

Figure 1. Sites used to model CWD in Urban and Non-urban land-use types.

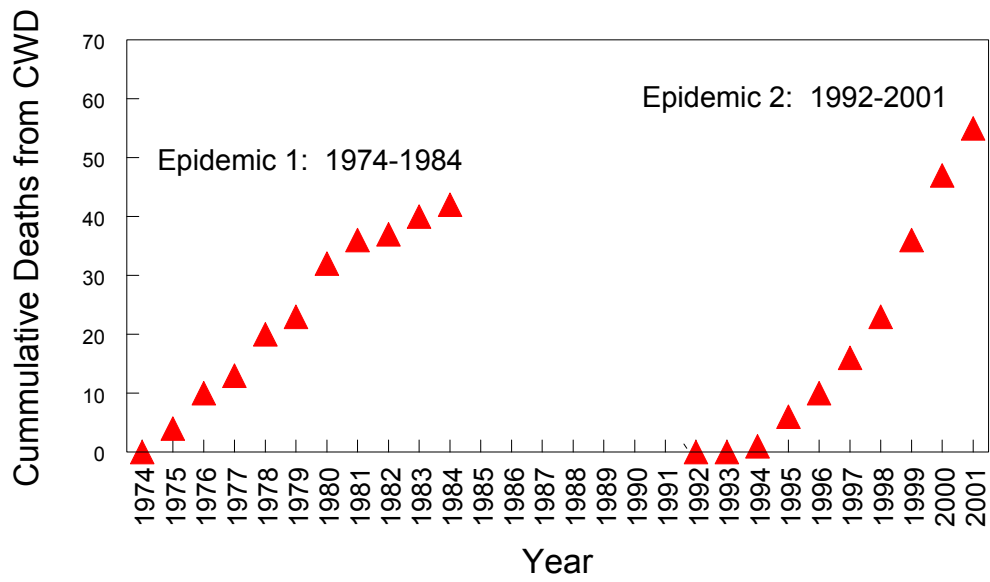


Figure 2. Time series of cumulative mortalities from chronic wasting disease at the Foothills Wildlife Research Facility during 1974-2001.

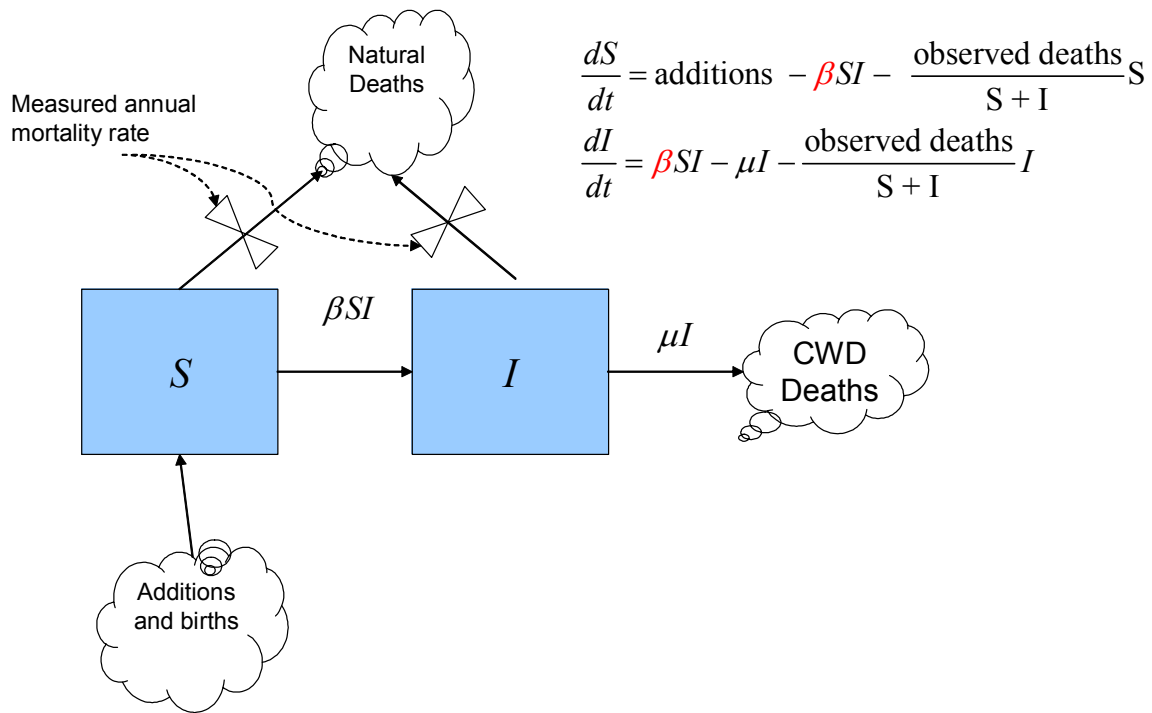


Figure 3. The horizontal transmission model assumes that all transmission occurs by direct contact between infected (*I*) and susceptible (*S*) animals. This model required estimating two initial conditions, the number of infected animals at the start of each epidemic, and a single parameter, the transmission rate (β). Estimates of the CWD mortality rate (μ) were derived from experimental studies.

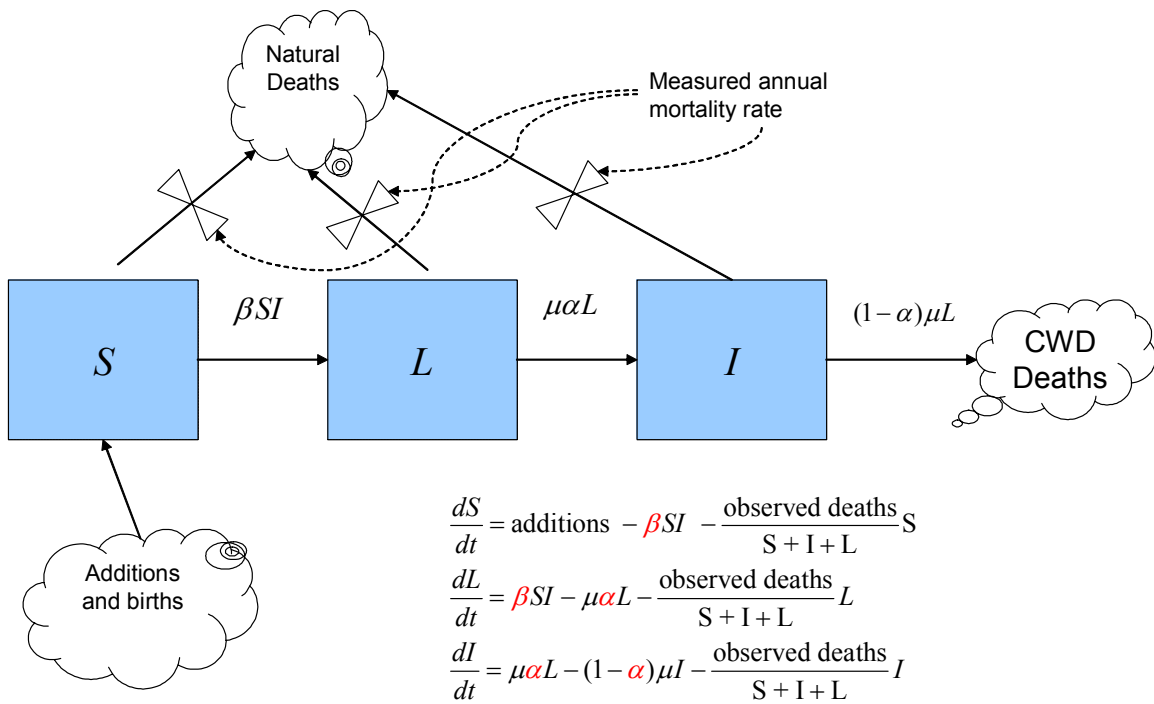


Figure 4. The horizontal transmission model with latency assumes that all transmission occurs by direct contact between infected (I) and susceptible (S) animals but that animals do not become infectious immediately after becoming infected. This model required estimating two initial conditions, the number of infected animals at the start of each epidemic, and a two parameter, the transmission rate (β) and proportion of the clinical course in latency (α). Estimates of the CWD mortality rate (μ) were derived from experimental studies.

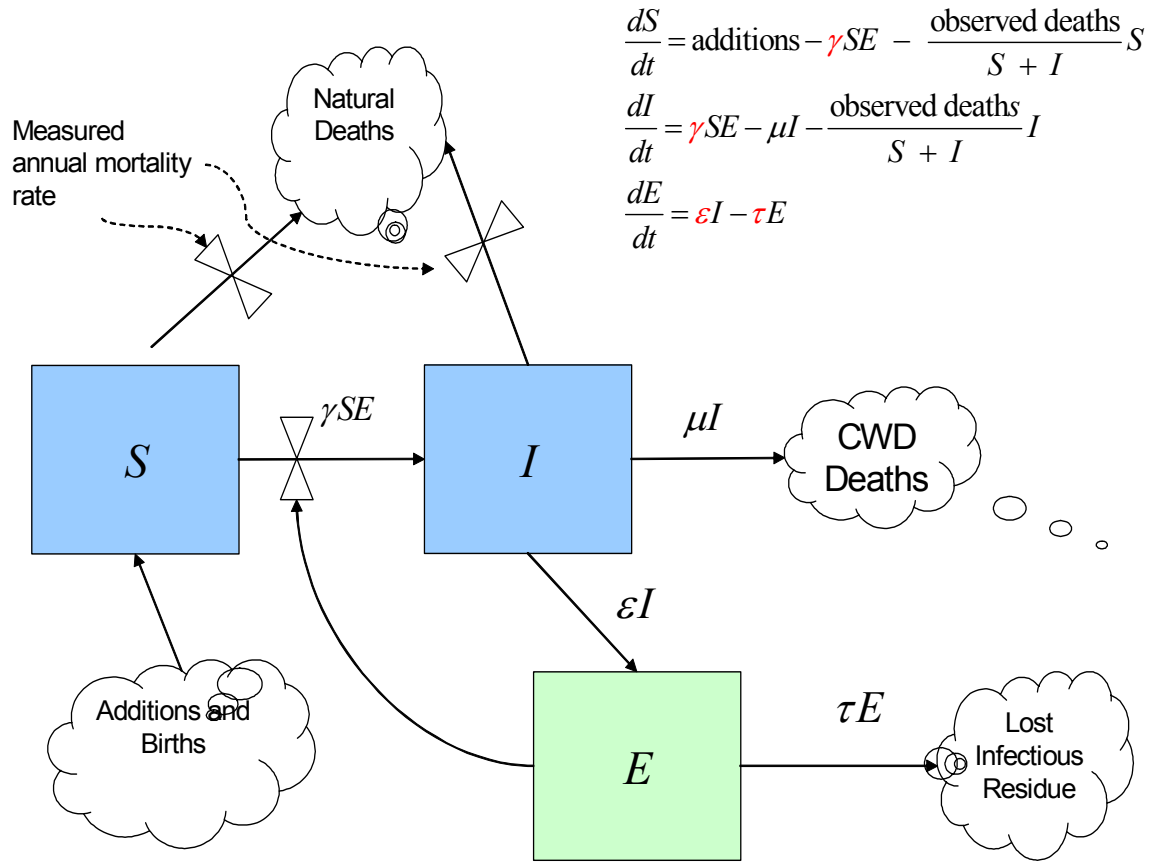


Figure 5. The environmental transmission model assumes that all transmission occurs between infectious environmental residues (urine, feces) and susceptible (S) and that the number of new infections per unit time per susceptible is directly proportionate to mass of infectious material in the environment. This model required estimating two initial conditions, the mass of infectious material at the start of each epidemic, and three parameters, the environmental transmission rate (γ), the rate of excretion of infectious material by infected animals (ε), and the rate of loss of infectious material from the environment (τ). Estimates of the CWD mortality rate (μ) were derived from experimental studies.

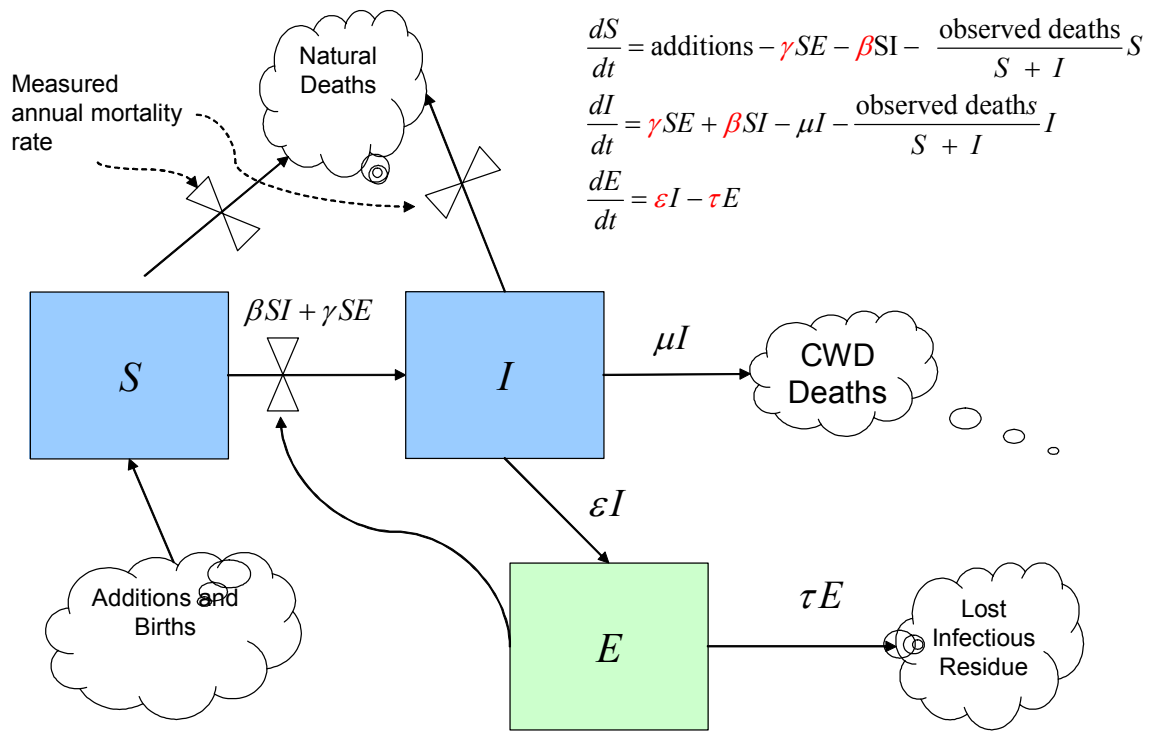


Figure 6. The environment and horizontal model represents transmission from the environment and among individuals as described in Figures 2 and 4.

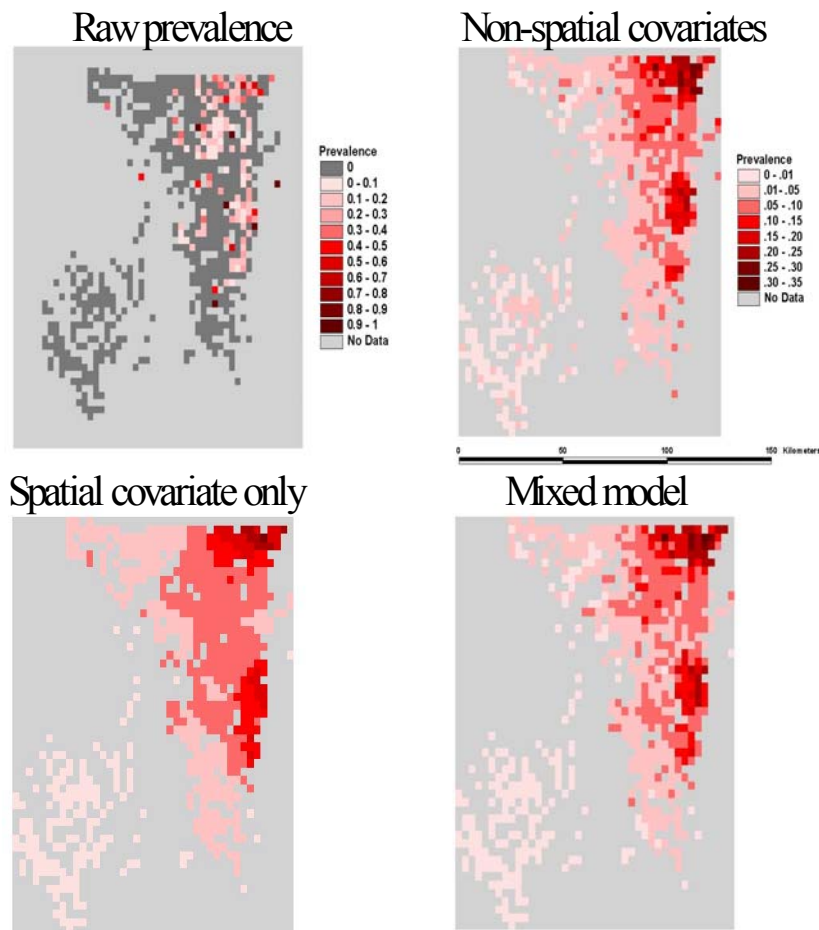


Figure 7. Preliminary estimates of the spatial distribution of prevalence in North-central Colorado.

- 1) Raw Prevalence reflects prevalence rates prior to modeling.
- 2) Non –spatial covariates shows predicted prevalence using non-spatial covariates.
- 3) Spatial covariate only surface uses only the spatial structure of the data to estimate prevalence.
- 4) Mixed Model uses both the non-spatial covariates and the spatial structure of the data to estimate CWD prevalence rates.

Model	AIC_c	Δ_r	$L(\text{model} \text{data})$	w_r
Environmental only	28.69	0	1	0.89
Horizontal	32.99	4.3	0.116	0.10
Environmental and horizontal	38.69	10.0	0.007	0.01
Horizontal with latency	79.00	50.3	0.000	0.00

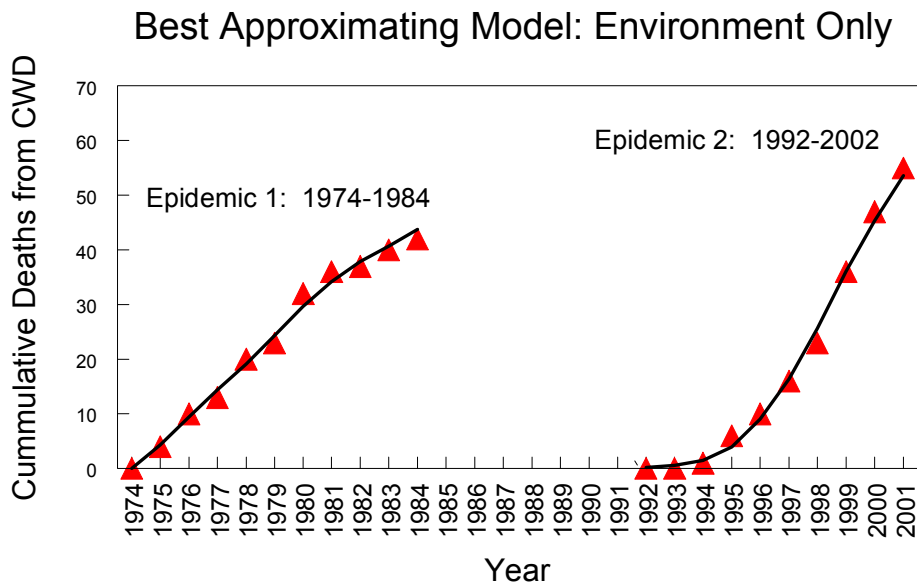


Figure 8. Results of model selection. The environmental transmission model had 8.9 times more support in the data than the next best model, which represented horizontal transmission. There was no support in the data for the combined environmental and horizontal model, or for the horizontal model with latency.

$$\frac{dS}{dt} = b(S + I) \left(1 - \frac{S + I}{K} \right) - \gamma ES - dS$$

$$\frac{dI}{dt} = \gamma ES - (\mu + d)I$$

$$\frac{dE}{dt} = \varepsilon I - \tau E$$

Assumptions

- transmission 1000 x less
- $K = 5000$ animals
- $N_0 = 3500$

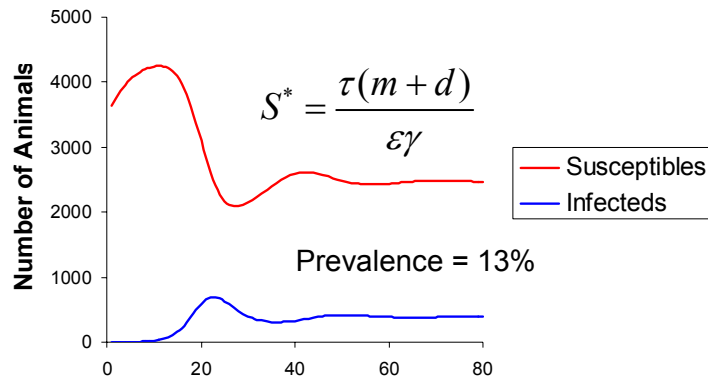


Figure 9. We developed a simple model of dynamics of CWD in mule deer populations regulated by effects of population density on recruitment and by mortality from CWD transmitted from environmental residues. The model assumed that transmission rates were 1000 times less in the wild than in the captive population. The carrying capacity, K was assumed to be 5000 animals, initial population size (N_0) was set at 3500 animals with one infected animal in the population. Maximum per capita birth rate was $.45 \text{ year}^{-1}$ and the per capita death rate was set at $.25 \text{ year}^{-1}$ which produced a maximum population growth rate (in discrete time) of about 20% per year, which is reasonable for mule deer populations.

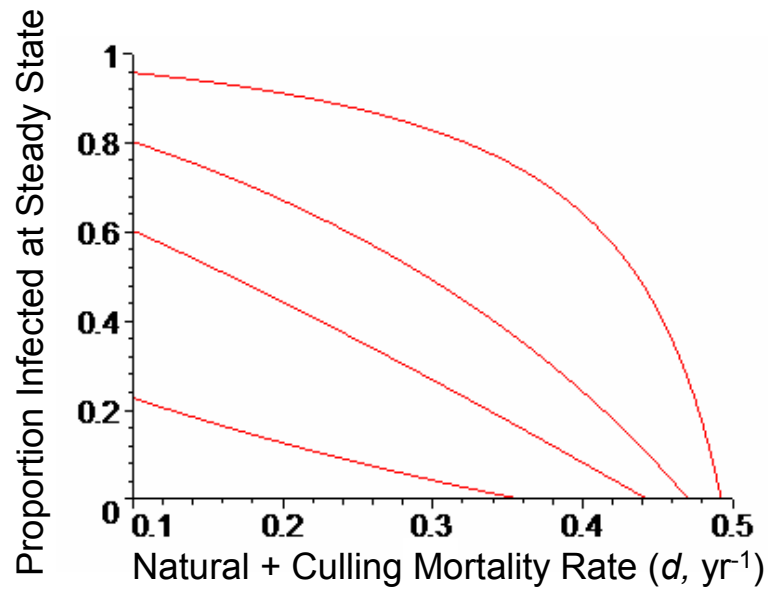


Figure 10. We obtained analytical solutions for the steady state of susceptibles and infected animals and used these solutions to examine the effect of culling on disease prevalence. Each curve represents a different mean residence time of infectious material in the environment, i.e., τ^{-1} . The point where the curves cross the x-axis is the mortality rate needed to eliminate the disease from the population.

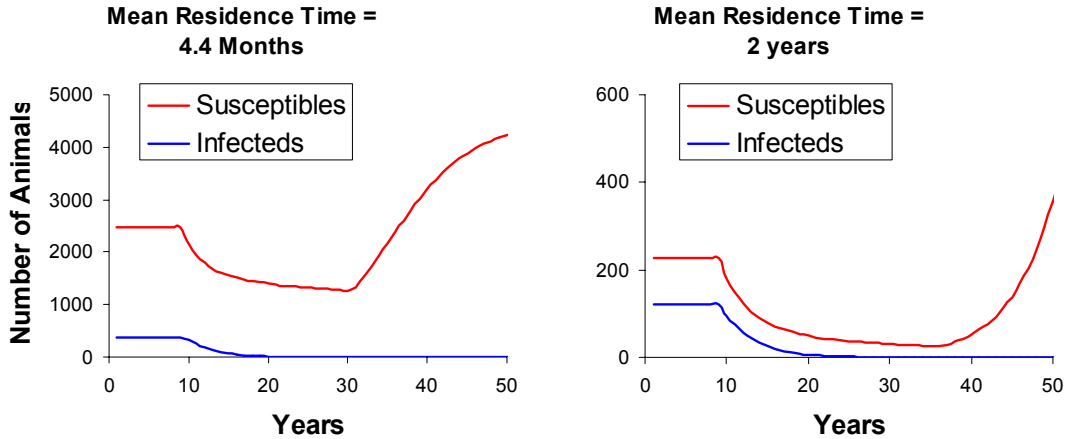


Figure 11. We exercised our population model (figure 7) to examine efficacy of culling as a technique for eradicating CWD in natural populations. Two simulation were conducted, one that assumed a mean residence time of infectious material in the environment of 4.4 months, the other assuming a residence time of 2 years. Initial conditions for susceptibles and infecteds were set to represent populations at equilibrium with the disease (Figure 7). We introduced culling rates necessary to eradicate the disease (Figure 8) during year 10. Simulation results suggest that sustained culling can eliminate the disease, although this may require 30 – 40 years of effort.