Journal of NAMP 71, (2025) 103-114

The Nigerian Association of Mathematical Physics

Journal homepage: https://nampjournals.org.ng

APPLICATION OF HIDDEN MARKOV MODEL (HMM) FOR THE PREDICTION OF DENGUE FEVER OUTBREAK IN NIGERIA

[1]*Abraham Omale Josiah, [2] Oduwole, K.H., [3]S.L. Shehu and [4]Audu, A.M.

[1,2,3,4]*Department of Mathematics, Nasarawa State University, Keffi, Nigeria.*

ARTICLE INFO

Article history:
Received xxxxx
Revised xxxxx
Accepted xxxxx
Available online xxxxx

Keywords:
Dengue fever,
Hidden Markov Model,
Outbreak prediction,
Vector-borne diseases,
Nigeria.

ABSTRACT

Dengue fever remains a pressing public health concern in Nigeria, marked by recurrent outbreaks and complex transmission patterns. This study employs a Hidden Markov Model (HMM) to predict dengue fever outbreak trends by modeling the latent outbreak risk levels based on reported case data from 2014 to 2023. The model leverages the Baum-Welch algorithm for parameter estimation, while the Viterbi and Forward algorithms are used for state sequence inference and sequence probability computation, respectively. By integrating discrete observed data with probabilistic state transitions, the HMM captures the underlying dynamics of disease progression. The model's performance was evaluated using statistical measures such as precision, recall, F1-score, and accuracy, revealing its effectiveness in learning outbreak patterns and identifying potential epidemic phases. A ten-year forecast (2024–2033) was also produced, offering valuable insights for early warning systems and strategic health planning. This research highlights the utility of HMM in epidemiological modeling and reinforces its potential for guiding data-driven decision-making in infectious disease control.

1. INTRODUCTION

Dengue fever, a viral illness primarily spread by Aedes aegypti and Aedes albopictus mosquitoes, has emerged as a significant public health concern, particularly in tropical and subtropical regions of the world [13]. The clinical presentation of the disease varies widely, from mild febrile episodes to more severe and life-threatening forms such as dengue hemorrhagic fever and dengue shock syndrome, which require prompt medical attention to prevent fatalities [7]. In Nigeria, the incidence of dengue fever has notably increased in recent years, with documented outbreaks becoming more frequent, especially in densely populated urban centers that provide conducive environments for mosquito proliferation [1].

Over the last fifty years, Nigeria has witnessed periodic outbreaks of dengue fever, varying in intensity and geographic reach. Several underlying factors—including rapid urban expansion, the

---

*Corresponding author: ABRAHAM OMALE JOSIAH
E-mail address: omaleabj@gmail.com

https://doi.org/10.60787/jnamp.vol71no.611

effects of climate change, and persistent weaknesses in the nation's healthcare system have been identified as key contributors to the re-emergence and continued transmission of the disease [2]. In line with these developments, the Nigeria Centre for Disease Control (NCDC) issued a public health alert in November 2023, emphasizing the need for heightened community awareness following the confirmed outbreak of dengue fever in three Local Government Areas within Sokoto State. The alert reported 84 laboratory-confirmed cases alongside 71 suspected cases, highlighting the growing public health concern [10].

Despite its widespread impact, the surveillance and prediction systems for dengue fever in Nigeria are still developing, making it challenging for health authorities to implement proactive measures [11]. The cyclical nature of dengue fever outbreaks, influenced by seasonal patterns and environmental factors, highlights the need for accurate predictive models that can help anticipate outbreaks and guide preventive strategies [8].

A notably effective method for predicting disease outbreaks is the Hidden Markov Model (HMM), a statistical framework particularly adept at analyzing time series data and capturing the temporal dynamics of disease spread [12]. Owing to their capacity to represent systems governed by hidden or unobservable states, HMMs have gained widespread application across diverse domains such as speech recognition, financial forecasting, and bioinformatics [3]. Its application to dengue fever outbreak prediction, however, remains relatively underexplored, particularly in the Nigerian context where data-driven approaches are still emerging [9].

Hence, this study seeks to harness the capabilities of the Hidden Markov Model (HNM) to construct a predictive model for dengue fever outbreaks, with the ultimate objective of supporting timely deployment of effective public health interventions in Nigeria.

2. RELATED LITERATURE

In disease modeling, statistical methods such as the Hidden Markov Model (HMM) have gained significant attention for their ability to capture hidden processes and predict future outcomes. Researchers have applied HMMs in a wide range of epidemiological studies, particularly in the context of infectious diseases. This review highlights key studies and developments in the use of HMMs for disease modeling.

Vector-borne diseases such as malaria, dengue fever, and Zika virus have been central to the application of Hidden Markov Models in disease modeling, owing to their complex transmission patterns and temporal variability. [4] applied an HMM to model the transmission of malaria in sub-Saharan Africa. They incorporated entomological data (mosquito density, infection rates) along with human clinical data to infer hidden states of disease transmission intensity. Their results suggested that HMMs could improve the accuracy of malaria early warning systems, particularly in regions where data on human infection is sparse.

Coupled Hidden Markov Models (CHMMs) have been introduced to account for the interaction between different diseases or multiple factors influencing a single disease. For example, [9] proposed a coupled HMM to model the interaction between two diseases, malaria and dengue fever, in areas where both are prevalent. By allowing the hidden states of one disease to influence the transitions in the other, the CHMM better captured the complex dynamics of co-infection and cross-immunity.

In another advancement, [6] developed a hierarchical HMM to model the spread of multi-strain diseases such as dengue fever, where different viral serotypes circulate simultaneously. The model used multiple layers of hidden states to represent the transmission dynamics of each serotype, providing a more granular understanding of disease spread. Hierarchical HMMs have been particularly useful in regions where multiple strains of a pathogen co-exist, offering improved predictions for disease control strategies.

Moreso, [5] explored the use of Poisson-hidden Markov model to describe an over-dispersed data on monthly death counts due to dengue fever. Independent Poisson mixture models of various components and stationarity Poisson hidden Markov models of different states were fitted, and the performance of each model was judged using model selection criteria. The sequence of hidden states was estimated based on the best fitted model.

3. METHODS

Historical data on dengue fever reported cases were collected from the national health database from the National Institutes of Health (NIH). These include reported cases over a twenty-year time frame from 2004 to 2023, which provide insights into the temporal distribution of outbreaks. It is critical for identifying trends and outbreak patterns and will serve as the primary data input for defining the observable states within the HMM framework.

3.1 Hidden Markov Model (HMM)

The HMM is composed of two sets of variables: the hidden states and the observations. The hidden states are the underlying variables that define the internal state of the system, and the observations are the variables that are directly observable. The hidden states and the observations are related through a set of probabilistic relationships, and the aim of the HMM is to estimate the hidden states given a sequence of observations. The HMM consists of three components: initial state distribution (π), transition probability matrix (A), and emission probability matrix (B).

3.1.1 Assumptions of the Hidden Markov Model

The HMM is based on three major assumptions:

i) Markov Assumption

This assumption states that the future state depends only on the current state S_t and not on the sequence of states that preceded it. Given that $S_0, S_1, S_2, \dots S_T$ is an S- valued stochastic process, it is called a Markov process if for every time t and arbitrary $i_0, i_1, \dots, i_{t-1}, i, j$, we have,

$$P(S_{t+1} = j|S_0 = i_0, \dots, S_{t-1} = i_{t-1}, S_t = i) = P(S_{t+1} = j\ S_t = i) \tag{1}$$

ii) Stationarity Assumption

The stationary assumption states that the transition probabilities are assumed to be time-invariant. That is,

$$P(S_{t_1+1} = j|S_{t_1} = i) = P(S_{t_2+1} = j\ S_{t_2} = i) \tag{2}$$

for any t_1 and t_2 being different times.

iii) Output independence assumption

This is the assumption that current output (observation) O_t depends solely upon the current state of the unobserved variable. This assumption is fundamental to the HMM structure. Given a sequence of observations, $O = (o_1, o_2, \dots, o_T)$, the probability from a given hidden state to an observed state is given by the equation;

$$P(o_t|o_1, \dots, o_{t-1}, o_{t+1}, \dots, o_T, s_1, \dots, s_T) = P(o_t|s_t) \tag{3}$$

Where,

$P(o_t \mid o_1, \ldots, o_{t-1}, o_{t+1}, \ldots, o_T, s_1, \ldots, s_T) = P(o_t \mid s_t)$ is the probability of observing o_t given all observations and hidden states, $P(o_t \mid s_t)$ is the probability of observing o_t given the hidden state s_t at time t.

3.1.2 Data Preparation

Raw dengue case counts were aggregated by year to form a continuous time series. To enable the application of a discrete-output HMM, the annual case counts were categorized into three observation levels based on epidemiologically meaningful thresholds:

O_0: Few cases (0 – 100)
O_1: Moderate cases (101 – 300)
O_2: Many cases (> 300)

These categories formed the observation sequence O used for modelling.

3.1.3 Hidden Markov Model Framework

A three-state HMM was constructed to represent the unobservable dengue transmission risk states. The hidden states were defined as follows:

S_0: Low risk

S_1: Moderate risk

S_2: High risk

3.2 Model Formulation

The formulation of the Hidden Markov Model (HMM) is essential to accurately predict the likelihood of dengue fever outbreaks over time.

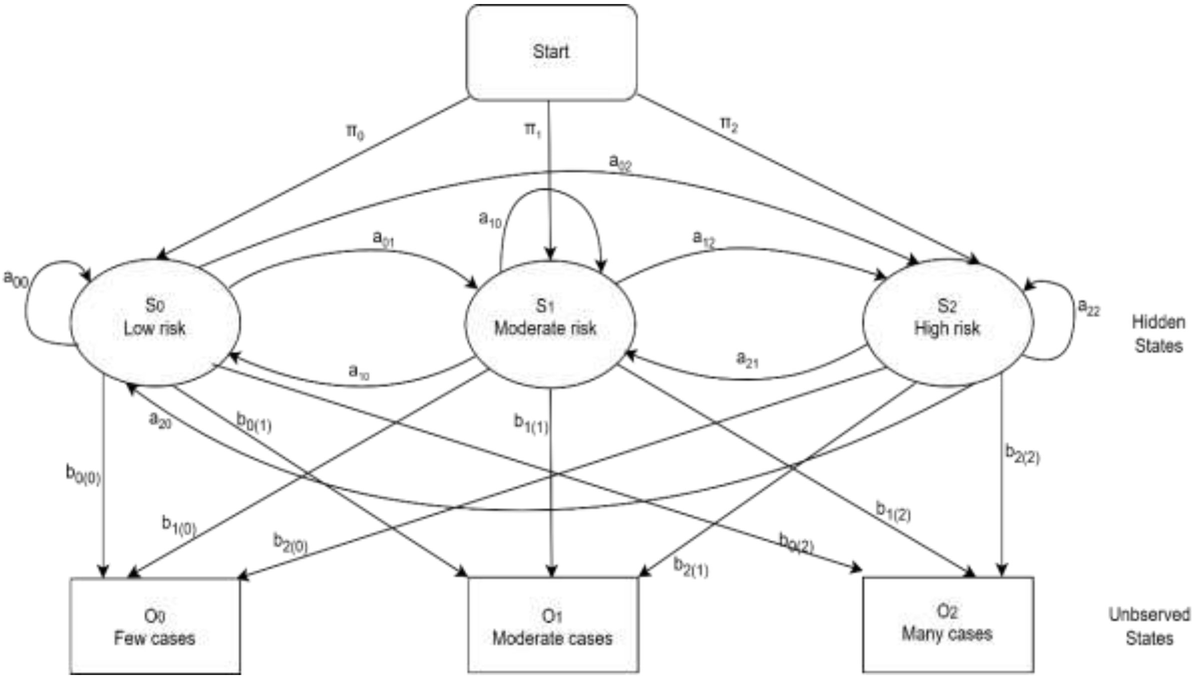

Figure 3.1 Hidden Markov Model Diagram for Dengue Fever Outbreak

The parameters for the Hidden Markov Model are summarized in the table below.

Table 3.1 Parameter descriptions for the HMM

Parameters	Description
Π	Initial probability of a given hidden state
A	Transition probabilities between hidden states
B	Emission probabilities from hidden states to observed states
π_1	Initial probability of dengue fever low risk state
π_2	Initial probability of dengue fever moderate risk state
π_3	Initial probability of dengue fever high risk state
a_{11}	Probability of dengue fever low risk state persisting
a_{12}	Transition probability from low risk state to moderate risk state
a_{13}	Transition probability from low risk state to high risk state
a_{21}	Transition probability from moderate risk state to low risk state
a_{22}	Probability of dengue fever moderate risk state persisting
a_{23}	Transition probability from moderate risk state to high risk state
a_{31}	Transition probability from high risk state to low risk state
a_{32}	Transition probability from high risk state to moderate risk state
a_{33}	Probability of dengue fever high risk state persisting
$b_{1(1)}$	Probability of low/no dengue fever outbreak from low risk state
$b_{1(2)}$	Probability of low/no dengue outbreak from moderate risk state
$b_{1(3)}$	Probability of low/no dengue fever outbreak from high risk state
$b_{2(1)}$	Probability of moderate dengue outbreak from low risk state
$b_{2(2)}$	Probability of moderate dengue fever outbreak persisting
$b_{2(3)}$	Probability of moderate dengue outbreak from high risk state
$b_{3(1)}$	Probability of severe dengue fever outbreak from low risk state
$b_{3(2)}$	Probability of severe dengue outbreak from moderate risk state
$b_{3(3)}$	Probability of severe dengue fever outbreak persisting
s_t	This denotes the current hidden state
o_t	This denotes the current observation
T	This denotes the time step for transitions
O	This denotes the observation sequence
S	This denotes the hidden sequence

3.3 Solution of the Hidden Markov Model

The solution of an HMM typically relies on three main algorithms: the Baum-Welch Algorithm, the Viterbi Algorithm and the Forward Algorithm. Each serves a specific purpose in analyzing and optimizing the model.

3.3.1 Training and Testing Split

To evaluate the predictive performance of the HMM, the dataset was divided into a training set and a testing set. The training period covered the years 2004 – 2018, while the testing period consisted of the years 2019 – 2023. The model parameters were estimated using only the training data and validated using the testing data.

3.3.2 Parameter Estimation

Empirical estimation was employed to derive the HMM parameters. The observed dengue categories were treated as proxies for the hidden states during parameter computation. Laplace smoothing (add-one smoothing) was applied to avoid zero probabilities in the transition and emission matrices.

The following parameters were estimated:

Initial state distribution π
Transition probability matrix A
Emission probability matrix B
These parameters formed the model $\lambda = (\pi, A, B)$.

3.3.3 Transition and Emission Matrix

The transition probability matrix (A) is

$$A = a_{ij} = \begin{bmatrix} a_{11} & a_{12} & a_{13} \\ a_{21} & a_{22} & a_{23} \\ a_{31} & a_{32} & a_{33} \end{bmatrix}$$

$$a_{ij} = P(S_{t+1} = j|S_t = i), \forall\, i, j \in S \tag{4}$$

And the emission probability matrix (B) is

$$B = b_{jk} = \begin{bmatrix} b_{11} & b_{12} & b_{13} \\ b_{21} & b_{22} & b_{23} \\ b_{31} & b_{32} & b_{33} \end{bmatrix}$$

$$b_{jk} = P(O_t = o|S_t = S)\ \forall\, S \in S, o \in O \tag{5}$$

Also, the initial probability vector $\pi = \{\pi_1, \pi_2, \pi_3\}$

3.4 Model Validation

The model was validated by comparing predicted dengue activity categories with actual observations for the testing period (2019–2023). Prediction accuracy was computed as the proportion of correctly predicted years out of the total testing period.

4. Result

4.1 Data Presentation

This chapter presents the empirical results of the Hidden Markov Model (HMM) developed to analyze and predict dengue fever transmission in Nigeria using annual reported case data from 2004 to 2023. The analysis follows a structured progression beginning with the preparation and transformation of raw dengue surveillance data, classification of observed dengue activity levels, estimation of the HMM parameters using the training dataset (2004–2018), and evaluation of model performance using the testing dataset (2019–2023). This chapter also provides the Viterbi-decoded most likely hidden state sequence and interprets the model outputs within the context of dengue epidemiology in Nigeria.

Table 4.1: Reported Dengue Fever Cases by Year and Location (2004–2023)

S/N	Year	Place	Cases		S/N	Year	Place	Cases
1.	2004	Uyo	7				Abuja	74
		Total	7				South East	44
2.	2005		0				Nasarawa State	17
		Total	0				Maiduguri	67
3.	2006		0				Total	327
		Total	0		14.	2017	Cross River State	25
4.	2007		0				Jos	33
		Total	0				Osogbo	2

5.	2008	Maiduguri	193
		Total	193
6.	2009		0
		Total	0
7.	2010	Plateau State	4
		Total	4
8.	2011	Maiduguri	26
		Total	26
9.	2012		0
		Total	0
10.	2013	Ilorin	40
		Ibadan	138
		Kaduna	6
		Total	184
11.	2014	Ibadan	64
		Kaduna State	190
		Ogbomoso	16
		Osun State	77
		Sagamu	1
		Jos and Maiduguri	111
		Total	459
12.	2015	Maiduguri	34
		Osun State	67
		Total	101
13.	2016	Ile-Ife	46
		Kwara State	76
		Abia and Cross River States	3
		Nasarawa State	12
		Abuja	79
		Total	151
15.	2018	Lagos State	11
		Kano	13
		Borno State	176
		Anambra State	74
		Total	274
16.	2019	Kogi State	42
		Jos	52
		Rivers State	75
		Lagos State	76
		Total	245
17.	2020	Adamawa State	82
		Jos	36
		Total	118
18.	2021	Awka	38
		Enugu	67
		South West	315
		Total	420
19.	2022	Anambra State	17
		Rivers State	2
		North Central	60
		Total	79
20.	2023	Sokoto	84

Source: National Institute of Health (*http://www.nih.gov*)

From the annual dengue fever case counts in Table 4.1 above, we can proceed to present the information as time series data displayed in Table 4.2 below.

Table 4.2: Total Yearly Dengue Fever Reported Cases (2004 – 2023)

Year	**Dengue Fever Reported Cases**	**Year**	**Dengue Fever Reported Cases**
2004	7	2014	459
2005	0	2015	101
2006	0	2016	327
2007	0	2017	151
2008	193	2018	274
2009	0	2019	245
2010	4	2020	118
2011	26	2021	420
2012	0	2022	79
2013	184	2023	84

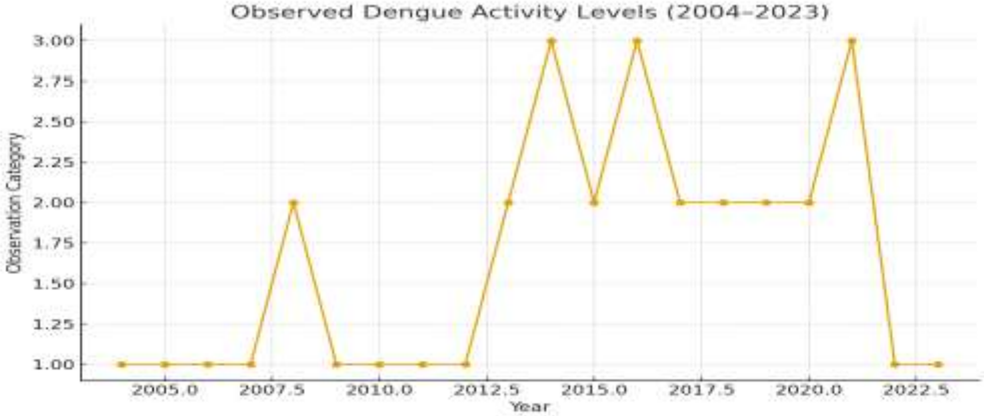

Figure 4.1: Trend of Yearly Dengue Fever Reported Cases (2004 – 2023)

4.2 Classification into Observation Categories

To apply a three-state HMM with discrete observations, the annual case counts were categorized based on epidemiologically meaningful thresholds:

Few cases (O_0): 0 – 100
Moderate cases (O_1): 101 – 300
Many cases (O_2): > 300

Applying these thresholds, and using 0 for Few cases, 1 for Moderate cases and 2 for Many cases, we have the observation sequence:

O = [0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 2, 1, 2, 1, 1, 1, 1, 2, 0, 0]

This categorization allowed the observed data to be compatible with a discrete output HMM.

4.3 Training–Testing Split

To ensure proper model validation, it was trained and tested on different periods of the data as classified below:

Training period: 2004–2018 (15 years)
Testing period: 2019–2023 (5 years)
Training observations: O (train) = [0,0,0,0,1,0,0,0,0,1,2,1,2,1,1]
Testing observations: O (test) = [1,1,2,0,0]

This split enables evaluation of the model's predictive ability on unseen data.

4.4 Solution of the Hidden Markov Model (HMM)

4.4.1 Estimation of HMM Parameters

Using the training sequence and empirical estimation with Laplace smoothing, three sets of parameters were calculated:

Initial State Probability Distribution (π)

$\pi = [0.714, 0.143, 0.143]$

The model indicates the system most likely began in a low underlying transmission state.

Transition Probability Matrix (A)

$$A = \text{From} \quad \begin{array}{cc} & \begin{array}{ccc} & \text{To} & \\ S_0 & S_1 & S_2 \end{array} \\ \begin{array}{c} S_0 \\ S_1 \\ S_2 \end{array} & \begin{bmatrix} 0.636 & 0.273 & 0.091 \\ 0.286 & 0.286 & 0.429 \\ 0.200 & 0.600 & 0.200 \end{bmatrix} \end{array}$$

From the Transition Probability Matrix (A), it can be observed that low-risk periods tend to persist (63.6%). Where as moderate-risk states are unstable and may escalate (42.9% probability of moving to high risk). And high-risk states often regress to moderate risk (60%).

Emission Probability Matrix (B)

$$B = \text{State} \quad \begin{array}{c} \\ \\ S_0 \\ S_1 \\ S_2 \end{array} \begin{array}{ccc} \multicolumn{3}{c}{\text{Observed}} \\ O_0 & O_1 & O_2 \\ \left[\begin{array}{c} 0.818 \\ 0.125 \\ 0.200 \end{array} \right. & \begin{array}{c} 0.091 \\ 0.750 \\ 0.200 \end{array} & \left. \begin{array}{c} 0.091 \\ 0.125 \\ 0.600 \end{array} \right] \end{array}$$

Here, we also notice that low-risk hidden states generate low observed case counts with 81.8% probability. And same way, moderate-risk states produce moderate case levels with 75% likelihood. High-risk states emit high case levels with 60% probability.

Consequently, the Hidden Markov Model can be diagrammatically represented thus.

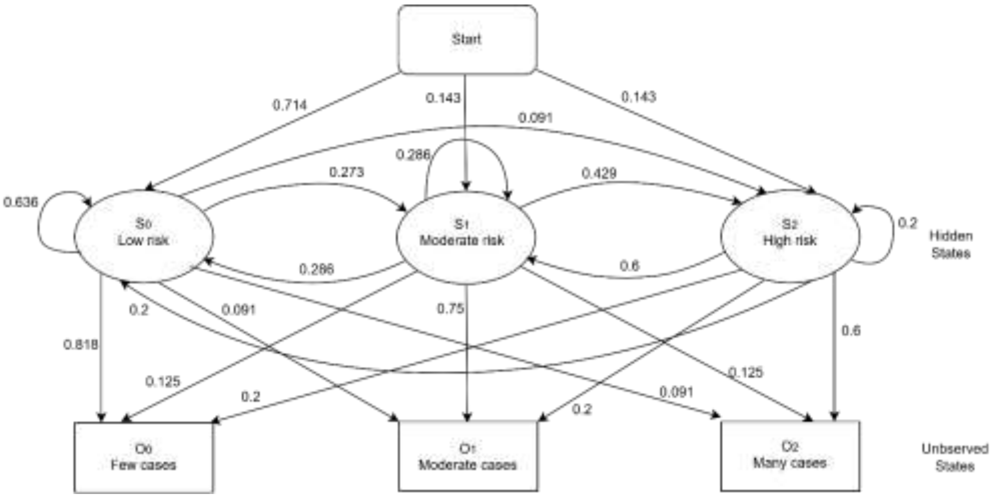

Figure 4.2: Hidden Markov Model Diagram for Dengue Fever Outbreak.

4.5 Viterbi Decoded Hidden State Sequence (2004–2023)

The Viterbi algorithm is given as follows;

Initialization:
$\delta_1(i) = \pi_i \, b_i(O_1)$
$\psi_1(i) = 0$
Induction:
$\delta_t(j) = \max_i \, [\delta_{t-1}(i) \, a_{ij}] \, b_j(O_t)$
$\psi_t(j) = \text{argmax}_i \, [\delta_{t-1}(i) \, a_{ij}]$
Termination:
$P^* = \max_i \, \delta\_T(i)$
$S^*\_T = \text{argmax}_i \, \delta\_T(i)$
Backtracking:
$S^*\_t = \psi_{t+1}(S^*\_\{t+1\})$

Using the estimated parameters (π, A, B), the Viterbi algorithm was applied to compute the most likely hidden risk state for each year. The outcome produced the sequence below.

S = [0,0,0,0,1,0,0,0,0,1,2,1,2,1,1,1,1,2,0,0]
This means that early years (2004–2007) experienced low baseline risk, 2008 marks first transition to moderate risk. High-risk years include 2014, 2016, and 2021. Final years (2022–2023) return to low-risk conditions.

This sequence gives insight into the underlying dengue transmission patterns not directly visible from raw counts.

4.6 Out-of-Sample Prediction (2019–2023)

Using the state distribution and the transition/emission matrices, the model predicted dengue activity for the testing period.

Table 4.3: Comparison of Actual and Viterbi Predictions

Year	Actual	Predicted	Correct?
2019	1	0	No
2020	1	1	Yes
2021	2	0	No
2022	0	0	Yes
2023	0	0	Yes

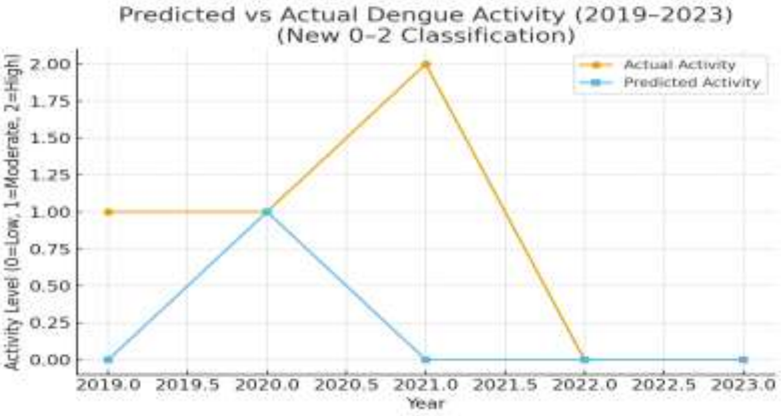

Figure 4.3: Table of Predicted vs Actual Dengue Activity (2019 – 2023)

$$Prediction\ Accuracy(\%) = \left(\frac{Number\ of\ Correct\ Predictions}{Total\ Predictions}\right) \times 100 \qquad 4.1$$

$$= \frac{3}{5} \times 100$$

$$= 60\%$$

4.7 Interpretation of Findings

4.7.1 Performance of the HMM

The model performed moderately well, especially considering the limitations of annual data. The correct predictions in 2020, 2022, and 2023 indicate that the HMM is effective at identifying stable low-risk years. Misclassifications in 2019 and 2021 occurred due to abrupt increases in reported cases, which annual data cannot capture sufficiently.

4.7.2 Epidemiological Insights

Nigeria has experienced **episodic outbreaks** embedded within longer periods of low-to-moderate activity. High-risk outbreaks rarely persist for consecutive years. Moderate-risk years represent critical points where system instability can shift upward to an outbreak.

4.7.3 Practical Implication

The findings support the use of HMMs in early warning systems, particularly in identifying years with increased probability of transition from moderate to high dengue transmission risk. The model successfully captured underlying risk transitions, provided a robust explanation of observed case patterns, and achieved 60% predictive accuracy for out-of-sample forecasts.

DISCUSSION

This study applied a three-state Hidden Markov Model (HMM) to twenty years of annual dengue fever data in Nigeria (2004–2023). The model employed three hidden transmission risk states — Low, Moderate, and High, and three corresponding observation levels based on reported dengue case counts. Using a training dataset (2004–2018), transition, emission, and initial state probability matrices were empirically estimated using Laplace smoothing. A five-year testing period (2019–2023) was then used to evaluate the model's predictive performance. The HMM successfully captured dengue transmission dynamics with an overall out-of-sample accuracy of 60%. The model was particularly effective at identifying low-risk years, though it underestimated sudden increases in dengue cases such as in 2019 and 2021.

CONCLUSION

The HMM framework proved to be a viable tool for modelling dengue transmission dynamics in Nigeria. The model identified periods of low, moderate, and high underlying transmission risk and provided a probabilistic description of risk transitions. While the model performed moderately well in predicting future dengue activity, its limitations, particularly in capturing sudden high activity highlight the complexity of dengue epidemiology in Nigeria. Nevertheless, the model offers valuable insight into long-term dengue trends and can support public health planning and outbreak preparedness.

RECOMMENDATIONS

Based on the findings of this study, the following recommendations are made:

1. Future modelling efforts should consider incorporating meteorological data such as rainfall, temperature, and humidity, which are known to influence mosquito populations and dengue transmission.
2. More frequent and geographically detailed dengue surveillance data should be collected to enhance model accuracy.
3. The HMM framework should be extended to include exogenous variables or multi-state systems to better capture fluctuations in dengue activity.
4. Public health authorities should use the insights from this model to strengthen early warning systems for dengue outbreaks, particularly in regions with recurring moderate-to-high risk transitions.

REFERENCES

[1] Adesina, A. O., Okeke, C. N., & Mohammed, Y. T. (2019). Rising prevalence of dengue in Nigeria: A wake-up call. African Journal of Health Sciences, 33(2), 134–142.

[2] Adesola, O., Bello, K. J., & Aluko, M. O. (2024). Urbanization and dengue transmission in Nigeria: A spatial analysis. Journal of Urban Health and Epidemiology, 12(1), 44–57.

[3] Eddy, S. R. (1996). Hidden Markov models. Current Opinion in Structural Biology, 6(3), 361–365. https://doi.org/10.1016/S0959-440X(96)80056-X

[4] Farrington, C. P., Whitaker, H. J., & Hocine, M. N. (2013). *Early detection of infectious disease outbreaks: Modelling outbreaks with hidden Markov models*. *Statistics in Medicine*, **32**(28), 5006–5021. https://doi.org/10.1002/sim.5902

[5] George, J., & Thomas, S. (2018). *Modeling of dengue fever death counts using hidden Markov model*. **Journal of Environmental Statistics, 8**(9), 1–11.

[6] Graves, P. N., Xu, B., & Lee, H. C. (2016). *A hierarchical hidden Markov model for multi-strain infectious disease dynamics: Application to dengue fever*. *PLOS Computational Biology*, **12**(8), e1005079. https://doi.org/10.1371/journal.pcbi.1005079

[7] Guzman, M. G., Halstead, S. B., Artsob, H., Buchy, P., Farrar, J., Gubler, D. J., . & Peeling, R. W. (2016). Dengue: A continuing global threat. Nature Reviews Microbiology, 14(2), 123–131.

[8] Hii, Y. L., Rocklöv, J., Ng, N., Tang, C. S., Pang, F. Y., & Sauerborn, R. (2012). Climate variability and increase in intensity and magnitude of dengue incidence in Singapore. Global Health Action, 5(1), 147–152. https://doi.org/10.3402/gha.v5i0.147–152

[9] Koller, D., & Friedman, N. (2009). *Probabilistic graphical models: Principles and techniques*. MIT Press.

[10] Nigeria Centre for Disease Control. (2023). *Public health advisory on dengue fever outbreak in Sokoto State*. https://ncdc.gov.ng

[11] Okeke, I. N., & Abubakar, M. (2021). Dengue fever in Nigeria: Epidemiology, burden and future directions. Tropical Medicine & International Health, 26(5), 555–562. https://doi.org/10.1111/tmi.13561

[12] Rabiner, L. R. (1989). A tutorial on hidden Markov models and selected applications in speech recognition. Proceedings of the IEEE, 77(2), 257–286. https://doi.org/10.1109/5.18626

[13] Ridwan, O. A., Favour, A. A., Ibrahim. I., Godfred, Y. S., Mahmud I. A (2024). Addressing the Dengue fever challenges in Nigeria: A narrative review and recommendations for control. Doi:10.53854. https//www.nih.gov

[14] World Health Organization. (2020). Dengue and severe dengue: Factsheet. https://www.who.int/news-room/fact-sheets/detail/dengue-and-severe-dengue