Murray G. Efford. 2011. Estimation of population density by spatially explicit capture–recapture analysis of data from area searches. *Ecology* **92:2202-2207.**

Appendix D. Likelihood-based spatially explicit capture–recapture models for linear searches.

A directly analogous formulation to that described for polygon searches in the main article exists for searches conducted along linear transects, for which the data are the positions y along one or more transects from which each individual is detected. Distances from the transect line are not included in the model. A transect may comprise multiple straight-line segments (straightness makes the numerical integration simpler). Note that y is a scalar distance from the start of a transect; as the absolute location and shape of the transect are known, y maps to a point in two dimensions. Detections are assumed to be independent. In addition to direct observations of animals, the data may be records of cues, as with polygon data; in this case it may be appropriate to search a narrow strip and model only longitudinal positions.

We assume a function $h'(u|\mathbf{X}; \theta^-)$ for the relative probability of detecting an animal at y if its home range is centered at $\mathbf{X}$. We can approach each transect as a one-dimensional version of the polygon detector, using κ in this case to refer to the set of straight line segments comprising each transect. We normalize h' by dividing by its integral along an infinite straight transect that passes through $\mathbf{X}$. This is not appropriate for transects that are highly convoluted (folded back on themselves), and more work is needed to determine

the limits of application of the method. Formulae are provided below. Potential extensions include the modeling of observed distances from the midline of transects (cf Johnson et al. 2010).

Here we state the formulae for independent transect detectors equivalent to those for polygons in Efford ms. Appendix A, using the same notation, with the addition of the scalar y_{ijks} for the observed distance along transect of j-th location of animal i on transect k on occasion s. The formulation for non-independent (exclusive) transect detectors follows that for non-independent polygon detectors in Appendix A, substituting h' for h.

$$h'_{sk}(\mathbf{X}) = \int_{\kappa_k} h'(u|\mathbf{X}; \theta^-) du$$

Binary (Bernoulli) transect data

$$p_{sk}(\mathbf{X}|\theta) = p_\infty h'_{sk}(\mathbf{X})$$

$$\Pr(\omega_{iks}|\mathbf{X}; \theta) = [p_{sk}h'(y_{i.ks}|\mathbf{X}; \theta^-)/h'_{sk}(\mathbf{X})]^{\delta_{sk}}[1 - p_{sk}(\mathbf{X}; \theta)]^{1-\delta_{sk}}$$

where $\delta_{sk} = 1$ if individual i was detected on transect k on occasion s and $\delta_{sk} = 0$, and using $\mathbf{y}_{i.ks}$ for the sole location.

Poisson counts along transects

As with polygon data, the number of observations J may be modelled as Poisson with parameter $v_{sk}(\mathbf{X}; \theta) = \lambda_\infty h'_{sk}(\mathbf{X})$. Then,

$$\Pr(\omega_{iks}|\mathbf{X}; \theta) = \frac{v_{sk}(\mathbf{X};\theta)^J \exp[-v_{sk}(\mathbf{X};\theta)]}{J!} \prod_{j=1}^{J} \frac{h'(y_{ijks}|\mathbf{X};\theta)}{h'_{sk}(\mathbf{X})},$$

where the product term is taken to be 1 when $J = 0$.

Literature cited

Johnson, D. S., J. L. Laake, and J. M. Ver Hoef. 2010. A model-based approach for

    making ecological inference from distance sampling data. Biometrics 66:310–318.