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A Simple Spatiotemporal Rabies Model for Skunk and Bat Interaction in Northeast Texas

Our research aims to develop an accurate model for the spread of rabies in skunk and bat populations. Simulations of the model show changes in the distribution and number of infected individuals over time. The study is based on information about skunks and bats in Northeast Texas and utilizes map data which displays the distribution of confirmed rabies cases in Texas. An accurate rabies distribution model will aid authorities by providing information about the most effective way to distribute rabies vaccine pellets. In addition, the visual qualities of our model simulations provide an engaging way to convey information about a known public health hazard to people from a variety of backgrounds.

Most existing models ignore reservoir species or model them with patchy models by ordinary differential equations. However, evidence for the influence of bats on the spatial distribution and rabies dynamics of skunks is supported by Texas map data of confirmed rabies cases. There appears to be a two to three year period in which initial dispersal is followed by a resurgence of infected individuals. This pattern is indicative of the skunk's role as a reservoir species for rabies.

Generally, the rabies virus spreads as infected individuals pass on the infection by biting susceptible individuals. Since infected bats can transmit rabies to susceptible skunks, we incorporate interspecies rabies infection by using a coupled system of differential equations for our model. Hence, the rate of infection for susceptible skunks is affected by the number of infected bats. Partial differential equations are used to account for general and rabid population random movement. Spatial modeling of rabies is particularly important because increased movement (lack of regard for territorial boundaries) is one of the symptoms of rabies.

Initial simulations of our model were applied to a Gaussian distribution of infected individuals. The result was that the peak of the infection decreased as infected individuals spread out from the center. Smaller waves of infection were indicated by periodic small increases in infected individuals. Simulations without bat to skunk infection only projected the decay of infected populations. The partial differential equation system is solved in MATLAB using an adaptive Runge-Kutta 4/5 order solver. No-flux Neumann boundary conditions are implemented.

After the trial simulations, confirmed case data from a $(300 \text{ km})^2$ region in northwest Texas was used to set the initial distribution of infected skunks and bats. Distributions of susceptible, exposed, and recovered individuals were initialized similarly. Most parameter values are obtained or computed from the literature. Simulations of our model with and without the additional infection contributed by bats are compared to the confirmed case data from Texas. The simulations which account for interspecies infection more accurately represent the distribution of infected skunks and bats in our region of study. Our model qualitatively describes the change in distribution of rabies infected bats and skunks over time.