

Discrete Model of Rabies in Raccoons

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Model

The objective of the model formulation is to provide a simple, readily modified framework to analyze alternative spatial control methods for vaccine distribution as it impacts the spread of rabies among raccoons.

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The epidemiological assumptions:

- no variance in time from infection to death
- random mixing assumed to be the only means of contact and transmission

Set-up and assumptions

Time scale: There is no population growth or immigration in this formulation, so the scale is assumed to be over a time period (say within a season) over which births do not occur.

* * *

Mortality occurs only due to infection.

The time step of each iteration is that over which all infected raccoons die (e.g. about 10 days).


Spatial set-up

Spatial scale: each box is uniform in size, arranged rectangularly

Movement: Raccoons are assumed to move according to a movement matrix from cell to cell, with distance dependence and without density-dependence in dispersal.

The matrix for infected raccoons has higher entries.

The coefficient a (less than 1) shows the effect of infecteds moving more than the other raccoons in their own box.



Vaccine/food packets are assumed to be reduced each time step due to uptake by raccoons, with the remaining packets then decaying due to other factors.

Then additional packets are added at the end of each time step.

Model Format

Model with (k,l) denoting spatial location, t time

- susceptibles at time $t = S(k,l,t)$
- infecteds at time $t = I(k,l,t)$
- removed (IMMUNE) at time $t = R(k,l,t)$
- vaccine at time $t = v(k,l,t)$

Order of events

Within a time step:

First movement: using range-diameter to get range of movement and using move ratio, which is larger for infected. See sum S, sum I and sum R to reflect movement.

—Then: some susceptibles become immune by interacting with vaccine

—Lastly: new infecteds from the interaction of the non-immune susceptibles and infecteds

* * * NOTE that infecteds from time step n die and do not appear in time step $n + 1$.

Model Equations

$$S(k, l, t + 1) =$$

$$\left(1 - e_1 \frac{v(k, l, t)}{v(k, l, t) + K}\right) \text{sum_}S(k, l, t)$$

$$- \beta \frac{\left(1 - e_1 \frac{v(k, l, t)}{v(k, l, t) + K}\right) \text{sum_}S(k, l, t) \text{sum_}I(k, l, t)}{a(\text{sum_}S(k, l, t) + \text{sum_}R(k, l, t)) + \text{sum_}I(k, l, t)}$$

$$I(k, l, t + 1) =$$

$$\beta \frac{\left(1 - e_1 \frac{v(k, l, t)}{v(k, l, t) + K}\right) \text{sum_}S(k, l, t) \text{sum_}I(k, l, t)}{a(\text{sum_}S(k, l, t) + \text{sum_}R(k, l, t)) + \text{sum_}I(k, l, t)}$$

Immune and Vaccine Equations

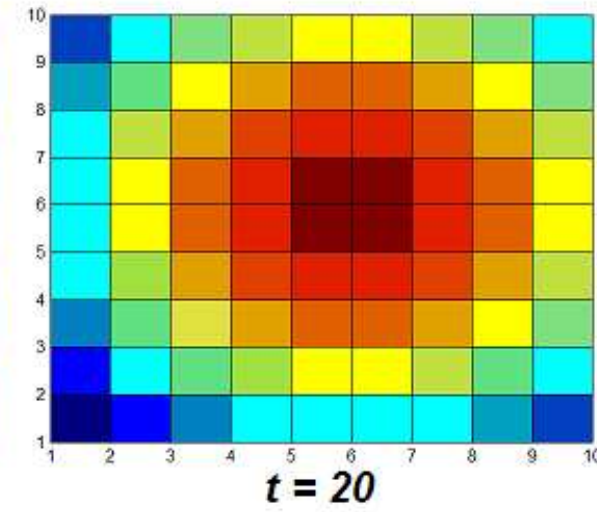
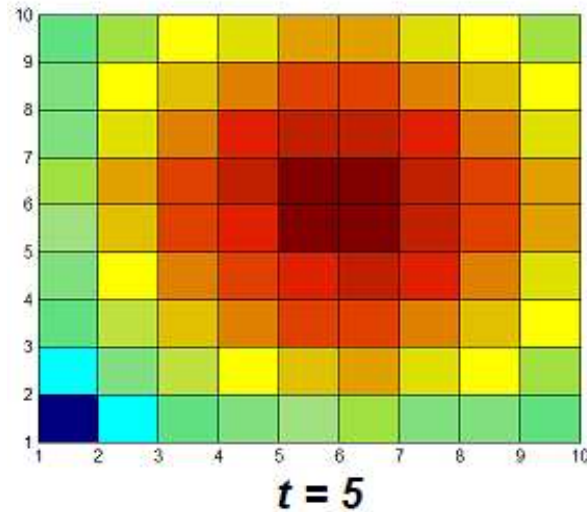
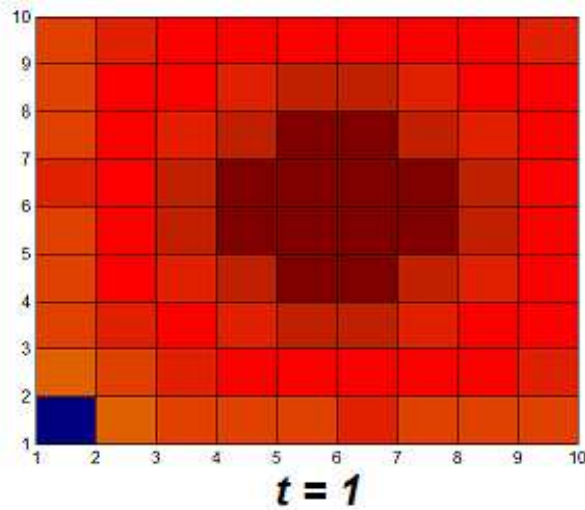
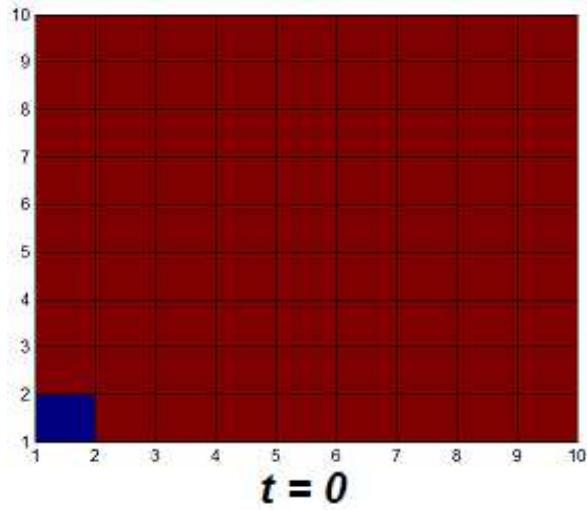
$$R(k, l, t + 1) =$$

$$\text{sum_}R(k, l, t) + e_1 \frac{v(k, l, t)}{v(k, l, t) + K} \text{sum_}S(k, l, t)$$

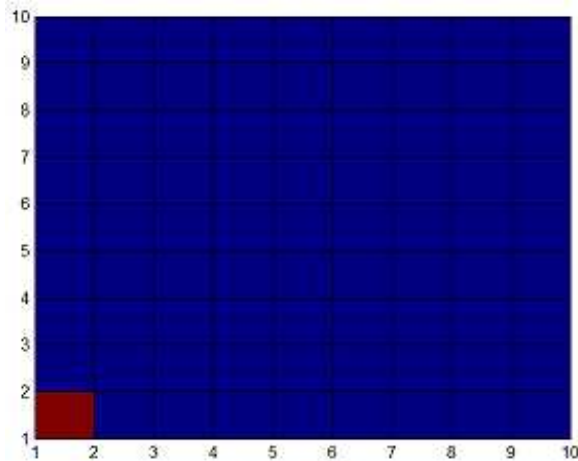
$$v(k, l, t + 1) =$$

$$.75v(k, l, t) \max[0, (1 - e_2(\text{sum_}S(k, l, t) + \text{sum_}R(k, l, t))) \\ + \text{control}(k, l, t)]$$

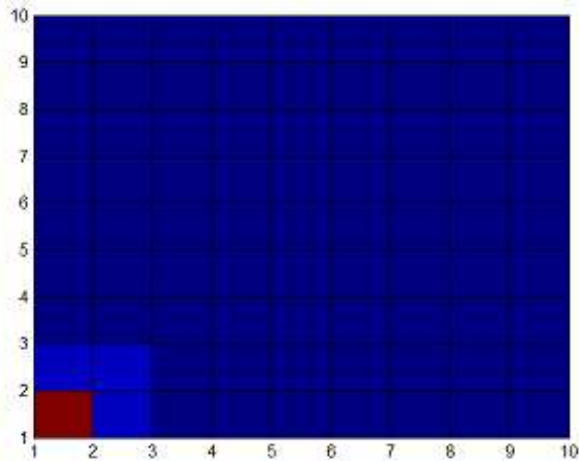
Susceptibles, disease starts at corner



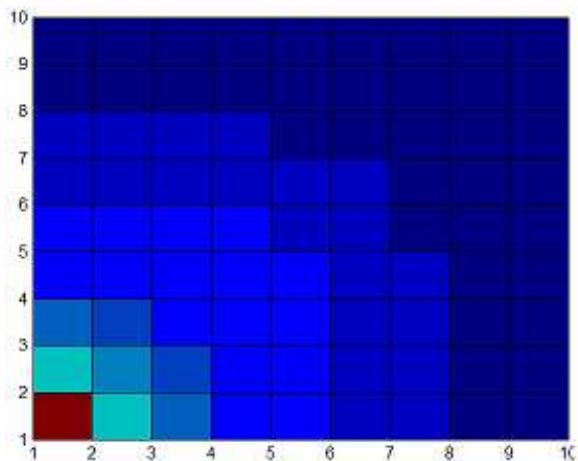
Infecteds



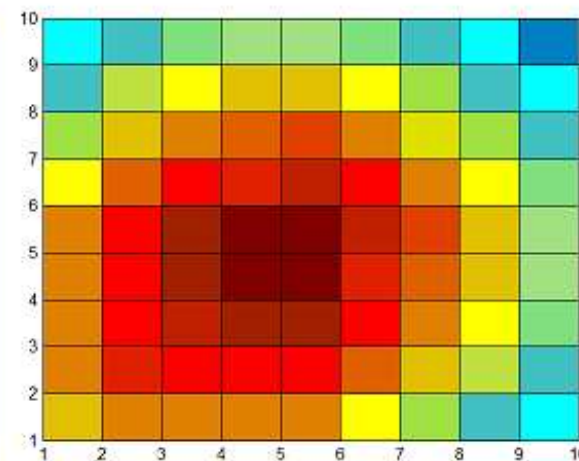
$t = 0$



$t = 1$

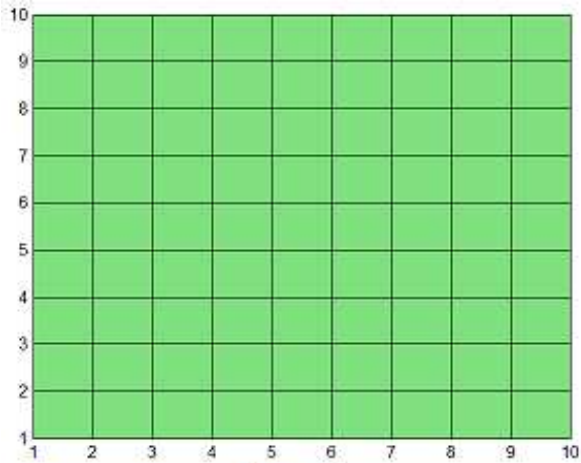


$t = 5$

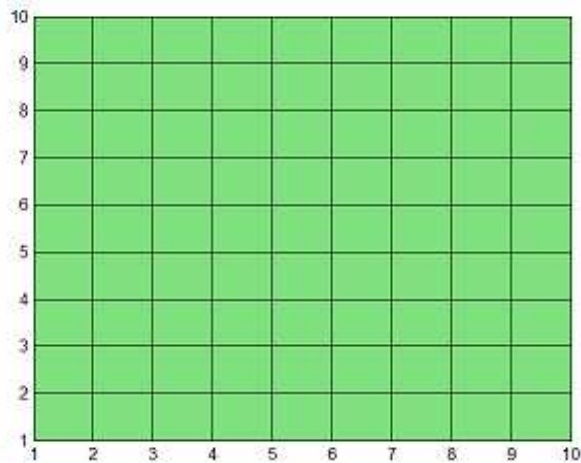


$t = 20$

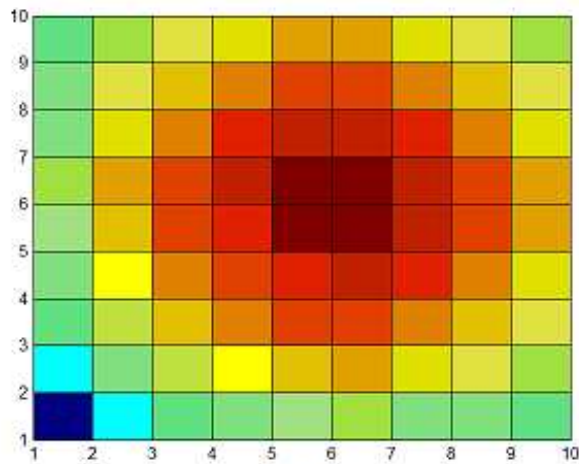
Immune



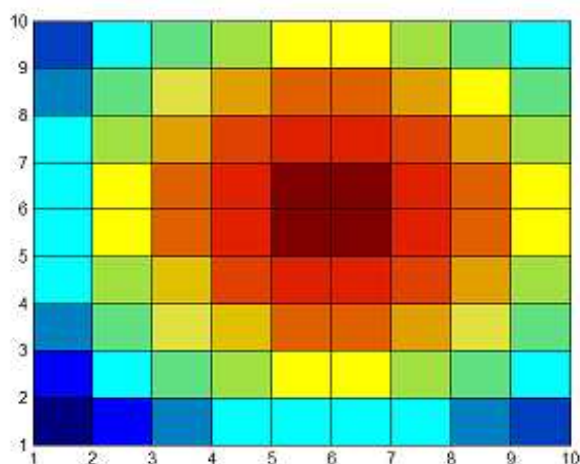
$t = 0$



$t = 1$



$t = 5$



$t = 20$