

A simplification of this filtering algorithm is possible for the case of single-state capture-recapture with one absorbing state. Once an animal is deceased, it is guaranteed to remain in that state thereafter, where $\mathcal{X} = \{\text{“alive”}, \text{“dead”}\}$ and $\mathcal{Y} = \{\text{“seen”}, \text{“not seen”}\}$. In this context we can express the likelihood of a capture history in terms of survival probabilities $\phi_t = \Pr(X_t = \text{“alive”} \mid X_{t-1} = \text{“alive”})$ and detection probabilities $p_t = \Pr(Y_t = \text{“seen”} \mid X_t = \text{“alive”})$ as

$$L(\theta \mid y) = \left(\prod_{t=1}^{t_{\text{final}}-1} \phi_t \right) \left(\prod_{t=2}^{t_{\text{final}}} p_t^{y_t} (1 - p_t)^{1-y_t} \right) \chi_{t_{\text{final}}}, \quad (6)$$

where we numerically assign $y_t = \text{“seen”}$ as $y_t = 1$ and $y_t = \text{“not seen”}$ as $y_t = 0$, t_{final} is the time index of the final observed sighting (*i.e.*, $t_{\text{final}} = \max\{t \mid y_t = 1\}$), $\chi_k = 1$, and $\chi_t = 1 - \phi_t + \phi_t(1 - p_t)\chi_{t+1}$ for $t < k$ (Lebreton et al., 1992). Use of this simplified calculation for single-state capture-recapture will dramatically speed up likelihood evaluations relative to (5), since the likelihood is expressed in closed form.

These filtering algorithms numerically integrate over sequences of latent states to directly calculate model likelihoods, removing the need to perform MCMC sampling of these latent variables. However, the MCMC sampling step for each component of θ now requires application of a filtering algorithm for each observed history y_i . Thus, this approach reduces the dimensionality of the MCMC sampling problem, but at the cost of increased computational complexity of each MCMC iteration.

Filtering MCMC with a reduced representation of the dataset

A further specialized approach arises when there are repeated instances of identical observation histories in the full observed dataset y . That is, multiple distinct individuals exhibited identical observation histories over the k observational periods. Let n^* be the number of unique observation histories in the original dataset y . We define a reduced representation (y^*, m^*) , where y^* contains the n^* unique histories appearing in y . An accompanying vector