Supporting Information. Gardner, B., B. T. McClintock, S. J. Converse, and N. J. Hostetter. 2022. Integrated animal movement and spatial capture-recapture models: Simulation, implementation, and inference. *Ecology*.

Appendix S2: Description of R code, custom functions, distributions, and samplers.

In this appendix, we describe the four R scripts (R Core Team, 2020) included in the supporting information that simulate data and fit the integrated spatial capture-recapture (SCR) – movement models described in the manuscript.

SCR WITH SIMPLE AND CORRELATED RANDOM WALKS

`sim_SCR_RandomWalks.R`: This R script simulates initial abundance, initial distribution, random walk movement processes, and SCR detection processes described in the manuscript. Current settings reflect scenario 7A in Appendix S1:Table S4. All other SCR with simple and correlated random walk models described in the manuscript and appendices are fit by changing σ (movement scale parameter), σ_{det} (detection scale parameter), λ_0 (encounter rate), γ (directional persistence parameter), and nTelem (number of telemetered individuals). Changing the current correlated random walk settings ($\gamma > 0$) to bivariate normal ("simple") random walk settings ($\gamma = 0$) requires (i) setting $\gamma = 0$ in the simulation settings, (ii) fixing $\gamma = 0$ in the `NIMBLE` model, and (iii) removing the initial value for γ in the initial values section (since it is fixed at 0). Section 2 within this script provides the `NIMBLE` models and Markov chain Monte Carlo (MCMC) settings to run the models in `NIMBLE` (de Valpine et al., 2017). The `NIMBLE` model references several functions and distributions in `SCR_RandomWalks_Distributions_Samplers_and_Functions.R` (described below), which improve MCMC efficiency.

`SCR_RandomWalks_Distributions_Samplers_and_Functions.R`: This R script provides the MCMC functions for the SCR with simple and correlated random walk movement processes described in `sim_SCR_RandomWalks.R`. While nearly all aspects of these models can be expressed in common BUGS language, these functions greatly improve MCMC efficiency. We briefly describe each of the functions below and note that they are annotated in the code.

GetLambdaStar: A function to derive the expected encounter rate for individual i across all J traps and T occasions ($\lambda_{i,1:J,1:T}$). i.e., the expected number of encounters given an individual's full trajectory ($s_{i,1:2,1:T}$). This function is used to evaluate augmented individuals, where an augmented individual is either part of the population and undetected ($z_i = 1$, $\sum_{j=1}^{J} \sum_{/t=1}^{T} y_{i,j,t} = 0$) or not part of the population and therefore cannot be detected ($z_i = 0$).

dpoisVec: A vectorized Poisson distribution for the detection process (eq 1). This function calculates the density of the observation process across all J traps given the location of individual i at time t ($s_{i,1:2,t}$) and the parameters influencing detection, here σ_{det} and λ_0.

dRW1: A custom distribution to jointly evaluate the x- and y-coordinates of an individual's location ($s_{i,1:2,t}$) using a bivariate normal random walk (eq 2) that is truncated at the state space.

dRW2: A custom distribution to jointly evaluate the x- and y-coordinates of an individual's location ($s_{i,1:2,t}$) using a (possibly) correlated random walk (eq 3) that is truncated at the state space. When $\gamma = 0$, this distribution reverts back to a simple bivariate normal random walk.

dRWTrajectory: A custom distribution to jointly evaluate the x- and y-coordinates of an individual's full trajectory ($s_{i,1:2,1:T}$) using a (possibly) correlated random walk (eq 3) that is truncated at the state space. This distribution allows the full movement path of augmented individuals ($s_{i,1:2,1:T}$) to be jointly evaluated. When $\gamma = 0$, this distribution reverts back to a simple bivariate normal random walk.

myRWtrajectorySampler: A custom sampler that proposes a candidate trajectory ($s_{i,1:2,1:T}$) for augmented individuals using a (possibly) correlated random walk (eq 3) that is truncated at the state space. When $\gamma = 0$, the proposal distribution reverts back to a simple bivariate normal random walk. This sampler currently does not adapt; thus, care must be taken to select a proper proposal scale value (see "SamplerScale" in `sim_SCR_RandomWalks.R`).

SCR WITH LANGEVIN MOVEMENT MODEL

`sim_SCR_Langevin.R`: This R script simulates initial abundance, habitat influenced initial distribution, Langevin movement processes, and SCR detection processes described in the manuscript. Current settings reflect scenario 13 in Appendix S1:Table S5. All other SCR with Langevin movement models described in the manuscript and appendices are fit by changing σ (movement scale parameter), σ_{det} (detection scale parameter), λ_0 (encounter rate), and δ (resource selection parameter).

Section 2 within this script provides the `NIMBLE` models and MCMC settings to run the models in `NIMBLE`. The `NIMBLE` model references several functions and distributions provided in `SCR_Langevin_Mvmt_Distributions_Samplers_and_Functions.R` (described below), which improve MCMC efficiency.

`SCR_Langevin_Mvmt_Distributions_Samplers_and_Functions.R`: This R script provides the sampler and functions for the SCR with Langevin movement processes described in `sim_SCR_Langevin.R`. While nearly all aspects of these models can be expressed in common `BUGS` language, these functions greatly improve MCMC efficiency. We briefly describe each of the functions below and note that they are annotated in the code.

GetLangExpectLoc: This function calculates the gradients given an individual's current location (eq. 5), and derives the expected location at time t given an individual's previous location ($s_{i,1:2,t-1}$), the associated gradients, resource selection parameter (δ), and movement variance (σ^2; see eq. 4).

GetLambdaStar: Same as previously described GetLambdaStar.

dpoisVec: Same as previously described dpoisVec.

dPointProcess: A custom distribution to jointly evaluate the x- and y-coordinates of an individual's location at occasion 1 ($s_{i,1:2,1}$) using an inhomogeneous point process model (eqs. 6 – 8). Specifically, this distribution evaluates locations at occasion 1 as a function of grid cell covariates and the resource selection parameter (δ), but assumes locations ($s_{i,1:2,1}$) within a grid cell are uniform (see details in the Langevin Movement Model section of the paper).

dRW: Same as previously described dRW1.

dRWTrajectoryLangevin: A custom distribution to jointly evaluate the x- and y-coordinates of an individual's full trajectory ($s_{i,1:2,1:T}$) using a Langevin resource selection and movement process (eq 4 – 8) that is truncated at the state space. This distribution allows the full movement path of augmented individuals ($s_{i,1:2,1:T}$) to be jointly evaluated. For reference, when $\delta = 0$, the distribution reverts back to a simple bivariate normal random walk movement process (i.e., habitat has no influence on initial distribution or movement).

myRWtrajectoryLangevinSampler: A custom sampler that proposes a candidate trajectory ($s_{i,1:2,1:T}$) for augmented individuals using a Langevin resource selection and movement process (eq 4 – 8) that is truncated at the state space. For reference, when $\delta = 0$, the proposal distribution reverts back to a simple bivariate normal random walk movement process (i.e., habitat has no influence on initial distribution or movement). This sampler currently does not adapt; thus, care must be taken to select a proper proposal scale value (see “SamplerScale” in `sim_SCR_Langevin.R`).

Literature Cited

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