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Empirical Validation of an Adaptive Spatial Hierarchical Bayesian Seir Model for HIV Transmission Dynamics in Kenya

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Abstract- ***This study presents the empirical validation of an adaptive spatial hierarchical Bayesian SEIR model developed for modeling HIV transmission dynamics in Kenya. Using comprehensive HIV surveillance data from 15 strategically selected Kenyan counties spanning 2015-2024 (1,620 county-month observations), the model was validated through comparative analysis with benchmark approaches, sensitivity testing, and policy scenario evaluation. Data sources included the Kenya AIDS Indicator Survey, National AIDS Control Council, Kenya Health Information System, and Kenya National Bureau of Statistics. The validation framework employed multiple performance metrics including Root Mean Square Error (RMSE), Mean Absolute Error (MAE), correlation coefficients, and Area Under the Curve (AUC) for hotspot detection. Results demonstrated that the proposed model achieved superior predictive accuracy with 48% improvement in prediction errors (RMSE = 0.035) compared to non-spatial approaches and 22% improvement over static spatial models. Diebold-Mariano tests confirmed statistically significant improvements ($p < 0.001$) across all benchmark comparisons. Sensitivity analysis revealed transmission rate as the most influential parameter (first-order Sobol index = 0.34), while the model maintained robust performance with up to 20% missing data. The validated model identified substantial spatial heterogeneity in basic reproduction numbers ranging from 0.3 in Wajir to 3.2 in Homabay counties. These findings validate the model for evidence-based resource allocation, early warning systems for emerging transmission hotspots, and adaptive HIV program management in Kenya and similar resource-limited settings.***

Keywords: ***HIV/AIDS modeling, Bayesian inference, spatial epidemiology, SEIR model, model validation, Kenya***

I. INTRODUCTION

HIV and AIDS remain a significant public health challenge globally, with Kenya bearing one of the heaviest burdens as the country with the third-largest HIV epidemic worldwide. According to UNAIDS (2023), approximately 1.3 million people are living with HIV in Kenya, representing a substantial healthcare and socioeconomic challenge. Despite considerable progress in prevention and treatment programs, the complex spatiotemporal dynamics of HIV transmission continue to challenge intervention strategies, necessitating advanced modeling approaches that can capture spatial heterogeneity and temporal evolution of the epidemic.

Traditional epidemiological models, while foundational, often fail to account for the spatial clustering of HIV infections and the dynamic nature of transmission patterns across different geographic regions (Cuadros et al., 2017). The recognition that HIV prevalence varies significantly across counties in Kenya, ranging from less than 1% in some northern counties to over 20% in western regions, underscores the need for spatially explicit modeling frameworks (National AIDS Control Council, 2022). Furthermore, the effectiveness of interventions such as antiretroviral therapy (ART), voluntary medical male circumcision, and pre-exposure prophylaxis varies across regions due to differences in healthcare infrastructure, population mobility, and socioeconomic factors.

The development of adaptive spatial hierarchical Bayesian models represents a methodological advancement in epidemiological modeling by integrating spatial correlation structures with temporal dynamics within a probabilistic framework (Blangiardo & Cameletti, 2015). Such models offer several advantages including rigorous uncertainty quantification, the ability to borrow strength across spatial units, and flexibility in incorporating complex

dependency structures. However, the practical utility of these advanced models depends critically on their empirical validation using real-world data.

This study addresses a critical gap in the literature by presenting comprehensive empirical validation of an adaptive spatial hierarchical Bayesian SEIR model specifically developed for HIV transmission dynamics in Kenya. The validation encompasses comparative performance assessment against benchmark models, sensitivity analysis to key parameters and assumptions, and evaluation of the model's practical utility for policy scenario analysis. The findings contribute to both methodological advancement in spatial epidemiology and practical guidance for HIV control programs in resource-limited settings.

II. LITERATURE REVIEW

The evolution of HIV modeling has progressed from simple compartmental models to sophisticated spatial-temporal frameworks incorporating Bayesian inference and machine learning techniques. The foundational SEIR (Susceptible-Exposed-Infected-Removed) framework, derived from the classical work of Kermack and McKendrick (1927), has been extensively adapted for HIV modeling with modifications to account for the chronic nature of HIV infection and the role of treatment (Hethcote, 2000).

Spatial modeling of HIV has gained prominence following recognition of significant geographic heterogeneity in transmission patterns. Cuadros et al. (2017) demonstrated substantial spatial clustering of HIV prevalence in sub-Saharan Africa, highlighting the importance of geographically targeted interventions. In the Kenyan context, studies by Odhiambo et al. (2020) and Mwangi et al. (2019) identified spatial hotspots requiring prioritized intervention, though these studies employed relatively simple spatial methods without full Bayesian uncertainty quantification.

Hierarchical Bayesian approaches have emerged as powerful tools for infectious disease modeling due to their ability to integrate multiple levels of variation and provide coherent uncertainty estimates (Gelman et al., 2013). The seminal work by Besag et al. (1991) on conditional autoregressive models established the foundation for spatial Bayesian inference, while subsequent developments by Rue et al. (2017) on Integrated Nested Laplace Approximations (INLA) have made these methods computationally tractable for large-scale applications.

Recent advances have integrated machine learning with traditional epidemiological models. Jewell et al. (2022) demonstrated ensemble machine learning approaches for HIV incidence prediction, while Park et al. (2021) applied spatial clustering algorithms to identify transmission networks. However, these approaches often lack the interpretability and uncertainty quantification of Bayesian methods, limiting their utility for policy decision-making.

Model validation in epidemiology has received increasing attention, with recognition that predictive accuracy alone is insufficient for assessing model utility (Hallett et al., 2019). Comprehensive validation frameworks should include sensitivity analysis to assess parameter influence, structural sensitivity to examine robustness to model assumptions, and practical validation through policy scenario testing. Despite these recommendations, few spatial HIV models have undergone rigorous empirical validation using comprehensive frameworks, representing a significant gap that this study addresses.

III. METHODOLOGY

3.1 Study Design and Data Sources

This study employed a quantitative research design integrating spatial-temporal SEIR modeling, hierarchical Bayesian inference, and comprehensive validation testing. The analysis utilized HIV surveillance data from 15 strategically selected Kenyan counties representing diverse epidemiological contexts across Kenya's five major regions. High-burden Western counties (Homabay: 21%, Siaya: 20.3%, Kisumu: 18.5%) were included alongside lower-prevalence Northern counties (Garissa: 2.1%, Wajir: 0.8%) to provide substantial variation for model validation.

Primary data sources included: the Kenya AIDS Indicator Survey (KAIS) providing county-level prevalence estimates (2015-2022); National AIDS Control Council (NACC) contributing incidence and ART coverage data (2015-2024); Kenya Health Information System (KHIS) supplying facility-level service delivery information (2015-2024); and Kenya National Bureau of Statistics (KNBS) providing population demographics (2015-2024). The comprehensive dataset encompassed 1,620 county-month observations with variables spanning demographic, epidemiological, and intervention domains.

3.2 Model Specification

The adaptive spatial hierarchical Bayesian SEIR model incorporates HIV-specific compartments, adaptive spatial weights, and time-varying parameters. The model extends the classical SEIR framework by including treatment compartments and spatial coupling between counties through mobility-informed connectivity matrices. The hierarchical structure allows county-specific parameters to be partially pooled toward regional means, enabling effective borrowing of information across spatial units while preserving local heterogeneity.

The Bayesian framework specifies prior distributions for all model parameters based on existing literature and expert knowledge. Spatial correlation is modeled using a Matérn covariance function with estimated range and smoothness parameters. Temporal dynamics are captured through time-varying transmission rates with seasonal components. Posterior inference was conducted using Hamiltonian Monte Carlo via Stan software (Carpenter et al., 2017), with INLA employed for spatial component approximation.

3.3 Validation Framework

The validation framework encompassed three complementary components: comparative performance assessment, sensitivity analysis, and policy scenario evaluation. For comparative assessment, model performance was evaluated against four benchmark approaches: non-spatial SEIR models, static spatial models with fixed weights, non-hierarchical Bayesian approaches, and standard geostatistical models. Performance metrics included Root Mean Square Error (RMSE), Mean Absolute Error (MAE), Pearson correlation coefficient, and Area Under the Curve (AUC) for hotspot detection capability.

Sensitivity analysis employed Morris screening for initial parameter ranking followed by Sobol variance decomposition to quantify individual and interaction effects of model parameters. Structural sensitivity examined model robustness to alternative specifications including different spatial weight formulations, correlation structures, temporal adaptation mechanisms, and prior distributions. Data quality sensitivity assessed model resilience to missing data and measurement noise through controlled simulation experiments.

Statistical significance of performance differences was assessed using Diebold-Mariano tests for comparing predictive accuracy between competing models. All computational analyses were conducted using R Statistical Software (version 4.2.0), Stan for Bayesian inference, and Python for machine learning integration and visualization.

IV. RESULTS AND DISCUSSION

4.1 Comparative Model Performance

The adaptive spatial hierarchical Bayesian model demonstrated superior performance across all evaluation metrics compared to benchmark approaches. Table 1 presents the comparative results showing the proposed model achieved the lowest RMSE (0.035) and MAE (0.027), representing a 48% reduction in prediction error compared to non-spatial SEIR approaches and a 22% improvement over the best-performing benchmark model (static spatial).

Table 1: Comparative Model Performance

Model	RMSE	MAE	Correlation	AUC	Log-likelihood
Non-spatial SEIR	0.067	0.052	0.71	0.65	-245.3
Static spatial	0.045	0.036	0.83	0.74	-187.2
Non-hierarchical Bayesian	0.052	0.041	0.78	0.71	-203.8

Geostatistical	0.048	0.038	0.81	0.73	-192.5
Proposed model	0.035	0.027	0.86	0.87	-156.4

The proposed model also achieved the highest correlation coefficient (0.86) with observed data and demonstrated superior discriminative capability for identifying transmission hotspots (AUC = 0.87). The significantly improved log-likelihood value (-156.4) confirms enhanced overall model fit to the empirical data. These improvements are attributable to the model's ability to capture both spatial clustering patterns and temporal dynamics through the adaptive hierarchical framework.

Table 2 presents formal statistical validation using Diebold-Mariano tests, confirming that all performance improvements are statistically significant at the 0.002 level or better. The largest effect was observed against non-spatial SEIR models (DM statistic = 8.42, $p < 0.001$), while more modest but still significant improvements were demonstrated against the static spatial model (DM statistic = 3.17, $p = 0.002$).

Table 2: Diebold-Mariano Test Results

Comparison	DM Statistic	p-value	95% CI (RMSE diff)
vs. Non-spatial SEIR	8.42	< 0.001	[0.025, 0.040]
vs. Static spatial	3.17	0.002	[0.004, 0.016]
vs. Non-hierarchical	4.85	< 0.001	[0.012, 0.028]
vs. Geostatistical	3.94	< 0.001	[0.007, 0.021]

4.2 Sensitivity Analysis Results

Comprehensive sensitivity analysis identified the transmission rate (β_0) as the most influential parameter with a first-order Sobol index of 0.34 and total effect index of 0.42, indicating it accounts for 34-42% of output variance. This finding aligns with epidemiological theory and emphasizes the critical importance of accurate transmission rate estimation for model reliability. Spatial parameters including spatial variance ($\sigma\theta$) and spatial range (ℓ) ranked second and third in influence, collectively accounting for 30-44% of variance and validating the importance of the spatial modeling approach.

Structural sensitivity analysis demonstrated that using fixed spatial weights instead of adaptive ones caused the largest performance decline (18% RMSE increase), confirming the value of dynamic connectivity modeling. Removing seasonal terms resulted in 15% performance degradation, while alternative prior specifications caused minimal impact (5% RMSE change), indicating robust Bayesian estimation. The model showed remarkable resilience to data quality issues, maintaining convergence and acceptable performance with up to 20% missing data, though systematic bias caused more substantial degradation (22% RMSE increase).

4.3 Spatial Heterogeneity in Transmission Dynamics

The validated model identified substantial spatial heterogeneity in HIV transmission dynamics across Kenyan counties. Basic reproduction numbers (R_0) ranged from 0.3 in Wajir County to 3.2 in Homabay County, reflecting the dramatic regional variation in epidemic potential. This ten-fold variation in R_0 has profound implications for intervention targeting and resource allocation, suggesting that uniform national strategies may be suboptimal compared to geographically differentiated approaches.

The model successfully captured spatial clustering patterns with residual Moran's I of 0.03 ($p = 0.45$), indicating adequate accounting for spatial autocorrelation. Temporal dynamics were well-represented with coefficient of determination (R^2) values exceeding 0.87 across all counties, while coverage probabilities for uncertainty intervals exceeded 85%, confirming reliable uncertainty quantification. These diagnostic results validate the model's ability to capture the complex spatial-temporal structure of HIV transmission in Kenya.

4.4 Discussion

The empirical validation results provide strong evidence for the utility of the adaptive spatial hierarchical Bayesian SEIR model for HIV transmission modeling in Kenya. The 48% improvement in predictive accuracy over non-spatial approaches is not merely a statistical accomplishment

but translates to more reliable prevalence forecasts that can meaningfully inform resource allocation and intervention planning. The ability to accurately identify transmission hotspots (AUC = 0.87) is particularly valuable for Kenya's HIV control program, enabling targeted deployment of prevention resources to areas of greatest need.

The sensitivity analysis findings have important practical implications. The dominance of transmission rate parameters suggests that intervention strategies targeting transmission reduction, such as behavioral change programs and pre-exposure prophylaxis, may have the greatest impact on epidemic trajectories. The substantial influence of spatial parameters validates the geographic targeting approach and emphasizes the importance of accounting for population mobility and cross-county transmission in intervention planning.

The model's robustness to data quality issues is encouraging for practical implementation in resource-limited settings where surveillance data often have substantial gaps and measurement errors. The finding that systematic bias causes greater performance degradation than random missing data highlights the importance of quality assurance protocols in HIV surveillance systems, particularly regarding consistent case definitions and reporting procedures across facilities and counties.

These findings align with and extend previous work on spatial HIV modeling in sub-Saharan Africa. While earlier studies by Cuadros et al. (2017) and Odhiambo et al. (2020) identified spatial clustering patterns, the current work advances beyond descriptive analysis to provide a validated predictive framework with formal uncertainty quantification. The hierarchical Bayesian approach addresses limitations of previous frequentist spatial analyses by providing coherent probabilistic statements about model parameters and predictions.

V. CONCLUSION

This study provides comprehensive empirical validation of an adaptive spatial hierarchical Bayesian SEIR model for HIV transmission dynamics in Kenya. The validation demonstrates statistically significant improvements over benchmark approaches, with 48% reduction in prediction error compared to non-spatial models and 22% improvement over static spatial approaches. The model successfully captures substantial spatial heterogeneity in transmission dynamics, with basic reproduction numbers varying from 0.3 to 3.2 across counties, while providing reliable uncertainty quantification with coverage probabilities exceeding 85%.

The sensitivity analysis confirms the model's robustness to reasonable ranges of parameter uncertainty, alternative structural specifications, and moderate data quality degradation. The identification of transmission rate as the dominant parameter influence provides valuable guidance for prioritizing intervention strategies. The validated model offers Kenya's HIV control program enhanced capabilities for evidence-based resource allocation, early warning systems for emerging transmission hotspots, and adaptive program management.

The methodological contributions extend beyond the Kenyan context to provide a generalizable framework for spatial epidemiological modeling in resource-limited settings. The successful integration of adaptive spatial weights, hierarchical Bayesian inference, and comprehensive validation protocols demonstrates that theoretically sophisticated models can be made practically useful for public health decision-making. As Kenya and similar countries progress toward HIV elimination goals, validated modeling frameworks such as that presented here will be essential tools for strategic planning and resource optimization.

VI. RECOMMENDATIONS

Based on the validated model findings, the following recommendations are proposed for HIV control program implementation and future research directions:

First, Kenya's National AIDS Control Council should adopt the validated spatial model for evidence-based resource allocation, prioritizing high-transmission counties ($R_0 > 2.0$) including Homabay, Siaya, and Kisumu for intensified prevention and treatment

interventions. The model's hotspot detection capability (AUC = 0.87) should be integrated into surveillance systems to enable early warning of emerging transmission clusters.

Second, HIV surveillance systems should strengthen data quality assurance protocols, particularly regarding consistent case definitions and timely reporting, given the model's sensitivity to systematic bias. Investment in facility-level data infrastructure would enable finer spatial resolution modeling and more precisely targeted interventions.

Third, intervention strategies should prioritize transmission-reducing approaches given the dominance of transmission rate parameters in model sensitivity. This includes scaling up pre-exposure prophylaxis programs, behavioral change interventions, and test-and-treat initiatives in identified hotspot areas.

Fourth, future research should extend the modeling framework to incorporate sub-county spatial resolution, integrate mobile phone and satellite-derived mobility data for improved connectivity estimation, and develop computationally efficient methods for real-time model updating. Development of user-friendly decision-support interfaces would enhance accessibility for non-technical public health practitioners.

Fifth, the validated framework should be adapted and tested in other high-burden countries in sub-Saharan Africa to assess generalizability and support regional HIV elimination efforts. Collaborative research networks could facilitate cross-country model calibration and validation using harmonized surveillance data.

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