

# Mathematical Model for Spatial and Temporal Risk Analysis of West Nile Virus Transmission in Bavaria, Germany

Oliver Chinonso Mbaoma<sup>1\*</sup>, Stephanie Margarete Thomas<sup>1,2</sup>, Carl Beierkuhnlein<sup>1,2,3</sup>

<sup>1</sup>Department of Biogeography, University of Bayreuth, Universitaetsstr. 30, 95447 Bayreuth, Germany;

\**oliver.mbaoma@uni-bayreuth.de*

<sup>2</sup>Bayreuth Center of Ecology and Environmental Research, BayCEER, University of Bayreuth, Universitaetsstr. 30, 95447 Bayreuth, Germany

<sup>3</sup>Geographical Institute of the University of Bayreuth, GIB, Universitaetsstr. 30, 95447 Bayreuth, Germany

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**Abstract.** The spatial and temporal trends of mosquito-borne diseases have been shifting. Recently, there has been an increase in cases of West Nile Fever across Germany. In this study, we investigated the spatial and temporal risk of West Nile virus transmission in Bavaria using a mathematical model. The model incorporated epidemiological, climatic, and bird distribution data. It generated spatially and temporally explicit graphs depicting the health states of mosquitoes and birds. Additionally, we produced risk maps identifying areas in Bavaria at heightened risk for West Nile virus transmission.

## Introduction

West Nile fever is an illness triggered by West Nile virus (WNV), a single strand RNA arbovirus from the Flaviviridae family and one of the most widely spread flaviviruses [1]. In 1937, the first case was isolated at West Nile district in Uganda and has since been occurred in all continents [2]. Although WNV normally circulates in a sylvatic cycle between mosquitoes and birds as hosts, mosquitoes can also spread the virus to humans and animals, including horses [2],[3]. Most of these animals and humans only experience mild viremia and are unable to serve as amplifying hosts for the virus [4]. In 2018, the virus was for the first time detected in 12 birds and 2 horses in eastern Germany [5]. The first human autochthonous case of the infection was detected in 2019 near Leipzig [6]. Suitable climatic conditions with high temperatures in summer was suspected to promote the spread of the virus.

While mosquitoes tend to spread the virus locally, migratory birds are suspected to play a role in disseminating the virus over long distances to new areas [5].

With information on bird surveillance for WNV, competence of vector mosquitoes and amplification suitability of hosts, we were able to develop a climate-driven process-based mechanistic model calibrated with functional traits of vector mosquito and host birds to predict the spatial and temporal risk of WNV infection in Bavaria.

## 1 Materials and Method

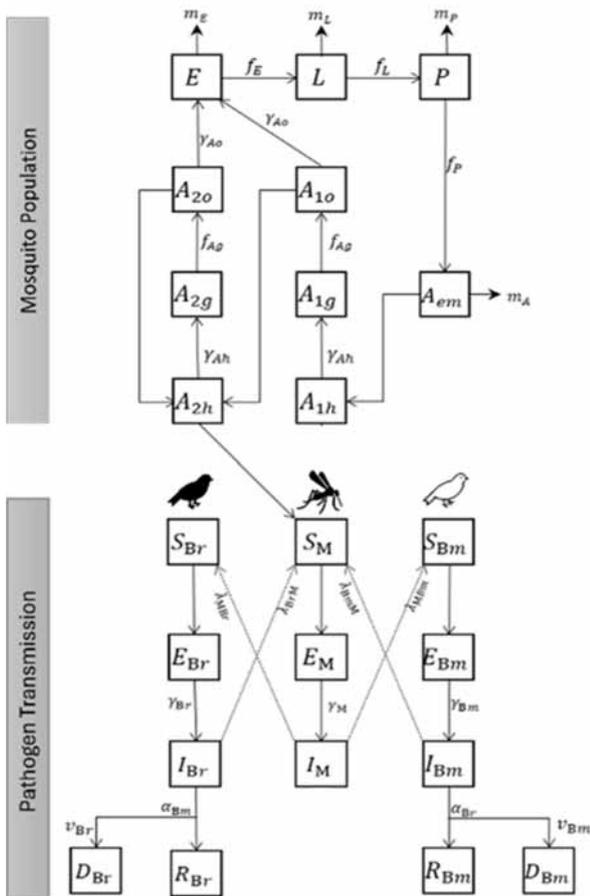
We adopted a similar approach applied to show the spatial and temporal pattern of WNV infection in Germany between 2018 and 2022 by Mbaoma et al, [7]. We applied the model in Bavaria and accounted for mosquito population, pathogen transmission in migratory and residential birds.

### 1.1 Materials

Climate and bird data were used to parameterize and force the model adequately. Cases of WNV infection were collected from the Animal Diseases Information System database of the FLI from 2018 to 2022 [5]. Bird distribution data was collected from E-bird online database [8]. Temperature, rainfall and humidity data used to drive our model were collected from E-OBS database [9].

### 1.2 Model Description

With a clear understanding of the entomology, life characteristics, and functional ecology of both the WNV vector and its hosts, we used the mechanistic approach which was developed by Mbaoma et al., 2024 [7] to generate spatial and temporal predictions of potential WNV infection outbreak in Bavaria.



**Figure 1:** WNV epidemic model showing two sections depicting mosquito population and pathogen transmission between mosquito, resident bird and migratory bird with compartments:

- Eggs ( $E$ ), Larvae ( $L$ ), Pupa ( $P$ ), New adults ( $A_{em}$ ),
- Host-seeking adults ( $A_{1h}$ ), Gravid adults ( $A_{1g}$ ),
- Ovipositioning adults ( $A_{1o}$ ),
- Older host-seeking adults ( $A_{2h}$ ),
- Older gravid adults ( $A_{2g}$ ), Older ovipositioning adults ( $A_{2o}$ ),
- Susceptible mosquitoes ( $S_M$ ), Exposed mosquitoes ( $E_M$ ),
- Infected mosquitoes ( $I_M$ ),
- Susceptible residential birds ( $S_{Br}$ ),
- Susceptible migratory bird ( $S_{Bm}$ ),
- Exposed residential birds ( $E_{Br}$ ),
- Exposed migratory birds ( $E_{Bm}$ ),
- Infected residential birds ( $I_{Br}$ ),
- Infected migratory birds ( $I_{Bm}$ ),
- Removed residential birds ( $R_{Br}$ ),
- Removed migratory birds ( $R_{Bm}$ ),
- ..Dead residential birds ( $D_{Br}$ ),
- Dead migratory birds ( $D_{Bm}$ ).

Mathematical epidemiology and population biology were used to formulate the fundamentals of the compartmental model driven by several ordinary differential equations. The model consists of two sections: the first describing mosquito population while the second described pathogen transmission.

As described in the paper by Mbaoma et al. [7], disease-free mosquito population was explained by the several equations.

$$\begin{cases}
 \dot{E} = d\gamma_{Ao}(\beta_1 A_{1o} + \beta_2 A_{2o}) - (\mu_E + df_E)E \\
 \dot{L} = df_E E - (m_L(1 + L/k_L) + f_L)L \\
 \dot{P} = f_L L - (m_P + f_P)P \\
 \dot{A}_{em} = f_P P \sigma e \left( -\mu_{em} \left( 1 + \frac{P}{k_P} \right) \right) - (m_A + \gamma_{Aem})A_{em} \\
 \dot{A}_{1h} = \gamma_{Aem} A_{1h} - (m_A + \mu_r + \gamma_{Ah})A_{1h} \\
 \dot{A}_{1g} = \gamma_{Ah} A_{1h} - (m_A + \mu_{pr} + f_{Ag})A_{1g} \\
 \dot{A}_{1o} = f_{Ag} A_{1g} - (m_A + \mu_r + f_{Ao})A_{1o} \\
 \dot{A}_{2h} = f_{Ao} (A_{1o} + A_{2o}) - (m_A + \mu_r + \gamma_{Ah})A_{2h} \\
 \dot{A}_{2g} = \gamma_{Ah} A_{2h} - (m_A + \mu_{pr} + f_{Ag})A_{2g} \\
 \dot{A}_{2o} = f_{Ag} A_{2g} - (m_A + \mu_r + f_{Ao})A_{2o}
 \end{cases} \tag{1}$$

The process of infection between mosquito and bird population is explained by the following sets of Ordinary differential equations, with Equation 2,3 and 4 explaining health states of mosquitoes, migratory birds and residential birds respectively.

$$\begin{aligned}
 \frac{dS_M}{dt} &= -(\lambda_{BrM}(T) + \lambda_{BmM}(T))S_M + A_{2h} - m_A(T)S_M \\
 \frac{dE_M}{dt} &= (\lambda_{BrM}(T) + \lambda_{BmM}(T))S_M - \gamma_M(T)E_M - m_A(T)E_M
 \end{aligned} \tag{2}$$

$$\begin{aligned}
 \frac{dI_M}{dt} &= \gamma_M(T)E_M - m_A(T)I_M \\
 \frac{dS_{Br}}{dt} &= \left( b_{Br} - (b_{Br} - m_{Br}) \frac{N_{Br}}{K_{Br}} \right) N_{Br} - \lambda_{MBr}(T)S_{Br} - m_{Br}S_{Br} \\
 \frac{dE_{Br}}{dt} &= \lambda_{MBr}(T)S_{Br} - \gamma_{Br}E_{Br} - m_{Br}E_{Br}
 \end{aligned} \tag{3}$$

$$\begin{aligned}
 \frac{dI_{Br}}{dt} &= \gamma_{Br}E_{Br} - \alpha_{Br}I_{Br} - m_{Br}I_{Br} \\
 \frac{dR_{Br}}{dt} &= (1 - v_{Br})\alpha_{Br}I_{Br} - m_{Br}R_{Br} \\
 \frac{dD_{Br}}{dt} &= v_{Br}\alpha_{Br}I_{Br}
 \end{aligned}$$

$$\begin{aligned} \frac{dS_{Bm}}{dt} &= \left( b_{Bm} - (b_{Bm} - m_{Bm}) \frac{N_{Bm}}{K_{Bm}} \right) N_{Bm} - \lambda_{MBm}(T) S_{Bm} - m_{Bm} S_{Bm} \\ \frac{dE_{Bm}}{dt} &= \lambda_{MBm}(T) S_{Bm} - \gamma_{Bm} E_{Bm} - m_{Bm} E_{Bm} \\ \frac{dI_{Bm}}{dt} &= \gamma_{Bm} E_{Bm} - \alpha_{Bm} I_{Bm} - m_{Bm} I_{Bm} \\ \frac{dR_{Bm}}{dt} &= (1 - v_{Bm}) \alpha_{Bm} I_{Bm} - m_{Bm} R_{Bm} \\ \frac{dD_{Bm}}{dt} &= v_{Bm} \alpha_{Bm} I_{Bm} \end{aligned} \tag{4}$$

Cross infection between mosquitoes and amplifying hosts which are birds of interest was defined in Equations 5 to 8.

$$\lambda_{MBr}(T) = \delta_M F_b k(T) p_{MBr} \phi_{Br} \frac{I_M}{K_M} \tag{5}$$

$$\lambda_{MBm}(T) = \delta_M F_b k(T) p_{MBm} \phi_{Bm} \frac{I_M}{K_M} \tag{6}$$

$$\lambda_{BrM}(T) = \delta_M F_b k(T) p_{BrM} \frac{I_{Br}}{K_{Br}} \tag{7}$$

$$\lambda_{BmM}(T) = \delta_M F_b k(T) p_{BmM} \frac{I_{Bm}}{K_{Bm}} \tag{8}$$

Basic reproductive number was computed based on the next-generation matrix approach applied in the precursor model by Mbaoma et al [7] using the equation below:

$$R_0 = \sqrt{\left[ \frac{\gamma_M(T) \beta_{Mbr}(T) + \beta_{Mbm}(T)}{(\gamma_M(T) + m_M(T)) m_M(T)} \left( \frac{S_{Br}}{K_{Br}} + \frac{S_{Bm}}{K_{Bm}} \right) \right] + \left[ \frac{\gamma_{Br} \beta_{Br}(T)}{(\gamma_{Br} + m_{Br})(\alpha_{Br} + m_{Br}) K_{Br}} \frac{S_M}{K_{Bm}} \right] + \left[ \frac{\gamma_{Bm} \beta_{Bm}(T)}{(\gamma_{Bm} + m_{Bm})(\alpha_{Bm} + m_{Bm}) K_{Bm}} \frac{S_M}{K_{Bm}} \right]}$$

### 1.3 State Variables, Parameters and Functions.

All state variables, parameters and functions used to develop this model, including calibration and validation processes have been described in a precursor publication for WNV epidemic model by Mbaoma et al. [7].

## 2 Results and Discussion

### 2.1 WNV Transmission Risk Projection for Bavaria

The inverse calibrated WNV epidemic model generated spatial and temporal abundance of mosquito. It also generated different health states for hosts of interests which include residential birds and migratory birds.

Due to limited occurrence recorded in Bavaria (just one case), we assumed our model was performing at optimum having been previously validated across Germany [7].

Functional traits of mosquito which includes fecundity, development rates, mortality rates, biting rates and extrinsic incubation rates of WNV pathogen all responded to deviations in temperature [10],[11]. The model was able to simulate various health states of mosquito and birds, with seasonal variation in Bavaria. Susceptible and parous host-seeking mosquitoes are especially of interest for the transmission potential (Figure 2). Also, we were able to simulate risk maps of WNV transmission for Bavaria between 2017 and 2022 at NUTS3 levels, identifying potential hotspots for WNV infection outbreaks (Figure 3).

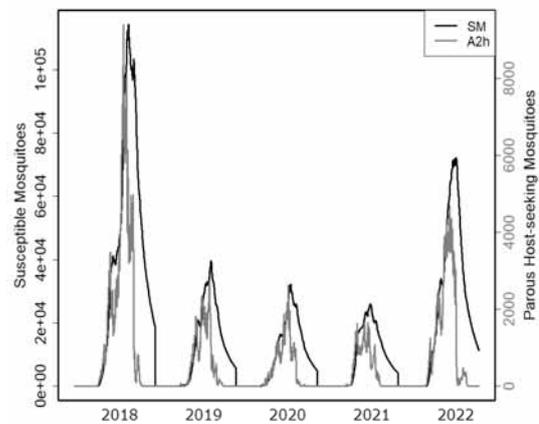
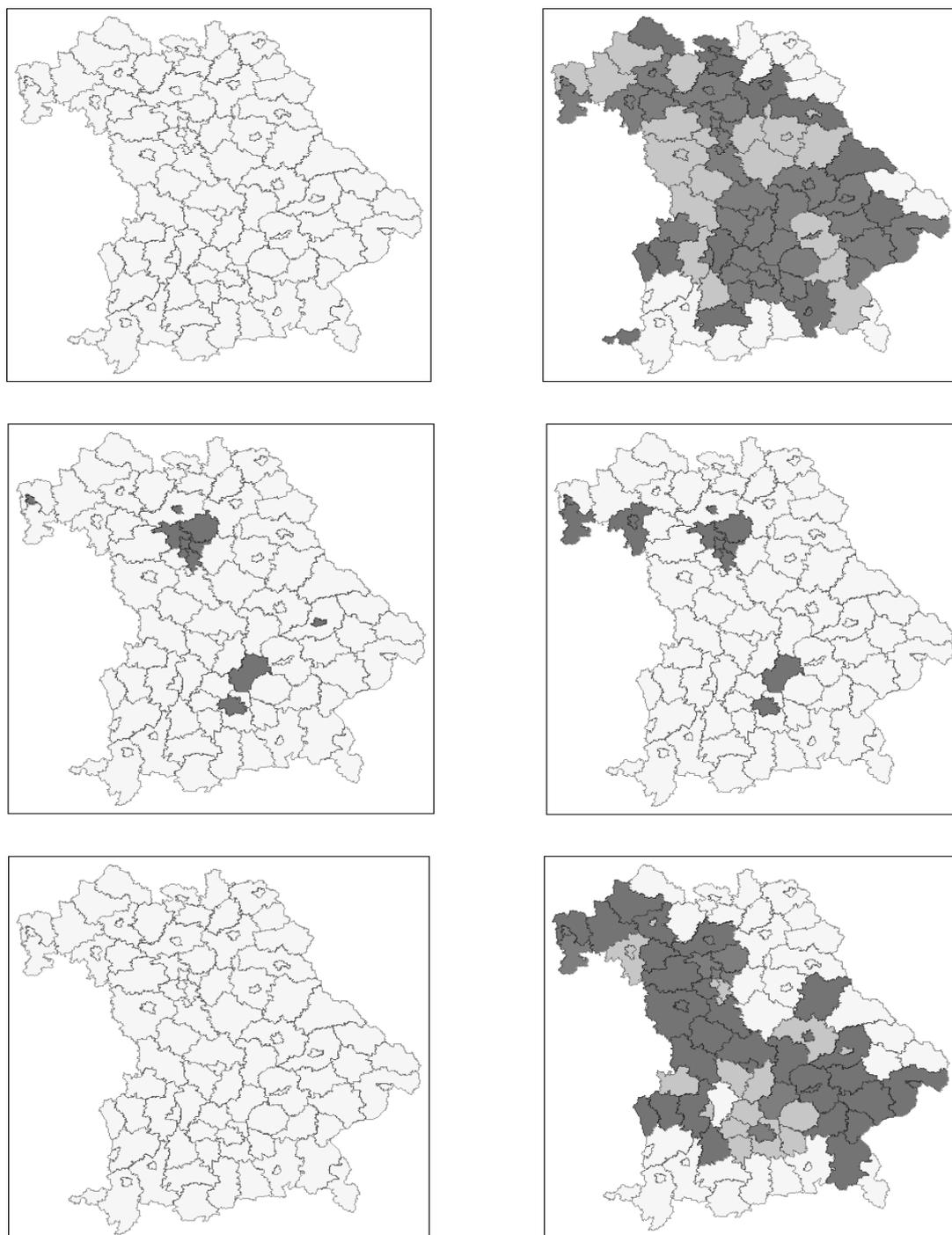


Figure 2: Simulated time series of health states for susceptible ( $S_M$ ) and parous host-seeking mosquitoes ( $A_{2h}$ ) between 2018 and 2022 in Bavaria.

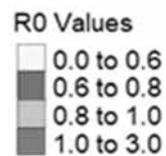
### 2.2 Seasonal Variation of WNV Infection Risk

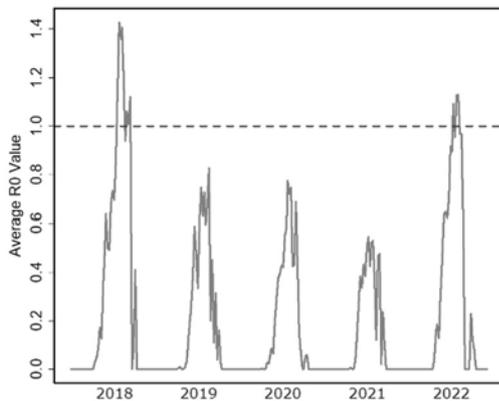
Several climate sensitive mosquito-borne diseases display seasonal variation [12]. In our model, several factors, including vector population, vectoral capacity, vector competence and amplifying host competence influenced  $R_0$  rates.

Infection parameters, such as mosquito biting rate and extrinsic incubation rate were important drivers which was consistent with the role of environmental suitability in driving infectious disease transmission [10]. The model reasonable simulates seasonal trend of  $R_0$  values. The  $R_0$  values averaged across Bavaria show a low risk of WNV transmission in 2018 and 2022 (Figure 4).



**Figure 3:** WNV transmission risk across Bavaria at NUT3 level from 2017 to 2022 estimated from daily R0 values between August and October (week 30 to 42) when the peak of the WNV infections were reported by FLI.





**Figure 4:** The risk of West Nile Virus (WNV) infection outbreaks, expressed as  $R_0$  values, was assessed across Bavaria from 2018 to 2022. The red line represents the simulated daily  $R_0$  values aggregated on a weekly basis, while the blue dashed horizontal line indicates the threshold at which secondary cases can be directly generated by the first case in a population where all individuals are susceptible to infection.

### 3 Conclusion

We developed a process based WNV epidemic model which was able to simulate areas prone to WNV transmission in Bavaria. From our results, it was obvious that WNV infection which is endemic in eastern Germany may likely spread to the South with several hotspots identified in Bavaria. Changing climate and migratory pattern of short distance migratory birds have been identified as key factors that could accelerate WNV infection spread. The model considered juvenile and adult stages of mosquito life cycle in several compartments, and two bird taxa with migratory and residential birds. Functional traits of mosquitoes were driven by climate. Host-feeding preference of vector, transmission probability and mosquito to host ratio were all accounted for in the model.

In addition, spatial heterogeneity of climate forcings, vectors and host species were considered. We developed a model that could be deployed at the backend of a warning system for *Culex pipiens* mosquito population occurrence and WNV transmission risk.

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