A Model for a Raccoon Rabies Epidemic in Connecticut

Andy Long

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Abstract

We seek a system of differential equations which are intuitively a good model of a raccoon rabies epidemic, and which simultaneously do a reasonable job of reproducing data associated with an actual epidemic in Connecticut.

1 The Two-State Model

1.1 The equations

Given that x is the healthy raccoon population density, and y the rabid animal density (densities relative to healthy raccoon equilibrium values).

We began by supposing that, in the absence of rabies, the raccoon population x would follow a logistic equation. If rabies is introduced, then we introduce a new state variable, y, the rabid population. Rabies takes awhile to develop, hence we used delay equations, to represent the time that it to develop. Generally the sort of interaction proposed is bi-linear, proportional to the product of each population: hence it is proportional to the populations of the healthy and rabid animals in the past. If the disease took three months to develop, then we would expect there to be a term in the model of the form $x(t-3)y(t-3)$ (if time were measured in months). More generally, however, we might expect that the disease has a variable time to expression, so that there are some rabid animals due to the state three months ago, two months ago, a month and a half ago, etc. More generally, animals are lost from the healthy population at time t due to interactions in past times s: $\kappa(s,t)x(s)y(s)$, where κ represents the strength of the loss at each time s.

Our system might then be written as

$$
\begin{aligned}
\dot{x}(t) &= \alpha x(t)(1 - x(t)) - \beta \int_{-\infty}^{t} \kappa(s,t)x(s)y(s)\,ds \\
\dot{y}(t) &= \beta \int_{-\infty}^{t} \kappa(s,t)x(s)y(s)\,ds - \gamma y(t)
\end{aligned}
\tag{1}
$$

The equations have already been scaled by the equilibrium population of animals in the absence of rabies, which accounts for the 1 in the logistic term. The last term to discuss is the loss to the rabid population: we assume that this is simply a dying exponential, with presumably large value of γ (rabid animals don't live very long).

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1.2 Interpretation of the parameters

- α - the logistic growth rate

- β - the rate of loss of animals to interactions between healthy and rabid animals

- γ - the rate of loss of the rabid animals

- κ - the weight function that determines how the interactions in the past turn into new rabid animals today.

2 The Linear Chain Trick

If one makes a clever choice of κ, then these apparently complex integral delay equations can be transformed into a system of ordinary differential equations, without delay. For the purposes of fitting the data (as shown in the plot, Figure (2)), we assumed that κ is of the form

$$\kappa(t,s) = \alpha(t-s)e^{-c(t-s)}$$

(as seen in Figure (2)). This function is 0 at t, rises to a maximum, then falls to zero as
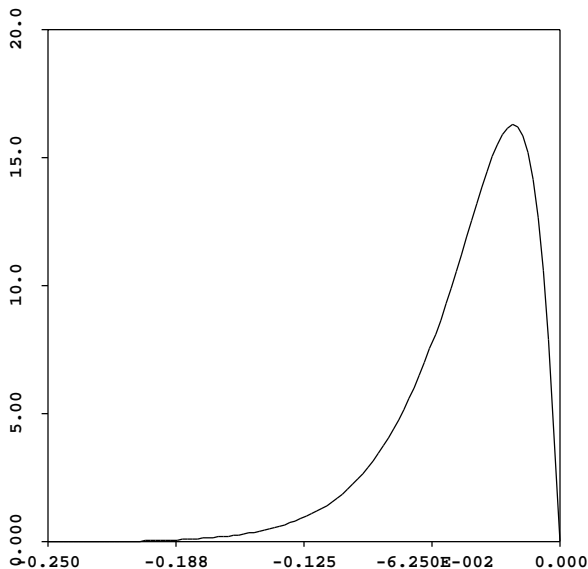
$t \to -\infty$ (as we look farther back into the past). The general kernel that relates to the "linear chain trick" is of the form

$$\kappa(t,s) = \alpha(t-s)^p e^{-c(t-s)}$$

where α is chosen so that κ is a density: that is,

$$\int_{-\infty}^{t} \kappa(t,s)ds = 1$$

Given our particular choice of kernel, we define a new variable, say u, as

$$u(t) = \int_{-\infty}^{t} c^2(t-s)e^{-c(t-s)}x(s)y(s)ds$$

(so $\alpha = c^2$ makes the kernel a density). If one uses Leibniz's rule to differentiate u, one sees that

$$\dot{u}(t) = c(w(t) - u(t))$$

where

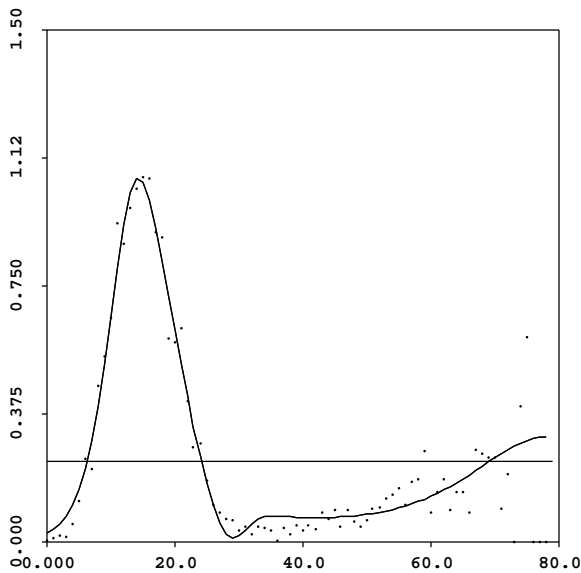$$w(t) = \int_{-\infty}^{t} ce^{-c(t-s)}x(s)y(s)ds$$

(again, $\alpha = c$ makes the kernel of w a density). Differentiating w with respect to time, we find that

$$\dot{w}(t) = c(x(t)y(t) - w(t))$$

We now can convert system (1) to a system of four equations with four state variables:

$$\begin{aligned}
\dot{x}(t) &= \alpha x(t)(1 - x(t)) - \beta u(t) \\
\dot{y}(t) &= \beta u(t) - \gamma y(t) \\
\dot{u}(t) &= c(w(t) - u(t)) \\
\dot{w}(t) &= c(x(t)y(t) - w(t))
\end{aligned} \qquad (2)$$

It is this system that was used to fit the data.

The parameter values used to fit this data are given in table (1).

3   Iterative Parameter Estimation

In order to estimate the parameters, we did non-linear regression: the data vector was provided by the towns of Connecticut (their time series averaged after being shifted so that their predicted start months were aligned); the difference between the data vector and the values predicted by the differential equations is then minimized (scaled appropriately, as described below).

When this process is carried out, we obtain the results compiled in table (1). These parameter results are fairly robust (with the exception of the initial duration parameter, as described below).

Table 1:

Birth rate of healthy	α	1.49
death rate of rabid	γ	2.26
healthy loss rate to rabies	β	12.54
kernel factor	c	44.33
initial healthy pop (proportion of carrying capacity)	x_o	0.985
initial rabid pop	y_o	1-x_o
scale factor	ϕ	1.75
initial duration of rabid background (months)		-0.261

The scale factor ϕ does not appear in the equations: it is a parameter which appears because I match the numerical solution of the rabid population from the system of differential equations to the levels of the data (given as cases per month). The scale factor is the amount by which I must multiply the solution to match the data.

The initial duration of rabid background (months) appears to be a relatively imprecise value (I get essentially the same fit with a value of -.05, for example). This value represents the initial values of u and w, the state variables appearing due to the linear chain trick. These come from integrating a constant, so the question is: for how long have they been integrating a constant value? The answer is this value.

All the other parameters have an explicit representation in the model.

4   Limitations and Future Work

The models that we propose are ordinary differential equations, and presuppose that the populations of raccoons continue to fail to interfere with one another (each town is effectively isolated from other towns). Our models would have raccoon populations bouncing in sync along the linear front for the rest of time. We recognize that the populations will interfere with each other, and the modeled local impact will lose its coherence. Partial differential equations could be constructed to attempt to capture this aspect, effectively allowing us to model the endemic period.