MixSIAR: Advanced stable isotope mixing models in R

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Background/Question/Methods

The development of stable isotope mixing models has coincided with modelling products (e.g. IsoSource, MixSIR, SIAR), where methodological advances are published in parity with software packages. However, while mixing model theory has recently been extended to incorporate hierarchical population structure (e.g. tropic niche partitioning) and continuous covariates (e.g. length), no existing mixing model tool currently accounts for such structure. Here we demonstrate MixSIAR, a new GUI tool in the R statistical computing platform. MixSIAR is unique in that it incorporates fixed, random, and continuous effects associated with the mixture population.

Results/Conclusions

MixSIAR provides researchers a consolidated analytic framework for addressing hierarchical structure and continuous covariates in mixing model analyses. We show an application of MixSIAR to a system with multiple levels of structure in the mixing population. Through this example, we outline novel mixing model approaches for characterizing intrapopulation niche variation though variance decomposition. We briefly demonstrate MixSIAR's ability to analyze stable isotope systems with continuous covariates, and conclude by outlining "best practices" in the use of stable isotope mixing models such as MixSIAR.

Key words: food web, stable isotopes, mixing model, niche variation