Explaining Environmental Distribution of *Aedes albopictus* using Machine Learning

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Abstract

The *Aedes albopictus* mosquito, known for its role in transmitting diseases such as dengue fever, Zika virus, and chikungunya, poses a significant public health threat globally. Understanding its distribution patterns is crucial for effective disease surveillance and control. This study employs machine learning techniques, specifically MaxEnt modeling, to elucidate the relationship between environmental factors and the distribution of *Aedes albopictus*. Using presence-only data and a suite of environmental variables, we trained MaxEnt models to predict the potential distribution of *Aedes albopictus* across a geographical region. The models were validated using independent datasets and evaluated for their predictive accuracy and robustness. Our results reveal significant associations between *Aedes albopictus* presence and environmental factors such as temperature related variables. Furthermore, we employed spatial analysis techniques to identify areas at high risk of Aedes albopictus presence, aiding in targeted vector control strategies and disease prevention efforts. MaxEnt models demonstrated high predictive performance, effectively capturing the complex relationships between environmental variables and mosquito distribution in Nepal, India and Myanmar, along with Spain and Italy. By integrating machine learning algorithms with environmental data, this study provides valuable insights into the ecological drivers of *Aedes albopictus* distribution, enhancing our ability to mitigate the risk of mosquito-borne diseases in affected regions.

1. Introduction

Vector-borne diseases (VBDs) are continuously impacting the world health on annual basis accounting 17% of the global disease burden due to parasites (Townson et al., 2005), for example, 50-100 million dengue cases (WHO, 2009a) and 300 million malaria cases (WHO 2009b) are recorded every year worldwide. The VBDs pose great threat to human health and are important as they have ever impacted, especially in developing nations. The contributing factors responsible for exponential rise in such cases in recent years are sue to unplanned urbanization, commensalism with humans, globalization of travel and trade, and environmental changes such as biodiversity loss and deforestation. The transmission and outbreak of VBDs are complex cycles due to essential interaction between vectors, pathogens, animal hosts and humans under the prerequisite of environmental factors with spatial and temporal permutations. The pathogens within vectors are environmentally sensitive because they exhibit distinct seasonal and regional patterns. The vector survival and vectorial capacity is greatly influenced when they interact with humidity in certain temperatures. Similarly, precipitation and seasonality in an area strongly encouraged the availability of breeding sites for mosquitoes as well as other species having aquatic immature stages. The Intergovernmental Panel on Climate Change listed VBDs that are more prone to change due to climate change and climate variability (IPCC, 2007). Recent studies highlighted that climate change is one of the most influential factors in vector-borne disease epidemiology (Dobson and Carper, 1992; Martens 1998; Epstein, 2000; Paaijmans et al., 2010; Rohr et al., 2011). This could be understood through an example of arthropod vectors, who are ectothermic, so if temperature fluctuates then its development time will be directly affected which may change their reproduction, behaviour, and population dynamics. This calls for understanding the ecology of the habitats, breeding grounds, and vector behaviours. The key components of this global fight involve identifying, tracking, and assessing the environmental elements linked to vector-borne illnesses. In the past 20 years, there has been a significant advancement in the field of spatial technologies, enabling individuals to swiftly and accurately identify and track environmental targets at a wide scale, including certain vectors' habitats and breeding grounds. Spatial information technologies offer a novel and potent way to analyse and forecast the spatiotemporal patterns of vector-borne diseases when combined with other statistical analysis toolboxes and algorithms.

Machine learning algorithms have proven adept at unravelling the complex relationships between environmental conditions and the distribution of the vector species. In recent years, statistical algorithms are being used in two ways to model species-distribution – one that predicts distribution using both presence and absence data of species, and other one is based on presence-only data (Gormley et al., 2011; Witten et al., 2005). Maximum Entropy (Maxent) is one of the popular algorithm for species distribution modelling, since its publish in 2006 by Phillips (et al., 2006). This algorithm ensemble background data by accounting environmental factors across the given space and fitted highly complex responses (Elith et al., 2011; Peterson et al., 2011). Furthermore, the Maxent's ability is extended by mapping the limiting factor and surface-mapping for range-shifting of species (Elith et al., 2010). This paper is focussing on implementing Maxent algorithm on understanding the distribution responses of one of primary vectors, *Aedes albopictus* mosquito, responsible for various diseases such as Zika, dengue, and chikungunya. Several studies have been carried out on assessing the role of environment in the distribution of Aedes albopictus. By feeding geospatial data on factors such as temperature, precipitation, land cover, and

elevation into sophisticated predictive models, researchers have been able to generate highly accurate maps of where this invasive mosquito species is most likely to thrive. These models not only enhance our fundamental understanding of Aedes ecology, but also provide public health officials with crucial insights to guide targeted surveillance and control efforts in regions at high risk of Aedes-borne disease outbreaks.

Several studies considered environment as an effective surrogate in defining large scale-species distributions (Holdridge, 1947; Pearson & Dawson, 2003; Guisan et al., 2013; Braunisch et al., 2013) with a stronger predictive capability than biophysical parameters. For the growth of alpine plants, low temperature has been considered as one of the most significant limiting climatic factors (Na et al., 2011). The study on the distribution of Chinese sea buckthorn on the Tibetan Plateau found that precipitation was the key climate that affected its distribution (Jia et al., 2016).

The rapid spread of *Ae. albopictus* in continental Europe are responsible for the cases of several diseases such as chikungunya fever in France (Gould et al., 2010), dengue in Croatia, Spain and France (Gjenero-Margan et al., 2011) and chikungunya in Italy (Rezza et al., 2007). *Ae. albopictus* is a rural invasive mosquito that can transmit more than 22 different viruses, experimented under laboratory conditions (Kamgang et al., 2012; Gratz 2004). These factors include temperature, humidity, vegetation cover, and water. Researchers have found that temperature plays a crucial role in the distribution of Aedes albopictus. At higher temperatures, the mosquito species tends to have a wider distribution range, while at lower temperatures, their distribution becomes more limited. The distribution of Aedes albopictus, commonly known as the Asian Tiger mosquito, is influenced by various environmental factors. Several studies have also shown that humidity is an important factor in the distribution of Aedes albopictus. Higher levels of humidity create favorable breeding and survival conditions for the mosquito species, leading to an increased distribution range. Furthermore, the availability of water sources is another essential factor influencing the distribution of *Ae. albopictus*. Areas with abundant water sources, such as stagnant ponds, puddles, and containers, provide ideal breeding habitats for Aedes albopictus. The Ae. albopictus raised an interest in estimating the probable risk and potential distribution, considering its invasiveness and public health threat. Machine learning (ML) techniques can be employed to model and predict the distribution of *Ae. albopictus* based on these environmental factors. Using historical data on mosquito populations and environmental variables, a machine learning model can be trained to identify patterns and relationships between these factors. By analysing and processing large datasets, machine learning algorithms can learn to accurately predict the distribution of *Ae. albopictus* based on environmental factors. Therefore, habitat suitability models could be used to investigate the risk and distribution at continental scale by evaluating its vulnerable environment variables.

The purpose of this study is to examine the relevant environmental factors dominating the ecology of *Ae. albopictus* in European continent and to simulate its suitability for other continents by incorporating the maxent algorithm on species occurrence and climatic datasets. The goals of this study are to: (1) identify the key climate factors and where these factors affect the species' distribution boundaries; (2) identify the climatic thresholds and locate *Ae. albopictus* habitats that are climatically suitable; and (3) explain the distribution patterns based on an understanding of the climates that are suitable in various geographic regions.

2. Materials and Methods

The habitat suitability model is constructed using maximum entropy modelling approach (MaxEnt) on the updated occurrence of *Ae. albopictus* species in Europe. Then, habitat suitability map is created demonstrating the low, medium and high risk of populations of *Ae. albopictus* in the country.

2.1 Occurrence data

According to the Global Invasive Species Database and Delivering Alien Invasive Species Inventories for Europe websites (www.iucn.org and www.europe-aliens.org), the prevalence of this Asian tiger mosquito is marked in top 100 worst invasive species in the Europe and the worldwide. This was first documented in Europe in 1979 in Albania and again in 1990 in Northern Italy, where it managed to establish itself in later years. These days, the species primarily inhabits Northern and Central Italy, however it is found throughout the Mediterranean (Medlock et al., 2006). Climate change is predicted to provide *Ae. albopictus* with more favourable habitat conditions in Central Europe, allowing it to expand its range farther north in Europe (Fischer et al., 2011; Koch et al., 2016). Therefore, occurrences of Aedes albopictus, sighted by humans in European continental, is obtained from Global Biodiversity information Facility (GBIF) repository (GBIF.org, 2024) whose total number was 20,749 including duplicate records of latitude and longitude. After, removal of duplicated records, the final number of occurrence records left for model construction is 15,383.

2.2 Environmental data

An important aspect influencing the spread of species is the environment. The bioclimatic dataset is obtained at the spatial resolution of 2.5 arc-minutes (~4.5 km at the equator) (Hijmans et al., 2005) from world climate repository (WorldClim, accessed at www.worldclim.org) for habitat suitability modelling. This dataset encompasses nineteen raster files as bio-climatic variables (bio1-bio19) representing temperature and precipitation for time series 1970-2000.

2.3 Model Construction

Maxent approach is insensitive to the spatial uncertainties, suitable for constructing a significant suitability model in few locations only and better than any other presence-only modelling approaches (Baldwin, 2009). These features may be useful in predictive the prevalence of invasive species in both native and non-native regions. The maxent is chosen over other ML algorithms because it is well versed in predicting the species distributions and tops other reputable methods (Dicko et al., 2014; Elith et al., 2011; Thibaud et al., 2014). Maxent (version 3.4.4) is used in this study for modelling through "dismo" package in R software. The occurrence data is divided into two sets – one is training set with 75% of records and remaining 25% is reserved as test set for testing the model's predictive capability. The Maxent's default setting is used for linear, quadratic and product features. The resulting model is then projected onto the wide geographical landscape of Europe and India to predict the prevalence of *Ae. albopictus*.

The ability of Maxent model is used to interpret the limiting climatic factors of novel species' habitat by increasing the

similar surface mapping of range-shifting species (Elith et al., 2010). The limiting mapping technique is then used to determine the climatic factors limiting the distribution range of species in predicted habitat. The output of this mapping are considered to examine which climatic factors are limiting physiological and ecological processes.

To validate the robustness of the model, threshold-independent receiver-operating characteristic analysis (ROC) is used for calibration. For more precise analysis, the receiver-operating characteristic curve's area under the curve (AUC) is opted. The range of AUC is used to measure the probability of occurrence point ranked above the randomly chosen background point. The AUC closer to 1.0 for better correlation and 0.50 for random selection. The ROC is to trade-offs between true positive rates (sensitivity) and false positive rates (specificity) with respect to model's probability threshold values. Then, jackknife test is an additional test to determine each variable's predictive performance. The high impact variables in model are determined by permutation importance. The model results are then projected to build suitability maps showing prevalence of species within study extent and worldwide to understand the distribution of *Ae. albopictus* mosquitos. The suitability maps are generated with probability scale bar which is customized as continuous dichotomy. The areas probability values close to 0 depicted with unsuitable state for mosquitos and areas with higher values indicated higher degree of prevalence for this species.

3. Results

The AUC value of trained model on 15,383 is 0.863 (Figure 1) depicting that the model is performing reasonable. The dominant environmental variables as per the percent contribution are annual mean temperature (bio1), temperature annual range (bio7), mean temperature of wettest quarter (bio8), and mean diurnal range (bio2) with 31.6%, 27.3%, 9.7% and 7.9% respectively.
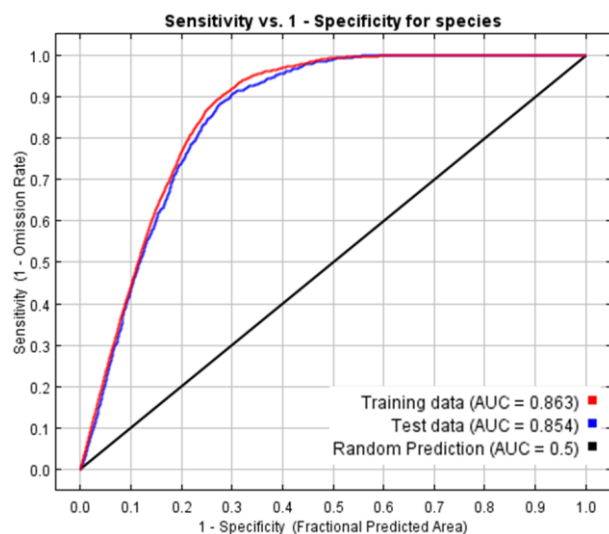

Figure 1. ROC AUC test of Maxent model

The mean temperature of warmest quarter (bio10) and mean temperature of coldest quarter (bio11) shares same percent contribution with 5.3%. According to permutation importance, the most influential variables are mean temperature of coldest quarter (bio11), mean diurnal range (bio2), temperature

seasonality (bio4), and annual mean temperature (bio1) with 33.5%, 11.3%, 9.2%, and 9.1% respectively.

The suitability assessment obtained through maxent model at European level has accurately predicted the present distribution of species and depicted the high risk of populations in Spain, France and Italy. The cities in northern Italy predicting medium level of suitability of Aedes ecology are Turin, Milan, and Trento, as shown in Figure 3. The highest suitable sites are predicted in following regions of Spain - Deltebre, Riumar, El Poble Nou del Delta, Els Muntells, LEucaliptus, and Parc Natural del Delta de l'Ebre (nature preserve), as shown in Figure 3.

The trained Maxent model is projected to global scale, depicted in Figure 4, that predicted major suitability in border regions of Nepal and Bihar (India), and Rakhine state of Myanmar v(Burma). These are Siliguri (West Bengal, India), Janakpur and Koshi Tappu Wildlife Reserve (Nepal), and few rehgions in centroid of Bihar state of India.
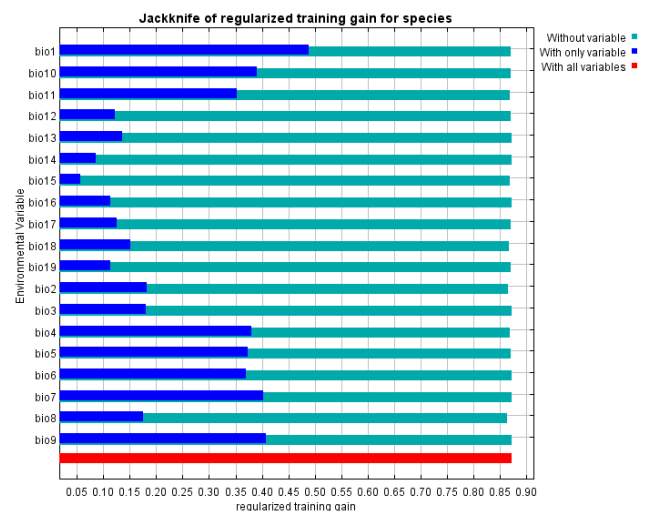

Figure 2. Jackknife test to demonstrate the impacts of environmental variables on the distribution gain of *Aedes albopictus*
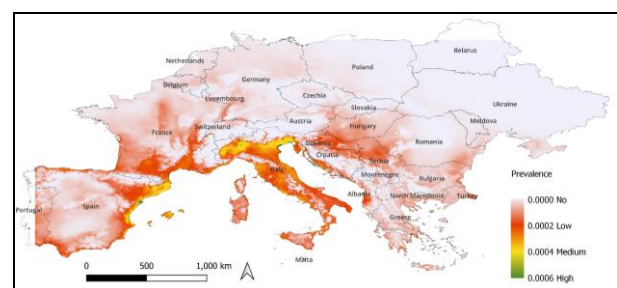

Figure 3. Potential distribution (prevalence) of *Aedes albopictus* in Europe

The limiting mapping of 19 bioclimatic variables for *Ae. albopictus* is shown in Figure 5 and 6. The results indicated that influential climatic variables, generated by permutation and percent importance, are limiting the potential distribution of Asian tiger mosquitos.
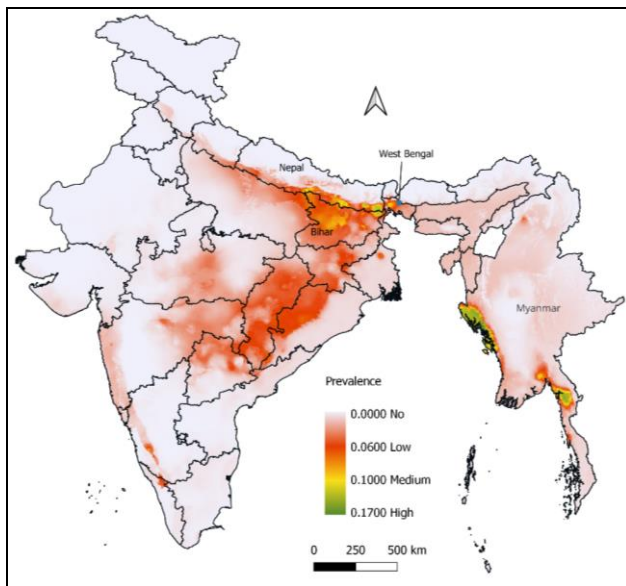
Figure 4. Predicted potential distribution (prevalence) of *Aedes albopictus* in different geographical regions
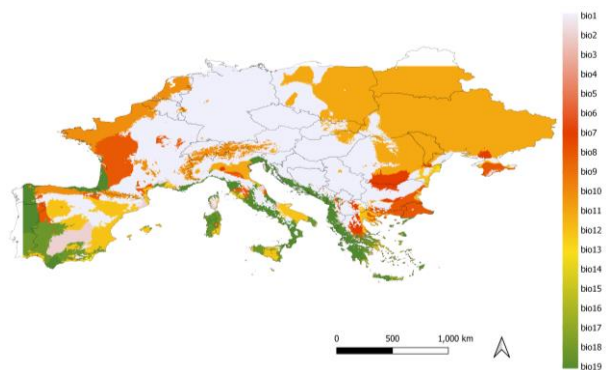

Figure 5. Limiting factor mapping of climates for distribution of *Aedes albopictus* in Europe
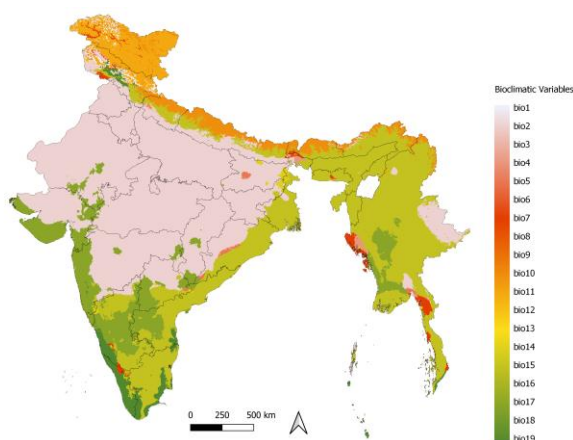

Figure 6. Spatial distribution of limiting mapping of climates for *Aedes albopictus* in India

4. Discussion

One of the key findings of this study is the identification of environmental factors significantly associated with the distribution of Aedes albopictus. The analysis reveals that variables such annual mean temperature (bio1), temperature annual range (bio7), mean temperature of wettest quarter (bio8), mean diurnal range (bio2), mean temperature of warmest quarter (bio10) and mean temperature of coldest quarter (bio11) play crucial roles in shaping the habitat suitability for the mosquito species. These findings are consistent with existing literature on *Ae. albopictus* ecology, confirming the importance of environmental drivers in determining its distribution patterns in Europe and India.

The utilization of MaxEnt modeling in this study proves to be a valuable tool for predicting the potential distribution of Aedes albopictus. MaxEnt's ability to handle presence-only data and integrate multiple environmental variables allows for a comprehensive analysis of the ecological niche of the mosquito species. The high predictive performance of the models underscores the effectiveness of machine learning approaches in understanding complex ecological systems and informing public health interventions. However, it is essential to acknowledge the limitations of the study. Despite the robustness of MaxEnt modeling, the accuracy of the predictions may be influenced by factors such as the quality and resolution of environmental data, as well as the spatial scale of analysis. Additionally, while the study identifies associations between environmental factors and *Ae. albopictus* distribution, it does not account for potential interactions with other ecological or socio-economic variables, which could further refine our understanding of mosquito habitat suitability.

Future research in this area could focus on refining the modeling framework by incorporating additional variables and employing more sophisticated machine learning techniques. Furthermore, longitudinal studies tracking changes in environmental factors and mosquito distribution over time could provide insights into the dynamics of *Ae. albopictus* populations and their response to environmental perturbations, including climate change. Overall, the integration of machine learning and MaxEnt modeling offers a promising approach for elucidating the complex relationship between environmental factors and the distribution of Aedes albopictus. By leveraging these advanced analytical tools, researchers can enhance our understanding of mosquito-borne disease transmission dynamics and inform targeted interventions to mitigate public health risks.

5. Conclusion

The application of machine learning in studying *Ae. albopictus* distribution represents a significant advancement in epidemiological research. It enhances our understanding of vector ecology, supports proactive public health measures, and contributes to global efforts in combating infectious diseases transmitted by mosquitoes. This study has demonstrated the effectiveness of machine learning in elucidating the distribution patterns of *Ae. albopictus* based on environmental factors. By leveraging advanced computational techniques, we have identified significant correlations between habitat characteristics and the presence of this mosquito species.

Through rigorous analysis and model validation, our findings underscore the complex interplay of variables such as temperature, precipitation, vegetation cover, and human settlement patterns in shaping the spatial distribution of Aedes albopictus. This knowledge is crucial for informing targeted mosquito control strategies and public health interventions, particularly in regions susceptible to vector-borne diseases like dengue fever and Zika virus.

The monitoring of *Ae. albopictus* is highly relevant in prevention and control of vector-borne diseases by mapping its potential distribution. The recommend action to study for the risks is to regularly update models using updated occurrence and climatic data. This information will be useful in controlling operations of mosquito by the authorities, especially at the predicted sites. The special measures should also be considered at breeding sites where species may inhibit artificial containers and catch basins.

Moving forward, further refinement of machine learning models and incorporation of additional environmental variables could enhance predictive accuracy and facilitate proactive mitigation efforts. By harnessing these technological advancements, we can better anticipate and respond to the ecological and epidemiological challenges posed by Aedes albopictus, ultimately contributing to improved public health outcomes globally.

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