

1       That's not the Mona Lisa! How to interpret  
2       spatial capture-recapture density surface  
3       estimates

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14    **Appendix A   Bayesian models**

15    Results presented in Section 4 in our manuscript were generated by fitting  
16    maximum-likelihood SCR models to simulated data. In this appendix we repro-  
17    duce results from Section 4 using Bayesian models fitted via MCMC to demon-  
18    strate that our conclusions are not simply a consequence of adopting a classical  
19    approach. We focus on reproducing Figures 7 and 9 from the manuscript; Fig-  
20    ures 6 and 8 are based on averages over 100 simulations, which would require  
21    considerable computation time given that fitting SCR models via MCMC is  
22    more time consuming than maximum likelihood.

23    In Section A1 we describe our Bayesian models, and in Section A2 we sum-

marise our results.

## A1 Model fitting

We fitted Bayesian versions of the maximum-likelihood models presented in Section 4 to each data set. Again, we used models with constant density to estimate realised AC and realised usage surfaces, and a model with inhomogeneous density characterised by a log-linear relationship with a spatial covariate to estimate expected AC density surfaces.

We fitted our models in NIMBLE (de Valpine, Turek, Paciorek, Anderson-Berman, Temple Lang & Bodik, 2017; Turek, Milleret, Ergon, Brøseth, Dupont, Bischof & de Valpine, 2021) using data augmentation (Tanner & Wong, 1987), which has become the prevailing way to fit SCR models under a Bayesian framework. This approach involves sampling a superpopulation of  $M$  activity centres, including those of the  $n$  animals detected on the SCR survey. We have an indicator variable  $z_i$  for the  $i$ th animal, denoting whether the  $i$ th animal in the augmented population is ‘exists’ in a given MCMC iteration. Rather than directly estimating  $N$ , the population size, we estimate the data augmentation parameter,  $\psi$ , the proportion of the animals in the superpopulation for which the indicator is equal to 1. For each MCMC iteration we obtain a sample from the posterior of  $N$  using  $\sum_{i=1}^M z_i$ . A sample from the posterior for animal density can be obtained by dividing by the area of the survey region. Further details on data augmentation can be found in Kéry & Schaub (2012, pp. 139–157).

We used the following uninformative priors for the detection function parameters, specifying a prior for  $\log\{1/(2\sigma^2)\}$  rather than  $\sigma$  directly:

$$\begin{aligned}\lambda_0 &\sim \text{Gamma}(0.001, 0.001) \\ \log\left(\frac{1}{2\sigma^2}\right) &\sim \text{Uniform}(-10, 10)\end{aligned}$$

For the constant density model, the activity centres were given a uniform prior distribution over the survey region and the data augmentation parameter

was given a uniform prior from 0 to 1. For the inhomogeneous density model, animal density at location  $\mathbf{x}$  is given by  $D(\mathbf{x}) = \exp\{\beta_0 + \beta_1 y(\mathbf{x})\}$ , where  $y(\mathbf{x})$  is a measurement of a covariate at location  $\mathbf{x}$ . We used the following uninformative priors for the coefficients  $\beta_0$  and  $\beta_1$ :

$$\beta_0 \sim \text{Uniform}(-10, 10)$$

$$\beta_1 \sim \text{Uniform}(-10, 10)$$

45 When we fit each constant density model, we ran 10 000 MCMC iterations,  
46 where we set M to be equal to 300. We also used an adaptation interval of  
47 1000, and discarded 500 iterations as burn-in.

48 When fitting each inhomogeneous density model, we ran 100 000 MCMC  
49 iterations, and used a value of 9000 for M. We didn't use an adaptation interval,  
50 and discarded 2500 iterations as burn-in.

## 51 A2 Results

52 We created trace plots for all parameters across all models, and none of them  
53 indicated a lack of convergence. Although we do not present them here for  
54 brevity, the point estimates (calculated using the posterior mean) of all param-  
55 eters were very similar to those obtained via maximum likelihood models fitted  
56 to the same data.

57 The plots based on our Bayesian models fitted via MCMC (Figures A1 and  
58 A2, respectively) were qualitatively similar to those based on maximum likeli-  
59 hood mdoels presented in the manuscript (Figures 7 and 9, respectively). We  
60 observed that the locations with the highest AC densities in Figure A2 were  
61 shifted slightly further from the detectors, relative to Figure 9. A potential ex-  
62 planation for subtle differences is that our Bayesian plots are constructed based  
63 on entire posterior distributions, whereas the maximum likelihood alternatives  
64 only use point estimates.

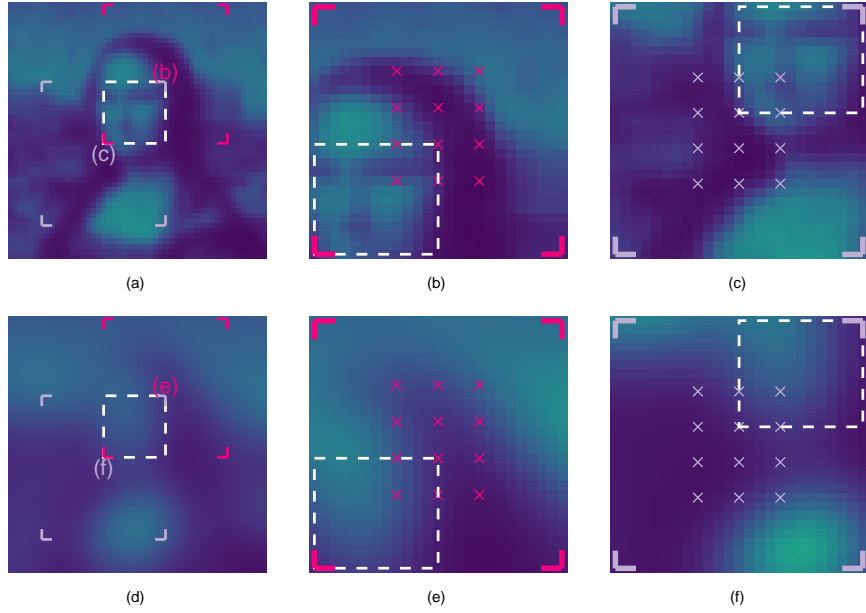


Figure A1: A version of Figure 7 from the manuscript based on our Bayesian models fitted via MCMC.

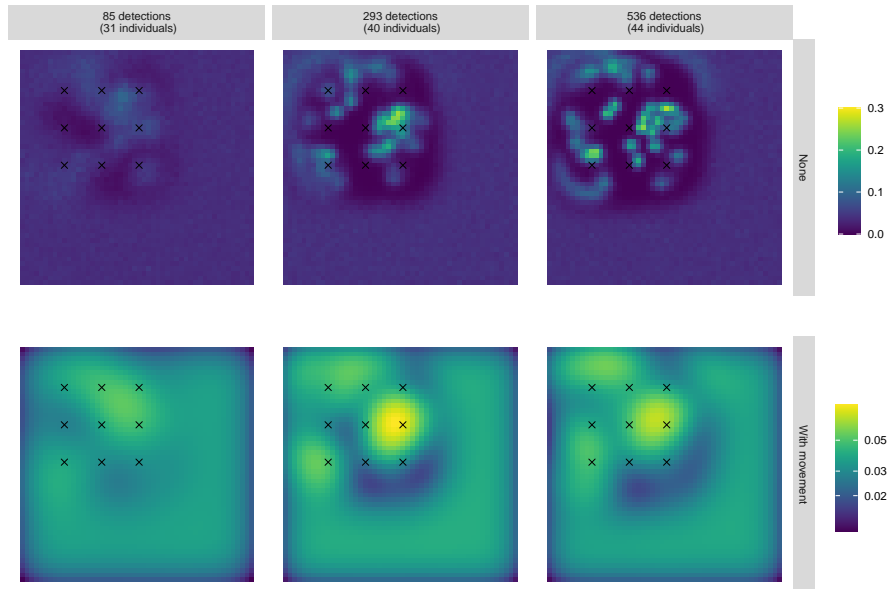


Figure A2: A version of Figure 9 from the manuscript based on our Bayesian models fitted via MCMC.

## Appendix B Realised usage density

Estimation of realised usage density is a similar process for both maximum likelihood and Bayesian approaches: we sum usage densities for each individual animal, each of which is calculated by convolving the posterior probability density function of its activity centre with an individual usage distribution.

### B1 The maximum likelihood approach

For maximum likelihood, the estimated usage density for the  $i$ th animal, with capture history  $\omega_i$ , is given by

$$f_{s|\omega}(s | \omega_i; \hat{\theta}) = \int f_{x|\omega}(x | \omega_i; \hat{\theta}) f_{s|x}(s | x; \hat{\theta}) dx, \quad (1)$$

where

- $\hat{\theta}$  is a vector containing the maximum likelihood estimates of the encounter function parameters;
- $f_{s|\omega}(s | \omega_i; \hat{\theta})$  is the estimated usage distribution, providing the probability density of finding an individual with capture history  $\omega_i$  at location  $s$  at a randomly selected point in time;
- $f_{x|\omega}(x | \omega_i; \hat{\theta})$  is the estimated PDF of the activity centre of an individual with capture history  $\omega_i$  (see Section 3); and
- $f_{s|x}(s | x; \hat{\theta})$  is the estimated usage distribution of the individual conditional on the activity centre, providing the probability density of the individual being at location  $s$  given that its activity centre is at  $x$ .

Estimated usage density at location  $s$  is then given by  $\hat{D}_u(s) = \sum_i f_{s|\omega}(s | \omega_i; \hat{\theta})$ , noting that the sum is over individuals that were not detected, with capture histories  $(0, \dots, 0)$ , along with those that were.

Here we constructed the individual usage distribution under the assumption that the density of an individual being at location  $s$  given its activity centre is

at  $\mathbf{x}$  is proportional to the encounter function  $h\{d(\mathbf{s}, \mathbf{x}); \hat{\boldsymbol{\theta}}\}$ , where  $d(\mathbf{s}, \mathbf{x})$  is the Euclidean distance between  $\mathbf{s}$  and  $\mathbf{x}$ , and so

$$f_{\mathbf{s}|\mathbf{x}}(\mathbf{s} | \mathbf{x}; \hat{\boldsymbol{\theta}}) = \frac{h\{d(\mathbf{s}, \mathbf{x}); \hat{\boldsymbol{\theta}}\}}{\int h\{d(\mathbf{s}', \mathbf{x}); \hat{\boldsymbol{\theta}}\} d\mathbf{s}'}, \quad (2)$$

where the denominator is a normalising constant.

## B2 The Bayesian approach

Bayesian models fitted via MCMC can directly sample activity centres of detected individuals, and also of undetected individuals using data augmentation, thus obtaining samples from  $f_{\mathbf{x}|\boldsymbol{\omega}}(\mathbf{x} | \boldsymbol{\omega})$  for each individual. We can use these samples directly to obtain the following approximation of the  $i$ th individual's usage distribution:

$$f_{\mathbf{s}|\boldsymbol{\omega}}(\mathbf{s} | \boldsymbol{\omega}_i) \approx \frac{1}{J} \sum_{j=1}^J f_{\mathbf{s}|\mathbf{x}}(\mathbf{s} | \mathbf{x}_{(j)}, \boldsymbol{\theta}_{(j)}), \quad (3)$$

where  $\mathbf{x}_{(j)}$  and  $\boldsymbol{\theta}_{(j)}$  are the activity centre and a vector of encounter function parameters that were sampled on the  $j$ th of  $J$  total MCMC iterations, respectively. The estimated usage distribution is therefore not conditional on one particular set of estimated parameter values, but instead considers the range of values across the posterior distribution of  $\boldsymbol{\theta}$ .

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