

Evaluating Statistical Modelling Methodologies of Disease Vector Abundances

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Declaration

Mosquito count data is from the VectDyn database of the VectorByte data platform. Meteorological data is from the NOAA Climate Data Online database. Meteorological data extraction from NetCDF files was adapted from protocols developed by Matthew Watts as part of the larger VectorByte project. All other data cleaning, processing, and analysis was my own work.

Abstract

Mosquito population dynamics directly affect disease incidence. Climate-based statistical models of abundance dynamics could provide early warnings of mosquito population growth and inform public health and mosquito management strategy. Existing attempts to model the relationship of temporally lagged meteorological variables on mosquito abundances tend to focus on single species in limited geographic areas and vary in their incorporation of auto régressive terms in the model. Conclusions about appropriate temporal lag lengths and significance of meteorological predictors are consequently highly specific and limited in their potential to inform wider reaching early warning models. The temporal resolution of these models also range from weekly to monthly time scales with little consensus on appropriate time scale of analysis. In this study I used comprehensive multi-species surveillance data from 5 Florida counties to compare the performance of temperature and precipitation based GAMs of abundance when aggregated at weekly, bimonthly, and monthly time scales. I also investigated the consistency of best fit temporal lag lengths and significance of temperature and precipitation in predicting abundance across multiple locations for the same species. Lastly I assessed the relative effect on model fit of incorporating an auto-regressive term into climate-based GAMs. I found that in most locations, models parameterised with monthly aggregated data explain the most deviance in mosquito abundance dynamics with the least absolute error. Lags and significance of meteorological drivers of mosquito abundance were commonly shared within species, but varied enough to recommend that statistical models should be location-specific. According to AIC selection, autoregressive models were, in a majority of cases, better fit than non-autoregressive models, but a substantial 31.4% of datasets were equally or better fit by climate-only models.

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Introduction

At the end of the 20th century, the world experienced a global resurgence of vector-borne disease (Gubler, 2001). Diseases that had been well-controlled in the early-to-mid 1900s surged under complacent public health policies and insufficient research funding (Gubler, 1998). Today, vector-borne diseases represent 17% of the total global infectious disease burden and cause millions of deaths annually. Mosquito-borne diseases, such as malaria, dengue, Zika, yellow fever, West Nile virus, and chikungunya, singularly infect more than an estimated 200 million individuals worldwide every year (WHO, 2017).

Surveillance of mosquito populations is a successful method to control the public health impacts of vector-borne disease (Vazquez-Prokopec et al., 2010). Intervention in growing populations through chemical control measures can effectively reduce disease incidence (Tomerini et al., 2011). Sampling methods are, however, often limited by resource constraints (Sedda et al., 2019). Many studies have attempted to develop early warning models of disease incidence through prediction, rather than surveillance, of mosquito abundance (Beck-Johnson et al., 2013; Li et al., 2019; Poh et al., 2019). Because localised arbovirus disease data is often lacking in quality, mosquito abundance models can offer an alternative method to estimate disease risk (Lowe et al., 2013). Predictive models of mosquito abundance could also offer a cost-effective strategy with which to plan control measures (Yang et al., 2009).

Mosquito abundances are affected by many factors, including land-use, elevation, and vegetation cover, but meteorological variables, such as temperature and precipitation, are particularly predictive of population dynamics and commonly used in abundance models (Trawinski and MacKay, 2008; Li et al., 2019; Wang et al., 2011; Yoo et al., 2016). The effects of temperature on mosquitoes are well characterised. As ectotherms, mosquito life history traits such as development rate, biting rate, fecundity, and survival, are temperature dependent and vary with changing temperatures (Mordecai et al., 2019). With increasing temperature, trait performance will increase until an optimal temperature is reached, after which, trait performance decreases according to physiological constraints (Amarasekare and Savage, 2012). Because these traits shape reproductive output, trait variation determines abundance of mosquito populations (Cator et al., 2020). Precipitation affects mosquitoes in more complex ways. Rainfall can create larval habitats in man-made containers or expand natural pooled breeding habitats (Keith, 2005; Koenraadt and Harrington, 2008). Inter-seasonal variability in larval carrying capacity, which is dependent on rainfall for habitat creation, has been shown to be a main driver of mosquito abundances (Marini et al., 2016). Heavy rainfall, however, can flush

immature mosquitoes from aquatic habitats, but the extent of this effect varies among species (Koenraadt and Harrington, 2008; Paaijmans et al., 2007). The effect of droughts on abundance is mixed; in some cases, drought is thought to benefit mosquito abundance by eliminating predators of larvae in drying water bodies (Chase and Knight, 2003). Other research have found that droughts simply increase sample collection, rather than true abundance of mosquitoes (Shaman et al., 2002). In light of projected increases in extreme weather events such as increased heavy rainfall frequency, droughts, and warming temperatures in this century due to climate change, it is vital that we understand the complex effects of temperature and precipitation on vector populations. (Seneviratne et al., 2012).

A wide variety mechanistic and statistical modelling techniques have been used to investigate the impact of climate on mosquito abundance (Ahumada et al., 2004; Cailly et al., 2012; Jian et al., 2014; Yoo et al., 2016; Wang et al., 2011). Mechanistic models based on trait responses to climate conditions may allow for longer term and more generalisable forecasting (Cator et al., 2020). The complexity of the relationship between precipitation and mosquito life history, however, complicates the inclusion of this important abundance driver in mechanistic models. Statistical models, on the other hand, may be more useful for understanding explanatory power of environmental variables (Mordecai et al., 2019). Mosquito abundances have been described phenomenologically by harmonic models, time series ARIMA models, Generalised Linear Models (GLMs), and Generalised Additive Models (GAMs) (Li et al., 2019; Trawinski and MacKay, 2008; Wang et al., 2011; Yoo et al., 2016). GAMs have recently been used to capture the complex and non-linear relationships between climate and abundance as linear models are likely to overestimate the effect of temperature on mosquito abundance at high temperatures (Li et al., 2019; Roiz et al., 2014; Xu et al., 2017).

Several unanswered methodological questions about the use of statistical models could limit the applicability of these methods as early warning systems of mosquito abundance and vector borne disease. Temperature and precipitation have both been found to have temporally lagged impacts on mosquito abundance at daily, weekly, and monthly scales (Chuang et al., 2012; Poh et al., 2019; Xu et al., 2017; Wang et al., 2011). In other words, past precipitation and temperature can drive contemporary mosquito population dynamics. Although lags of different time scales capture different effects of environmental drivers, tested methodologies for appropriate temporal resolutions to use for lagged models are non-existent (Mordecai et al., 2019). Most statistical models have also focused on characterising lags and dependence on meteorological variables in single species and limited geographic areas (Chuang et al., 2012; Wang et al., 2011; Poh et al., 2019; Yoo et al., 2016). Because abundance responses to meteorological drivers are also dependent on local land characteristics such as elevation, vegetation cover, and urban structures, climate effects are likely to be location-specific (Ahumada et al.,

2004; Yoo et al., 2016). In order to understand the applicability of early warning systems for vector species abundances across geographies, the consistency of temporal lag lengths and meteorological abundance drivers in abundance models needs to be assessed across several locations. The inclusion of a first-order auto-regressive term (AR) of lagged abundance in analysis of GAMs can improve model fits by capturing density dependence of mosquito population dynamics and auto-correlative structure of mosquito abundances. (Da Cruz Ferreira et al., 2017; Li et al., 2019; Xu et al., 2017). The need for nearly contemporary abundance data for this AR term, however, could limit the real-time forecasting ability of these methods. Research is needed into the trade off in model fit with the use of AR terms to understand how applicable these models are in real time. This study aims to address these gaps in statistical modelling of mosquito abundance dynamics by answering the following questions:

1. Which level of temporal resolution of temperature and precipitation data is best able to predict mosquito abundances?
2. How consistently can temporal lags and significant meteorological drivers be characterised for species specific abundance models across multiple locations?
3. How does incorporation of an auto-regressive term affect the predictive ability of temperature and precipitation driven models of mosquito abundance?

To answer these questions, I will be evaluating temperature and precipitation dependent multivariate GAMs of mosquito abundance constructed using surveillance datasets from five geographically dispersed locations in Florida. This study is novel for its use of comprehensive multi-species and multi-location datasets. The insights gained from this investigation should help to inform the development of cost-effective early warning systems of increases of mosquito abundances and vector-borne-disease.

Methods

Mosquito Abundance Data

Mosquito count data was obtained from the VectDyn database from the open source VectorByte data platform (www.vectorbyte.org). VectDyn is a global database containing spatially and temporally explicit abundance data of mosquitoes and other arthropod vectors from published data and surveillance program records. Mosquito counts from 205 global locations was narrowed down to seven data-rich counties in Florida, U.S.A. Florida has a long history of mosquito-borne disease epidemics, including yellow fever, dengue, and malaria (Connelly et al., 2014). Since the start of the 21st century, this state has seen a re-emergence of dengue fever, geographically novel emergence of West Nile Virus, and locally transmitted outbreaks and incidences of Eastern Equine Encephalitis, St. Louis Encephalitis, Zika, and Chikungunya fever (Connelly et al., 2014; Florida Department of Health, 2017). I decided to use data from five of these counties which had multi-year surveillance records and nearly year-round sampling from which fairly continuous time series of mosquito abundances could be formed.

Each location contained multiple trap sites. A variety of trap types were used, including BG-Sentinel traps, CDC light traps, animal-baited traps, and CDC gravid traps. Trap type can affect the efficacy of trapping for different mosquito species (Li et al., 2016). At locations with multiple traps, proportionality of each trap type was inconsistent across the time series. This would complicate conclusions of species abundances aggregated across multiple trap types. Thus, for locations with multiple types of traps, I identified the most common trap type and removed observations from all other trap types. Table 1 summarises the characteristics of mosquito trap records at each location.

I averaged species-specific count data in each location and at weekly, biweekly, and monthly temporal resolutions. This transformed integer count values to averaged indicators of county-level abundance and allowed me to account for frequent variation in the number of traps deployed at each location. I aggregated species that are morphologically indistinguishable from one another according to the ontology used by VectorBase (**list in SI**). Species counts that were identified only to the genus or family level were also removed. After this processing, I had 161 datasets of unique species and location combinations aggregated at weekly, biweekly, and monthly resolutions. I then removed datasets where fewer than 10% of the data points were greater than zero. This left me with 111 weekly, 119 bimonthly, and 129 monthly datasets. Because abundance values of zero would be undefined in log transformations used in the model fitting, all abundance values were then increased by 1 unit. Because abundance really represents mosquito detection rather than true abundance, zero counts do not necessarily mean absence of mosquitoes. Zero counts rather mean that mosquito abundances were

below a detectable threshold with the employed trapping methods.

County	Trap Type	Years of Data	Number of Species
Lee	CDC Light Trap	2008 - 2017	18
Manatee	CDC Light Trap	2012 - 2016	48
Orange	CDC Light Trap	2012 - 2017	31
St. Johns	baited light trap	2004 - 2015	38
Walton	New Jersey Trap	2014 - 2017	28

Table 1. Locations of abundance data and associated length of data collection, trap type, and number of species at each location. Individual species in these locations may have abundance records that are shorter than the overall years of data of each location.

Meteorological Data

Temperature and precipitation datasets were obtained from the NOAA Climate Data Online database as global NetCDF raster files at a spatial resolution of 0.50 degrees latitude and 0.50 degrees longitude. Rasters were rotated 180 degrees to match coordinate rotation of trap locations. Maximum daily temperature and total precipitation values were then extracted by taking the unweighted mean of the bilinear interpolation of the 4 closest raster cells to each trap location. Each raster file contained one year of meteorological data, and so this procedure was repeated for each year of the surveillance period. I then mapped the extracted daily maximum temperature and total daily precipitation to corresponding mosquito abundances by date and trap location.

Data Pre-Processing

I spatially and temporally aggregated maximum temperature data by averaging both at county-level and at weekly, biweekly, and monthly time scales. Consequently, temperature in this study refers to the average maximum daily temperature across respective temporal scales. Multiple temperature indices, including minimum, maximum, and average temperatures have all been shown to be significant drivers of mosquito abundances (Chaves et al., 2013; Roiz et al., 2014; Xu et al., 2017). Maximum temperature was chosen to capture the maximum extreme of ambient temperatures mosquitoes were exposed to as high temperatures can have detrimental effects on adult survival (Marini et al., 2016).

Number of days of rainfall has been shown to be a more effective predictor of mosquito-borne disease incidence than cumulative precipitation (Xu et al., 2017). This is likely due to the maintenance of humid conditions over time with frequent rainfall. Humidity has been independently assessed as a significant predictor of abundance dynamics (Trawinski and MacKay, 2008), and so this representation

of precipitation may capture both humidity and precipitation effects. With this in mind, I aggregated precipitation to weekly, biweekly, and monthly scales by summing the number of days in each temporal period with non-zero cumulative precipitation. Consequently precipitation as I will further refer to it refers to a discrete number of days of rainfall, with a maximum of 7, 16, or 31 days dependent on temporal scale.

In order to investigate the effect of autoregressive predictors of abundance, I created an explanatory variable of abundance by shifting the continuous time series of response abundance by a lag of one time period; this was one week, bimonth, or month in each respective aggregation. Finally, I removed rows of data with missing values in any response or explanatory variables. By the end of this pre-processing, I had obtained three different temporally aggregated groups of species and location specific datasets. Each dataset contained explanatory variables of temperature, precipitation, and lagged abundance, as well as response variable abundance, at weekly, bimonthly, and monthly time scales.

Model Structure

I used univariate GAMs for each dataset to determine the best-fit temporal lags between abundance and temperature as well as between abundance and precipitation. Because aggregated abundance values were positive, non-normally distributed and non-integer, I used Gamma family distribution GAM.. These models had the form:

$$\log(\mathbb{E}(V_t + 1)) = a_0 + f_1(T_{t-l_T}) \quad (1)$$

$$\log(\mathbb{E}(V_t + 1)) = a_0 + f_1(P_{t-l_P}) \quad (2)$$

V_t is abundance at time t . a_0 is the intercept, T_{t-l_T} and P_{t-l_P} are the temperature and precipitation at l_T and l_P , respectively, time periods prior to time t . f_1 is a smooth function comprised of cubic polynomial basis functions. Each smooth function was allowed up to nine degrees of freedom, equal to 9 basis functions, to allow for flexibility in the model fit. The penalisation process in GAM fitting reduces the degrees of freedom to an optimised number for each smooth function. If a smooth function had fewer than ten unique data points, such as with weekly precipitation datasets with values between zero and seven, this upper limit needed to be lowered. The maximum degrees of freedom in these cases was set to one less than the number of unique values for that smooth function.

The use of cubic polynomial basis functions is an effective way to avoid the underestimation of standard error caused by concurvity with non-parametric basis functions (Dominici et al., 2002;

Ramsay et al., 2003). Concurvity is the extent to which each smooth function can be approximated by other smooth function predictors and is analogous to multicollinearity in linear models. Because of the way variances are estimated in GAMs, concurvity can cause underestimation of p-values and thus lead to Type I errors (Ramsay et al., 2003). I used shrinkage methods to allow for full penalisation of spline complexity and REML for optimising smooth parameter estimates. Both of these smooth function estimation methodologies have been shown to maximise the predictive ability of GAMs (Marra and Wood, 2011).

Each dataset was also fit with two multivariate models, each incorporating temperature and precipitation, and one of which incorporating an autoregressive term.

$$\log(\mathbb{E}(V_t + 1)) = a_0 + f_1(T_{t-l_T}) + f_2(P_{t-l_P}) \quad (3)$$

$$\log(\mathbb{E}(V_t + 1)) = a_0 + f_1(T_{t-l_T}) + f_2(P_{t-l_P}) + f_3(V_{t-1} + 1) \quad (4)$$

In Equation 4, V_{t-1} is the abundance one time step prior to abundance at time t .

Model Selection and Evaluation

Models 1 and 2 were used to determine the best-fit lags of temperature and precipitation for each dataset at each temporal aggregation. At the weekly scale, lags of zero to twelve weeks were considered. At the bimonthly and monthly scales, lags were considered between zero, one, and two months. Because, on average, zero to two months is approximately the same number of days as zero to twelve weeks, this allowed equivalent time periods to be considered at each temporal scale. This wide range of lags were tested in order to avoid making strict assumptions about the relationship of meteorological variables with abundance and to account for wide variation in mosquito development time (Barrera and Medialdea, 1996; Beck-Johnson et al., 2013). Best-fit lags for each temporal scale were chosen by finding the minimum corrected Akaike’s Information Criterion (AIC) value among models fit with each possible lag length.

$$AIC = -2\ln[L(\hat{\theta}_p|y)] + 2p \quad (5)$$

AIC (Equation 5) determines the likelihood of a given model while penalizing model complexity (Johnson and Omland, 2004). Models that maximise both fit and simplicity are selected by choosing the model with the lowest AIC score. Corrected AIC fulfils the same goals as AIC, but uses likelihoods relevant to GAM models and corrects the over-selection of complex models that is typical of AIC methods for GAMs (Greven and Kneib, 2010; Wood et al., 2016). The Akaike weight of each

best fit model was calculated in order to indicate the confidence in this lag as compared to other univariate lagged models. Once best-fit lags of meteorological variables for each dataset and temporal scale were determined, these lags were incorporated into multivariate models 3 and 4.

In order to compare equivalent datasets across resolutions, datasets were removed from the 119 bimonthly and 129 monthly datasets to match the species and location composition of the 111 weekly datasets. Mean Absolute Error (MAE, Equation 6) and deviance explained were used to compare the performance of lagged models at different temporal resolutions. Deviance explained is a relative measure that compares the likelihood of the proposed model to the likelihood of a saturated model with a parameter for each term and has a functionality equivalent to R^2 for non-Gaussian distribution families, such as the Gamma distribution that was used in this study (Nelder and Wedderburn, 1972). MAE (Mean Absolute Error) is an absolute measure that can be interpreted as the average error in the number of mosquitoes predicted for each dataset. Because it is non-directional, I also calculated mean bias (MB, Equation 7) to understand the overall under and overestimation of the data by the fitted model.

$$MAE = \frac{1}{N} \sum |O_i - P_i| \quad (6)$$

$$MB = \frac{1}{N} \sum (O_i - P_i) \quad (7)$$

N is the number of data points and O_i and P_i are observed and predicted points, respectively. MAE and mean bias for each dataset were found through 10-fold cross validation. This is a form of out-of sample model validation. The dataset is randomized then split into 10 equal sections, or folds. One fold is withheld while the model is trained on the remaining nine sections. The model is then tested on the out-of-sample fold and measures of fit, in this study, MAE, are calculated. This procedure is repeated nine more times and the 10 resultant MAE values are averaged. MAE thus is representative of the out-of-sample predictive power of the model. I used MAE over residual mean square error (RMSE) because RMSE increases with number of data points and is only appropriate for comparison of equally sized datasets. This would make comparisons across equivalent datasets at different temporal resolutions biased against higher resolution data, fit notwithstanding. After finding the temporal resolution that best fit and predicted the data using deviance explained and MAE, datasets at this temporal resolution was used for all further analysis.

A subset of species that were present in all five locations were used to examine the consistency of best fit lags and significance of meteorological drivers across locations. Covariates were considered

significant if smooth functions had p values of less than 0.05.

Corrected AIC and deviance explained were used to compare the performance of the autoregressive and non-autoregressive models for each dataset. Relative change in deviance explained between the two multivariate models was be found through differencing. Comparison of model fit was assessed also by finding the minimum corrected AIC between the two models. Models with differences in AIC of less than two were considered to be equally best fit (Johnson and Omland, 2004).

Results

Time series of temperature, precipitation, and abundance data for two sample datasets can be found in Fig 2. Temperature ranges in each location varied by a minimum of 15 °C in Manatee county to to a maximum of 27 °C in St. Johns county. Frequency of rainfall in all counties tended to peak in wet summer rainy seasons.

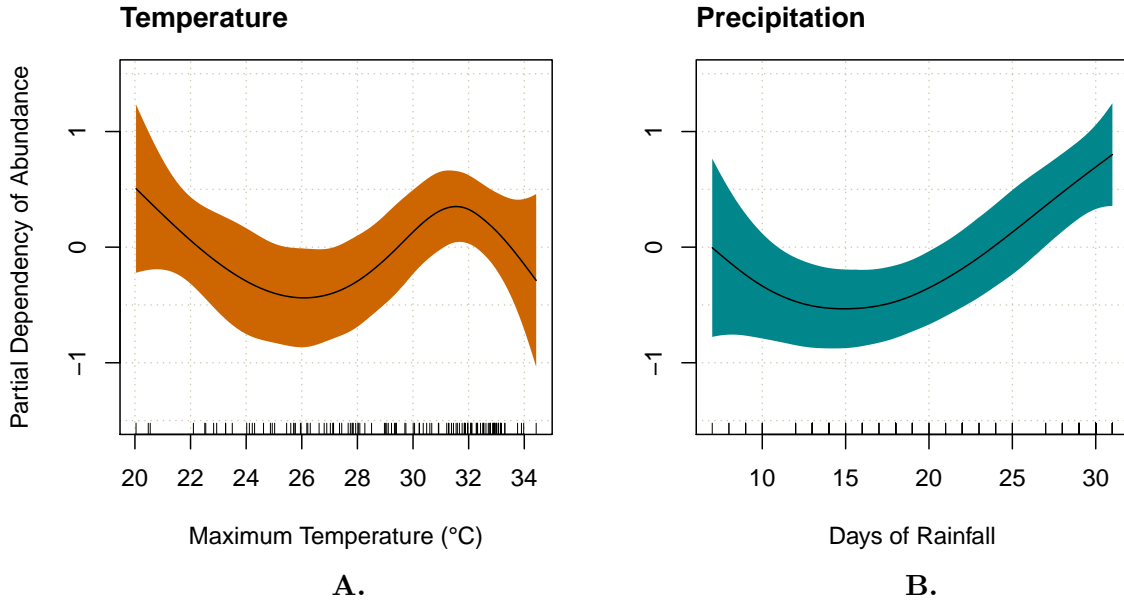


Fig. 1. Sample of multivariate model fitting showing the partial dependency of *Anopheles quadrimaculatus* abundance in Lee County, Florida on temperature and precipitation at the monthly temporal aggregation. Both temperature and precipitation are significant and best fit at a lag of two months.

Which level of temporal resolution of temperature and precipitation data is best able to predict mosquito abundances?

The fit of multivariate models (Fig 1) of temperature and abundance at best fit lags were compared across weekly, bimonthly, and monthly resolutions (Table 2) using MAE and deviance explained. In all locations besides St. Johns, monthly aggregated datasets had a higher median deviance explained than the median deviance explained at weekly and bimonthly resolutions. Three out of five locations had the lowest median MAE at the monthly resolution, indicating that monthly datasets had tended to have less prediction error than other resolutions. St. Johns datasets had equal median MAE at every resolution, while Lee datasets had the lowest median error at the weekly resolution. Because monthly datasets could explain the most deviance in four out of five locations, and had the lowest median MAE in three out of five locations, this resolution was used for the rest of the analysis.

At this time, I would also talk about mean bias. I'm still mulling over my mean bias results,

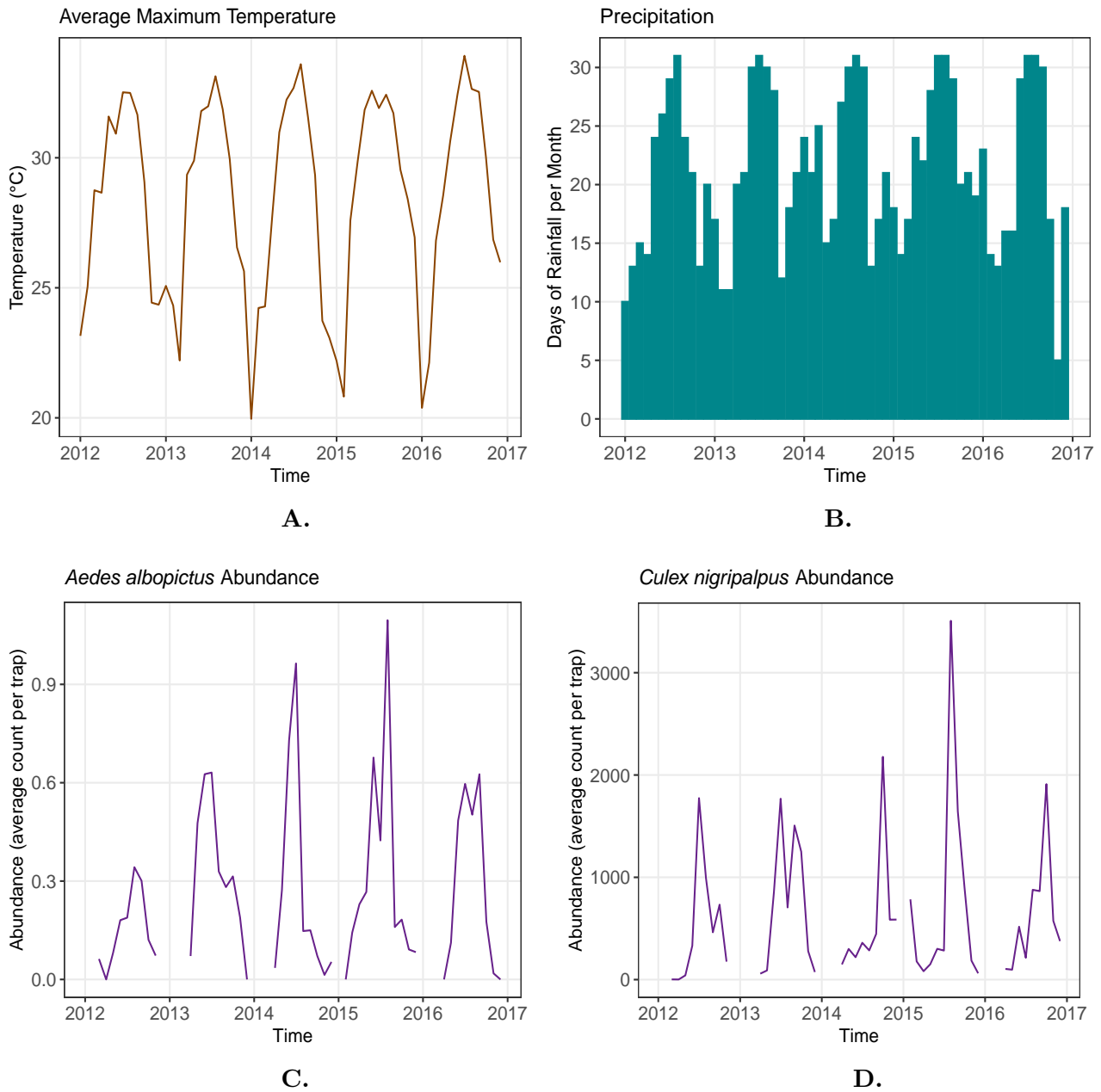


Fig. 2. Time series data of temperature, precipitation, and two vector species from Manatee County, Florida, 2012-2016. Data shown here are aggregated at the monthly scale. In **A.**, average daily maximum temperature per week shows regular seasonality with a range of about 15 °C. In **B.**, precipitation is very frequent during during a summer rainy season. This is common in all locations. **C.** and **D.** show patterns of abundance for two vector species, *Aedes albopictus* and *Culex nigripalpus*. Abundance datasets were non-continuous over winter periods where abundances are assumed to be low so traps are not employed. These missing data points were removed from datasets prior to analysis.

however, so this will be updated in my final draft.

Median Deviance Explained and Median MAE at Various Temporal Resolutions			
County	Weekly	Bimonthly	Monthly
Lee	37.7% (3.60)	45.8% (9.66)	52.2% (11.87)
Manatee	30.2% (1.04)	35.5% (0.92)	40.1% (0.90)
Orange	26.2% (0.50)	29.0% (0.44)	35.0% (0.43)
St. Johns	13.0% (0.20)	*25.9% (0.20)	12.6% (0.20)
Walton	31.7% (0.26)	40.2% (0.22)	49.9% (0.19)
All Counties	28.6% (0.76)	33.0% (0.83)	37.9% (0.78)

Table 2. Deviance explained and MAE by the best fit multivariate model of temperature and precipitation for each dataset summarised by the median value at each location and temporal resolution. MAE is in parentheses. Median was used because the distribution of deviance explained and MAE was left skewed.

How consistent are best fit temporal lags and the influence of temperature and precipitation on mosquito abundance across locations?

I used corrected AIC selection in univariate models of temperature and precipitation to find the best fit lags of temperature and precipitation for each dataset. Temperature in the contemporary time period ($l_T = 0$) was most frequently the best fit lag across all temporal resolutions. For precipitation models (Equation 2), lags of one and two weeks at the weekly scale were nearly equally most frequent (selected in 14 and 13 datasets, respectively). At the bimonthly scale, best fit lags of zero lags were most frequent but were favoured in only one more dataset than precipitation with one half month lag (31 and 30 datasets, respectively). At the monthly scale, the contemporary month was most frequently the best fit lag.

In order to assess the consistency of best-fit meteorological model characteristics in individual species across locations, I narrowed my monthly dataset to eleven species that occurred in all five locations and examined the frequency of best-fit lags and significant variables in each species. Nine out of eleven species (81.8%) had single temperature lag that was preferred in a majority of locations (Fig 4A.). Only one species, *Psorophora ciliata*, had consistent best fit lags for temperature across all locations. Eight of the eleven species had a precipitation lag that was best fit for a majority of the locations, but only 1 species, *Aedes infirmatus*, had a single lag length consistently chosen across all locations (Fig 4B.).

Across 128 monthly that successfully converged in a multivariate model of abundance, models with significance in both temperature and precipitation was slightly more common than other combinations of variables. Variable categories were sorted by number of datasets where only temperature (25.8%), only precipitation (25.0%), both variables (30.5%), or neither variable (18.8%) was significant (Fig 4C.). In the focal eleven species, there were no species with a single category of significant pre-

dictors consistent across locations. Eight out of eleven species (72.7%), however, had a single category of significant predictors in at least a majority of locations.

How does incorporation of an autoregressive term affect the predictive ability of temperature and precipitation driven models of mosquito abundance?

I used relative comparison of deviance explained and corrected AIC to understand the change in multivariate model fits with the addition of an autoregressive term of lagged abundance (Equation 4). From 129 monthly datasets, 8 were removed that failed to converge in either multivariate model. As expected, the autoregressive term tended to improve model fit with a mean change in deviance explained of +16.7% and median change in deviance explained of +10.9% across all locations. Four datasets had a decrease in deviance explained with incorporation of an autoregressive term (range of [-2.1%, -0.2%]). Surprisingly, according to selection through corrected AIC, almost a third of datasets (31.4%) were equally or better fit by the model with only meteorological predictors.

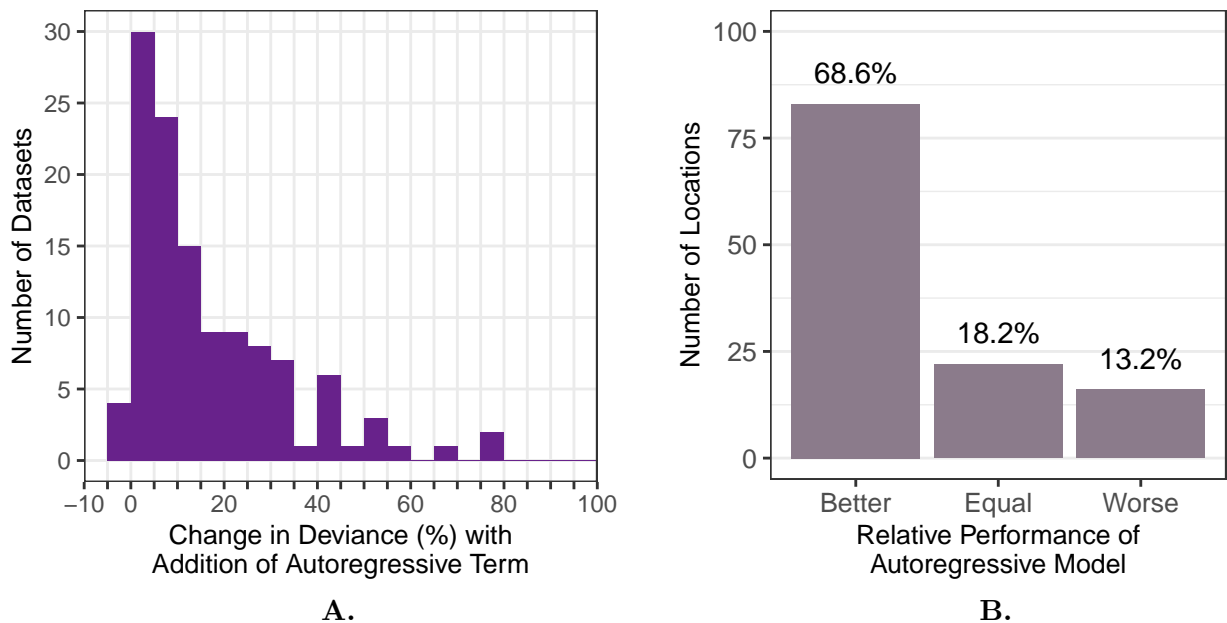


Fig. 3. Comparison of the fit of autoregressive versus non-autoregressive meteorological models of mosquito abundance for each monthly dataset. After removing 8 datasets where the autoregressive model did not converge, 121 datasets were compared. **A.** is a histogram of the relative change in deviance explained with the incorporation of an autoregressive term to the multivariate model for each dataset. Four datasets had a decrease (range of [-2.1%, -0.2%]) in deviance explained with incorporation of an autoregressive term. In **B.**, the number of datasets where the autoregressive model was a better, equal, and worse fit than the non-autoregressive model is shown.

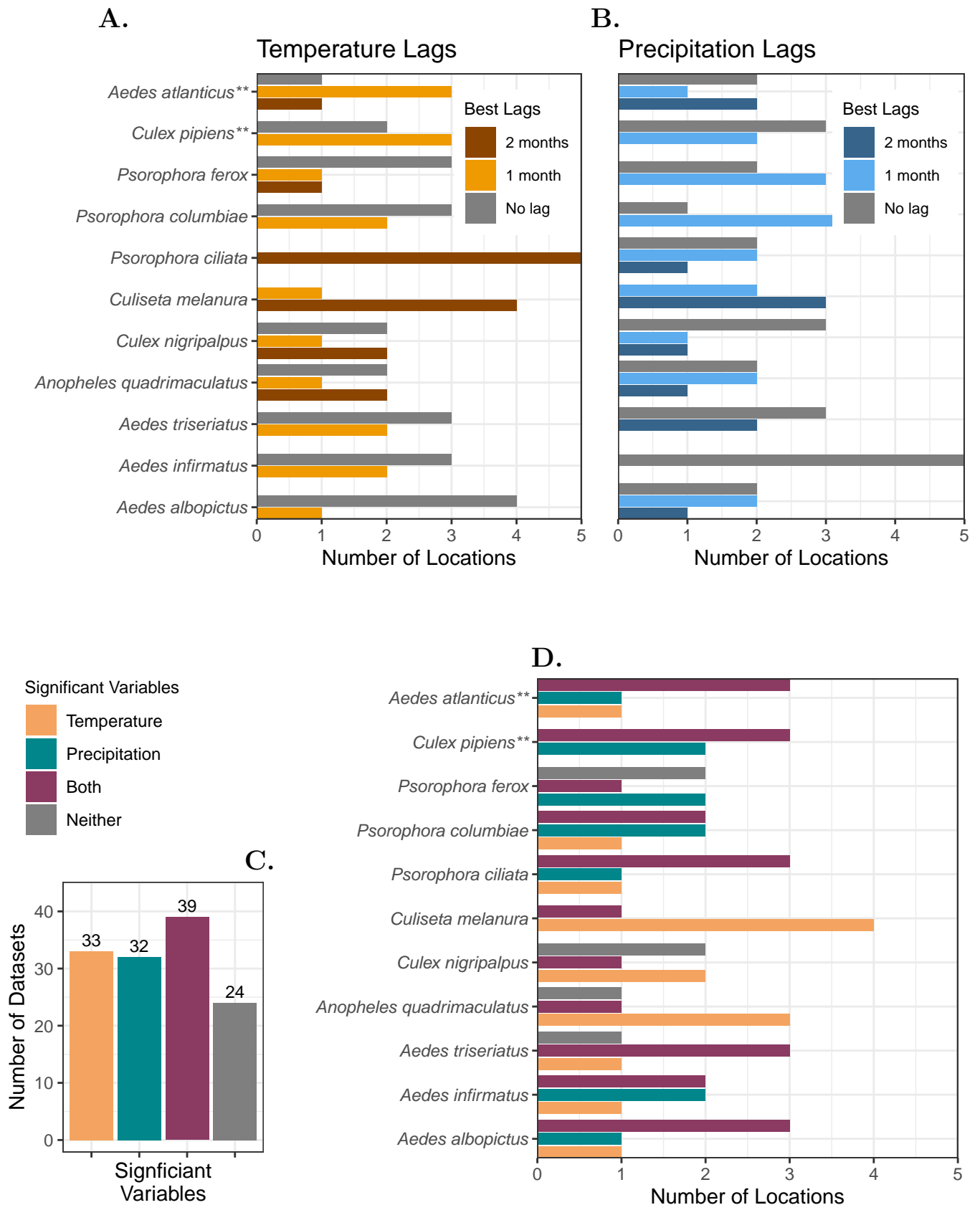


Fig. 4. Frequency of best fit lags and significant variables across locations for monthly datasets. Morphological groups are marked with asterisks. In **A.** and **B.**, frequency of best fit temperature and precipitation lags chosen by corrected AIC from univariate models of abundance are shown for eleven species that were present in all locations. **C.** shows the frequency of significant predictors for 128 abundance datasets fit with multivariate models of temperature and precipitation. In **D.**, the eleven species are shown with the frequency of significant variables in datasets across all locations.

Discussion

Mosquito-borne disease transmission is dependent on both natural and human environmental factors, such as climate, land use, health infrastructure, host demographics- using only climate will overestimate impact of climate change on populations (Parham et al., 2015)

Aggregation of precipitation will lose the importance of quick torrential rains likely to flush immature mosquitoes (Koenraadt and Harrington, 2008)

Even if monthly aggregated data captures more of the variation, we're talking aggregation not surveillance protocol. Studies have shown lower sampling error when doing more frequent (1/week) sampling versus less frequent but more sampling (2/fortnight) (Magbity and Lines, 2002)

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