Estimation Procedure for Maximum Likelihood Estimates of Prey Contributions to Predator Diets

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**Purpose:**

This is an online supplement for:

Moriarty, P.E., T.E. Essington, E.J. Ward. 2016. A Novel Method to Estimate Prey Contributions to Predator Diets. Canadian Journal of Fishery and Aquatic Sciences. *In review*.

This document demonstrates an example of the mixture model described in the above article. In this supplement, we provide a simulated dataset and an actual dataset used in the article above. We use the provided R code to run our mixture model in order to estimate the model parameters for the datasets. Code was built and tested under R version 3.1.0.

**File Descriptions:**

-‘README.doc’: Explanation of the contents of this supplement and directions on running the model.

-‘PredatorExample.Rdata’: Contains 1 simulated example dataset and 1 real dataset (lingcod) from Moriarty et al. (*in review*).

-‘MixtureModelExample.R’: Contains R code to run the simulated and real examples.

-Main R functions: see descriptions in table at end of this document

**Packages Needed:**

plotrix

stats4

optimx

numDeriv

MASS

fitdistrplus

**Model Execution:**

*Required Data Format:* The data must be in two columns, where one is a vector of the proportion of each stomach that is the prey type of interest (prey type *i*) and the other column is the corresponding total stomach contents mass for that stomach. There must be at least one stomach for each of the three cases: proportion of the prey type (*pi*) is 0, *pi = 1, 0 < pi < 1*.

*Run Mixture Model Examples:*

To see examples of the mixture model, open the file called ‘MixtureModelExample.R’. Once the necessary packages are installed and loaded, this file will load the example datasets. As demonstrated in the example, to run the mixture model, use the function called ‘run.model.R’. The arguments are the proportion of each stomach that is the prey type (called ‘prop’) and the total stomach contents mass for each stomach (called ‘total.mass’). Inputting these two columns of data into ‘run.model.R’ returns maximum likelihood estimates for all parameters in the mixture model.

Additionally, to compare the estimates and error from the mixture model to other methods, use the function ‘model.comparison.R’. The arguments are the same as for ‘run.model.R’.

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**Support, Liability and Copyright:**

Support in using this software is available from Pamela Moriarty, pmoriart@uw.edu. The code and files contained in this package may be copied and distributed for non-commercial purposes. If it is used in a publication, please cite Moriarty et al. (2016) (full citation at top of this document). The authors, University of Washington, and National Oceanic and Atmospheric Administration accept no liability for the use of this software.

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**Main Function Descriptions**

|  |  |  |  |
| --- | --- | --- | --- |
| **Name** | **Purpose** | **Inputs** | **Outputs** |
| run.model | runs the mixture model | **prop** = column of data of the proportion of each stomach that is prey type *i*; **total.mass** = column of corresponding total stomach contents masses | maximum likelihood estimates of all mixture model parameters |
| model.comparison | compares estimates between previously existing analysis methods and the mixture model | **prop** = column of data of the proportion of each stomach that is prey type *i*; **total.mass** = column of corresponding total stomach contents masses; **mat** = whether output as a matrix is desired (F); **CI** = whether error output as 95% confidence intervals is desired (F); **yaxis** = whether the yaxis should be shown on the output plot (T); **ybnd** = maximum value for y axis (1.0); **…**=other arguments to be passed to the plotting function | table or plot showing the estimates using the mixture model, a conventional mean and weighted mean, and standard error for all 3 methods |

**Internal Function Descriptions**

|  |  |  |  |
| --- | --- | --- | --- |
| model.par | cleans input data, calculates starting values for the mixture model, then compares estimates from the mixture model to estimating each parameter individually to ensure they match | **prop** = column of data of the proportion of each stomach that is prey type *i*; **total.mass** = column of corresponding total stomach contents masses | table of mixture model parameter estimates |
| find.mle | calculates parameters for the gamma and beta distributions from their mean and variance, then runs the optimization procedure to find the maximum likelihood estimates | **data** = cleaned data as a 2 column matrix, starting values for all parameters (**p.bin, p.full, mean.pres, var.pres, var.abs, beta.mean, beta.sd, p.pop**) | output of the optimization function (optimx) |
| par.mle | calculates the maximum likelihood estimate for each mixture model parameter individually | **data** = cleaned data; **prey.est** = estimates from estimating parameters simultaneously; **width** = bounds for how close the two estimates for *ci* should be | estimate for *ci* from estimating parameters individually and the upper and lower bound of the chosen range |
| Bmean | calculates the mean of a beta distribution | **alpha1** = beta parameter 1; **alpha2** = beta parameter 2 | mean of beta distribution |