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IsoPOPd Web Interactive: Interactive software to understand how elements in a population matrix model influence the asymptotic population growth rate

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Overview of the software application

Population matrix models decompose life history traits into mathematical expressions. These mathematical expressions form a matrix, which provides the analytical machinery to calculate the growth rate (λ) of the population (Caswell, 2001).

But how does the matrix transform information from a life history into information on population dynamics? This software application is designed to allow users to visualize the interplay between life history traits (vital rates) and the population growth rate.

This interactive app allows users to:

- 1) Visualize how life history characteristics aggregate into p and q and r superparameters, and then how those superparameters aggregate into the population growth rate.
- 2) Visualize the contribution of each life history trait to the characteristic equation, $\lambda^3 + p\lambda^2 + q\lambda + r = 0$.
- 3) Understand how targeted managerial alteration of one (or more) life history traits will influence the growth rate.
- 4) Understand how targeted managerial alteration of one (or more) life history traits will change the influence of other life history traits to the growth rate.

Interactive Software User Tutorial

Preparing the app for use on your computer:

- Step 1: Identify the appropriate structure of a 3-stage model matrix for your species.
- Step 2: Gather data from your species for each vital rate.
- Step 3: Download the IsoPOPd software code.
- Step 4: Install three packages: “shinyBS”, “rgl”, and “rmarkdown”. To install packages, type `install.packages(“shinyBS”)` to the console and hit run. Repeat with the other packages.
- Step 5: Open the IsoPOPd file in R studio.
- Step 6: Click “Run All” and begin interacting with the software application.

Using the IsoPOPd interactive software app:

- Step 1: Enter all nine vital rates for your system of interest. Zero should be entered when the transition is not biologically plausible in your species. Save your entries by clicking “Save vital rate entries”. This click will activate all the tabs.
- Step 2: View the outputs on each tab. The code will automatically produce graphics of an eigenvalue cube, the p volume, the q volume, and the r volume. Help and interpretation are obtained by clicking the buttons at the bottom of each tab.

User Inputs:

The user must input all nine vital rate magnitudes. Vital rates must be positive real numbers. Zero is a valid input for any vital rate magnitude.

Reproduction parameters: The top row represents the reproduction traits in the life history. Each element may be parameterized as fertility (actual reproduction) or fecundity (maximum reproduction). Reproduction elements are in the units of number of female offspring per breeding female, per time period. Reproduction in the ith column corresponds to reproduction in the ith stage.

Transition parameters: All entries that do not appear in the top row represent transitions through the life stages. A transition that begins at one stage and ends in a different stage represents the average probability that a female will survive the time unit and transition to the latter stage. Alternatively, a transition that begins at one stage and ends in the same stage represents the average probability that a female will survive the time unit and remain in that same stage.

For further information on user inputs, please see:

Caswell, H. (2001). - *In: Matrix population models: Construction, analysis, and interpretation*. 2nd edition. Sinauer Associates. Sunderland, Massachusetts, USA.

Technical Details of the Software

This app was written under R Studio Version 1.1.463 – © 2009-2018 RStudio, Inc. This code requires three R Shiny packages: “shinyBS”, “rgl”, and “rmarkdown”.

Acknowledgements

We’d like to thank Mathew Plourde and the online R troubleshooting community for the code segment used to create the sequentially illuminated tabs in the user interface. We would also like

to thank Jennifer Peaslee and Nick Hollingshead for help with wordings of this readme file and on the corresponding Cornell Wildlife Health Lab webpage.

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Suggested Citation for this Software:

Hanley, B., Connelly, P., & Dennis, B. 2019. IsoPOPd: Interactive software to understand how elements in a population matrix model influence the asymptotic population growth rate [Software]. Cornell University Library eCommons Repository.
<https://doi.org/10.7298/bcmg-7w08>