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Mapping eastern equine encephalitis virus risk for white-tailed deer in Michigan

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Abstract

Eastern equine encephalitis (EEE) is a mosquito-borne viral disease that is often fatal to humans and horses. Some species including white-tailed deer and passerine birds can survive infection with the EEE virus (EEEV) and develop antibodies that can be detected using laboratory techniques. In this way, collected serum samples from free ranging white-tailed deer can be used to monitor the presence of the virus in ecosystems. This study developed and tested a risk index model designed to predict EEEV activity in white-tailed deer in a three-county area of Michigan. The model evaluates EEEV risk on a continuous scale from 0.0 (no measurable risk) to 1.0 (highest possible risk). High risk habitats are identified as those preferred by white-tailed deer that are also located in close proximity to an abundance of wetlands and lowland forests, which support disease vectors and hosts. The model was developed based on relevant literature and was tested with known locations of infected deer that showed neurological symptoms. The risk index model accurately predicted the known locations, with the mean value for those sites equal to the 94th percentile of values in the study area. The risk map produced by the model could be used refine future EEEV monitoring efforts that use serum samples from free-ranging white-tailed deer to monitor viral activity. Alternatively, it could be used focus educational efforts targeted toward deer hunters that may have elevated risks of infection.

Keywords

arbovirus; disease mapping; GIS; *Odocoileus virginianus*; wildlife

INTRODUCTION

Eastern equine encephalitis (EEE) is a mosquito-borne disease caused by the EEE virus (EEEV). EEEV is endemic to the eastern United States and infects a variety of vertebrate species. EEEV is primarily found along the Atlantic and Gulf coasts, although it also occurs in some inland areas near the Great Lakes. An estimated 30-70% of human cases and 90% of horse cases of EEE are fatal, and survivors often suffer severe neurological complications (CDC 2014). Mortality rates are also high for some species of exotic birds, such as ring-necked pheasants (*Phasianus colchicus*) (Williams et al., 2000) and emu (*Dromaius novaehollandiae*) (Tengelsen et al., 2001). Mortality from EEE has been reported in some native wildlife, including the endangered whooping crane (Dein et al., 1986). EEEV infections have been reported in domestic pigs (Elvinger et al., 1996), cattle (McGee et al., 1992), sheep (Bauer et al. 2005), dogs (Farrar et al., 2005), and chickens (Griffiths & McClain, 1985), although these species typically do not show signs of disease and instead develop detectable antibodies against the virus. Similar resistance to EEEV has been observed in a variety of wildlife, including some passerine birds (Sun et al., 2013), wading birds (Gottdenker, Howerth, & Mead, 2003), ungulates (Berl et al., 2013; Lubelczyk et al., 2014; Schmitt et al., 2007), and snakes (Bingham et al., 2012).

EEEV is maintained in ecosystems through an enzootic cycle that involves mosquitoes (vectors) and competent avian reservoirs (hosts) that amplify the virus. Throughout much of the eastern US, this cycle primarily involves mosquitoes of the genus *Culiseta* (*Cs. melanura* and *Cs. morsitans*) and the bird species that they feed upon, such as northern cardinals (*Cardinalis cardinalis*) and other song birds (Cohen et al., 2009; Estep et al., 2011; McLean et al., 1985; Molaei, Andreadis, & Armstrong, 2007; Molaei et al., 2010; Estep et al., 2013). EEEV is then transmitted to humans, horses, and other susceptible species via bridge vectors—mosquitoes that feed on both birds and mammals. Common bridge vectors include *Aedes vexans*, *Coquillettidia perturbans*, *Ochlerotatus sollicitans*, and *Ochlerotatus canadensis* (Armstrong & Andreadis, 2010a, 2010b). In the Northeast and Great Lakes regions, EEEV transmission peaks during summer and early fall, and not every year, while transmission is typically observed year-round in Florida (CDC 2014).

Though EEE is relatively rare, high fatality rates in humans, horses, and other susceptible species prompt many government agencies to implement prevention, monitoring, and control programs. A vaccine is commercially available to prevent EEE in horses (Pandya et al., 2012). As the equivalent is unavailable for humans, reducing exposure to mosquitoes is the most reliable way to prevent human EEEV infections. Recommended approaches include using insect repellents, wearing protective clothing, installing screens on windows and doors, and removing mosquito breeding sites from yards and gardens. Monitoring efforts typically involve testing blood samples from collected mosquitoes or avian sentinel flocks of chickens (Loftin et al., 2006; Morriset al., 1994; Oprandy, Olson, & Scott, 1988; Ottendorfer & Stark, 2006) or wild birds (Williams et al., 1971). A recent innovation in EEEV surveillance involves screening free-ranging wildlife that are resistant to the disease for antibodies. Serum samples can be collected from hunter harvests, road kill surveys, or other methods (Berl et al., 2013; Eisen et al., 2011). If EEEV is detected by any of these means, attempts to curb its transmission generally involve aerial spraying of insecticides

over impacted areas in order to kill any potentially infected mosquitoes (Carpenter, Lee, & Chancy, 1981; Howard & Oliver, 1997). Programs like these are vital for protecting public health, although the costs incurred can be large, reaching more than \$100 million annually in some states.

A potential way to reduce costs is to target efforts in locations with higher risks of transmission. Predictive modelling using GIS offers one approach for identifying priority areas. A popular approach involves the development of index models. Typically, these models measure physical, biotic, or human variables for spatial units—either raster cells or polygons—and combine them mathematically to derive final index values that measure the outcome of interest. Index models have found utility in a variety of geographic applications, such as assessing the suitability of lands for wildlife habitat (Downs, Gates, & Murray, 2008), agricultural production (Wilson et al., 1992), and urban activities (Rybarczyk & Wu, 2010). Index models are also widely applied for measuring socio-economic (Weber et al., 2015) and environmental vulnerability (Malcomb, Weaver, & Krakowka, 2014; Kovarik & van Beynen, 2015), as well as quantifying risk associated with natural hazards (Platt, 2014), environmental dangers (Santini et al., 2010), and a host of other threats. Index models are particularly useful for mapping risk of disease and predicting future outbreaks. Index models and closely related approaches have been widely used to map high risk locations for a variety of mosquito-borne diseases, such as West Nile Virus (LaBeaud et al., 2008; Rochlin et al., 2011; Young, Tullis, & Cothren, 2013) and Dengue (Machado-Machado, 2012; Wen et al., 2015). Once high risk areas are identified using these approaches, efficient monitoring and control strategies can be developed and implemented (Chu, Chan, & Jao, 2013).

This paper develops and tests a risk index model for mapping EEEV risk for white-tailed deer (*Odocoileus virginianus*) in Michigan. EEEV can cause encephalitis and abnormal behaviour in white-tailed deer (Schmitt et al., 2007), though mortality is thought to be relatively uncommon. The first fatal infection was reported in a single deer in Georgia during 2001 (Tate et al., 2005) and subsequently a small number of other cases have been documented in Michigan (Schmitt et al., 2007). It is generally thought that EEEV poses only a minimal threat to deer populations, since they are generally resistant to the virus and produce antibodies upon infection. EEEV antibodies are widespread in deer populations in the Northeast, with 7.1% of sampled deer testing positive in Maine (Eisen et al., 2011) and 10.2% in Vermont (Berl et al., 2013), further suggesting mortality is insignificant. The antibodies produced by white-tailed deer can be detected using plaque-reduction neutralization assay methods in the laboratory, and testing free-ranging individuals for antibodies can be a cost-effective way to monitor viral activity over a large geographic area as is commonly done in Maine (Eisen et al., 2011) and Vermont (Berl et al., 2013). The model developed in this paper is designed to map EEEV infection risk for white-tailed in order to target surveillance, prevention, or control efforts.

MATERIALS AND METHODS

A risk index model was developed to evaluate EEEV risk to white-tailed deer in the state of Michigan. Since 1980, 16 human cases of EEE have been documented in Michigan, the highest incidence in the Great Lakes region. The state has also recently experienced high

numbers of equine cases, including 8 in 2005 and 58 in 2010. Additionally, 8 white-tailed deer cases and their geographic locations were reported for 2005 in a study by (Schmitt et al., 2007). The free-ranging deer in the sample displayed signs of chronic wasting disease or other neurological symptoms. The individuals were subsequently euthanized in the field, and tissue samples were sent for analysis. Eight individuals tested positive for EEEV. The three-county area where those deer were located was selected as the study area for this research included Kent, Ionia, and Montcalm counties in the Lower Peninsula (Figure 1). These counties support some of the highest deer densities in the nation, estimated at 30-40 deer per square mile or larger (QDMA 2009). Ten of the reported horse cases also occurred within these three counties, suggesting it is an ideal region for model testing.

The risk modelling approach used in this paper mirrors that of habitat suitability index (HSI) modelling. HSI models measure relevant environmental data and incorporate them into a mathematical equation that rates habitat suitability for wildlife species on a continuous scale from 0.0 (unsuitable) to 1.0 (optimal) (Roloff & Kernohan, 1999). Risk index models use similar techniques to measure risk on a scale from 0.0 (no measurable risk) to 1.0 (highest possible risk). The model developed here follows the same basic structure as a risk index model used to predict EEEV risk to horses in Florida (Vander Kelen et al., 2014), but the inputs (termed risk variables) are adapted to reflect habitat preferences of white-tailed deer and the relevant vector mosquito species in Michigan. The model quantifies EEEV risk to white-tailed deer at individual locations in a map (represented as raster cells) based on the habitat type at that location and the composition and configuration of surrounding land cover types. The risk variables were identified from a number of published papers detailing habitat use of white-tailed deer, as well as habitats associated with EEEV vectors and hosts. The model is composed of five risk variables (RVs) hypothesized to be associated with EEEV transmission: likelihood of cover type to support white-tailed deer (RV1), distance to nearest wetland (RV2), percentage of wetlands in surrounding landscape (RV3), distance to the nearest lowland forest (RV4), and percentage of lowland forest in the surrounding landscape (RV5). The final risk index is computed using an equation that combines the variables, as described below.

Risk variable 1 (RV1): local habitat

RV1 measures EEEV transmission risk associated with the habitat type at each cell in terms of supporting white-tailed deer. Values for RV1 were derived based on the relative likelihood of white-tailed deer using particular cover types, as measured in a study by (Hiller, Campa, & Winterstein, 2009), which reported the percentage of time white-tailed deer in south-central Michigan spent in each habitat type during the growing season, the time period corresponding to EEEV activity. The habitat type used most often was upland deciduous forest (27.12%). As per Vander Kelen et al. (2014), this cover type was assigned the highest risk value of 1.0. Risk values for remaining cover types were calculated by dividing the reported percentage for that type by that of the highest class to create a ratio of relative risk. For example, lowland shrub was used 17.49% of the time, so its calculated RV1 value would be 0.645 (17.49% / 27.12%). RV1 values for remaining cover types are shown in Table 1.

Risk variable 2 (RV2): wetland proximity

Wetlands are associated with EEEV activity as they support mosquitoes which transmit the virus, as well as numerous avian reservoir hosts (Gottdenker et al., 2003), so areas closer to wetlands have an elevated risk. RV2 measures EEEV transmission risk associated with the distance to wetlands.

The same formulation for RV2 used by Vander Kelen et al. (2014) is used here. RV2 is calculated based on the distance from the focal raster cell (the raster cell being evaluated) to the nearest wetland in meters, d_w , where:

$$RV2 = \begin{cases} 1 & \text{if } d_w \leq 400 \\ 1 - \left(\frac{d_w - 400}{1500 - 400} \right) & \text{if } 400 < d_w < 1500 \\ 0 & \text{if } d_w \geq 1500 \end{cases}.$$

If a cell is located less than 400 m from the nearest wetland, it is assigned the highest possible risk value of 1.0. If it is located between 400 and 1500 m, it receives a scaled value between 0.0 and 1.0, inversely proportional to the measured distance. The cell is assigned a value of 0.0 if it is located greater than 1500 m away from the nearest wetland. The 1500 m threshold was based on the distance that many of the EEEV vectors typically disperse (Estep et al., 2010).

Risk variable 3 (RV3): wetland composition

As wetlands support mosquitoes that transmit EEEV, areas with abundant wetlands have an elevated risk. RV3 measures EEEV risk associated with the percentage of wetlands within the neighbourhood of the focal raster cell. The same formulation for RV3 used by Vander Kelen et al. (2014) is used here. RV3 is calculated from the percentage of wetlands within a 1500-m radius of each focal cell, p_w , where:

$$RV3 = \begin{cases} 1 & \text{if } p_w \geq 18\% \\ \frac{p_w}{18\%} & \text{if } p_w < 18\% \end{cases}.$$

In other words, if the calculated percentage of wetlands within 1500 m of the focal raster cell is greater than 18%, then that cell is assigned a value of 1.0 for RV3. If the cell is surrounded by less than 18% wetlands, it is assigned a value proportional to the percentage observed relative to 18%. For example, if the cell is surrounded by 6% wetlands, it receives a value of 0.33. Similar to RV2, 1500 m was used as it measures the distance that EEEV vectors typically disperse [39]. The threshold of 18% was based on that observed in a study by Vander Kelen et al., (2012).

Risk variable 4 (RV4): lowland forest proximity

In the much of the eastern U.S., including the Great Lakes region, EEEV activity is thought to be associated with bottomland or lowland forests. These habitats support primary and bridge vector species (Snow, 1955; Rey, et al., 2012), as well as avian hosts (Estep et al., 2011; Molaei et al., 2013). White-tailed deer in Michigan also heavily utilize lowland forests

during spring and summer (Hiller et al., 2009), which coincides with peaks in EEEV transmission. As locations nearer to lowland forests would be expected to have a higher risk of transmission, RV4 measures the proximity to lowland forests. RV4 is calculated based on the distance from the focal raster cell to the nearest lowland forest in meters, d_l , where:

$$RV4 = \begin{cases} 1 & \text{if } d_l \leq 250 \\ 1 - \left(\frac{d_l - 250}{1500 - 250} \right) & \text{if } 250 < d_l < 1500 \\ 0 & \text{if } d_l \geq 1500 \end{cases}.$$

If a cell is less than 250 m from the nearest lowland forest, it is assigned a value of 1. If it is located between 250 and 1500 m, it receives a value that extends from 0.0 to 1.0, inversely proportional to the calculated distance. For example, if the distance is 500 m, then $RV4 = 0.8$. If a cell is more than 1500 m away, it is assigned 0.0. The distance parameters were modelled after Vander Kelen et al. (2014).

Risk variable 5 (RV5): lowland forest composition

RV5 measures risk identically to RV3, except it measures the abundance of lowland forests instead of wetlands. RV5 is calculated from the percentage of lowland forest within 1500 m of each focal cell, p_l , where:

$$RV5 = \begin{cases} 1 & \text{if } p_l \geq 20\% \\ \frac{p_l}{20\%} & \text{if } p_l < 20\% \end{cases}.$$

If the calculated percent of lowland forests in the focal area is greater than 20%, the focal cell receives a value of 1.0 for RV5. For values less than 20%, the cell receives a value proportional to the amount calculated.

Risk index (RI): EEEV transmission risk

The final risk index model assesses EEEV transmission to white-tailed deer based on the five risk variables identified above. The model consists of two parts that are multiplied together to generate a final risk index (RI) value for each grid cell, where:

$$RI = RV1 \times \left[\frac{RV2 + RV3 + RV4 + RV5}{4} \right].$$

The first term, $RV1$, measures the local transmission risk at the grid cell based on the likelihood of being occupied by white-tailed deer, as determined from its cover type. The second term, which is calculated as an average of the remaining four risk variables measures transmission risk for the surrounding landscape in terms of distance and abundance of wetlands and lowland forests, which support vectors with their normal dispersal distance. These four variables are averaged since they play similar roles in supporting mosquitoes, and high values for some can compensate for lower values in others. The final risk index is calculated as the product of the two main terms. Multiplication ensures that cells only

receive high index values if high risk values are calculated for both terms—in other words, if both white-tailed deer and vectors are likely to interact at that location.

Risk index model application

The model was applied to the three-county study area using land cover data at a 30 m spatial resolution with ArcMap v. 10.0 (ESRI, Inc). The data set was published for 2001 and supplied by the Michigan Geographic Data Library (<http://www.mcgi.state.mi.us/mgdl/>). This dataset was the most recent land cover layer available and the closest in time to the 2005 deer cases used to test the model. The land cover classification included 31 types that were aggregated into 13 classes for the purposes of applying the model: (1) *Coniferous Forest*—Aspen Association, Mixed Upland Deciduous, Other Upland Deciduous, Upland Mixed Forest; (2) *Lowland Shrub*; (3) *Agriculture*—Forage Crops / Non-tilled Herbaceous, Non-vegetated Farmland, Orchards/Vineyards/Nursery, Row Crops; (4) *Coniferous Forest*—Mixed Upland Conifers, Other Upland Conifers, Pines; (5) *Lowland Forest*—Lowland Deciduous, Lowland Mixed, Lowland Coniferous; (6) *Northern Hardwood Association*; (7) *Wetland*—Emergent Wetland, Floating Aquatic, Mixed Non-Forest Wetland; (8) *Oak Association*; (9) *Open Water*; (10) *Herbaceous Open Land*—Herbaceous Open Land, Parks/Golf Courses; (11) *Urban*—High Intensity Urban, Low Intensity Urban, Roads/Paved; (12) *Upland Shrub*; and (13) *Other*.

The risk index model was tested using the spatial locations of the eight white-tailed deer documented with EEEV; the latitude and longitude of the locations were reported by (Schmitt, et al., 2007). First, the locations of the deer were plotted in the GIS. Then, the risk variable and index values were extracted at those locations using standard GIS functions. Individual values and summary statistics were reported. Risk index values were also compared to those recorded for random locations in order to test if the known sites had higher risk values than expected by chance. For this purpose, 300 samples of 8 random points were generated. The mean risk index of each random sample was calculated, and a *t*-test was used to determine if the means were different from that calculated for known locations. This analysis was repeated using the maximum values found within a 100-m radius of both the known and random locations. This was done to account for a small degrees of spatial error associated with the known locations. This distance also reflects that the deer were more likely to have been infected by EEEV near the recorded location but not exactly at that site (Berl et al., 2013; Eisen et al., 2011).

RESULTS

Individual risk variables and the final risk index are mapped in Figure 2. The map of RV1 reflects the distribution of land cover types in the study area. The three counties are predominantly composed of agriculture, lowland shrub, and a variety of forest types, most of which are suitable to white-tailed deer. The patch of low RV1 values in the southern portion of Kent County is the city of Grand Rapids. RV2 values are relatively high throughout much of the study area, though there are widely distributed small groups of low values. RV3, which measures wetland composition, shows a very patchy spatial distribution of high values, with relatively few areas dominated by large expanses of wetlands. High RV4

values, which measure proximity to lowland forests, are widespread but slightly less so than RV2. RV5, which measures lowland forest composition, shows a relatively restricted spatial distribution of high values. The final risk map reflects the combination of the five individual risk variables at each grid cell. Risk index values are not evenly distributed across the study area. The mean of 0.18 ($s = 0.15$) indicates the study area is largely comprised of relatively low risk areas. Risk is lowest around the city of Grand Rapids and highest in preferred white-tailed deer habitats that are near to an abundance of wetlands and lowland forests. The highest value calculated in the map is 0.84.

Individual risk variables and the final index values extracted from the locations of the eight known white-tailed deer infected with EEEV are recorded in the first several columns of Table 2. Risk maps zoomed to a finer scale centred on each location are shown in Figure 3. Risk variables for the deer locations were very similar whether they were extracted from the exact locations or using the 100 m radius, with the exception of RV1. RV1 values were relatively low directly at the sites, some of which were directly on or next to roads (mean of 0.12). When the error radius was considered, RV1 values for the locations increased substantially to a mean of 0.88, indicating all were located very near habitats highly suitable for deer. RV2 and RV4 values were high for all deer locations, with averages of 0.95 or higher regardless of how they were extracted. This indicates the locations were in close proximity to both wetlands and lowland forests. RV3 and RV5 averaged 0.12 and 0.18, respectively, indicating they were located in areas with moderately abundant wetlands and lowland forests. The risk index values extracted from the direct locations ranged from 0.0 to 0.25, with a mean of only 0.07. However, when an error radius of only 100 m was used, computed risk values for the deer locations ranged from 0.23 to 0.62, with a mean of 0.55. Compared to other values in the map, these rank highly; the mean of the deer sample marks the 94th percentile in the risk index map, with the lowest value ranking 65th percentile. If urban areas and other habitats not often used by deer (i.e. $SV \leq 0.05$) are excluded the analysis, the mean of the deer sample still ranks highly at 89th percentile. Removing these habitats from the analysis removes potential bias of including Grand Rapids and other cities in the analysis. The comparison between the 8 deer locations and 300 sets of 8 random points confirms the values for the deer locations were significantly higher than average ($t = 7.6$, $p < 0.001$) using the 100-m error radius for both sets of points (while excluding urban areas and other habitats not often used by deer).

DISCUSSION

This study developed and tested a risk index model designed to predict EEEV activity in white-tailed deer in the Lower Peninsula of Michigan. High risk areas were defined as those with habitats supporting white-tailed deer that are in close proximity to an abundance of wetlands and lowland forests. The model was tested with known locations of infected deer in a 3-county study area. Though the test sample was relatively small, it represented the best data available. The results confirmed that the deer were collected from areas predicted to have a relatively high risk of EEEV transmission, as the mean risk index within 100 m of those sites was equal to the 94th percentile of computed values within the entire study area. The resulting risk map could be used target future EEEV monitoring efforts that use plaque-reduction neutralization assay methods to detect antibodies from serum samples of free-

ranging white-tailed deer, as per (Berl, et al., 2013; Eisen, et al., 2011), or to target aerial insecticide spraying aimed to reduce vector populations and the spread of the virus. Additionally, though EEE is generally not fatal to white-tailed deer, they sometimes show signs of illness, which could potentially impact herd health during outbreaks. The map could be used to identify locations of potential health concern for deer populations. Alternatively, it could be used focus educational efforts targeted toward deer hunters that may have elevated risks of infection. For example, since deer hunters are unlikely to use insect repellent due to the strong scent which might deter deer, those hunting in high risk areas might be encouraged to wear protective clothing.

The results of the index model application yield an important finding relevant to Michigan. The mean of the risk map was 0.18, which indicates risk is moderately low on average throughout the study area. The largest index value observed was 0.84 out of a possible 1.0 which indicates no locations exhibited the maximum possible risk. Computed values were largely limited by RV3, which measures wetland abundance and had maximum recorded value of 0.57. If these results are compared to those from Vander Kelen' et al.'s model for Florida—which is structured identically but rates habitats for horses instead of deer and uses conifers instead of lowland forests—then this range of values is not unexpected. Florida is the state with the highest rate of EEEV activity. Florida supports large numbers of horses and contains large amounts of wetlands and conifers, so high risk index values are very widespread across most regions of the state. In contrast, Michigan displays much lower EEEV activity and fewer large expanses of wetlands. This suggests the computed values for Michigan are meaningful, even if the highest level of risk is not detected. Relative to horses in Florida, risk of infection to white-tailed deer in Michigan is expected to be relatively lower. Despite the smaller range of computed values, areas in Michigan that have elevated levels of risk can be easily identified based on their relative values.

In terms of utilizing the risk index map in practice, there are number of limitations or potential improvements worth mentioning. First, as in any GIS modelling exercise, the quality of the output reflects that of the input. In this case, land cover data of a similar year to the test data was used. However, land cover datasets are subject to attribute error, and habitat data derived from more recent satellite imagery would be desirable for future applications. Second, the model predicts likely locations for EEEV transmission, though deer are mobile and can be harvested some distance from the actual location where they are infected. However, deer, especially females with fawns during summer or those in dense populations, often have small home ranges (Burroughs et al., 2006) (Kilpatrick, Spohr, & Lima, 2001), often about 1 km² in size (Walter et al., 2009). It is thought that deer harvested or collected from a particular location were likely to have been infected nearby (Eisen et al., 2011; Berl et al., 2013). In this study, high risk values were found within 100 m of the deer carcass locations, supporting that claim. Third, the model was developed based on results from previous studies, some of which were not specific to the study area. Any new data collected within the state could be used to further test or refine the model. Fourth, like Vander Kelen et al.'s model, this one only predicts where EEEV activity is likely to occur and not when. As mosquito populations fluctuate in time depending on precipitation (Lubelczyk et al., 2013), this model could be combined with meteorological forecasts to predict EEEV transmission in both space and time. Fifth, the model was developed for the

Great Lakes region, but the basic modelling approach—which was also used successfully in Florida—could be extended to other regions. For example, future work might develop and test similar models specific to the Northeast, where EEEV activity is also prevalent.

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- A GIS model was developed to EEEV risk in white-tailed deer.
- The model was applied and validated using data for Michigan.
- The model accurately predicted deer cases in a 3-county area.
- The results can be used to guide EEEV control efforts.

Figure 1.
Map of the three-county study area in Michigan.

Figure 2.
Maps of individual risk variables and the final risk index model.

Figure 3.
Maps of final risk index values for eight deer cases (black stars in centre of maps).

Table 1

Risk values for local habitat (RV1) for 13 land cover types.

Land cover type at raster cell	RV1
Upland deciduous forest	1.000
Lowland shrub	0.645
Agriculture	0.414
Coniferous forest	0.302
Lowland forest	0.173
Northern hardwood	0.108
Mixed wetland	0.101
Oak association	0.052
Water	0.049
Herbaceous open land	0.010
Urban	0.004
Upland shrub	0.000
Other	0.000

Table 2

Risk variable and risk index values extracted directly from and within 100 meters of the locations of 8 white-tailed deer cases in Michigan.

Case	Value at location					Maximum value within 100 m of location						
	RV1	RV2	RV3	RV4	RV5	RI	RV1	RV2	RV3	RV4	RV5	RI
1	0.30	1.00	0.16	0.90	0.25	0.17	1.00	1.00	0.16	0.97	0.26	0.60
2	0.11	1.00	0.03	1.00	0.07	0.06	1.00	1.00	0.03	1.00	0.08	0.53
3	0.00	0.93	0.09	1.00	0.13	0.00	0.41	1.00	0.10	1.00	0.14	0.23
4	0.41	1.00	0.27	1.00	0.16	0.25	0.65	1.00	0.28	1.00	0.16	0.39
5	0.00	0.96	0.18	0.64	0.11	0.00	1.00	1.00	0.11	0.71	0.11	0.44
6	0.11	1.00	0.05	1.00	0.21	0.06	1.00	1.00	0.05	1.00	0.23	0.57
7	0.00	1.00	0.17	1.00	0.31	0.00	1.00	1.00	0.18	1.00	0.32	0.62
8	0.05	1.00	0.05	1.00	0.15	0.03	1.00	1.00	0.05	1.00	0.15	0.55