Climate Change & Mosquito Spread Diseases: Modeling Malaria and Dengue

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Vector-borne diseases such as malaria and dengue are strongly influenced by climatic factors, making their future dynamics sensitive to climate change. This study develops predictive models to estimate monthly malaria and dengue cases using a climate-driven simulation framework. The dataset incorporates simulated climate variables, including temperature, precipitation, air quality index, UV index, temporal factors, and geographic information such as country and region.

A Random Forest model was implemented as a flexible, non-parametric baseline capable of capturing complex nonlinear relationships and interactions. To better accommodate the count nature of disease incidence, Poisson regression and Generalized Additive Models (GAMs) with a Negative Binomial link were employed to address potential over dispersion and nonlinear climate effects.

Model evaluation indicates that Poisson regression consistently achieved the strongest predictive performance across both malaria and dengue outcomes, while Random Forest produced competitive results, all while GAMs provided additional flexibility. Overall, predictive accuracy remained moderate, suggesting that additional unmeasured factors likely contribute to disease variability.

Climate change simulation experiments were conducted across multiple warming scenarios. The simulations indicate modest increases in predicted disease incidence under elevated temperature and climate variability, with malaria and dengue cases increasing or decreasing by approximately 4% to 7% depending on the scenario and modeling approach. These findings highlight both the potential health impacts of climate change on vector-borne disease transmission and the challenges involved in modeling complex disease-environment relationships.

I. INTRODUCTION

Vector-borne diseases (VBDs), including malaria and dengue, are significant public health concerns worldwide. The transmission dynamics of these diseases are highly sensitive to climatic and environmental factors that can influence both mosquito population dynamics and incubation cycles. Rising global temperatures, shifting precipitation patterns, air pollution, and ultraviolet radiation levels all play critical roles in determining where and when these diseases may emerge or expand.

Climate change is expected to alter these environmental drivers, potentially expanding the geographic range of disease-carrying vectors into regions that have historically been unaffected or minimally affected. As a result, health systems in newly vulnerable areas may face unexpected outbreaks without adequate budget, disease surveillance systems, or vector control measures in place. While much of the current focus in public health remains on containing disease in traditionally high-burden regions, anticipating how future extreme climate conditions may shift disease burden into previously unprepared regions is increasingly important.

Accurately forecasting the combined impact of climate change and healthcare capacity on malaria and dengue incidence is critical for informing policy decisions, resource allocation, and early intervention strategies.

The primary research question guiding this study is:

How might projected changes in climate, environmental conditions, and healthcare system capacity influence the future incidence of malaria and dengue across diverse regions?

To address this question, several specific objectives were pursued:

1. Develop climate change simulation scenarios by systematically modifying key environmental variables, including temperature, precipitation, UV index, air quality index, and healthcare budget.

2. Build predictive models capable of estimating malaria and dengue incidence under both current and simulated climate conditions using a combination of statistical and machine learning approaches.

3. Quantify the potential changes in disease burden across scenarios, and assess the relative impact of both environmental shifts and healthcare system interventions on disease outcomes.

II. LITERATURE REVIEW

Malaria is caused by the *Plasmodium* parasite and is transmitted through bites from the *Anopheles* mosquito. This disease is most prevalent in Sub-Saharan Africa and tends to thrive in warm, humid envrionemnts that support mosquito life cycle and parasite development. In contrast, dengue is caused by the flavivirus that is transmitted by the *Aedes Aegypti* mosquito, which are commonly found in urban settings where stagnant water, such as puddles post rainfall, provides abundant breeding sites. Dengue transmission typically increase under conditions of high temperatures and elevated rainfall, both of which promote mosquito reproduction and enhance viral transmission efficiency.

According to the Centers for Disease Control and prevention, the CDC, malaria infections typically present with flu-like symptoms that include fever, chills, sweats, nausea, vomiting, and body aches. In severe cases, malaria could result in neurological symptoms, anemia, multi-organ failure, and death in rare cases. The severity of malaria certainly depends on a multitude of factors, specifically access to treatment (Centers for Disease Control and Prevention, 2023b).

Alternatively, the CDC report that dengue infection may also present with fever, nausea, rash, joint pain, but more specifically pain behind the eyes. Once again, the dengue infection heavily relies on access to treatment, and dengue can turn severe, with patients developing plasma leakage, hemorrhagic manifestations, organ impairment, and fatal shock. Early detection is key for dengue, and appropriate supportive care is critical for managing it (Centers for Disease Control and Prevention, 2023a).

The scientific community has increasingly recognized the importance of environmental factors, especially those linked to climate change, in shaping the dynamics of these diseases.

Evidence suggests that climatic conditions play a large, central roll in determining the geographical distribution and seasonal effects of malaria and dengue transmission. Temperature affects both mosquito life cycles as well as the incubation period of pathogens, while precipitation patterns can influence the availability of mosquito breeding sites.

(Morin *et al.*, 2013) conducted a review of the relationships between climate variables and dengue virus transmission. Their study highlights how climate can influence dengue transmission directly and indirectly by affecting mosquito vector development, virus replication, mosquito survival, and mosquito-human interaction. Specifically, temperature was identified as a particularly important factor which could accelerate virus replication and shortening the incubation period, while also affecting mosquito development and mortality. The author emphasizes that these relationships are nonlinear and context specific as extreme temperatures could potentially limit vector survival.

This study took massive inspiration from (Carlson *et al.*, 2022) and their study on how climate change may drastically increase the risk of viral cross-species transmission. In the article, the authors simulate projected shifts in the geographic ranges of 3,139 mammalian species by 2070 under multiple climate and land-use scenarios. Their model estimated that climate induced changes could potentially yield more than 15,000 new viral transmission events, specifically in high - elevation biodiversity hotspots in tropical areas; these areas are currently known to have high cases of dengue.

According to (Ryan *et al.*, 2019), under worst case global warming scenarios, nearly one billion additional people may face new suitable conditions for *Aedes Aegypti* mediated transmissions by 2080. This large expansion shows a major potential increase in dengue exposed populations globally, which highlights the importance of incorporating climate projections into long term forecasting. On a brighter note, the study also indicates that some areas may potentially become too warm to sustain transmission via *Aedes Aegypti*.

III. EXPLORATORY DATA ANALYSIS

Prior to modeling, exploratory data analysis was conducted to examine distributional trends and relationships among variables. Visual summaries such as density plots, histograms, and boxplots were used to assess variation in disease counts. Correlation analysis revealed moderate associations between predictors, with no major concerns regarding multicollinearity. These preliminary observations guided the next steps for the selection of modeling techniques used in the analysis.

A. Descriptive Summary

The dataset was obtained from Kaggle, it is important to note, this is simulation dataset. This dataset is comprised of 34,560 observations recorded between 2000 and 2020, spanning multiple countries and five major geographic regions. To improve accuracy and reduce noise from ecologically implausible regions, we excluded cases corresponding to Antarctica and Greenland, yielding a sample of 33,866 observations. This cleaned dataset shows climate conditions, disease incidence, and socioeconomic information for the diverse ecological settings. Malaria and dengue exhibited comparable monthly averages, 70.52 and 75.94 cases, respectively. Monthly precipitation exhibited a highly skewed distribution (median = 195.30 mm; maximum = 485.70 mm), suggesting intermittent periods of heavy rainfall.

B. Distribution Properties

A side-by-side boxplot (Figure 1) illustrates the differences in central tendency and dispersion between malaria and dengue case counts. Both diseases exhibit overlapping interquartile ranges, though dengue has a slightly higher median and marginally wider distribution.

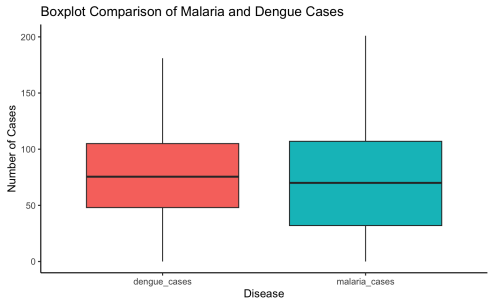

FIG. 1. Boxplot comparison of malaria vs. dengue incidence (2000–2020).

C. Seasonality

Monthly trends for malaria and dengue were examined to asses seasonality. As shown in Figure 2, both show consistent variation across the yearly trends. Dengue shows peaks in the early months of February to May, where there is a no-

TABLE I. Summary statistics for disease incidence, climate variables, and socioeconomic indicators across all regions from 2000 to 2020 (after removing observations from Antarctica and Greenland; $n = 33{,}866$).

Statistic	Malaria	Dengue	Precip (mm)	Temp (°C)	AQI	UV	Pop. Dens.	Health $
Min.	0.00	0.00	0.00	−2.56	0.00	0.87	50.00	205.00
1st Qu.	32.00	48.00	125.13	14.32	15.65	8.90	134.00	1395.00
Median	70.00	75.50	195.38	20.31	41.17	10.74	276.00	2817.00
Mean	70.62	75.94	192.81	20.36	44.13	10.20	264.97	2745.74
3rd Qu.	107.00	105.00	259.89	26.31	68.82	12.00	383.00	3989.00
Max.	201.00	181.00	485.70	44.58	168.85	12.00	498.00	4969.00

table dip at the end of summer around August to September. Malaria does show a slightly more lagged pattern, with peak levels between March and June, where there is a decline in September. These trends do appear consistent with the temperature and precipitation dependencies of a mosquito life cycle.

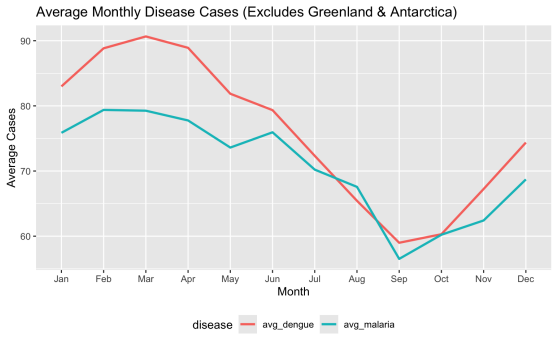

FIG. 2. Average monthly malaria and dengue incidence (2000–2020).

D. Geographic Variation

Figure 3 shows the total number of cases by region over the set study period. The Western and Central regions show the highest amount of disease burden for both malaria and dengue, whereas the Eastern and Southern Regions show fewer amounts of cases. This highlights the importance of including fixed regional effects or smoothing terms in downstream modeling to so that we may account for unmeasured geographic confounders.

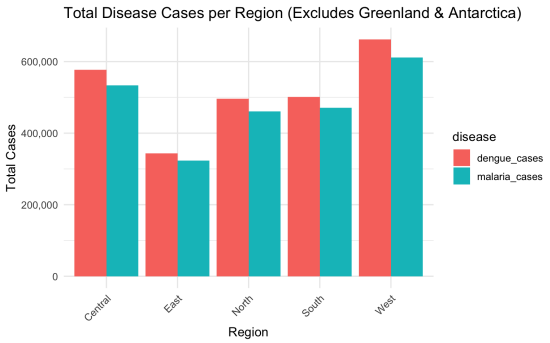

FIG. 3. Total malaria and dengue case counts by region.

E. Climate Disease Relationship

To better understand potential nonlinear associations between the conditions and diseases, we visualized average case counts across precipitation and temperature.

As shown in Figure 4, both malaria and dengue show an increase with higher records of precipitation, particularly when recorded between $100 - 300$mm per month. Figure 5 shows similar trends with respect to temperature. Disease counts seem to rise steadily with temperature until $\sim 34°C$, after which there is a plateau or decline. As mentioned previously, this suggests an ecological thresholds for mosquito viability and viral transmission. This this as well motivates the use of smoothing terms in the modeling frameworks.

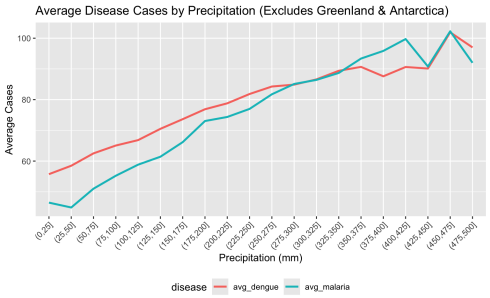

FIG. 4. Average malaria and dengue incidence by precipitation bin.

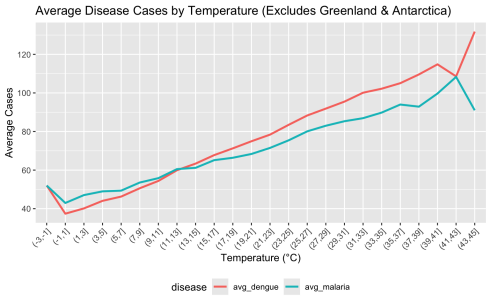

FIG. 5. Average malaria and dengue incidence by temperature bin.

F. Correlation Structure

A correlation heatmap was examined among the continuous predictors and response variables. Figure 6 shows a heatmap of Pearson correlation coefficients. Dengue cases shows to be moderately correlated with temperature (r = 0.45), whereas malaria has a weaker positive correlation (r = 0.26). Precipitation displays a weak but positive correlation with both diseases.

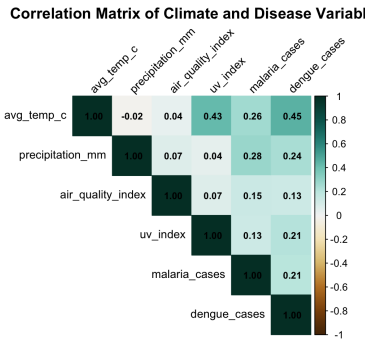

FIG. 6. Correlation matrix of climate and disease variables.

IV. METHODOLOGY

The analysis utilized a simulated dataset containing monthly malaria and dengue case counts alongside multiple climate and environmental variables. Predictors included lagged temperature, lagged precipitation, UV index, air quality index, temporal variables (month and year), and geographic indicators (region and country). Disease incidence counts were modeled as the response variable. To minimize noise from regions unlikely to experience endemic transmission, the dataset was filtered to exclude countries with low historical malaria and dengue risk, such as Antarctica and Greenland.

Categorical predictors, including `region`, `country`, `month`, and `year`, were made as factor variables. Lagged climate variables were computed to account for the delayed biological effects of climate on mosquito populations and pathogen development. The final modeling dataset excluded the dengue response variable when modeling malaria outcomes, and vice versa.

The dataset was partitioned into training and testing sets. A 60/40 split was employed, with 60% of the data allocated for model training and 40% reserved for evaluation.

A. Random Forest

Random Forest models were implemented as a flexible, non-parametric approach to capture nonlinear relationships between predictors and disease incidence. The Random Forest algorithm constructs an ensemble of decision trees, each trained on the data and using a random subset of predictors at each split. Predictions from individual trees are aggregated to form the final model output.

In this study, Random Forest regression models were trained using the `tidymodels` framework in `R`. All categorical predictors were converted into dummy variables via one-hot en-

coding using the `recipes` package. The Random Forest models were implemented via the `ranger` engine, specifying 500 trees and tuning the number of variables sampled at each split (`mtry`). No prior distributional assumptions were required for this model.

B. Poisson Model

Poisson regression models were employed to take advantage of the count nature of the response variable. This approach assumes that the variance of the response equals its mean, making it appropriate for count data that exhibit relatively stable dispersion patterns.

Similar to the Random Forest pipeline, categorical predictors were first converted to dummy variables. Poisson regression models were implemented using the `glm()` function in `R`, specifying the Poisson family with a log link function. No normalization or transformation of the predictor variables was applied prior to model fitting.

C. GAM - Negative Binomial

The GAM–Negative Binomial model was implemented using the `mgcv::gam()` function in R, specifying `family = nb()` to account for overdispersion in count data. Smooth terms were included for key continuous climate predictors, namely lagged temperature (`s(avg_temp_c_lag1)`), lagged precipitation (`s(precipitation_mm_lag1)`), UV index (`s(uv_index)`), and air quality index (`s(air_quality_index)`). These smoothing functions enable the model to capture anything nonlinear, and potentially threshold-based relationships without requiring prespecifications.

In addition to the smoothing terms, linear covariates for population density and healthcare budget have been included, while categorical variables for region, country, and year were modeled as fixed effects to account for structured variation. Smoothing parameters were selected via restricted maximum likelihood (REML), and predictor scaling was handled internally by the `mgcv` framework.

Model performance was evaluated using pseudo-R^2, following methods suggested by Nakagawa and Schielzeth (2013), to account for the proportion of variance explained while accommodating non-Gaussian error structures and penalized smoothing.

D. Evaluation Metrics

Model performance was assessed using Root Mean Squared Error (RMSE) and coefficient of determination (R^2) on the held-out test dataset. These metrics were used to compare predictive accuracy across models while avoiding overfitting on the training data.

V. RESULTS

A. Random Forest Results

Random Forest models were fit separately on both the malaria and dengue cases; climate and environmental predictors were used for the regression. Model performance was assessed on the test data using Root Mean Squared Error (RMSE) and the coefficient of determination (R^2). The full results can be seen in Appendix A, Table II.

For malaria, the Random Forest model achieved a RMSE of 43.5666 and an R^2 value of 0.132. The RMSE provides an estimate of the average magnitude of error between the model's predicted case counts and the observed cases counts. These are measured in the same units as the outcomes, (i.e., the number of cases). In context of the report, an RMSE of 43.5666 in terms of malaria cases suggests that on average, the model's prediction deviated from the observed malaria case counts by approximately 44 cases per month. For dengue, the model performed better, with an RMSE of 33.598 and an R^2 of 0.230. Using the same context as the malaria

cases, for dengue, the random forest model deviated by approximately 34 cases per month.

The coefficient of determination (R^2) reflects the proportion of variance in the observed data that is explained by the model. While the random forest model captured some of the variability in malaria cases ($R^2 = 0.132$), substantially more variability remained unexplained. The higher R^2 value observed for dengue ($R^2 = 0.230$) indicates that the model explained a larger portion of variability for dengue relative to malaria.

B. Poisson Regression Results

Poisson regression models were applied to both malaria and dengue case counts. Similar to the random forest results, model performance was evaluated using RMSE and R^2. The full results can be seen in Appendix A, Table III.

For malaria, the Poisson model yielded an RMSE of 42.819 and an R^2 of 0.139. For dengue, the Poisson model achieved an RMSE of 32.423 and an R^2 of 0.243. The RMSE values indicate that for malaria, the model's prediction deviated from the observed case counts by approximately 43 cases per month, while for dengue, predictions deviated by approximately 32 cases per month on average. The RNSE results are slightly lower relative to the random forest model, which suggest improved prediction accuracy for both cases.

The R^2 values also indicate that the Poisson model explains a greater proportion of variance in both malaria and dengue incidence relative to the random forest model. As seen previously, predictive performance remains stronger for dengue than for malaria across both models.

C. GAM - Negative Binomial

The GAM–Negative Binomial model was implemented using the `mgcv::gam()` function in R, specifying `family = nb()` to account for overdispersion in count data. Smooth terms were included for key continuous climate predictors, namely lagged temperature (`s(avg_temp_c_lag1)`), lagged precipitation (`s(precipitation_mm_lag1)`), UV index (`s(uv_index)`), and air quality index (`s(air_quality_index)`). These smooth functions enabled the model to capture nonlinear, potentially threshold-based relationships without requiring prespecified functional forms.

In addition to the smooth terms, linear covariates for population density and healthcare budget were included, while categorical variables for region, country, and year were modeled as fixed effects to account for variation.

VI. SIMULATED SCENARIOS

To investigate how climate change can affect the number of future cases of malaria and dengue, multiple scenarios were constructed by systematically modifying key environmental and health system variables. The simulated scenarios were designed to reflect both climate and public health shifts that could potentially occur. Four scenarios were considered:

- **Case 1 (Warming Only):** A uniform 10°C increase in average temperature.
- **Case 2 (Warming + Rain Variability):** A 10°C temperature increase combined with ±20% variability in precipitation.
- **Case 3 (Extreme Climate Change):** A comprehensive extreme weather scenario incorporating a 10°C increase in temperature, ±20% precipitation variability, an increase of 3 units in UV index, and an increase of 10 points in air quality index.
- **Case 4 (Health Investment):** A 50% increase in simulated healthcare budget to assess the potential mitigating effects of increased health system capacity. This was

modeled separately using the GAM - Negative Binomial model.

Given that both models demonstrated previously improved fit for dengue relative to malaria, subsequent climate change simulations were conducted using dengue case predictions only. The Random Forest and Poisson models were only applied to the first three climate based scenarios to evaluate changes in the projected number of dengue cases. The health budget scenario was modeled independently with just the GAM-Negative Binomial model.

A. Random Forest Simulation Results

The Random Forest model was applied to the simulated climate scenarios (Cases 1 - 3) to predict the projected number of dengue cases. The full results can be seen in Appendix A, Table V. In Case 1, the projected number of dengue cases increased relative to the baseline, with total predicted cases rising from $1,024,420$ to $1,067,440$, corresponding to a 4.20% increase. When adding precipitation variability, in Case 2, there was a comparable increase in cases of 4.10% relative to the baseline. Finally, in Case 3, under extreme climate change, total cases reached $1,086,119$, which reflected a 6.02% increase from the baseline.

B. Poisson Model Simulation Results

The Poisson model was similarly applied to the first three climate scenarios using dengue data. Across all simulated conditions, changes in predicted total cases were relatively small compared to the Random Forest model. The full results can be seen in Appendix A, Table VI

In Case 1, total predicted dengue causes decreased by 0.14%. With the addition of precipitation, or Case 2, it produced a decrease of approximately 0.13% compared to the baseline. Finally, in Case 3, it yielded a 0.12% reduction in cases.

In addition to the performance metrics, model diagnostics were examined to better understand the differences in predictive behavior between Random Forest and Poisson regression. Variable importance analysis via the Random Forest model indicated that the climate variables contributed substantially to the model's predictive accuracy. Essentially, the Random Forest captured the nonlinear relationships between climate variables and dengue incidence.

In contrast, the Poisson regression model assigned more weight to non-climate features such as country and months. This suggests that the Poisson model has primarily learned regional or seasonal baseline levels of disease incidence, rather than placing weigh on climate predictors to explain variability. One may argue for one model or another; while the Poisson model is primarily used for count data, the obvious negligence towards climate variables suggests the model's inability to capture climate-driven changes, thus contributing less to smaller simulated changes in dengue incidence across global warming scenarios.

C. GAM - Negative Binomial Simulation Results

The GAM-Negative Binomial model achieved an RMSE of 43.393 and an R^2 of 0.116 for malaria, and an RMSE of 33.140 and an R^2 of 0.213 for dengue. While this models has a lower in R^2 value than the Poisson and Random Forest models, the GAM-NB offers an improved flexibility when modeling nonlinear patterns and handing overdispersion.

Scenario simulations revealed a increase of disease burden under warming conditions. When in comparison to the baseline, malaria cases rose by 21.7% under warming, 22.1% with the addition of precipitation, and 24.9% under the worst case scenario of extreme climate stress.

Dengue outcomes followed similar trends. Compared to the baseline, under warming con-

ditions cases increased by 21.6%, with the addition of precipitation cases increased by 21.8%, and under the worst case scenario for extreme climate stress cases increased by 24.1%.

In contrasts to these climate stress scenarios which project a steady rise in disease burden, when a targeted healthcare budget intervention was implemented. Wherein, we saw the GAM-Negative Binomial model show a 7.0% reductions in total malaria cases and a 6.4% reduction in dengue cases when compared with the baseline model. These decreases suggest increasing healthcare investments can potentially offset the rise in disease burden brought on by climate stressors. Which reinforces the the value of integrating socioeconomic interventions preemptively

Although the GAM-NB model is found to have lower R^2 values, its ability to model nonlinear dynamics and simulate interventions (i.e. increase of healthcare budget) make it well suited for public health forecasting. Full scenario results can be found in Appendix A Table VII

VII. FUTURE WORK

To further improve climate sensitive disease modeling, research shows several methodological extensions are recommended. Firstly, incorporating a biological lag into the models, this may improve temporal alignment between the climate variables and the observed case outcomes. For instance, taking into account incubation delays, such as, the $7-14$ day development period for mosquito eggs and the $10-14$ day incubation period for positive human infection. These would help predictors reflect the possible exposure windows.

Furthermore, future studies should explore the use of Generalized Linear Mixed Models (GLMMs) to account for un-scene heterogeneity (Nakagawa and Schielzeth, 2013). With the introduction of random intercepts, we can potentially capture differences across regions, while allowing for climate effects to vary. This flexibility is essential for building complex ecological models.

Lastly, moving towards building an early warning system. By integrating climate forecasts with disease models will provide proactive surveillance particularly in disease vulnerable regions.

VIII. CONCLUSION

This study assessed how changes in climate and health system capacity may affect the incidence of malaria and dengue. Using a combination of Random Forest, Poisson regression, and GAM–Negative Binomial models, we evaluated model performance and simulated future disease trends under various climate scenarios.

Overall, the Poisson model offered the strongest predictive performance, especially for dengue, although Random Forest and GAM-NB models provided competitive results and added interpretability. All models agreed that climate change—particularly increases in temperature and precipitation—could moderately raise disease burden, with GAM-NB showing the most pronounced effects. Importantly, increased healthcare investment was associated with reductions in predicted cases, highlighting its potential role in mitigating climate-related health risks.

While predictive accuracy remained moderate, these results underscore the importance of incorporating climate variables and health system considerations into disease forecasting. As environmental conditions continue to shift, data-driven models like those developed here will be crucial tools for anticipating disease risks and guiding public health responses.

ACKNOWLEDGMENTS

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All code, data, and acknowledgment of authors collaboration can be found in STAT 209 Project GitHub.

APPENDIX A: SUPPLEMENTARY VISUALS

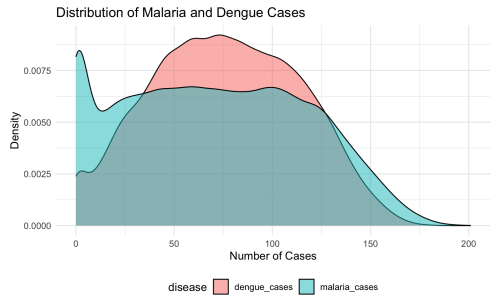

FIG. 7. **Figure A1.** Distribution of malaria and dengue case counts (kernel density overlay).

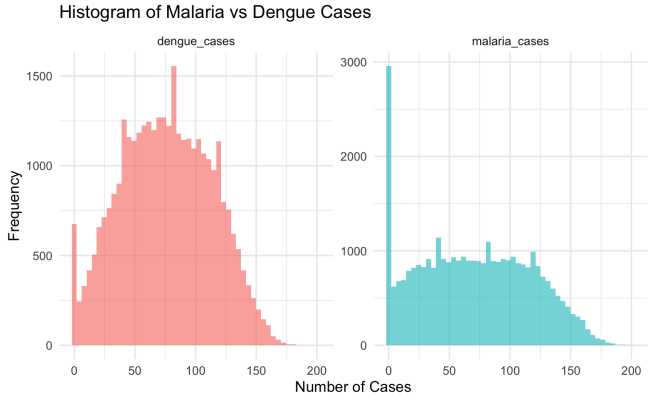

FIG. 8. **Figure A2.** Histograms of monthly malaria (right) and dengue (left) cases.

TABLE II. Random Forest model performance for malaria and dengue predictions.

Metric	Malaria	Dengue
RMSE	43.566	33.598
R^2	0.132	0.230

TABLE III. Poisson regression model performance for malaria and dengue predictions.

Metric	Malaria	Dengue
RMSE	42.819	32.423
R^2	0.139	0.243

TABLE IV. GAM–Negative Binomial model performance for malaria and dengue predictions.

Metric	Malaria	Dengue
RMSE	43.393	33.140
R^2	0.116	0.213

TABLE V. Random Forest Simulation Results for Dengue Cases.

Scenario	Mean Predicted	Total Cases	% Change
Baseline	75.62	1,024,420	0.00%
Case 1	78.80	1,067,440	4.20%
Case 2	78.72	1,066,430	4.10%
Case 3	80.17	1,086,119	6.02%

TABLE VI. Poisson Model Simulation Results for Dengue Cases.

Scenario	Mean Predicted	Total Cases	% Change
Baseline	75.48	1,022,462	0.00%
Case 1	75.37	1,021,135	-0.14%
Case 2	75.37	1,021,140	-0.13%
Case 3	75.37	1,020,986	-0.12%

TABLE VII. GAM–Negative Binomial model scenario predictions for malaria and dengue.

Model	Scenario	Mean Predicted	Total Cases	% Change
Malaria	Baseline	76.20	1,028,367	0.00%
Malaria	Case 1: Warming	92.70	1,250,706	+21.7%
Malaria	Case 2: Warm + Precip.	93.01	1,254,637	+22.1%
Malaria	Case 3: Extreme Climate	95.18	1,283,594	+24.9%
Malaria	Case 4: Budget Increase	70.90	956,880	**−7.0%**
Dengue	Baseline	76.09	1,015,929	0.00%
Dengue	Case 1: Warming	92.58	1,234,831	+21.6%
Dengue	Case 2: Warm + Precip.	92.73	1,236,835	+21.8%
Dengue	Case 3: Extreme Climate	94.50	1,261,143	+24.1%
Dengue	Case 4: Budget Increase	71.33	951,114	**−6.4%**

APPENDIX B: REFERENCES

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