# Efficient and flexible MCMC algorithms for capture-recapture using the NIMBLE software package 

Daniel Turek<br>Department of Environmental Science, Policy, and Management University of California, Berkeley dturek@berkeley.edu

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#### Abstract

Capture-recapture analyses have a long history in the field of ecological statistics, providing inference for a variety of population parameters. In the absence of individual random effects, a closed-form likelihood function for capture-recapture models is often available, providing a direct means for likelihood-based calculations. However, the inclusion of random effects for individuals, sites, or sampling occasions often leads the analyst to rely upon MCMC algorithms. The use of mainstream MCMC software (e.g. WinBUGS) requires specifying a binomial response for each sampling occasion, along with latent states when individuals are not detected, rather than directly evaluating the capture-recapture likelihood. MCMC sampling of the population parameters of interest is thereafter hampered by the inefficient calculation of capture history likelihoods and the interlaced sampling of latent states, which may lead to poor mixing and slow convergence. Using the new NIMBLE software package, we show how capture-recapture likelihoods can be built directly into a BUGS model specification to greatly improve algorithmic performance. This native specification also allows the unrestricted use of other numerical algorithms, in addition to MCMC. In models with individual state uncertainty, such as multi-state capture-recapture, we show how a hybrid "MCMC-filtering" algorithm can be implemented, in which MCMC sampling is used for some parameters, but individual capture history likelihoods are calculated via direct filtering. This MCMC-filtering algorithm is applied to the well-known European dippers dataset (Lebreton et al., 1992), and results are compared to those using WinBUGS.


## References

Lebreton, J.-D., Burnham, K. P., Clobert, J., and Anderson, D. R. (1992). Modeling survival and testing biological hypotheses using marked animals: A unified approach with case studies. Ecological Monographs, 62:67-118.

