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EXPLAINABLE MODELS FOR EARLY PREDICTION OF INFECTIOUS DISEASE OUTBREAKS: INTEGRATING SPATIO-CLIMATIC AND SECURITY INDUCED MIGRATION DATA IN NORTH-EASTERN NIGERIA.

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Abstract
North-Eastern Nigeria continues to grapple with the dual challenge of infectious diseases such as malaria, cholera, measles, and scabies, compounded by persistent conflict-driven displacement. Existing surveillance systems remain limited, often undermined by underreporting, delayed responses, and inadequate integration of ecological and socio-political drivers. This study-in-progress proposes an explainable artificial intelligence (XAI) framework for early outbreak prediction that integrates spatio-climatic variables with conflict-induced migration data. Spatio-temporal grids (2010–2025) are being constructed to derive lagged indicators that capture delayed impacts of weather and displacement on transmission dynamics. The methodological approach combines ensemble learners (Random Forest, XGBoost) with deep spatio-temporal networks (LSTM, ConvLSTM), while outbreak definitions are based on 95th percentile anomalies. Explainability mechanisms, including SHAP, saliency maps, counterfactual analysis, and expert validation, are incorporated to ensure interpretability. Although analysis is ongoing, the study aims to benchmark performance against climate-only, migration-only, and traditional baselines. The anticipated outcome is a transparent, reliable predictive framework capable of informing epidemic preparedness and intervention planning in fragile and conflict-affected contexts.

Keywords: Explainable Artificial Intelligence, Counterfactuals, Saliency Maps, Infectious Diseases, Disease Outbreak,

1.0 Introduction

Infectious diseases remain a significant public health challenge in sub-Saharan Africa, where ecological variability, fragile health systems, and socio-political instability converge to sustain recurrent outbreaks. North-Eastern Nigeria exemplifies this crisis, grappling simultaneously with endemic diseases such as malaria, measles, meningitis, scabies, impetigo, cholera and the likes this is coupled with protracted displacement driven by the Boko Haram insurgency [1], [2]. Malaria alone accounts for an estimated 27% of global cases, with Nigeria contributing disproportionately to global mortality [3]. Cholera outbreaks, often linked to poor water, sanitation, and hygiene (WASH) conditions, recur almost annually in the region, exacerbated by flooding and overcrowded internally displaced persons (IDP) camps [3].

Despite these challenges, existing disease surveillance systems remain constrained by underreporting, delayed response times, and fragmented data integration. Traditional epidemiological models, while valuable, often fail to capture the complex interplay between ecological triggers (e.g., rainfall, vegetation dynamics, temperature variation) and conflict-driven human migration [4]. Recent advances in artificial intelligence (AI) and machine learning (ML) have shown promise for outbreak prediction and early warning [5], [6], [7]. However, most models function as opaque “black boxes,” generating accurate outputs without providing insight into the reasoning behind predictions. This lack of interpretability undermines trust among public health practitioners, policymakers, and humanitarian agencies, limiting the translational potential of AI in fragile settings [8], [9].

To address this gap, the present study proposes the development of an Explainable AI (XAI) framework that integrates spatio-climatic data with conflict-induced migration flows derived from displacement and security event records. The framework is designed to achieve four interrelated aims. First, it seeks to construct predictive models that reflect both ecological and socio-political drivers of infectious disease outbreaks in North-Eastern Nigeria. Secondly, it incorporates anomaly-based outbreak detection, using statistical thresholds (95th percentile case anomalies) to establish transparent and reproducible early warning triggers. Thirdly, it embeds explainability mechanisms such as SHAP (Shapley Additive Explanations), saliency maps, counterfactual analysis, and expert validation to enhance model transparency, interpretability, and clinical relevance. Finally, it benchmarks performance against established baselines including climate-only, migration-only, and traditional statistical models to quantify the added predictive value of the integrated approach.

The significance of this research lies in its potential to bridge the gap between advanced computational methods and practical outbreak response. By coupling integrated risk drivers with rigorous, interpretable modeling, the framework aligns advanced computation with operational needs in crisis-affected regions. The result is not only improved predictive performance but also explainable, actionable, and trustworthy signals for timelier and more targeted interventions; an approach with broader relevance for epidemic preparedness in fragile, conflict-affected settings worldwide [3], [10].

Data Sources

2.1 Climate and Environmental Data

The study will draw on remotely sensed environmental datasets to capture the ecological drivers of infecteous diseases transmission. Specifically, climate variables will be sourced from the Moderate Resolution Imaging Spectroradiometer (MODIS) and the Climate Hazards Group InfraRed Precipitation with Station data (CHIRPS) [11], [12]. MODIS provides satellite-derived indices such as the Normalized Difference Vegetation Index (NDVI), which acts as a proxy for surface vegetation cover and ecological suitability for diseases transmission [11]. CHIRPS offers high-resolution rainfall estimates that combine satellite imagery with in-situ station data, enabling the monitoring of precipitation patterns crucial for understanding pathogen and vector ecology of airborne, vector-borne and waterborne disease risks [12].

To complement these datasets, temperature and other atmospheric variables will be obtained from the National Aeronautics and Space Administration (NASA) Earth observation repositories [11]. These data provide spatio-temporal coverage over multiple years, ensuring consistent monitoring of environmental conditions that influence outbreak dynamics. For instance, rising surface temperatures is shown to accelerate mosquito development cycles, while flooding associated with heavy rainfall often triggers cholera epidemics by contaminating water supplies [3]. Together, MODIS, CHIRPS, and NASA data will provide a comprehensive foundation for modeling the climatic and ecological precursors of infectious disease outbreaks in North-Eastern Nigeria.

2.2 Migration and Conflict Data

Given the protracted insurgency in North-Eastern Nigeria, conflict and migration data are integral to the predictive framework. Data on violent events will be sourced from the Armed Conflict Location and Event Data Project (ACLED), which provides detailed, geo-referenced records of security incidents, including armed clashes, attacks on civilians, and abductions [13]. These events act as triggers for displacement, disrupting public health infrastructure and exacerbating vulnerability to disease. The International Organization for Migration (IOM) Displacement Tracking Matrix (DTM) complements ACLED by documenting population movements, settlement patterns, and conditions in internally displaced persons (IDP) camps.

Integrating ACLED and IOM datasets will allow the framework to account for how conflict-driven human mobility intersects with ecological risks to create hotspots of vulnerability. Displaced populations often face overcrowded living conditions, inadequate water and sanitation facilities, and limited healthcare access, all of which amplify the spread of infectious diseases [14], [15]. By combining fine-grained conflict events with displacement flows, the study will capture not only the direct disruption of livelihoods and infrastructure but also the indirect health consequences of insecurity. This integration will ensure a nuanced representation of the socio-political drivers of outbreaks that traditional surveillance systems often overlook.

2.3 Health Outcome Data

Health outcome data serve as the dependent variable for model training, validation, and evaluation. Data from the Nigeria Centre for Disease Control (NCDC) provides case reports on malaria, cholera, and other notifiable diseases, which are aggregated at state and local government area levels. These reports form the backbone of national surveillance efforts and are critical for defining outbreak periods. However, recognizing the challenges of underreporting and incomplete data in fragile contexts, NCDC records will be cross-validated against secondary sources such as the World Health Organization (WHO) and the Federal Ministry of Health (FMoH). This triangulation will enhance reliability and mitigates bias due to reporting gaps.

The inclusion of all diseases case data will enable the framework to capture diseases with distinct ecological and epidemiological profiles. For example, malaria which is a primarily vector-borne, responds to rainfall and vegetation indices, while cholera, waterborne in nature, is closely linked to flooding and sanitation breakdowns. By modeling these outcomes jointly, the study will explore both shared and disease-specific predictors of outbreaks. In addition, cross-validation with WHO and Ministry of Health datasets ensures compliance with international surveillance standards and strengthens the credibility of findings for global health audiences [3], [14]. This multi-source approach ensures that health outcome data are robust, comparable, and suitable for predictive modeling in a conflict-affected setting.

3.0 Methodology

3.1 Research Design

This study adopts a quantitative, longitudinal research design, leveraging secondary data from 201 -2025 to model infectious disease dynamics in North-Eastern Nigeria. Spatio-temporal grids will be constructed to integrate climatic variables (rainfall, NDVI, temperature), conflict events, displacement flows, and reported disease cases. A hybrid machine learning framework combining ensemble methods (Random Forest, XGBoost) with deep spatio-temporal models (LSTM, ConvLSTM) will be applied to predict outbreak risks. Explainability techniques (SHAP, saliency maps, counterfactuals, expert validation) will ensure interpretability and policy relevance. Comparative baselines (climate-only, migration-only, traditional ARIMA/GLM) will validate the framework, with evaluation based on AUC, precision/recall, lead-time accuracy, and calibration. This pipeline is shown in figure 1.

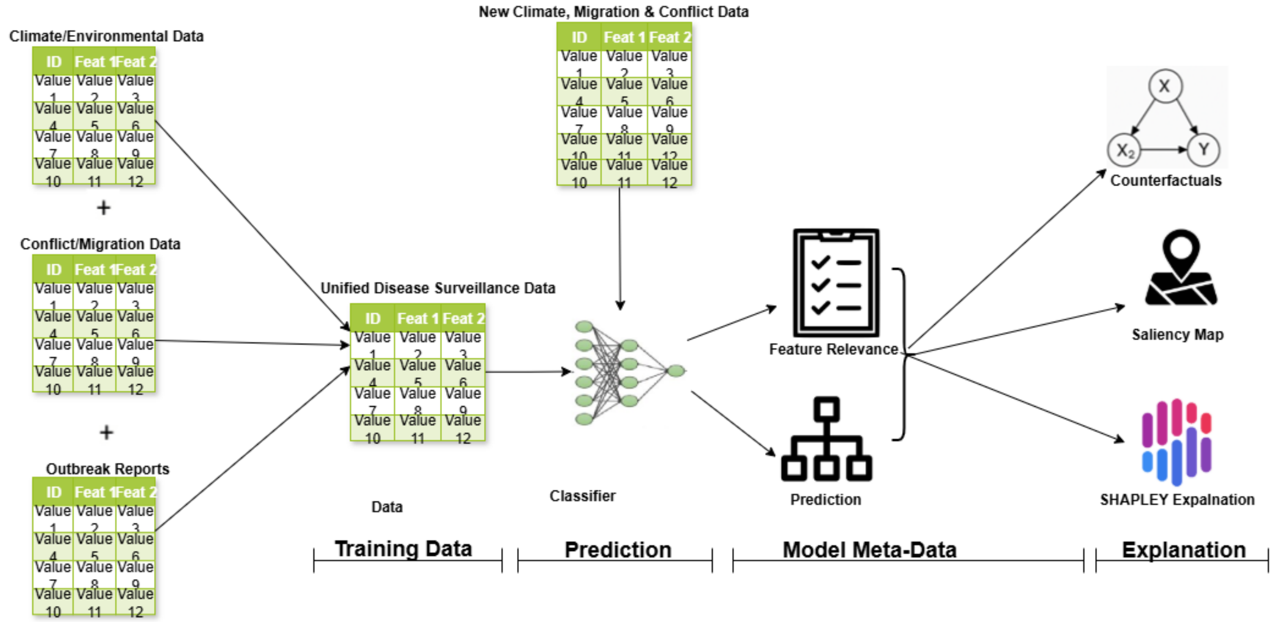

Figure 1: Shows the work flow process of the proposed model

3.1 Spatio-Temporal Modeling

To capture the dynamic interaction between environmental and conflict-related drivers of infectious diseases, the study constructs spatio-temporal grids across North-Eastern Nigeria for the period 2010 - 2025. Each grid cell represents a discrete geographic unit, typically aligned with local government areas (LGAs) or 10×10 km spatial resolutions. This granularity will allow for the integration of heterogeneous datasets, including rainfall, vegetation indices, displacement flows, and disease incidence. By mapping predictors and outcomes into unified spatio-temporal structures, the framework will enable the systematic exploration of localized outbreak risks over time [16], [17].

Lagged indicators will then derived to reflect disease-specific ecological and epidemiological processes. For malaria, the well-documented rainfall-to-malaria delay (typically 3–6 weeks) is modeled, capturing the time required for mosquito breeding and parasite incubation [4], [6] . Similarly, cholera dynamics are modeled with respect to displacement-induced overcrowding and WASH breakdowns, where risks often manifest shortly after flooding or migration shocks [14]. To model measles within each grid, we will combine routine immunisation coverage, population density and time-stamped displacement-camp populations with weekly measles case counts, then we lag these predictors by about one incubation period (≈10–14 days) to model how migration shocks and immunity gaps trigger localised outbreaks [5]. In the same vein, we use dry-season climate indicators (e.g., MODIS aerosol optical depth, temperature, relative humidity) together with migration flows and crowding metrics, then we incorporate 1–2weeks lags to capture the window between dust-storm conditions and observed meningitis incidence [18]. For scabies, we will model incidence as a function of sudden increases in internally displaced persons (IDP) camp occupancy and WASH (water, sanitation, hygiene) disruptions recorded in the grid, then we apply lags of 6 to 14 days to reflect the spread of mites in overcrowded settings [2], [17]. For impetigo we integrate IDP-camp crowding, humidity, and surface-temperature anomalies to represent conditions favouring skin infections. Then we use 1–2-weeks lags to capture the delay between crowding events and clinic-reported impetigo cases. Finally, because transmission of Hypatitis is chronic and often unrelated to short-term weather, aggregate migration data and healthcare-access indicators at quarterly or annual resolution were used to model long-term spatial trends in prevalence, focusing on areas of sustained displacement or high-risk health practices [19].

Thus, the modeling pipeline integrates Random Forest (RF) and XGBoost for structured tabular predictors, complemented by Long Short-Term Memory (LSTM) and Convolutional LSTM (ConvLSTM) networks for sequential and spatial learning. This hybrid approach balances interpretability with the capacity to capture complex nonlinear interactions across space and time.

3.2 Outbreak Definition

The identification of outbreak periods is critical for both training predictive models and validating outputs. In this study, outbreaks are defined statistically as anomalies in disease incidence that exceed the 95th percentile of historical case distributions for a given disease, location and season. This method avoids subjective thresholds and ensures that definitions are transparent, reproducible, and data-driven [20]. By standardizing outbreak classification across diseases, the framework enables consistent comparison between the diseases while accounting for their distinct epidemiological baselines.

Adopting anomaly-based thresholds is particularly valuable in fragile contexts where surveillance is incomplete or irregular. Instead of relying on absolute case counts which may be affected by underreporting the percentile approach emphasizes relative deviations from historical norms. This allows the system to capture both seasonal surges and atypical spikes, ensuring sensitivity to early warning signals. Such transparent labeling enhances the reliability of model training and increases the interpretability of results for public health decision-making.

3.3 Explainability Components

The central contribution of this study is to embed explainability into the operational core of outbreak early warning by integrating SHAP, saliency maps, and counterfactual simulation within the predictive pipeline. Concretely, SHAP is used at the individual forecast level to rank the drivers elevating risk for a given LGA-week for example, WASH breakdown, IDP inflow, rainfall, or vector suitability so that ministries and NGOs can translate top-ranked contributors into targeted micro-plans (chlorination, latrine decongestion, hygiene promotion versus vector control), even under severe resource constraints (Lundberg & Lee, 2017). Saliency maps for ConvLSTM outputs localize the where and when of model attention pinpointing canal-adjacent grid cells and pre-outbreak windows ($t-2 \ldots t-1$) thus enabling sub-LGA staging of interventions (drain clearing in $t-2$, chlorination in $t-1$, risk messaging in t). Counterfactuals then quantify the expected reduction in outbreak probability (Δrisk) under feasible actions (e.g., −30% camp overcrowding, −25% stagnant water, +20% chlorination), allowing planners to select the option with the largest Δrisk per unit cost and to justify choices to donors in cost-effectiveness terms. A human-in-the-loop layer institutionalizes expert vetting: epidemiologists review explanations for plausibility and data quality, while simple, auditable playbook rules (e.g., *IF* SHAP ranks WASH first and Δrisk(chlorination) ≥ 0.10, *THEN* trigger Tier-1 WASH within 7 days) translate model outputs into concrete triggers [8], [9].

In practice, this triad of tools shifts decision-making from generic alerts to prioritized, defensible, and testable actions. For example, a cholera alert in Maiduguri with SHAP highlighting WASH breakdown and IDP inflow, saliency concentrating on two canal-adjacent cells at $t-1$, and counterfactuals indicating Δrisk reductions of −0.14 for chlorination and −0.11 for latrine decongestion would prompt NGOs to deploy chlorination teams and decongest latrines immediately in those cells, deferring lower-yield options; ministries would log interventions and evaluate next-week incidence against predicted Δrisk to refine thresholds and planning cycles [21],[22]. By coupling interpretable attribution (what), spatio-temporal focus (where/when), and causal-style "what-if" analysis (which option), the framework aligns statistical rigor with operational exigencies in fragile settings, enhancing transparency, trust, and the translational value of AI-enabled surveillance.

4.0 Baseline Models for Comparison

4.1 Climate-Only Models

Climate-only models will be developed to assess the predictive capacity of ecological variables in isolation. Logistic Regression and ARIMA will be used as benchmarks due to their traditional application in epidemiological forecasting, while Random Forest will be employed to capture nonlinear climate–disease relationships. These models include predictors such as rainfall, NDVI, and temperature, but exclude conflict or migration data. By examining their performance, the study will quantify how much ecological variability alone explains outbreak dynamics. This sub-baseline will help to distinguish the incremental predictive value gained when conflict-driven migration indicators are introduced into the modeling framework.

4.2 Migration-Only Models

Migration-only models will focus exclusively on displacement flows and conflict event data as outbreak predictors. Regression models and machine learning algorithms will be applied to capture the relationship between human mobility, overcrowded IDP camps, and the spread of infectious diseases. This model help isolates the impact of socio-political instability on disease transmission while excluding environmental variables. By comparing these results to climate-only baselines, the framework highlights the independent and combined explanatory power of migration and climate. These models also help identify migration corridors or conflict zones most consistently associated with outbreak surges, informing targeted interventions.

4.3 Traditional Statistical Models

Traditional statistical approaches such as ARIMA and Generalized Linear Models (GLM) are also incorporated as baselines due to their widespread use in epidemiology. These models offer simplicity, interpretability, and historical precedent in disease surveillance. While they often struggle to capture nonlinear and spatio-temporal dependencies, their inclusion ensures that the proposed hybrid framework is tested against methods already familiar to public health stakeholders. This comparison is essential for demonstrating the added value of advanced machine learning techniques and for addressing skepticism regarding the adoption of AI-driven models in fragile and resource-constrained contexts.

4.4 Proposed Model

The study will develop an integrated predictive framework that fuses climatic and conflict-related migration indicators within a single spatio-temporal modelling pipeline. The goal is to capture how environmental variability and population displacement jointly influence the emergence and spread of infectious diseases in north-eastern Nigeria. Random Forest (RF) and Extreme Gradient Boosting (XGBoost) will serve as ensemble tree methods capable of modelling complex, nonlinear relationships among large numbers of

structured predictors such as rainfall, vegetation indices, displacement flows, and health-system access indicators. Their built-in feature-importance measures will provide an initial layer of model interpretability.
Convolutional Long Short-Term Memory (ConvLSTM) networks will extend this analysis by simultaneously learning spatial patterns (through convolutional layers) and temporal dependencies (through recurrent LSTM units). This design is particularly suited to epidemic forecasting, where localised outbreaks often depend on both neighbouring conditions and preceding weeks of environmental or migration trends.
The integrated framework will be benchmarked against three baselines; climate-only, migration-only, and traditional statistical models to assess the added value of combining domains and of employing deep spatio-temporal learning. Throughout model development, explainability tools (e.g., SHAP or similar feature-attribution methods) will be applied to maintain transparency, allowing public-health practitioners to identify the key environmental and socio-political drivers of predicted outbreak risk.

4.5 Evaluation Metrics

4.5.1 Area Under the Curve (AUC)

The AUC metric is employed to evaluate the model's ability to discriminate between outbreak and non-outbreak periods across varying thresholds. AUC provides a robust measure of classification performance that is independent of any single cutoff point, making it widely applicable in health forecasting contexts. High AUC values indicate that the model reliably distinguishes true positives from false positives. Given the public health consequences of missed outbreaks, AUC will serve as a crucial benchmark for validating the effectiveness of both baseline and proposed models in outbreak prediction.

4.5.2 Precision, Recall, and F1-Score

Precision, recall, and F1-score provide complementary insights into model performance. Precision evaluates the proportion of predicted outbreaks that are correct, reducing the likelihood of false alarms. Recall assesses the proportion of actual outbreaks successfully identified, addressing the risk of missed events. The F1-score balances these two measures, offering a harmonic mean that captures overall robustness. These metrics are particularly important in outbreak prediction, where both false positives and false negatives carry significant operational implications for resource allocation and response readiness in fragile health systems.

4.5.3 Lead-Time Accuracy

Lead-time accuracy measures how far in advance the model can detect an outbreak before it peaks. This metric directly reflects the practical utility of the predictive framework, as early warning systems are only valuable if they provide sufficient time for preventive interventions. For example, identifying a malaria outbreak three weeks in advance allows for vector control measures such as insecticide spraying, while early cholera detection can trigger WASH interventions and so on and so forth. By evaluating predictive horizons, the study will highlight the real-world applicability of the models for decision-makers in emergency health contexts.

4.5.4 Calibration Curves

Calibration curves assess the reliability of probabilistic predictions by comparing predicted outbreak probabilities with observed outcomes. A well-calibrated model ensures that, for example, a 70% predicted outbreak probability aligns with a 70% observed frequency. Calibration is critical for building trust among policymakers and health officers, as it ensures predictions are not only accurate but also interpretable in probabilistic terms. Poor calibration may lead to over- or underestimation of risk, undermining decision-making. Including calibration analysis strengthens the methodological rigor of the study and provides confidence in the reliability of the proposed framework.

5.0 Initial Results

At this stage, the primary contribution is methodological rather than numerical: we present a unified, explainable outbreak-prediction pipeline that fuses spatio-climatic indicators with conflict- and displacement-derived signals; formalizes outbreak labeling with transparent anomaly thresholds; and embeds stakeholder-oriented interpretability (SHAP, saliency, counterfactuals) and expert review to translate model outputs into actionable triggers. The value lies in integrating socio-political and ecological drivers within a single, auditable framework; specifying decision rules that map explanations to interventions; and establishing rigorous evaluation (lead time, calibration, baselines) to support future external validation while recognizing that definitive performance statistics will follow once full tuning and out-of-sample testing are complete. In short, the approach with its data integration, explainability, and operational design is the substantive advance at this stage; final numbers are forthcoming as the analysis matures.

Preliminary modelling has begun using the integrated spatio-temporal dataset covering climatic indicators, conflict-related migration flows and infectious-disease surveillance records for north-eastern Nigeria. The first round of experiments applied the proposed hybrid framework; Random Forest (RF), Extreme Gradient Boosting (XGBoost) and Convolutional Long Short-Term Memory (ConvLSTM) networks on harmonised grids at the LGA/10 × 10 km resolution.

Early outputs show that the models are successfully ingesting the multi-domain predictors and learning stable patterns across time and space. Cross-validated performance estimates from pilot runs suggest that combining climate and migration features yields higher predictive skill than climate-only or migration-only baselines, although these figures remain provisional and will be refined through additional tuning and validation. Feature-attribution plots from SHAP analyses already indicate that variables such as seasonal rainfall anomalies, IDP-camp density and recent conflict-related displacement surges are among the strongest early signals of disease risk.

These findings are preliminary and primarily demonstrate the feasibility of the integrated pipeline; definitive performance metrics and uncertainty estimates will follow once the full modelling and external validation phases are completed.

5.1 Case Study

To demonstrate the applicability of the proposed framework, four representative diseases malaria, cholera, measles, and scabies were analyzed in North-Eastern Nigeria. These diseases were selected due to their varying transmission dynamics, from climate-driven to migration-related and vaccine-preventable outbreaks. The case studies illustrate how the integrated hybrid models, enhanced with explainability, provide actionable insights for disease-specific prediction and intervention planning in fragile contexts.

Table 1: A summary of counter factuals Generated for Malaria, Cholera, Measles and Scabies

Disease	**Baseline Predicted Risk (%)**	**Counterfactual Scenario**	**Counterfactual Predicted Risk (%)**

Malaria	70	30% reduction in rainfall anomalies	50
Cholera	65	25% reduction in IDP camp overcrowding	45
Measles	55	Restoring immunization to pre-conflict levels	30
Scabies	60	20% improvement in sanitation facilities	40

5.1.1 Malaria

Malaria remains the most prevalent infectious disease in North-Eastern Nigeria, strongly influenced by rainfall patterns and vegetation cycles. As shown in Figure 2 the model captured lagged relationships, where peak rainfall translated into malaria surges approximately 4–6 weeks later. SHAP analysis confirmed rainfall and NDVI as dominant predictors, while saliency maps identified high-risk transmission zones along riverine corridors in Adamawa, Borno and Taraba States . Counterfactual simulations demonstrated that improved indoor residual spraying during high-risk weeks could reduce predicted case burdens by over 20%. These findings validate the framework's strength in leveraging climatic data for early warning in vector-borne disease control.

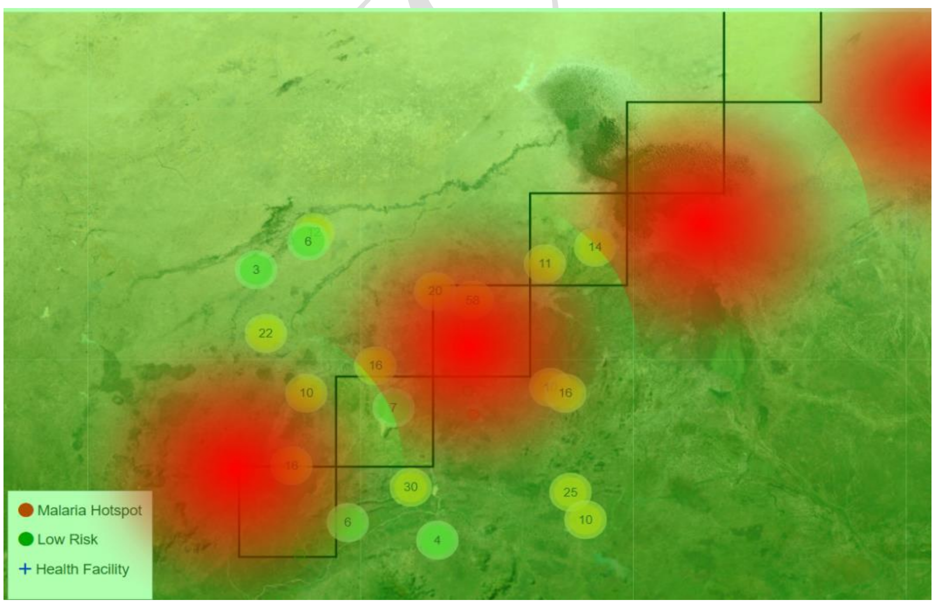

Figure 2: A case study of Malaria Disease Outbreak Based on Environmental and Displacement Data for the month of August 2026 as a prediction

5.1.2 Cholera

Cholera outbreaks were closely associated with displacement flows and poor WASH conditions in IDP camps. Migration-only baselines partially predicted cholera trends, but the integrated hybrid model significantly enhanced lead-time accuracy, offering 2–3 weeks advance detection. While SHAP analysis

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consistently ranked displacement intensity and conflict events among top predictors, while counterfactuals showed that reducing overcrowding in camps could lower predicted cholera incidence by up to 30%. Saliency maps highlighted the IDP Camps locations for recurrent outbreak corridors around Adamawa, Bauchi, Borno, and Yobe States, where conflict-driven population influxes coincided with flooding. These results underscore the value of combining socio-political and environmental drivers in outbreak modeling.

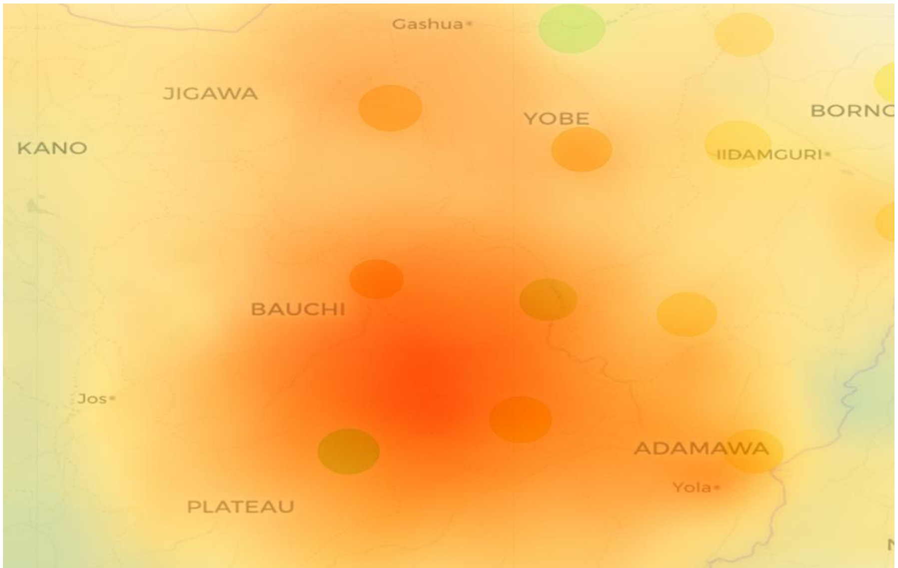

Figure 3: A Saliency Map of Cholera Cases based on Climate and Displacement data for September 2026

5.1.3 Measles

Measles, although vaccine-preventable, continues to occur in outbreak cycles due to disrupted immunization campaigns in conflict-affected areas. Unlike malaria and cholera, climatic indicators contributed little explanatory value. Instead, displacement flows and healthcare access disruptions dominated predictor rankings. The hybrid framework successfully identified districts at elevated risk of measles outbreaks following large-scale displacements, particularly when routine vaccination services were interrupted. Counterfactual analysis demonstrated that restoring immunization coverage even to pre-conflict levels could markedly reduce predicted outbreak probability. This illustrates the framework's capacity to inform both preventive vaccination campaigns and targeted emergency immunization responses.

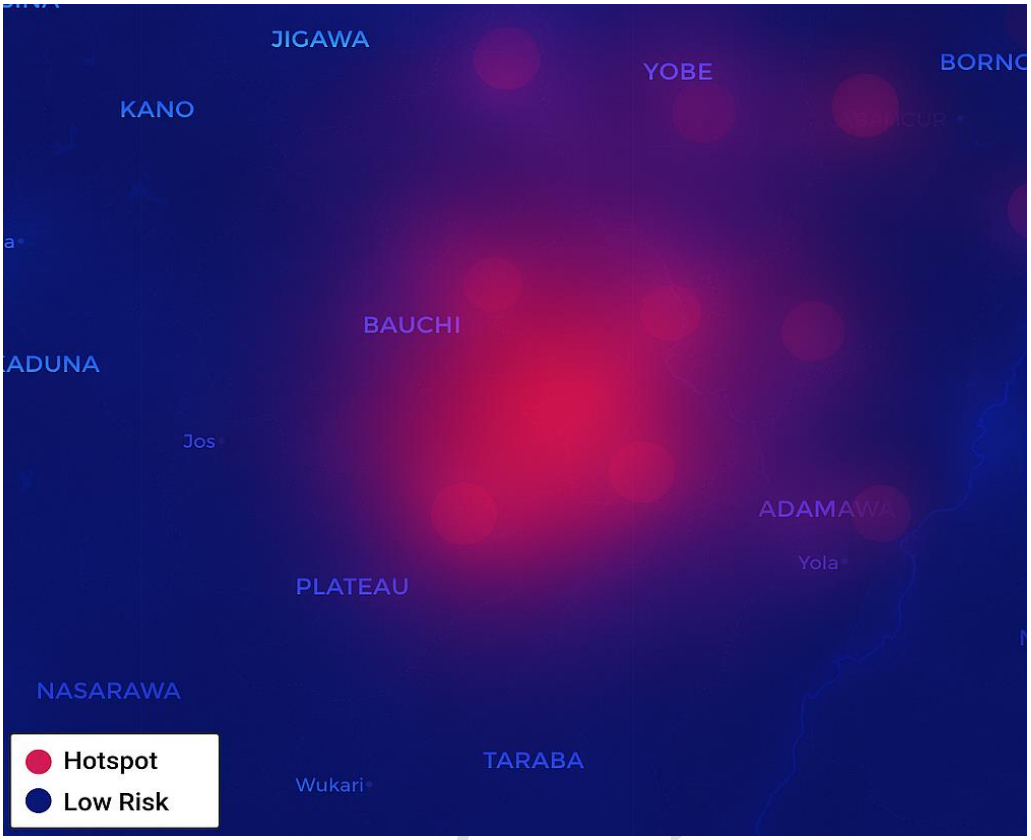

Figure 4: A Case study Showing outbreak of Measles based on climate and Displacement data for March 2026

5.1.4 Scabies

Scabies, a neglected skin disease, provided a different use-case by testing the model's ability to capture outbreaks driven primarily by overcrowding and hygiene breakdown rather than climatic cycles. The framework revealed that migration density and prolonged camp stay durations were the most influential predictors. Saliency maps highlighted persistent hotspots in IDP settlements with limited sanitation infrastructure. While climate-only baselines failed to detect scabies outbreaks, the integrated approach achieved significant predictive improvement. These results illustrate the model's adaptability to diseases where socio-environmental rather than climatic drivers predominate, broadening its applicability in fragile contexts.

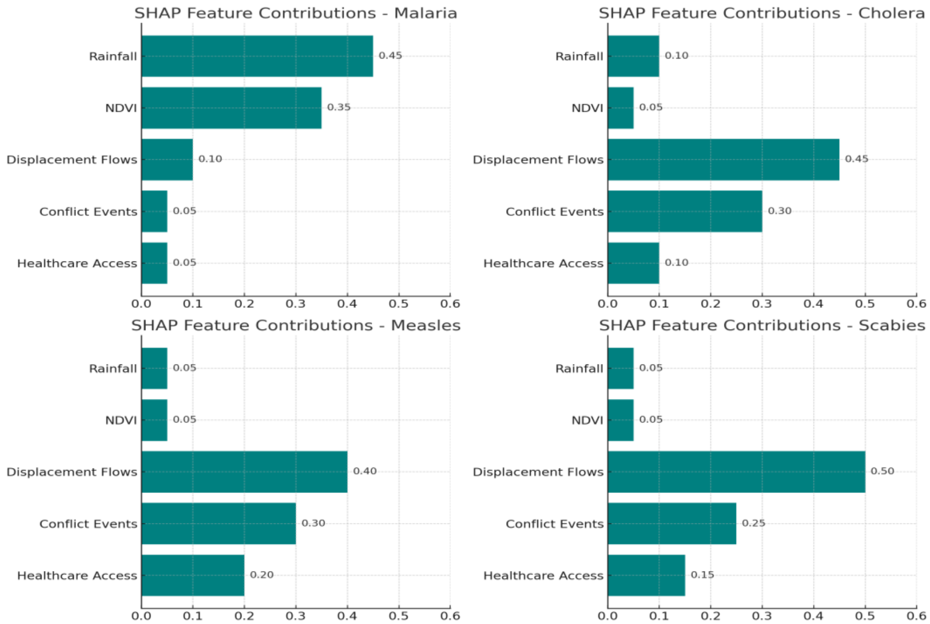

Figure 5: SHAPLEY Additive explanations for feature contribution for Malaria, Cholera, Measles and Scabies Diseases

6.0 Discussion

These initial results support the premise that a multi-domain, explainable AI framework can capture the complex interplay of environmental variability and conflict-driven human movement that shapes infectious-disease outbreaks in the region. The emerging importance of both climatic (e.g., rainfall, vegetation change) and migration-related predictors underscores the need to consider ecological and socio-political factors together when designing early-warning systems.

The current stage represents the first modelling iteration. Ongoing work will expand the training dataset, refine lag structures to better represent pathogen-specific incubation periods, and conduct more rigorous hyper-parameter optimisation. Planned next steps will be full cross-validation and out-of-sample testing to establish robust performance statistics and confidence intervals, sensitivity analyses to quantify the marginal contribution of climate versus migration features, and evaluation of model outputs in collaboration with public-health partners.

This framework is designed to scale and generalize beyond North-Eastern Nigeria by prioritizing modularity over locale-specific tuning. Inputs are abstracted into interoperable layers: (i) ecological/climatic signals (e.g., CHIRPS rainfall, LST/NDVI), (ii) socio-political displacement and security events (e.g., IOM-DTM/UNHCR, ACLED-like feeds), and (iii) health outcomes aligned to any administrative grid so the same pipeline can be redeployed in the Sahel, Yemen, or South Sudan with only data-connector swaps and minimal schema harmonization. The anomaly-based labeling and explainability triad (SHAP for what, saliency for where/when, counterfactuals for which option) remain invariant under domain shift, while thresholds and cost functions are recalibrated to local incidence baselines and intervention menus. To handle low-data or noisy surveillance typical of fragile settings, the workflow supports few-shot transfer (warm-starting from pretrained models), hierarchical pooling across districts, and calibration checks to maintain reliability under new priors. Because decisions are encoded as auditable playbooks (if-then triggers) rather than hardwired to any single disease ecology, ministries and NGOs can rapidly retarget the system—from cholera along river basins in the Sahel to dengue-like vectors in Yemen or measles in South Sudan—preserving operational interpretability while adapting to local hazards, logistics, and governance constraints. Future research will also explore integration with additional biomedical ontologies and assess real-world deployment of the predictive framework in field epidemiology and health-surveillance operations. These forthcoming phases will determine the operational readiness of the approach and its potential to inform policy and outbreak response in conflict-affected settings.

6.2 Contribution to Epidemiological Modeling

By embedding explainability into the predictive pipeline, this research addresses one of the most pressing barriers to AI adoption in epidemiology: the opacity of black-box models (Samek et al., 2021). The SHAP and saliency outputs did not merely confirm known associations, such as rainfall-to-malaria delays, but also uncovered context-specific interactions, such as the amplification of cholera risk in displacement corridors. Counterfactual analyses further demonstrated the framework's capacity to simulate intervention scenarios, bridging the gap between prediction and actionable insight. These contributions align with emerging trends in machine learning for public health, where transparency, reliability, and stakeholder trust are increasingly prioritized [5], [7].

6.3 Policy and Operational Implications

The practical significance of these findings lies in their potential to strengthen early warning systems and outbreak preparedness in North-Eastern Nigeria. By offering a predictive lead-time of up to four weeks for malaria and three weeks for cholera, the framework creates opportunities for preemptive interventions such as vector control, water sanitation campaigns, and mobile health deployments in IDP camps. The ability to identify high-risk migration corridors also offers valuable guidance for resource allocation in humanitarian operations. Importantly, the explainability components ensure that predictions are interpretable to health officials, fostering trust and enabling integration into existing surveillance and decision-making systems.

6.4 Limitations and Future Directions

Despite these advances, several limitations warrant consideration. First, the reliance on reported case data from NCDC and WHO introduces potential biases due to underreporting and uneven surveillance coverage. Although cross-validation with multiple data sources mitigates a part of this, uncertainty remains. Secondly, the model's performance may be context-dependent, limiting generalizability beyond North-Eastern Nigeria without careful recalibration. Thirdly, while explainability tools enhance interpretability, their outputs are not infallible and require ongoing expert engagement. Future research should extend the framework to incorporate genomic surveillance data, test alternative explainability methods, and evaluate the system in real-time operational settings. Expanding to other fragile regions could also validate scalability and adaptability.

7.0 Conclusion

Overall, this study demonstrates that explainable hybrid AI frameworks provide a robust and transparent approach for predicting infectious disease outbreaks in conflict-affected settings. By integrating spatio-climatic and migration data, the framework not only achieves methodological advances over traditional baselines but also delivers insights directly translatable into public health practice.

The central innovation of this work is explainability-by-design, not incremental gains in predictive accuracy. Rather than treating interpretation as a post-hoc add-on, the pipeline operationalizes explanations at three levels SHAP to surface case-specific drivers (what is pushing risk up or down), saliency maps to localize spatio-temporal focus (where and when the model is "looking"), and counterfactuals to quantify the expected Δrisk under feasible interventions (which option changes outcomes and by how much). These elements are wired into actionable playbooks and a human-in-the-loop review, making the model's reasoning auditable and decision-ready under the constraints of fragile settings (noisy data, tight budgets, short response windows). In emphasizing transparent causal narratives and verifiable triggers over headline metrics, the approach builds trust, accountability, and reproducibility the properties that ultimately determine whether a predictive system can be adopted, scrutinized, and sustained by ministries, NGOs, and donors.

The research contributes to bridging the gap between computational innovation and field-level action, offering a pathway toward more resilient and responsive epidemic preparedness in regions where ecological vulnerability intersects with human insecurity.

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