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## Metadata S3

Code to simulate and analyze individual diet specialization at the population level

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## File list

Supplementary\_Data\_S3.R

## Description

**Supplementary\_Data\_S3.R**– The R code contained in Data S3 simulates and analyzes the relative diet specialization of individuals within populations using three metrics: IS, WIC/TNW, and the concentration parameter of the Dirichlet distribution  $w$  (see main text). The R code simulates individual diets in populations of 100 individuals whose preferences and amount of diet specialization are randomly pulled from uniform distributions. The individual diets are pulled from a multinomial distribution with the probabilities determined by their true preferences and the number of items the individual is observed feeding on determined by a draw from a uniform(3,50) distribution. The code provided allows individuals to feed on up to four prey types. The code then estimates the relative diet specialization among individuals by using the maximum likelihood method in the R package ‘RInSp’ to estimate the WIC/TNW and IS indices (Zaccarelli et al. 2013) and the Bayesian hierarchical method implemented in ‘OpenBUGS’ using the R package ‘R2OpenBUGS’ to estimate  $w$  (Lunn et al. 2000; Sturtz et al. 2005). The code also calculates WIC/TNW and the IS index using the true preferences of individuals. The true value of  $w$  is known, as it is used to simulate the original data. The output provides: 1) the true values of  $w$ , 2) the estimated values of  $w$ , 3) the true values of the population preferences, 4) the true and estimated values of WIC/TNW, and 5) the

true and estimated values of IS. Annotations provide explanations of each step of the simulation and analysis. The code can be modified to simulate different numbers of populations, different numbers of individual per populations, different distributions for the number of prey items observed per individual, and different numbers of prey types across which individuals can feed.

The R code was run on R version 3.2.4. It requires the R packages ‘R2OpenBUGS’ (Sturtz et al. 2005), ‘RInSp’ (Zaccarelli et al. 2013), ‘MCMCpack’ (Martin et al. 2011), and the program OpenBUGS to be installed on the machine being used. The code was developed and run using OpenBUGS version 3.2.3.

## References

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- Zaccarelli, N., G. Mancinelli, and D. I. Bolnick. 2013. RInSp: an R package for the analysis of individual specialisation in resource use. *Methods in Ecology and Evolution* **4**:1018–1023.