Forecasting West Nile Virus Infections: A Machine-Learning Approach to Epidemiological Monitoring

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Abstract

Mosquitoes are vectors for a number of serious illnesses, such as Dengue, Zika, Malaria, and West Nile Virus. In the United States, West Nile Virus (WNV) is the leading mosquito-borne disease (CDC 2022). As there are currently no vaccines to prevent WNV nor medications to cure it, government agencies must sustain financially taxing programs to monitor mosquito populations and WNV infections in an effort to prevent WNV outbreaks. In this study, we develop four machine learning models that forecast WNV infections in humans, enabling government and healthcare officials to take proactive action instead of reacting to real-time infection data. Our models take in data on ecological variables – such as humidity, wind, air quality, and vegetation — and use that data to predict future WNV infections five weeks in advance. We then present a comparative analysis of two types of machine learning models – support vector machine regressors and random forest regressors – to evaluate which is best suited for the task. Our results provide a streamlined solution for government agencies as they monitor WNV, enabling effective and low-cost preventative action.

Keywords: West Nile virus, machine learning, disease prevention, epidemiological monitoring

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Research Question

Which machine learning models and climatic inputs are most effective for predicting West Nile Virus infections in humans?

Introduction and Literature Review

Our study presents machine learning models whose predictive capabilities provide healthcare and government officials early warning in their disease monitoring and prevention efforts by forecasting WNV infections five weeks in advance. Current scientific consensus is that early warning systems for WNV outbreaks are critical, as they can estimate future outbreak risk months before virus activity is discovered by traditional land surveys (Barker 2019). Prior work informed our decision to use Random Forest (RF) and Support Vector Machine (SVM) models for this task. Genoud et al. (2020) proposed that machine learning can be used in the field of classifying mosquito sex, gravidity, and species using machine learning models such as SVM and RF. Früh et al. (2018) used SVMs and RFs when modeling invasive mosquito species abundance and achieved the highest levels of precision through these models. Wieland et al. (2021) used a SVM to determine the importance of climatic variables in a classification task modeling mosquito habitats. The methodology of Lorenz et al. (2020) demonstrates the practicality of using remote sensing data in machine learning processes to predict infection rates by outlining its use in various operations, including the evaluation of urban habitats similar to Los Angeles and its surrounding counties for disease vectors. Franklinos et al. (2019) also emphasized the utility of remote sensing technologies in evaluating and predicting the effects of mosquito-borne disease, supporting our use of Enhanced Vegetation Index (EVI) data derived from NASA's Aqua and Terra satellites. To improve accuracy, Wieland et al. (2021) trained models on weather and land use data in order to build mosquito habitat models for assessing outbreak risk. Hoffmann et al. (2003) concluded that as wind speed increased, the number of mosquitoes caught in traps decreased significantly. We hypothesized that the correlation between wind speed and mosquito flight suppression would be valuable to our work, as limiting flight could lead to a decline in virus transmission rates because of the inability of vectors to fly and spread disease. Project AEDES used weather variables such as temperature and rainfall to predict Dengue cases per month in specific locations (Ligot et al. 2021). Similarly, precipitation, temperature, and humidity were found to be important factors correlated with mosquito abundance in a study of land cover data in Georgia (Buckner et al. 2011). Not only do weather conditions affect mosquito abundance, but according to Chuang et al. (2011), they also influence virus dynamics within the mosquito, such as its ability to transmit WNV. Thiruchelvam et al. (2018) analyzed how AQI affected the spread of disease, finding little correlation. However, another study conducted by Massad et al. (2010) concluded that poor air quality in severely smokey conditions is able to reduce the transmission of vector-borne diseases. In an assessment of weather factors on dengue incidence, Gui et al. (2021) observed that poor air quality and high wind speed could reduce the risk of dengue transmission. We decided to incorporate AQI in our models because of contradicting conclusions from multiple studies as we were curious to see what results we would observe. Several studies also touched on the advantages of citizen science data; Carney et al. (2022) and Früh et al. (2018) point out that citizen science programs such as the GLOBE Observer app's Mosquito Habitat Mapper and Land Cover facilitate consistency and utility for researchers and mosquito control personnel. Based on these findings, we also included GLOBE data in our dataset.

Methodology

Area of Interest

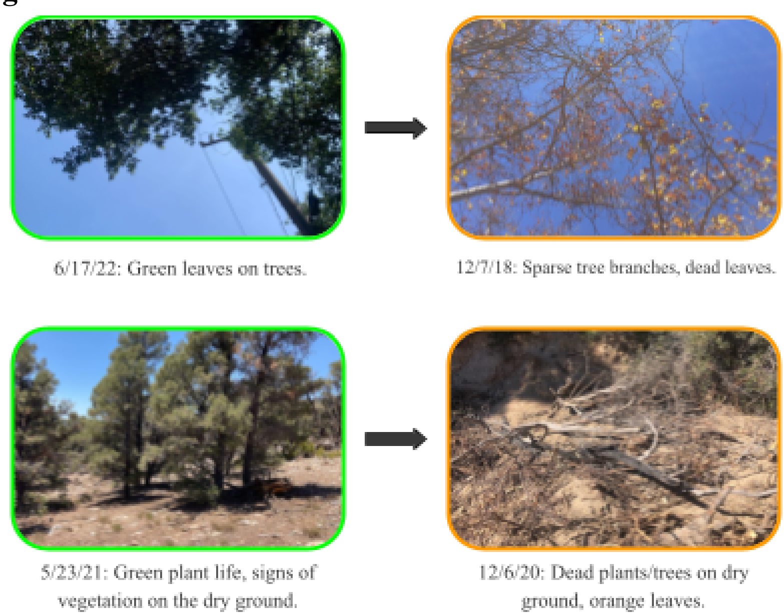
Los Angeles, Riverside, and Orange county are all located in southern California. They have climates ranging between 45°F to 85°F with summers averaging in the 70's and high 80's, as well as winters in the high 60's, and an average of 14 inches of precipitation across the three counties (US Climate Data, 2022). The topography of these three southern California counties ranges from 9 ft below sea level to the 10,068 ft peak of Mount Baldy in the San Gabriel Mountains. The vegetation across our AOI varies, but the counties have abundant shrubs and oak trees. Densely populated urban areas are located in the coastal cities while sparse population densities are located near the San Rosa and the San Jacinto Mountains.

We chose the Los Angeles, Riverside, and Orange counties as our AOI as they contain significant mosquito populations and West Nile Virus (WNV) infection instances that are documented in open access datasets. We used ArcGIS to select our AOI by plotting GLOBE Mosquito Habitat Mapper (MHM) data instances on the map tool (Figure 1). In doing so, we found that Los Angeles, Riverside, and Orange counties had a significant amount of GLOBE MHM data. The consistent GLOBE MHM data available in these areas, despite the opportunistic nature of citizen science data collection, demonstrates the significant impact of the local mosquito population on the community. As described, the Californian government also provides ample data on West Nile Virus infections in these counties. As a result of these two factors, we decided to focus our study on Los Angeles, Orange, and Riverside Counties. Furthermore, the GLOBE Land Cover Observations in our AOI revealed variable vegetation throughout the mosquito season, providing ecological patterns we could use to predict West Nile Virus infections. For example, two sets of Land Cover Photo data entries in our AOI submitted from locations within 20 miles of each other document seasonal changes in vegetation like the process of leaves changing color and falling from trees as a result of cooling temperatures (Figure 2).

Figure 1. GLOBE MHM Observations Map

Note: ArcGIS Map of larvae count in LA, Orange, and Riverside counties.

Figure 2. Land Cover Photos



Note: Land cover photos of vegetation changes throughout the year

Data Pre-processing:

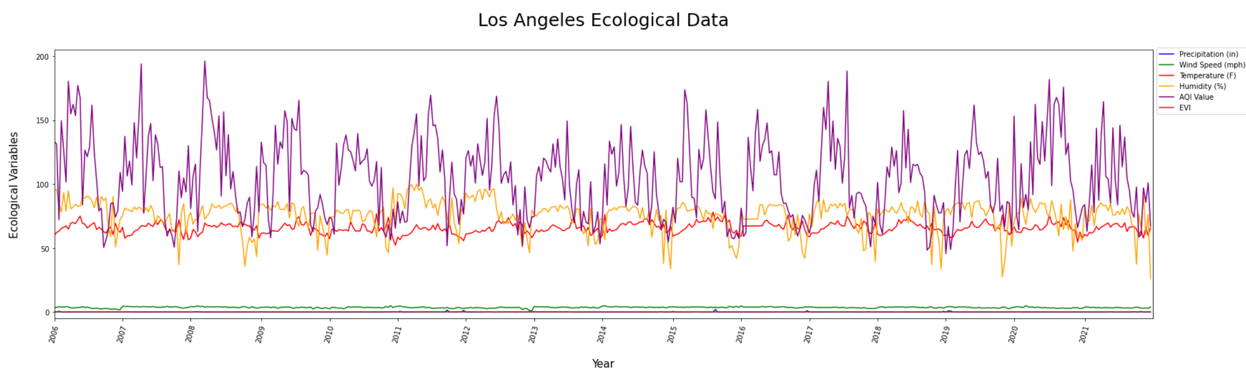
Ecological variables pre-processing. In order to evaluate the effects of ecological variables on mosquito oviposition through our models, we processed environmental data collected from the California Department of Water Resources Irrigation Management Information System (CIMIS) and the United States Environmental Protection Agency (Table 1). To incorporate this data into our models, we cleaned the data using Python and Pandas, isolating our ecological variables and averaging the daily data into weekly data. We also added weekly dates based on the CDC's MMWR Epidemiological Week format and limited each year's data to weeks 24-53. We padded missing values in our time series using the mean calculated across each year's mosquito season. We then graphed the pre-processed data in order to evaluate shared trends between the various ecological variables (Figure 3). Figure 4 depicts our ecological variables on a log scale to aid the visibility of variables with smaller ranges, such as precipitation, wind speed, and EVI. Our Enhanced Vegetation Index (EVI) preprocessing strategy built on that of Schneider et. al (2021). We gathered our daily EVI data from a Google dataset using Google Earth Engine. This dataset contained daily MODIS sensor outputs recorded on the NASA Aqua satellite. As our AOI was over 50 times larger than that of Schneider et. al, we collected daily EVI data in areas of 50 kilometers squared, instead of 1 kilometer squared. We then averaged the EVI points for each week, creating a single EVI value for each epidemiological week described by our WNV dataset.

Table 1. Table of Ecological Variables

Ecological Variable	**Unit**
Average Relative Humidity	Percentage (%)
Average Air Temperature	Fahrenheit (F)
Precipitation	Inches (in)
Average Wind Speed	Miles Per Hour (mph)
Air Quality Index	Fine Particles (PM $_{2.5}$)
MODIS Enhanced Vegetation Index (EVI)	Spectral Index (Band Ratio)

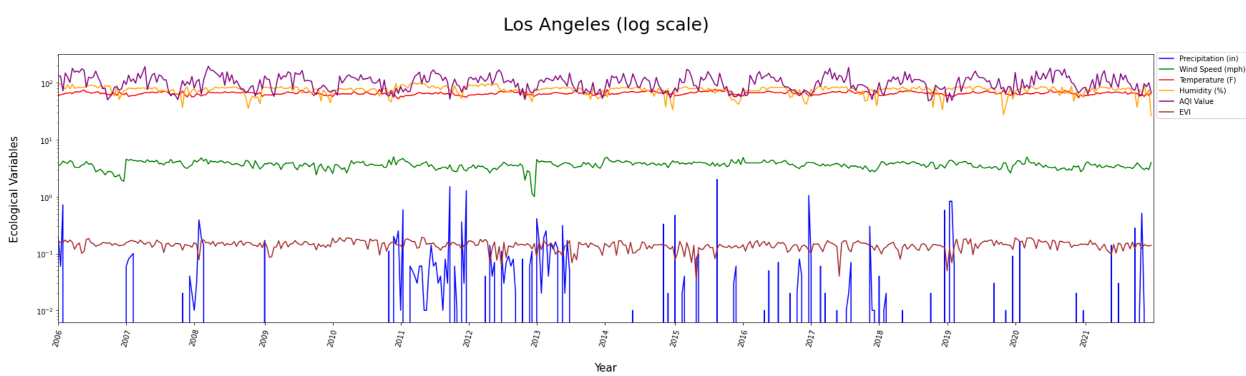
Note: Table of Ecological Variables used in machine learning models along with their units

Figure 3. Los Angeles Ecological Variables Graph



Note: Los Angeles Ecological Variables Graph from data collected from 2006-2021 with a five week lag

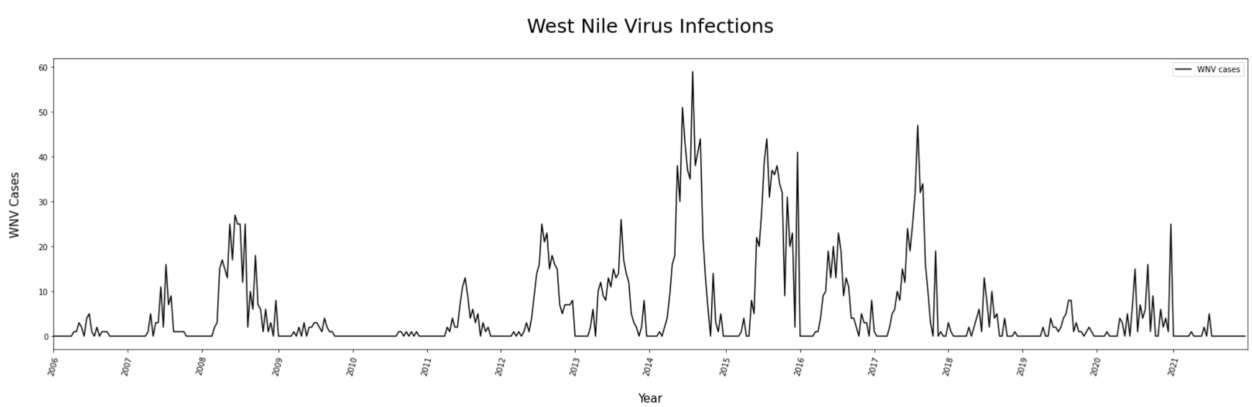
Figure 4. Los Angeles Ecological Variables Graph (Log Scale)



Note: Los Angeles Ecological variables from 2006-2021 graphed with a log scale with a five week lag

West Nile Virus infection data preprocessing. The CHHS California Department of Public Health West Nile Virus Cases, 2006-present open dataset serves as our West Nile Virus (WNV) infections dataset. It details WNV cases in every Californian county from 2006 till present (2022). Data was recorded on a weekly timestep, according to the CDC's MMWR Epidemiological week format – only weeks with nonzero WNV case records were included. Counting the number of WNV records in each county across the time series, we found that Los Angeles, Kern, Stanislaus, Orange, and Riverside counties were the top five. Since Los Angeles County, Riverside County, and Orange County were in the top five and had a consistent and frequent number of GLOBE Mosquito Habitat Mapper records, we defined our AOI as being composed of those three counties and filtered for data from those counties alone. After preprocessing this filtered data, we found that CDC MMWR weeks 24-53 was the largest range with a semi-consistent quantity of WNV infections recorded, so we limited every year's range of CDC weeks to 24-53 and padded our data with zeros to create a continuous time series between weeks 24 to 53 in all 15 years of data. A graph of this data is seen in Figure 5.

Figure 5. West Nile Virus Infections Graph

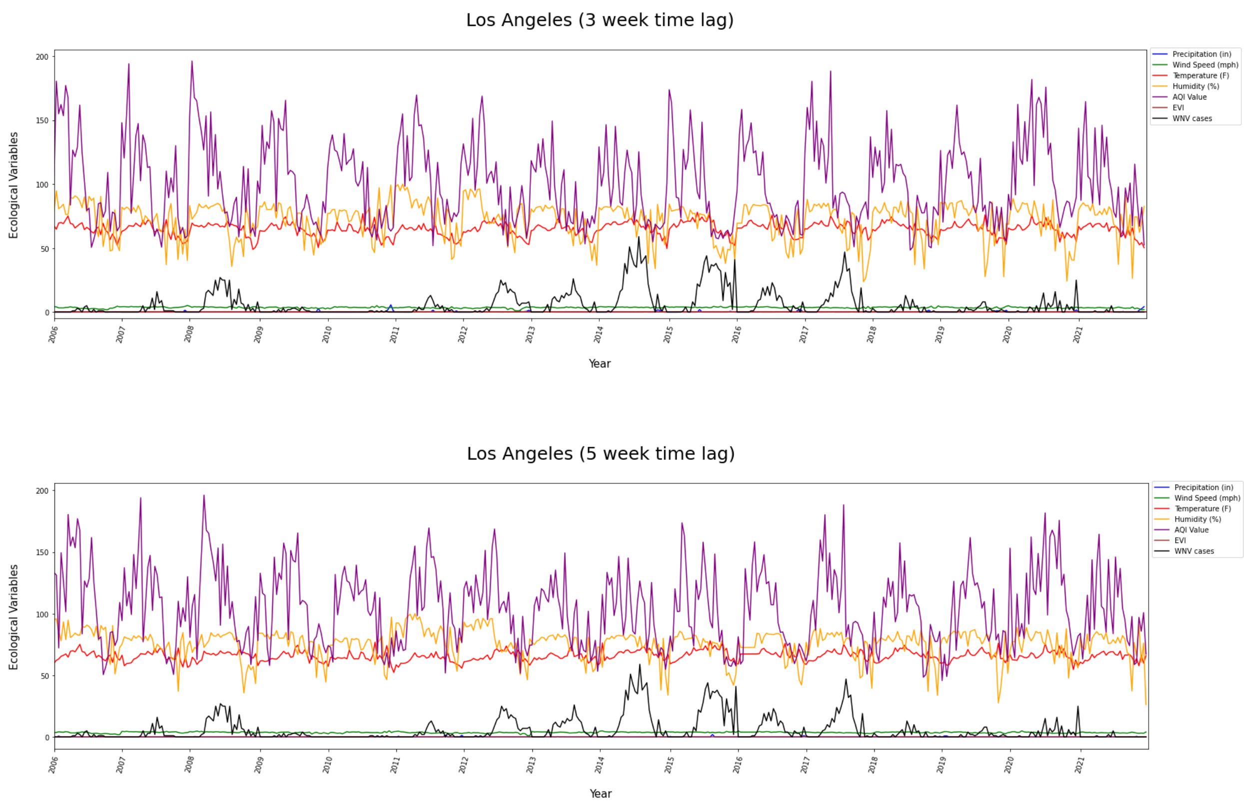


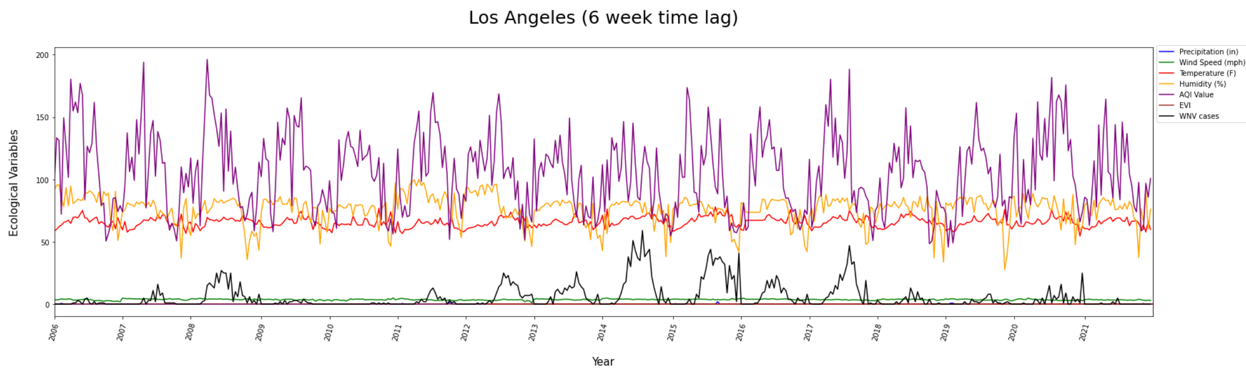
Note: Graph of West Nile Virus Infections from 2006-2021

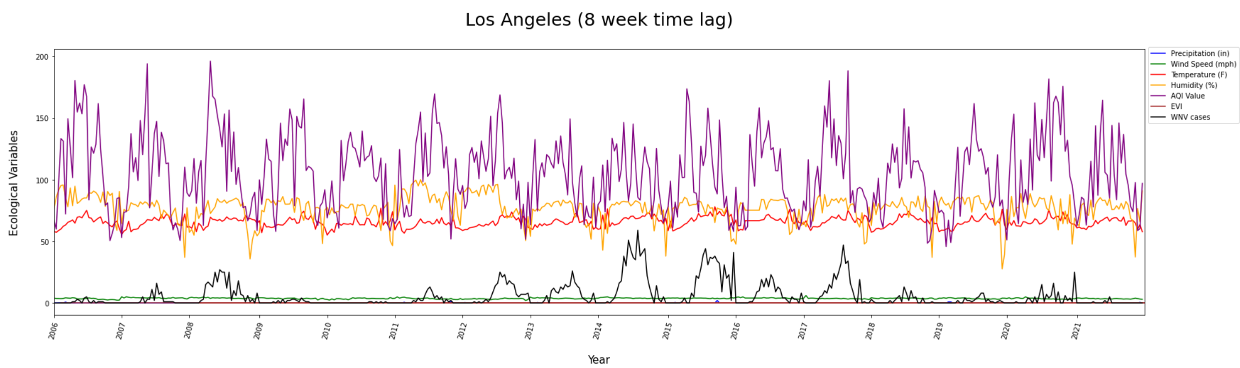
Time lag. Previous studies by Lopez et al. (2014) and Ligot et al. (2021) that were successful in evaluating the correlations between ecological variables and vector transmission of

Dengue virus emphasized the importance of time lag in obtaining accurate virus predictions. We graphed the pre-processed ecological data in order to evaluate time lag and observed the correlation between various ecological factors and WNV. We started by testing out a three week time lag and found that the ecological data's peaks still failed to align with WNV peaks, so we also tested and graphed a five week lag, which was closer to Ligot et al. one month lag, along with a six week lag and an eight week lag as Lopez et al. found that a lag of one month or more resulted in increased correlations. As seen in Figure 6, the WNV peaks and ecological variable peaks are best aligned during the 5 week lag, hence we chose it.

Figure 6. Ecological and WNV Graphs with Various Time Lags







Note: Graphs of the various time lags tested between Ecological Variables and WNV cases from 2006-2021. (Top to bottom: 3 week time lag, 5 week time lag, 6 week time lag, 8 week time lag)

Training and testing. Using the aforementioned ecological inputs and WNV outputs, we trained four machine learning models: three support vector machine (SVM) regressors and one random forest (RF) regressor. All models were built using SciKit-Learn: the RF's hyperparameters were tuned using SciKit-Learn's randomized search cross validation tool and the RBF and sigmoid SVM's hyperparameters were tuned using SciKit-Learn's grid search cross validation tool. Our test-train split was 67% to 33% and randomized to reduce the risk of overfitting. Since SVMs are not scale invariant, we used SciKit-Learn's preprocessing package to scale the SVM's training and testing data. In contrast, RFs are scale-invariant, so no transformations were applied to the training and testing data for that model.

Results

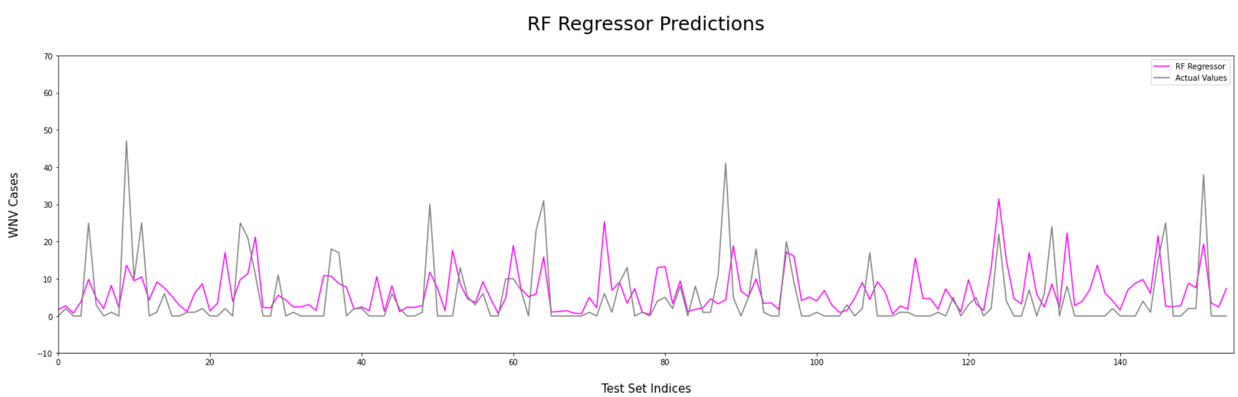
Table 2 details the performance of our four machine learning models in terms of overall mean absolute error (MAE), overall root mean squared error (RMSE), minimum RMSE, and maximum RMSE. While overall MAE and overall RMSE are overall error metrics, minimum RMSE and maximum RMSE describe the smallest and largest error values between any two points in the test set, providing another perspective on model performance. When comparing RMSE as a proportion of the desired output range for each model, the RF regressor clearly displays stronger performance than the SVMs. However, when comparing MAE as a proportion of the desired output range for each model, the four models display rather similar performance, with the RBF SVM ultimately outperforming all other models. This trend persists in the minimum RMSE value, where all models perform closely but the RBF SVM still outperforms its counterparts. In contrast, the maximum RMSE value as a proportion of the desired output range describes the RF regressor as notably stronger than its counterparts. This variation is likely a result of the nature of MAE and RMSE. MAE is linear in nature; therefore, it penalizes all errors equally, while RMSE is nonlinear in nature and weights errors that are larger in absolute value more heavily (Chai & Draxler, 2014). With this understanding of error, we can conclude that the RF regressor is indeed stronger than the SVMs as it is less likely to produce an error that is large in magnitude. This fact is also visually clear when viewing Figures 7 and 8 side-by-side: the RF regressor more closely approximates the actual case values, even when there are sudden and extreme changes from a norm of 0 cases. Table 3 and Figure 9 display the ecological variables' feature importances for the RF regressor's predictions. Temperature emerges as the most important feature and precipitation as the least important, while EVI, AQI, wind speed, and humidity are all of similar importance.

Table 2. Machine Learning Model Error Metrics

Model	Overall MAE	Overall RMSE	Minimum RMSE	Maximum RMSE	Range of Desired Output
RBF SVM	0.514808	0.91283	9.0204e-05	0.37031	5.6596
Linear SVM	0.55336	1.0024	0.000167	0.39182	5.6596
Sigmoid SVM	0.54848	1.0086	0.00012	0.39083	5.6596
RF Regressor	5.74241	8.18072	0.00401	2.9433	59

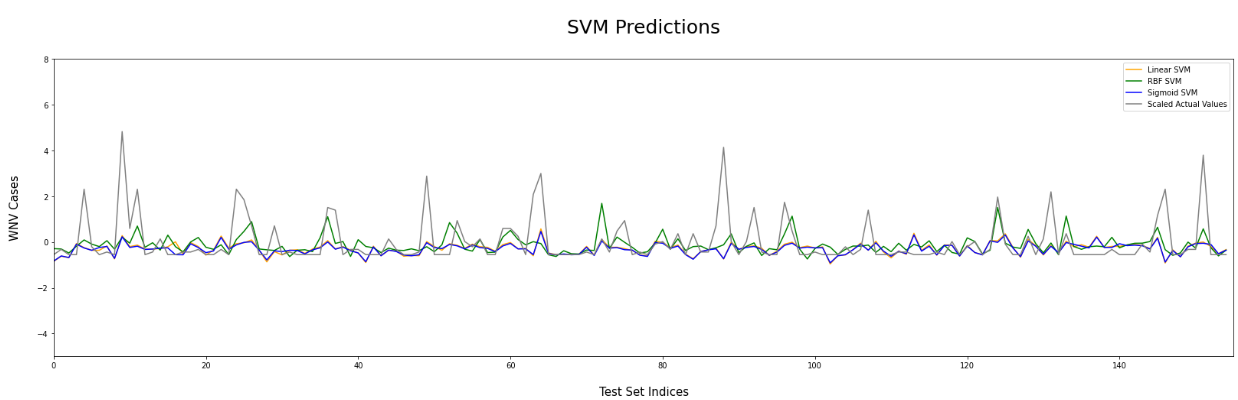
Note: This table details a variety of error metrics used to contextualize our 4 models' performance.

Figure 7. RF Regressor Predictions vs Actual WNV Cases



Note: This graph describes our RF regressor's predictions in magenta and the actual WNV cases recorded in gray.

Figure 8. SVM Regressor Predictions vs Actual WNV Cases



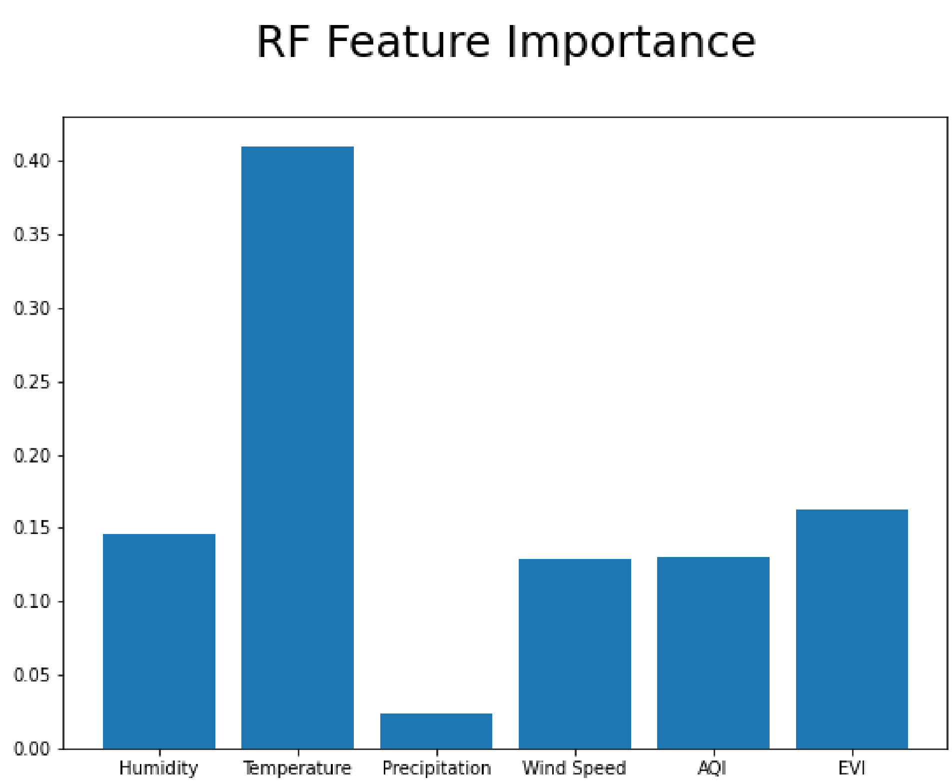
Note: This graph describes our linear SVM regressor’s predictions in orange, RBF SVM regressor’s predictions in green, sigmoid SVM regressor’s predictions in orange, and the actual WNV cases recorded in gray.

Table 3. RF Feature Importance Table

Ecological Variable	RF Feature Importance
Average Relative Humidity	0.14559
Average Air Temperature	0.41017
Precipitation	0.02372
Average Wind Speed	0.12840
AQI	0.12990
EVI	0.16222

Note: This table details our RF regressor’s feature importances.

Figure 9. RF Feature Importance Graph



Note: This figure depicts our RF regressor’s feature importances.

Discussion

In this study we develop four different machine learning models using two different machine learning architectures for the purpose of forecasting the absolute value of West Nile Virus infections in humans across our AOI. Our results indicate that random forest regressors are the best machine learning architecture for this task; however, support vector machine regressors perform comparably well and even exceed random forest regressors when the magnitude of error is unweighted. Our results are particularly strong given the challenge of predicting absolute values in a dataset that varies significantly week-to-week, due to delays between infection and reporting and the life cycle of Culex pipiens.

The RF regressor's feature importances reveal noteworthy correlations between our ecological variables and WNV infections. Most notably, EVI, AQI, wind speed, and humidity rank almost equal in importance. This is significant as, as detailed in our literature review, there is a lack of consensus on the importance of AQI and wind speed in mosquito prediction tasks. Our work suggests that AQI and wind speed are almost as important as vegetation and humidity metrics when aiming to predict disease characteristics in the southern California area.

Such findings and others described in our paper reveal new research directions and provide a solid foundation for the continued development of early warning systems for forecasting WNV infections. However, our work also has potential for growth. First, our models would benefit from more frequent WNV testing, as a dataset with more frequent time steps would likely reveal new patterns that are currently obscured behind the weekly reporting structure and thereby reveal new opportunities to improve our predictions. Second, our models were trained with WNV case data collected through passive surveillance where healthcare providers report cases to public health authorities following the diagnosis of a person who sought care after experiencing symptoms. This system inevitably underestimates the true incidence of disease by the number of people who are undiagnosed and unreported (Krow-Lucal et al. 2017). Because our models were trained with this data, they are limited to predictions of the number of reported cases, which may not necessarily represent the true number of cases. Improvements in healthcare diagnosis efforts will therefore simultaneously present opportunities to improve our models.

Conclusion

In summary, our machine learning models forecast the absolute number of WNV infections five weeks in advance using open access ecological variables and remote sensing data. Our methodology and results hold valuable insight for the development of early warning systems that aid healthcare and government officials in preparing for and preventing incoming WNV outbreaks. Our predictions are particularly valuable when assessed from a resource allocation standpoint, as the five-week lead time they provide can aid healthcare providers in predicting when they must prepare to increase capacity. This early notice is critical to avoiding preventable deaths. Directions for future work center around such collaborations between data scientists and healthcare and government officials. Data scientists must continue improving predictive capabilities – particularly when working with variable data described via large timesteps – while the healthcare sector continues providing open access data to fuel this forward progress. We look forward to continuing to work towards maximizing our models' positive impact by effectively embedding them in existing healthcare initiatives, streamlining and improving these processes.

Appendix A

IVSS Badges

I am a Collaborator

We are a strong team that worked diligently with each other and used each member's unique skill sets to best improve our research. With our combined expertise we developed new ways to predict WNV predictions. By working with students from multiple schools across the country, we created a project that each of us could not do alone. We are applying for this badge because we collaborated in a team environment driven by helping one another during the project.

I am a Data Scientist

We collected, cleaned, and processed multiple data sets for our models, including the GLOBE Mosquito Habitat Mapper data (which contains our contributions as NASA SEES interns), EVI data from remote sensing, WNV cases, and LA humidity, temperature, AQI, wind speed, and precipitation. We examined several other databases based on our task, but since our AOI was in southern California (LA, Riverside, and Orange counties) we stuck to databases gathered in that region. Once graphed, we were able to pinpoint patterns in our data and made accurate predictions using SVM and random forest regressors.

I am a STEM Professional

We worked with professionals in the STEM field through the NASA SEES internship. We talked with Dr. Russanne Low who provided us with guidance throughout our project. She shared a paper she co authored with about the usefulness of citizen science to researchers. We also collaborated with Dr. Erika Podest by sharing her team's paper about the identification of correlations between Dengue outbreaks and ecological factors in Brazil. She helped us by suggesting we add similar time lags in our variables. We also talked to Julianna Schneider and Alessandro Greco who were authors in a paper with very similar goals. In all, all of our mentors' guidance helped us with understanding and expanding the viewpoints we had for our project.

The Team

Rachel Chen: Data Visualization Specialist, Environmental Data Preprocessing, Data Management, Writing

Aidan Schneider: Machine Learning Specialist, Epidemiological Data Preprocessing, Remote Sensing Data Preprocessing, Data Visualization, Data Management, Writing

Francisco Rodriguez: Documentation Specialist, Data Management, Writing

Starlika Bauskar: Citizen Science Data Specialist, Data Management, Writing

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Code and Datasets

Unless previously approved, code and datasets are available upon request at this link: https://drive.google.com/drive/folders/1zk1vBAcw64MJQGkPrW5rDLd3ZnWQpUWT?usp=sharing

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