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## Metadata S2

Code to simulate and analyze individual diet data with heterogeneity in sample sizes among individuals

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## File list

Supplementary\_Data\_S2.R

## Description

Supplementary\_Data\_S2.R– The R code contained in Data S2 simulates individual diet data from a population with a random population preference and degree of diet specialization among individuals. To simulate the data, individuals feeding on up to four prey types draw a multinomial sample from the Dirichlet distribution describing the population diet. The code in Data S2 simulates individuals with heterogeneity in the sample size per individual. Three scenarios of heterogeneity among individuals are simulated: i) sample sizes per individual are uniformly distributed (drawn from a Beta(1,1) distribution), ii) sample sizes per individual are skewed towards many observations per individual (a Beta(1,0.5) distribution), or iii) sample sizes are skewed towards few observations per individual (a Beta(0.5, 1) distribution). The resulting values of the Beta distribution draw per individual are then multiplied by 100 and rounded to the next highest integer leading to a total sample size ranging from 1 to 101 items per 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, the number of prey types across which individuals can feed, and the Beta distribution from which the sample sizes are drawn. 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

- Lunn, D. J., A. Thomas, N. Best, and D. Spiegelhalter. 2000. WinBugs – a Bayesian modeling framework: concepts, structure, and extensibility. *Statistics and Computing* **10**:325–337.
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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.