

MixSIAR: A Bayesian stable isotope mixing model for characterizing intrapopulation niche variation

Background/Question/Methods

The science of stable isotope mixing models has tended towards the development of modeling products (e.g. IsoSource, MixSIR, SIAR), where methodological advances or syntheses of the current state of the art are published in parity with software packages. However, while mixing model theory has recently been extended to incorporate hierarchical structure in mixture populations (e.g. trophic niche partitioning across levels of population structure), no existing mixing model tool currently accounts for such structure. Here we introduce MixSIAR, a new GUI tool based on the R statistical computing platform. MixSIAR is unique in that it incorporates both fixed and random effects associated with the mixture population.

Results/Conclusions

MixSIAR provides researchers a consolidated analytic framework for addressing hierarchical structure in mixing model analyses. To demonstrate the tool, we show an application to a source/mixture system with multiple levels of structure in the mixing population. Through this example, we outline novel mixing model approaches for characterizing intrapopulation niche variation through variance decomposition. We also outline “best practices” associated with data collection and analysis when applying mixing models studies to systems with hierarchical structure.