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An Application to Elk in the Greater Yellowstone Area

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Managing a Portfolio of Spatial Wildlife Infection Risks: An Application to Elk in the Greater Yellowstone Area

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Background and Research Questions

The Greater Yellowstone Area (GYA) is the last known natural reservoir of *Brucellosis abortus* in the U.S. More than 50% of the elk population are infected, and elk can easily pass the disease to local cattle ranches (NAS 2020). Brucellosis causes abortions in infected female animals, so elk hunters and conservationists are also affected. Additionally, mule deer herds have recently introduced chronic wasting disease (CWD) into the GYA, where it has spread to elk primarily via environmental transmission (Maloney et al. 2020). CWD, which is not transmissible to cattle, always kills the host animal.

Elk-elk and elk-cattle interactions depend on elk and habitat management and disease mitigation activities across GYA's many land uses, including hunting areas, feedgrounds, ranching, and conservation areas. The result is a portfolio of endogenous risks that vary across a spatially diverse landscape.

Our main research question is how to efficiently manage the spatio-temporal portfolio of disease risks. In particular, what is the optimal mix of population controls and land use choices, and how are these actions influenced by spatial considerations?

A secondary question is how to simplify spatial bioeconomic modeling to improve the tractability of dynamic optimization in a spatial setting.

Most prior bioeconomic analyses of wildlife disease are aspatial, but those that are spatial are often based on metapopulation models that divide the landscape into "patches". Each patch has its own populations (e.g., susceptible, infected) whose members can move across patches over time to join other populations. This means the number of state and control variables increases multiplicatively in the number of patches. To offset this complexity, policy analyses are often simplified in some manner - often by placing restrictions on the variables being optimized (e.g., to make them invariant over time or space). Such restrictions increase tractability but reduce the efficiency of any solution, along with the benefits of spatial analysis.

An Epidemiological Model with Endogenous, Within-Patch Heterogeneity

Standard Metapopulation Model Assumptions: No Within-Patch Heterogeneity
 Populations within each patch consist of uniform individuals, distributed uniformly over a homogeneous landscape. This distributional process occurs instantaneously at each point in time, even as individuals move across patches. Within this setting, each individual animal is equally likely to be affected by any ecological or anthropogenic process. Additional patches are required to model heterogeneity.

Modeling Within-Patch Heterogeneity

If it is reasonable to assume that, at each point in time, animals instantaneously distribute themselves uniformly within a patch, then it is reasonable to assume they could instantaneously distribute themselves in an alternative way. There is some precedent for this assumption. Ecological models have used non-linear interaction functions to capture non-uniform distributions, but these functions reflect heterogeneities implicitly: they do not explicitly relate to different land uses. We assume different land uses within a patch, and we adopt distribution functions as weights that determine how many animals locate themselves on the different land use areas. The various ecological and human activities on each land type are then applied only to the animals occupying that land type. We aggregate these processes to determine changes in each aggregate population within a period, and then use the distribution functions to redistribute animals in the next period.

Our model consists of four state variables (susceptible, infected with brucellosis, infected with CWD, and the stock of Prions that cause CWD) across four land types (hunting areas, feedgrounds, ranches, and conservation areas), with three controls (hunting on public and private lands, supplemental feeding on feedgrounds, and biosecurity on ranches). A standard metapopulation model would require four patches (one for each land type), each with four state variables and the relevant controls: in this case, 16 states and 4 controls. Our approach allows modeling a single patch with 4 states and 4 controls.

Example

Let $k_i(t)$ denote the human-augmented carrying capacity of land use i .

Let $\gamma_i(\mathbf{k}) = \frac{k_i}{\sum_j k_j}$ be the relative attractiveness of land use i . We use this as an endogenous distribution function. If N is the total population, then $N_i = \gamma_i(\mathbf{k})N$.

Logistic growth on land use i is $G_i(N, \mathbf{k}) = r\gamma_i(\mathbf{k})N \left(1 - \frac{\gamma_i(\mathbf{k})N}{k_i}\right) = r\gamma_i(\mathbf{k})N \left(1 - \frac{\gamma_i(\mathbf{k})N}{\sum_j k_j}\right)$.

Then total growth takes the standard form $G(N, \mathbf{k}) = \sum_i G_i(N, \mathbf{k}) = rN \left(1 - \frac{N}{\sum_j k_j}\right)$.

Epidemiological Dynamics

Elk Population Growth

$$\dot{S} = r_S S \left(1 - \frac{N}{\sum_j k_j}\right) - \beta_B C_B(\mathbf{k}) I_B S - \beta_C C_C(\mathbf{k}) P S - [q_{hunt} + q_{ranch}] S$$

$$\dot{I}_B = r_B I_B \left(1 - \frac{N}{\sum_j k_j}\right) + \beta_B C_B(\mathbf{k}) I_B S - [q_{hunt} + q_{ranch}] I_B$$

$$\dot{I}_C = r_C I_C \left(1 - \frac{N}{\sum_j k_j}\right) + \beta_C C_C(\mathbf{k}) P S - \alpha_C I_C - [q_{hunt} + q_{ranch}] I_C$$

where

S = susceptible elk population

I_B = brucellosis-infected elk population

I_C = CWD-infected elk population

$C_B(\mathbf{k}) = \sum_i \gamma_i(\mathbf{k})^2$ = land use-weighted brucellosis contact function

$C_C(\mathbf{k}) = \sum_i \gamma_P \gamma_i(\mathbf{k})$ = land use-weighted CWD contact function

Prion Stock Growth

$$\dot{P} = r_P I_D - \delta_P P$$

where I_D is the equilibrium infected mule deer population, which is the leading contributor to prion deposition in the environment. Mule deer management and dynamics are not modeled, but current infection rates have stabilized.

Endogenous Host-Density Thresholds

Infectious contacts are density dependent, and so there is a population threshold below which infection levels decline. We can write

$$\dot{I}_B = M_B(I_B, \mathbf{k}) [N - \tilde{N}_B(I_B, I_C, \mathbf{q}, \mathbf{k})]$$

$$\dot{I}_C = M_C(I_C, P, \mathbf{k}) [N - \tilde{N}_C(I_B, I_C, P, \mathbf{q}, \mathbf{k})]$$

where

$\tilde{N}_i(\cdot)$ is the threshold for pathogen i

$M_i(\cdot)$ is the speed of adjustment of pathogen i

The thresholds are endogenous, as they depend on human choices and state variables that are influenced over time by human choices.

Managing the disease means managing both the population and the threshold, rather than managing the population relative to a fixed threshold. If population reduction is costly, then invest in increasing the threshold.

An endemic equilibrium with both diseases requires $\tilde{N}_B(\cdot) = \tilde{N}_C(\cdot)$. Otherwise, it is likely that one disease will outcompete the other for hosts. Which outcome occurs is influenced by human choices.

Bioeconomic Model

Social net benefits (SNB) at any point in time are defined as economic surplus to hunters (on public lands and on ranches), plus WTP for elk viewing and conservation, less the costs of habitat augmentation (expansion on on feedgrounds and conservation areas; contraction on ranches) and expected damage costs to ranchers from brucellosis transmission from elk.

Given a discount rate of ρ , the efficient management strategy solves

$$\max_{\mathbf{q}, \mathbf{k}} \int_0^{\infty} SNB e^{-\rho t} dt \quad \text{s.t.} \quad \dot{S}, \dot{I}_B, \dot{I}_C, \dot{P}, \quad S(0), I_B(0), I_C(0), P(0)$$

The controls allow managers to influence population levels and the distribution of animals. But the controls are imperfect because an elk's disease status is unobservable.

Application to the Pinedale Area in the Wyoming GYA

We investigate elk management in the Pinedale area of the GYA, which is home to four feedgrounds as well as a valuable ranching sector.

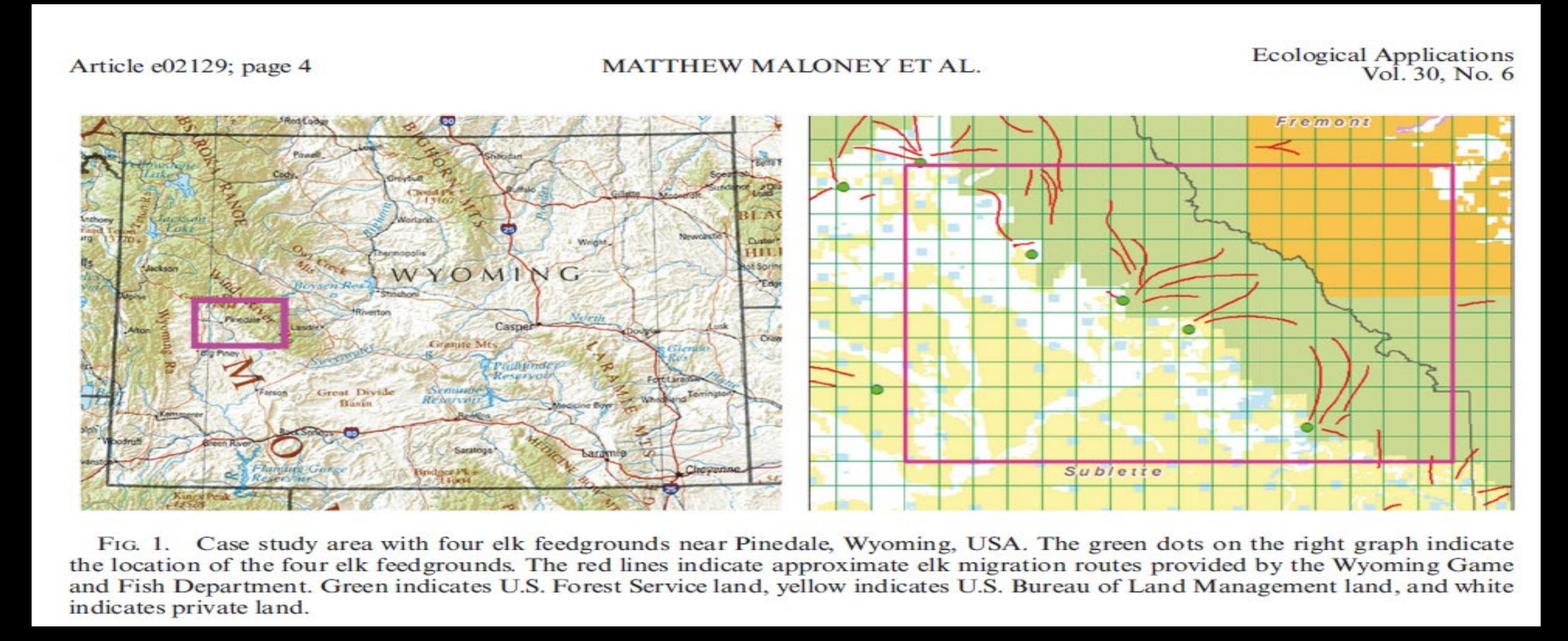


FIG. 1. Case study area with four elk feedgrounds near Pinedale, Wyoming, USA. The green dots on the right graph indicate the location of the four elk feedgrounds. The red lines indicate approximate elk migration routes provided by the Wyoming Game and Fish Department. Green indicates U.S. Forest Service land, yellow indicates U.S. Bureau of Land Management land, and white indicates private land.

Some Preliminary Results

We present steady state results for two management scenarios: (i) manage harvests and feedgrounds (Table 1), and (ii) manage harvests, feedgrounds, and on-farm biosecurity (Table 2). Harvests in each case only include those on public lands. We have yet to solve the model to include harvests on private lands (outfitting businesses).

The pre-CWD baseline outcomes presented in the tables are based on historical feedground activity that has significantly boosted the carrying capacity. Specifically, the carrying capacity allocated to feedground areas under historical feeding levels is $k_{feed} = 10,904$ elk (absent feeding, the carrying capacity allocated to this land area is $k_{feed} = 3,099$ elk). Given this carrying capacity and assuming a harvest rate of 0.4, the steady state prevalence of brucellosis in elk is 0.67.

The remaining columns in Tables 1 and 2 present results for three disease cases: (i) only brucellosis is present, (ii) only CWD is present, and (iii) both diseases are present (the multi-disease case, for which we always find co-existence is optimal). Comparing outcomes across the columns indicates the effects of the two diseases on optimal management. Comparing outcomes across the tables indicates the effects of having an additional policy instrument (biosecurity).

Table 1. Steady State Results: Managing Harvests and Feeding

Variable	Pre-CWD Baseline	Brucellosis Only	CWD Only	Brucellosis and CWD
N	3,726	3,890	4,760	3,982
q_{hunt}	0.4	0.39	0.35	0.39
I_B/N	0.67	0.007	----	0.006
(Brucellosis prevalence)				
I_C/N	----	----	0.044	0.043
(CWD prevalence)				
k_{feed}	10,904	3,606	3,933	3,600
(γ_{feed})	(0.7)	(0.43)	(0.46)	(0.43)
k_{ranch}	1,427	1,427	1,427	1,427
(γ_{ranch})	(0.18)	(0.17)	(0.17)	(0.17)
k	15,613	8,315	14,050	8,309

Feedground activity is reduced significantly for each scenario, with feedgrounds almost closed in the brucellosis-only and multi-disease scenarios. CWD is less costly (no rancher losses) and so, in the CWD-only case, a larger population and slightly greater feedground activity.

When both diseases are present, then brucellosis has a dominant effect on management. Specifically, the population level and the harvest rate are only slightly greater than in the brucellosis-only case, and feeding is about the same.

Table 2. Steady State Results: Managing Harvests, Feeding, and Biosecurity

Variable	Pre-CWD Baseline	Brucellosis Only	CWD Only	Brucellosis and CWD
N	3,726	3,886	7,726	3,195
q_{hunt}	0.4	0.33	0.57	0.32
I_B/N	0.67	0.034	----	0.03
(Brucellosis prevalence)				
I_C/N	----	----	0.036	0.05
(CWD prevalence)				
k_{feed}	10,904	3,535	3,933	3,529
(γ_{feed})	(0.7)	(0.51)	(0.28)	(0.51)
k_{ranch}	1,427	124	6,835	112
(γ_{ranch})	(0.18)	(0.02)	(0.49)	(0.02)
k	15,613	6,941	14,050	6,923

In the brucellosis-only case, the only significant change relative to Table 1 is that a great deal of biosecurity has been implemented to keep elk off ranches. Brucellosis prevalence, while relatively small in relation to the baseline, increases relative to the brucellosis-only scenario in Table 1. This result stems from more animals dispersing to feed areas as ranches invest heavily in biosecurity. Feed levels are further reduced in this scenario to offset some of these spillover effects.

In the CWD-only case, the population is larger although equilibrium prevalence levels have been reduced due to greater harvest rates. In this case, farm habitat has optimally been increased, thereby moving elk away from feedgrounds.

In the multi-disease case, we again find that brucellosis has a dominant effect on management, with feedlots almost closed and a great deal of biosecurity in place.

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