

County and Health-Service Sector Variation in Malaria Diagnostic Positivity in Liberia: A Longitudinal Multilevel Analysis of Routine Surveillance Data, 2021–2025

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DOI: 10.46609/IJSSER.2026.v11i10.002 URL: <https://doi.org/10.46609/IJSSER.2026.v11i10.002>

Received: 17 August 2026 / Accepted: 25 September 2026 / Published: 10 October 2026

ABSTRACT

Malaria surveillance records describe diagnostic activity across geographic and health-service settings, but positivity in routine records is not a direct measure of population prevalence. This study examined temporal, county, and health-service-sector variation in malaria diagnostic positivity in Liberia from 2021 to 2025. A retrospective longitudinal ecological analysis was conducted using routine malaria surveillance data supplied by the Liberia Ministry of Health/National Malaria Control Program. The dataset contained 300 county-sector-year observations covering all 15 counties and four service sectors; 220 observations had complete diagnostic information. Diagnostic positivity was calculated from positive microscopy and RDT results among all recorded positive and negative tests. Across complete observations, 7,097,294 tests were recorded, including 3,914,734 positive results. Observed positivity declined from 59.1% in 2021 to 51.2% in 2025 while testing increased from 1,463,900 to 1,624,400 tests. Private services recorded the highest positivity (62.9%) and Concession services the lowest (44.9%). In the beta-binomial mixed-effects model, the odds of a positive recorded result were higher in Private than Public services (OR 1.450, 95% CI 1.220–1.722) and in Faith Based than Public services (OR 1.195, 95% CI 1.022–1.396); the year effect was not statistically supported (OR 0.963, 95% CI 0.921–1.005). The findings show that routine diagnostic positivity varied across counties, sectors, and years and should be interpreted with testing volume and reporting completeness in view.

Keywords: malaria; diagnostic positivity; routine surveillance; multilevel model; beta-binomial; Liberia; health-service sector

1.0 Introduction

Malaria continues to place a substantial burden on sub-Saharan Africa. The World Health Organization (WHO) estimated 282 million malaria cases and 610,000 deaths globally in 2024, with the African Region accounting for most of this burden [1]. Liberia remains malaria-endemic, and national surveillance and survey data indicate continued transmission despite progress in malaria control [2,3]. Routine diagnostic records are therefore useful for examining how malaria testing and recorded positive results are distributed across the health system [6].

Parasite-based diagnosis is a central part of malaria case management and surveillance. WHO recommends prompt diagnosis by microscopy or a quality-assured rapid diagnostic test (RDT) for people with suspected malaria before treatment [4,5]. Routine surveillance can generate repeated observations across counties and service sectors, but diagnostic positivity depends on the circumstances in which testing takes place [6]. The proportion of positive tests may reflect malaria transmission as well as the characteristics of people seeking care, diagnostic practices, service availability, and reporting completeness [6]. For this reason, positivity in routine diagnostic records should not be equated with population prevalence, particularly when the data are aggregated by county and service sector [6].

The Liberian dataset used here contains repeated county-by-service-sector observations for five years across Concession, Faith Based, Private, and Public services. These repeated observations create a hierarchical structure because records from the same county may be related. Differences in reporting completeness between sectors can also change the number and distribution of recorded tests and positive results. Descriptive counts and percentages show the surveillance pattern, but they do not account for county clustering or determine whether the variability in aggregated counts is greater than expected under a conventional binomial model.

The longitudinal multilevel framework was used to examine changes over time and differences between service sectors while accounting for repeated observations within counties. Model checking was also necessary because aggregated surveillance counts may be more variable than a standard binomial model assumes, a concern documented in routine malaria surveillance data [11,16]. Descriptive summaries were therefore complemented by multilevel models and a beta-binomial specification, allowing the sector and temporal findings to be examined after allowing for extra-binomial variation.

The study examined changes in malaria diagnostic positivity in Liberia from 2021 to 2025, variation between counties, differences among health-service sectors after accounting for county clustering, and whether temporal changes differed by sector. The analysis used aggregated

routine surveillance data from all 15 counties and retained an ecological interpretation because the records represent county-sector-year observations rather than individual patients.

2.0 Literature Review

2.1 Malaria Diagnosis and Routine Surveillance

Parasite-based diagnosis is central to malaria case management and surveillance. WHO recommends prompt testing by microscopy or a quality-assured rapid diagnostic test (RDT) for people with suspected malaria before treatment [4,5]. Both methods are used in routine services, with their relative use shaped by service availability, laboratory capacity, clinical practice, and the setting in which patients receive care [4,5].

Routine diagnostic records capture both malaria test results and patterns of service use. The availability of microscopy and RDTs, the number of people tested, and the type of provider contributing records can all affect the composition of surveillance data [4–6]. Comparisons across counties and service sectors therefore require attention to these differences rather than assuming that each observation represents the same patient population or service conditions [6].

2.2 Interpretation of Diagnostic Test Positivity

Routine health information systems allow malaria testing to be followed repeatedly across places and service settings, but the records have important limitations. Reporting may be incomplete in some sectors or locations, people who reach diagnostic services may differ from the wider population, and changes in testing practice can alter the proportion of positive results without a corresponding change in transmission [6,11,16]. These factors make diagnostic positivity different from a population-based prevalence measure [6].

Facility-based studies illustrate this distinction. Francis et al. found that malaria test positivity varied with age, area of residence, and diagnostic method, showing that facility-based results depend partly on who is tested and how testing is performed [10]. Kamau et al. also found an association between facility-based test positivity and community parasite prevalence, while noting that the relationship is affected by the population presenting for care [13]. Routine diagnostic positivity is thus useful for describing patterns within the health system, but it cannot replace population-based measures of malaria infection [6,10,13].

2.3 Malaria Surveillance Context in Liberia

National aggregates can mask differences between counties and service sectors. A county may account for a large share of testing without having the highest positivity, while a smaller sector may record higher positivity despite contributing relatively few tests [11,16].

Evidence from Liberia and other malaria-endemic settings shows important geographic and service-sector differences. Recent Liberia-specific work by Koko et al. identified missing data, inconsistent reporting, variable data-entry practices, and unreliable testing rates in routine malaria data used for subnational stratification [16]. Rozelle et al. used Liberia HMIS data to show that malaria diagnostic activity can shift between community and facility providers, affecting the composition of recorded diagnoses [17]. In Western Kenya, Alegana et al. used routine surveillance data to examine malaria risk at subnational level and highlighted reporting completeness, population distribution, spatial structure, and facility characteristics as important considerations [12]. In mainland Tanzania, Thawer et al. used routine health-facility data to examine spatial and temporal variation and emphasized uncertainty and incomplete reporting when interpreting routine records [14]. Diagnostic access also differs between public and private providers; the ACTwatch analysis documented differences in malaria diagnostic availability and market share across public and private providers in several sub-Saharan African countries [15]. Together, these studies support examining county and service-sector patterns separately rather than relying only on a national aggregate [12,14–17].

2.4 Research Gap

Because each county appears repeatedly across the study period, observations from the same county are not necessarily independent. This dependence needs to be considered when estimating temporal and service-sector associations.

The analysis accounts for this structure by treating county as the clustering level in a longitudinal multilevel model. The repeated county-sector-year observations allow temporal and sector differences to be examined without treating all records as independent. The analysis also tests for extra-binomial variation with a beta-binomial model because aggregated surveillance counts may show greater variability than the conventional binomial distribution permits. The two approaches are used alongside descriptive surveillance measures to separate the observed pattern from uncertainty related to county clustering, reporting completeness, and service-sector differences.

3.0 Research Methodology

3.1 Study Design

This retrospective longitudinal ecological study used aggregated routine malaria surveillance data for Liberia covering 2021–2025.

3.2 Study Setting

The analysis included all 15 counties: Bomi, Bong, Gbarpolu, Grand Bassa, Grand Cape Mount, Grand Gedeh, Grand Kru, Lofa, Margibi, Maryland, Montserrado, Nimba, River Gee, Rivercess, and Sinoe. Four health-service sectors were represented: Concession, Faith Based, Private, and Public.

3.3 Data Source and Dataset Structure

The Liberia Ministry of Health/National Malaria Control Program supplied the dataset [7]. It contained 300 rows and 57 variables, structured as 15 counties $\times$ 4 health-service sectors $\times$ 5 years. Each row represented one county-sector-year combination and did not identify an individual patient or named health facility.

3.4 Diagnostic Variables and Outcome Definition

The diagnostic component contained 12 variables covering microscopy-positive, microscopy-negative, RDT-positive, and RDT-negative counts for children younger than five years, persons aged five years and older, and pregnant women. Microscopy testing was calculated from microscopy-positive and microscopy-negative counts across the three groups; RDT testing was calculated in the same way. Total diagnostic testing was the sum of microscopy and RDT tests, and total positive tests were the sum of microscopy-positive and RDT-positive results.

Diagnostic positivity (%) = (Total positive diagnostic tests / Total recorded diagnostic tests) $\times$ 100

Diagnostic positivity was defined as the proportion of recorded diagnostic tests that were positive. It was not treated as malaria prevalence because the dataset contains no individual-level population denominator and does not capture people who did not reach diagnostic services.

3.5 Data Completeness and Handling of Missing Observations

Of the 300 structural observations, 220 contained complete information for all 12 microscopy/RDT diagnostic variables, while 80 had all 12 variables missing. A missing diagnostic block was retained as missing surveillance information rather than coded as zero testing. This avoids interpreting an unreported observation as evidence that no testing occurred. Missingness was summarized by year and service sector before model fitting; the detailed year-by-sector pattern is presented in Supplementary Table S1.

3.6 Statistical Analysis

The analysis began with summaries of testing volume, positive and negative results, diagnostic positivity, and RDT share by year, health-service sector, and county. Since counties were observed repeatedly, mixed-effects models were used for inference. The response was specified as a binomial count with positive tests and negative tests forming the two components.

Potential sources of bias were addressed during analysis. Reporting completeness differed between service sectors, and incomplete diagnostic blocks were kept as missing rather than zero. Recorded positivity may also reflect differences in the people reaching services, testing practices, referral patterns, and diagnostic availability across counties and sectors. Because the data are aggregated, residual confounding and ecological bias cannot be ruled out; the estimates should not be interpreted as individual-level associations or population prevalence. Reporting was prepared with reference to STROBE recommendations for observational studies [8].

3.7 Longitudinal Multilevel Models

Models were fitted sequentially to examine year, health-service sector, and county-level clustering.

Null model: $\text{logit}(p_i) = \beta_0 + u_c$

Temporal model: $\text{logit}(p_i) = \beta_0 + \beta_1 \text{Year}^c + u_c$

Adjusted sector model: $\text{logit}(p_i) = \beta_0 + \beta_1 \text{Year}^c + \beta_2 \text{Sector} + u_c$

Year-by-sector model: $\text{logit}(p_i) = \beta_0 + \beta_1 \text{Year}^c + \beta_2 \text{Sector} + \beta_3 (\text{Year}^c \times \text{Sector}) + u_c$

Random-slope model: $\text{logit}(p_i) = \beta_0 + \beta_1 \text{Year}^c + \beta_2 \text{Sector} + u_{0c} + u_{1c} \text{Year}^c$

Here, p_i denotes the probability that a recorded diagnostic test was positive; c identifies the county; Year^c is calendar year centered at 2021; and u_c is the county random intercept. Public services were the reference sector.

3.8 Beta-binomial Model

Model checking showed that the conventional binomial specification did not reproduce the observed variability adequately. A beta-binomial mixed-effects model was therefore fitted with year, health-service sector, and a county random intercept to allow for extra-binomial variation. The model was specified as:

$$Y_{csy} \sim \text{Beta-Binomial}(N_{csy}, p_{csy}, \phi)$$
$$\text{logit}(p_{csy}) = \beta_0 + \beta_1 \text{Year}^c + \beta_2 \text{Sector} + u_c$$

Here, Y_{csy} is the number of positive diagnostic tests, N_{csy} is the total number of positive and negative tests, and ϕ is the beta-binomial dispersion parameter. The fitted beta-binomial model had a dispersion parameter of 18.4. This fitted-model parameter is distinct from the residual dispersion statistic reported by the DHARMA diagnostics.

3.9 Clustering Measures

For the null county random-intercept model, the estimated county-level variance was $\sigma^2_{county} = 0.0333$. The logistic intraclass correlation coefficient (ICC) was calculated as:

$$ICC = \sigma^2_{county} / (\sigma^2_{county} + \pi^2/3)$$

$$ICC = 0.0333 / (0.0333 + 3.2899) = 0.0100 \approx 1.0\%$$

The ICC of 0.0100 indicates that approximately 1.0% of the latent logistic-scale variance in the null model was attributable to differences between counties.

The median odds ratio (MOR) was calculated as:

$$MOR = \exp[\sqrt{(2\sigma^2_{county})} \times \Phi^{-1}(0.75)]$$

$$MOR = \exp[\sqrt{(2 \times 0.0333)} \times 0.6745] = \exp(0.1741) = 1.19$$

The MOR of 1.19 indicates that, when comparing two randomly selected counties, the median difference in the odds of a positive recorded diagnostic result attributable to county membership was approximately 1.19-fold in the null model.

Together, the ICC and MOR indicate relatively limited county-level clustering, with a small proportion of the latent logistic-scale variance attributable to county differences.

3.10 Model Diagnostics and Sensitivity Analyses

Model fit was evaluated with convergence checks, AIC, BIC, log-likelihood, and DHARMA simulation-based residual diagnostics. For the conventional adjusted binomial model, residual uniformity, dispersion, and outliers were examined. Because a county-year may contain several service-sector observations, DHARMA residuals were reduced to one residual per county-year with ``recalculateResiduals()`` for descriptive assessment of temporal patterns. The same procedure was applied to the beta-binomial model as a robustness check. No formal county-specific temporal autocorrelation p-value was reported because the resulting county-year residual series was not used for unsupported formal inference. Sensitivity analyses included categorical year, a beta-binomial year-by-sector interaction model, and random-intercept versus random-slope structures. Model-based predicted probabilities were estimated with estimated marginal means.

3.11 Software and Reproducibility

The analysis package uses R version 4.6.1 and retains the raw and cleaned data, model objects, scripts, tables, figures, diagnostic outputs, and analysis logs. The revised workflow produces county-year DHARMA residual tables, the corresponding temporal residual trajectory figure, and the formal diagnostic outputs. Models were fitted with glmmTMB [9].

The aggregated routine surveillance data were supplied by the Liberia Ministry of Health/National Malaria Control Program and are not publicly available.

4.0 Results

4.1 Dataset Completeness and Analytic Sample

The structural dataset comprised 300 county-sector-year observations. Complete diagnostic information was available for 220 observations (73.3%), while 80 (26.7%) were incomplete. Missingness was concentrated in non-public sectors: 60.0% of Concession observations, 13.3% of Faith Based observations, and 33.3% of Private observations were incomplete; no Public observations were incomplete.

Table 1. Data completeness of the 300 county-sector-year observations

Group	Records	Complete diagnostic	Incomplete diagnostic	Incomplete (%)
Overall	300	220	80	26.7
Concession	75	30	45	60.0
Faith Based	75	65	10	13.3
Private	75	50	25	33.3
Public	75	75	0	0.0
2021	60	42	18	30.0
2022	60	43	17	28.3
2023	60	45	15	25.0
2024	60	45	15	25.0
2025	60	45	15	25.0

Note. The 80 incomplete observations had the full diagnostic block missing. Missing diagnostic observations were not treated as zero tests.

4.2 Overall Temporal Pattern

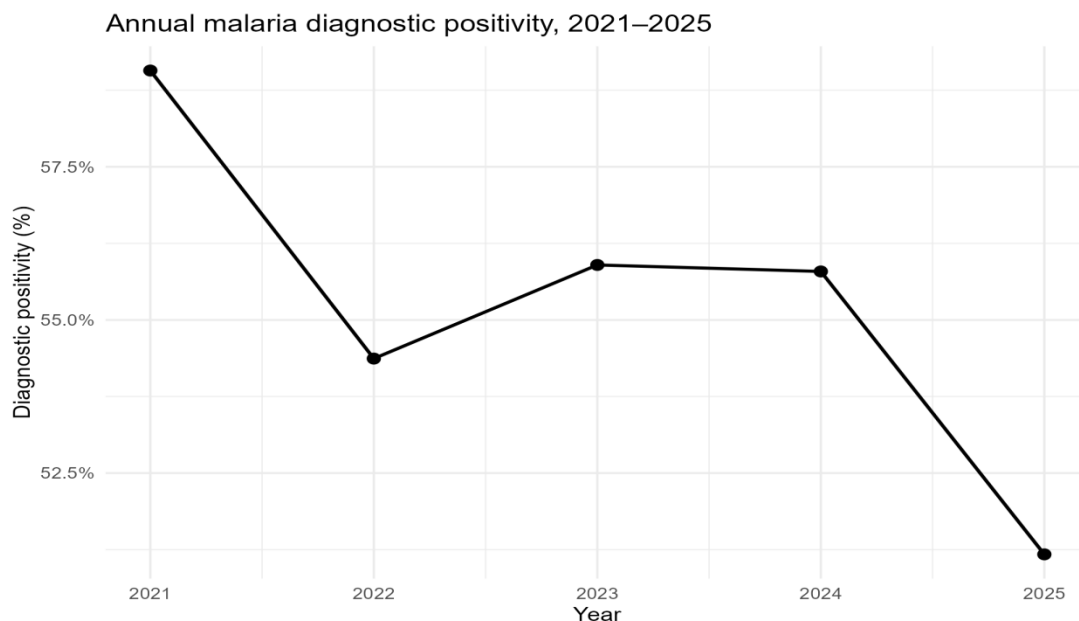
Among the 220 complete diagnostic observations, 7,097,294 tests were recorded: 3,914,734 were positive and 3,182,560 were negative, giving an overall positivity of 55.2%. Testing volume was lowest in 2023 (1,188,755) and highest in 2025 (1,624,400). Recorded positivity fell from 59.1% in 2021 to 51.2% in 2025.

Table 2. Annual malaria diagnostic testing and positivity, Liberia, 2021–2025

Year	Diagnostic observations	Total tests	Positive	Negative	Positivity (%)	RDT share (%)
2021	42	1463900	864748	599152	59.1	64.7
2022	43	1350262	734127	616135	54.4	62.8
2023	45	1188755	664485	524270	55.9	45.3
2024	45	1469977	820123	649854	55.8	55.7
2025	45	1624400	831251	793149	51.2	64.0

Note. RDT, rapid diagnostic test. Positivity is positive diagnostic tests divided by total recorded positive and negative diagnostic tests.

Figure 1. Annual malaria diagnostic positivity in Liberia, 2021–2025. Values are based on aggregated positive and negative diagnostic counts in observations with complete diagnostic information.



Positivity was highest in 2021 and was lower by 2025. The later years therefore contained a smaller proportion of positive recorded tests than 2021. This is a pattern in the surveillance records and should not be read as a direct estimate of malaria prevalence.

4.3 Health-Service Sector Variation

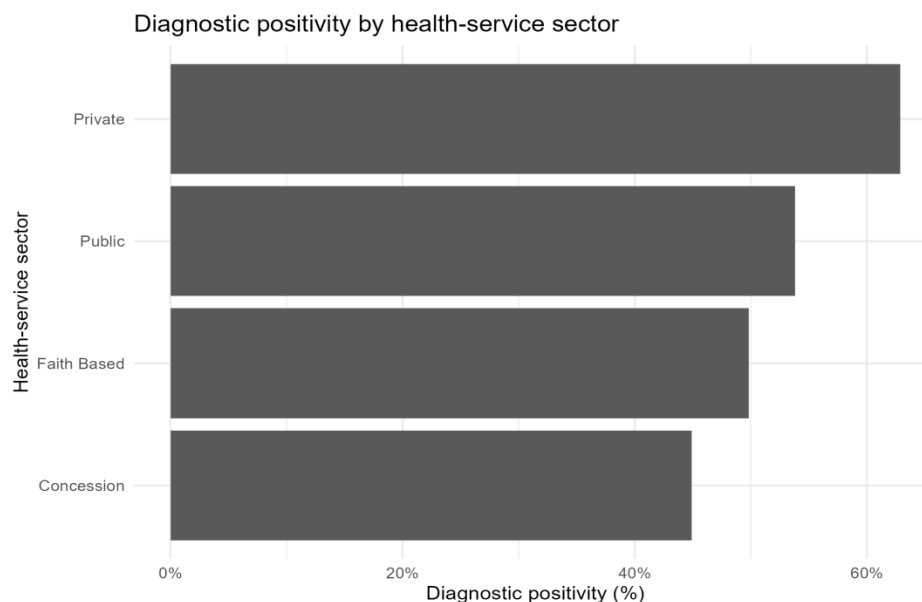
The four service sectors differed in observed diagnostic positivity. Private services recorded the highest aggregate positivity (62.9%), followed by Public (53.8%), Faith Based (49.8%), and Concession (44.9%). Public services accounted for 4,588,593 tests, or 64.7% of recorded testing, whereas Concession services accounted for 3.5%.

Table 3. Malaria diagnostic testing and positivity by health-service sector

Health-service sector	Observations	Total tests	Positive	Negative	Positivity (%)	RDT share (%)
Concession	30	250764	112633	138131	44.9	39.3
Faith Based	65	668790	333204	335586	49.8	35.2
Private	50	1589147	999140	590007	62.9	35.1
Public	75	4588593	2469757	2118836	53.8	71.9

Note. Values are aggregated across counties and years with available diagnostic data.

Figure 2. Observed malaria diagnostic positivity by health-service sector, aggregated across 2021–2025.

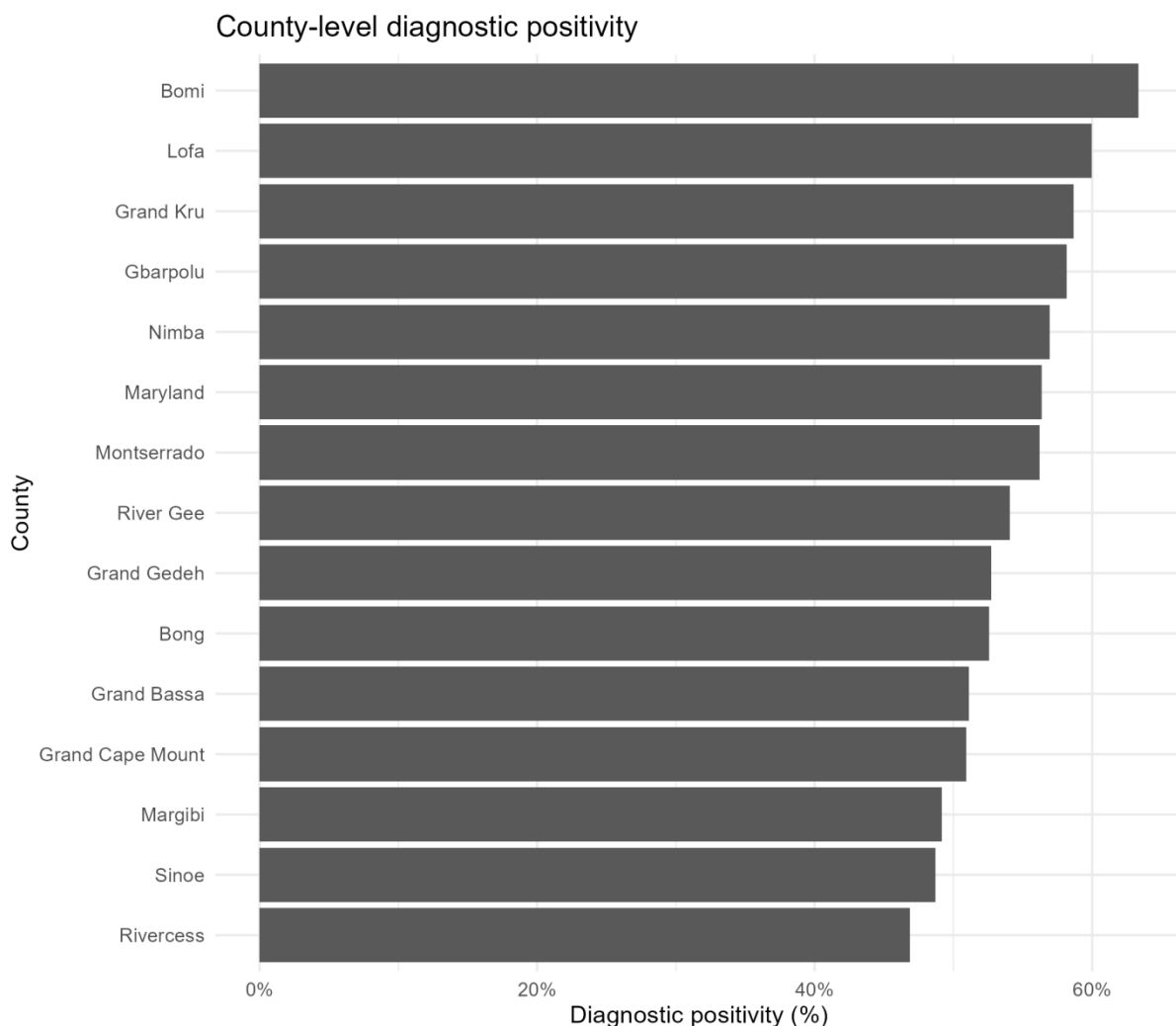


The sectors differed in both positivity and testing volume. Private services had the highest observed positivity and Concession services the lowest, while Public services contributed most of the recorded tests. The distribution of positive results was therefore not the same as the distribution of testing activity.

4.4 County-Level Variation

County-level observed positivity ranged from 46.9% in Rivercess to 63.4% in Bomi. Montserrado contributed 2,568,959 tests, representing 36.2% of all recorded testing, and had an observed positivity of 56.2%. These values describe the surveillance records and are not population prevalence estimates.

Figure 3. Observed malaria diagnostic positivity by county, aggregated across 2021–2025.



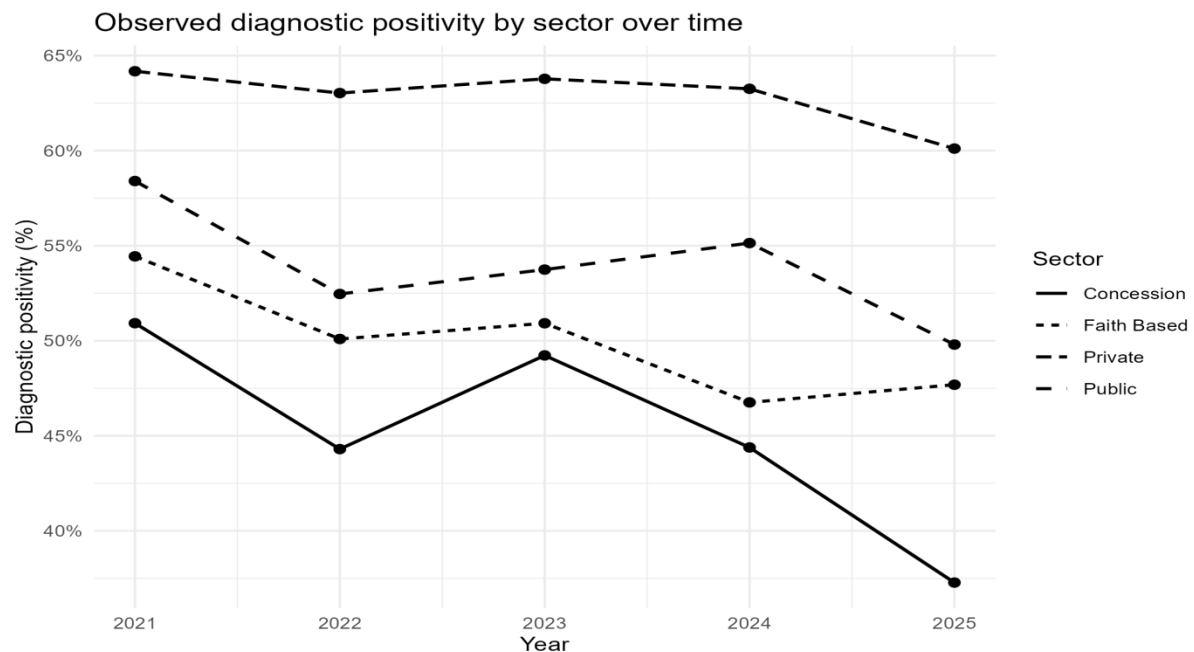
Observed positivity differed across counties, with Bomi highest and Rivercess lowest in the aggregated records. The geographic differences do not, by themselves, establish corresponding differences in population malaria prevalence because the volume and composition of testing may vary between counties.

The complete county-level results are in Supplementary Table S2, and the county-by-sector results are in Supplementary Table S3.

4.5 Observed Sector Trajectories

Positivity differed between sectors across the study period. Private services remained above the other sectors in years with available observations, while Concession services had lower positivity and declined from 50.9% in 2021 to 37.3% in 2025. Public-sector positivity declined from 58.4% to 49.8%. These patterns were examined further in the multilevel models; annual sector results are listed in Supplementary Table S4.

Figure 4. Observed malaria diagnostic positivity by health-service sector over time. Lines summarize aggregated diagnostic counts within each sector and year.



The sector trajectories were not identical over time. Private services remained relatively high, whereas Concession and Public services declined. The figure describes the observed pattern and was used to motivate the formal assessment of year and sector effects.

4.6 Multilevel Model Results

All fitted models met the recorded convergence checks. The null model gave a county-level variance of 0.0333, a logistic ICC of 0.0100, and an MOR of 1.19. Within the conventional binomial models, adding year reduced AIC, and adding health-service sector reduced it further. The year-by-sector model produced another AIC reduction. The beta-binomial model was then examined because the residual diagnostics indicated extra-binomial variation in the conventional specification.

Table 4. Comparison of longitudinal multilevel models

Model	AIC	BIC	Log-likelihood	Parameters	Converged
M0: Null	186,435.6	186,442.4	-93,215.8	2	True
M1: Year	172,712.5	172,722.6	-86,353.2	3	True
M2: Year + sector	98,745.4	98,765.7	-49,366.7	6	True
M3: Year $\times$ sector	97,647.4	97,678.0	-48,814.7	9	True
M4: Beta-binomial	3,734.0	3,757.8	-1,860.0	7	True
M5: Categorical year $\times$ sector	88,979.2	89,050.5	-44,468.6	21	True
M6: Random slope	92,535.4	92,562.6	-46,259.7	8	True

Note. AIC and BIC are reported for models fitted to the same 220 complete diagnostic observations. AIC and BIC were used for comparisons within the conventional binomial model family; the beta-binomial model was evaluated as an alternative distributional specification because residual diagnostics indicated extra-binomial variation, so its AIC and BIC should not be interpreted as a direct ranking against the conventional binomial models.

Table 5. Adjusted associations with malaria diagnostic positivity from the beta-binomial mixed-effects model

Term	Adjusted OR	95% CI	P-value
Year (per one-year increase)	0.963	0.921–1.005	0.086
Concession vs Public	0.827	0.671–1.020	0.075
Faith Based vs Public	1.195	1.022–1.396	0.025
Private vs Public	1.450	1.220–1.722	<0.001

Note. Reference sector: Public. Year is centered at 2021. OR >1 indicates higher odds of a positive recorded diagnostic result; OR <1 indicates lower odds. The model included a county random intercept and had a beta-binomial dispersion parameter of 18.4.

The beta-binomial model was used for the primary adjusted inference. The year effect was not statistically supported at the 0.05 level (OR 0.963 per year, 95% CI 0.921–1.005, $p=0.086$). Compared with Public services, the odds of a positive recorded diagnostic result were higher in Private services (OR 1.450, 95% CI 1.220–1.722, $p<0.001$) and Faith Based services (OR 1.195, 95% CI 1.022–1.396, $p=0.025$). The Concession estimate was lower than Public but was not statistically supported (OR 0.827, 95% CI 0.671–1.020, $p=0.075$).

Table 6. County-level heterogeneity from the null random-intercept model

Measure	Estimate
County random-intercept variance	0.0333
Logistic ICC	0.0100
Median odds ratio (MOR)	1.19

Note. ICC and MOR were calculated from the conventional binomial null model. They quantify county-level clustering on the latent logistic scale.

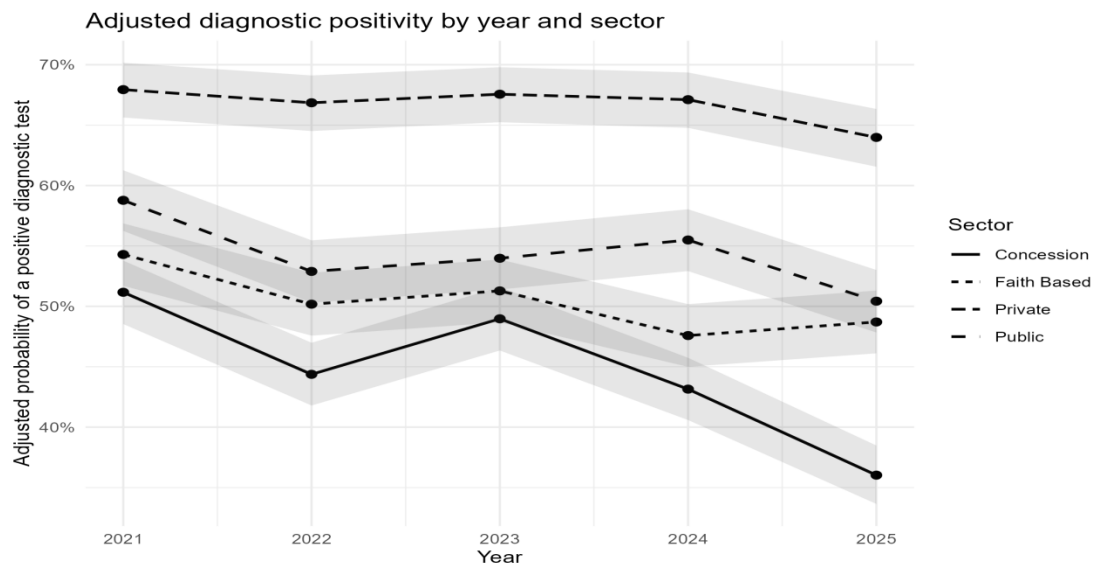
The null random-intercept model estimated a county-level variance of 0.0333, corresponding to a logistic ICC of 0.0100 (1.0%) and an MOR of 1.19. These measures indicate that a small proportion of the latent logistic-scale variance was attributable to county clustering.

4.7 Adjusted Predicted Probabilities

The categorical-year model generated adjusted predicted probabilities for graphical comparison. Across sectors, the estimated probabilities were 66.7% for Private, 54.3% for Public, 50.4% for Faith Based, and 44.5% for Concession. The corresponding year-specific estimates declined

from 58.2% in 2021 to 49.8% in 2025. Because the conventional binomial diagnostics indicated poor residual fit, these estimates are presented as model-based descriptive contrasts and are interpreted alongside the beta-binomial analysis.

Figure 5. Adjusted predicted probability of a positive diagnostic test by year and health-service sector from the categorical-year binomial mixed-effects model. Shaded bands are model-based 95% confidence intervals.



The figure shows model-adjusted probabilities rather than observed percentages. After adjustment for the variables in the categorical-year mixed-effects model, Private services had the highest predicted probability and Concession services the lowest. The year-specific adjusted probability also declined from 58.2% in 2021 to 49.8% in 2025. The shaded bands represent the 95% confidence intervals. Given the residual misfit of the conventional binomial model, these estimates are descriptive contrasts and should be considered with the beta-binomial results.

4.8 Sensitivity Analyses and Diagnostics

For the conventional adjusted binomial model, DHARMA showed non-uniform residuals (Kolmogorov–Smirnov $D=0.498$, $p<0.001$), significant residual dispersion (1.021, $p<0.001$), and a high frequency of model-level residual outlier flags (209 of 220 observations; 95.0%, $p<0.001$). For the beta-binomial model, the DHARMA residual dispersion statistic was 1.146 ($p=0.194$), indicating no statistically significant evidence of residual dispersion. Full results are in Supplementary Table S11 and Supplementary Figure S1. County-year residuals for both models are provided in Supplementary Tables S12 and S13, with the consolidated summary in Supplementary Table S14 and trajectories in Supplementary Figure S2.

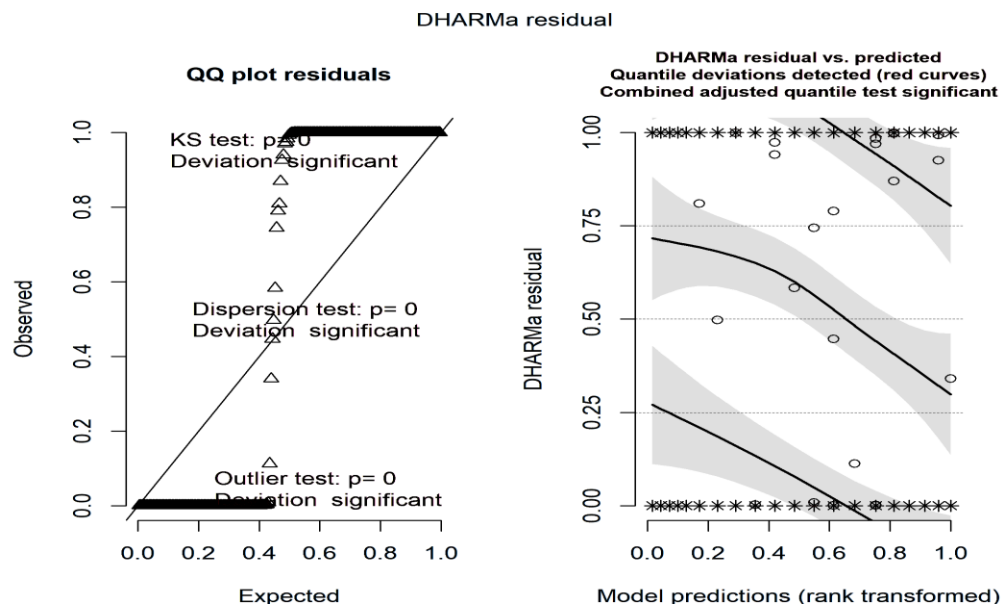
The beta-binomial model showed no statistically significant evidence of residual dispersion in the DHARMA diagnostic (dispersion statistic 1.146, $p=0.194$).

Supplementary Table S11. DHARMA residual diagnostic results for the conventional adjusted binomial and beta-binomial models.

Model		Diagnostic	Statistic	P-value	Interpretation
Conventional binomial	adjusted	Uniformity (Kolmogorov–Smirnov)	$D = 0.498$	<0.001	Residuals departed from the expected uniform distribution
Conventional binomial	adjusted	Dispersion	1.021	<0.001	Evidence of residual dispersion
Conventional binomial	adjusted	Outliers	209/220 (95.0%)	<0.001	High model-level residual outlier frequency
Beta-binomial		DHARMA residual dispersion	1.146	0.194	No statistically significant evidence of residual dispersion

Note. The outlier count refers to DHARMA model-level residual outlier flags among the 220 analytic observations; it does not represent individual patient-level outliers.

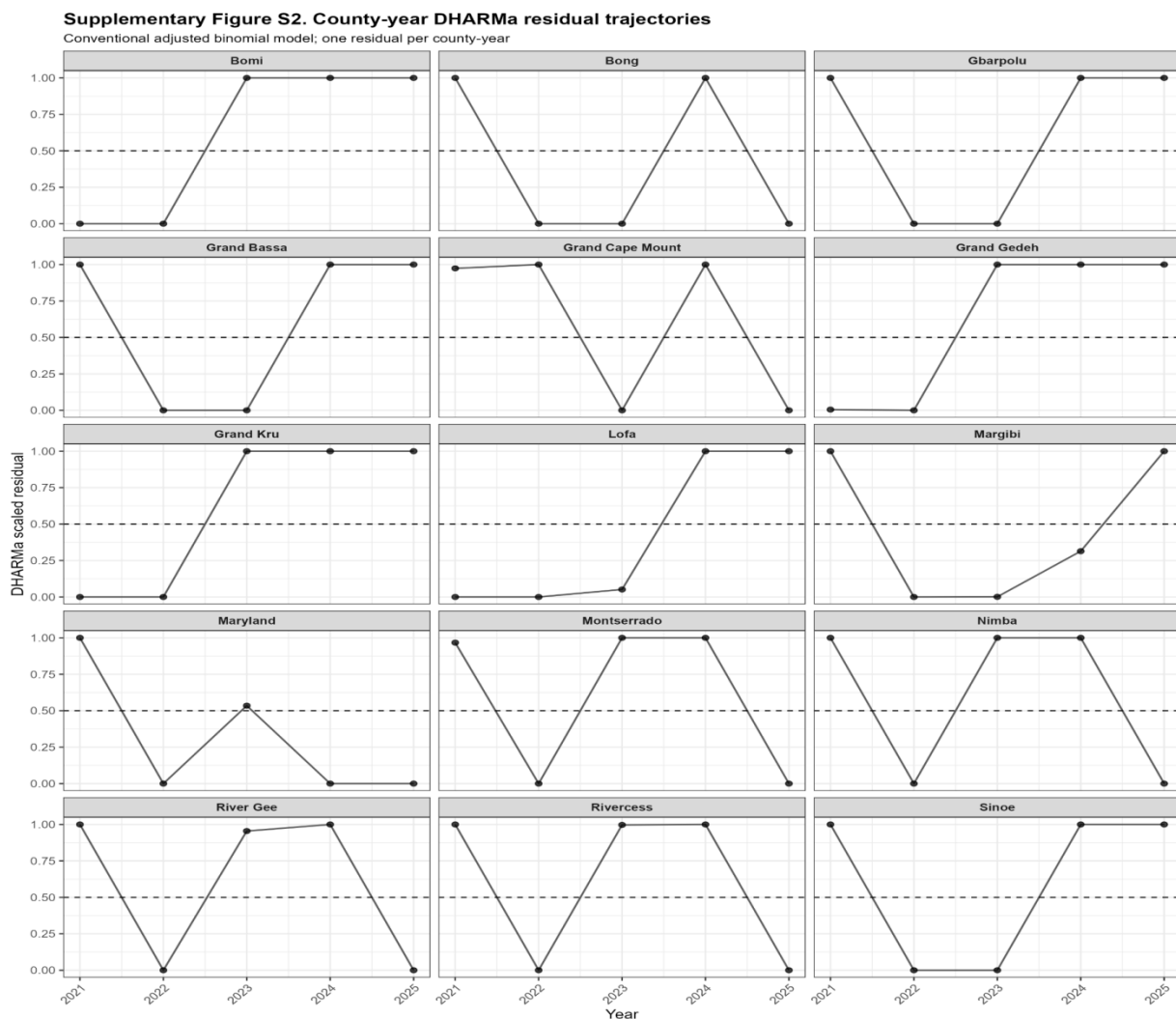
Supplementary Figure S1. DHARMA residual diagnostics for the conventional adjusted binomial model (M2)



The figure is a visual assessment of the conventional binomial model. The residuals depart markedly from the pattern expected under adequate fit, in agreement with the uniformity and dispersion tests in Supplementary Table S11. The 209 model-level outlier flags should not be interpreted as 209 individual patient outliers; they indicate that the conventional model does not reproduce the aggregated diagnostic data adequately.

Supplementary Figure S2. County-year DHARMA residual trajectories.

The plot gives a descriptive county-year assessment from the conventional adjusted binomial model, with one residual per county-year. It is not accompanied by a formal county-specific temporal autocorrelation p-value.



The panels show the simulated residual position for each county across the five study years. Residual behavior differs among counties and years rather than following a single pattern. With only five annual observations per county and residuals aggregated to the county-year level, the figure is descriptive and does not establish a formal temporal autocorrelation effect.

The diagnostic plots show substantial departures from the residual behavior expected under the conventional binomial model, consistent with the uniformity, dispersion, and outlier tests in Supplementary Table S11.

The beta-binomial model reduced the evidence of residual dispersion seen with the conventional binomial model and was used for the primary adjusted inference.

The categorical-year conventional binomial sensitivity model produced statistically detectable year-by-sector interaction terms. Because its residual diagnostics were poor, those estimates were interpreted cautiously; the complete results are reported in Supplementary Table S8.

The random-slope binomial model had a lower AIC than the random-intercept binomial model (92,535.4 versus 98,745.4), indicating additional county-specific temporal heterogeneity within that model family. Because the conventional binomial framework showed substantial residual misfit, the random-slope comparison was retained as a sensitivity analysis rather than the primary model. The full comparison is in Supplementary Table S10.

5.0 Discussion

The national surveillance records show differences in diagnostic positivity over time, between counties, and across health-service sectors. Positivity declined while the number of recorded tests increased, so changes in the testing denominator and in the population reaching diagnostic services need to be considered when reading the temporal pattern. Francis et al. reported that facility-based malaria test positivity varies with age, residence, and diagnostic method, showing why changes in facility positivity cannot be attributed to transmission alone [10]. Kamau et al. also found a relationship between facility-based positivity and community parasite prevalence, but the relationship depended on the population presenting for care [13]. The Liberian results should therefore be read as changes in recorded diagnostic positivity within the surveillance system rather than direct measures of population-level transmission.

The county pattern is consistent with findings from other malaria-endemic settings in which routine diagnostic data show substantial geographic variation. In Western Kenya, Alegana et al. found marked differences in malaria test positivity across sub-counties and showed the value of accounting for reporting completeness, population distribution, spatial structure, month, and facility type when estimating local risk [12]. Thawer et al. reported similar spatial variation in

routine malaria test positivity across wards in mainland Tanzania and highlighted the effects of incomplete reporting and uncertainty on empirical estimates [14]. The Liberian data add another national example of why county-level patterns can be obscured by national summaries. Montserrado's large testing volume without the highest positivity also shows why testing volume and positivity should be examined together.

The service-sector differences in Liberia were retained in the beta-binomial model: Private and Faith Based services had higher odds of a positive recorded result than Public services, while the Concession contrast was not statistically supported. ACTwatch reported substantial differences in malaria diagnostic availability, market share, and the organization of testing between public and private providers across sub-Saharan Africa [15]. Such differences may reflect variation in care-seeking, referral pathways, illness severity, access to testing, and diagnostic practice. The sector estimates should therefore be interpreted as associations within the surveillance system, not as effects of ownership or management. The beta-binomial year-by-sector model also did not support the interaction terms, so the data do not provide strong evidence that the sectors followed different temporal changes.

The conventional binomial model also showed more variability than its assumed distribution could accommodate. Its residual diagnostics were poor, whereas the beta-binomial model showed less evidence of residual dispersion. For routine malaria surveillance, this distinction matters because reporting completeness, testing practices, denominators, and service use can differ by place and time. Alegana et al. described similar challenges in using routine malaria morbidity data in Africa, particularly the need to account for reporting completeness, denominators, and the populations represented by health-facility records [11]. The Western Kenya and Tanzania studies addressed related problems through spatial and spatiotemporal models [12,14]. The present analysis retained county-level clustering while allowing extra-binomial variation with a beta-binomial model, resulting in more cautious adjusted inference.

The analysis covers all 15 counties and five consecutive years of surveillance observations, allowing geographic and temporal patterns to be examined within one national dataset. The large number of recorded diagnostic tests supports detailed description of routine testing activity. Repeated county observations were handled with a multilevel structure, and extra-binomial variation was assessed rather than relying only on conventional binomial inference. The analysis package also retains the data, scripts, model objects, tables, figures, diagnostic outputs, and logs, allowing the analytical steps to be reproduced.

6.0 Policy Implications

The results point to several practical considerations for malaria surveillance. County, service sector, testing volume, diagnostic method, and reporting completeness should be reviewed together when interpreting changes in positivity. Improving reporting from non-public sectors would strengthen the completeness of national surveillance. Monthly data, population denominators, suspected-case counts, and service-utilization measures would also allow more detailed assessment of changes in diagnostic positivity.

7.0 Limitations of the Study

The analysis has several limitations. The data are aggregated and ecological, so individual-level associations cannot be drawn, and the records do not identify individual patients or named facilities. Diagnostic information was missing from 80 of the 300 structural observations, with the missing observations concentrated in non-public sectors. Annual observations prevent assessment of seasonality and short-term changes; adjusted predictions and sensitivity estimates are reported in Supplementary Tables S5–S10. The denominator consists of recorded positive and negative diagnostic tests rather than all persons suspected of malaria or the population at risk. Testing practices, referral patterns, diagnostic availability, and service use may differ between counties and sectors and were not measured directly. The observational design also prevents causal interpretation of the reported associations.

8.0 Conclusion

From 2021 to 2025, malaria diagnostic positivity in Liberia's routine surveillance records differed by year, county, and health-service sector. Testing volume increased while observed positivity declined, and the surveillance data showed clear geographic and sector differences. The conventional binomial mixed-effects model did not adequately represent the variability in the aggregated counts. A beta-binomial multilevel model provided a better basis for adjusted inference and gave more conservative estimates of temporal and sector effects. Routine diagnostic positivity should be interpreted together with testing volume, service sector, county clustering, and reporting completeness rather than as a direct measure of population prevalence.

Acknowledgements

The author thanks the Liberia Ministry of Health/National Malaria Control Program for providing the aggregated routine malaria surveillance dataset used in this analysis.

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