

## EEB 2208 LECTURE TOPIC 15

### POPULATION VIABILITY ANALYSIS

#### Reading for this lecture and the next one

Primack: Chapters 13 and 14

#### Additional optional reading:

[Reed, D. H. et al. 2003. Estimates of minimum viable population sizes for vertebrates and factors influencing those estimates. Biological Conservation 113:23-34.](#)

### 1. Population viability analysis (PVA)

#### A) THE BASICS OF DEMOGRAPHIC MODELING

- i) Population viability analysis is really just a special case application of the typical population modeling that is done by ecologists all the time (you might have encountered this in general ecology or in a course on wildlife management). Human demographers use similar methods to determine the rate of change of human population sizes.
- ii) In its simplest terms all that needs to be done is to figure out how big a population is now, and to predict how its size will change. To do this we need to know how many individuals will be added and how many will be lost. Sounds simple, eh?
- iii) To figure out how many to add, we need to estimate the number of breeders in the population and how many young each of those breeders will produce.
- iv) To determine how many are lost, we need to know the mortality rate (i.e., how many will die), preferably with some sort of breakdown for different age classes (e.g., juveniles usually have much higher death rates than adults).
- v) Then, just to complicate things, we also have to account for whether there will be immigrants (which get added) or emigrants (which get subtracted). If an entire population is being modeled (as is often the case with endangered species), immigration/emigration can be ignored.
- vi) To put this in simple mathematical terms,  $N_{t+1} = N_t + \text{Births} - \text{Deaths} + \text{Immigrants} - \text{Emigrants}$ . ( $N_t$  is the current population size;  $N_{t+1}$  is the population size one time step in the future; usually time steps are measured in years, but they don't have to be.) In very simplistic terms, if (B+I) is larger than or equal to (D+E) then the population will be OK. If (D+E) is larger than (B+I), the population will decline.

#### B) INCORPORATING VARIATION

- i) A key element of any PVA is that it should provide information about the potential variability in the system. When we estimate the numbers that go into a model, we know that there is uncertainty about each of them. This uncertainty arises both because we often do not have very good information (i.e., our estimates have error), but also because of stochasticity inherent in the system. For example, not every individual produces exactly the same number of young, not every individual gets to breed, not every year is as good as the others, ....
- ii) This stochasticity is incorporated by telling the computer not to use a single number for each part of the equation, but rather to pick a number from a range of possible numbers. Some numbers may be more likely to be picked than others (can you think which kind of numbers these might be – e.g., in terms of mean, mode, median?), but it is not certain how any particular simulation will turn out. Models that incorporate variability in this way are referred to as **stochastic**, rather than **deterministic** (a deterministic model will produce exactly the same result every time – i.e., the result is “determined” by the model's design and input data).

- iii) **Genetic stochasticity** was covered in some detail in the conservation genetics lecture. To recap, drift is a random process by which genetic variation is lost from a population. As populations get smaller, variation is lost at an increasingly rapid rate. Mutation is another random process that restores variation, but the mutation rate does not vary with population size. The smaller the population size, the more the losses due to drift will outweigh the gains through mutation.
- iv) **Demographic stochasticity** refers to random variation in birth and death rates. For example, imagine you have a population in which there is a high chance of an individual failing to breed in any one year. If the population is large then there will almost certainly be some breeding every year (just as if you roll a pair of die 1000 times then you will almost certainly get two sixes at least once). But if population size is sufficiently small then it is possible that no one will breed in some years – simply due to chance (i.e., if you only roll a pair of die ten times, then you could easily not get two sixes at all).
- v) **Environmental stochasticity** refers to the effects of random variation in environmental conditions. For example, there might be a string of “bad” years for a species. If the population is big, this might be no big deal – there will be a decline in population size, but nothing that the population cannot recover from once conditions improve. But, if the population is small, a string of bad years might be just enough to cause it to decline to zero – and there’s no recovery from zero.
- vi) Finally, many models incorporate a final type of variation: **catastrophes**. These are major events that have a drastic impact on a population (e.g., they cause total reproductive failure, or they kill a large proportion of the population). Catastrophes are really just the extremes that arise from of environmental variation and could be included within environmental stochasticity. But, for several reasons it is often easier to incorporate them into models separately (if you want to know the details, ask me about it).

#### C) ESTIMATING EXTINCTION RISK

- i) Once the model has been created, all the researcher needs to do is run repeated simulations and determine how many simulations end with the population going extinct.
- ii) To determine the probability that a population of a given size will go extinct within a given number of years, one simply needs to set the starting population size and then determine the proportion of the model runs that went extinct within that time frame. E.g., if 1000 separate simulations are each run for 50 years, and the computer population went extinct in 423 of the simulations, then the probability of extinction is predicted to be 0.423 (i.e., just over 40%) over a 50 year period.
- iii) To determine how extinction risk changes with population size, one can simply repeat this process with different starting population sizes, and compare the number of extinctions at each size.
- iv) Equally, to determine how effective different management actions are likely to be, you can simply change the numbers in the model (the “parameter estimates”) based on how they are expected to change with the target management action, and compare the extinction probabilities under each scenario.

#### D) CASE STUDY: HAWAIIAN STILT

- i) Once a model has been created we first need to ask if we can trust the model results. One way to do this is to see if the model accurately predicts what has happened in the past. Another alternative is to see whether plausible (i.e., accounting for error in the way the estimates were made) changes in the numbers that go into the model radically change the results.
- ii) In the PVA on Hawaiian stilts that is described in the text book, the model predicted that the population would increase over time until all the habitat was filled. This matched reality – populations have steadily increased on all of the islands where stilts are found and have subsequently leveled off, suggesting habitat saturation.
- iii) When the model was constructed, some of the numbers had to be made up. For example, there was no information on survival rates in these birds, so data from other similar species was used instead (assuming that survival in stilts would be similar to survival in these closely related birds). A “**sensitivity analysis**” was conducted in which the survival values were

- systematically varied to see how much they affected the model result. This analysis suggested that the survival estimates would have to be wrong by quite a lot for it to alter the conclusions.
- iv) Hence, although the model is far from perfect, the conclusion was that it probably did an OK job of predicting extinction risk.

## 2. So how big do populations need to be?

### A) ESTIMATES BASED ON GENETIC CONSIDERATIONS

- i) Some of the first attempts to estimate MVP in general terms focused on the genetic issues faced by small populations. This work resulted in what was known as the “50/500 rule.”
- ii) The idea was that at least 50 individuals are needed to protect a species from inbreeding effects over the short-term, and at least 500 were needed to avoid serious effects of drift over the long term.
- iii) Lots of people jumped on this and saw it as a nice easy guideline. Unfortunately the rule was misinterpreted in several ways. First, the focus was on the “50” part, whereas the number 500 was more important for long-term conservation. Second, some users of the rule ignored the fact that these numbers refer to the **effective population size** ( $N_e$ ), which is usually much smaller than the real population size (see lecture on conservation genetics).
- iv) In fact, it is estimated that  $N_e$  is often 1/5 to 1/10 of  $N$ . Hence, the 50/500 rule basically means that MVP on average should be about 2,500 - 5,000 based on genetic considerations alone. Subsequent research suggests that to avoid losing evolutionary potential within the population, this number should be even higher (up to 10,000 or more).

### B) ESTIMATES BASED ON GENERIC POPULATION DYNAMICS

- i) Studies of real populations show that some species can last for a long time with very small populations.
- ii) But, in most cases, at least a few 100 individuals are needed for a population to last > 100 years.
- iii) Realistic (but generic) computer simulations suggest that typically at least 500 individuals are needed, and that if the population size is relatively variable this number can rise to > 5,000.

### C) ESTIMATES BASED ON PVA

- i) Most recently, people have used actual population models for specific species to estimate MVP. In the largest study 102 vertebrate species were modeled to estimate MVP for 99% persistence over 40 generations. (Why do you think they used generations, instead of years?)
- ii) This study found that the mean MVP was about 7300 adults, while the median was about 5800 adults.
- iii) Similar results were found for different types of animals.
- iv) Another result was that MVP was larger for species that have been studied for a long time. This is probably because long studies do a better job of describing variability in the system. One consequence of this result is that it suggests that MVP estimates based on short-term studies are probably underestimates of the true MVP.

### D) CONCORDANCE OF ESTIMATES

Overall, this collection of studies, using a variety of techniques and focusing on different threats, tend to converge on a single result: For a population to be viable over the long term it needs to number at least several thousand individuals.