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Subnational Inequities in Measles Vaccination Coverage in Kenya: A Bayesian Geostatistical Modelling Analysis

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Abstract

Background

Subnational inequalities in measles vaccination coverage remain a major barrier to elimination, particularly in low- and middle-income countries. In Kenya, national averages mask substantial geographic and socioeconomic disparities in measles-containing vaccine (MCV) coverage. We aimed to generate high-resolution estimates of first- and second-dose measles coverage (MCV1 and MCV2), identify subnational inequities, and quantify gaps relative to WHO targets.

Methods

We analysed vaccination data for 7,307 children aged 12–35 months from the 2022 Kenya Demographic and Health Survey using Bayesian geostatistical modelling. Cluster-level vaccination data were combined with environmental, socio-economic, and health-system covariates to produce MCV1 and MCV2 coverage estimates at 5x5km resolution, aggregated to county and sub-county levels. We estimated probabilities of achieving 80% and 95% coverage and the number of unvaccinated children by location and dose.

Findings

Design-adjusted DHS estimates showed 53.2% of counties achieved $\geq 90\%$ MCV1 coverage, including 27.7% meeting the WHO $\geq 95\%$ target. MCV2 coverage was markedly lower: no county reached $\geq 95\%$, and just over one quarter exceeded 80%. Model-based estimates indicated national coverage of 86.1% (95% credible interval [CrI] 84.5–87.4) for MCV1 and 63.0% (60.4–64.8) for MCV2, representing a drop-off of more than 20 percentage points between doses. Spatial heterogeneity was observed, with persistently low coverage in northern and north-eastern Kenya and pockets of underperformance within higher-coverage counties. The probability of attaining $\geq 95\%$ coverage was uniformly low across nearly all counties and sub-counties. Higher maternal literacy and shorter motorized travel time to health facilities were consistently associated with higher uptake of both doses.

Conclusion

Despite high first-dose measles coverage in many counties, large second-dose gaps and pronounced subnational inequities threaten elimination efforts in Kenya.

Introduction

Despite the availability of a safe and highly effective vaccine for over five decades, measles remains one of the leading causes of vaccine-preventable morbidity and mortality globally¹. Caused by the measles virus which is transmitted via airborne droplets and contaminated surfaces, measles is highly infectious, with up to 90% of susceptible individuals becoming infected upon exposure². Measles continues to pose a major public health threat, particularly in low-resource settings. In 2018, an estimated 9.7 million measles cases and over 140,000 related deaths were reported globally, mostly among children³. Although mortality declined by 2023, the annual incidence rose to 10.3 million cases, highlighting persistent gaps in the measles control efforts⁴.

Vaccination remains the primary intervention for preventing measles. The measles-containing vaccine (MCV) is delivered in two doses: the first (MCV1) through routine immunization at 9 months of age, and the second (MCV2) at 15 to 18 months or through supplementary immunization activities when the coverage is sub-optimal (<95%)². MCV is administered as a monovalent vaccine or in combination with mumps and rubella⁵.

As of 2023, global efforts have achieved MCV1 and MCV2 coverage rates of 83% and 74% respectively⁶. Between 2000 and 2018, these efforts reduced measles-related mortality by 73% and cases by 76%³. However, due to its high infectivity, measles requires population immunity of 89% to 94% to interrupt transmission, levels that cannot be attained with MCV1 alone⁷. As such, the World Health Organization (WHO) recommends achieving 95% coverage with both doses across all sub-national regions to ensure population-level immunity⁷. Yet, current global coverage remains below this target⁴.

Under the WHO's Immunization Agenda 2030 (IA2030), measles is recognized as a tracer of immunization system performance and equity, helping to identify missed communities and broader gaps in primary health care⁸. In Kenya, the Expanded Programme on Immunization (KEPI) delivers MCV1 at 9 months and MCV2 at 18 months, with periodic supplementary campaigns targeting high-risk populations⁹. MCV is commonly administered as a measles-rubella (MR) vaccine in public health facilities and as measles-mumps-rubella (MMR) in private facilities but for consistency, we refer to them as MCV1 and MCV2 in this study. While national MCV1 coverage has averaged 89% in recent years, MCV2 coverage lags at 70% with substantial regional disparities¹⁰. Remote and underserved communities continue to report low coverage, contributing to recurrent outbreaks.

National and regional averages often obscure critical subnational variation, particularly in low- and middle-income countries (LMICs) where routine health information systems may be incomplete or outdated. Coverage estimates frequently rely on household surveys such as the Demographic and Health Surveys (DHS), which are conducted approximately every five years and are typically representative only at national or first administrative levels¹¹. While

useful for trend monitoring, these surveys are ill-suited for generating reliable estimates at lower administrative units, such as sub-counties, where granular data are essential for targeted programming and resource allocation¹².

To address these gaps, fine-scale spatial estimates are increasingly needed to identify under-vaccinated communities and guide tailored interventions. Using data from the 2022 Kenya DHS and Bayesian geostatistical modelling, this study estimates the magnitude and spatial distribution of MCV1 and MCV2 coverage at high resolution across all 47 counties and their constituent sub-counties. We characterise the subnational and local heterogeneities obscured by national averages, identify the socio-demographic and environmental factors driving population-level inequities in coverage, quantify the remaining immunity gaps relative to programmatic and elimination targets, and highlight settings where children remain at heightened risk of under-immunisation. The findings are intended to support equity-focused, geographically targeted immunisation strategies in Kenya and comparable low- and middle-income settings where aggregate national figures mask critical local gaps.

Methods

In this study, we first derive design-adjusted estimates of MCV1 and MCV2 coverage from the 2022 Kenya DHS, using statistical weights that account for the survey design with cluster sampling, stratification, and probability of selection. These results are reported as the county-level estimates. Secondly, we derive population-weighted model-estimated sub-national coverage by fitting a Bayesian spatial model to the survey data, incorporating socio-economic and environmental variables, and borrowing statistical strength from neighbouring areas. Using this approach, we generate predictions of MCV1 and MCV2 coverage at a fine 5x5Km grid resolution across the entire country, and aggregated back up to sub-county, county and national level weighted by population size. The details of the data and methods are provided below.

Data

Data on coverage of the first (MCV1) and second (MCV2) doses of the measles-containing vaccine were obtained from the 2022 Kenya Demographic and Health Survey (KDHS)¹¹. The DHS program conducts nationally representative household surveys approximately every five years, providing data on key health indicators including fertility, child health, and immunization coverage, particularly in LMICs¹¹. The 2022 KDHS employed a two-stage stratified sampling design, first selecting clusters (enumeration areas) from a national household master sample frame, followed by random sampling of households within each cluster¹¹. Stratification was achieved by dividing each of Kenya's 47 counties into rural and urban strata.

Vaccination status was assessed among children aged 12-23 months for MCV1, and 24-35 months for MCV2, using information recorded on vaccination cards or, where unavailable, caregiver recall. Geographic coordinates of each sampled cluster were included, along with the urban or rural classification. Individual level data were aggregated at the cluster level to compute the number of children surveyed, the number vaccinated, and the proportion vaccinated for each dose within each cluster.

Geospatial covariates

To improve the predictive accuracy of vaccination coverage estimates, we incorporated a suite of geospatial covariates informed by prior literature¹²⁻¹⁴, categorized into socioeconomic, environmental, and health infrastructure factors (Supplementary Table S1, Figure S5,S6). Socioeconomic covariates included population density; the age structure of children aged 1–4 years; night-time light intensity as a proxy for urbanization; literacy rates among men and women aged 15–49; proportion of the population practising open defecation; and the proportion of population in the lowest wealth quintile derived from a spatially continuous surface estimated using a separate Bayesian geostatistical model fitted to Kenya DHS 2022 data¹⁵.

Using demographic data from the 2019 Kenya Population and Housing Census, we derived age-specific ratios of children aged exactly 1 and 2 years relative to the broader 1–4-year age group. These ratios were applied to population raster to estimate the size of the target populations eligible for MCV1 and MCV2 respectively. These estimates were used in both population-weighted aggregations and in calculating the number of unvaccinated children per dose.

Environmental covariates included daytime land surface temperature and precipitation. Health infrastructure and access factors included travel time to cities with populations of 20,000 - 50,000, motorized travel time to the nearest health facility, facility and nurse density per 10,000 population obtained from the Kenya Health Facility Assessment¹⁶ and included as a sub-county level areal covariate, percentage of live births occurring in a health facility, and coverage of children aged 12–23 months who received Pneumococcal 3, first and third doses of Diphtheria, Pertussis, and Tetanus vaccine (DPT), and those with a vaccination card. All covariates were processed and standardized at a spatial resolution of 5 by 5 Kilometres (km), consistent with the resolution used for pixel-level model estimates generated in this study.

To extract covariate values for each survey cluster while accounting for positional displacement, we applied the displacement-adjustment method described by Perez-Haydrich et al¹⁷. Because pixel-level urban–rural classification data were unavailable, we derived urban–rural stratification using the approach by Dong et al.¹⁴, which was then included as a covariate in the final models (figure S3 in the supplementary materials).

Covariate pre-processing and selection

We calculated pairwise correlation coefficients and removed highly correlated covariates (with > 0.9 correlation) to address potential multicollinearity. Secondly, all continuous covariates were standardized by centring and scaling to have mean zero and unit variance prior to model fitting. This improves numerical stability and facilitates the specification and interpretation of weakly informative priors on regression coefficients. Travel time to health facilities, travel time to cities, population density, and facility density were first log-transformed before centring and scaling, given their right-skewed distributions. Covariate selection was done in an initial screening step using backward Akaike Information Criterion (AIC) selection in

Variable screening was conducted prior to fitting the Bayesian geostatistical models, and all substantive inference was based on the final spatial models that explicitly account for spatial correlation and uncertainty. The covariates selected for each model are reported in Table S2 in the supplementary materials. We also examined evidence of residual spatial correlation, after adjusting for covariate effects, by computing empirical variograms of the residuals from a non-spatial binomial regression model using the empirical variograms (figure S2 in the supplementary materials).

Geostatistical modelling framework and validation

Let $A \subset R^2$ denote the geographic extent of Kenya and let $s_1, s_2, \dots, s_n \in A$ represent the cluster locations, given by longitude and latitude. For each cluster i at location s_i we modelled the number of vaccinated children $Y(s_i)$, out of $N(s_i)$, eligible children, where:

$$Y(s_i) \sim \text{Binomial}(N(s_i), p(s_i))$$

Here, $p(s_i)$ is the true vaccination coverage at location s_i . The logit-transformed coverage was modelled as:

$$\text{logit}(p(s_i)) = x(s_i)^T \beta + \psi(s_i) + \epsilon(s_i)$$

Where $x(s_i)$ is a vector of pre-processed geospatial covariates, $\psi(s_i)$ is a spatially correlated Gaussian random effect ($\psi \sim N(0, \Sigma_\psi)$) to account for unexplained spatial variation in vaccination coverage across locations, with covariance assumed to follow a Matérn function with smoothness parameter set to 0.5. $\epsilon(s_i) \sim N(0, \sigma_\epsilon^2)$ is a set of independently and identically distributed (i.i.d) gaussian random effects (nugget) capturing the non-spatial residual variation or between-cluster variation.

We adopted a fully Bayesian framework using the Integrated Nested Laplace Approximation (INLA) for posterior inference, combined with the Stochastic Partial Differential Equation (SPDE) approach for spatial random field approximation, implemented through the `inlabru`¹⁸ package in R (version 4.4.0)¹⁹. A weakly informative prior, $N(0, 10^3)$, was assigned to the

regression parameter β . A Penalized Complexity (PC) prior²⁰ was placed on the standard deviation of the i.i.d gaussian random effects σ_ϵ , such that $p(\sigma_\epsilon > 1) = 0.01$. Following Fuglstad et al.²¹, a joint PC prior was used for the covariance structure of the spatial random effect ψ , specified such that $p(r < r_0) = 0.5$ and $p(\sigma_\psi > 1) = 0.01$, with r_0 chosen to be $\frac{1}{5}$ of the extent of Kenya in the north-south direction¹².

We assessed model performance using four-fold out-of-sample cross-validation. In each iteration, 25% of clusters were randomly withheld, and the model was trained on the remaining 75%. Predictions for the withheld data were compared to observed values. This was repeated four times without replacement. Performance was evaluated using Mean Absolute Error (MAE), Mean Squared Error (MSE), and Root Mean Square Error (RMSE). We also assessed the calibration of the fitted geostatistical models using the average non-randomized Probability Integral Transform (AnPIT), originally proposed by Czado et al. and adapted to binomial geostatistical models by Giorgi et al.^{22,23}. Full validation results and model calibration diagnostics are provided in the Supplementary Materials (Table S3, Figure S1,S2 in the supplementary materials).

Spatial predictions, aggregation and posterior estimates

Vaccination coverage predictions were first generated at the 5×5 km grid-cell level. These predictions were then aggregated to county and sub-county levels using population-weighted averages. For the k^{th} posterior sample in each administrative unit u (either a sub-county or a county) the population-weighted coverage $p_k(u)$ was computed as;

$$p_k(u) = \int p d(s) p_k(s) d(s) \approx \sum_{j=1}^{m_u} p d_{prop}(s_j) \times p_k(s_j)$$

Where $p d_{prop}(s_j) = \frac{p d(s_j)}{\sum_{j=1}^{m_u} p d(s_j)}$ is the proportion of the population at grid cell s_j , and m_u is the number of grid cells within administrative unit u .

For each administrative unit u and posterior sample k , the number of unvaccinated children was estimated as;

$$\bar{N}_k(u) = (1 - p_k(u)) \times N_u$$

Where N_u is the estimated population of children eligible for MCV1 or MCV2 in unit u . The mean number of unvaccinated children and 95% credible intervals were calculated to capture uncertainty in these estimates.

Results

Study population and vaccine coverage

The analysis included 7,307 children drawn from two age cohorts: 3,677 children aged 12–23 months (from 1,447 clusters) for MCV1 estimation, and 3,630 children aged 24–35 months (from 1,411 clusters) for MCV2, consistent with the 2022 Kenya Demographic and Health Survey (KDHS) age groupings. Overall, 3117 (84.8%) had received MCV1 and 2,135 children (58.8%) had received MCV2. Substantial spatial heterogeneity in vaccine uptake was evident at cluster-level (Figure 1a for MCV1; Figure 1e for MCV2).

At the county level, the design-adjusted estimates of MCV1 coverage varied widely. Just over half of counties (59.6%) achieved $\geq 90\%$ MCV1 coverage, including 13 (27.7%) that reached the WHO-recommended target of $\geq 95\%$, and a further 15 (31.9%) with coverage between 90–94% range (Figure 1b). Eleven counties (23.4%) had coverage of 80–89%, and the remaining eight counties fell below 80%: four (8.5%) at 70–79%, two (4.3%) at 60–69%, and two (4.3%) below 50%.

In contrast, MCV2 coverage was markedly lower and more variable. No county met the WHO $\geq 95\%$ target, and only two counties (4.3%) achieved 90–94% coverage (Figure 1f). Ten counties (21.3%) reached 80–89%, while coverage in the remaining counties was distributed across lower coverage brackets: 10 counties each (21.3%) in the 70–79% and $<50\%$ categories, 9 (19.2%) in the 60–69% category, and five counties (10.6%) in the 50–59% range.

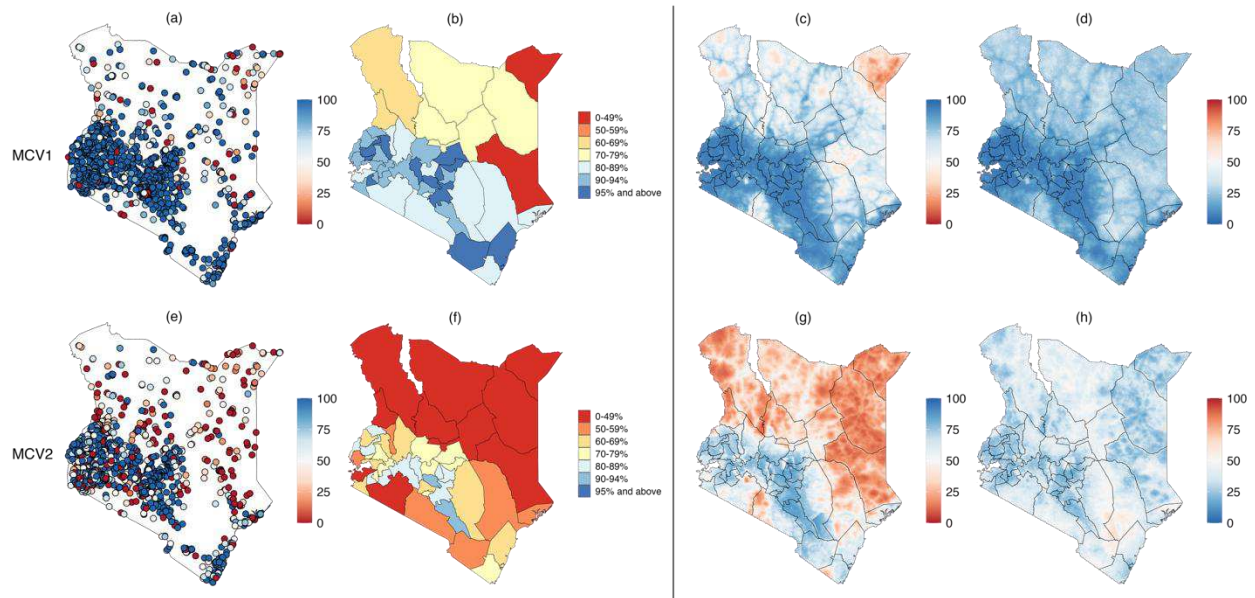


Figure 1: Cluster level observed coverage for MCV1 and MCV2 are shown in Figures 1a and 1e respectively. County-level design-adjusted coverages categorized by coverage thresholds are presented in Figures 1b and 1f respectively. High-resolution (5x5 km) predictions of MCV1 and MCV2 vaccination coverages are displayed in Figures 1c and 1g respectively, together with their associated uncertainties (95% Credible Interval widths) in Figures 1d (MCV1) and 1h (MCV2).

Factors associated with vaccination coverage

In multivariable Bayesian models, higher maternal literacy and receipt of DPT1 were each positively associated with MCV1 coverage, while greater motorized travel time to health facilities and higher proportion of the population in the lowest wealth quintile were negatively associated, corresponding to odds ratio less than one, with posterior credible intervals excluding 1. Population density and urban residence showed no significant association with MCV1 uptake. For MCV2, maternal literacy was positively associated with coverage, while travel time to health facilities and population density were each negatively associated, with all credible intervals excluding unity. Pneumococcal 3 coverage, DPT1, facility density, urban residence, and household wealth showed no significant independent association with MCV2 uptake (Figure 2).

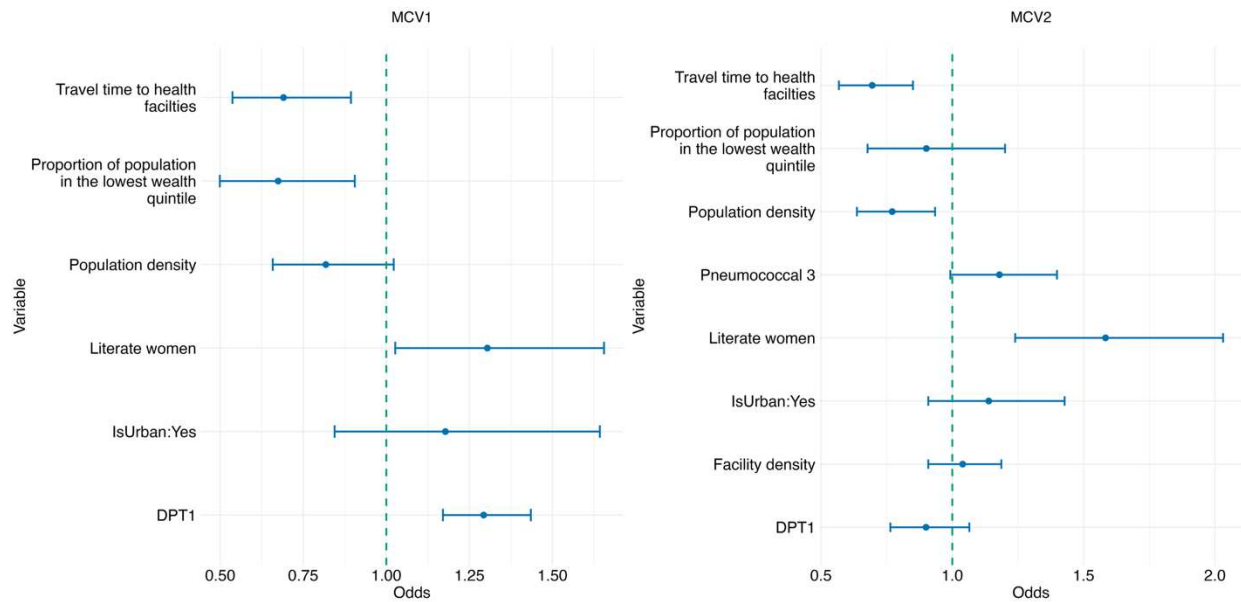


Figure 2: Regression parameters for the MCV1 model (left) and MCV2 model (right), presented as odds ratios with 95% posterior credible intervals. All continuous covariates were centred and scaled prior to model fitting; therefore, each odds ratio represents the change in odds associated with a one-standard-deviation increase in the corresponding covariate.

Geographical distribution of MCV1 and MCV2 coverage

High-resolution (5×5km) predictive maps revealed pronounced geographic heterogeneity (Figure 1c). MCV1 coverage above 75% was concentrated in western and central Kenya, while the northeastern areas consistently recorded coverage levels below 50%. Pockets of low coverage were also observed within otherwise high-performing areas, highlighting localized inequities. MCV2 displayed even more pronounced spatial inequality, with a clear north-south divide: moderate coverage (50–75%) was limited to central and southwestern areas, while north and northeast regions fell below 25% (Figure 1g).

Distinct linear corridors of relatively higher coverage were apparent in eastern and northern regions, likely reflecting road-network-mediated access to health facilities. Uncertainty maps (Figure 1d for MCV1; Figure 1h for MCV2) showed that, for MCV1, uncertainty was lowest in central and south-western areas, where predicted coverage was highest, and greatest in the east and north. For MCV2, uncertainty was relatively low in parts of the northwest and east, despite persistently low coverage estimates in those areas.

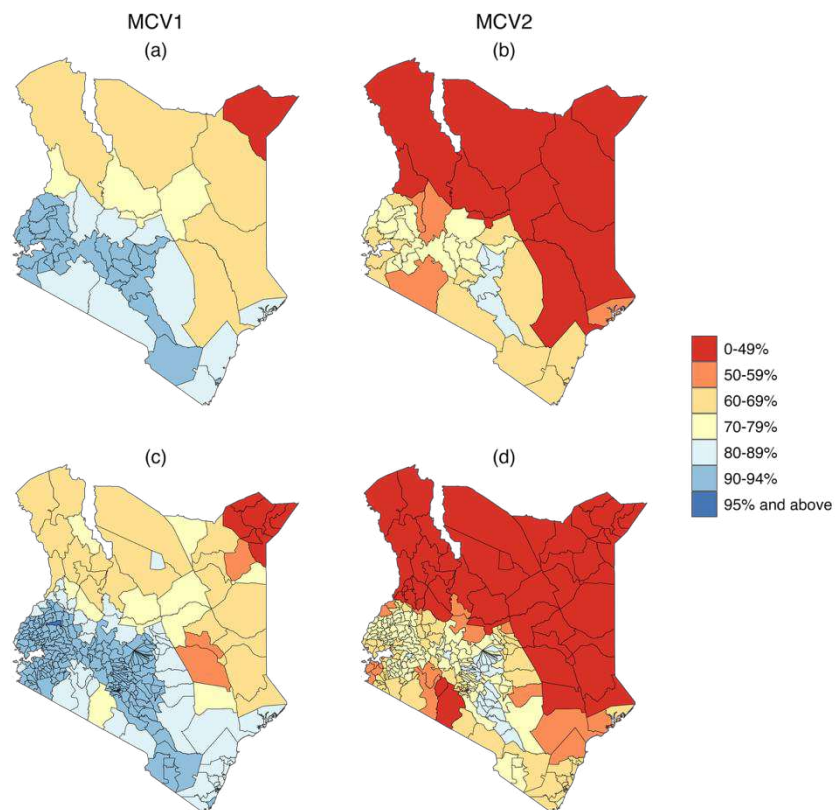


Figure 3: Estimated population-weighted vaccination coverage for MCV1 and MCV2 at County (Figures 2a and b), sub-county (Figures 2c and d) levels.

Population-weighted national and sub-national coverage

Population-weighted national coverage was estimated at 86.1% (95% credible interval [CrI] 84.5–87.4%) for MCV1 and 63.0% (60.4–64.8%) for MCV2, representing a national drop-off of more than 20 percentage points between the first and the second doses, and both below the WHO $\geq 95\%$ elimination threshold.

At the county level, model-estimated MCV1 coverage was broadly high: 28 (59.6%) of the counties achieved 90-94% coverage and 10 (21.3%) fell within 80-89% (Figure 3a). Lower

coverage was confined to a minority of the counties: 3 (6.4%) at 70-79%, 5 (10.6%) at 60-69%, and one county below 50%.

MCV2 county average was uniformly suboptimal. No county exceeded 90%, and only four (8.5%) achieved 80-89% (Figure 3b). Most of the counties recorded coverage of 70-79% (36.2%, n=17) or 60-69% (27.7%, n=13), with four counties (8.5%) at 50-59% and nine counties (19.1%) below 50%.

Sub-county analyses revealed similar gradients at finer resolution. For MCV1, eight sub-counties (2.7%) achieved coverage $\geq 95\%$, 206 (68.7%) achieved 90-94% and 46 (15.3%) achieved 80-89% coverage (Figure 3c), with only 40 (13.3%) falling below 80%. For MCV2, sub-county coverage was skewed toward lower uptake: 28 (9.3%) of sub-counties reached 80-89%, 133 (44.3%) recorded 70-79%, 76 (25.3%) recorded 60-69%, and 21.0% fell below 60%, including 45 (15.0%) that fell below 50% (Figure 3d; Table 1).

Table 1: MCV1 and 2 coverage by threshold, administrative level and method of estimation

Coverage threshold	County level (n = 47)				Sub-county level (n = 300)	
	MCV1		MCV2		MCV1	MCV2
	Design-based n (%)	Model-based n (%)	Design-based n (%)	Model-based n (%)	Model-based n (%)	Model-based n (%)
$\geq 95\%$	13 (27.7%)	0 (0%)	0 (0%)	0 (0%)	8 (2.7%)	0 (0%)
90-94%	15 (31.9%)	28 (59.6%)	2 (4.3%)	0 (0%)	206 (68.7%)	0 (0%)
80-89%	11 (23.4%)	10 (21.3%)	10 (21.3%)	4 (8.5%)	46 (15.3%)	28 (9.3%)
70-79%	4 (8.5%)	3 (6.4%)	10 (21.3%)	17 (36.2%)	11 (3.7%)	133 (44.3%)
60-69%	2 (4.3%)	5 (10.6%)	9 (19.1%)	13 (27.7%)	19 (6.3%)	76 (25.3%)
50-59%	0 (0%)	0 (0%)	6 (12.8%)	4 (8.5%)	3 (1.0%)	18 (6.0%)
0-49%	2 (4.3%)	1 (2.1%)	10 (21.3%)	9 (19.1%)	7 (2.3%)	45 (15.0%)

Probability of achieving coverage thresholds

The predicted probability of achieving $\geq 95\%$ coverage was low (<0.25) across virtually all counties and sub-counties for both doses (Figures 4a, 4b, 4e, and 4f). A localized cluster of higher probability for MCV1 was observed in the central and western regions at sub-county level (Figure 4e), suggesting isolated areas nearing elimination-level coverage. Figure 4

presents the predicted probabilities of achieving the 95% and 80% coverage thresholds for MCV1 and MCV2 at both county and sub-county levels in Kenya.

For the 80% threshold, geographic variation was more pronounced. MCV1 attainment probabilities showed a north-south gradient, with higher probabilities concentrated in southern regions (Figure 4c, 4g). MCV2 probabilities at the 80% threshold were highest in central and lower eastern Kenya, while sub-counties across the north and northeast remained well below this benchmark (Figure 4d, 4h).

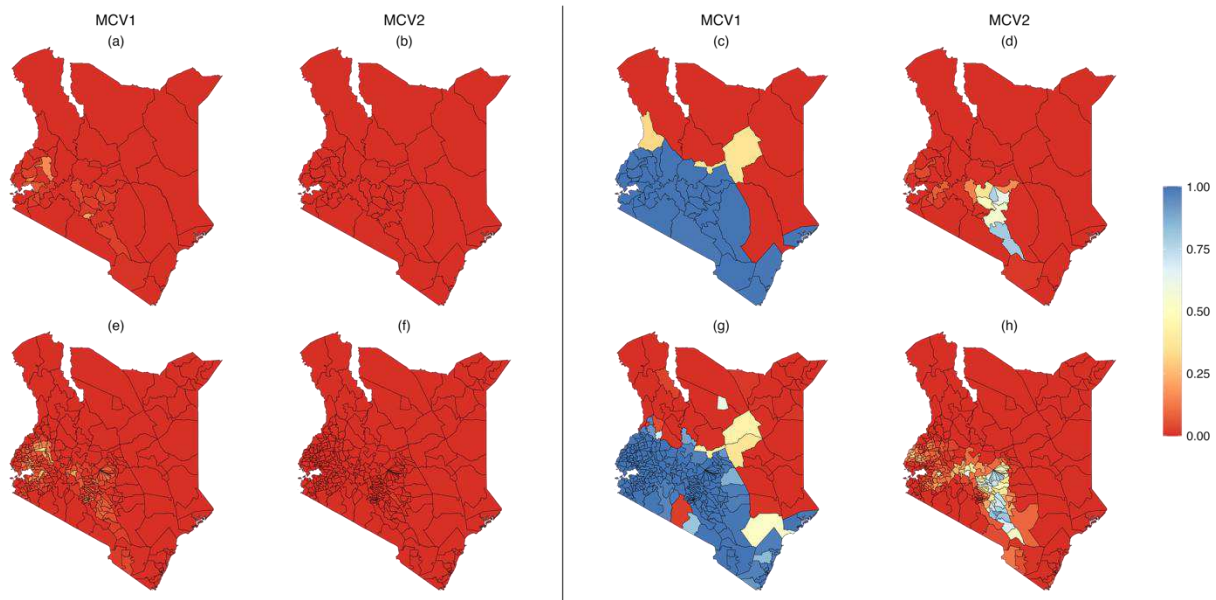


Figure 4: Probability of achieving 95% (Figures 3a, b, c and d) and 80% (Figures 3e, f, g and h) vaccination coverage for MCV1 and MCV2 at county and sub-county levels in Kenya, with a vertical line separating 95% (left) from 80% (right) plots.

Vaccination inequalities

Ridgeline plots of posterior county-level coverage distributions (Figure 5) revealed three broad strata for each dose. For MCV1, counties clustered around 30-50% (low), 50-80% (intermediate), and >80% (high), with Mandera County distinguished by a markedly low distribution peaking around 35% (Figure 5a). For MCV2, the three-stratum pattern was evident but with lower overall levels: 10-30%, 30-50%, and a higher-coverage group ranging from 70-90%. Across both vaccine doses, counties with higher proportions of residents in the lowest wealth quintile consistently exhibited lower predicted coverage, reinforcing a socioeconomic gradient in under-immunization.

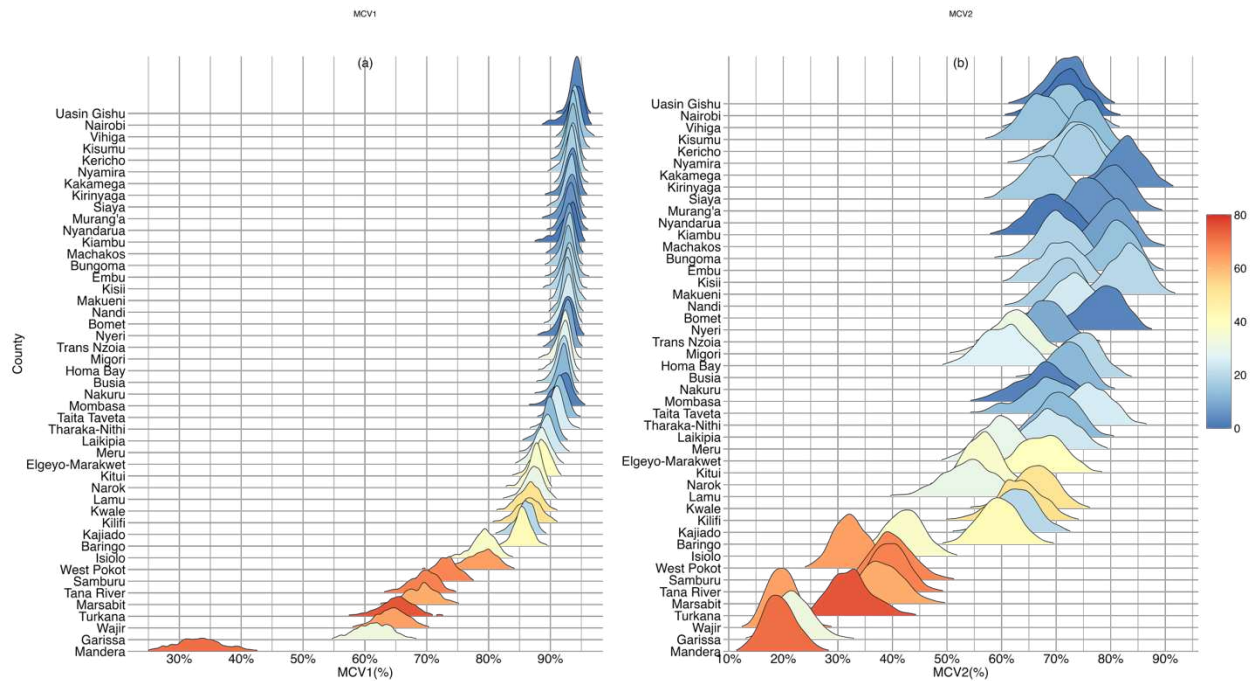


Figure 5: Ridgeline plots showing the posterior distributions of vaccination coverage estimates for MCV1 (Figure 5a) and MCV2 (Figure 5b) across Kenyan counties. Coverage percentages are plotted on the x-axis, with counties ordered by median MCV1 coverage from highest to lowest. For MCV2, counties maintain the same order as in MCV1. Colour gradients indicate the percentage of population in the lowest wealth quintile in each county from the 2022 Kenya Demographic Health Survey.

Number of unvaccinated children

We estimated the number of unvaccinated children at county level by applying the complement of model-estimated coverage to the target population. Nationally, an estimated 193,468 children aged 12–23 months remained unvaccinated for MCV1 and 552,029 for MCV2.

The burden of unvaccinated children was highly concentrated geographically. For MCV1, Mandera county alone accounted for 40,742 (95% CrI: 35,660–45,338) unvaccinated children, followed by Wajir (14,631; 12,636–16,835) and Garissa (14,612; 12,410–16,937), together accounting for a disproportionate share of the national unvaccinated burden. For MCV2, the same counties dominated; Mandera (52,349; 48,352–56,052), Wajir (34,935; 32,396–37,060), and Garissa (31,351; 28,354–33,751); with Nairobi (29,892; 22,565–38,727) also contributing substantially, reflecting its large population size despite relatively higher coverage. Full county-level estimates with 95% credible intervals are provided in Supplementary Table S6, S7 respectively.

Discussion

In this study, we used Bayesian geostatistical modelling to generate high-resolution estimates of first- and second dose measles-containing vaccine (MCV1 and MCV2) coverage across Kenya and to characterize the socioeconomic, environmental, and health system factors shaping subnational disparities. By integrating design-adjusted survey estimates with spatial modelling, our analysis reveals substantial heterogeneity (Figure S4 in the supplementary materials) in measles vaccination coverage that is obscured by national averages and provides actionable insights for identifying and addressing persistent immunity gaps.

Our findings demonstrate that although moderate to high MCV1 coverage has been achieved in several counties, this progress has not translated into comparable uptake of the second dose. More than half of counties achieved at least 80% MCV1 coverage, yet most fell below this threshold for MCV2, and the probability of achieving the WHO-recommended 95% coverage target remained uniformly low across both county and sub-county levels. The national drop-off exceeding 20 percentage points between MCV1 and MCV2 highlights structural weaknesses in sustaining engagement with routine immunisation services beyond infancy²⁴. Evaluations following the introduction of MCV2 across the African region suggests that such gaps may reflect a combination of factors, including gaps in health worker training, limited awareness among caregivers about the need for a second dose and challenges in recording and tracking vaccinations²⁵. Given the high transmissibility of measles, these gaps are sufficient to sustain outbreaks even in settings with relatively strong first-dose performance. Closing them will therefore require more than periodic supplementary immunisation activities (SIAs), including emphasis on community engagement, more locally driven and decentralised strategies, and better systems for tracking children missed after the first year of life, together with the political will to address the structural inequities that perpetuate these gaps²⁶.

Spatial clustering of coverage revealed three strata of low, intermediate, and high coverage that were geographically patterned. Coverage was consistently lowest in northern and north-eastern Kenya, where several counties recorded very low predicted MCV1 and MCV2 uptake. These geographic gradients likely reflect longstanding inequities in health system access and performance, including remoteness, population mobility and historical underinvestment in health infrastructure²⁷. Importantly, the fine-scale estimates also revealed localized pockets of low coverage within otherwise higher-performing counties, reinforcing the limitations of county-level averages for programmatic planning and vaccine allocation as have been reported across other studies²⁸.

Interpretation of the observed spatial patterns is further informed by contrasts in the estimated spatial structure of the MCV1 and MCV2 models. For MCV1, the estimated spatial

variance was small and weakly identified, with a broad posterior for the spatial range, suggesting that once the selected covariates were accounted for, relatively little residual spatial structure remained for the random field to capture. This is consistent with several key covariates, including DPT1 coverage, maternal literacy, and household wealth, being spatially smooth surfaces that likely absorb much of the large-scale geographic variation in first-dose uptake. As a result, MCV1 predictions are largely covariate-driven, with the spatial random field acting primarily as a minor smoothing component.

For MCV2, by contrast, the spatial random field was more clearly identified, indicating the presence of genuine residual spatial structure beyond what the included covariates explain. This suggests that unmeasured, spatially structured factors such as local health-system capacity, service continuity, or community-level demand, contribute meaningfully to variation in second-dose uptake. This distinction has important implications for interpretation: while MCV1 estimates may be more sensitive to covariate specification, MCV2 estimates are comparatively more robust to potential covariate misspecification due to the stronger role of the spatial random field.

We found that counties with higher proportions of residents in the lowest wealth quintile consistently had lower predicted vaccination coverage for both MCV1 and MCV2, highlighting persistent socioeconomic disparities in immunization^{29,30,31}. These patterns were most pronounced in counties such as Mandera, Wajir and Garissa, where geographic isolation and fragile service delivery interact with poverty to compound barriers to access³². While our models did not directly assess the effects of shocks such as drought or displacement, such stresses are common in these regions and may further disrupt routine immunisation by limiting household mobility, reducing contact with health services, and interrupting vaccination schedules³³.

Maternal literacy was a consistent predictor of measles vaccination uptake across both doses, aligning with evidence from other settings in Sub-Saharan Africa, demonstrating that maternal education is strongly associated with improved adherence to vaccination schedules^{34,35}. Literate caregivers are more likely to understand immunisation schedules, recognize the benefits of timely vaccination, and respond effectively to health communication³⁶. Beyond knowledge, maternal literacy may enhance autonomy and decision-making power within households, facilitating completion of multi-dose vaccination schedules^{34,37}.

The positive association between receipt of first dose of diphtheria-pertussis-tetanus vaccine (DPT1) with MCV1 coverage reflects the importance of early engagement with routine child health services^{38,39}. DPT1 uptake can be viewed as a marker of both caregiver trust in vaccination services and health system performance at early contact points, increasing the likelihood of completing subsequent vaccinations⁴⁰. This reinforces the value of

strengthening the immunization cascade from the earliest contacts, rather than addressing individual antigens in isolation.

For MCV2, access constraints played an important role. The negative association between motorised travel time to health facilities and MCV2 uptake was statistically supported in our analysis and is epidemiologically meaningful. Unlike MCV1, which is administered at nine months, MCV2 is scheduled at 18 months, a period characterized by fewer routine interactions with the health system. Under these circumstances, distance, transport costs, and opportunity costs may act as deterrents to caregivers, particularly in rural and underserved areas^{41–43}. Improving MCV2 coverage will therefore require delivery strategies that reduce access barriers, such as outreach services, integration with other child health contacts, and improved defaulter tracing ⁴⁴.

Understanding these geographical inequalities requires examining the structural and social barriers that contribute to vaccination gaps. Vaccine stockouts, frequently driven by insufficient cold chain infrastructure, fragmented distribution systems, delayed procurement process and poor supply chain management, are a recurring challenge in these rural areas⁴⁵. Further, these failures are embedded within the broader systemic neglect of peripheral regions in healthcare systems, requiring a combined approach on targeted investments to strengthen the resilience of vaccine supply systems, and broader policy commitments to address long-standing geographic and socioeconomic imbalances in health service delivery in Kenya^{46,29}.

This study had several limitations. First, vaccination data were obtained either from vaccination cards or, where unavailable, through caregiver recall, which may introduce recall bias. Second, estimates are based on the 2022 Kenya KDHS and may not capture more recent changes in coverage. Third, we did not enforce monotonicity in vaccination coverage between MCV1 and MCV2 because estimates were derived from different age cohorts (which assumes that coverage for MCV2 should not exceed that of MCV1, since only children who receive MCV1 are eligible for MCV2). However, no county or sub-county showed MCV2 coverage exceeding MCV1, suggesting minimal impact on interpretation.

In conclusion, Kenya has made important gains in first-dose measles vaccination, but substantial second-dose gaps and subnational inequities continue to undermine elimination efforts. High-resolution spatial modelling reveals critical localized immunity gaps that are invisible in national summaries yet central to outbreak risk and efficient resource allocation. In the context of constrained health resources and competing priorities, maximizing the effectiveness of immunization programs requires precise identification of where children are being missed and why⁴⁷. Equity-focused, geographically targeted strategies, particularly those strengthening MCV2 delivery in underserved sub-counties, are essential to closing immunity gaps and advancing measles elimination in line with Immunization Agenda 2030 and the principle of leaving no one behind ^{48, 49}.

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Author contributions

Conceptualization: BN, NM, SMT. Data curation: BN, NM, SS, SMT. Formal analysis: BN, NM, SMT. Funding acquisition: LO, SMT. Investigation and Methodology: BN, NM, RJ, SS, EO, GPO, HK, TNK, MCM, CF, LO, SMT. Project administration: RJ, EO, HK. Supervision and validation: RJ, EO, GPO, HK, TNK, MCM, CF, LO, SMT. Visualization: BN, NM, SS, CF, SMT. Writing – original draft: BN, NM, SMT. Writing – review and editing: All authors had full access to the data and had final responsibility for the decision to submit for publication. All authors read and approved the final version of the manuscript.

Competing interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this article.

Data availability

The datasets used and/or analysed during the current study available from the corresponding author on reasonable request.

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