SECTION I

SAVING SPECIES THROUGH POPULATION BIOLOGY AND VIABILITY ANALYSES: A MORASS OF MATH, MYTH, AND MISTAKES?

Population biology will always be the core of conservation biology. The reason for this is simple. Ultimately, we aim to save species, and this task requires that we consider reproduction, survival and dispersal rates, evolutionary vigor, and extinction risks. These factors are the domain of population biology. Indeed, anyone receiving an advanced degree in conservation biology is likely to have been exposed to course work in population biology; many will have used some form of population viability analysis (affectionately known as "PVA"). But these standard subjects have become much more sophisticated than treatments in most textbooks suggest. We asked a wide range of population biologists engaged in everything from academic research to "on-the-ground" conservation to review their area of population-oriented conservation biology. The response overwhelmingly indicates a rejection of the simplicity of our early applications of population theory.

It is not the case that early ideas in conservation population biology were wrong, however. Smaller populations *have* greater extinction risks. Fragmentation and habitat loss *is* bad. Demographic rates summarized in transition matrices *can* be informative. But these truisms do not get us very far in the practice of conservation. The question should not be whether small populations are at greater risk than large populations, but rather, what is the marginal gain (in terms of reducing extinction risk) of each incremental increase in population size? Similarly, while it is easy to appreciate the merits of a diverse seed bank, it is much harder to decide on a practical protocol for gathering seeds to be included in a seed bank (i.e., if there is space for 100 seeds of each species, how should the sample be apportioned among individual plants, families of plants, populations, and regions?). Similarly, when collecting demographic data a plea is always made for long-term studies, but those studies are expensive. Exactly how much insight is gained by going from a two-year to a three-year demographic study? These are the sorts of questions asked by contributors to this section—hard practical questions that bring somewhat vague theory into the realm of real-world practical constraints.

The answers to these hard questions will not be pleasing to those who hope for simple rules to follow. It turns out in all cases that the answers depend on the details, although the influence of details is nicely illuminated by general theory. Guerrant and Pavlik show how strategies for collecting seeds and reintroducing plants depend critically on details regarding a plant's breeding system, life cycle, and habitat requirements. Similarly Menges points out that the extinction risks faced by plants depend on variance-to-mean ratios in demographic rates. Fiedler and her colleagues discover that a clear-cut demographic distinction between rare versus common plants is not apparent—instead the distinction takes form only after careful analyses of projection matrices in all their arcane detail. The management conclusions to emerge from PVA, even when using the same baseline data, is shown by Groom and Pascual to depend on the source of variation and on the mechanics of how variation is incorporated into models. Similarly, the effects of fragmentation can depend on exactly what variables are considered. For example, Freidenburg points out that whereas edge effects with respect to light penetrate only 50 meters into forest fragments, edge effects with respect to airflow commonly penetrate at least 200 meters into forests. When one realizes that many forest patches have diameters of less than a half a kilometer, these specific differences translate into huge contrasts with respect to how much core habitat we conclude is remaining for many of our North American forests.

A second advance evident in this section is a greatly sharpened view of variability. Certainly the importance of variation was not lost on the founders of conservation biology; however, earlier treatments tended to be anecdotal and casual—at best distinguishing between demographic stochasticity and environmental stochasticity. Contemporary viability analyses, investigations of genetic viability, and studies of fragmentation all deal with a much more elaborate classification and portrait of variability. Indeed, most of the contributions to this section include analyses that show precisely how the magnitude and character of variability alter a population's likely fate and dictate different management solutions.

Finally, although the dependence on detail is unarguable, equally clear is the realization that all detail is not crucial, or that in some situations the details will not matter. Thus, Groom and Pascual report that the results of PVA are typically insensitive to exactly how many stage-classes are used in the projection matrices. Menges finds (through exhaustive computer simulation) that environmental stochasticity matters little to extinction risks once population grow by more than 15% per year. And Fiedler and her colleagues demonstrate that the same basic format for a projection matrix aptly captures the demographic processes of nearly a dozen different species, albeit species in one taxonomic group.

The protection and management of single species is the branch of conservation biology most steeped in abstract theory—life history theory, metapopulation theory, minimum viable population theory, and so forth. Although these general models rarely help solve particular problems, this does not mean that population theorists are without value to the practice of conservation. Indeed, conservation practitioners have much to gain from combining forces with theoreticians to determine the optimal level of detail and specificity for studies aimed at protecting species.