Explanation for PopulationExampleModelt.txt

Supplement to Chapter 8 in book on Ranaviruses (Gray and Chinchar, eds.) published in 2014 by Springer.

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This model is a stage-structured population matrix model for exploring the effects of ranavirus exposure in the premetamorphic stage on population dynamics. The model requires input of demographic parameters (survival [p], fecundity [f]) for uninfected populations, survival given ranavirus exposure (dissurv), adult carrying capacity (K), and average frequency of ranavirus exposure (disprob). The current form of the model is based on wood frogs (*Lithobates sylvaticus*), but a different stage structure could be implemented by altering the population matrix (LX). Simulations based on this model have been published in (Earl and Gray 2014).

This is a female-only, post-breeding model, meaning that the numbers of individuals in each class for a year are censused just after eggs are laid. In this model, the population size for stage *i* (where *i* = pm, 1, 2, and 3+ for pre-metamorphosis and years 1, 2 and ≥ 3) at time *t* [$N_i(t)$] is calculated by multiplying the population matrix at time *t* – 1 by the transition matrix containing parameter estimates for survival (p) and fecundity (F; Eq. 1).

$$\begin{pmatrix} N_{pm}(t) \\ N_1(t) \\ N_2(t) \\ N_{3+}(t) \end{pmatrix} = \begin{pmatrix} 0 & F_1 & F_2 & F_3 \\ p_1 & 0 & 0 & 0 \\ 0 & p_2 & 0 & 0 \\ 0 & 0 & p_3 & p_4 \end{pmatrix} \text{ x } \begin{pmatrix} N_{pm}(t\text{-}1) \\ N_1(t\text{-}1) \\ N_2(t\text{-}1) \\ N_{3+}(t\text{-}1) \end{pmatrix} \qquad \text{(Eq. 1)}$$

Parameter estimates are drawn at from a normal distribution for each parameter in order to simulate stochasticity in a continuous manner. In each year of the model simulations, a random value is drawn from a normal distribution (described by the mean [p and f] and standard deviation [psd and fsd]) for each parameter. The stochasticity can be eliminated from the model by setting all of the standard deviations (psd and fsd) to zero. The model also includes an adult carrying capacity (K), which works as a ceiling such that when the number of adults exceeds the carrying capacity the adult population size is reduced to K, split evenly between year 2 and year 3+.

To simulate mortality in years with ranavirus exposure, the model multiplies the pre-metamorph to year-one transition probability (p_1) times the ranavirus survival probability (specified in the model as dissurv). The model assumes that individuals that are exposed and survive are not exposed again during a subsequent life stage. For the pathogen interval exposure, intervals are treated probabilistically such that years with pathogen exposure are randomly determined using a binomial distribution appropriate for the exposure interval (specified in the model as disprob). Thus, when disprob = 0.1, or every ten years, ranavirus is not introduced exactly every ten years but on average every ten years.

The model is set to run simulations for a specified number of runs (called runs in the model) over a specified amount of time (years as specified in the model). The output includes the extinction probability and the average and standard error of the time to extinction, the final population size, and the final adult population size after the specified number of years.

Extinction is defined very conservatively as zero living individuals. The model also exports the data as a .csv file with the year of extinction, final population size, extinction status (1 for extinct, 0 for not extinct), and the final population size for each model run.

Literature Cited

Earl JE, Gray MJ (2014) Introduction of ranavirus to isolated wood frog populations could cause local extinction. EcoHealth DOI: 10.1007/s10393-014-0950-y.