Efford MG, Dawson DK, Jhala YV, Qureshi Q. 2015. Density-dependent home-range size revealed by spatially explicit capture–recapture. Ecography (in press)

Abstract

The size of animal home ranges often varies inversely with population density among populations of a species. This fact has implications for population monitoring using spatially explicit capture–recapture (SECR) models, in which both the scale of home-range movements σ and population density D usually appear as parameters, and both may vary among populations. It will often be appropriate to model a structural relationship between population-specific values of these parameters, rather than to assume independence. We suggest re-parameterizing the SECR model using $k_p = \sigma_p \sqrt{D_p}$, where k_p relates to the degree of overlap between home ranges and the subscript p distinguishes populations. We observe that k_p is often nearly constant for populations spanning a range of densities. This justifies fitting a model in which the separate k_p are replaced by the single parameter k and σ_p is a density-dependent derived parameter. Continuous density-dependent spatial variation in σ may also be modelled, using a scaled non-Euclidean distance between detectors and the locations of animals. We illustrate these methods with data from automatic photography of tigers (*Panthera tigris*) across India, in which the variation is among populations, from mist-netting of ovenbirds (*Seiurus aurocapilla*) in Maryland, USA, in which the variation is within a single population over time, and from live-trapping of brushtail possums (*Trichosurus vulpecula*) in New Zealand, modelling spatial variation within one population.

Possible applications and limitations of the methods are discussed. A model in which k_p is constant, while density varies, provides a parsimonious null model for SECR. The parameter k of the null model is a concise summary of the empirical relationship between home-range size and density that is useful in comparative studies. We expect deviations from this model, particularly the dependence of k_p on covariates, to be biologically interesting.