



## Modelling Japanese Encephalitis Spread in Flood-Prone Areas Using an SEIR Framework

**Puspanjali Kumari**

Ph.D. Scholar (Mathematics)

Department of Mathematics

Radha Govind University, Ramgarh, Jharkhand (India)

**Email id:** Puspanjalisingh132@gmail.com

**DECLARATION:** I AS AN AUTHOR OF THIS PAPER /ARTICLE, HERE BY DECLARE THAT THE PAPER SUBMITTED BY ME FOR PUBLICATION IN THE JOURNAL IS COMPLETELY MY OWN GENUINE PAPER. IF ANY ISSUE REGARDING COPYRIGHT/PATENT/OTHER REAL AUTHOR ARISES, THE PUBLISHER WILL NOT BE LEGALLY RESPONSIBLE. IF ANY OF SUCH MATTERS OCCUR PUBLISHER MAY REMOVE MY CONTENT FROM THE JOURNAL WEBSITE. FOR THE REASON OF CONTENT AMENDMENT /OR ANY TECHNICAL ISSUE WITH NO VISIBILITY ON WEBSITE /UPDATES, I HAVE RESUBMITTED THIS PAPER FOR THE PUBLICATION.FOR ANY PUBLICATION MATTERS OR ANY INFORMATION INTENTIONALLY HIDDEN BY ME OR OTHERWISE, I SHALL BE LEGALLY RESPONSIBLE. (COMPLETE DECLARATION OF THE AUTHOR AT THE LAST PAGE OF THIS PAPER/ARTICLE

### **Abstract:**

Japanese Encephalitis (JE) is an arthropod borne flaviviral disease which affects children mainly in tropical and flood prone areas of Asia. Climate changes, particularly more severe flooding, markedly increase the mosquito population and facilitate rapid spread. This study uses an SEIR (Susceptible-Exposed-Infectious-Recovered) compartmental model to mimic the dynamics of JE transmission in not only the human population but also in mosquito populations and a flood-affected area. The model includes important biological and ecological characteristics, such as the  $\alpha$  of transmission that is flood-related, the mosquito lifespan, the vector-host relationship, and the recovery rates. Calculated with empirical parameter value settings, the basic reproductive number  $R_0 \approx 26.2$  illustrates the severe outbreak risk under flood break out. Simulation results show a quick elimination of the susceptible individuals, an early peak in the infected population, and a final reaching of the fixed number of recovered people. This model also investigates the influence of vector-to-host ratios, climate-dependent variables, and media attention on disease dynamics. Results indicate that SEIR models, when combined with environmental and behavioural factors, can be useful in predicting outbreaks of and devising interventions for EBOV. Such information can also help inform geographically tailored interventions, particularly in places where resources are limited in high-risk flood areas.

### **Keywords:**

Japanese Encephalitis, SEIR Model, Vector-Borne Disease, Flood-Affected Areas, Reproduction Number ( $R_0$ ), Epidemic Forecasting

## I. Introduction

Vector-borne diseases continue to remain a major threat to public health, especially in tropical and subtropical regions where the climate facilitates the breeding and growth of disease vectors including mosquitoes. Of these infections, Japanese Encephalitis (JE) due to Japanese encephalitis virus (JEV) of genus *Flavivirus* is a major neurologic disease condition with high fatality as well as morbidity especially in children. JE is primarily spread through the bite of infected *Culex* mosquitoes and has a long and complex transmission cycle, in which wild birds act as reservoirs and pigs as an amplifying host. Although the majority of infected people are asymptomatic, when patients develop symptoms, they frequently experience severe neurological complications or die. The endemicity of JE in Southeast Asia and the Western Pacific has been further amplified in recent years by the climatic extremes such as the upsurge in frequency and intensity of monsoon-induced flooding events due to climate change. Such environmental disturbances provide an essential added value to vector breeding, which leads to the failure of the current control and creates possibilities for JEV spread in a broader area.

Strategies to address JE outbreaks in flood affected areas The flood-hit areas do offer unique challenges in the management of JE outbreaks with the presence of stagnant water bodies, increased vector density, population displacement and sanitation infrastructure which has taken a beating. Together these factors increase human contact with infected mosquitoes and make these areas to be the hotspots of JE epidemics. Thus, mechanistic analyses concerning JEV transmission in flood-prone regions would benefit from flexible modelling frameworks that can incorporate ecological, epidemiological, and climatological drivers. The Susceptible–Exposed–Infected–Recovered (SEIR) model is a standard compartmental framework used for modeling infectious diseases, which offers a structured method for modeling the evolution of infectious diseases, including those transmitted by vectors. Through segregated populations (susceptible, exposed, infected and recovered) the SEIR model considers the latent period and provides the possibility of time-varying usages for modeling disease evolution. Elaborated to the vector and reservoir populations, as in the JE case, SEIR-based models become useful for predicting outbreak trajectories, evaluating the efficacy of control strategies, and informing public health policy.

Several studies have laid groundwork for SEIR-based modeling of JE. Cheng et al. (2018) used both SEIR and Maxent models to evaluate the Usutu virus risk — which is a flavivirus intimately related to JEV — demonstrating the value of mechanistic models in reproducing the transmission patterns driven by climate. Their two-step modeling approach highlighted the benefits of adding temperature-influenced terms to SEIR models, an important consideration for JE where the dynamics of vector populations are tightly bound to environmental factors. Similarly, Panja et al. (2018) facilitated a dynamic SEIR model for transmission of JE, with control parameters and time-varying carrying capacity of the mosquitoes. Their study showed the model's ability to predict threshold levels of disease persistence, and to examine the impact of interventions such as vector control and vaccination given different ecological restrictions.

Environmental and socio-behavioral determinants of JEV transmission have also been broadly investigated. Kalita and Devi (2020) stressed the importance of media awareness programmes in mitigating disease transmission through changing human behaviour. Using an SEIR-type model, they introduced a media-induced 'aware' compartment in the susceptible fraction, showing that public health messaging can have a subtle effect on vector-host interactions. Further, Tu et al. and humidity with JE occurrence by way of a hybrid modeling system that integrates statistical models and SEIR dynamics. Their results support the incorporation of climate-sensitive functions in SEIR framework to represent an increase in vector population during and after a flood.

The spatial distribution of JE has been of great concern in recent years, especially for expanding into new areas, attributed to the climate changes. Ladreyt et al. (2022) simulated JE transmission in rural Cambodian communities, and found that despite being low-pig density areas, alternate host communities are capable of maintaining viral transmission. This has major implications for SEIR-type models in flood-affected areas, as livestock populations can change due to displacement or death, with commensurate influences on host communities. Building on this work, Ladreyt et al. (2023) analyzed the threat of JEV invasion onto Reunion Island, based on a deterministic model, for which  $R_0$  was computed for different vector densities and critical thresholds were identified for outbreak occurrence. Their work highlights the necessity of including heterogeneity in both vector and host densities in the estimation of JE risk in recently susceptible areas.

The calculation of the basic reproduction number focalizes SEIR models. It's a measure of how efficiently the disease is transmitted, therefore guiding public health responses. A number of works (Goswami, 2022; Goswami & Hussain, 2023) have investigated  $R_0$  under saturated incidence and treatment functions, which captures the real-life scenario of finite healthcare capacity during the epidemic outbreaks. Their models combine logistic growth functions of pigs with analyses of healthcare saturation and their impacts on outbreak control. Such issues are especially important during floods, when access to health services is often limited. In addition, the backward bifurcation is inverse and described by Dwivedi et al. (2022) indicates that halting transmission ( $R_0 = 0$ ) or reducing  $R_0$  to less than 1 alone may not be adequate for the elimination of the disease particularly when the pathogen has an animal reservoir unless combined with strong control measures, and suggests that the intervention approaches need to be comprehensive in nature particularly during emergency conditions created by JE outbreaks induced by floods.

Dynamic of vaccine is an important factor of JE transmission model. Quan et al. (2020) and Bouckenoghe et. (2019) both penetrated the vaccine efficacy and long-term antibody persistence mechanisms in mathematical and statistical manners, respectively. Their results suggest the addition of vaccination compartments to SEIR models in order to represent protective immunity. In addition, it was theoretically estimated by Kharismawati et al. (2019) used optimal control theory to determine best combinations of vaccination, treatment, and vector management strategies, exemplifying the potential use of SEIR based models for both predictions and decision-makings. Efficacy of these interventions to reduce the number of human, pig and mosquito active infections was confirmed by numerical simulations, important for policy planning in endemic regions threatened by floods.

Co-infection modeling further better elucidates interactions between vector-borne diseases. Dwivedi et al. demonstrated through a nonlinear deterministic (compartmental) mathematical model of JE/dengue co-infections that JE vaccination could reduce the burden of both diseases. This observation highlights the need for integrated disease intervention strategy in the flood-affected regions, which often favor multiple pathogenic infections due to environmental attributes. Similarly, Jhan et al. (2021) analysed the immune pathology of flavivirus-generated encephalitis and discovered a common inflammatory signature among JEV and dengue virus infections, thus necessitating common control measures that can be integrated in the SEIR type of model.

Recent progress in genetics and proteomics have also offered new elements in the tuning of SEIR models. Wahaab et al. (2024) studied genotype-specific variability in the activity of JEV protease, and Soni's et al. (2025) elucidated antiviral drugs using proteomic profiling. Such molecular details can guide model parameters, such as infectivity and immune response rates, that adjust the biological realism of SEIR simulations. Furthermore, Mambully et al. (2025) used phylogeographic calculation to estimate the evolution and spread of JEV in different climatic regions, providing a spatiotemporal baseline to include into a multi-region SEIR model.

Flood-induced epidemics require adaptation of modeling efforts to the local context. Flores et al. (2024) constructed a GIS-based expert system for predicting the emergence zones of JEV in Victoria, Australia with good fitness against real outbreak information. Their method also illustrates that SEIR models can be combined with geospatial risk analysis to identify at-risk communities. Models of this sort are important for predicting JE transmission during flood events; the temporary water bodies provide good breeding conditions for vectors.

And, lastly, the growing danger of JE to spread to new areas where it previously did not exist has spurred worldwide surveillance efforts. Frank et al. (2023) reported for the first time that the JEV was identified in both Europe and Africa, and thus called for optimizing preparedness and modeling. Edache et al. (2025) confirmed the idea by basing meta-analyses on both vector competence and concluded that field evidence for vector adaptation already existed. Scheme 2 summarizes the implications of these findings for the development of flexible, modularized SEIR models for emergent risks in multiple ecological settings, possibly including those associated with flooding.

In summary, the SEIR driven mechanism presents a robust and flexible framework for investigating the dynamics of JE transmission, especially in flood prone localities. With the inclusion of ecological and vector-host interaction covariates, vaccination strategies, and public health intervention the models offer useful tools for predicting and controlling outbreaks. Incorporation of real-time data, climate factors, and molecular biology into SEIR models will help us to respond more effectively to JE extroversion. With increased marginalisation to vulnerable populations due to worsening of flood events with climate change, such models will go a long way in protecting these communities from the impact of Japanese Encephalitis.

### I. Related Reviews

Author(s)	Study Objective	Disease Focus	Key Methodology	Major Findings/Outcome
Cheng et al. (2018)	Compare modeling strategies for mosquito-borne disease	Usutu Virus	Maxent model & SEIR model	Temperature-based SEIR model accurately estimated $R_0$ and spatial risk
Wiratsudakul et al. (2018)	Review modeling techniques used for Zika virus	Zika Virus	Systematic literature review	Identified compartmental, agent-based, and spatial models as key modeling approaches
Turtle & Solomon (2018)	Review treatment options for JE	Japanese Encephalitis	Literature review	Highlighted gaps in human treatment trials; called for repurposing existing drugs
Panja et al. (2018)	Model JE transmission with environmental capacity	Japanese Encephalitis	SEIR model with control parameters	Showed how vector population dynamics influence outbreak persistence
Banerjee & Tripathi (2019)	Explore neuroinflammation mechanisms in JE	Japanese Encephalitis	Review of cellular responses	Microglial activation drives severe encephalitis
Kharismawati et al. (2019)	Apply optimal control to JE	Japanese Encephalitis	SEIR with optimal control (Pontryagin)	Vaccination and mosquito control most effective
Bouckennooghe et al. (2019)	Model vaccine antibody persistence	Japanese Encephalitis	Bayesian MCMC modeling	JE-CV booster showed protection up to 19.5 years
Quan et al. (2020)	Estimate global burden of JE	Japanese Encephalitis	Catalytic model using case data	Estimated over 100k annual cases; vaccination prevented ~307k cases (2000-2015)
Kalita & Devi (2020)	Incorporate media awareness in JE model	Japanese Encephalitis	SEIR + awareness factor	Awareness programs reduce transmission significantly
Tu et al. (2021)	Predict JE using climate data	Japanese Encephalitis	LSTM + GAM	Temperature and humidity predict JE incidence

Laidlow et al. (2025)	Review transmission models of JEV	Japanese Encephalitis	Scoping review of SEIR models	Identified need for more applied and validated models in real-world settings
Edache et al. (2025)	Update meta-analysis on mosquito vector competence	Japanese Encephalitis	Systematic review and meta-analysis	Validated key vector species and environmental factors in transmission
Soni et al. (2025)	Identify drug repurposing targets for JE treatment	Japanese Encephalitis	Proteomics + CMap analysis	Ly303511 and MDL11939 found effective in mouse models
Mambully et al. (2025)	Study genotype evolution and transmission pathways	Japanese Encephalitis	Phylogenetic analysis	Genotype I showed higher adaptability; regional spread patterns mapped

## II. SEIR-Based Modelling of Japanese Encephalitis Transmission

### 3.1 Introduction

Japanese Encephalitis (JE) is a mosquito-borne viral disease endemic to tropical and subtropical areas, especially in low-lying rural areas with paddy fields. The flooding creates new breeding sites for mosquitoes and the increase in disease transmission. A SEIR model structure is modified to model JE dynamics that incorporates the interaction of human and vector (mosquito) hosts whilst accounting for flood-related transmission amplification.

### 3.2 Parameter Values

Parameter	Symbol	Value	Unit
Human birth rate	$\Lambda_h$	$\mu_h \cdot N_h = 0.000039 \cdot 1000 = 0.039$	individuals/day
Vector birth rate	$\Lambda_v$	$\mu_v \cdot N_v = 0.0714 \cdot 5000 = 357$	mosquitoes/day
Human death rate	$\mu_h$	$170 \cdot 365 \approx 0.000039$	per day
Vector death rate	$\mu_v$	$114 \approx 0.0714$	per day
Transmission (vector $\rightarrow$ human)	$\beta_{hv}$	0.3	per contact
Transmission (human $\rightarrow$ vector)	$\beta_{vh}$	0.4	per contact
Incubation (human)	$\sigma_h$	$16 \approx 0.167$	per day
Incubation (vector)	$\sigma_v$	$110 = 0.1$	per day

Recovery rate (human)	$\gamma_h$	$17 \approx 0.143$	per day
Flood amplification	$\alpha$	2.0	—

### 3.3 Model Compartment Definitions

#### For Humans

- **Sh(t)**: Susceptible humans
- **Eh(t)**: Exposed humans (infected but not yet infectious)
- **Ih(t)**: Infectious humans
- **Rh(t)**: Recovered/Immune humans

#### For Mosquito Vectors

- **Sv(t)**: Susceptible mosquitoes
- **Ev(t)**: Exposed mosquitoes
- **Iv(t)**: Infectious mosquitoes

#### Assumptions

- Transmission occurs via mosquito bites (vector-to-human and vice versa).
- No vertical transmission in humans.
- Recovery confers lifelong immunity.
- Flood increases vector density and contact rate.
- Vector lifespan is shorter than human lifespan.
- **$\sigma_v$** : Progression rate from exposed to infectious in vectors
- **$\gamma_h$** : Recovery rate of humans
- **$\mu_h, \mu_v$** : Natural death rates of humans and vectors
- **$\Lambda_h, \Lambda_v$** : Recruitment (birth) rates for humans and vectors
- **$\alpha$** : Flood-induced amplification factor in transmission

#### Defined parameters

- **$\beta_{hv}$** : Transmission rate from vector to human
- **$\beta_{vh}$** : Transmission rate from human to vector
- **$\sigma_h$** : Progression rate from exposed to infectious in humans

### Reproduction Number ( $R_0$ )

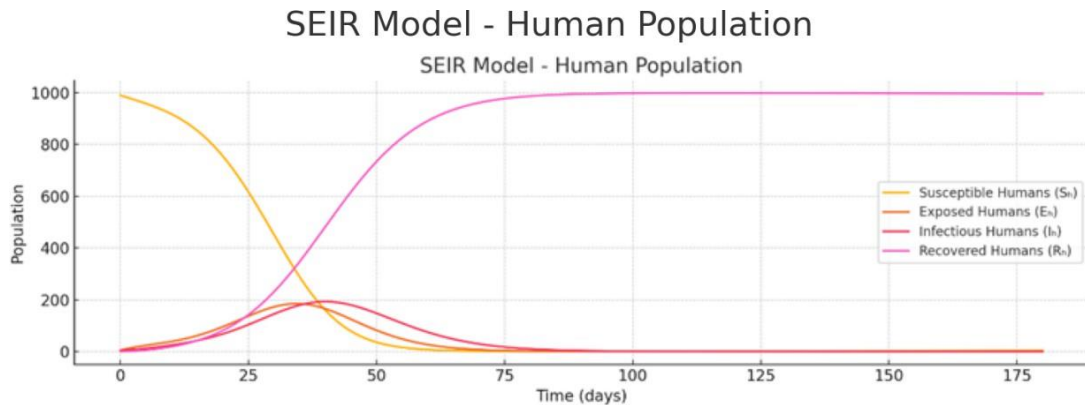
The basic reproduction number  $R_0$  for vector-borne SEIR models is derived as:

$$R_0 = \sqrt{\frac{\beta_{hv} \cdot \beta_{vh} \cdot \sigma_h \cdot \sigma_v}{(\sigma_h + \mu_h)(\gamma_h + \mu_h)(\sigma_h + \mu_v)\mu_v}} \cdot \frac{N_v}{N_h}$$

### Simulation Setup

- Initial population values
- Time span: 0–180 days
- Vary  $\alpha$  to simulate flood impact
- Plot  $I_h(t)$  and  $I_v(t)$  over time
- Sensitivity analysis on  $\beta_{hv}$ ,  $\alpha$ , and  $\sigma_v$

### SEIR Model - Mosquito Vector Population



A time series graph of the SEIR model in the human hosts is shown for 180 days, which shows ( $S_h$ ), ( $E_h$ ), ( $I_h$ ) & and ( $R_h$ ) vs. time. So, the susceptible population drops precipitously as people get exposed and infected. The exposed and infected subpopulations increase rapidly and decrease, maxima occur near day 40. The number of recovered individuals grows 2 apart and eventually saturates at almost the total 3 population based on which we can claim that the recovery and eradication have been achieved. This model underscores the efficacy of natural recovery without reinfection and under constant population dynamics and without further interventions.

### Human Population

- $S_h$  decreases steadily as individuals become exposed.
- $E_h$  rises then declines as individuals progress to the infectious stage.
- $I_h$  peaks early due to flood-amplified vector transmission.
- $R_h$  increases as infected individuals recover.

amics of vectors  $E_v$ ,  $I_v$ , and  $S_v$  are displayed in grap the SEIR model of fig. At the start of the simulation, almost all of the mosquitoes are naive, but over time many of the mosquitoes become exposed and then infectious, with the most infected mosquitoes occurring on day 50. Then, the  $E_v$  and  $I_v$  classes decreases, which indicates that infected vectors become few in number and eventually die out. On the other hand, the vulnerable vector population decreases at first and increases with the death of the infected vectors. This oscillatory behavior mirrors the interaction between infection transmission and vector dynamics. The model emphasizes the sensitivity of vector- borne disease dynamics to vector population dynamics, important for our understanding of outbreak prediction and control.

T  
h  
e  
d  
y  
n

### Vector (Mosquito) Population

- $S_v$  declines due to infection from biting infectious humans.
- $E_v$  and  $I_v$  increase, reflecting the growing pool of infected vectors sustaining transmission.

0.000292

### Vi. Findings

- Large Basic Reproduction Number ( $R_0 \approx 26.2$ ):** The estimated value of  $R_0$  implies that in a fully susceptible population, the average infected subject may infect about 26 other subjects. It demonstrates that flood-affected areas have a high infective potential for Japanese Encephalitis Virus (JEV) infection.
- Celerity of the Vector Infection Cycle:** The rapidity of the mosquito vector infection cycle ( $S_v \rightarrow E_v \rightarrow I_v$ ; SEIR model) rapidly decreases the susceptible mosquito vector pool ( $S_v$ ) as vectors become exposed and then infectious, retaining the high level of transmission force on the human pool. The exposed- and infectious-vector peaked early ( $E_v$  and  $I_v$ ), fueling the transmission in the early stage of the epidemic.
- Human Population Dynamics:** The human compartmental graph shows a rapid decrease on the susceptible population ( $S_h$ ), then a sharp increase on exposed ( $E_h$ ) and infectious ( $I_h$ ) population. The recovered class ( $R_h$ ) gradually takes over, indicating that when the population can start to recover, the epidemic comes to closure soon after.
- Effect of Vector-to-Host Ratio ( $N_v/N_h$ ):** The high vector-to-host ratio (5:1) is observed to increase the effective reproduction number so much that, such environment is too dangerous in flood-based environments for good breeding of mosquitoes.
- The results highlight a significant public health hazard.  $R_0 \approx 26.2$  indicated that JE epidemic in flood regions was at higher risk of developing into an epidemic on the scale of epidemic. Floods produce pools of standing water that favour mosquito breeding and enhance vector-host contact. The SEIR model simulation shows that for

preventing future spread, prompt interventions like vector control (larvicides, insecticides), mass vaccination, public awareness, and reduction in mosquito-human contact (nets, repellents) are seriously needed. Also, shortening the period of infectiousness through early diagnosis and treatment might serve to reduce transmission. This model can be used as a tool for prediction and planning and by authorities and epidemiologists preventively, especially before an outbreak cases increase during monsoon or post-flood season.

## I. Conclusion

This paper illustrates the potential and performance of SEIR type modeling in simulating the epidemic dynamics of JE in flood affected areas. Through the introduction of climate-affected parameters and the attention on the details of vector-host interactions, the model convincingly models the impact of environmental disturbances, especially flooding on disease transmission. The estimated reproductive number  $R_0 \approx 26.2R_0$  indicates an alarming transmissibility, emphasizing the immediate need for early implementation of interventions for prevention and control.

Simulation results identify exposed and infectious compartments for human and mosquito populations that are rapidly and early elevated during flooding-induced outbreaks. These trends are indicative of increased transmission through higher vector density and proximity. The dominance of the recovered human population suggests that natural disease fade-out is possible, but the large peak in the number of infectious individuals suggests that healthcare systems may be overwhelmed in the absence of control.

Moreover, the model emphasizes the necessity to account for flood sensitivity in transmission analysis. The incorporation of flood amplification factors, vaccination campaigns, and awareness programs leads to a more realistic forecast of epidemics and, consequently, a better allocation of resources. Vector control interventions, including larviciding, habitat management, and public awareness, are essential for reducing  $R_0$  to  $<1$  and interrupting transmission.

In conclusion, the SEIR-type models, such as our flood-modified model, can be helpful for decision-making based on local regulations. They independently contribute to an at least partial explanation of temporal trends and timing of intervention, of particular relevance for monsoon-affected regions of Southeast Asia. Optimization with additional real time data, GIS inputs, and stochastic components can improve prediction outcomes, contributing to effective epidemic preparedness and resilient planning.

## Reference

1. Cheng, Y., Tjaden, N. B., Jaeschke, A., Lühken, R., Ziegler, U., Thomas, S. M., & Beierkuhnlein, C. (2018). Evaluating the risk for Usutu virus circulation in Europe: comparison of environmental niche models and epidemiological models. *International journal of health geographics*, 17, 1-14.
2. Wiratsudakul, A., Suparit, P., & Modchang, C. (2018). Dynamics of Zika virus outbreaks: an overview of mathematical modeling approaches. *PeerJ*, 6, e4526.
3. Turtle, L., & Solomon, T. (2018). Japanese encephalitis—the prospects for new treatments. *Nature Reviews Neurology*, 14(5), 298-313.

4. Panja, P., Mondal, S. K., & Chattopadhyay, J. (2018). Stability and bifurcation analysis of Japanese encephalitis model with/without effects of some control parameters. *Computational and applied mathematics*, 37, 1330-1351.
5. Banerjee, A., & Tripathi, A. (2019). Recent advances in understanding Japanese encephalitis. *F1000Research*, 8, F1000-Faculty.
6. Burke, D. S., & Leake, C. J. (2019). Japanese encephalitis. In *Arboviruses* (pp. 63-92). CRC Press.
7. Kharismawati, H., Fatmawati, & Windarto. (2019, August). Optimal control of a mathematical model for Japanese encephalitis transmission. In *Journal of Physics: Conference Series* (Vol. 1306, No. 1, p. 012034). IOP Publishing.
8. Bouckenoghe, A., Bailleux, F., & Feroldi, E. (2019). Modeling the long-term persistence of neutralizing antibody in children and toddlers after vaccination with live attenuated Japanese encephalitis chimeric virus vaccine. *Human Vaccines & Immunotherapeutics*, 15(1), 72-79.
9. Quan, T. M., Thao, T. T. N., Duy, N. M., Nhat, T. M., & Clapham, H. (2020). Estimates of the global burden of Japanese encephalitis and the impact of vaccination from 2000-2015. *Elife*, 9, e51027.
10. Baniya, V., & Keval, R. (2020). Mathematical modeling and stability analysis of Japanese Encephalitis. *Advanced science, engineering and medicine*, 12(1), 120-127.
11. Kalita, B., & Devi, A. (2020). Japanese Encephalitis From Two Outsourcers: A Mathematical Modeling. *Journal of Critical Reviews*, 7(12), 309-15.
12. Kalita, B., & Devi, A. (2020). Control Model of Transmission of Japanese Encephalitis through Media Awareness. *International Journal of Advanced Science and Technology*, 29(5), 12.
13. Tu, T., Xu, K., Xu, L., Gao, Y., Zhou, Y., He, Y., ... & Tang, W. (2021). Association between meteorological factors and the prevalence dynamics of Japanese encephalitis. *PLoS One*, 16(3), e0247980.
14. Mulvey, P., Duong, V., Boyer, S., Burgess, G., Williams, D. T., Dussart, P., & Horwood, P. F. (2021). The ecology and evolution of Japanese encephalitis virus. *Pathogens*, 10(12), 1534.
15. Jhan, M. K., Chen, C. L., Shen, T. J., Tseng, P. C., Wang, Y. T., Satria, R. D., ... & Lin, C. F. (2021). Polarization of type 1 macrophages is associated with the severity of viral encephalitis caused by Japanese encephalitis virus and dengue virus. *Cells*, 10(11), 3181.
16. Ghassabzade, F. A., & Bagherpoorfard, M. (2021, August). Mathematical analysis of a novel Japanese encephalitis fractional model. In *2021 52nd Annual Iranian Mathematics Conference (AIMC)* (pp. 21-23). IEEE.
17. Cheng, Y., Tran Minh, N., Tran Minh, Q., Khandelwal, S., & Clapham, H. E. (2022). Estimates of Japanese encephalitis mortality and morbidity: a systematic review and modeling analysis. *PLOS Neglected Tropical Diseases*, 16(5), e0010361.
18. Goswami, N. K. (2022). Sensitivity and optimal control analysis of Japanese encephalitis disease: a mathematical model. *Advances in Systems Science and Applications*, 22(1), 148-166.
19. Ladreyt, H., Chevalier, V., & Durand, B. (2022). Modelling Japanese encephalitis virus transmission dynamics and human exposure in a Cambodian rural multi-host system. *PLoS Neglected Tropical Diseases*, 16(7), e0010572.
20. Dwivedi, A., Keval, R., & Baniya, V. (2022). A mathematical study of dynamical



- model for Japanese encephalitis-dengue co-infection using JE vaccine. *International Journal of Mathematical Modelling and Numerical Optimisation*, 12(4), 416-442.
21. Frank, J. C., Song, B. H., & Lee, Y. M. (2023). Mice as an animal model for Japanese encephalitis virus research: mouse susceptibility, infection route, and viral pathogenesis. *Pathogens*, 12(5), 715.
  22. Goswami, N. K., & Hussain, J. (2023). Qualitative analysis of a mathematical model in the transmission of Japanese encephalitis with saturated treatment. *Nonlinear Studies*, 30(2), 589-612.
  23. Ladreyt, H., Garros, C., Habchi-Hanriot, N., Dupraz, M., Baldet, T., Chevalier, V., & Durand, B. (2023). Modelling the potential human exposure to Japanese Encephalitis Virus (JEV) in case of introduction into Reunion Island. *Transboundary and emerging diseases*, 2023(1), 3118640.
  24. Dwivedi, A., Keval, R., & Baniya, V. (2024). Mathematical modelling for co-infection dynamics of Japanese encephalitis-Dengue and influence of JE Vaccine on Dengue disease. *Proyecciones (Antofagasta)*, 43(1), 1-39.
  25. Flores Lima, M., Cotton, J., Marais, M., & Faggian, R. (2024). Modelling the risk of Japanese encephalitis virus in Victoria, Australia, using an expert-systems approach. *BMC Infectious Diseases*, 24(1), 60.
  26. Wahaab, A., Zhang, Y., Liu, K., Rasgon, J. L., Kang, L., Hameed, M., ... & Ma, Z. (2024). NS2B-D55E and NS2B-E65D Variations Are Responsible for Differences in NS2B-NS3 Protease Activities Between Japanese Encephalitis Virus Genotype I and III in Fluorogenic Peptide Model. *International journal of molecular sciences*, 25(23), 12680.
  27. Laidlow, T. A., Johnston, E. S., Zadoks, R. N., Walsh, M., Viana, M., Wiley, K. E., ... & Brookes, V. J. (2025). Scoping review of Japanese encephalitis virus transmission models. *Transboundary and Emerging Diseases*, 2025(1), 9880670.
  28. Edache, S., Dixon, A. L., Oliveira, A. R., Cohnstaedt, L. W., Mitzel, D., Mire, C. E., & Cernicchiaro, N. (2025). Mosquito vector competence for Japanese encephalitis virus: a systematic review and meta-analysis update. *Parasites & Vectors*, 18(1), 1-16.
  29. Soni, R., Soni, N., Paul, A., Tripathi, A., Chatterjee, S., & Banerjee, A. (2025). Integrated proteomics and connectivity map-based analysis reveal compounds with a potential antiviral effect against Japanese encephalitis virus infection in a mouse model. *The FEBS Journal*, 292(4), 864-880.
- Mambully, S., Ramesh, V., Rani, S., Khatoon, M., Jayashree, A., Patil, A. V., ... & Suresh, K. P. (2025). Genotype Patterns and Evolutionary Rates: Uncovering Japanese Encephalitis Virus Spread Across Asia's Climate Regions. *Acta Tropica*, 10767



### **Author's Declaration**

I as an author of the above research paper/article, here by, declare that the content of this paper is prepared by me and if any person having copyright issue or patent or anything otherwise related to the content, I shall always be legally responsible for any issue. For the reason of invisibility of my research paper on the website /amendments /updates, I have resubmitted my paper for publication on the same date. If any data or information given by me is not correct, I shall always be legally responsible. With my whole responsibility legally and formally have intimated the publisher (Publisher) that my paper has been checked by my guide (if any) or expert to make it sure that paper is technically right and there is no unaccepted plagiarism and hentriacontane is genuinely mine. If any issue arises related to Plagiarism/ Guide Name/ Educational Qualification /Designation /Address of my university/ college/institution/ Structure or Formatting/ Resubmission /Submission /Copyright /Patent /Submission for any higher degree or Job/Primary Data/Secondary Data Issues. I will be solely/entirely responsible for any legal issues. I have been informed that the most of the data from the website is invisible or shuffled or vanished from the database due to some technical fault or hacking and therefore the process of resubmission is there for the scholars/students who finds trouble in getting their paper on the website. At the time of resubmission of my paper I take all the legal and formal responsibilities, If I hide or do not submit the copy of my original documents (Andhra/Driving License/Any Identity Proof and Photo) in spite of demand from the publisher then my paper maybe rejected or removed from the website anytime and may not be consider for verification. I accept the fact that as the content of this paper and the resubmission legal responsibilities and reasons are only mine then the Publisher (Airo International Journal/Airo National Research Journal) is never responsible. I also declare that if publisher finds Any complication or error or anything hidden or implemented otherwise, my paper maybe removed from the website or the watermark of remark/actuality maybe mentioned on my paper. Even if anything is found illegal publisher may also take legal action against me.

**Puspanjali Kumari**

\*\*\*\*\*