Can Selective Predation Slow the Spread of CWD?

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

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Acknowledgement

FOREST AND WILDLIFE ECOLOGY
COLLEGE OF AGRICULTURAL & LIFE SCIENCES

Prof. Tim Van Deelen

The setting: **Wisconsin**

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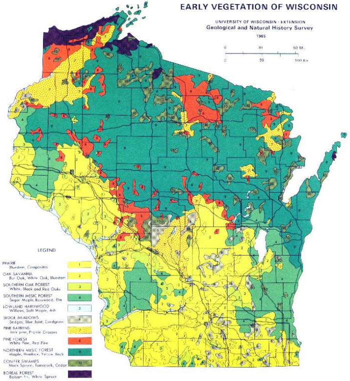
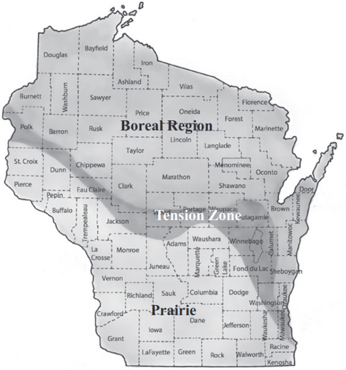
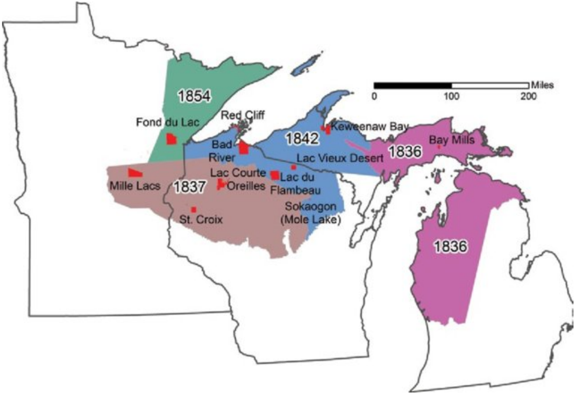




- **Southwest:** Mainly agricultural / ex-prairie and oak savanna.
- **Northeast:** Conifer-hardwood forest / bogs / also agriculture

The setting: **Wisconsin**



Wildlife management and fishing rights largely retained by Ojibwe tribes in the North.

Three characters

1. White-tailed deer
2. Chronic wasting disease
3. Wolves

White-tailed deer in Wisconsin

Odoiceulus virginiacus

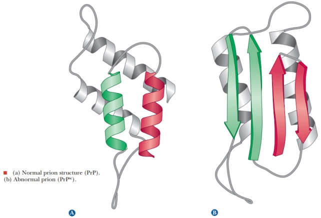
- (over)-abundant: 1.9-2.1 million ind.
- major ecological impacts
- $\approx$ 350,000 hunted annually (and falling)
- \$1.4 billion dollars / year to economy
- a big chunk of which funds research / mitigation of those ecological impacts

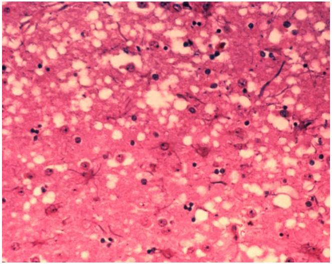
Todd Hubler - *The Isthmus*

Chronic Wasting Disease

Transmissible spongiform encephalopathy

- Turns brains into sponges
- Invariably fatal
- Caused by **prion**
  - misfolded protein found in nervous system
- Only affects cervids
  - only TSE in *wildlife*
- Major focus of concern / research among agencies





Chronic Wasting Disease

Clinical Signs

"Zombie Disease"

- Emaciation
- Lack of coordination
- Drooping head/ears
- Excessive drooling
- Excessive drinking
- Excessive urination

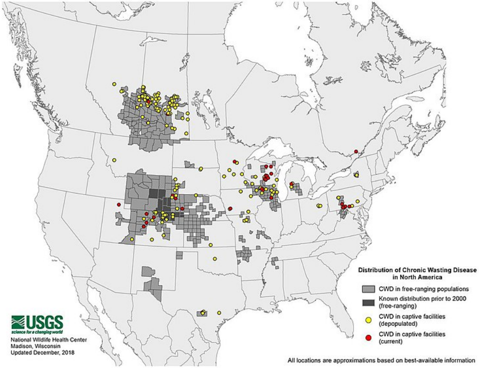
Incubation: (asymptomatic) period lasts on average 18 months

Transmission: urine, feces, blood. Direct contact. Long-term environmental persistence (even uptake by plants).

Chronic Wasting Disease

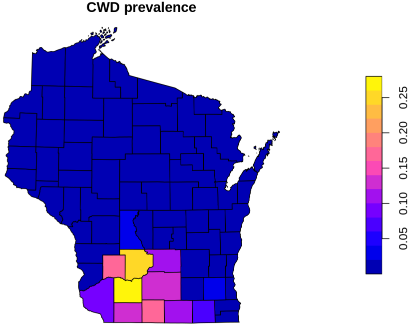
Global Expansion

- 1967 - First detected (mule deer) in research facility Colorado.
- 1981 - First wild animal (elk) detected in Colorado
- 2002 - Found in wild WTD in Wisconsin
- 2011 - Found in wild WTD in Maryland
- 2017 - Appeared in 3 reindeer in Norway (!) - entire 2000 animal herd summarily executed



Chronic Wasting Disease: In Wisconsin

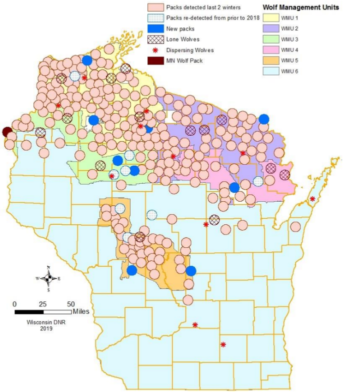
Concentrated in southern counties, up to 25% prevalance.

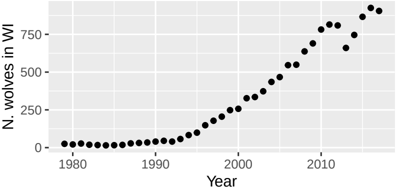


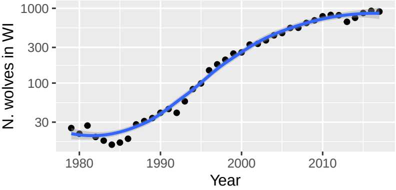
Good data: In affected counties, all hunted carcasses need to be tested. In non-affected counties, a sample of carcasses is tested.

Wolves in Wisconsin

Extirpated early 1900's. Re-colonized from Minnesota post-ESA.







Currently, approx. 1000 ind. mainly in North. Expansion slowing. ***Good Data.***

The question

Wolves selectively predate on old, young, weak or **infirm(?)** individuals . . . though there is no direct evidence w.r.t. CWD (or - actually - other diseases).

Given that CWD is concentrated in the SW - and expanding - and wolves are concentrated in NE - and maybe still expanding? - What happens when they meet?

Specifically, how do wolf presence and selective predation influence:

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

Approaches to look at this question

Lots of ***Mathematical Modeling!!*** Mainly, continuous-time, non-spatial SEIR-type ODE's.

Journal of Wildlife Diseases, 47(1), 2011, pp. 78–93

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]

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

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

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

Very influential, but no data (and no spatial structure)

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[5] & C. Gortázar[2]

$$\frac{dP_S}{dt} = b_A(Y+A)(1-qN) - mP_S - d_P P_S - \beta_{DP} P_S \frac{G}{N} - \omega\beta_{FP} P_S F - a_P P_S W \quad (1a)$$

$$\frac{dP_I}{dt} = \beta_{DP} P_S \frac{G}{N} + \omega\beta_{FP} P_S F - mP_I - d_P P_I - \varepsilon_P P_I - a_P P_I W \quad (1b)$$

$$\frac{dP_G}{dt} = \varepsilon_P P_I - mP_G - \alpha P_G - d_P P_G - a_{PG} P_G W \quad (1c)$$

$$\frac{dY_S}{dt} = mP_S - mY_S - d_Y Y_S - \beta_{DY} Y_S \frac{G}{N} - \omega\beta_{FY} Y_S F - cY_S - a_{YA} Y_S W \quad (1d)$$

$$\frac{dY_I}{dt} = \beta_{DY} Y_S \frac{G}{N} + \omega\beta_{FY} Y_S F + mP_I - mY_I - d_Y Y_I - \varepsilon_Y Y_I - cY_I - a_{YA} Y_I W \quad (1e)$$

$$\frac{dY_G}{dt} = \varepsilon_Y Y_I + mP_G - mY_G - \alpha Y_G - d_Y Y_G - cY_G - a_G Y_G W \quad (1f)$$

$$\frac{dA_S}{dt} = mY_S - d_A A_S - \beta_{DA} A_S \frac{G}{N} - \omega\beta_{FA} A_S F - cA_S - a_{YA} A_S W \quad (1g)$$

$$\frac{dA_I}{dt} = \beta_{DA} A_S \frac{G}{N} + \omega\beta_{FA} A_S F + mY_I - d_A A_I - \varepsilon_A A_I - cA_I - a_{YA} A_I W \quad (1h)$$

$$\frac{dA_G}{dt} = \varepsilon_A A_I + mY_G - \alpha A_G - d_A A_G - cA_G - a_G A_G W \quad (1i)$$

$$W = W(t) \quad (1j)$$

Lots of compartments - and some data (but no spatial structure)

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

Basic model structure:

Discrete time / discrete space

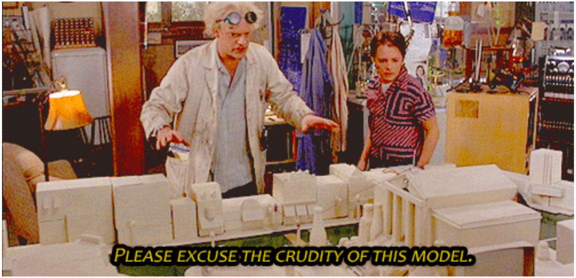
- **Annual** - matches data collection and deer biology (birth / seasonal mortality / dispersal?)
- **County-level metapopulation** - matches data reporting and collection

Two classes: Susceptible and Infected

$$
\begin{aligned}
S_{i,t+1} &= S_{i,t} - \textit{infected} + \textit{recruited} - \textit{died} + \textit{immigrated} - \textit{emigrated} \\
I_{i,t+1} &= I_{i,t} + \textit{infected} - \textit{died} + \textit{immigrated} - \textit{emigrated}
\end{aligned}
$$

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

Mortality

Non-Wolf:

Annual mortality rate: μ_S and μ_I :

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

Mortality

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* $\left(\frac{I}{S+I}\right)$ and the *preference* $\left(\frac{\alpha}{1+\alpha}\right)$.

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

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!

Disease dynamics

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

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

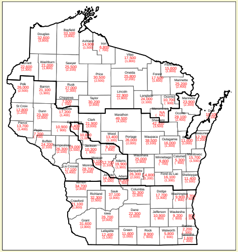
- **Exponential** ($\beta = 1$) or **Gaussian** ($\beta = 2$) dispersal kernel with mean λ
- κ - normalization, so that probability of emigrating from site j sums to 1
- Assumes homogenous dispersal in all directions, dependent only on distance.
- *Estimable (and refinable) from movement data!?*

Data

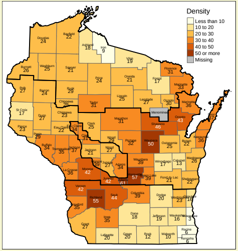
Deer Abundance

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

2018 Winter Deer Population Estimates (SD)



2018 Winter Deer Pop Estimate Per Sq. Mile



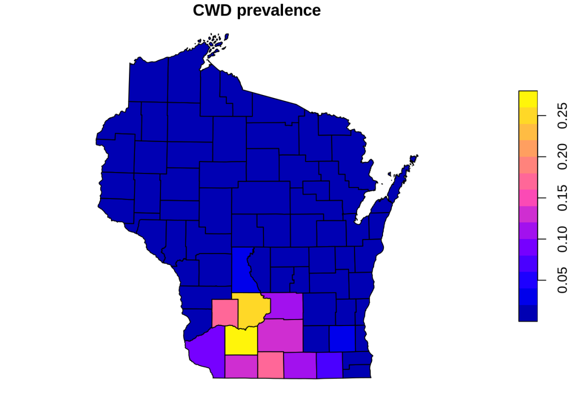
Fall population estimates - total harvest, by county.

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

Data

CWD prevalence

Wisconsin DNR CWD monitoring efforts (by county)

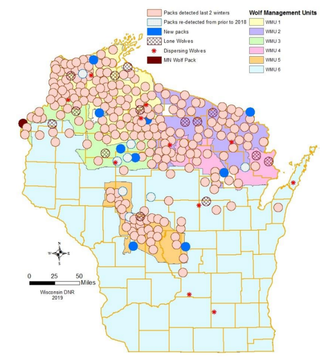


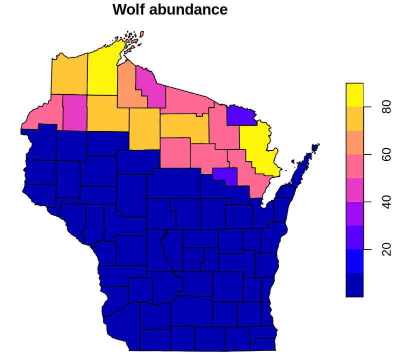
https://dnr.wi.gov/wmcwd/Summary/YearCounty/2019

Data

Wolves

Latest estimate from DNR: 950 ind.





,,,

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

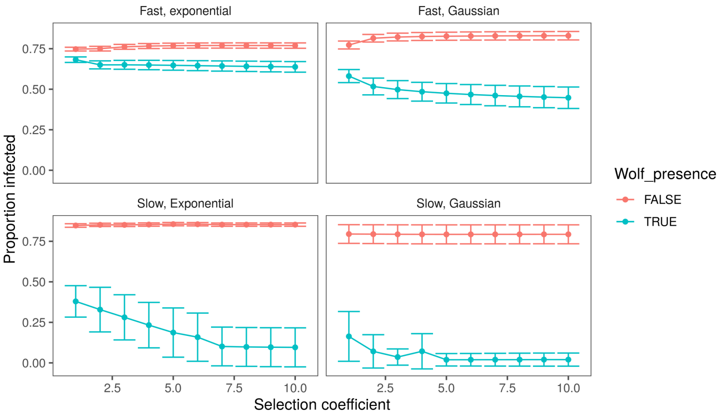
Model

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.

`rho = 0.5, gamma = .02, mu_S = 0.06, mu_I = 0.06, W_max = 60, lambda = 10 or 80`

Next steps

Model structure

- Add **Male / Female** sex classes!
- Separate **Infected / Asymptomatic** from **Infected / Symptomatic**
- Assess assumptions: Density dependence? | Disease transmission?

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Data

- Obtain better **wolf distribution** and **predation** data
- Use **Harvest** for mortality!
- Use **GPS data** for dispersal portion
- Fit to historical data!?
  - Infer γ by matching to observed CWD spread?

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Larger strategy

- Thoroughly analyze / explore parameter space
- Find PhD student to do the work!?
- Get funding!

Thanks!