Spatially Explicit Capture-Recapture Disease Uncertainty Models

F. Ketwaroo, E. Matechou, M. Silk and R. Delahay

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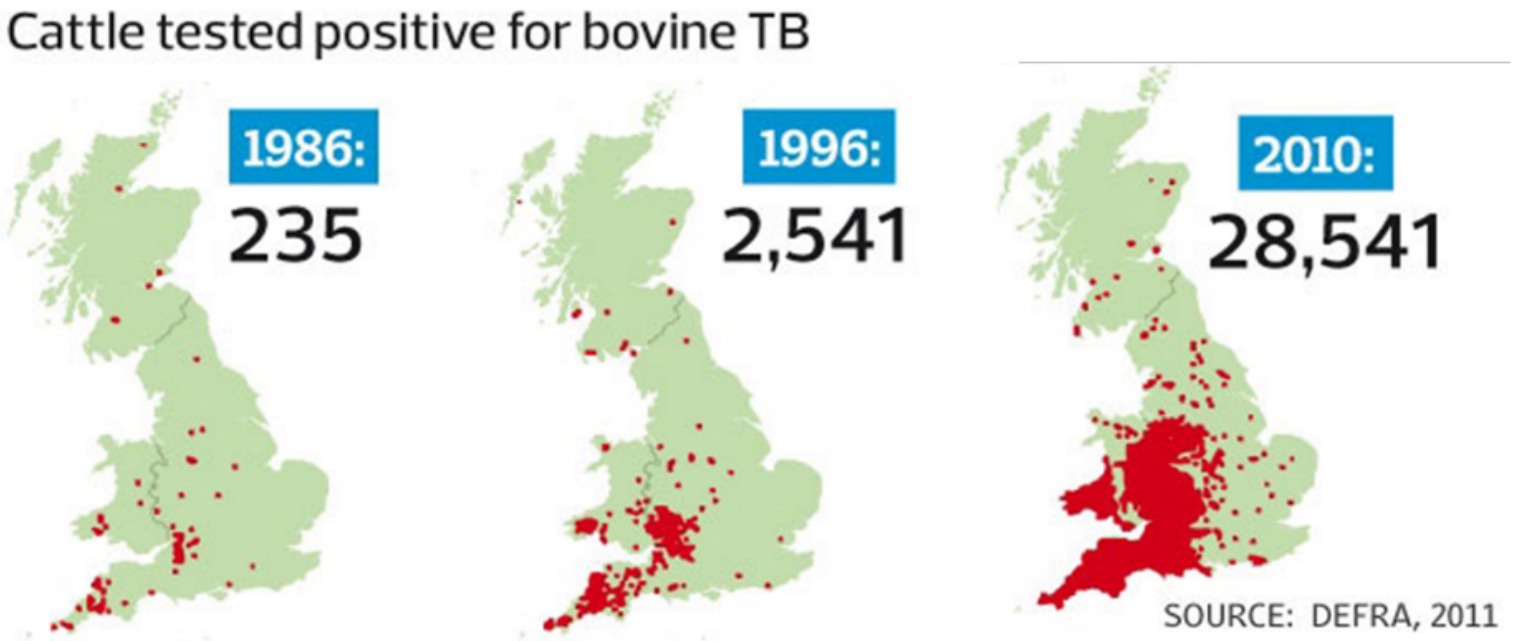
Outline

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.



- 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) [1].
- 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.

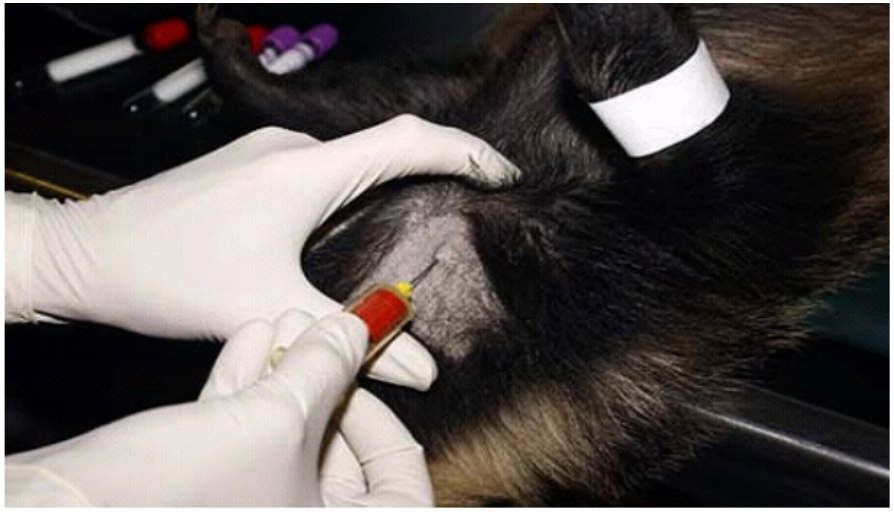
[1] Donnelly, Christl A., et al. "Positive and negative effects of widespread badger culling on tuberculosis in cattle." Nature 439.7078 (2006): 843-846.

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 $i = 1, \ldots, M$ individuals, $k = 1, \ldots, K$ sampling occasions and $t = 1, \ldots, T$ 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

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

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

$$\delta = \begin{matrix} \text{infected} & \text{unifected} \end{matrix} \\ \begin{pmatrix} \delta_I & (1-\delta_I) \end{pmatrix}$$

- δ_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

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

- $\phi_{d_{k,t}}$ 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

$$\Gamma_{d|z}^{(k,t)} = \begin{array}{c} \\ \text{infected} \\ \text{unifected} \end{array} \begin{array}{c} \begin{array}{cc} \text{infected} & \text{unifected} \end{array} \\ \begin{pmatrix} 1 & 0 \\ \psi & 1-\psi \end{pmatrix} \end{array}$$

- ψ 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:

$$p(x_j, s_i) = p_{0_{d_{i,k,t}}} \exp\Big(- \frac{1}{2\sigma^2_{d_{i,k,t}}} \parallel x_j - s_i \parallel^2 \Big)$$

where p_0 is the baseline encounter probability and σ 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.

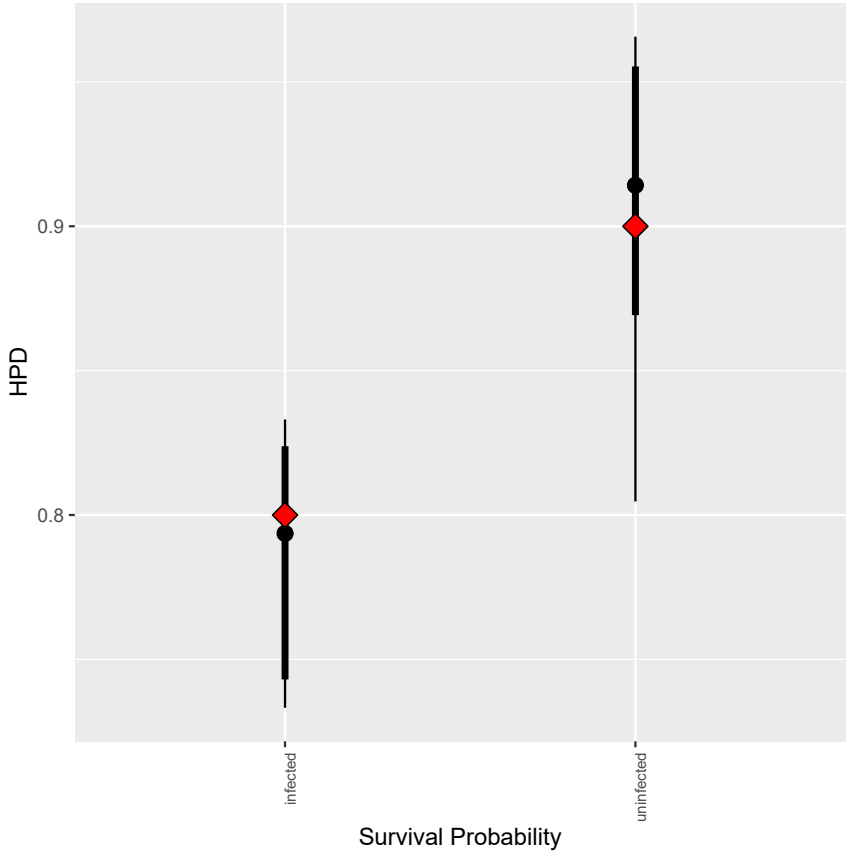
Test result combination	Test 1 (StatPak)	Test 2 (IFNγ)	Test 3 (Culture)	Probability of the combination of test results	
				if uninfected	if infected
1	-	-	-	$Sp_1*Sp_2*Sp_3$	$(1-Se_1)*(1-Se_2)*(1-Se_3)$
2	+	-	-	$(1-Sp_1)*Sp_2*Sp_3$	$Se_1*(1-Se_2)*(1-Se_3)$
3	-	+	-	$Sp_1*(1-Sp_2)*Sp_3$	$(1-Se_1)*Se_2*(1-Se_3)$
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	+	+	+	$(1-Sp_1)*(1-Sp_2)*(1-Sp_3)$	$Se_1*Se_2*Se_3$

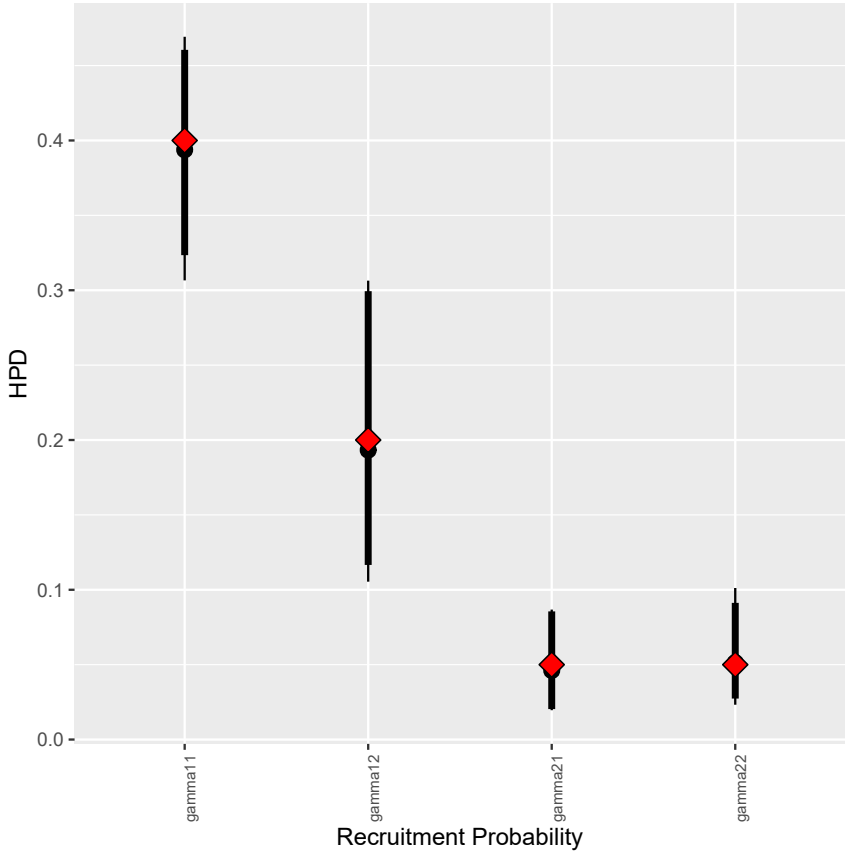
+ = positive test result; - = negative test result

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

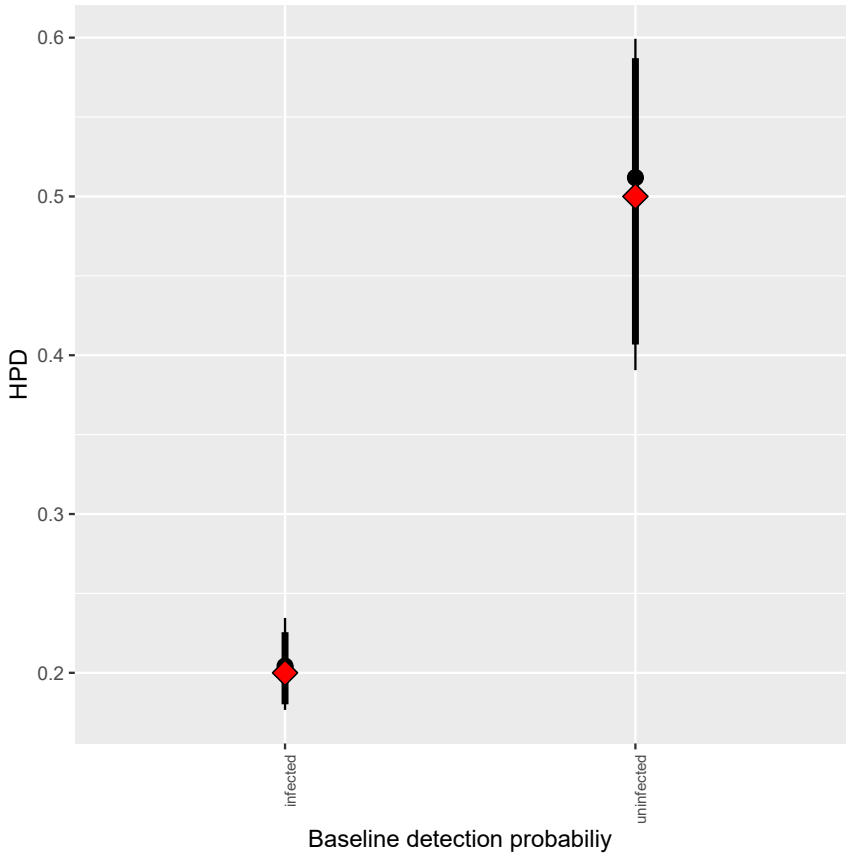
Simulation results

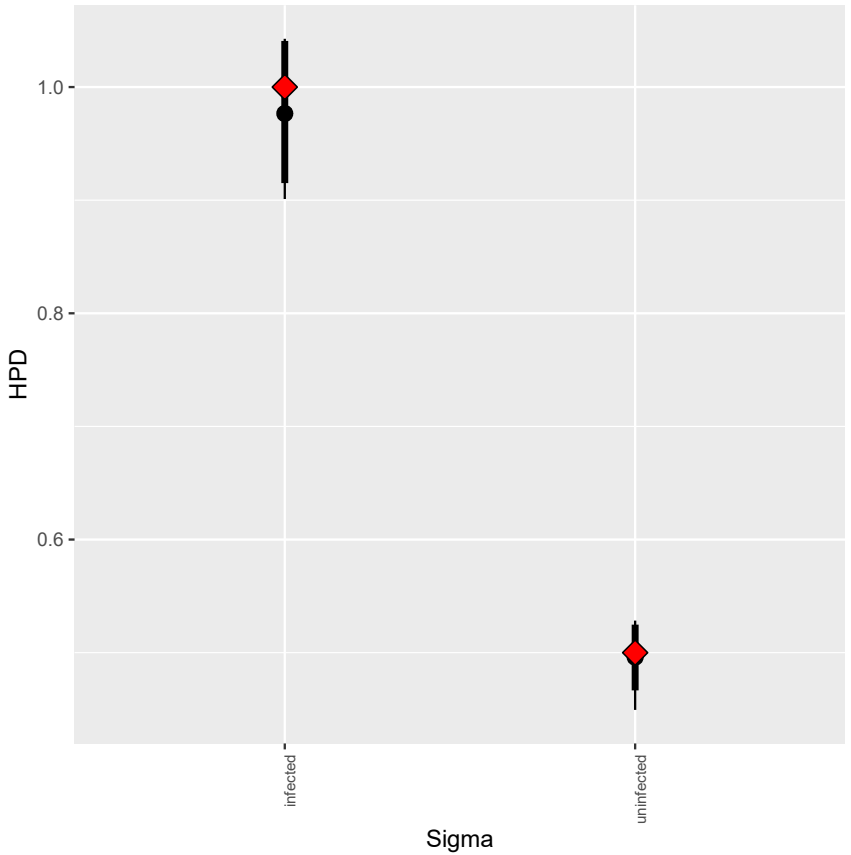
Number of simulation runs: 30, $T = 2, K = 4$



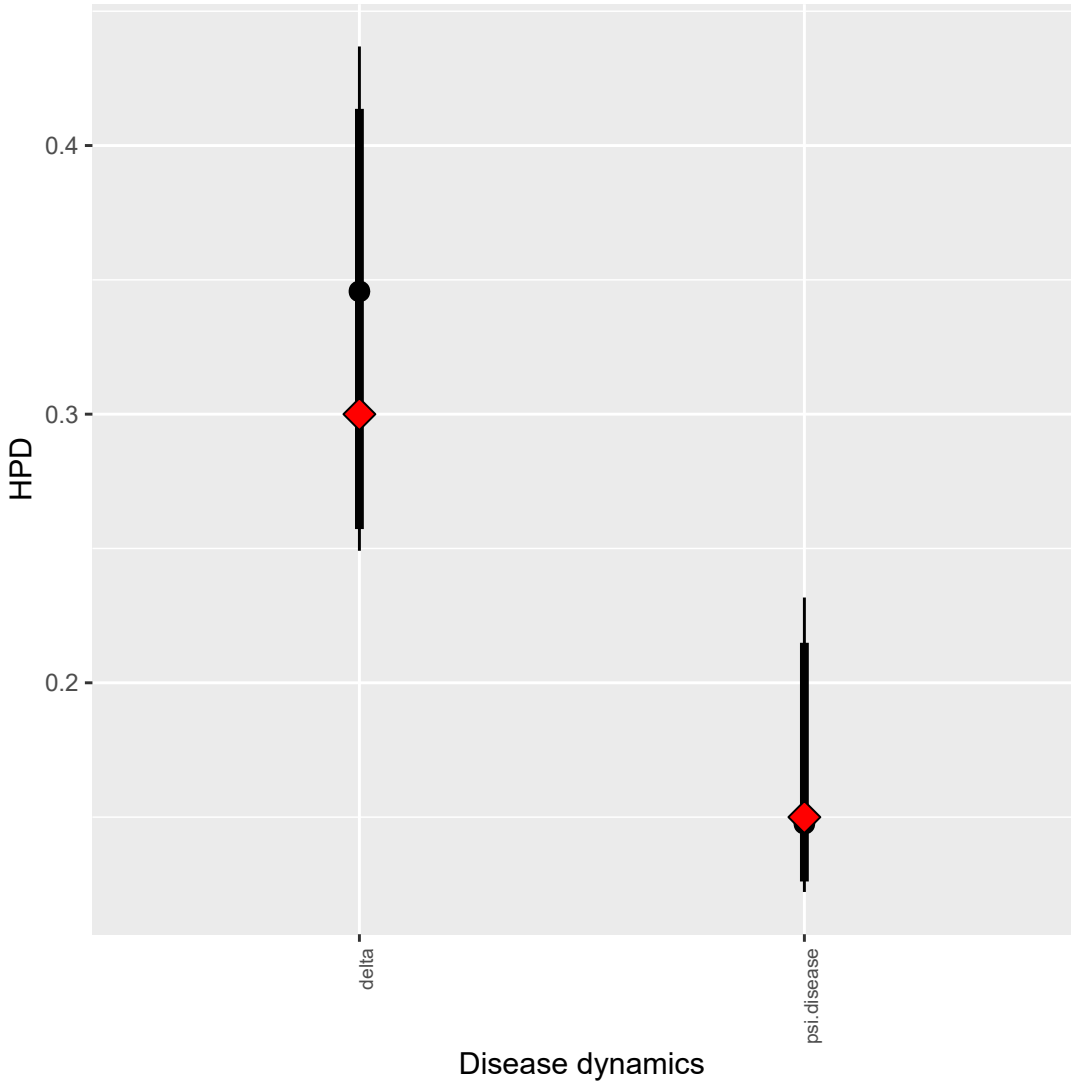


Simulation results





Simulation results



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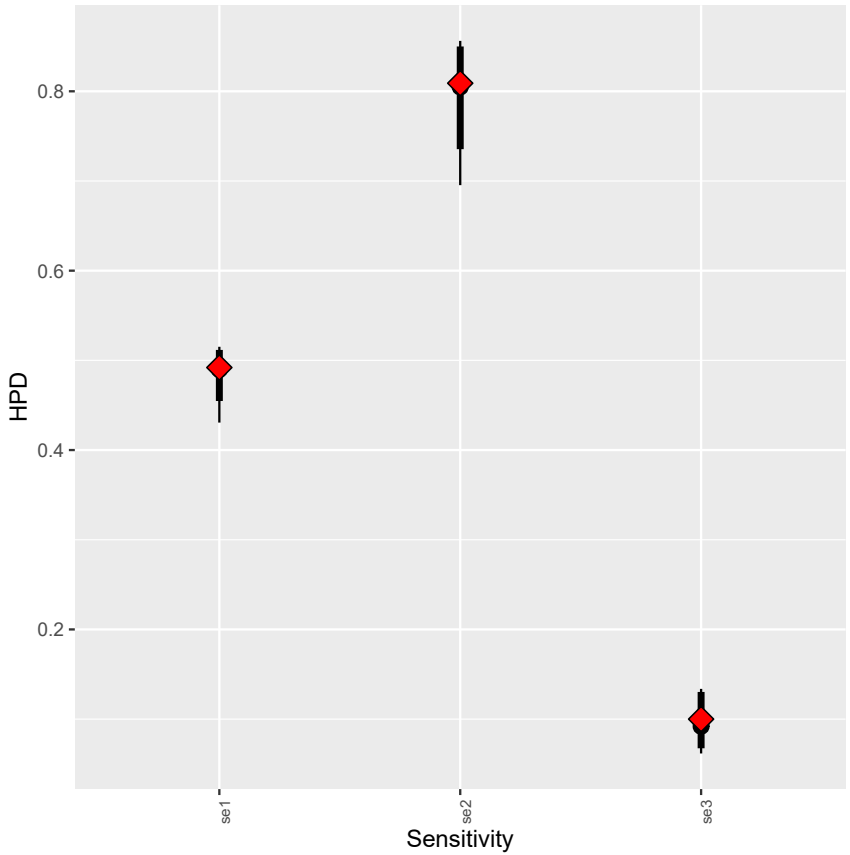
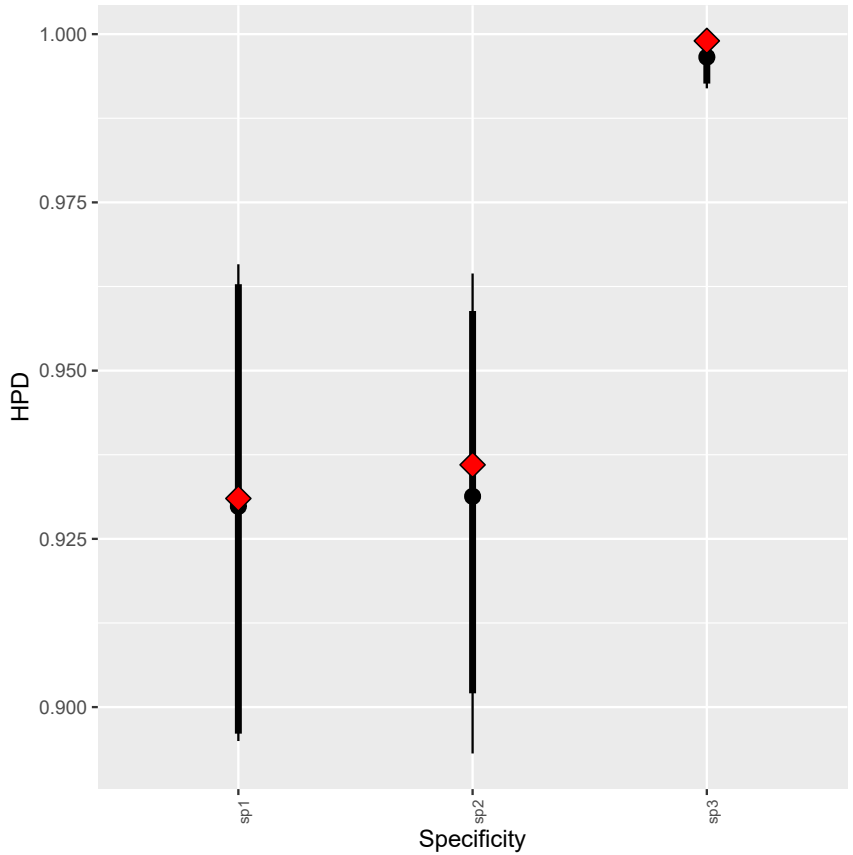




Modelling Disease transmission

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:

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

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

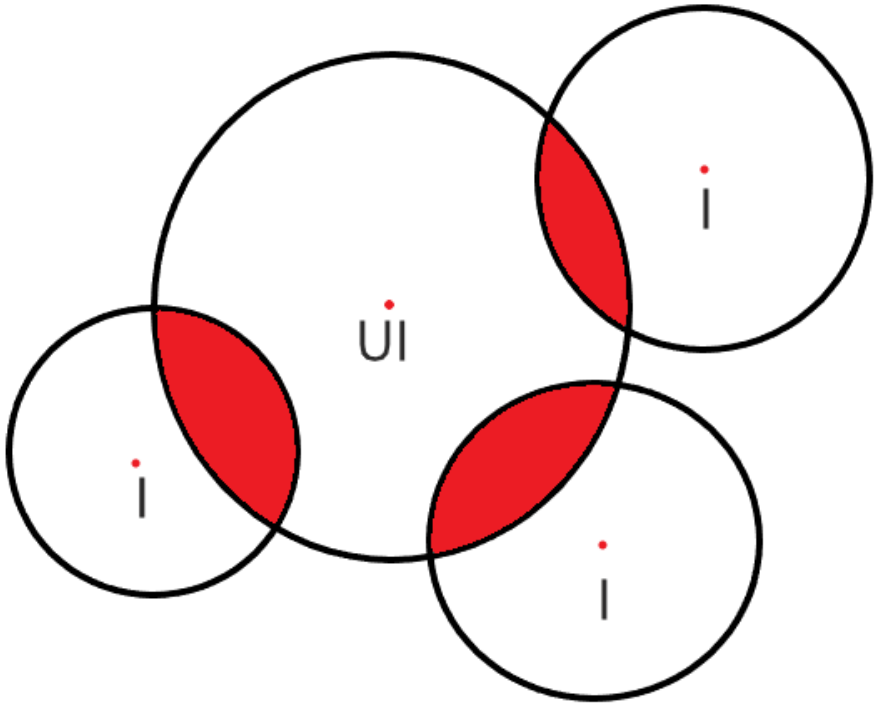
$$\psi_{i,k,t} = 1 - \Big(\prod_{l=1}^{L} 1 - \theta_{i,l} \Big)$$

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?

Contact: **fk231@kent.ac.uk**