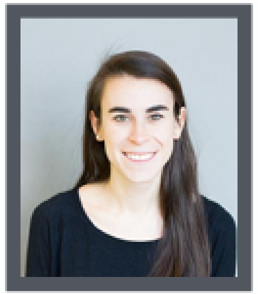


PennState

Matt Ferrari (co-PI)

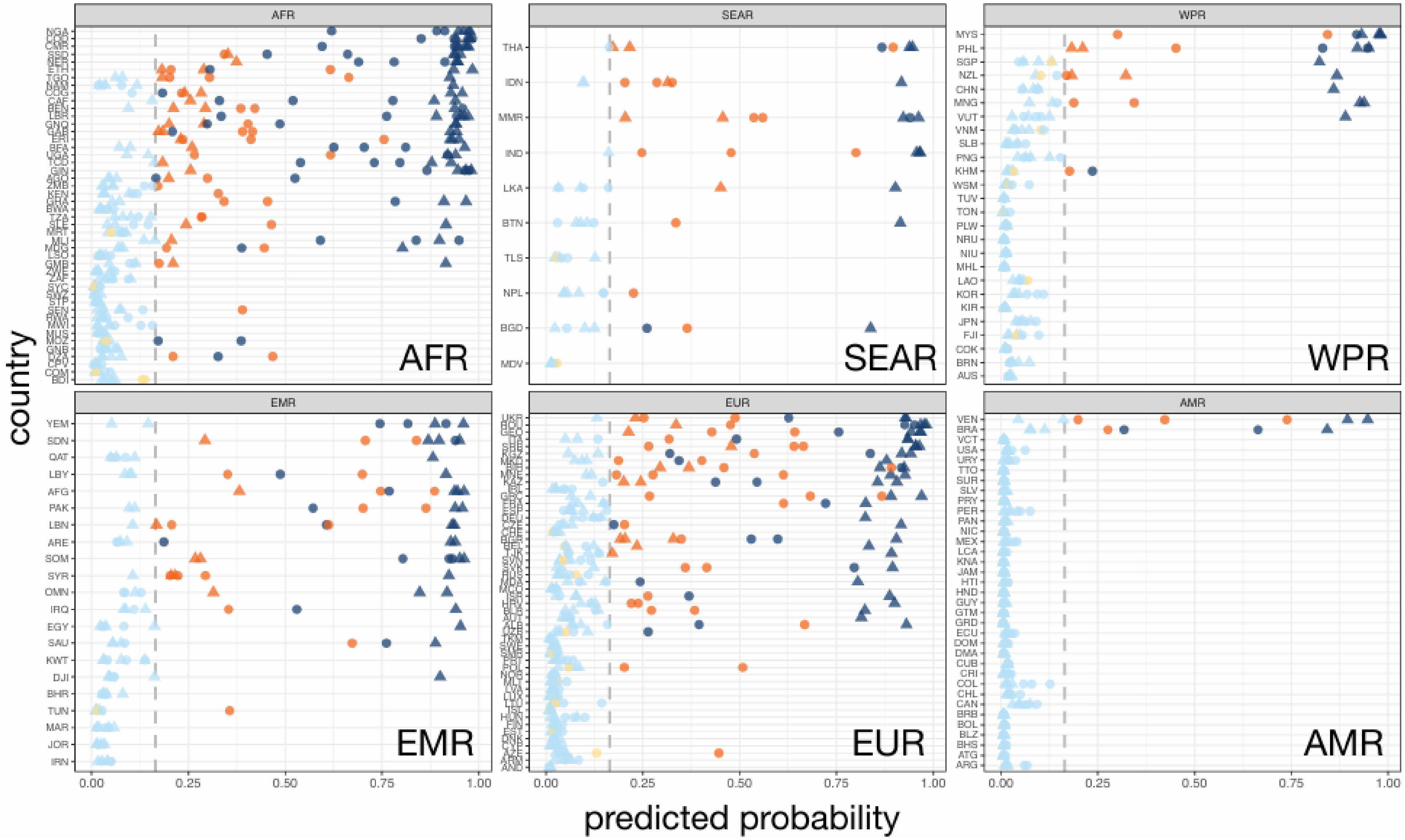
Objective:

To build global scale measles outbreak prediction model using classification machine learning (ML) methods

Using ML to predict outbreaks

Step 0: Collate the data	Monthly measles case data Jan 2011 - Dec 2024 for 187 countries; data on predictors
Step 1: Define prediction target (time step, outbreak definition, prediction horizon)	Annual (12 month) time step; outbreak definition $\geq C$ cases per one million population; prediction horizon of T years ahead
Step 2: Define training, test, and validation sets	Model was trained on 2011-2018 data, with classification threshold optimized using test data 2018-2023 and validated on 2021-2024 data
Step 3: Dichotomize time series of cases into outbreak (yes/no)	
Step 4: Quantify performance of the baseline model	Baseline outbreak probability is the proportion of previous time steps with an outbreak
Step 5: Lag and summarize predictors by time step	Taking into account temporal changes in predictors
Step 6: Train ML model on training set and evaluate model performance on test and validation sets compared to baseline	Hyper-parameter tuning; early assessment of other ML models (RF, gradient boosting, etc)

Predicted probabilities illustrate 3 country groupings



Legend

TP	FP
FN	TN

data type:

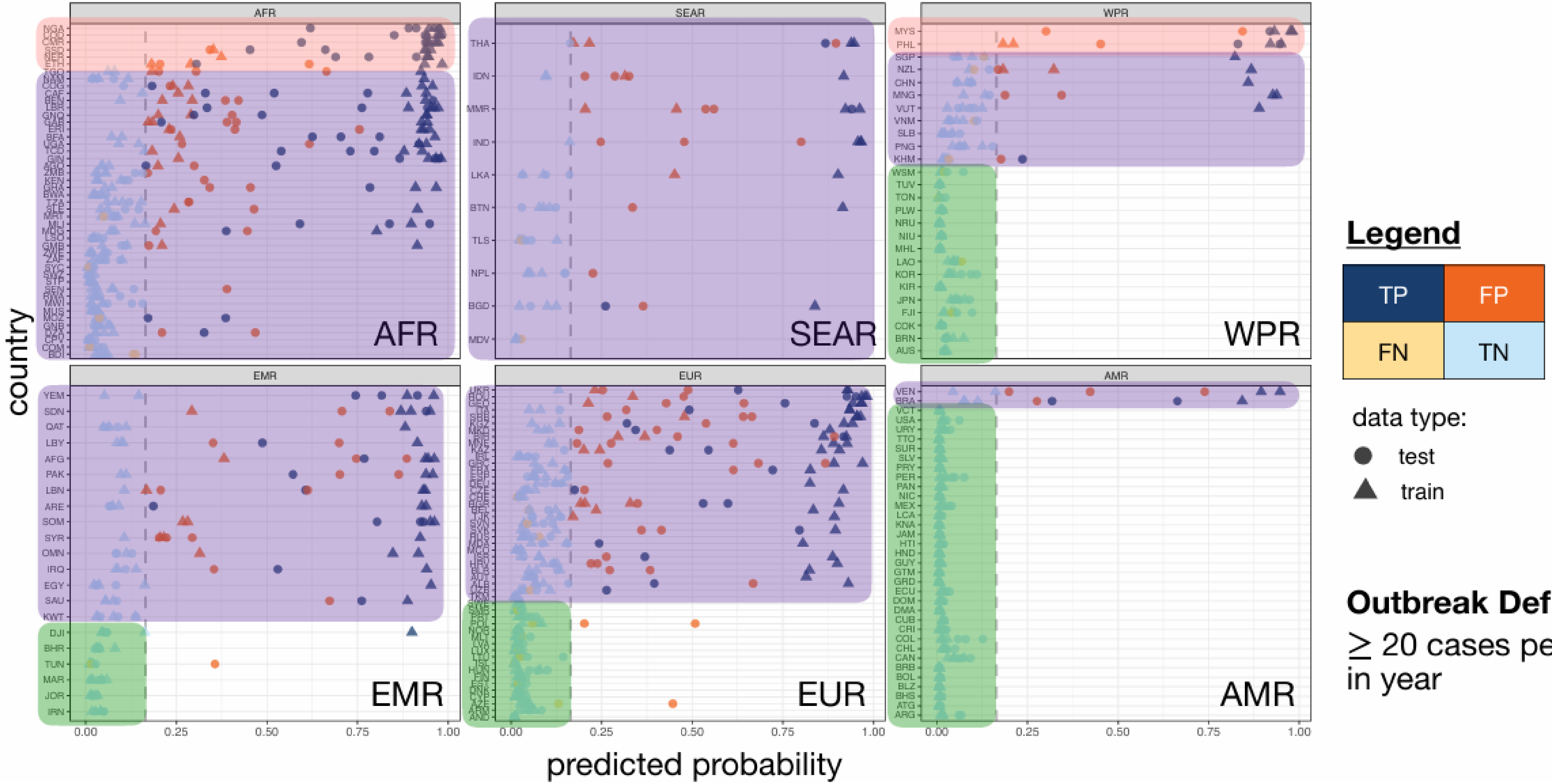
● test

▲ train

Outbreak Definition:

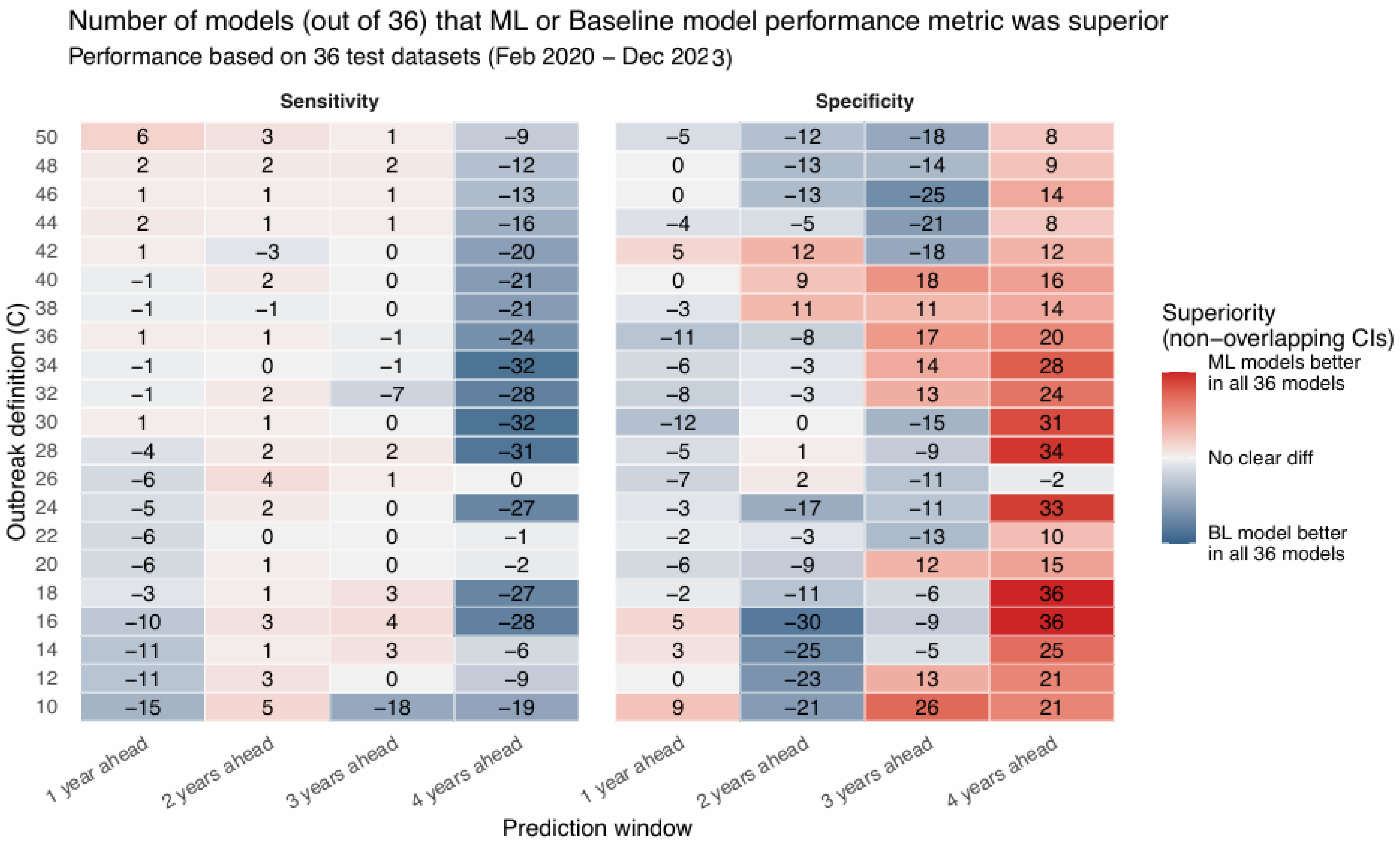
≥ 20 cases per million in year

ML meant to predict for purple countries



Outbreak Definition:
≥ 20 cases per million in year

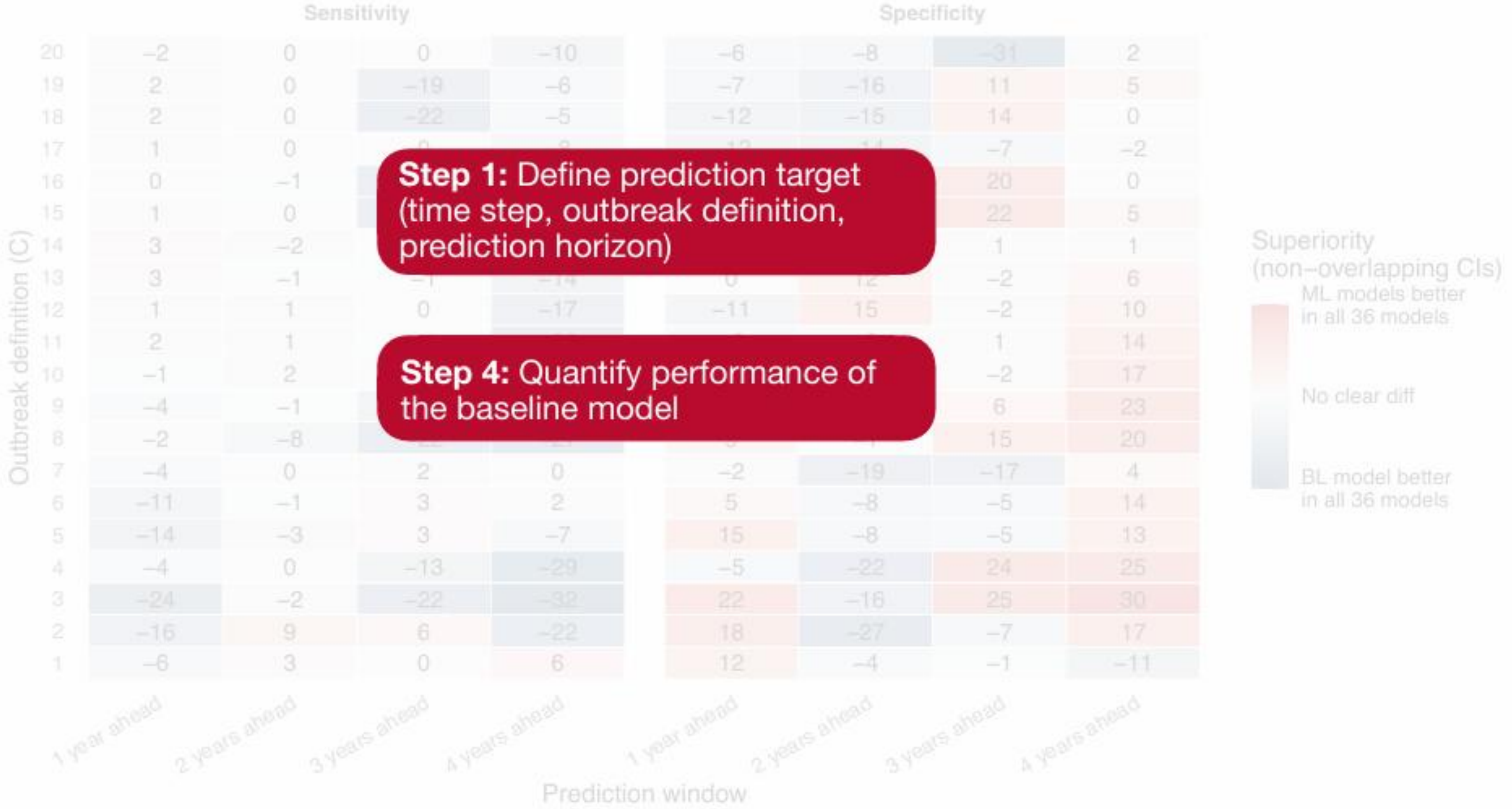
ML model not consistently better than baseline



ML model not consistently better than baseline

Number of models (out of 36) that ML or Baseline model performance metric was superior

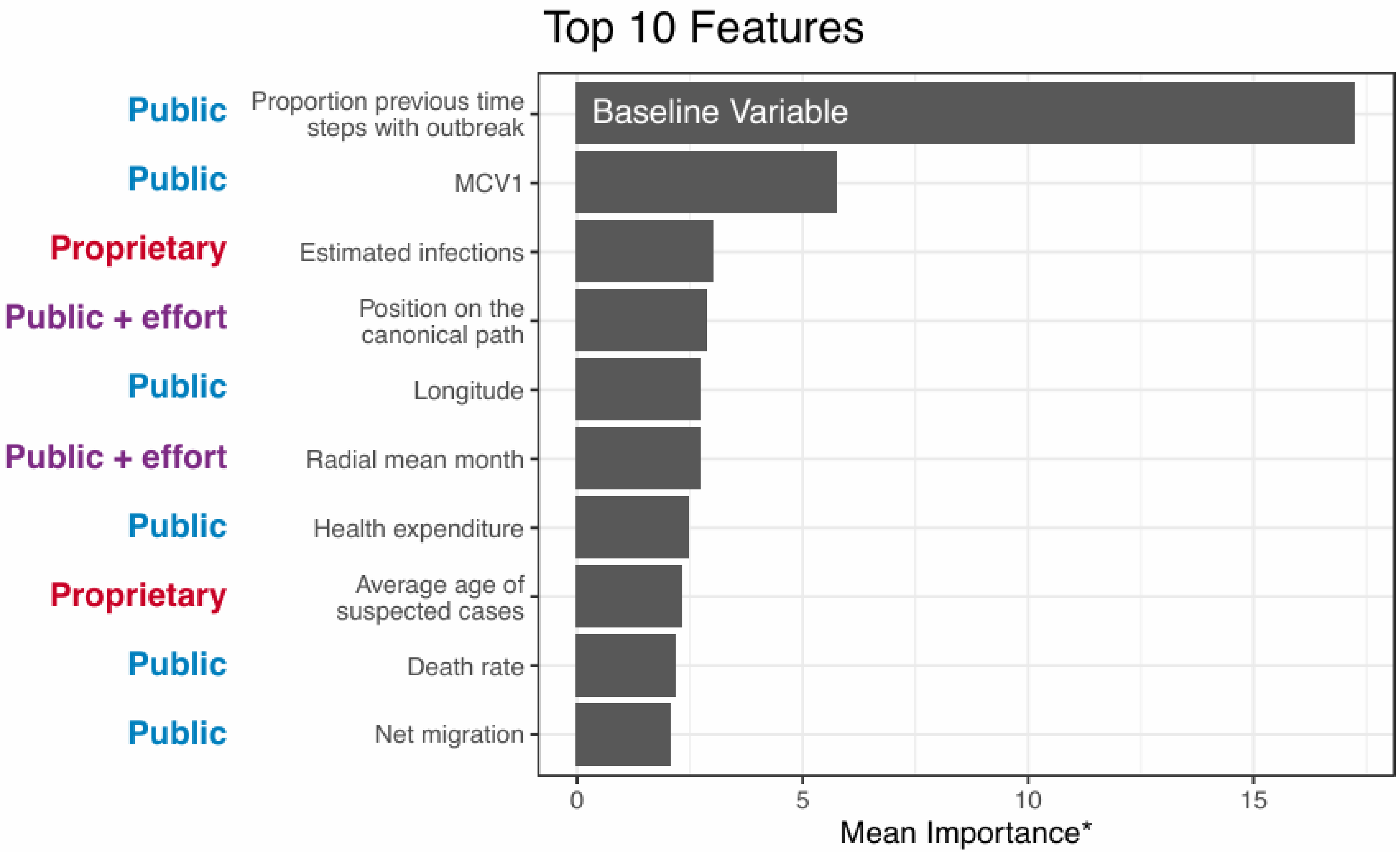
Performance based on 36 test datasets (Feb 2020 – Dec 2024)



Step 1: Define prediction target (time step, outbreak definition, prediction horizon)

Step 4: Quantify performance of the baseline model

Variable importance plots can be used to quantify the value of measles data streams



Challenges and Next Steps

- ML model is not consistently better than baseline
  - Poor noise to signal ratio in the data
  - Potentially national scale hiding subnational dynamics
- ML forecasting national measles outbreaks work is ending

Measles Immunity Profiles

Gates Foundation project just beginning

UNIVERSITY OF GEORGIA

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Saki Takahashi

Simon Mutembo

Chrissy Prosperi

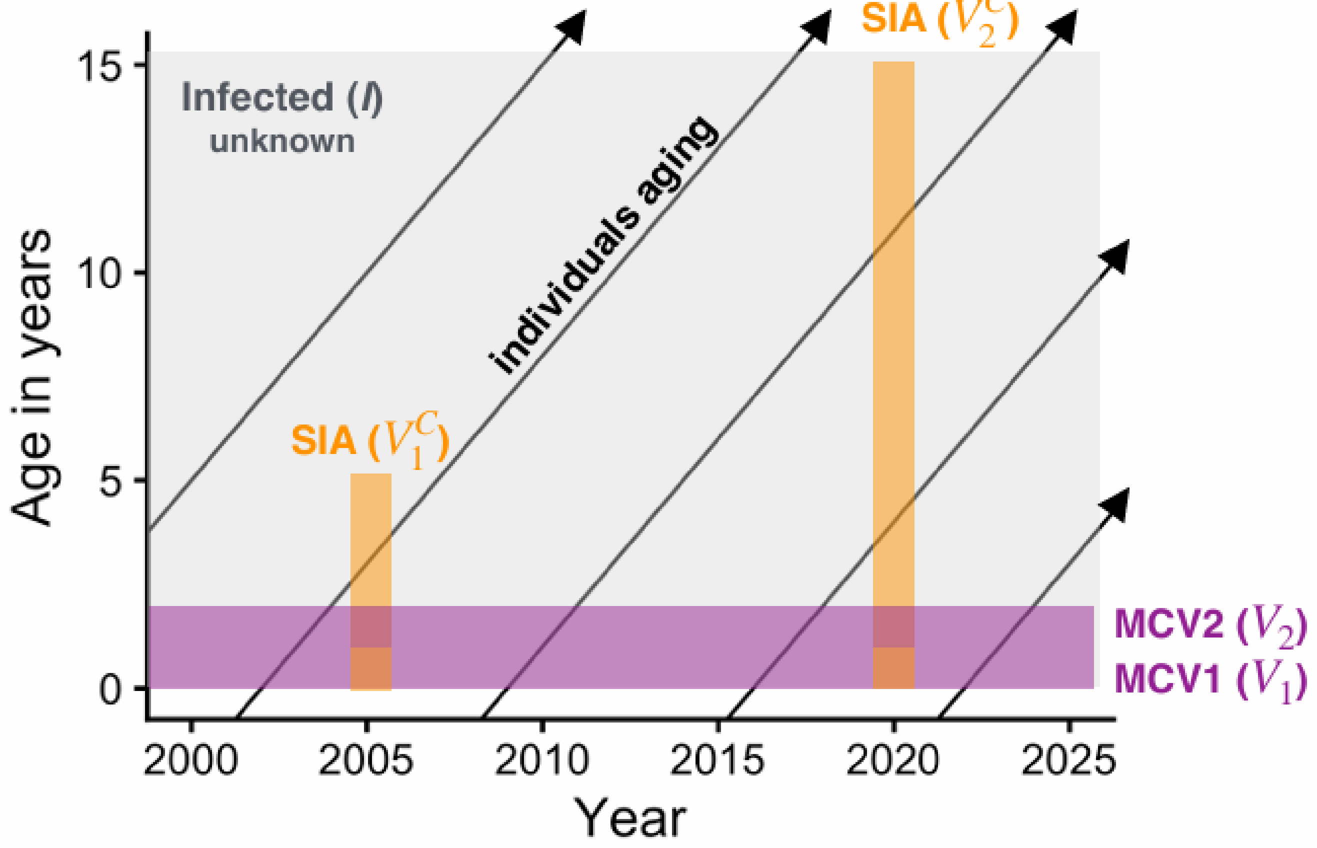
Objectives:

1. To build scalable approach for incorporating infection derived immunity into country level indirect estimates of age-specific immunity

2. To pilot approach for deriving admin1 level indirect estimates of age-specific immunity (including vaccine and infection derived immunity)

Indirect cohort based estimates

Combines infection, routine vaccination, campaign vaccination, and vaccine effectiveness



Sources of immunity

$$s \in \{I, V_1, V_2, V_1^c, ..., V_M^c\}$$

Each birth cohort is divided among mutually exclusive immunity sources whose proportions sum to 1.

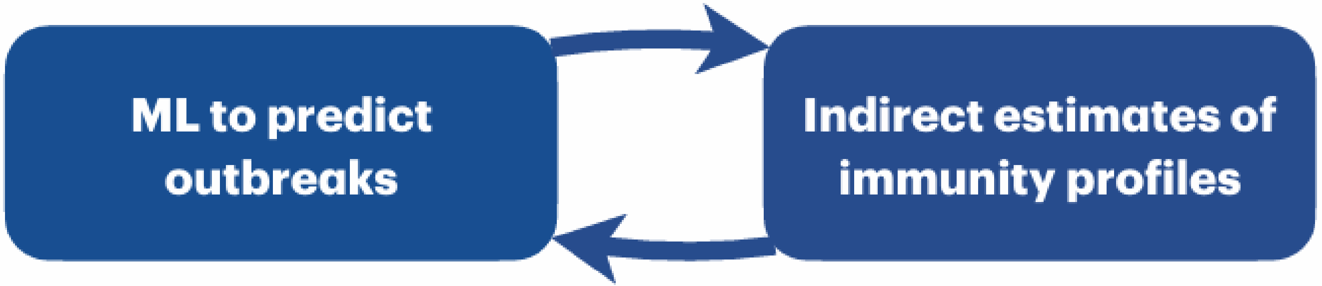
$$\sum_s p(s \mid b) = 1.$$

Infection-derived immunity is solved so that the cohort partition sums to 1

Thakkar et al. 2026, Plos ONE

Conclusions

	"Risk" indicator	Spatial Scale	Time Scale	User & Operation
Project 1. ML to predict outbreaks	Probability of outbreak	National	Predict 1-4 years ahead	International organizations - Resource prioritization
Project 2. Indirect estimates of immunity profiles	Proportion susceptible	National and Admin1	Nowcast	Country EPI - Setting preventative SIA schedule



Endemic Measles Forecasting with **EpiFlowML**

James Schlitt, Amanda J. Meadows, Vikram Sridharan, Nicole Stephenson, Nita K. Madhav

[MARCH 2026]

Measles Forecasting to Inform Response Activities

Funding: Gates Foundation

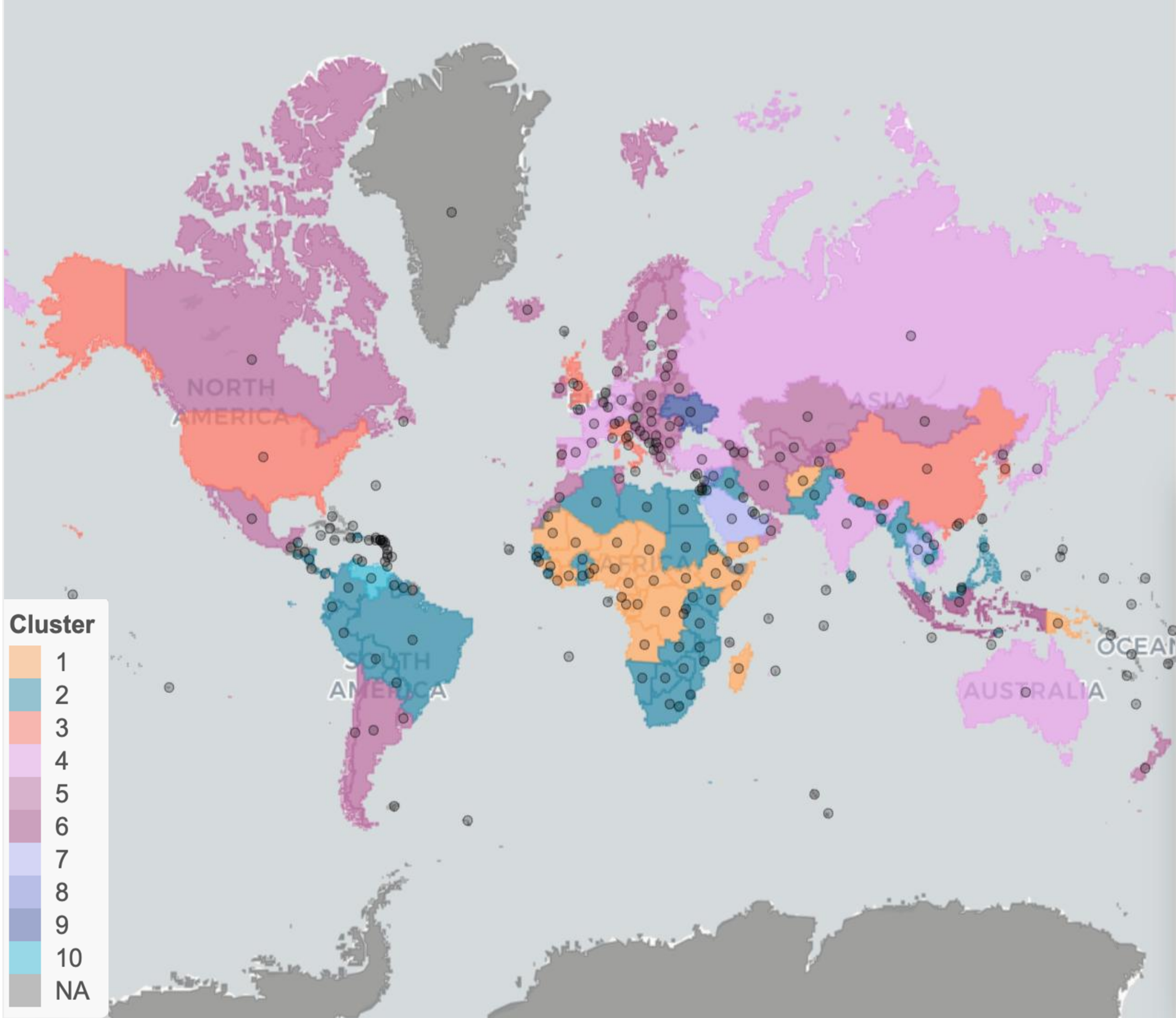
- **Objective:** To develop a country-level measles forecasting model to prioritize countries by their risk of outbreaks over a 9-month prediction window.
- **Policy goal:** To inform supplemental immunization activity (SIA) to prevent outbreaks before they occur.
- **Problem:** Traditional measles models rely on granular datasets that are resource intensive to generate and vulnerable to data scarcity and fragility.
- **Approach:** Pipeline the application of wrapped machine-learning (ML) algorithms, preprocessing routines, and outcome metrics on readily-available, diverse data streams to develop a model which forecasts a coming measles outbreak.

Epidemiologically Relevant Country Grouping

Grouped countries via cluster analysis (case and environmental predictors)

Applied pooled models to enhance performance in regions with limited data

Cluster	Qualitative Description (relative)
1	High birth rate, low vax, low travel, high temps with low variation
2	High birth rate, high vax, low travel, high temps with moderate variation
3	Low birth rate, high vax, high travel, moderate temps
4	Low birth rate, high vax, moderate travel, moderate temps with high variation
5	Moderate birth rate, moderate vax, low travel, extreme variation in temps



Outcome Variable

- Defined an outbreak month as >= 5 reported measles cases per million
- Prediction windows set to 9 months
- Models were evaluated based up on their ability to predict outbreak prioritization tiers

Prioritization Tier	Number of outbreak months in the prediction window
A - Higher	7 or more months
B - Moderate	4 – 6 months
C - Lower	1 – 3 months
None	0 months

Model Fitting

Swept all possible combinations of:

Geography binning method

- Single country and cluster

ML models

- Random Forest, Bagging Regressor, CatBoost, Gradient Boosting, XGB Regressor, boosted heavy ensemble, diverse ensemble

Predictors: All models contained temp and precipitation plus up to 3 additional predictors

- Additional predictors were chosen based on univariate associations with outbreak status
- Predictors were evaluated for multicollinearity

Selection of Best Model Configuration

The **single country fit + single model** was the **best configuration**

- Best balance between proportion of acceptable countries and the total number of countries able to be modeled
- 74.8% of 111 modeled countries yielded an acceptable prediction

Although the single country fit + ensemble model configuration had a higher percentage of acceptable countries, seven fewer countries were able to be modeled through the validation window with this configuration.

Top 10 Most Common Predictor Variables in the Final Models

Variable/Variable group	**Proportion of selected country models containing the variable or variable group**
Proportion of previous *N* months (rolling window) in outbreak (5 cases per M) - 12 months (0.189) / 24 months (0.171) / 60 months (0.126)	0.486
Months since last outbreak (20 cumulative cases per M) (0.162) Months since last outbreak (20 cases per M) (0.117)	0.279
Monthly air passengers arriving from countries with seasonal measles outbreaks (0.153) Monthly air passengers visiting countries with seasonal measles outbreaks (0.117)	0.270
Cases per M 12-month z-score (0.153) Cases per M 36-month z-score (0.072) Cases per M 60-month z-score (0.036)	0.261
Months since last SIA campaign	0.216
MCV2 coverage (0.135) MCV1 coverage (0.063)	0.198
Migrations per thousand population	0.171
Birth rate per thousand population	0.144

Notes: *The top model for each country could contain up to three predictors (in addition to mean temperature and precipitation). Since the models are multivariate, the proportions in the table will not sum to 1.*

Final Model Assessment: Configurations Considered

Each possible subset (rows) of possible model configurations considered, the number of countries able to be modeled through the validation test window, and the proportion of countries with acceptable predictions. To illustrate which fits and models are included in the subset, cells are shaded and marked with a ✓ to indicate inclusion. The selected configuration is bolded.

Model configuration	Countries modeled through validation	Proportion acceptable	Single country fit	Cluster fit	Single Model	Ensemble
Single country fit + single model	**111**	**0.748**	✓		✓	
Single country fit + ensemble	104	0.769	✓			✓
Single country fit (any model)	109	0.734	✓		✓	✓
Cluster fit + single model	101	0.693		✓	✓	
Cluster fit + ensemble model	22	0.773		✓		✓
Cluster fit (any model)	96	0.698		✓	✓	✓
Single model (any fit)	105	0.705	✓	✓	✓	
Ensemble model (any fit)	75	0.733	✓	✓		✓
Any fit, any model	103	0.728	✓	✓	✓	✓

Final Model: Validation of Predictions

- A Fisher's exact test reveals a highly significant correlation between the observed and predicted tiers (*p* = 1.397 x 10-7).
- Removing the 57 "None-None" countries from this analysis still results in a significant correlation between the observed and predicted tiers (*p* = 0.016)
- Final model produces acceptable predictions for 6 more countries than the alpha model

- Over-prediction: two or more groups above the observed group.
- Acceptable prediction: observed group or one group higher to bias the model against under-prediction
- Under-prediction: one or more groups lower than the observed group.
- We saw under-prediction as more detrimental to public health than over-prediction

Prioritization Tier		Observed			
		A	B	C	None
Predicted	A-Higher	6	5	3	6
	B-Moderate	0	2	2	4
	C-Lower	0	5	5	6
	None	0	3	7	57

Prediction	Number of countries	Proportion of total
Over-Predicted	13	0.117
Acceptable	83	0.748
Under-Predicted	15	0.135

Comparison to Simple Baseline

Baseline: the observed case data for each country in a period one year prior to the validation window

	ML Model		Baseline	
Prediction	**Number of countries**	**Proportion of total**	**Number of countries**	**Proportion of total**
Over-predicted	13	0.117	15	0.135
Acceptable	83	0.748	81	0.730
Under-predicted	15	0.135	15	0.135

ML was not able to overcome the data limitations

Exhaustion of methods

- Pooled model fitting (global local)
- Ensembles
- Fuzzing
- ML models (e.g. Random Forest, Gradient Boosting, Bagging Regressor, CatBoost, and XGBoost)
- Imputation of missing data
  - Neural Prophet, AutoETS
- Experimental grid
  - 115 countries assessed (single fit + cluster fit)
  - 14 predictors assessed (permutations up to 3 predictors per country)
  - 5 models assessed, plus 2 additional ensembles
  - 15 replicates of each configuration
  - In total, 800k+ simulations performed

Discussion and Commentary: Generalizability

- **Additional pathogens/ or health outcomes**
  - The model workflow could be adapted to other infectious diseases, particularly those with a strong seasonal component.
  - Would require altering outcome definitions and retraining on appropriate surveillance, social, and environmental datasets.
- **Different levels of geographic resolution (provided availability of data)**
  - Data pipelines transform data sets into consistent country-level inputs
  - Given the availability of appropriate subnational data, the same approach could be reconfigured to aggregate information at regional, state, or district levels.
- **Expansion to different time steps (provided availability of data)**
  - Time step flexibility is embedded in model architecture and preprocessing, allowing for configuration changes to shift the models' timeframe
  - Adaptations from monthly to weekly, quarterly, or annual outcomes are feasible
  - Seasonal clustering and dynamic window selection methods ensure that predictive alignment can be maintained even as the temporal granularity changes.

Scientific Publication

EpiFlowML: A Modular Framework for Standardized and Reproducible Epidemiological Forecasting

INPUT

Model training dataset

- Data ingestion pipeline → Processed training dataset containing:
  - Epidemiological time series
  - Climate variables
  - Social variables
  - Travel variables
- All data aligned to 1 row per country and time step

Configuration files

- Three optional files:
  - Preprocessor rules
  - Model feature specification (metadata workflow)
  - Country-specific train/test split cutoff dates

MODEL TRAINING

Data Loading

- MD5 hashing
- Completeness and uniqueness checks
- Assemble pooled training data
- Data sufficiency filters

Preprocessing

- Missing data handling
- Transformations
- Quality filters

Model fitting

- Scikit-learn model ecosystem
- Model configs parsed from metadata
- Generates forecast for prediction window or *N* months forward

EVALUATION

Standardized outputs

- Projection output: Dates, observed and predicted values, country identifiers
- Summary output: Evaluation metrics, country identifiers
  - Test and train: MSE, MAE, R2, Sensitivity, Specificity, F1
- Metadata workflow: A configuration ID linking results back to metadata files

Visualization dashboard

- Shiny-based interface
- Exploration of observed vs. predicted values, performance metrics, and configuration details
- Supports model review and validation

Risk Mapping of Measles in Niger

Predicting High-Burden Districts

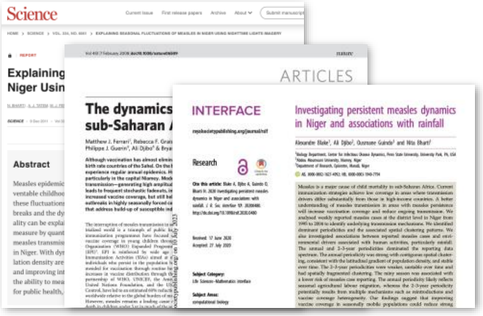
Anton Camacho

MAH Q1 meeting – 9 March 2026

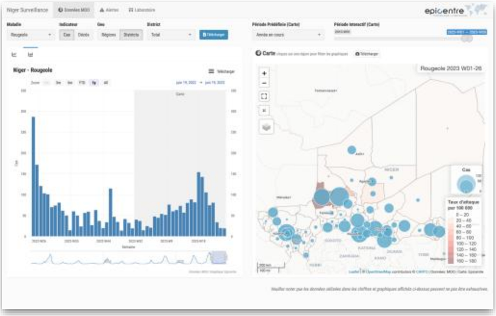
epicentre ÉPIDÉMIOLOGIE • EPIDEMIOLOGY

MEDECINS SANS FRONTIERES

Long-standing scientific/operational collaboration on measles in Niger



> 10 publications since 1994



National surveillance dashboard

DSRE
Dr ELH Ibrahim Tassiou
Mr Zaneidou Maman
Ms Aicha Arzika

Epicentre
Dr Ousmane Guindo
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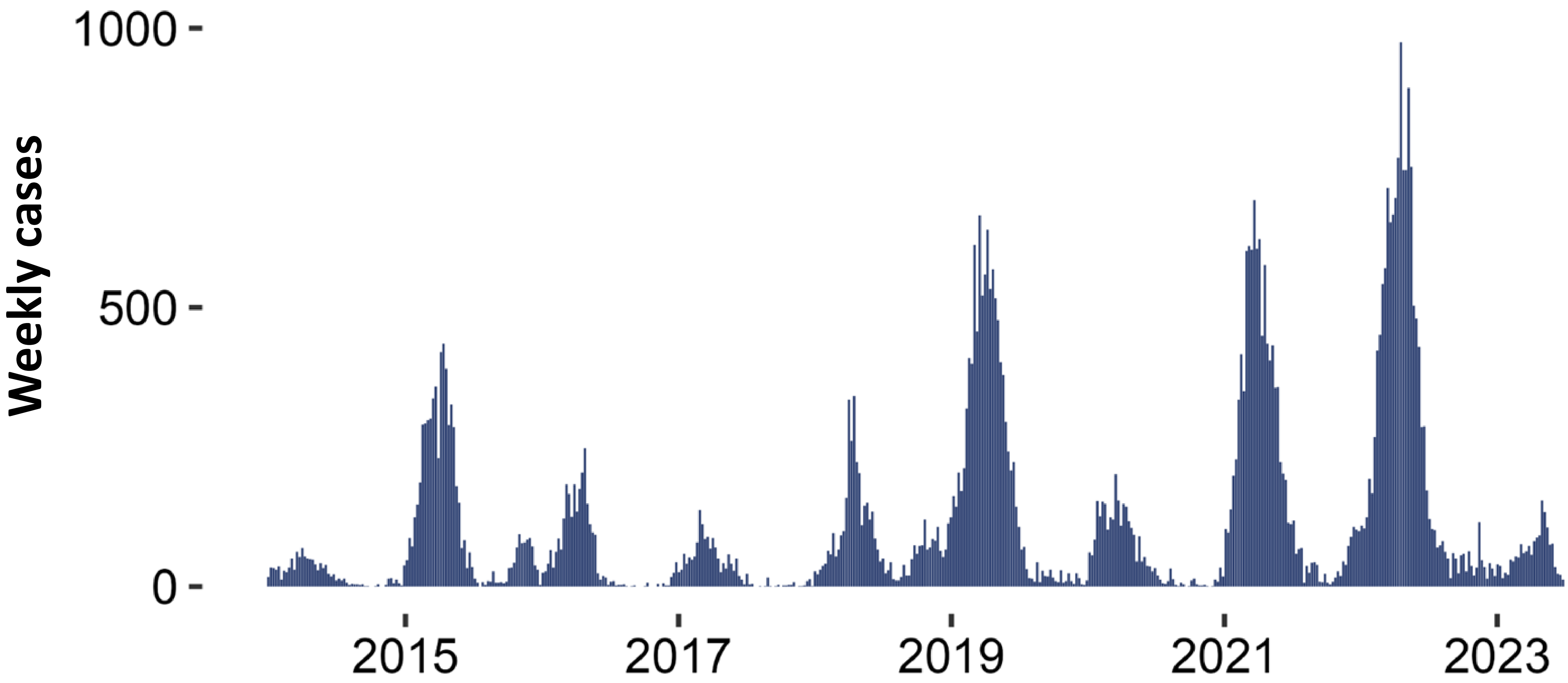
Mr Kimba Moussa Harouna

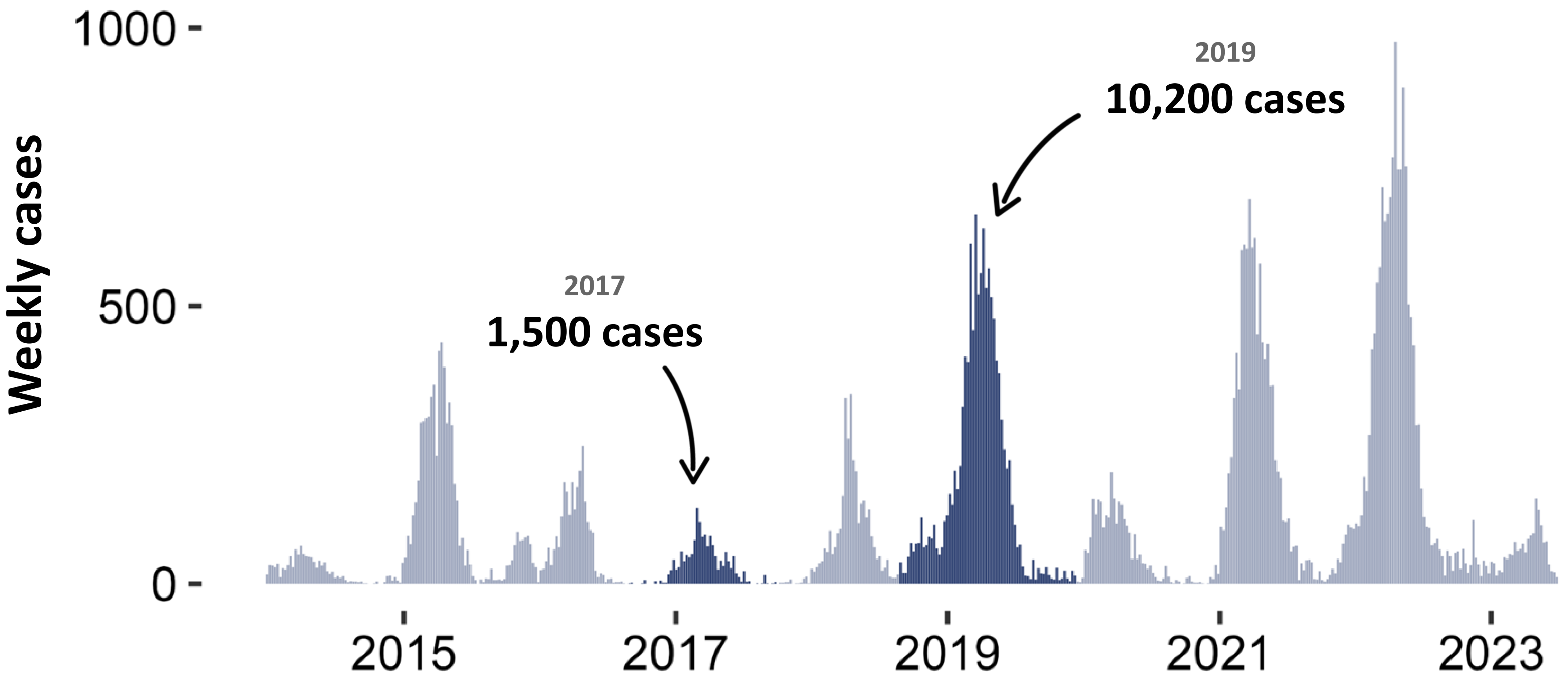
LSHTM
Dr Sebastian Funk
Dr Alexis Robert
Dr Manuel Stapper

Significant variability in the size and location of epidemics



Data source: MDO

Significant variability in the size and location of epidemics



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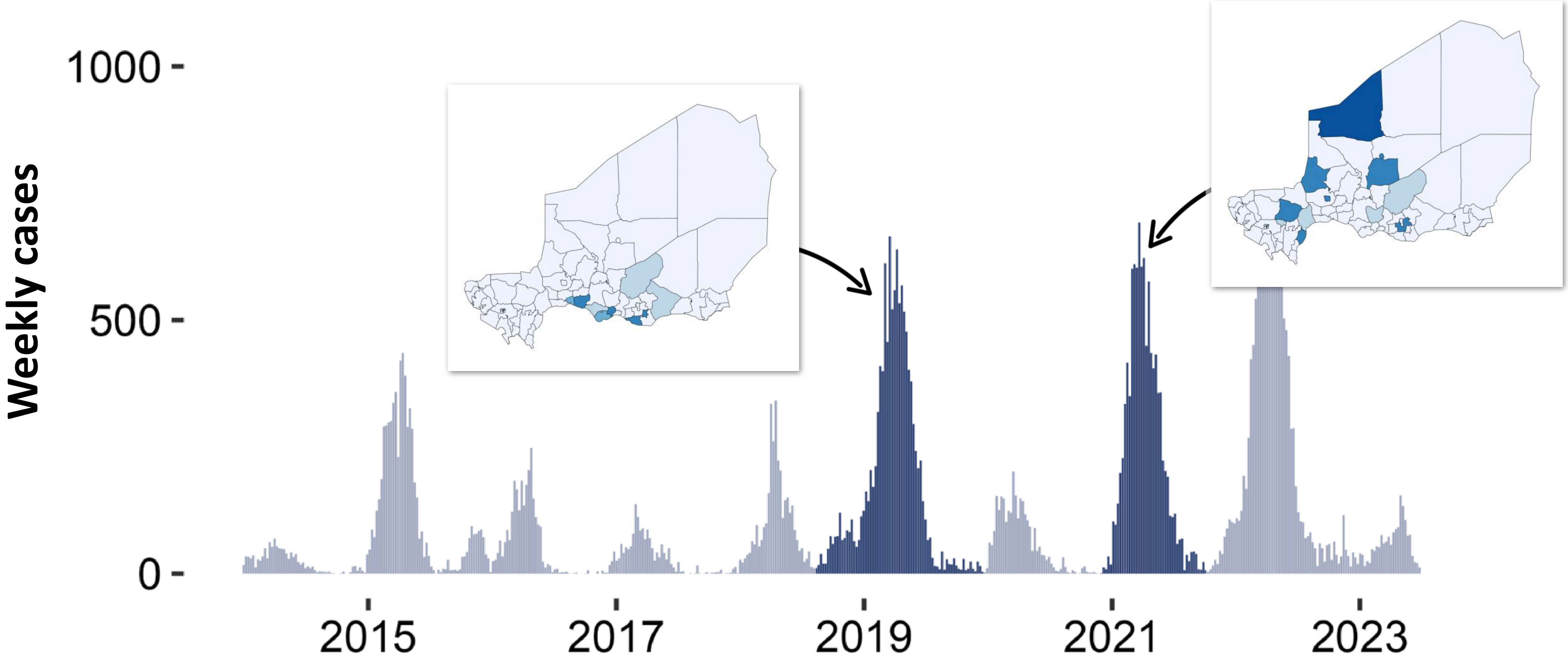
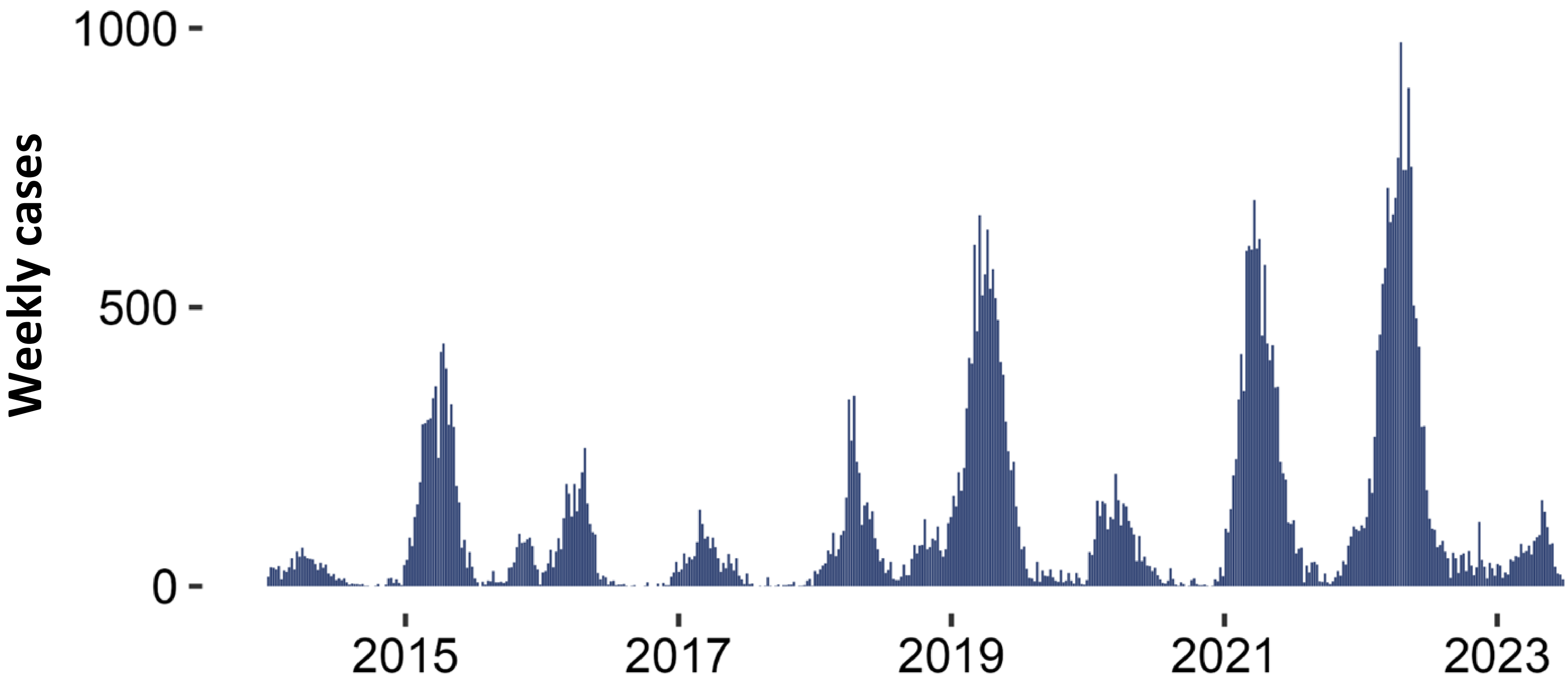
Significant variability in the size and location of epidemics



Data source: MDO

Significant variability in the size and location of epidemics **poses challenges for operational planning**



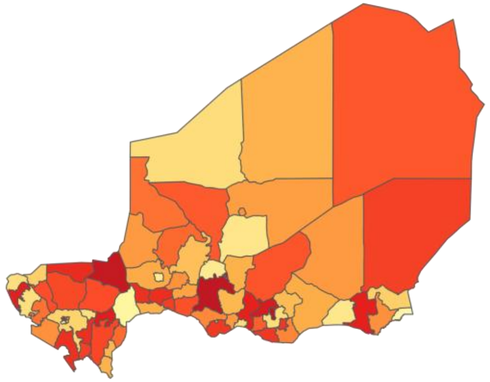
Data source: MDO

PURPOSE OF THE TOOL

Which districts are most likely to experience high measles burden next season?

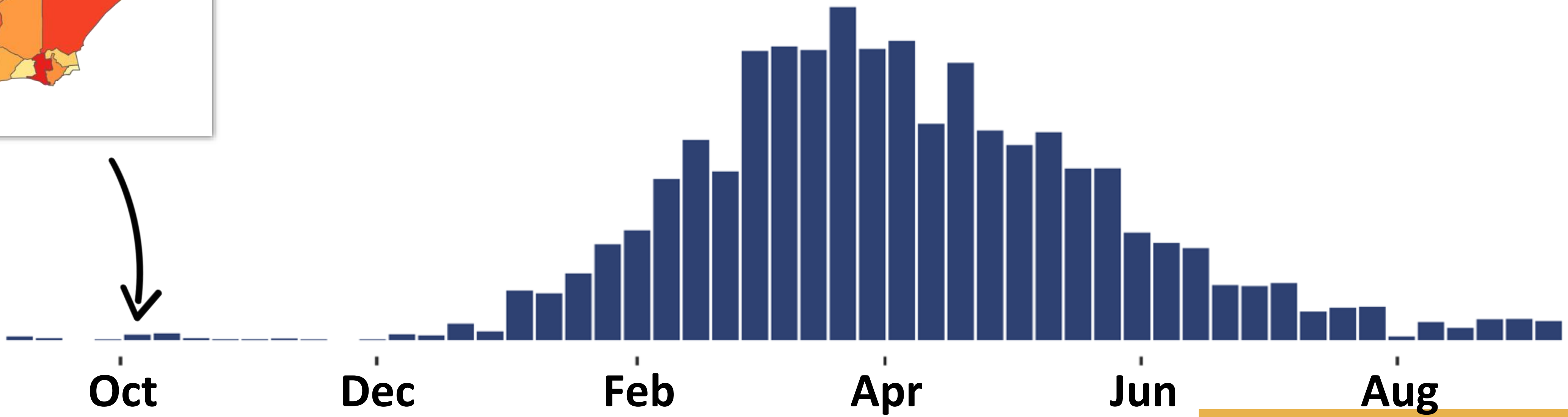
RISK MAP

ahead of season



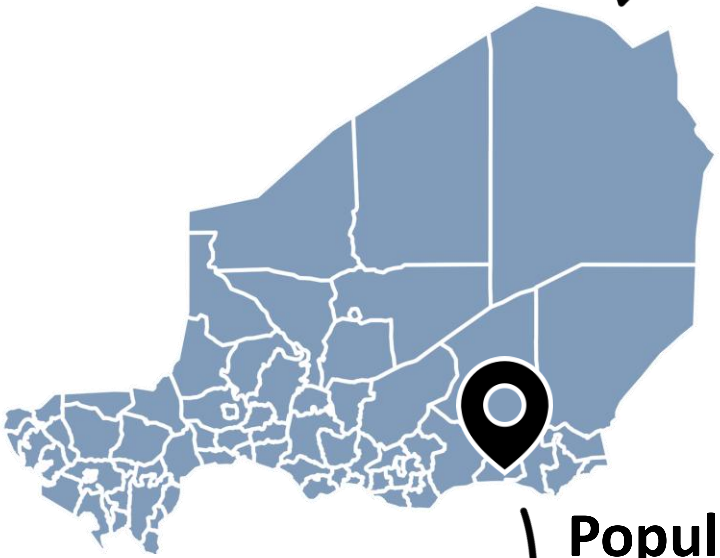
POLICY DECISION

Dimensioning and pre-positioning of vaccine stocks, outbreak preparedness, surveillance prioritisation.

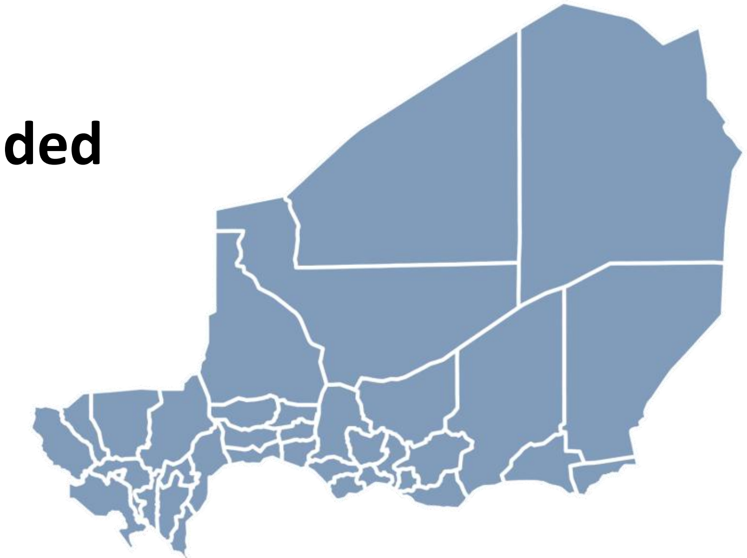


SPATIAL GRANULARITY

Niger: 8 Regions > **72 Districts** > 883 Integrated Health Centers (CSI)

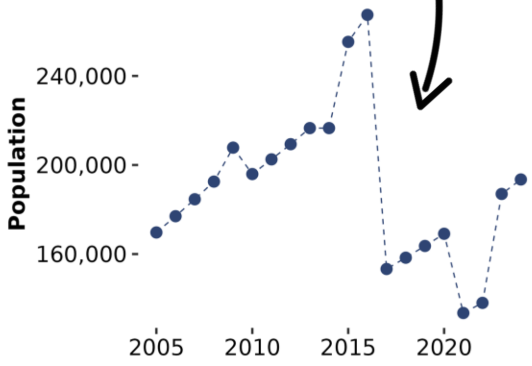


Before 2017: 42 districts



Districts were sub-divided in 2014 and 2017

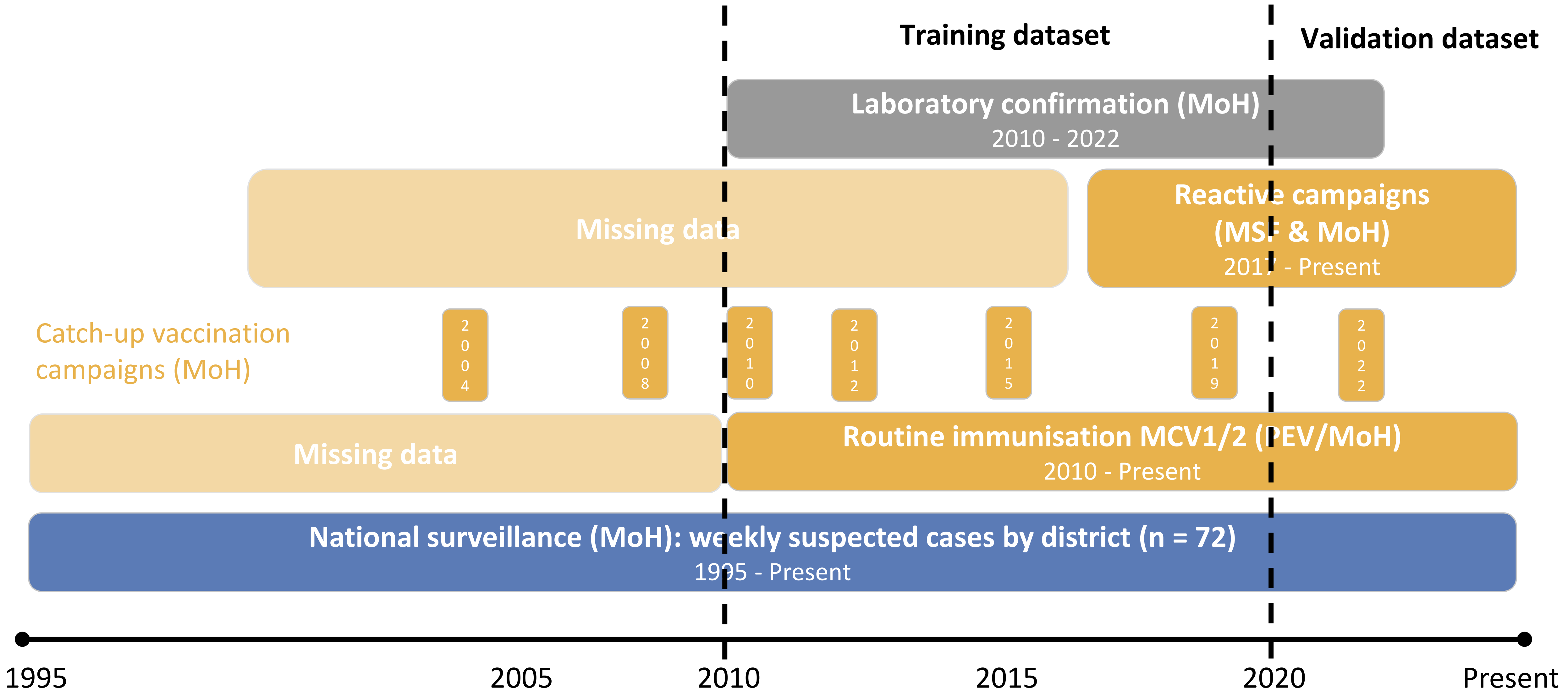
Population



CONSTRAINTS

Although surveillance data is available from 2005 onwards, training the risk mapping tool has been challenging due to district discontinuities.

Key data inputs



Core methods

Model	Target	Variable
Baseline	Number of cases, converted in Top 5/10/15 districts	Median number of cases over past 4 years
NegBin regression	Number of cases, converted in Top 5/10/15 districts	See table below
Random forest	Top 5/10/15 districts	See table below
Ensemble model	Top 5/10/15 districts	6 different aggregations of ranks

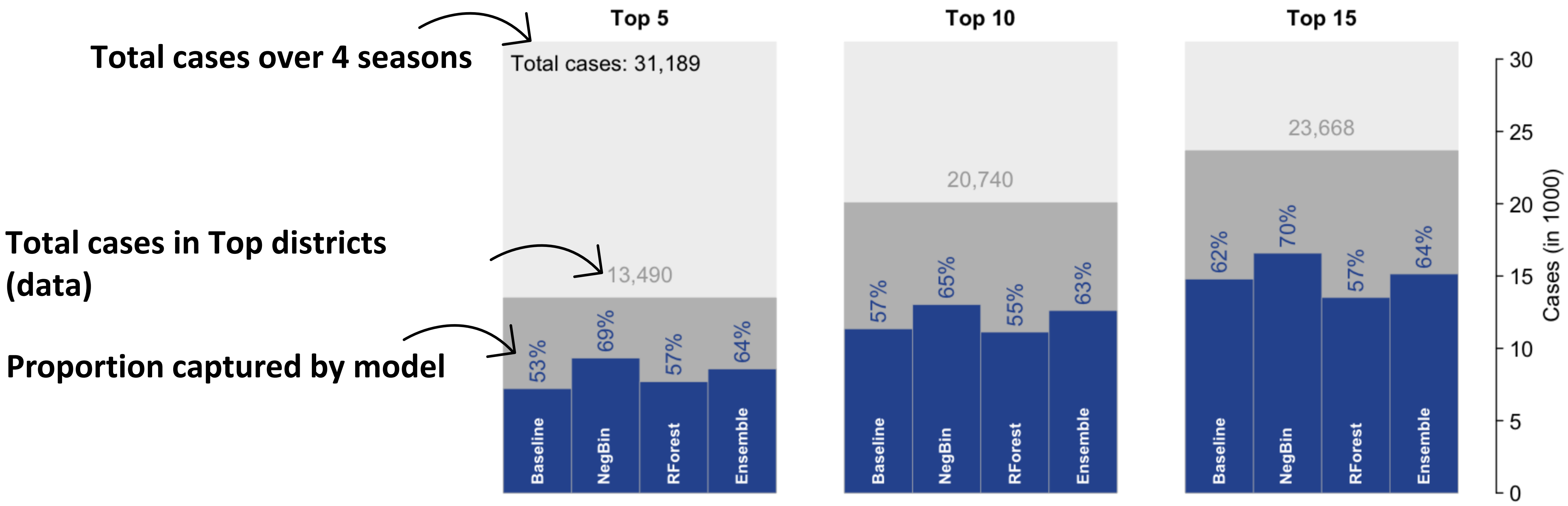
Hyperparameters (e.g. lags) tuned on training data (2010-2019)

Variable	Number	Values	Temporally constant
Historical cases (1-2 seasons)	2	Count data	No
Routine vaccination coverage (1-6 seasons)	6	Proportion	No
Past outbreak occurrence (1-2 seasons)	2	Binary	No
Years since last vaccination campaign	4	Categorical (0-3)	No
Cumulative outbreak count	1	Count data	Yes
Nigeria border indicator	1	Binary	Yes
Population density	1	Continuous	Yes
Population within radius (0, 1, 5, 10km)	4	Continuous	Yes
District indicators	72	Binary	Yes
Distance to hotspots	72	Continuous	Yes

Evaluation on 4 seasons: 2020-2024

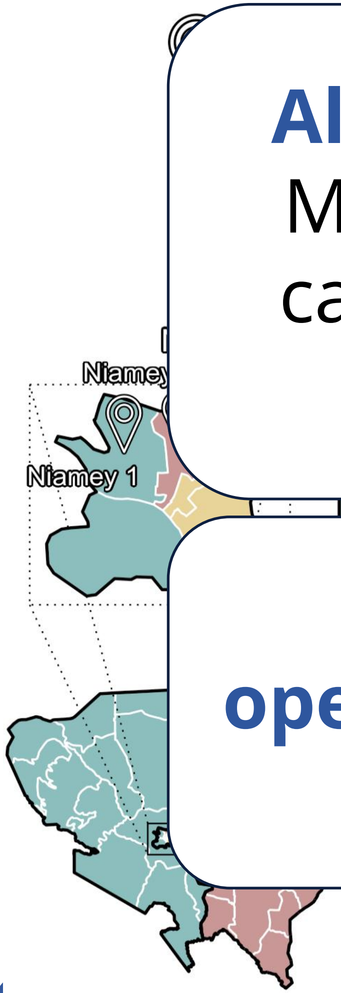
PROPORTION OF CASES CAPTURED

The Neg-Bin regression performed best, capturing 65–70% of cases in the top district sets



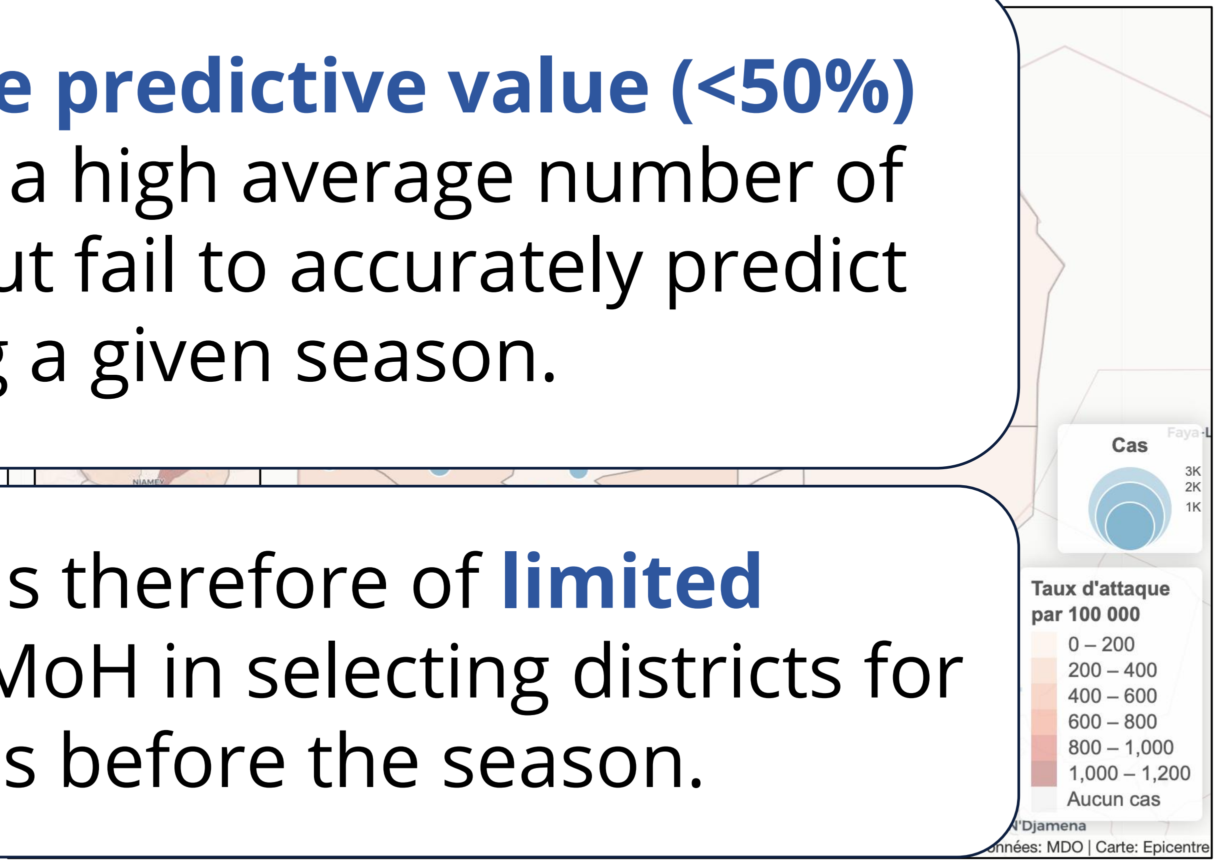
Evaluation on 2024/25 season

Measles cases reported in 2025: only **6 districts** predicted in the Top 15 are within the Top 15



All models have low positive predictive value (<50%)
Models identify districts with a high average number of cases (the most populous), but fail to accurately predict Top districts during a given season.

The risk mapping tool was therefore of **limited operational use** for MSF and MoH in selecting districts for preventive interventions before the season.



MoH data until week 23 (8 June 2025)

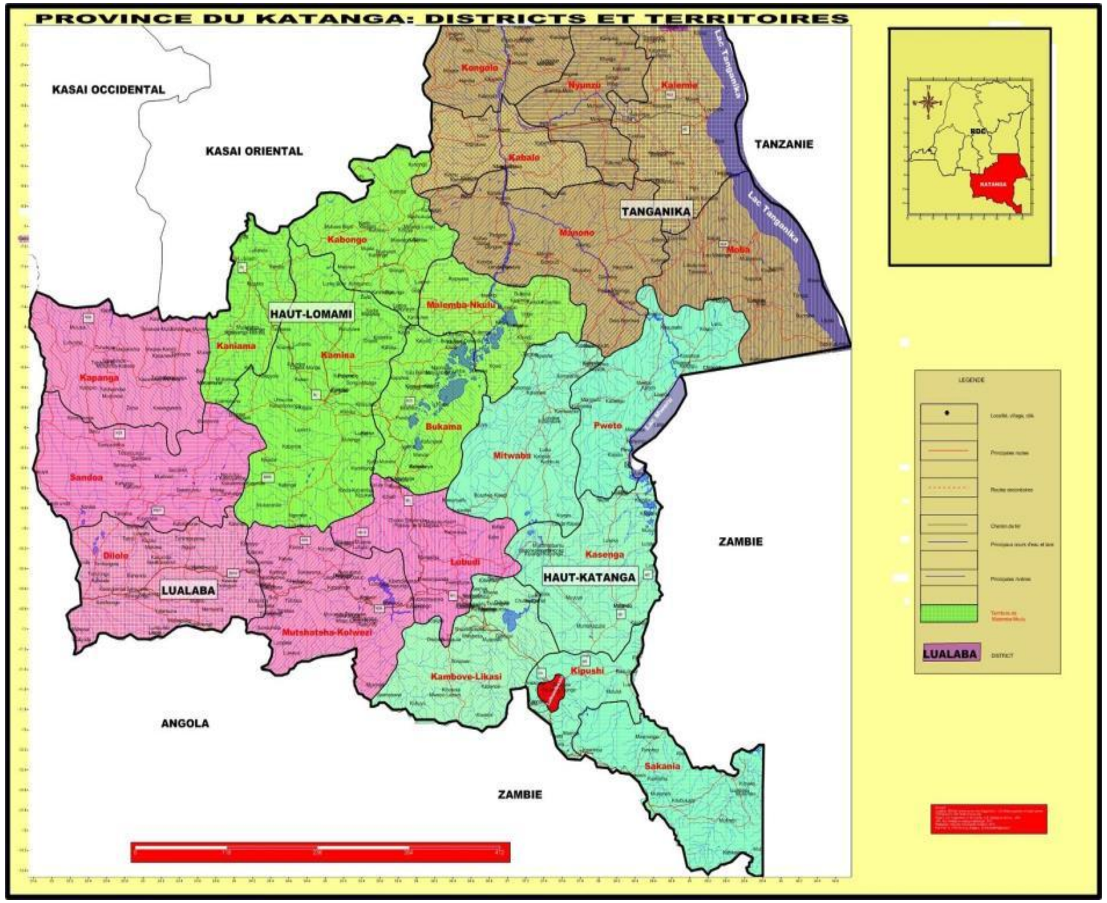
Discussion

- Lessons learned:
  - Complex models performance comparable to baseline.
  - Limited signal from vaccination coverage data.
- Strength: Utility for broad planning. Uses routine data.
- Limitation: Modest PPV. Data quality & completeness.
- Future directions:
  - Include new datasets (mobility, climate).
  - Benchmark performance of other risk mapping tools.

Epicentre / PSU

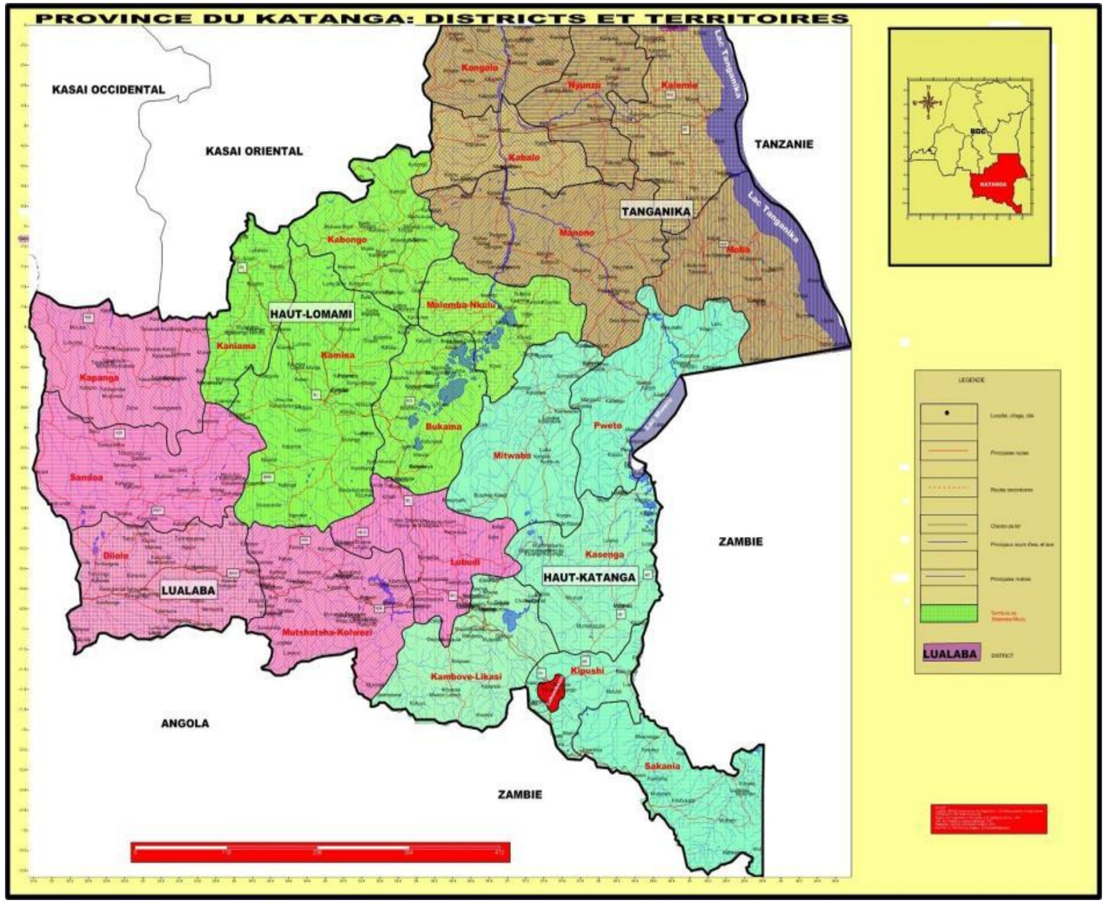
MEASLES ANALYTICS HUB

Objective



- URGEPI was developed to support measles outbreak response by MSF-OCP in 4 provinces in southeastern DRC
  - ~15 million population
  - 68 health zones
- Epidemiological context
  - Low RI coverage
  - Frequent outbreaks
  - Weak seasonality
  - Large IDP population

Initial Activities

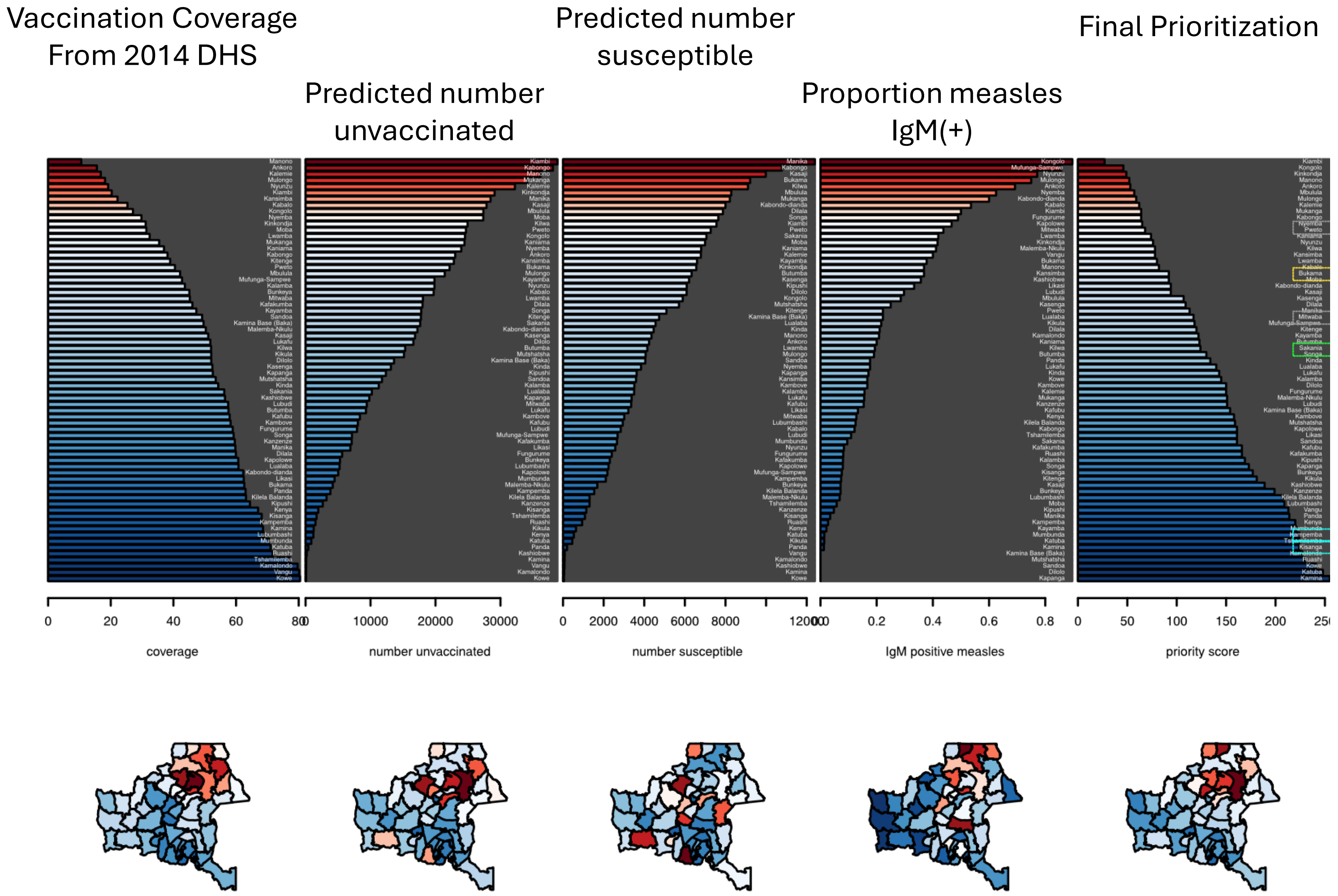


Starting in 2017

- Developed a diagnostic laboratory in Lubumbashi
- Developed sentinel sites to monitor for measles outbreaks. These sites had enhanced support for routine case-based surveillance.
  - Local staff visiting health facilities and digitizing line-lists. Communicated to MSF and to MoH.

Prioritization, not Prediction

Mulitiple Indicator Prioritization



Ranked Health Zones across multiple indicators and took a consensus risk score.

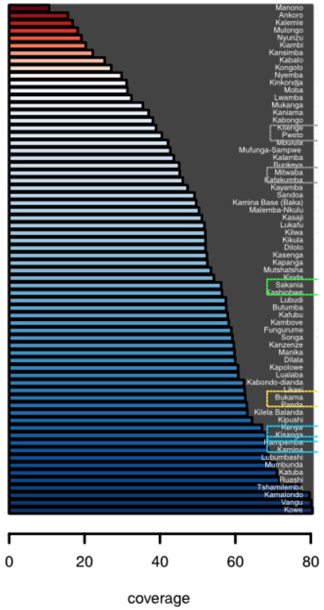
1. Historical vaccination coverage
2. Recent population at risk (projected using recent campaigns and outbreaks)
3. Recent surveillance

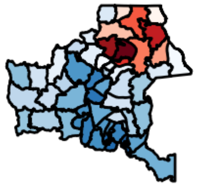
Rank is qualitative indicator of risk.

Not a statement of outbreak risk because we did not have reliable historical case-surveillance on which to train.

Prioritization for Sentinel Sites

Vaccination Coverage
From 2014 DHS





A large outbreak in 2018-2020 provides an out-of-sample test of prioritization

Prioritization for Sentinel Sites

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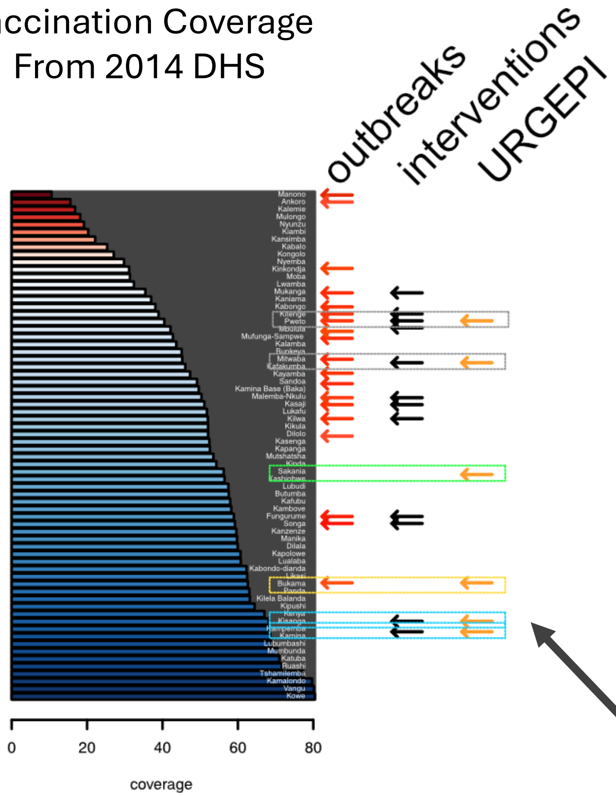
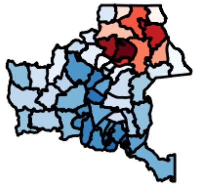
From 2014 DHS



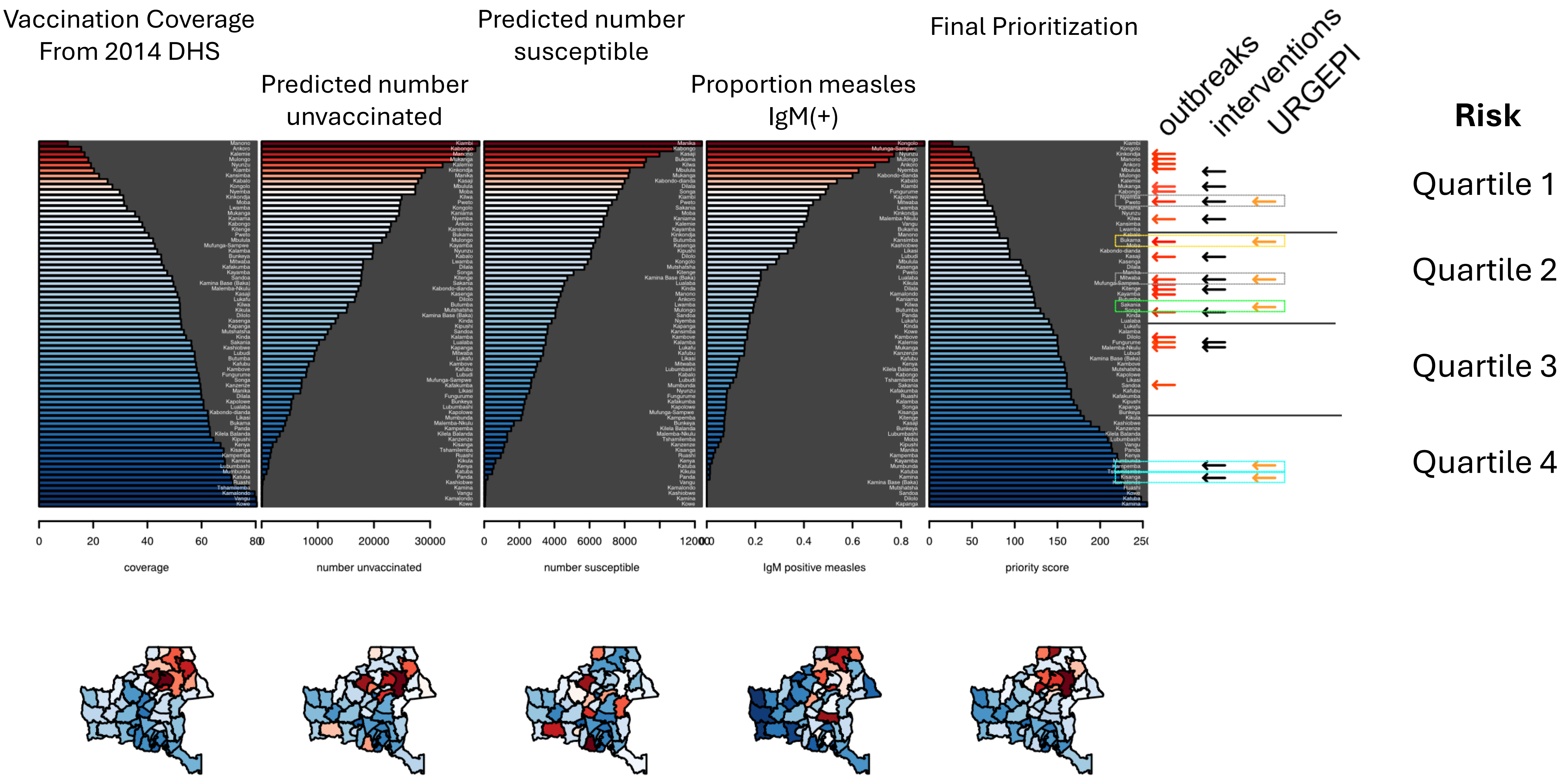


Zones de Sante ranked from HIGH RISK to LOW RISK

- ZdS with outbreaks
- ZdS with MSF interventions
- URGEPI Sentinel Sites

Note that we intentionally chose sites in low-priority health zones as comparators

Prioritization of Sentinel Sites



Distribution of Outbreaks

Priority	Outbreak	No Outbreak	% Outbreak
Top 25%	8	9	42
Bottom 75%	11	40	58

Sensitivity = .42
Specificity = .82
Negative Predictive Value = .78

Priority	Outbreak	No Outbreak	% Outbreak
Top 50%	15	19	78
Bottom 50%	4	30	22

Sensitivity = .79
Specificity = .61
Negative Predictive Value = .88

Conclusions

URGEPI Project was a "*natural experiment*" at outbreak prediction … assessment was truly **out of sample**

A priori risk assessment *was* predictive of outbreak risk, though weak sensitivity … it is hard to predict outbreaks

A priori risk assessment *was* **highly specific for low-risk areas,** it is easier to predict where outbreaks won't occur

Evolution of URGEPI: supporting MSF activities

In 2021, 21 health zones were selected as **Priority.**

Preventive vaccination campaigns were carried out in 9 of the 21 Priority health zones

	Vaccinated	Not
Outbreaks	3/9	9/10
Attack Rate	123/100k	418/100k

Note: 2 health zones excluded because of reactive campaigns

	All 68 Health Zones	**Priority Health Zones**
Preventive vaccination		+ Preventive vaccination in selected priority health zones
Surveillance	- **Data:** weekly health-zone level data from national system - **Laboratory confirmation:** laboratory support in Lubumbashi	+ Enhanced data (health area-level data, linelists) + Sample shipment support
Alert detection & Investigations	- **Alert detection:** Weekly threshold-based detection - **Alert prioritization:** Scoring to identify most pertinent alerts - **Investigations:** In collaboration with MoH	+ More sensitive alert thresholds + Higher weights assigned
Interventions	- **Vaccination campaigns & Case management:** in health zones selected for interventions	

Evolution of URGEPI: supporting MSF activities

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Over period 2021-2023, there were alerts in 66/68 health zones. MSF responded to 24 measles outbreaks. Priority designation uses more sensitive alert criterion and increased weight on "alert score".

Conclusions

URGEPI is a prioritization scheme to guide operational activities. In high-burden, high-risk settings, need for vaccination exceeds capacity.

Prioritization can help focus activities to settings most in need.

Institute for Health
Metrics and Evaluation

Subnational measles modeling - IHME

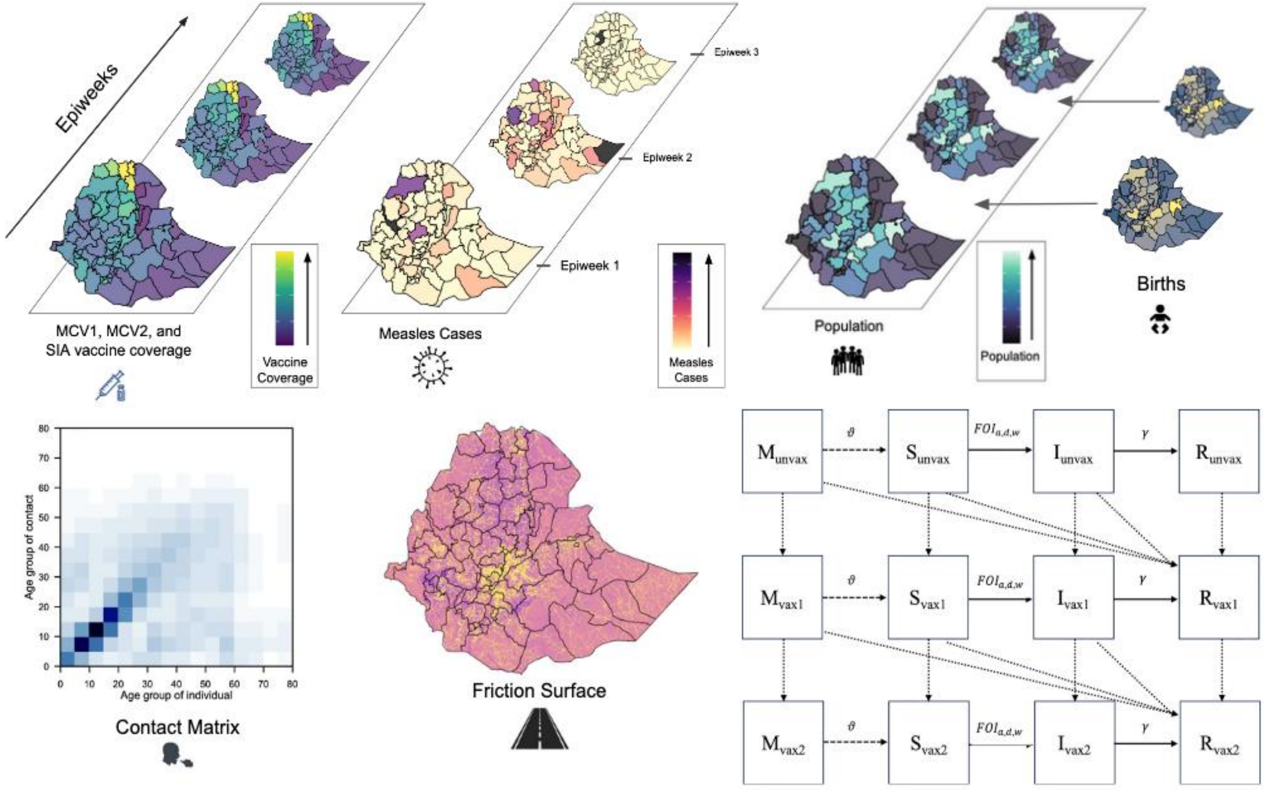
March 9, 2026

Overview

- District-level **MSIR transmission-dynamic model** fit to surveillance data
- Aims to produce **subnational, age-specific susceptibility** estimates to complement subnational vaccine coverage estimates
- Tested using data from six countries shared by WHO but **would need deeper partnership to co-develop further and operationalize**
- Technical capacity for short-term projections under various RI / SIA scenarios but has not been tested or validated
- Computational requirements:
  - Fitting: running on HPC cluster, takes around 24-48h to fit regional models
  - Prediction / simulation: less than a minute (depends on # cores)

Input data

- **Case data:** district-level case data collected by WHO, 2013-2024, supplemented by cases from MOH and other sources where possible
- **Population:** WorldPop surfaces calibrated to GBD population estimates
- **Births**: WorldPop surfaces of surviving infants calibrated to number of GBD live births
- **Contact matrices**: synthetic contact matrices adapted from POLYMOD[1], standardized for location and week
- **Mobility matrices** informed by a gravity model, based on district-district travel time from friction surfaces[2]
- **RI + SIA coverage** (MCV1 + MCV2) from IHME subnational coverage estimates (admin2 level)
    - Assumptions about SIA locations & dose information from technical reports where available



1. Prem, Cook, and Jit (2017) https://doi.org/10.1371/journal.pcbi.1005697
2. Weiss DJ, et al. (2018) https://doi.org/10.1038/nature25181

Model specifications

- **MSIR** + **vaccination status** (MCV 0,1,2+) compartments
- Weekly **time steps** from 1980 – 2024 (1980-2013 = burn-in)
- 24 **age groups** (n = 24):
  - Monthly for 0-11-month-olds, yearly for 1-4-year-olds, 5-9-year-olds, 10-14-year-olds
  - 10-year age bins for 15-64+ year-olds
- **Time/location/age-specific probability of infection**, reflecting cases from other age groups & locations based on mobility & contact matrices
- Fit to r**eported number of cases** via negative binomial distribution
  - "True" cases downscaled by underreporting rate (ρ)
  - Aggregate across weeks, ages, etc. if needed to match data prior to calculating the likelihood

Model assumptions – fixed but modifiable

Assumption	Notes
Single-dose vaccine efficacy	93-95% (represents maximum efficacy of each dose; model can optimize additional scalars for RI vs SIA doses)
Transmission parameters	Constant over time (aside from seasonal variation) and within model region
Seasonal offset	Determined prior to fitting model using a harmonic regression fit to case data (represents typical timing of outbreaks in a model region)
Serial interval	2 weeks
TSIR discretization parameter (α)	99%
Maternal immunity	Wanes exponentially at beginning at 13 weeks old

Model Parameters – able to be optimized

To minimize the NLL and refine the model's fit, the user has the option to either optimize or fix the following parameters:

Parameter	Model Variable Name	Starting Value	Optimization Bounds
Under-reporting rate	Rho (ρ)	0.26	0.005 - 1.0
Vaccine Efficacy	*VE*	0.75	0.4 - 1.0
Minimum Transmission Parameter*	β_{min}	Varies	Varies
Maximum Transmission Parameter*	β_{max}	Varies	Varies
Dispersion parameter in negative binomial distribution	*nb_size*	5.0	0.1 - 50
Ratio of SIA to RI vaccine efficacy	*VE_ratio*	1.0	0.1 - 1.0
Probability of staying of staying within home district	θ	0.99	0.98 - 1

* Initial value and bounds for βmin and βmax are determined by calculating the β values that would yield a plausible R_0 range (ie ~12-18) using a next-generation matrix approach, then applying a buffer to the upper & lower bounds.

Note: practically, some of these need to be fixed and/or tightly bounded (generally not possible to allow all to vary at once)

Other Model Options

Parameter	Description
Admin fit level	1. National – run models including all admin 2 units in the country together 2. Regional – run separate models by region (admin 1)
Buffer districts	If running regional models, can choose to include a percentage of other districts (based on ranking of linkage from mobility matrix), with option to downweight likelihood for buffer districts if desired
Input case smoothing method	1. No smoothing – use raw input cases 2. Loess smoothing – fit to input cases smoothed using loess() 3. Moving average – fit to an average of the input cases over a set number of epi-weeks
Seasonality	Can either assume constant beta value throughout the year or allow for seasonal variation
Importation rate	Define a rate at which cases are being brought in from outside the modelled geographies (e.g., imported cases from outside the country)
Temporal aggregation	Fit cases at the weekly or yearly level
Missing case handling	1. Missing cases do not contribute to the likelihood 2. Missing cases contribute to the likelihood as if they were zeros, but only if the model's prediction implies a high incidence rate (censored likelihood). The threshold is based on a user-defined percentile of the distribution of reported non-zero incidence rates in the model.
Optimization method	1. NMKB – Nelder-Mead gradient-based optimization algorithm for derivative free optimization (with box constraints) 2. PSO – particle swarm optimization (with or without hybrid approach using L-BFGS-B)

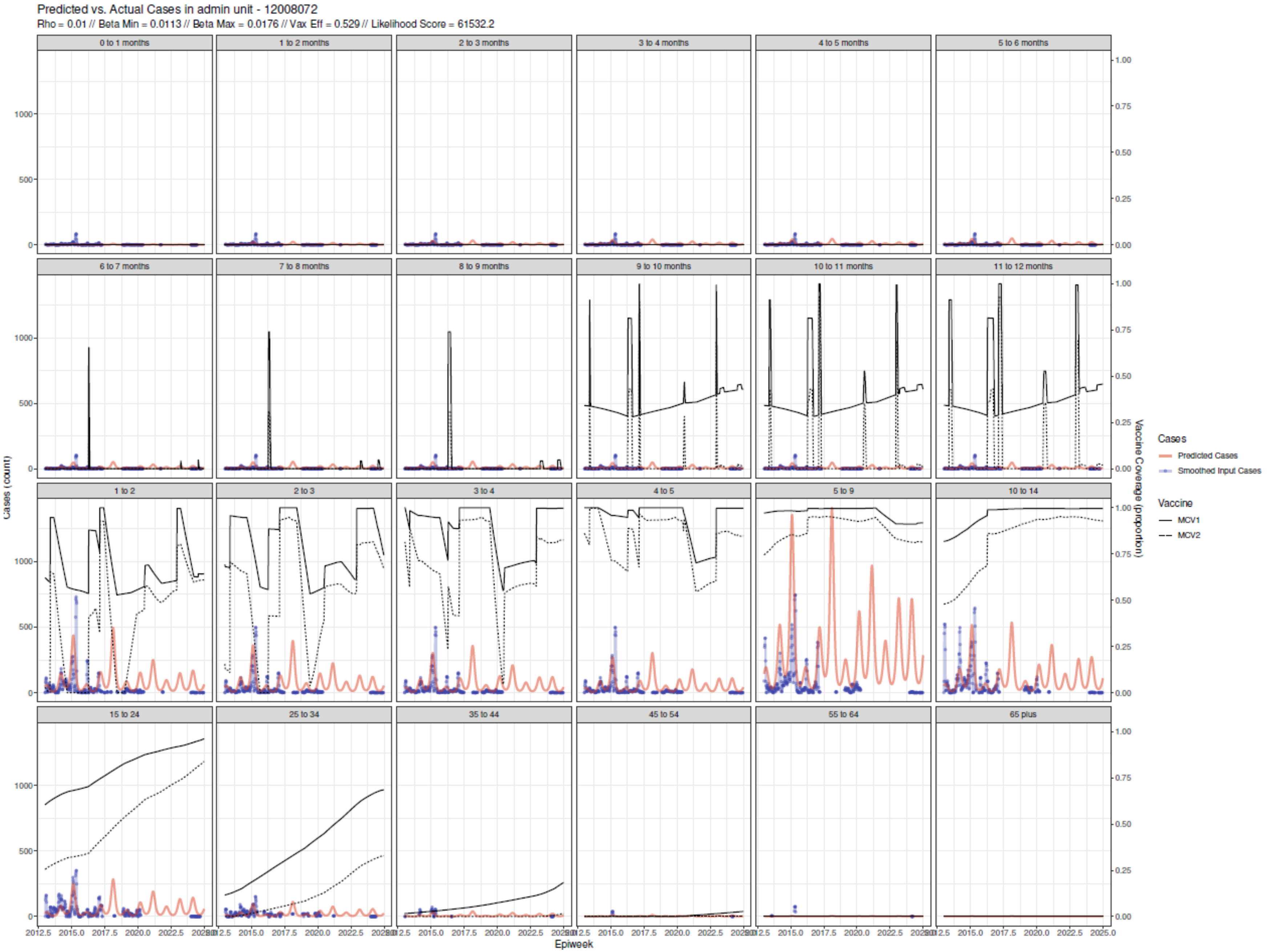
Particle swarm optimization

- Based on the social behavior of **flocks of birds** or **schools of fish**
- A “swarm” of “particles” is launched into the multi-dimensional parameter space, and each moves about the space based on three factors:

- **Inertia**: the tendency of the particle to move in its current direction
- **Cognitive component**: the “self-confidence” of the particle, pulling it back towards the best position that it has personally discovered
- **Social component**: the “swarm confidence”, pulling the particle towards the best position found by any member of the swarm

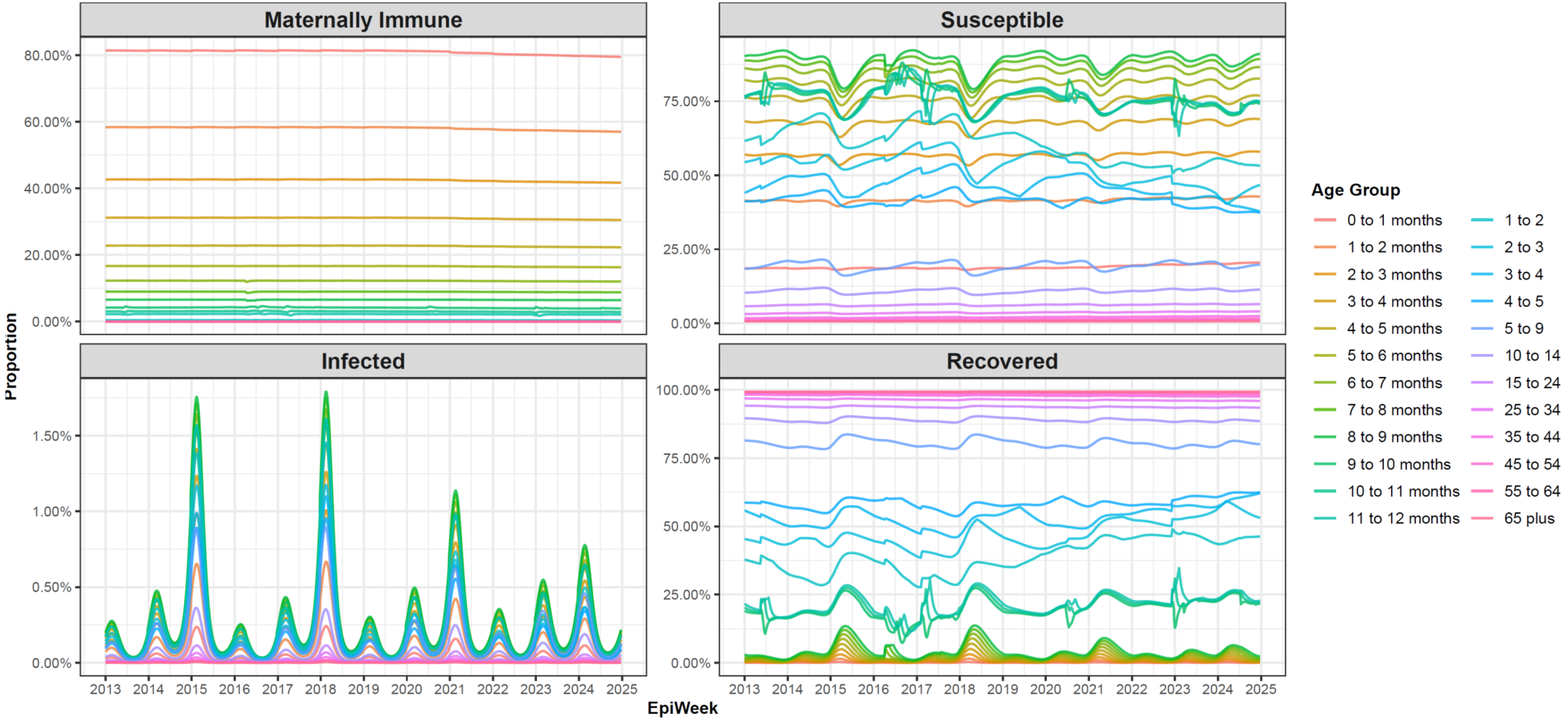
Predicted vs. actual cases and vaccine coverage, by age group

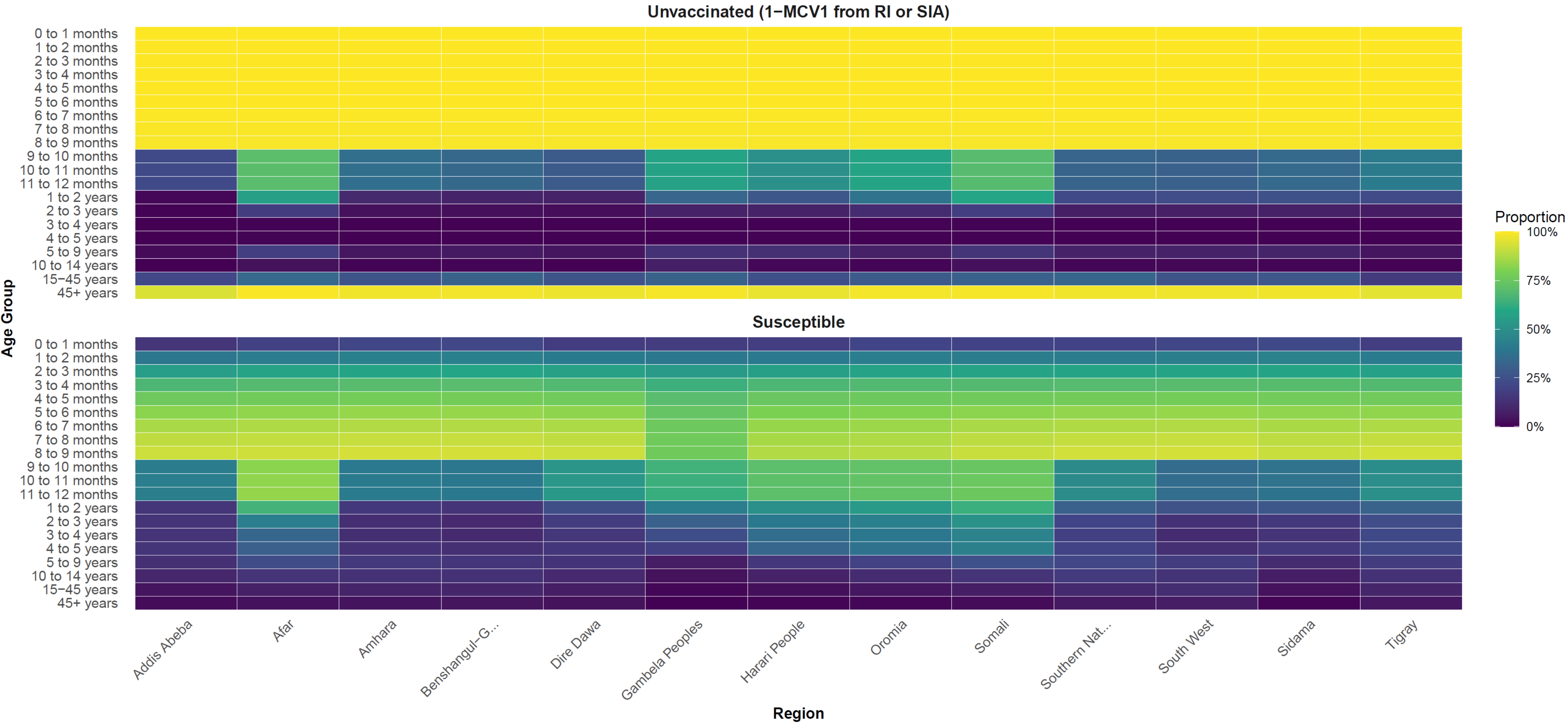
Note: input cases are smoothed using a simple moving average prior to fitting due to sporadic biweekly reporting



Region: Oromia (Aggregated)

Recent History (2013+) | Version: jm_test_regional_pso_auto_beta_ve_risia_fixdata_wideve




Unvaccinated (1−MCV1 from RI or SIA)
Susceptible
Age Group
0 to 1 months
1 to 2 months
2 to 3 months
3 to 4 months
4 to 5 months
5 to 6 months
6 to 7 months
7 to 8 months
8 to 9 months
9 to 10 months
10 to 11 months
11 to 12 months
1 to 2 years
2 to 3 years
3 to 4 years
4 to 5 years
5 to 9 years
10 to 14 years
15−45 years
45+ years
Region
Addis Abeba
Afar
Amhara
Benshangul−G...
Dire Dawa
Gambela Peoples
Harari People
Oromia
Somali
Southern Nat...
South West
Sidama
Tigray
Proportion
100%
75%
50%
25%
0%

Opportunities and limitations

- Flexible, (relatively) fast, easy-to-run modeling framework
- Have tested fitting to case data from 6 countries shared by WHO
- Currently set up to primarily be a susceptibility profiling tool, though forward projection possible (would need to be validated)
- **Limitations:**
  - Major challenge: initial model developed with a set of GBD collaborators from Ethiopia; paused plans for further bilateral collaborations while MAH being developed.
    - **Would need partnership with experts, deep dives into data, & ideally co-development with other modelers to optimize platform / validate results.**
  - Substantial computational requirements; uncertainty via bootstrapping (computationally expensive)
  - Can be challenging to fit depending on data and assumptions, co-linearity (need to make assumptions about ranges of parameters → expert input and guidance)

Safinea

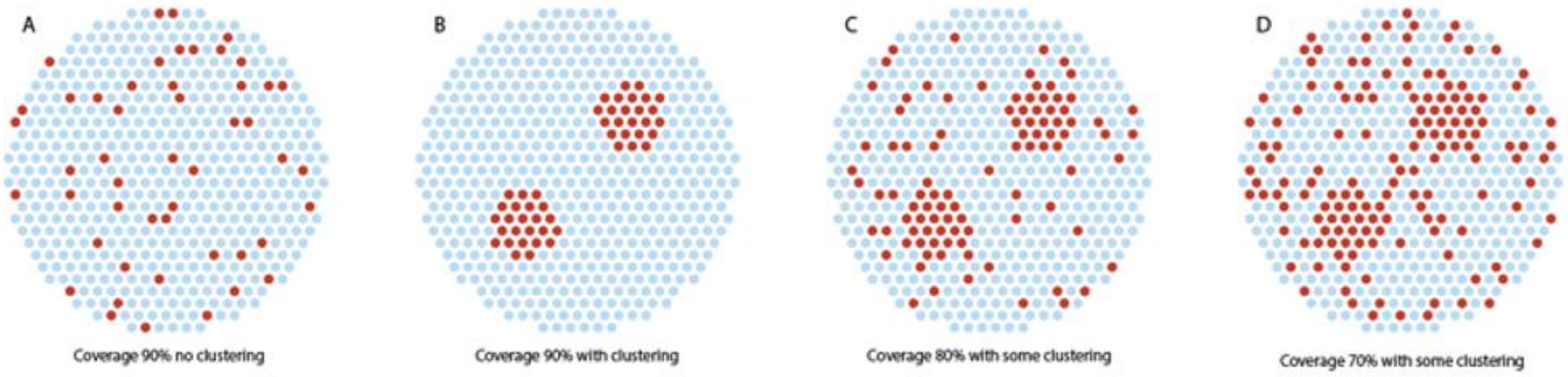
MEASLES ANALYTICS HUB

High-level overview of your risk mapping tool

Purpose of the Tool

- Estimates measles outbreak risk (probability of sustained transmission and distribution of resultant outbreak sizes) given introduction

- Quantifies how clustering of under-vaccinated groups influences outbreak risk. The model explicitly accounts for mixing within and between different social groups and for differences in vaccination coverage



When unvaccinated people cluster with other unvaccinated people, they don't just miss out on the direct protection, but the indirect protection too

SAFINEA

High-level overview of your risk mapping tool

Purpose of the Tool

- Estimates measles outbreak risk (probability of sustained transmission and distribution of resultant outbreak sizes) given introduction

- Quantifies how clustering of under-vaccinated groups influences outbreak risk. The model explicitly accounts for mixing within and between different social groups and for differences in vaccination coverage

Policy Questions Supported

- How much do immunity gaps in specific social groups increase the risk of large outbreaks?

- How would improving coverage in targeted groups reduce transmission and outbreak probability?

- Where would increasing vaccination coverage yield the greatest marginal reduction in outbreak risk?

- What is the marginal health and health-economic benefit of increasing vaccination coverage in higher-risk populations?

SAFINEA

Subnational representation

- Limitations on subnational representation are data-driven
- Highest spatial resolution of the model architecture is 1km grid, derived from WorldPop population estimates
- A crosswalk is defined between the 1km grid and admin boundaries (GeoBoundaries), allowing the model to be run at a user-specified spatial resolution
- In practice, the highest resolution to date has been admin 2 / district level
- The model is containerised and configured to run on Azure instances so parallelisation is straightforward and computational constraints are, in principle, budgetary

SAFINEA

Core methods

Mechanistic framework:

- Age-structured stochastic branching-process model
- Transmission informed by R0, with heterogeneity defined by overdispersion

Heterogeneous mixing:

- Population stratified by age and social group
- Adjustable assortativity parameter informs within- and between-group mixing
- Composite age–social contact matrix defines “who acquires infection from whom” probabilistically

Population-level susceptibility:

- Flexible state-space model to reconstruct susceptibility from historical vaccination coverage and surveillance data.
  Option for hierarchical learning
- Observation model accounts for trends in reporting and testing

SAFINEA

Core methods

Outputs:

- Distribution of outbreak sizes, given introduction
- Number of cases in each age and social group
- Proportion of transmission attributable within and between age and social groups
- Scenario-based impact analysis for potential interventions
- Marginal benefit of vaccinating targeted population subgroups

Uncertainty:

- Stochastic uncertainty: overdispersion in R0
- Parametric uncertainty: MCV coverage, maternal protection, population susceptibility (including older age groups), waning of protection (natural and vaccine-mediated), vaccine efficacy
- Structural uncertainty: choice of number of social groups
- Sensitivity analysis: contact patterns within and between social groups, other assumptions could be assessed
- Scenario-based uncertainty: interventions targeted by age and social group, waning protection, (future) population mobility

SAFINEA

Key data inputs

The model framework is flexible and robust to different input sources / formats. The input components are:

- Size of each social group, as per definition
- Age structure of each social group (default: WorldPop age-population estimates)
- MCV1 / 2 coverage in each age and social group (state-space model can incorporate routine and SIA)
- Measles surveillance data (state-space model can account for reporting rate / quality over time)
- Serology could, in principle, be included in the state-space model to estimate population susceptibility
- Age- and social-group specific contact patterns! In the absence of observed data, user-defined values can be used to assess sensitivity of outcomes

To facilitate operational use, we are coding the model to accommodate certain standardised data formats e.g.

- Multiple Indicator Cluster Surveys (MICS)
- WorldPop vaccination coverage estimates

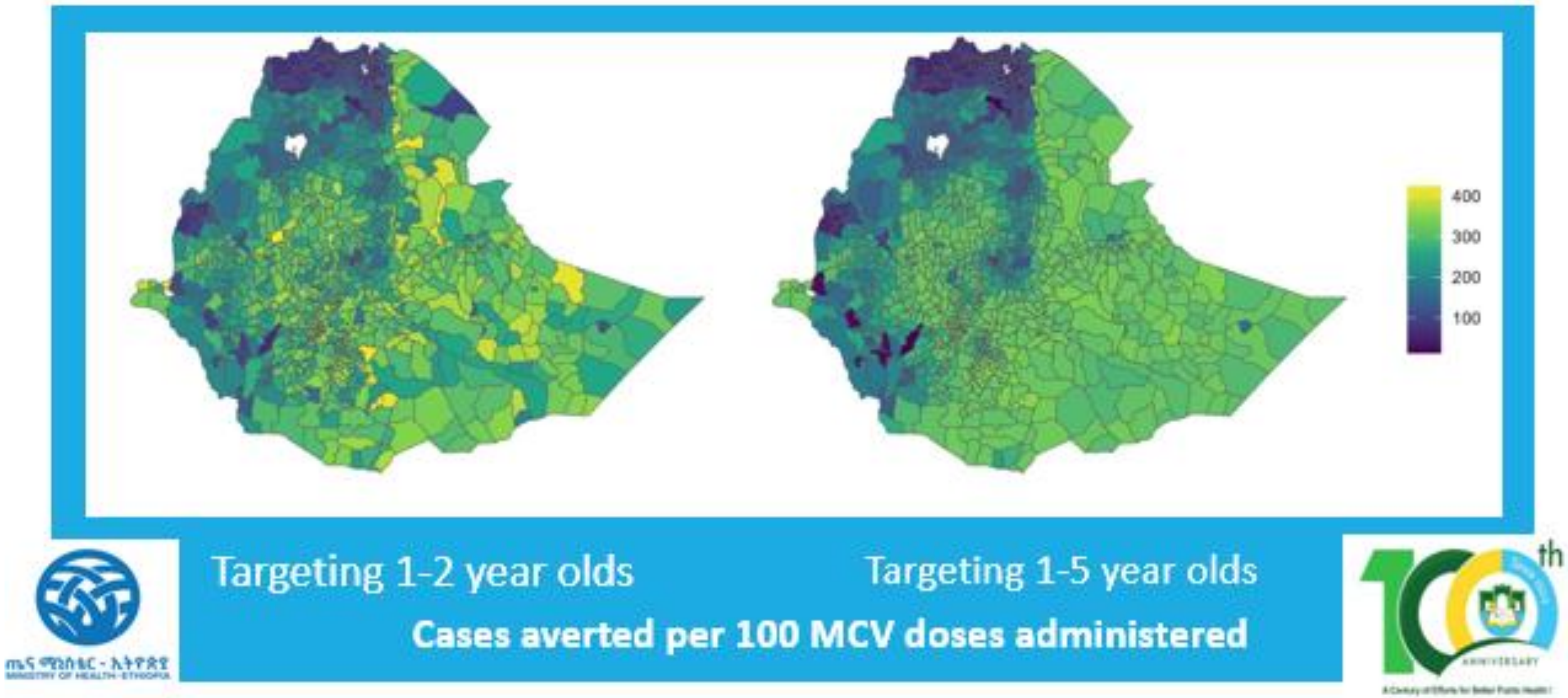
  etc.

SAFINEA

Where the tool has been applied and validated

Settings where implemented:

- Ethiopia: Woreda (Admin-2) level modelling to inform 2025 SIA planning
- Karachi, Pakistan: Informal settlements to assess outbreak risk by ethnicity / language group
- England: Evaluating impact of income-related inequalities on measles transmission



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Validation approaches (ongoing):

- Retrospective assessment in Ethiopia
- Retrospective assessment in Laos and Tunisia **MICS surveys conducted before and after major outbreaks**
- Country engagement to assess plausibility

Key lessons learned:

- Social clustering of under-vaccinated groups strongly amplifies outbreak risk, even when overall coverage appears high
- High flexibility of the model allows for context specific questions
- High-resolution data is critical for identifying risk pockets and understanding where each additional dose has the greatest effect

Key strengths and known limitations

Key Strengths:

- Explicit incorporation of social-group mixing and clustering of susceptibility
- Flexible, modular framework adaptable to different data availability contexts
- Supports scenario analysis and comparison of marginal impact in different population subgroups and geographical locations
- Generates full uncertainty distributions, not only point estimates
- Operationally relevant outputs (e.g., per-dose impact, probability of outbreaks larger than a given size)
- The model is currently being developed into an accessible tool for ongoing analysis, including integration to DHIS2 frameworks

Known Limitations:

- More nuanced output requires detailed input e.g. vaccination coverage and contact patterns by social group
- Where empirical data are limited, relies on user-defined assumptions about age- and social-group mixing

SAFINEA

MAH Updates

MEASLES ANALYTICS HUB

MAH annual meeting

- 10-12 June, Jakarta, Indonesia
    - Indonesia is a strategically important location for the meeting given the country's ongoing measles outbreaks and its strong example of best-practice co-creation of modelling projects with the Ministry of Health through the MAH working group.
- Sample agenda:
    - Networking with modellers from high burden countries
    - Regional showcase of measles modelling work (WPRO/SEARO)
    - Discussions around modelling that can inform programmatic needs
    - Breakout sessions – modeller & stakeholder co-creation of modelling projects
        - **Call for Abstracts**: now OPEN – deadline 1st April – more info can be found on the MAH website