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Metadata S1

Code to simulate and analyze individual diet data

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File list

Supplementary_Data_S1.R

Description

Supplementary_Data_S1.R– The R code contained in Supplementary Data S1 simulates individual diet data from a population with a random population preference and degree of diet specialization among individuals. To simulate the data, individual's feeding on up to four prey types draw a multinomial sample from the Dirichlet distribution describing the population diet. The code provided shows an example where each individual draws 10 items to compose its diet. Annotations provide directions for altering the number of items drawn in the multinomial sample for each individual. After simulating the data, the code then analyzes the data using the maximum likelihood method using the R package 'RInSp' (Zaccarelli et al. 2013) and a two-level Bayesian hierarchical model using 'OpenBUGS' through the R package 'R2OpenBUGS' (Lunn et al. 2000; Sturtz et al. 2005). The program produces an array containing for each population simulated: i) each individual's true preferences for the prey types, ii) the true PS_i value for each individual, iii) the Bayesian estimate of PS_i and its variance, iv) the maximum likelihood estimate of PS_i and its variance, and v) a 95% credible interval for the Bayesian PS_i estimate. Alterations to the code can change the number of populations simulated and the number of prey types across which individuals can feed. Annotations within the code provide explanations for each step of the code.

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.