

# Spatially Explicit Capture-Recapture Disease Uncertainty Models

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# OUTLINE

Introduction

Model

Simulation Results

Disease Transmission

Discussion

# MOTIVATION

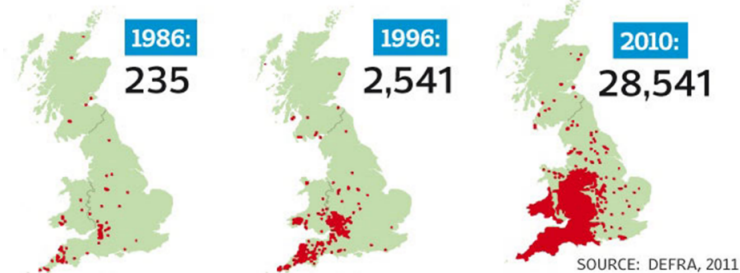
This work is motivated by the study of European badgers (*Meles meles*) naturally infected with bovine tuberculosis (bTB) at Woodchester Park in Gloucestershire (UK).



# BOVINE TB IN THE UK

- ▶ Bovine TB is a serious disease of UK cattle.

Cattle tested positive for bovine TB



- ▶ It is estimated to cost millions/billions to tax payers.

# BOVINE TB IN THE UK

- ▶ There is evidence suggesting that it is European badgers that act as a major reservoir of bTB and play an important role in the transmission of bTB to cattles (Donnelly et al., 2006)<sup>1</sup>.
- ▶ This has resulted in the controversial culling of badgers.
- ▶ Hence, for effective control of bTB there is a need to accurately monitor population level as well as to better understand disease dynamics among badgers.

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<sup>1</sup> Donnelly, Christl A., et al. "Positive and negative effects of widespread badger culling on tuberculosis in cattle." *Nature* 439.7078 (2006): 843-846.

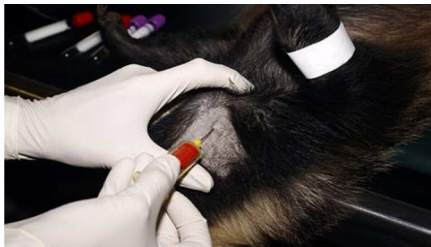
# SAMPLING

- ▶ The badger population is monitored by CR sampling.
- ▶ Trapping is done year round excluding February to April inclusive to avoid trapping breeding females.
- ▶ The study area has been divided into three zones of approximately equal size and each zone is trapped four times during each year.



# DISEASE TESTING

- ▶ Three test are done on captured individuals to infer the disease status:
  1. Interferon-Gamma immunoassay
  2. Serological tests
  3. BrockTB Stat-Pak test
  
- ▶ Each test is imperfect, resulting in false positive and false negative errors, making it difficult to infer an individual's disease state.



## MODEL OVERVIEW

- ▶ With the aim of monitoring populations levels as well as better understanding disease dynamics, we have develop a novel open spatial capture recapture (OSCR) model that uses a hidden Markov model (HMM) to account for imperfect observations of true epidemiology states.
- ▶ This OSCR model allows individuals to survive and to be recruited between sampling occasions.
- ▶ This framework enables a better understanding of how disease dynamics are linked to population dynamics within a spatial context, giving estimates of critical parameters, such as abundance, survival probabilities, disease transmission probabilities, local density and disease density maps, etc..



# UNOBSERVED STATES

Let  $i = 1, \dots, M$  individuals,  $k = 1, \dots, K$  sampling occasions and  $t = 1, \dots, T$  years.

$$z_{i,k,t} = \begin{cases} 1 & \text{alive} \\ 0 & \text{unrecruited/dead} \end{cases}$$

$$d_{i,k,t} = \begin{cases} 1 & \text{infected} \\ 0 & \text{uninfected} \end{cases}$$

# INITIAL DISTRIBUTIONS

$$\gamma = \begin{matrix} & \text{alive} & \text{unrecruited} \\ \left( \begin{matrix} \gamma_{1,1} & (1 - \gamma_{1,1}) \end{matrix} \right)$$

- ▶  $\gamma_{1,1}$  is the recruitment probability that a “pseudo-individual” enters the population at the start of the study.

$$\delta = \begin{matrix} & \text{infected} & \text{uninfected} \\ \left( \begin{matrix} \delta_I & (1 - \delta_I) \end{matrix} \right)$$

- ▶  $\delta_I$  is the probability of being infected at the start of the study conditional on being alive the start of the study.

# STATE TRANSITION PROBABILITIES

$$\Gamma_z^{(k,t)} = \begin{array}{c} \text{alive} \\ \text{unrecruited} \\ \text{dead} \end{array} \begin{array}{c} \text{alive} \\ \text{unrecruited} \\ \text{dead} \end{array} \begin{pmatrix} \phi_{d_{k,t}} & 0 & 1 - \phi_{d_{k,t}} \\ \gamma_{k,t} & 1 - \gamma_{k,t} & 0 \\ 0 & 0 & 1 \end{pmatrix}$$

- ▶  $\phi_{d_{k,t}}$  is the probability of survival from one sampling occasion to the next conditional dependent on disease status.
- ▶  $\gamma_{k,t}$  represents the recruitment probability that an “pseudo-individual” may enter the population at sampling occasion  $k$  time  $t$ .

# STATE TRANSITION PROBABILITIES

$$\Gamma_{dz}^{(k,t)} = \begin{array}{c} \text{infected} \\ \text{uninfected} \end{array} \begin{array}{cc} \text{infected} & \text{uninfected} \\ \left( \begin{array}{cc} 1 & 0 \\ \psi & 1 - \psi \end{array} \right) \end{array}$$

- ▶  $\psi$  is the probability of an uninfected individual becoming infected.
- ▶ Transition of disease status is conditional on  $z_{k,t}$ . That is, only alive and uninfected individuals can become infected.

# INDIVIDUAL ACTIVITY CENTER ( $s_i$ )

Badgers at Woodchester park are highly site-attached species that do not change activity centers much over their lifetime.

$$s_i \sim \text{Uniform}(S)$$

where  $S$  is the region of interest.

# STATE-DEPENDENT OBSERVATION PROCESS

Let  $y_{i,j,k,t}$  be the observation event for individual  $i$  at trap  $j$  on sampling occasion  $k$  during time  $t$ .

$$y_{i,j,k,t} | z_{i,k,t} \sim \text{Bernoulli}(p(x_j, s_i) z_{i,k,t})$$

where  $p(x_j, s_i)$  is the Gaussian model:

$$p(x_j, s_i) = p_{0_{d_{i,k,t}}} \exp\left(-\frac{1}{2\sigma_{d_{i,k,t}}^2} \|x_j - s_i\|^2\right)$$

where  $p_0$  is the baseline encounter probability and  $\sigma$  represents the rate at which detection probability declines as a function of distance. Both are dependent on the individuals disease status.

# STATE-DEPENDENT OBSERVATION PROCESS

Let  $\omega_{i,k,t}$  be the disease test results for individual  $i$  on sampling occasion  $k$  time  $t$ .

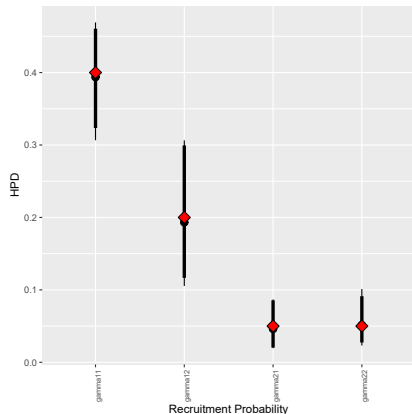
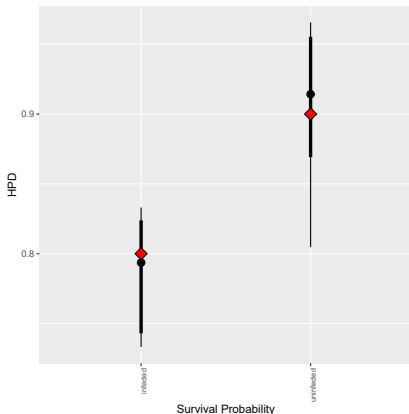
Test result combination	Test 1 (StatPak)	Test 2 (IFN $\gamma$ )	Test 3 (Culture)	Probability of the combination of test results	
				if uninfected	if infected
1	-	-	-	$Sp_1 * Sp_2 * Sp_3$	$(1-Se_1) * (1-Se_2) * (1-Se_3)$
2	+	-	-	$(1-Sp_1) * Sp_2 * Sp_3$	$Se_1 * (1-Se_2) * (1-Se_3)$
3	-	+	-	$Sp_1 * (1-Sp_2) * Sp_3$	$(1-Se_1) * Se_2 * (1-Se_3)$
4	-	-	+	$Sp_1 * Sp_2 * (1-Sp_3)$	$(1-Se_1) * (1-Se_2) * Se_3$
5	+	+	-	$(1-Sp_1) * (1-Sp_2) * Sp_3$	$Se_1 * Se_2 * (1-Se_3)$
6	+	-	+	$(1-Sp_1) * Sp_2 * (1-Sp_3)$	$Se_1 * (1-Se_2) * Se_3$
7	-	+	+	$Sp_1 * (1-Sp_2) * (1-Sp_3)$	$(1-Se_1) * Se_2 * Se_3$
8	+	+	+	$(1-Sp_1) * (1-Sp_2) * (1-Sp_3)$	$Se_1 * Se_2 * Se_3$

+ = positive test result; - = negative test result

$$\omega_{i,k,t} | d_{i,k,t} \sim \text{Categorical}(8, p_{d_{i,k,t}})$$

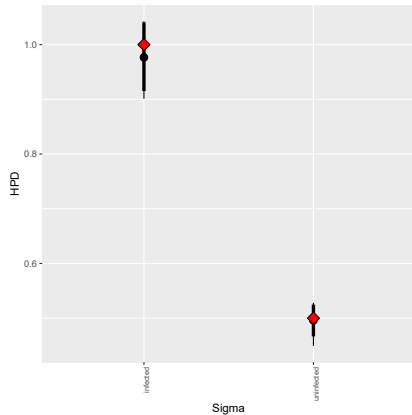
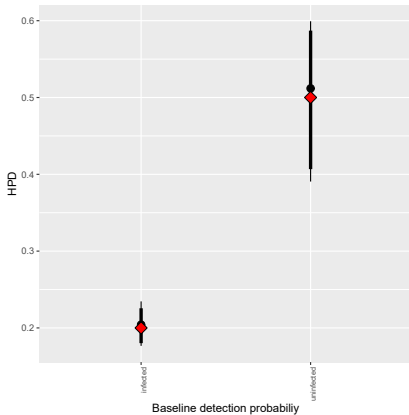
# SIMULATION RESULTS

Number of simulation runs: 30,  $T = 2$ ,  $K = 4$

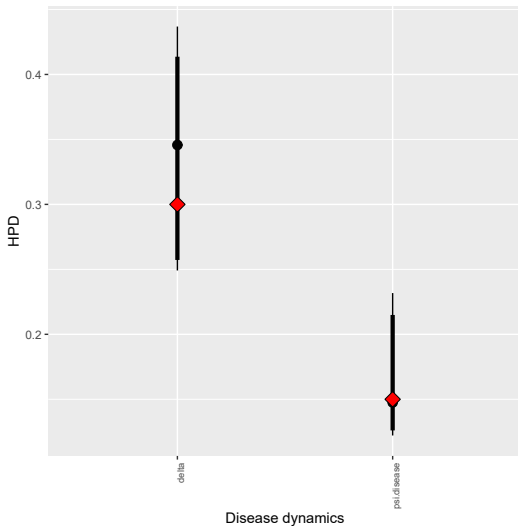




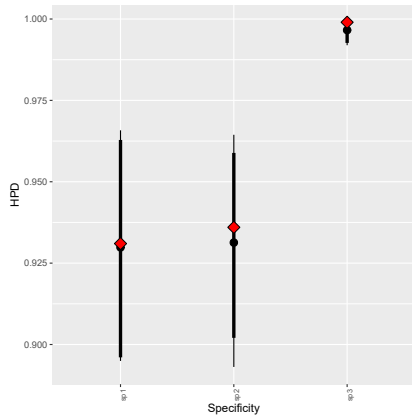
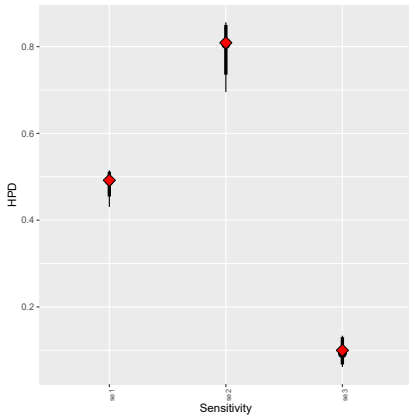
# SIMULATION RESULTS



# SIMULATION RESULTS



# SIMULATION RESULTS



# MODELLING DISEASE TRANSMISSION

## Half Normal

Let  $\theta_{i,l}$  be the probability that individual  $i$  is infected by individual  $l$ .  
We let  $\theta_{i,l}$  follow a half normal distribution:

$$\theta_{i,l} = \exp\left(-\frac{1}{2\sigma^2} \|s_i - s_l\|^2\right)$$

Then the probability of individual  $i$  being infected at occasion  $k$ , time  $t$  ( $\psi_{i,k,t}$ ) can be written as

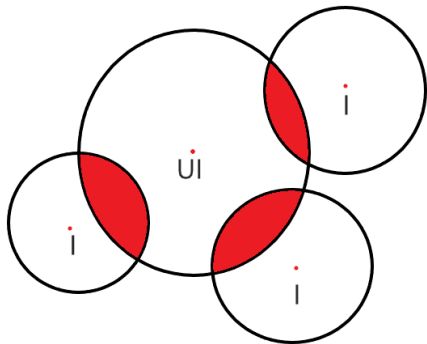
$$\psi_{i,k,t} = 1 - \left(\prod_{l=1}^L 1 - \theta_{i,l}\right)$$

# MODELLING DISEASE TRANSMISSION

## Intersection of Home Range Area

$$\text{logit}(\psi_{i,k,t}) = \beta_0 + \beta_1 \cdot A_{i,k,t}$$

$A_{i,k,t}$  is the sum of intersection area between uninfected individual  $i$  and all infected individuals at the previous time point.



# DISCUSSION

- ▶ These models are computational expensive and future work will be focused on making these models more computational efficient.
- ▶ Another area of focus will be how to choose between the different models of disease transmission.
- ▶ The limitation of the half normal approach is that infected individuals are “treated” like traps i.e. we don’t account for the fact that they also move.
- ▶ Any suggestions on how to account for how close/far an individual is from infected individuals will be much appreciated.

Thank you!  
Any questions/comments?

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