

Use and abuse of mixing models (MixSIAR)

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Background/Question/Methods

Characterizing trophic links in food webs is a fundamental ecological question. In our efforts to quantify energy flow through food webs, ecologists have increasingly used mixing models to analyze biological tracer data, often from stable isotopes. While mixing models are based on simple concepts, incorporating important biological complexity complicates analysis. In order to spur the implementation of advances in mixing model theory, we recently developed MixSIAR, a GUI tool written in R. Here, we address common questions and pitfalls in mixing model analyses we have seen from our work on MixSIAR.

Results/Conclusions

We explain and suggest “best practices” to ecologists implementing mixing models on the following: 1) Markov Chain Monte Carlo (MCMC) parameters, 2) incorporating prior distributions and the influence of priors, 3) alternative error structures, 4) source aggregating/splitting, 5) incorporating fixed, random, and continuous covariates, 6) effects of the number of tracers included, and 7) application to fatty acid data as well as stable isotope data. We conclude by outlining unresolved research questions in the use of mixing models such as MixSIAR.