Forecasting Disaster:
Adding a Human Touch to Animal Disease Predictions

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Background

The implementation of mechanistic mathematical models with probabilistic assumptions has shown success in improving the prediction and forecasting capabilities of Cervid prion disease modeling. By accounting for stochastic processes and sources of measurement error these models reach closer to the reality of the data generating process[3].

Forecasting models such as these have shown to be only applicable to the species that they were designed for as well as expressing a general disregard for the pathobiological principles at play in the data generating processes[3,4]. Yet, as far as human knowledge has taken us, we understand that the mechanisms of prion diseases are fundamentally the same in all species[1,2].

This model expands on the Chronic Wasting Disease model developed by Hefley et al. by incorporating the process of vertical transfer[5] for prion diseases in Cervids and other susceptible animal species. The primary intent of this study is to answer the following two questions:

(1) Does vertical transfer play a scientifically significant role in prion disease forecasting?
(2) Does the separation of disease transfer pathways enable this model to forecast outbreaks in species beyond Cervids?

Methods

Data
Chronic Wasting Disease data, acquired due to the extensive surveillance efforts of the Wisconsin Department of Natural Resources, will be fit to the model after initial simulations confirm sufficient computational optimization. Data from additional species will be sought out periodically throughout the project.

Model Ideation and Development
The model is designed to extend stronger infectious disease principles to the Chronic Wasting Disease forecasting model developed by Hefley et al.
All model development is being done in R programming and designed with the consideration of being placed into an end-user friendly application.

Selection and Validation
Model selection will be conducted by comparing against the original Hefley et al. model as well as a Generalized Additive Model for disease incidence. The horizontal transfer variable will be retained or rejected via a Bayesian Indicator Variable Selection (BIVS) model.

Hierarchical Bayesian Model

Data Model:

$$y_i \sim Bern(p_i)$$

Process Model:

$$g(p_i) = u(\boldsymbol{s}_i, \boldsymbol{t}_i) e^{\boldsymbol{x}_i'\boldsymbol{\beta}} e^{(\boldsymbol{q}_i'\boldsymbol{\tau})\cdot 1\{v\} V}$$

$$\frac{\partial}{\partial t} u(\boldsymbol{s}, \boldsymbol{t}) = \left(\frac{\partial^2}{\partial s_1^2} + \frac{\partial^2}{\partial s_2^2}\right)[\mu(s)u(s,t)] + \lambda(s)u(s,t)$$

$$\log\big(\mu(\boldsymbol{s})\big) = \alpha_0 + \boldsymbol{z}(\boldsymbol{s})'\boldsymbol{\alpha}$$

$$\lambda(s) = \gamma_0 + \boldsymbol{w}(\boldsymbol{s})'\boldsymbol{\gamma}$$

Parameter Model:

$$1\{v\}: \begin{cases} 1 & \text{if birth in } t \\ 0 & \text{o.w.} \end{cases} \qquad V \sim Bern(\varphi)$$

$$u(\boldsymbol{s}, 0) = \frac{\theta e^{\frac{-|s-d|^2}{\phi^2}}}{\int_s e^{\frac{-|s-d|^2}{\phi^2}} ds}$$

$$\boldsymbol{\beta} \sim N(\mu_\beta, \sigma_\beta^2)$$
$$\boldsymbol{\tau} \sim N(\mu_\tau, \sigma_\tau^2)$$
$$\boldsymbol{\alpha} \sim N(\mu_\alpha, \sigma_\alpha^2)$$
$$\boldsymbol{\gamma} \sim N(\mu_\gamma, \sigma_\gamma^2)$$

Hyper-Parameters:

$$\phi \sim TN(\mu_\phi, \sigma_\phi^2) \quad \theta \sim TN(\mu_\theta, \sigma_\theta^2) \quad \varphi \sim Unif(a_\varphi, b_\varphi)$$

Expected Results

- Addition of the vertical transfer parameter should account for incidents of positive cases that are not inherently captured by the data collection process.
- The intended result of this project is a back-end program with the validated model framework, designed with the consideration of being placed into an application.
- Output of the model will be displayed visually in GIS software to allow for adjustment of management practices for spatial locations.

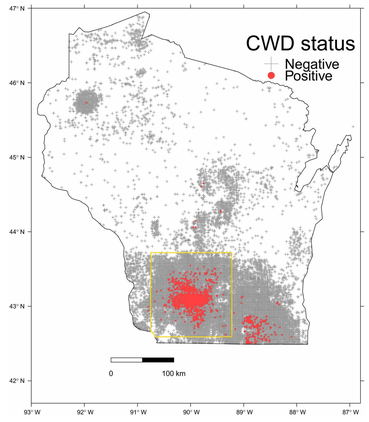
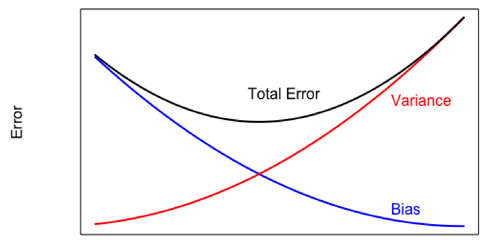


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Discussion

- Creation of a generalized model for prion diseases presents the opportunity to expand to other pathogens. Any disease that follows a similar transfer process, such as *Rabies lyssavirus*, could be applied to the model given it's proven to be effective.
- Cross-species transmission has not been built into the model considerations. Building past the assumption of within-species infection could create a more realistic model.
- Incorporation of other movement models, besides ecological diffusion, in the process model may be necessary to allow livestock and domesticated animal species data to be used in this framework.
- Adding complexity to this model could push it into deeper bias and create problematic outputs. Due to this, checking the model using out-of-sample data is necessary but costly.



References

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Let's Collaborate!

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