Can Selective Predation Slow the Spread of CWD?

Modeling disease, predation, dispersal, and population dynamics in Wisconsin

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March 4, 2020

The question

It is widely asssumed that wolves selectively predate on old, young, weak or infirm individuals.

Given that CWD is concentrated in the SW Wisconsin (but expanding rapidly), and wolves are concentrated in NE Wisconsin (and - maybe expanding? more slowly?), how does wolf presence and selective predation influence:

- **CWD prevalence**
- **CWD spread**
- **Deer abundance**

Modeling goals

- Capturing dynamics of:
  - **disease**,
  - **predation**,
  - **population**
  - **dispersal**
- Biologically meaningful parameters
  - independently estimated / estimable?
- Provide spatially and temporally explicit predictions
- Balances realism with tractability

Other models . . .

Continuous-time, non-spatial SIR-type:

$$\frac{dS}{dt} = a(S+I)\left(1 - \frac{S+I}{K_a}\right) - S(\gamma E + m)$$
$$- (1-p)\delta(S+I),$$

$$\frac{dI}{dt} = \gamma SE - I(m+\mu) - p(1-c)\delta(S+I),$$

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

Journal of Wildlife Diseases, 47(1), 2011, pp. 78–93
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THE ROLE OF PREDATION IN DISEASE CONTROL: A COMPARISON OF SELECTIVE AND NONSELECTIVE REMOVAL ON PRION DISEASE DYNAMICS IN DEER

Margaret A. Wild,[1,5] N. Thompson Hobbs,[2] Mark S. Graham,[1,4] and Michael W. Miller[3]

SCIENTIFIC REP⚙RTS

OPEN | **Wolves contribute to disease control in a multi-host system**

E. Tanner[1], A. White[1], P. Acevedo[2], A. Balseiro[3,4], J. Marcos[1] & C. Gortázar[2]

Basic model structure:

Discrete time / discrete space

- **Annual** - matches data collection and deer biology (birth / seasonal mortality / dispersal?)
- **County-level metapopulation** - matches data reporting and collection

Two classes: Susceptible and Infected

$$S_{i,t+1} = S_{i,t} - \textit{infected} \quad + \textit{recruited} - \textit{died} + \textit{immigrated} - \textit{emigrated}$$

$$I_{i,t+1} = I_{i,t} + \textit{infected} \qquad\qquad\quad - \textit{died} + \textit{immigrated} - \textit{emigrated}$$

Complete model

	Susceptible ($S_{i,t+1}$)	Infected ($I_{i,t+1}$)
disease	$-\gamma\frac{S_{i,t}I_{i,t}}{area}$	$\gamma\frac{S_{i,t}I_{i,t}}{area}$
predation	$-\left(\frac{S_{i,t}}{S_{i,t}+I_{i,t}}\right)\left(\frac{1}{1+\alpha}\right)W_{max}$	$-\left(\frac{I_{i,t}}{S_{i,t}+I_{i,t}}\right)\left(\frac{\alpha}{1+\alpha}\right)W_{max}$
other mortality	$-\mu_s S_{i,t}$	$-\mu_I I_{i,t}$
recruitment	$\rho S_{i,t}(1 - S_{i,t}/K_i)$	
immigration	$\sum_j M_{S,ij}$	$\sum_j M_{I,ij}$
emigration	$-\sum_j E_{s,ji}$	$-\sum_j E_{i,ji}$

Recruitment

Approximate number of new (non-infected) individuals entering population annually:

$$\rho \, S_{i,t}(1 - S_{i,t}/K_i)$$

Assumptions:

1. Logistic, density dependent growth with carrying capacity: K
2. Intrinsic adult recruitment rate, ρ, uniform across range

Non-Wolf:

Annual mortality rate: μ_S and μ_I :

- Equal (!?)
- Constant across range (?))

Wolf:

Assume: **Wolves gonna kill what wolves gonna kill** - (almost entirely deer).

- e.g. 10 wolves, each kills 20 deer / year = 200 deer/year/county killed

Apportioning of S and I killed is proportional to the *availability* ($\frac{I}{S+I}$) and the *preference* ($\frac{\alpha}{1+\alpha}$).

- $P(I\ killed) \propto P(I) \times P(killed \mid I) = \left(\frac{I}{S+I}\right)\left(\frac{\alpha}{1+\alpha}\right) N_w K_{rate}$
- $P(S\ killed) \propto P(S) \times P(killed \mid S) = \left(\frac{S}{S+I}\right)\left(\frac{1}{1+\alpha}\right) N_w K_{rate}$

where α is the odds of selecting infected over non-infected deer, i.e. the Predation Selection Coefficient (presumably > 1).

This is the key, unobservable parameter of interest!

Number of infected . . .

(by county by year)

$$-\gamma \frac{S \times I}{area}$$

- γ is infection rate per encounter
- Total number of infections is higher if areas are smaller (densities are higher).
- Lots of mechanism and structure swept under rug here!

Dispersal

Necessary for disease to spread! (or not spread)

Immigration

$$M_i = \kappa_m \sum_j S_j \exp\left(-\frac{d_{ij}}{\lambda}\right)^\beta$$

Emigration

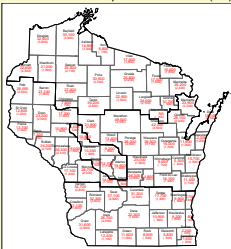$$E_j = \kappa_e S_i \sum_j \exp\left(-\frac{d_{ij}}{\lambda}\right)^\beta$$

- **Exponential** ($\beta = 1$) or **Gaussian** ($\beta = 2$) dispersal kernel with mean λ
- κ - normalization, so that probability of emigrating from site j sums to 1
- Assumes homogenous dispersal in all directions, dependent only on distance.
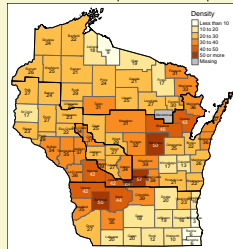- *Estimable (and refinable) from movement data!?*

Deer Abundance

Wisconsin DNR winter population survey:
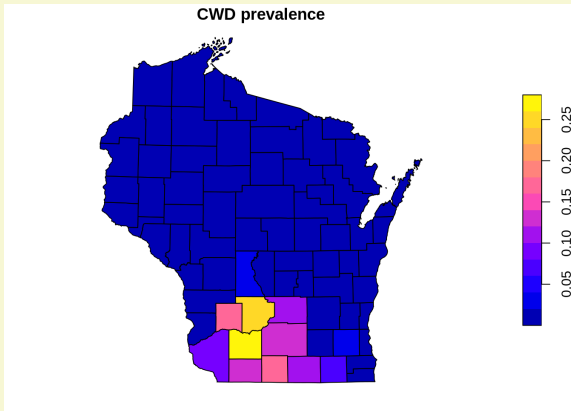https://dnr.wi.gov/topic/hunt/maps.html

Fall population estimates - total harvest, by county.

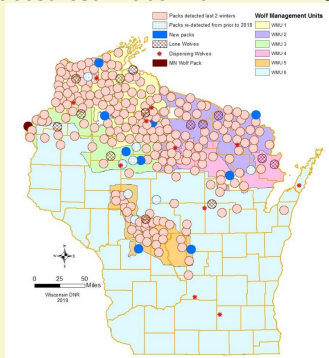Working assumption: Carrying Capacity $K_i = 2N_i$.

Data

CWD prevalence

Wisconsin DNR CWD monitoring efforts (by county)
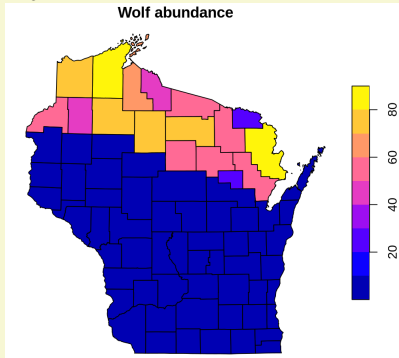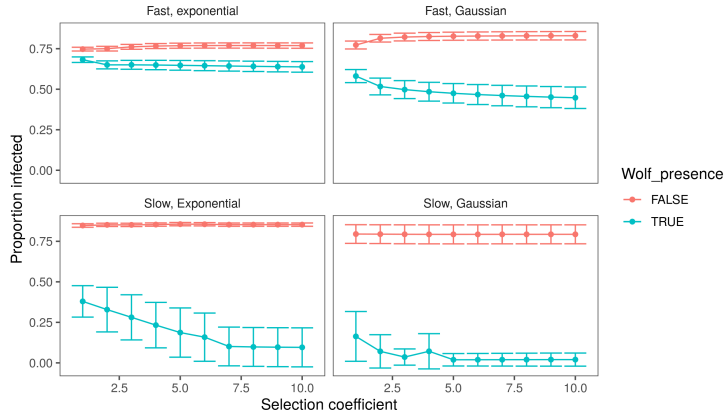
Wolves

Latest estimate from DNR: 950 ind.

County data not readily available ... so I allocated 1000 wolves across the counties north of this line.

Model

Shiny App.

A brand new skill! Facilitates exploring parameters and visualizing results.

(enjoy demo)

A Result: Selective Predation Decreases CWD Prevalence!

In ALL parameterizations, wolves depress CWD. Note - dispersal scale (10 and 80 km) AND shape both important.

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rho = 0.5, gamma = .02, mu_S = 0.06, mu_I = 0.06, W_max = 60,
lambda = 10 or 80
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- Literature review
- Assess / discuss assumptions:
  - Density dependence?
    - Disease transmission?
- Thoroughly analyze / explore parameter space
- Inform with other monitoring data
  - Correct wolf distribution data
  - Mortality - Harvest? Spatially explicit?
  - Movement and dispersal?
- Fit to historical data!?
  - Infer γ by matching to observed CWD spread?
- Get funding!
- Add pictures to presentation!

Thanks!