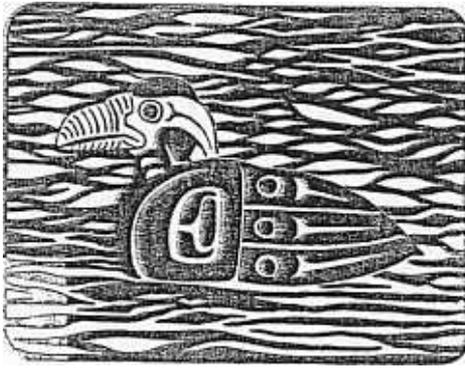


Characterizing Species at Risk

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Introduction

For at least the past three decades, researchers and managers have used various forms of risk and decision analysis for assessing the status and effects of management practices on populations or habitat. Early methods that continue to be practiced today use habitat relationships information to assess changes in macro- or microhabitat area from land management practices or other human activities.^{36, 147, 171} Other forms use risk analysis to identify and rank species of conservation concern.^{58, 77, 107, 120} Quantitative population viability models have received extensive attention for analyzing probabilities of extinction for single species under current or future conditions,^{1, 80} but they are just one of many tools in the risk analysis toolbox. Decision models have used risk analysis to compare extinction likelihood of wildlife populations to the economic cost of their conservation.⁴⁹ Many other examples can be found in the literature.

In this chapter, we attempt to describe some of those risk analysis tools, but also strive to provide readers with a basic understanding of the underlying theory and criteria for identifying species at risk. We focus on analytical tools that might be used with available datasets, like the CD-ROM in this book, to meet the risk analysis challenge at different levels of geographic and ecological scale. We define the components of risk analysis, describe the criteria for identifying species at risk, review methods of species risk analysis, examine the attributes of species currently considered at risk, and work several examples of risk analysis using the life history and habitat relationships information in this book.

Defining Risk

In much of the biological literature, the term "risk" really means "likelihood" of some event or condition occurring.¹ However, formally, ecological risk analysis typically differentiates the estimation of outcome likelihood (possibility of change or loss) from management values (or utilities) placed on those outcomes. Outcome likelihood can be estimated quantitatively (e.g., 90% persistence of a nonzero population over 100 years) from simulation modeling (rarely from empirical study), qualitatively from simpler habitat or life history models, or from expert judgment as an ordinal scale (rank order) of outcomes. "Risk" is the likelihood that some

management objective will not be met. Risk is the likelihood of an outcome occurring multiplied by the value given to an outcome. This means that to fully evaluate the "risk" of any course of action, management objectives first must be articulated in terms that can be clearly analyzed.

Distinguishing Risk Analysis from Risk Management

In risk analysis, researchers list possible outcomes, estimate their likelihood under one or more management alternatives, and then weight each outcome with a value. Outcome values are assigned by managers based on social, economic, political, or other goals. Defining what is desired (outcome values) and the likelihood of achieving it (outcome likelihood) helps determine the risk of a decision (Figure 1). In risk management, the manager first describes the values they place on possible outcomes, ideally in conjunction with the risk analysis. Then the manager describes their risk attitude towards seeking or avoiding particular kinds of outcomes. Then, they apply this attitude to the risk analysis results and choose an acceptable course of action that best fits their risk attitude and the outcome values.

Data that fuel risk analyses can be uncertain in several ways. There can be errors of measurement, sampling errors, and natural variation. Data errors of these kinds can result in greater variances in the estimation of the biological factor of interest, which can add some degree of confusion to the risk management phase. How these errors add up and interact is typically ignored in risk analyses, but the problem of error propagation is not to be neglected. Methods to negate the effects include stochastic simulation analysis and sensitivity analysis,¹⁴⁴ use of meta-analysis techniques,^{34, 38, 56} partitioning or bootstrapping samples,¹¹¹ and, when the problem is simple enough, outright analytic solutions.¹¹⁵

A common erroneous view of uncertainty (variance) in risk analysis outcomes is that it appears as a lack of evidence of adverse effects, or even as evidence of no effect. This can be a biologically, and politically, hazardous approach leading, in the worst cases, to species extirpation or extinction. What can the risk analyzer do in the face of such unknowns? True data unknowns mean that no

statistical estimation or population projection is even possible, even by using expert judgment. The risk analyzer can skirt the issue by borrowing data from a related species, time period, or geographic location, or can conduct a sensitivity analysis, letting an unknown variable vary over some biologically reasonable range of values and determining the degree to which the outcome (e.g., population persistence likelihood) is influenced by that variable. A more formal analysis of the value of additional information also can be conducted to determine the worth of expending time and money in seeking values of unknown variables, or refining estimates of ones known.

Criteria for Identifying Species at Risk

If current trends in human behavior continue, the twenty-first century may come to be known as a mass extinction event rivaling the extinction event of 65 million years ago. Some estimates suggest that up to one quarter of all species now living may be lost in the next fifty years,¹⁰² mainly through habitat alteration, but also through introduction of invasive species, pollution, and other human activities. Clearly, to avoid such a catastrophe, natural resource professionals must better understand the process of extinction, how humans can affect species' extinction risks, and the attributes that make species particularly extinction-prone. In particular, decision makers and risk analyzers need theory and predictive tools to make wise land-use decisions in short time frames and otherwise data-poor environments, particularly in the next fifty years, when the world's human population is expected to peak. Below, we outline some of what we know and do not know about the process of extinction.

The viability of populations is driven by two basic types of processes: systematic and stochastic. Systematic processes generally reduce the size of populations,¹³⁵ and result from the removal of something essential from the environment, such as space, shelter, or food, or from the insertion of something lethal, such as a new predator or poison. Systematic processes tend to reduce population sizes to levels that make them susceptible to stochastic processes that lead to extinction. Stochastic processes, on the other hand, are random events or a series of events that can dramatically affect birth and death rates within populations.

Systematic Extinction Processes

Primary processes. Of the 485 animals and 584 plant species that have been certified as extinct since 1600,¹⁰² approximately 61% of the animal extinctions and 27% of the plants are island endemics. Most of these island extinctions resulted from Diamond's²⁹ "evil quartet" of systematic processes: habitat destruction and fragmentation, introduction of exotic species, over-exploitation by humans, and chains of extinction. Although this same evil quartet affects mainland species, island endemics, having evolved in the absence of predators or competitors including humans, are particularly vulnerable to extirpation when exotic predators or competitors are introduced. The spread of

exotic species will only increase with the growth of the global economy.

Landscape change (habitat loss, degradation, and fragmentation) is the primary cause of endangerment for two-thirds of the world's vertebrates currently considered at risk of extinction.¹²⁸ Some major habitat types such as the North American tallgrass prairie have been virtually eliminated (converted to other uses) while others such as the heathlands in the United Kingdom and thorn scrub in Sri Lanka have been reduced to less than 30% of their original extent.¹⁴¹ Currently some of the highest rates of forest conversion to agricultural and urban land are found in the humid tropics,¹⁸⁶ our great storehouses of biodiversity. Other habitat types are changed in less obvious ways. For example, while the amount of forest cover is increasing in Europe and the former USSR, the clearing of virgin forest worldwide has increased exponentially since the 1500s.⁹⁹ Of the 4 billion hectares estimated to be in forest cover today, 1.7 billion are secondary forests or plantations.¹⁸⁵

As an area is converted from natural vegetation to some other use, the remaining habitat is commonly divided into smaller parcels. The effects of these actions on biodiversity are diverse,^{32, 131, 146, 181} but often discussed in terms of three related effects: fragmentation, edge, and isolation. It is important to note that although human alterations to the environment are often considered deleterious to most species, the effects of landscape change including fragmentation, isolation, and the creation of edge habitat are species-specific. What constitutes a patchy

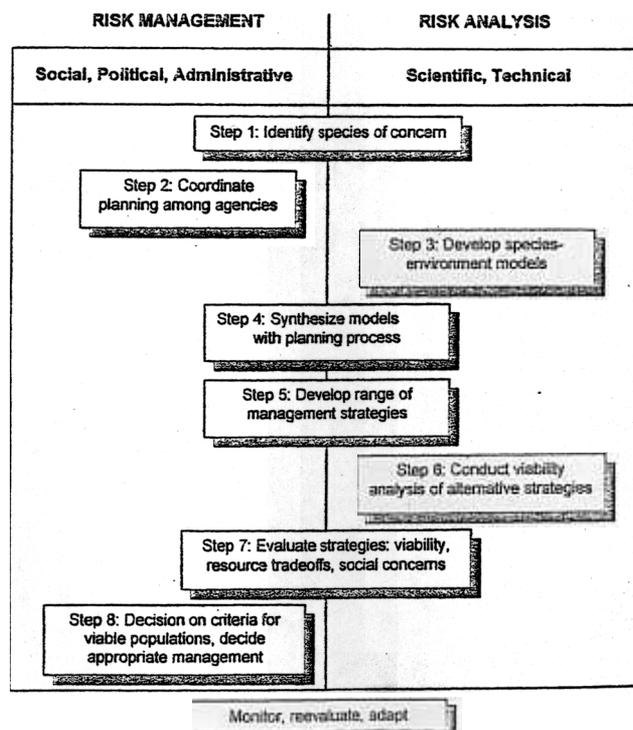


Figure 1. Example of risk management and risk analysis as applied to population viability planning (from Marcot et al. 1986).

environment for one species may constitute a homogeneous environment for another species. Likewise, degraded habitat for one species may constitute ideal habitat for another. Moreover, some species will benefit from human activities either directly by the creation of habitat (edge for example) or through indirect effects such as reducing competition or predation pressure.

• **Fragmentation.** Habitat loss results in the reduction of habitat and in discontinuities in the distribution of remaining habitat, that is, fragmentation. Fragmentation can be viewed as the creation of remnant vegetation patches surrounded by a matrix composed of different habitat or land/uses.¹⁴⁶ For illustrative purposes, consider a single species on a landscape where each parcel of land is either classified as habitat or non-habitat. At one end of the fragmentation spectrum and in the simplest case, patches of habitat may be so small that they support no individuals (i.e. smaller than a single home range, or missing some important habitat feature such as nesting substrate). In areas that are slightly less fragmented, small populations may persist in some of the larger habitat patches. However, these small populations may be at increased risk of extirpation due to stochastic processes described below.

A collection of small populations (or subpopulations) each inhabiting its own patch may constitute a metapopulation. Although there are many variations on the metapopulation theme, the distinguishing characteristic of metapopulations is that population dynamics within a patch are relatively independent of dynamics in other patches. That is, dispersal among patches is a relatively rare event that has little effect on the extant population's growth rate. In theory, persistence of a metapopulation is related to the rate at which each patch (subpopulation) goes extinct and is recolonized by individuals from another patch. The metapopulation persists if recolonization is greater than extinction rate.

Edge effects. As patches of habitat become smaller (and the matrix expands), the ratio of edge habitat to interior habitat increases. Edges can be thought of as areas of abiotic and biotic gradients between patch habitat and the matrix. For example, in a clear-cut matrix with forest patches, the outside edge of the forest patch has conditions (e.g. light humidity, temperature, plant species composition) more like those in the clear-cut than in any other part of the forest patch. Edges essentially reduce the amount of habitat for species requiring interior conditions of the patch. Shade tolerant species may become restricted to the interior parts of the habitat patches, with different species requiring different distance from the edge.^{73, 136} Edge habitat may have different types of species interactions than either the matrix or the patch interior. For example, nest predators and avian brood parasites are more common along forest edges than in patch interiors.^{169,}

¹⁸⁰ The importance of this phenomenon depends on the scale of edge effects: some outside influences penetrate only a few meters from the boundary (e.g. sunlight),⁸² whereas others infiltrate hundreds of meters in to the interior (e.g., wind,²⁵ nest predators).¹⁸⁰

Isolation. Isolation refers to the accessibility of habitat patches to organisms, and mostly is related to two measures: distance between patches and the composition of matrix lands surrounding those patches. All else being equal, as distance between patches increases, or suitability of the matrix land as habitat decreases, the more isolated a patch becomes to a particular species. Demography within and dispersal among patches, which is a function of isolation, will often determine the response of individual species to fragmentation.⁶³

Upon isolation, a patch is likely to have more species than it can sustain in the long-term. Species may be lost from the patch in a process called species relaxation.¹¹² The most rapid extinctions are likely to occur in species that depend entirely on native vegetation, require large (relative to the patch size) territories, and those that exist at low densities and are thus vulnerable to stochastic processes.¹⁴⁶

Stochastic Extinction Processes

Demographic stochasticity. Stochastic, or random, processes are usually the proximate causes¹⁵⁵ of extinction for populations already small from systematic processes. There are four types of stochasticity: demographic, environmental, natural catastrophes, and genetic.^{37, 160, 161, 164} Demographic stochasticity is the result of chance variation in vital rates. This form of stochasticity affects individuals randomly and increases the variance in mortality and/or natality rates and thus increases the probability of extinction.^{43, 74, 101} For example, a species consisting of very few breeding pairs by chance alone could produce offspring all of the same sex, effectively reducing the rate of successful reproduction in the next generation. Alternatively, consider a species where the annual probability of mortality based on the population as a whole is 50%. If we represent the fate of individuals as the result of a coin toss, it is easy to demonstrate that 5 tails in row (where tails equal death) are easier to obtain than 100 tails in a row. The smaller the number of coin tosses (smaller the population) the more likely they will all come up tails. Demographic uncertainty is an important consideration usually only for relatively small populations¹⁵²—on the order of 100s.

Environmental stochasticity. Environmental stochasticity is the variation in mean fecundity and survivorship rates across space and time, although it is most commonly thought of as temporal variation at a single site. It results from changes of environmental or habitat quality and interspecific interactions with competitors, predators, parasites and diseases.¹⁰¹ In contrast to demographic stochasticity, environmental stochasticity can affect individuals in the population more or less equally to increase the variation in birth and death rates, and thus variation in abundance.^{43, 74} Natural catastrophes, such as floods, fires, and droughts, often occur at random intervals and can have dramatic and usually adverse effects on small populations. Also, because some catastrophes such as hurricanes are very large, they can adversely affect even very large populations. However, as the geographic range

of a species increases (i.e. larger population) there is less likely to be spatial correlation of environmental variation across that range. Thus, large populations may be buffered against environmental stochasticity occurring at relatively small spatial scales.

Genetic stochasticity. Genetic stochasticity is the variation in frequency of alleles within a gene pool. The type of genetic stochasticity that conservation biologists are most concerned with is loss of allelic diversity. This arises from a reduction in the "effective population size" (that is, the effective number of breeding adults) with consequential deleterious short-term effects of random allele fixation, founder effects, inbreeding or outbreeding on reproductive success, and long-term losses of genetic variation (heterozygosity) and adaptability to environmental change from genetic drift.^{37, 148} Inbreeding has been shown to reduce reproductive success in small or isolated populations, including rainbow trout,⁷⁰ ungulates,^{6, 133, 134} red-cockaded woodpeckers,⁴⁸ and pit vipers.⁸⁴ In the past few years, the emphasis on genetics in conservation biology has decreased for a variety of reasons, the most important being the conclusion that populations large enough to be demographically self-sustaining are likely to remain genetically viable indefinitely.^{55, 74, 110} However, the relationship between long-term viability and genetic diversity remains unclear and is an active area of research.

Interactive effects on populations. The population size at which stochastic processes become important is likely to vary over time and space according to factors affecting successful reproduction and dispersal.⁴⁴ For example, given two populations of equal size, high rates of reproduction or immigration in one population would allow faster recovery from disturbance than where reproduction or immigration are slow. Such population size thresholds also are species-specific and largely determined by the interaction among the particular characteristics of a species life history and population structure, and environmental conditions.⁴² Birth and death models of population demography indicate that the risk of extinction declines rapidly with increasing population size.⁴⁴ As an example, Morrison et al.¹¹⁵ analyzed the exponential rate of decline of native Hawaiian bird populations, and demonstrated that species with very small populations decline at a far faster rate than do larger populations. Extinction risk as a function of environmental stochasticity and large-scale catastrophes also will decrease with increasing population size, but at a slower rate than with demographic effects. In reality, extinction of small populations is probably the result of interactions among these four processes,⁴² although their relative contribution to extinction is largely unknown and possibly quite complex.

For example, consider the extinction of the heath hen (*Tympanuchus cupido cupido*), a species that was fairly common in the New England States at the time of European settlement.¹⁵⁷ By 1900, there were fewer than 100 birds, all of which were found on Martha's Vineyard

(systematic processes). In 1907, a portion of Martha's Vineyard was set aside as a refuge for the bird and a program of predator control was implemented. The population responded, and by 1916 had reached the size of more than 800 birds. In 1916 a fire (natural catastrophe) destroyed most of the heath hens' nests and during the following winter the birds suffered unusually heavy predation (environmental stochasticity) from a relatively high concentration of a common heath hen predator, the goshawk. The combined effect of these events reduced the population to 100-150 individuals. In 1920, after the population had increased to about 200, disease (environmental stochasticity) reduced the population to below 100. Though the species persisted a while longer, by 1932 the last survivor was gone. In the final stages of the population decline, the birds appeared to have become increasingly sterile (inbreeding depression) and the proportion of males increased (demographic stochasticity). Which of these events served as the *coup de grace* is unknown. Theory suggests that in general, the probability of extinction for small populations is highest from environmental effects, followed by demographic stochasticity, longer-term genetic effects, and lastly catastrophes,^{42, 72} although this hierarchy itself varies by species and condition.

In contrast to systematic pressures, the magnitude of stochastic threats depends more on population size than on life history traits of a species. In part, this is because life history traits are generally selected traits imparting persistence of the species within particular bounds of environmental conditions. Thus, a general theory of stochastic processes has been developed based on population size alone. Systematic processes, on the other hand, are likely to be as different from each other as the life history traits of species affected by those processes. It may not be possible to construct a universal theory of population decline comparable to the stochastic theory of small populations.²⁴ However, understanding the mechanisms of extinction (i.e. why some species and not others decline in the face of systematic extinction processes) is fundamentally important to conservation biologists and wildlife managers.

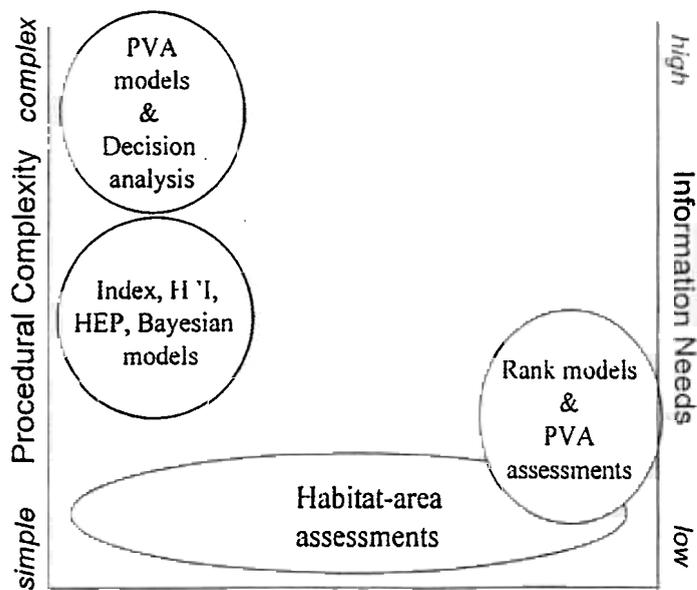
Criteria of Species at Risk

Population vulnerability analysis. The basic question is: why do some populations decline and others do not? We can use the conceptual "population vulnerability analysis" framework to determine criteria and processes for assessing extinction risk.⁴² The risk of extinction due to systematic processes is likely a function of the interaction of: (1) the physical and biotic environment of the individual and population; (2) the population phenotype, including the species life history, behavior, morphology, physiology, and habitat requirements; and (3) how the first two factors interact to determine population distribution and individual fitness.^{42, 174} The relative importance of these three factors is a matter of debate and probably depends on the particular blend of species characteristics and environmental characteristics. Despite the potential

the effective size of threatened populations as rapidly as possible.⁵⁵ Additionally, in some cases, it is advantageous to establish more than one population center to avoid losing the entire population to single environmental stochastic influences or catastrophes. In extreme cases, captive propagation followed by reintroduction into restored habitats, although terribly expensive, may be one of the best recourses.¹⁴⁹

Methods for Determining Species at Risk

Methods for wildlife risk assessment vary in taxonomic scope, procedural complexity, and objective. The scope of assessments ranges from single-species assessments to multi-species ecosystem or biodiversity assessments in which many species are considered in the same effort. Procedural complexity varies from simple deterministic estimates of risk (e.g., consistent loss of habitat area, and use of ordinal risk rankings) to complex probabilistic estimates for explicit time periods that incorporate uncertainty related to demographic and environmental stochasticity, or management processes (Figure 2). Risk assessments also vary in their objectives, from estimates only of extinction risk to estimations of management risk that integrate extinction risk with social, economic, or other biological considerations. Several of the methods to assess risk of habitat or population loss described below, such as habitat relationships assessments and models, are covered in detail elsewhere in this book; here, we give an overview of these and other methods for analyzing risk of loss.



single-species Taxonomic Scope *multi-species*
 Figure 2. Methods of risk assessment for animal and plant species vary along gradients of taxonomic scope and procedural complexity. Additionally, methods vary in objective from estimating ecological risk of extinction to management risk.

Habitat Relationships Assessments

Wildlife habitat relationships (WHR) assessments or models use a variety of procedures to estimate the effects of changes in habitat quantity or quality under management alternatives. The objective of WHR models is to assess how changes in vegetation composition or structure from management might result in habitat loss for one or more species. Multiple species typically are analyzed in guilds or groups of species with similar habitat relationships, foraging or nesting behavior, movement, or other life-history attributes. Habitat relationship assessments can be applied at stand, landscape, and regional scales, although Raphael and Marcot⁹⁰ found such models most accurate and appropriate for use with some species at landscape or larger scales.

The methodological roots of wildlife habitat relationships programs for vertebrates are in the work of Patton,¹²² Thomas et al.,¹⁷¹ Lehmkuhl and Patton,⁷⁵ and Brown,¹⁴ among others. Indexed WHR models include the habitat suitability models (HSI),¹⁴⁷ the habitat evaluation procedures (HEP),^{36, 178} and habitat effectiveness models (e.g., elk models by Thomas et al.,¹⁷¹ Wisdom et al.,¹⁸⁴ Thomas et al.)¹⁷³ Morrison et al.¹¹⁵ review these models.

Habitat is typically defined as the sum of area in plant communities and their structural variants (macrohabitats). Adding to the suitability of an environment are habitat elements (microhabitats) used for feeding, nesting, and resting. Analysis usually determines the change in area of available habitats under management alternatives and describes the implications for associated species. Versatility indices of habitat use are the number, or breadth, of macrohabitats or habitat elements used by individual species. Versatility indices are used to assess implications of habitat change for species that use few habitats (low versatility) or several to many habitats (higher versatility). Index models (HEP, HSI) independently describe or index the value (typically scaled 1 to 10 or 0 to 1) of several macrohabitat and microhabitat attributes (e.g., westside conifer forests and snag density therein) then calculate a summary index of habitat value. Risk is determined from HEP and HSI approaches by comparing model index values against an independently determined threshold of habitat change considered to put the species at risk.

It is problematic, however, in HEP and HSI models to identify such thresholds. Thus, HEP and HSI type models are better used to qualitatively assess alternative conditions in a rank order comparison, rather than to estimate absolute population response. In some cases, historical and projected trends in area of forest habitats have been related to population density in habitat types to depict potential trends in the abundance of vertebrate taxa and functional groups over large areas.^{137, 139} Similar trends and analyses pertain to other, non-forest environments.

Rank Models

Rank models work within a population vulnerability framework to evaluate risk.^{9,42,150} These models provide a ranking of extirpation or management risk, using attributes of population structure and distribution, life history, habitat-use versatility, or habitat area and spatial pattern. For ordinal-rank models, each factor is usually assigned an integer score, or rank, relative to its contribution to extirpation or management risk, for example, on a scale of 1 to 10. Quantitative data on habitat area or population size, as well as qualitative information on life history attributes, can be used to develop the scores. In this approach, multiple species typically are evaluated at the same time using the same variables. The scale of application is most often regional or larger, but could be applied down to watershed or smaller scales. Ordinal-rank models have been developed to assess the impacts of large-scale habitat loss and fragmentation on potential population persistence.^{51, 61, 77}

The International Union for the Conservation of Nature and Natural Resources (IUCN) developed a categorical rank system⁵⁷ for their Red Lists^{58, 59} to assess worldwide species extinction risk based on population size and distribution (see Mace and Collar⁶³ for an application) (Figure 3). The IUCN system has been further developed for local application to assess extinction and associated management risk within individual countries or other artificial management units.^{41, 124}

The Nature Conservancy (TNC) developed a global categorical-rank extinction and management rating system for the Natural Heritage Program that is based primarily on qualitative estimates of plant and animal population abundance and distribution.⁹⁸ The system also ranks "site biodiversity significance" and "site protection urgency" on a rank scale of 1-5 for use in developing management priorities. Other ordinal-rank models have

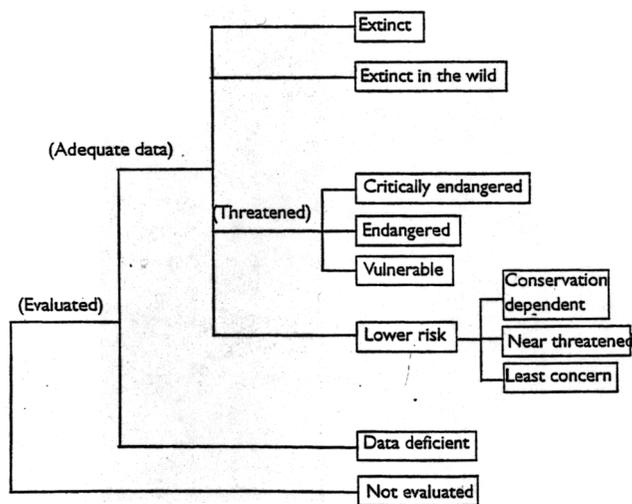


Figure 3. Rank categories of ecological risk developed by the International Union for the Conservation of Nature and Natural Resources (IUCN 1994) for the Red List of threatened and endangered species.

been developed that integrate extinction and management risk attributes to set state-wide or global management priorities for individual species.^{4, 20, 62, 81, 114, 120, 135}

Population Viability Analyses and Assessments

Population viability analysis (PVA) is a formal modeling process for quantifying the likelihood that a species will persist for a given time into the future.^{1, 9, 42, 150, 152} In PVA, attributes of population structure and demography, life history, genetic structure, and habitat quality and quantity typically are used in models combining population demography and geographically referenced metapopulation dynamics to assess viability likelihood and extinction risk. A very significant innovation that distinguishes this form of risk assessment from that based on WHR models and rank methods is a consideration of uncertainty arising from natural variation or unpredictability in population and environmental processes. Sometimes, uncertainty is addressed by depicting viability as likelihoods of extinction over a specified period of time, rather than as a single deterministic estimate for an unspecified time period as with rank methods, sensitivity analysis of population parameters, or estimating the variance of modeling analysis outcomes. However, the formal PVA approach seldom accounts for propagation of error terms and general lack of scientific knowledge on the ecology of a species.

For some authors, the process of PVA has been associated with determining the "minimum viable population" (MVP), which is presumed to be the minimum number of individuals that ensure a population's persistence for a specified length of time.¹⁵⁰ The value of the MVP concept has proven very limited, however, because the "minimum" population size is not a simple number, but varies with population parameters, the acceptable probability of persistence, the length of planning period,^{42, 79} and how populations and their environments change unpredictably. Also, acceptable persistence likelihoods and planning period durations are functions of the amount of risk managers are willing to accept in trading species viability for other values; thus, the "minimum" viable population size largely is a function of conservation policy instead of pure science.

Typically, quantitative PVA models are developed for single species because of model complexity and the need for detailed data on population dynamics and habitat relationships. Several less-quantitative approaches have been developed to assess viability for multiple species—these may be termed Population Viability "Assessments" to distinguish them from the more stochastic and demographic modeling-based PVA process. The scale of analysis in population viability assessments can vary from regions for wide-ranging species with sparse populations, such as the northern spotted owl^{94, 177} to local site conditions for less-mobile species with locally disjunct populations.

Population viability assessment was developed to accommodate the varying availability of species data and

the needs and constraints of scientists and managers while meeting the basic criterion for estimating the likelihood of persistence over a specified period of time. For example, expert-opinion approaches were used to estimate the likelihood of persistence of the northern spotted owl and other species associated with late-successional forests in the coastal Pacific Northwest.^{33, 61, 94, 172, 177} Subsequent regional assessments of multiple species for the interior Columbia River basin,⁷⁶ and southeast Alaska¹⁵⁴ adapted and modified methods developed for the Pacific Northwest.³³

These approaches typically have had expert panelists score the relative abundance and distribution of habitats or populations at particular points in time under alternative management scenarios. The scores are described by several outcome classes to depict the likelihood of persistence under management alternatives. Uncertainty of viability likelihood in one approach⁷⁶ was estimated as the variance among and within viability scores of expert panelists. In a current effort, however, this "black box" of expert opinion is being opened by using Bayesian belief network models of species' interactions with their key environmental correlates as a way to measure habitat or population potential across landscapes over time (B. Marcot, pers. comm., USDA Forest Service, Portland, Oregon).

Model forms of PVA quantify the probability of persistence for single species by using mathematical and simulation models. Those forms explicitly model the probability of persistence as a function of population structure and distribution, genetic structure or processes, habitat quality and quantity, or life history attributes. Uncertainty can be evaluated with sensitivity analysis that varies parameter values within a range of known or hypothesized values.^{1, 79, 104, 167} Random, or stochastic, effects are modeled from hypothesized (or, less commonly, empirically fit) probability density functions. Several programs have been developed to model PVA, each with particular strengths and weaknesses.^{78, 79, 113} Examples of PVA can be found in the literature for birds,^{3, 7, 11, 12, 13, 23, 45, 48, 89, 103, 142} mammals,^{3, 16, 21, 22, 39, 52, 67, 69, 72, 80, 97, 121, 159, 187} reptiles,¹⁶² fish,^{8, 26, 31, 100, 140} invertebrates,¹¹⁶ and plants.^{10, 17, 19, 109, 117}

It is our considered opinion that the quantitative PVA approach is useful primarily in uncommon cases where species have been previously screened to be at high risk, and where data on their population demography and genetics, and variations in their environment and habitats are known and can be adequately modeled. For most cases, however, the more qualitative population viability assessment approach is likely to be adequate for policy decision-making at broad scales.

Decision Analysis and Knowledge-Based Systems

Decision analysis integrates extinction risk assessment with management risk assessment. Biological and management uncertainty, in terms of probabilities and their variation, are used to calculate expected values of species abundance under several management

alternatives.^{79, 87, 132} Decision and knowledge-based systems differ from quantitative PVA models by using rigorous steps to capture and quantify expertise, and by explicitly incorporating management (as opposed to ecological) risk. As with PVA, decision analysis models are usually too complex to use with more than 1 species at a time, and are useful at watershed to regional scales.

Decision-tree risk analysis is the most commonly used procedure, and has been done for grizzly bear,⁸⁸ black-footed ferrets,⁸⁵ tigers,⁸⁶ and Sumatran rhinos.⁸⁷ Expected value of perfect and sample information, and Bayesian statistics^{46, 168} are other methods that may be useful for wildlife risk analysis.⁹³ Expert systems and other expert advisory approaches are gaining acceptance as important tools when used to analyze risk related to specific problems of wildlife resource management.^{93, 108}

Toxicological risk assessments

The literature on toxicological risk assessments for wildlife is relatively well established.^{124, 143, 175, 176} Procedural standards have been set by the U.S. Environmental Protection Agency for laboratory and field risk assessment of environmental contaminants on wildlife.^{35, 176} Risk is quantified¹⁷⁵ as (1) dose-response evaluated by, (a) the ratio of environmental concentration over lethal concentration resulting in 50% mortality of test individuals (LC_{50}), and (b) the ratio of toxicant consumption over the lethal dose resulting in 50% mortality of individuals (LD_{50}); and (2) by the environmental exposure quantified as the amount of toxicant in the environment over the amount required for LD_{50} . Environmental exposure is a function of population and life history attributes, as used for other risk assessments. Risk increases as these ratios approach 1. Those metrics of risk do not quantify, however, the interaction of toxicants with other factors or the important population consequences of sub-lethal effects.

Single species are the focus of toxicological assessments. Application is usually at small scales of individual contaminant sites or treatment areas, as in the case of pesticides. Watershed or regional applications would sum the lower-order effects at individual sites. Population models are increasingly being used to assess toxicological risk.^{30, 40, 50, 68, 127, 158, 179}

Advantages and Disadvantages of Methods

WHR and rank models. Simple WHR habitat models or rank models that rate species risk to develop priorities for conservation or assess generalized risk from specific threats (e.g. forest fragmentation) have the advantages of being broadly applicable, rapid, and incorporating ecological data, theory, and local expert knowledge when research data are few. Simple ranking techniques usually are easily understood by managers in other disciplines, and can be applied to estimate risk for many species over large areas.

However, the generality of the procedure brings with it disadvantages. Information based on expert opinion may be biased by personal experience or tacit motivational bias of the contributors. When a common set of life history,

population, or habitat attributes are used to examine risk for a group of species, there is the potential that an attribute that is critical for the persistence of one species might be missing because it was generally considered not important. Likewise, a model developed for one place might fit poorly in other areas. Simple WHR and rank models do not incorporate variation in risk associated with variability of species populations, environmental conditions, or uncertainty in species responses that is necessary for application to small scales of management, such as stands and sub-watersheds.

PVA models. Quantitative risk analyses, such as single-species PVA models, require detailed life history and population information, consider variation in assessing risk, and often examine effects of management alternatives. Variation in management and species responses to risk factors is specifically estimated as likelihood, or through sensitivity analysis. PVA models can help clarify assumptions, create testable hypotheses relative to model parameters and processes, synthesize and integrate knowledge, and demand explicit and rigorous reasoning.⁹

These potential advantages of PVA models are often offset by poor documentation, high cost, or limitations of the methodology, which have been amply discussed in the literature.^{2, 11, 24, 47, 66, 74, 104, 105, 113, 167} At the heart, too, persistence likelihood is not strictly an empirically verifiable parameter—you cannot conduct a field study or experiment to verify the risk levels stated in a PVA without putting at risk the very populations you are trying to conserve. Thus, PVA is used under the presumption that its mosaic of models and concepts, which individually can be derived from sound theoretical or empirical evidence on other species, together constitute a useful approach for describing changes in some scarce species of interest.

Decision analysis. Alternatively, highly structured procedures of risk assessment using decision analysis have the advantage of explicitly stating key assumptions and possible management alternatives in a standard format.^{85, 87, 90, 92} Management actions and species responses are expressed as probabilities with a defined range of expected values and variation. Different types, sources, and units of management and ecological information can be incorporated to facilitate management decisions.

However, there are several disadvantages of decision analysis when used in population viability assessments.^{92, 118} Probabilities are often difficult to accurately assess by use of expert opinion, and assumptions to quantitatively estimate probabilities may inject too much additional uncertainty. Also, small changes in probabilities may greatly affect the results of the analysis. Not all management alternatives and future environmental conditions may be foreseen, thus biasing the management decision. Also, it may be difficult to define specific management objectives for individual species and to quantify outcomes with respect to habitat conditions from biological, and especially social and political, viewpoints.

Improvements Needed in Assessing Wildlife Risk

Improvements in wildlife risk assessment can be made in several areas. There is an enduring need for better information on species' population structure and the range of variability and response to environments over space and time. Also needed for model development are data on habitat selection and the impacts of management on both population structure and habitat selection. Data also are needed for verification of models—a critical and often overlooked aspect of model building because of the difficulty of obtaining independent data at appropriate spatial or temporal scales. Long-term datasets, such as Breeding Bird Surveys, waterfowl surveys, and other data from formal monitoring programs may provide useful data for model verification. Data for model building and verification can be gained through conventional research, but also through better monitoring of management outcomes within the framework of adaptive management.⁵⁴ Both approaches aim to provide reliable knowledge using basic scientific methods; hence, the perception that research is for scientists and adaptive management for managers is a false dichotomy that hinders progress in the field.

Just as important is the need for methods to better estimate economic and social values of wildlife, and explicitly incorporate the costs incurred by alternative management practices.^{118, 165} Central to the goal of ecosystem management is defining essential ecosystem components, linking processes, and endpoints or desired future conditions of those properties.¹¹⁸

Characterizing Risk Species and Their Attributes

Below are several examples of methods for characterizing species at risk, determining the specific attributes that distinguish high-risk species from other species, and comparing risk from several management alternatives. The examples are not the only ways risk analysis might be done (see the methods section of this chapter), but are intended to illustrate approaches to the problems. The first two examples use different but related procedures to differentiate and classify imperiled, secure, and intermediate-risk species, and develop a rule set for classifying other species. A third example uses principles discussed in the section of this chapter on criteria for identifying species at risk to score and rank potential risk based on life history characteristics, when prior knowledge of risk is unavailable. That same approach could be used to rank management priorities. A fourth example describes a population viability assessment used to assess land management alternatives.

For the first three examples, we developed a database for a sample of 60 species that were selected based on criteria shown in Appendix 1. A sample of 20 threatened, endangered, or sensitive (TES) species in Oregon and Washington (e.g., Photo 1) were combined with a sample of 20 species we considered secure (e.g., Photo 2) and 20



Photo 1. Bobolink (*Dolichonyx oryzivorus*) in Shrub-steppe habitat. An example of a "Group I" species, i.e., species known to be imperiled. (Photo: Bruce G. Marcot)



Photo 2. *Ensatina* (*Ensatina eschscholtzii*) in Westside Lowlands Conifer-Hardwood Forest habitat. An example of a "Group II" species, i.e., species very likely secure. (Photo: Bruce G. Marcot)

species that had potentially intermediate viability risk (e.g., Photo 3).

For the species in the example database, we extracted a subset of the life history and habitat relationships fields from the matrixes (CD-ROM with this book) that correspond to attributes associated with variation in viability; as discussed in the section of this chapter on criteria for identifying species at risk. We combined some matrix values for a few fields to somewhat simplify the example analyses. Where field values were given as "unknown" we used the most likely value, based on our knowledge of species, to completely fill the data matrix for the example analysis. We designated primary fields in the example database as those most likely to account for risk levels based on our experience, and some secondary life history fields that could be important attributes of species at risk. Other fields were purely for information to interpret the analysis. We calculated two "versatility" indices of habitat cover and structural-type use from the data given in the habitat matrixes. The indices were calculated as the percentage of all habitat cover or structural types that the animal is known to use.



Photo 3. Sharptail snake (*Contia tenuis*) in Southwest Oregon Mixed Conifer-Hardwood Forest habitat. An example of a "Group III" species, i.e., species with intermediate security. (Photo: Bruce G. Marcot)

Using Classification Trees to Determine Influences on Species Risk

This first example shows how a classification tree procedure¹⁸³ can be used to determine the relative contribution of life history, population distribution, and versatility attributes in the matrixes to known risk-group membership. The results of that analysis, then, can be used to develop a rule-set to predict risk-group membership for species with unknown risk potential. Our example concentrates on comparing the attributes of TES species with species in secure or potential intermediate-risk categories. It is important to remember that this and the following examples are merely illustrations of what can be done with the larger list of species and attributes that might be used in a real situation.

The classification tree procedure worked in a way similar to a dichotomous key used for plant identification: it started with all the species in a group, then sequentially split each subsample based on the most discriminating variable until no significant splits could be performed. The "proportional reduction in error" (PRE) statistic described the goodness-of-fit, or strength, of the model, similar to the conventional R^2 statistic, varying between 0 and 1, with 1 indicating a perfect fit of the model. The classification tree figure showed the splits and relative number of species within each subsample. Crosstabulation and t-tests also were used to examine the relationship between each life history and versatility field and risk group

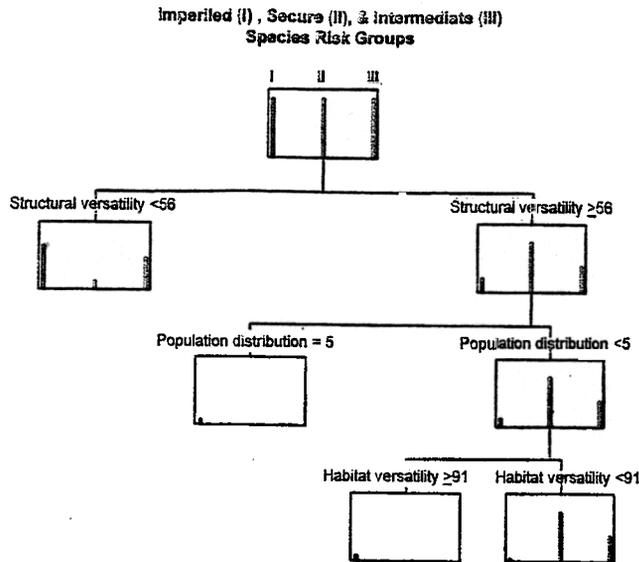


Figure 4. Classification tree of 60 vertebrate species in Oregon and Washington known to be imperiled, secure, or of potential intermediate viability risk. The classification used life history and habitat versatility attributes from the matrices. See text for an explanation of the species and variable selection processes. Risk groups are represented by bars in the order of imperiled, secure, and intermediate; the height of the bars indicates the number of species in each group and box, starting with 20 species in each group.

membership. Differences among groups were reported if significant at $P \leq 0.05$.

Imperiled species in our sample dataset were best distinguished from the other species by their use of few structural habitat types, as reflected by low structural habitat versatility ($PRE=0.125$; Figure 4). Structural habitat versatility of imperiled species (mean=41%) was almost half that of secure species (mean=75%), and somewhat less than secure and intermediate species combined (mean=55%). Intermediate-risk species when considered alone could not be neatly separated from imperiled or secure species. That pattern was evident in the classification tree (Figure 4) where intermediate-risk species were split nearly equally between imperiled and secure groups on the basis of structural versatility. Although not appearing critical for separating risk groups, habitat cover-type versatility had the same pattern of differences among groups, which might be expected with a high correlation between structural and habitat versatility ($r=0.76$).

In some cases, population distribution and habitat cover versatility could be used to distinguish imperiled from other species. Imperiled and intermediate-risk species with low structural versatility on the left side of tree appeared to have similar life history and distribution traits and could not be easily separated by additional attributes from the sample dataset (Figure 4). However, among the species with high versatility on the right side of the tree, scarce population distribution and relatively low habitat cover versatility distinguished most of the few imperiled species from secure or intermediate species.

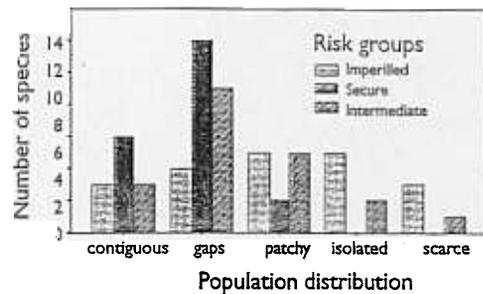


Figure 5. Numbers of vertebrate species in the risk analysis sample dataset by population distribution category and viability risk group.

Other than habitat and structural versatility, population distribution was the only other variable that differed among risk groups (Figure 5). Imperiled species largely had patchy, isolated, or scarce distributions; whereas, secure species mostly were contiguously distributed or had gaps in their distribution. Distributions of intermediate species varied between those 2 extremes.

A Rule Induction Approach: SARA—Species At Risk Advisor

This example discusses the use of a rule induction approach developed by B. Marcot to identify species at risk based on their life history attributes. Rule induction is a knowledge-base modeling approach for devising an optimal rule to distinguish among categories based on a set of example cases. For example, Stockwell et al.¹⁶⁶ used rule induction to predict different density levels of gliders (*Petauroides volans*) in Australia. In our example, the rule distinguishes among the three risk levels (imperiled, secure, and intermediate) and the examples are the 60 sample species used in the data set.

There are many kinds of rule induction algorithms, particularly in the area of knowledge-base and expert systems programming and statistical analysis.⁶⁰ Used here is the Quinlan ID-3 rule-induction algorithm.^{123, 129} This approach is similar to the classification tree example presented above in that it identifies an optimal division of the known cases based on successively identifying variables and their values that best distinguish among remaining cases. What results is an optimal rule, much like a botanical key, that leads to final categories of the three species risk levels. The ID-3 rule-induction algorithm and other related knowledge-base approaches, however, differ from the classification tree analysis in that they can handle both categorical and ordinal data, as well as continuous (ratio-scale) data.

The knowledge-base expert system programming package 1st Class (1st Class Expert Systems, Inc., Wyland, MA; Release 3.65) was used to do the rule-induction analysis. In general, rule induction and use of knowledge base modeling differ from classification tree analyses in several ways. First, a knowledge base programming approach can produce a user-friendly interactive query system based on the optimal rule. In this example, the query system produced is named SARA—the Species At

Risk Advisor. Second, the knowledge base programming approach can account for uncertainty and unknowns that cannot be included in a classification tree analysis. Uncertainty is handled by depicting likelihood of assigning each example to each outcome category. It then uses these likelihoods to calculate a probability of an unknown case (e.g., a species not included in the example data set) belonging to each outcome category (each risk level). Third, during the interactive query, a knowledge base model such as produced by 1st Class can allow the user to enter "do not know" or "no information" to any question, and from there the program determines the next best sequence of as-yet-unasked questions to optimally determine the outcome category. Fourth, because it is not limited to statistical assumptions inherent in the parametric classification tree approach, the ID-3 rule-induction algorithm is not limited to a specific number of variables given a fixed number of example cases (e.g., 5-10 example cases are needed for each variable considered in the classification tree approach). Fifth, "classification trees," being a strictly parametric statistical analysis procedure, provides confidence values describing the degree to which each factor accounts for classification; knowledge base approaches typically do not. Thus, rule induction and classification trees type classification analyses are complementary approaches (see Conclusions section).

SARA uses 29 life history attributes, 1 taxonomic attribute, and 60 example species. Its optimal rule is displayed in Figure 6. It should be remembered that this analysis is only an example of the kind of assessment that can be done to determine how life history attributes might contribute to viability risk levels. Similar analyses can be done on other species' attributes such as population size, trend, density, and so on, if data are available. Results of this analysis, and the SARA model, should not be interpreted as definitive analyses of the influence of life history attributes on risk levels; at best, this analysis poses testable hypotheses, and urges a fuller assessment of a fuller set of species.

Analysis results suggest that 9 life history attributes and 1 taxonomic attribute can account for, and differentiate among, the 3 viability risk levels for the 60 example species. These attributes are population distribution, foraging substrate, elevational range, age at first reproduction, structural versatility, habitat versatility, landscape use, migration distance, and taxonomic order. It should be noted that rule induction algorithms generate results whether or not they are statistically valid, so the relative power with which each of these life history attributes contributes to predicting viability risk levels is not known. This is where the parametric statistical analysis of classification trees can complement this analysis.

An example of how SARA can be used is for identifying a species of unknown risk level. For example, suppose a species has a population distribution consisting of gaps with habitat broadly distributed but with interruptions causing some population isolation ($\text{PopnDistrb} = \text{pop2}$, as in Figure 6 and Appendix 3), that it is an owl (Order =

Strigiformes), and that it uses only 20% of all available habitat types ($\text{HabVers} < 34.5\%$). The SARA rule set, and the knowledge base expert system, would key this species out to belonging to Group I, that is, a potentially imperiled species. This is because at least 1 known case from the set of 60 example species had these conditions and was known to be imperiled (state or federally listed), the northern spotted owl. Whether another owl with these same attributes would be similarly imperiled is postulated by the SARA analysis but would bear further evaluation. So the purpose of the SARA model, particularly if developed among a broader set of species, is to provide a tool for initially screening species for further evaluation.

An analysis was also done that combined the secure and intermediate categories and compared this combination to the imperiled category. This more simply determined which life history attributes might be used to identify imperiled species although it could not differentiate between secure and intermediate categories. In this analysis, a somewhat different set of attributes were identified as key differentiating factors: habitat versatility, structural versatility, clutch or litter size, summer site fidelity, breeding status, population distribution, and taxonomic order. That a different set of factors resulted in this analysis as compared with the above analysis is not unexpected when the same example species cases were combined in a different way. In this example, one possible combination of attributes that would lead to identifying the imperiled category is if a species had a structural versatility $< 54\%$ ($\text{StrucVers} < 54$), a mean litter or clutch size of 3 or less ($\text{NLitt_Clut} = \text{nlit3}$), and documented or suspected breeding in both Washington and Oregon ($\text{BreedStatus} = \text{bs3}$). Again, this should be taken only as an example of the kind of analysis possible; a fuller evaluation with more species would likely produce more reliable results that could be evaluated against a larger set of species with known population status.

A Rank-Model Example

This example shows how population and life history attributes can be used to develop a simple rank model (see methods section of this chapter) to evaluate potential extirpation risk when there is no *a priori* knowledge of risk, as was known in the previous examples. We scored risk for each value of the primary life history and versatility fields in the example dataset on a scale of 1 to 10 (Appendix 2), with 10 being the highest risk, using the principles discussed in the section of this chapter on criteria for identifying species at risk. For example, species with high annual production of offspring or numbers of litters were scored lower risk for that attribute than species with low productivity. The rationale was that a population of species with high fecundity likely would more easily recover from disturbance in their environment, i.e., be more resilient, and less susceptible to local extirpation than species with low productivity. We then summed the scores of each field to calculate a total score for each species. Species with high scores would potentially be at greater risk of extirpation than species with low scores. Differences

- A. Population distribution is contiguous.
 - B. The organism forages underwater or aerially, or foraging substrate is unknown.
 - C. The upper elevation range of typical or regular occurrence is up to 1000 ft. (no identification)
 - CC. The upper elevation range of typical or regular occurrence is up to 3000 ft. (no identification)
 - CCC. The upper elevation range of typical or regular occurrence is up to 5000 ft. Group III
 - CCCC. The upper elevation range of typical or regular occurrence is >5000 ft. Group I
 - BB. The organism does not forage underwater or aerially, and foraging substrate is not unknown.
 - C. The average age at first breeding (females) is <6 months. (no identification)
 - CC. The average age at first breeding (females) is 1 year. Group II
 - CCC. The average age at first breeding (females) is 2 years.
 - D. The structural versatility of the species is <99. Group II
 - DD. The structural versatility of the species is >=99. Group III
 - CCCC. The average age at first breeding (females) is 3 years. Group III
 - CCCCC. The average age at first breeding (females) is 4+ years. Group II
- AA. Population distribution consists of gaps.
 - B. The taxonomic order is Caudata.
 - C. The structural versatility of the species is <90.50. Group II
 - CC. The structural versatility of the species is >=90.50. Group III
 - BB. The taxonomic order is Anura. (no identification)
 - BBB. The taxonomic order is Squamata. Group III
 - BBBB. The taxonomic order is Falconiformes.
 - C. The average age at first breeding (females) is <6 months. (no identification)
 - CC. The average age at first breeding (females) is 1 year. Group II
 - CCC. The average age at first breeding (females) is 2 years. Group III
 - CCCC. The average age at first breeding (females) is 3 years. Group I
 - CCCCC. The average age at first breeding (females) is 4+ years. (no identification)
 - BBBBB. The taxonomic order is Charadriiformes. Group II
 - BBBBBB. The taxonomic order is Strigiformes.
 - C. The habitat versatility of the species is <34.50. Group I
 - CC. The habitat versatility of the species is >=34.50 and < 50.00. Group III
 - CC. The habitat versatility of the species is >=50.00. Group II
 - BBBBBBB. The taxonomic order is Apodiformes.
 - C. The habitat versatility of the species is <53.50. Group II
 - CC. The habitat versatility of the species is >=53.50. Group III

Figure 6. The example, optimized rule from the SARA (Species At Risk Advisor) example knowledge base model that determines species' viability risk levels based on their life history attributes. This rule was induced from analysis of 60 example wildlife species in Washington and Oregon, and is only an example of the type of analysis possible by using knowledge base, rule-induction analysis. The decision points in the rule correspond to the questions and states shown in Appendix 3. Group I = imperiled species; Group II = secure species; Group III = intermediate species. See text for explanation of methods.

among species or species groups in risk score or life history attributes were considered significant at $P \leq 0.05$.

The distribution of risk scores was very normally distributed, ranging from 33 to 94 points with a mean of 65 (Figure 7). A preponderance of low scores would have indicated few species likely to be negatively affected by management; whereas a preponderance of species with high risk scores would indicate a potentially large risk of action. Ranking species by their risk score from high to low would indicate priorities for further analysis or field work to accurately determine the impacts of management.

How well does this risk scoring and ranking method coincide with the species risk group, as defined in the sample dataset and analyzed in earlier examples? Risk scores for species showed a similar relationship among risk groups to those found with the classification and SARA procedures. Imperiled species on average had higher risk scores (mean=72) than secure species (mean=56) (Figure 8). Intermediate-risk species (mean=68) did not differ from imperiled species in average risk score, but did have higher scores than secure species. That pattern was largely a result of similarly high values for

- BBBBBBBB. The taxonomic order is Piciformes.
 C. The habitat versatility of the species is <50.00. Group III
 CC. The habitat versatility of the species is >=50.00. Group II
- BBBBBBBBBB. The taxonomic order is Passeriformes.
 C. It is a "patch" species, likely using only 1 homogenous habitat patch during the life cycle. Group III
 CC. It is a "mosaic" species, likely using an aggregate of habitat patches but 1 structural stage.
 D. The migration or seasonal movement is <100 km. (no identification)
 DD. The migration or seasonal movement is 100 - 1000 km. Group I
 DDD. The migration or seasonal movement is >1000 km. Group II
 DDDD. The species is non-migratory. Group II
 CCC. It is a "generalist" species, likely using all or many patch types, & >1 structural stage. Group III
 CCCC. It is a "contrast" species, likely requiring contrast between 2 structural stages in close proximity.
 (no identification)
- BBBBBBBBBBB. The taxonomic order is Rodentia.
 C. The structural versatility of the species is <28.50. Group I
 CC. The structural versatility of the species is >=28.50. Group III
- BBBBBBBBBBBB. The taxonomic order is Carnivora. Group II
- AAA. Population distribution consists of patchily distributed populations.
 B. The average age at first breeding (females) is <6 months. Group II
 BB. The average age at first breeding (females) is 1 year. Group I
 BBB. The average age at first breeding (females) is 2 years. Group III
 BBBB. The average age at first breeding (females) is 3 years.
 C. The habitat versatility of the species is <34.50. Group I
 CC. The habitat versatility of the species is >=34.50. Group II
 BBBB. The average age at first breeding (females) is 4+ years. Group III
- AAAA. Population distribution consists of isolated population(s).
 B. The migration or seasonal movement is <100 km. Group III
 BB. The migration or seasonal movement is 100 - 1000 km. Group III
 BBB. The migration or seasonal movement is >1000 km. Group I
 BBBB. The species is non-migratory. Group I
- AAAAA. Population distribution is scarce.
 B. The habitat versatility of the species is <16.00. Group III
 BB. The habitat versatility of the species is >=16.00. Group I

both imperiled and intermediate species in the life history field describing population distribution, as noted in the classification tree example.

Could we use risk scores to create our own, perhaps better, risk groups instead of using existing legal or administrative definitions of risk, which might reflect political as much as ecological conditions? We used cluster analysis to create three new "risk" clusters, or groups, of species based only on our risk scores, and then we compared the clusters with the previously defined risk groups to see how well they matched the old groups.

Cluster analysis identified low- (mean=51), intermediate- (mean=68), and high-risk (mean=84) species clusters (Table 1); but, cluster membership did not always match the *a priori*-assigned risk groups. That result might be expected considering the inability to perfectly separate species in imperiled, intermediate-risk, and secure risk groups in the earlier examples. The low risk cluster included about 60% of the secure species, 20% of the intermediate-risk species, and 10% of the imperiled species. Most species clustered as moderate-risk, with nearly equal numbers of imperiled and intermediate-risk

species, and some secure species. Only 9 of the 60 species clustered as high-risk, with equal numbers of imperiled and intermediate risk species. The poor match between cluster and *a priori* risk group, in some cases, indicates that legal definitions of risk may not always be adequate to define risk, and unlisted species might also need to be analyzed.

Population Viability Assessments: The Interior Columbia Basin

A final example is taken from the population viability assessment of draft management alternatives for the Interior Columbia Basin Ecosystem Management Project.⁷⁶ The purpose of the assessment was to determine the degree to which habitat conditions on lands administered by the Forest Service and Bureau of Land Management within the interior Columbia River basin contribute to long-term persistence (at least 100 years) of select plant and animal species of conservation concern. Secondly, they examined the extent to which other lands and other influences might affect populations.

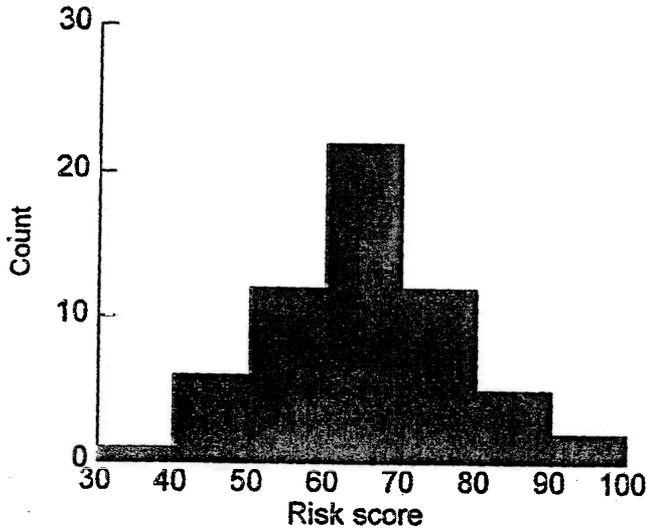


Figure 7. The distribution of risk scores for 60 species in the example dataset using the methodology described for rank model procedures. Risk scores were estimated by scoring each life history, population, or habitat attribute in the example dataset for its potential contribution to extirpation risk, then summing the attribute scores for a single risk estimate.

Table 1. Crosstabulation of risk group memberships based on clustering risk scores of life history attributes and habitat versatility, compared with risk groups in the sample dataset based on legal or administrative designations of threatened, endangered, or sensitive status and expert opinion.

Risk group (sample dataset)	Risk Score Cluster			Total
	1 (low)	2 (high)	3 (moderate)	
I (Imperiled)				
Count	2	4	14	20
% within Group I	10%	20%	70%	100%
II (Secure)				
Count	12	7	7	20
% within Group II	60%	35%	35%	100%
III (Intermediate)				
Count	4	4	12	20
% within Group III	20%	20%	60%	100%
Total				
Count	18	9	33	60
% within Group	30%	15%	55%	100%

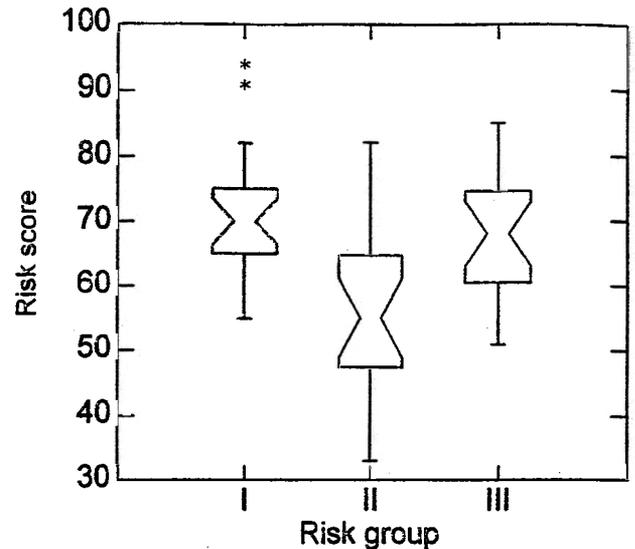


Figure 8. The distribution of risk scores, estimated by the rank model procedure, by viability group (imperiled [I], secure [II], intermediate [III]) determined a priori for the example dataset of 60 species. Boxes indicate the mid-range (50% quartile) of data values around the median; notches in the box are the confidence interval around the median. Whiskers on the boxes show the outside quartiles, and asterisks show outliers.

The assessment was not a quantitative population viability analysis, as it did not employ an explicit model of genetic or demographic risk to species persistence. Rather, the qualitative assessment was a structured and reasoned series of judgments about projected amounts and distributions of habitat and the likelihood that such habitat would allow populations to persist over the long term. Thus, it met the essential criterion of a population viability assessment to provide an estimate of the likelihood that a population will persist to some arbitrarily chosen future time.

Species assessments were based on expert opinion about the likely outcome for species and their habitats under a variety of possible management alternatives. Expert judgments were solicited from eight expert panels. The panels were provided with information on the species distributions, habitat relationships, and known population trends, and with information on the effects of management alternatives on species macro- and micro-habitat elements. Based on that information, the experts were asked to make two judgments. The first judgment rated the species' likely distribution based only on habitat conditions on the federal lands and the natural history characteristics of the species. The second was a cumulative effects analysis of the likely condition of species populations across all ownerships. Factors considered included demographic characteristics, responses to varying qualities of habitat for specific life functions, types and ranges of seasonal and permanent movements, genetic characteristics, and biotic interactions (e.g., competition, predation, herbivory).

Expert judgments were registered through a process of likelihood voting using a structured outcome scale. The

Table 2. Viability outcomes used for the population viability assessment of draft management alternatives for the Interior Columbia Basin Ecosystem Management Project.⁷⁶

Outcome 1.

Habitat is broadly distributed across the planning area with opportunity for continuous or nearly continuous occupation by the species and little or no limitation on population interactions.

Outcome 2.

Habitat is broadly distributed across the planning area but gaps exist within this distribution. Disjunct patches of habitat are typically large enough and close enough to other patches to permit dispersal among patches and to allow species to interact as a metapopulation.

Outcome 3.

Habitat exists primarily as patches, some of which are small or isolated to the degree that species interactions are limited. Local subpopulations in most of the species' range interact as a metapopulation but some patches are so disjunct that subpopulations in those patches are essentially isolated from other populations.

Outcome 4.

Habitat is typically distributed as isolated patches, with strong limitation in interactions of populations among patches and limited opportunity for dispersal among patches. Some local populations may be extirpated and rate of recolonization will likely be slow.

Outcome 5.

Habitat is very scarce throughout the area with little or no possibility of interactions among local populations, strong potential for extirpations, and little likelihood of recolonization.

outcome scale depicted 5 distinct possible outcomes for the habitat or population, each representing points along a gradient ranging from a broadly distributed condition with high likelihood of persistence to a poorly distributed condition with high likelihood of extirpation (Table 2). For each judgment, each expert spread 100 likelihood votes across these 5 outcomes (Table 3). Placing 100 votes on a single outcome indicated certainty in that outcome; whereas, spreading the votes among several outcomes indicated less certainty in any one outcome. Consensus among panelists was not an objective of the process; moreover, the independence of experts' judgments was necessary to assess the uncertainty (standard deviation) of viability likelihood. Uncertainty included two components, variation of likelihood distributions among panelists and the spread of likelihood points among outcomes by each panelist.

There were 2 primary analyses performed on the data derived from the panels. First, the mean likelihood scores for all experts for each of the outcomes was calculated. For example, if there were 4 experts on a panel, and their likelihood votes for outcome 2 for a particular species were 30, 30, 60, and 40, then the mean likelihood score was 40. Next, to summarize mean likelihood for each species, a

weighted mean outcome was also calculated. This was calculated by assigning a value to each of the outcome categories (Outcome 1 value=1, Outcome 2 value=2, etc.), multiplying the mean likelihood of that outcome by its assigned value, adding these products for all outcomes, and then dividing by 100. Outcomes were considered improving or declining from the historical to current, or from current to future, periods if they changed at least 0.5, a value corresponding to one standard deviation of the mean outcome. The assessment did not provide a simple determination of what does and does not constitute a "viable" population. This was considered a strength of the process rather than a weakness, as there are no simple thresholds for viability, particularly when assessments are done on a broad array of taxa. Rather than providing a simple determination, this assessment described likely future conditions for species and habitats and provided for comparison of those conditions to current and historical conditions. Lack of a simple determination, however, added complexity to the job of interpreting the results and using them in a decision-making framework. The authors recommended that interpretation of the results emphasize comparison of the projected future conditions under the alternatives to historical and current conditions.

A variety of cautions must be applied to the interpretation of this form of assessment. These cautions fall into four areas: (1) the broad geographic and temporal scale of the analysis limits local inference; (2) the resolution of the data and planning guidance define the level of confidence in results; (3) limitations on the ability to infer population results from habitat analysis; and (4) gaps in knowledge limit confidence or geographic scope of inference. Lehmkuhl et al.⁷⁶ give a detailed discussion of these cautions and assumptions.

Conclusions Drawn from the Example Analyses

The examples were meant to illustrate a practical range of risk analysis methods that would be relatively easy to implement using the data matrixes in this book and conservation theory. The examples focused on frequently encountered situations when the taxonomic scope is fairly broad (i.e., many species need to be analyzed), and when procedural, or analytical, complexity may be limited by available data. The geographic scale (extent) of application would usually be large—at watershed or larger scales.

The first two examples used data in related procedures to differentiate and classify imperiled, secure, and intermediate-risk species, and to develop a rule set for classifying other species of unknown risk. The third example used species risk theory and data to score and rank potential risk based on attributes of life history and population distribution, when prior knowledge of risk was unavailable. That same type of model could be used to rank management priorities based on criteria other than extirpation risk, e.g. social or economic value. The fourth example described a qualitative population viability assessment that linked in the data matrixes with expert

Table 3. Example of the likelihood voting system used to assess viability outcomes for selected species of conservation concern for the Interior Columbia Basin Ecosystem Management Project.*⁷⁶

Species: <i>Flammulated Owl</i>	Management Alternative				
	Historic	Current	Traditional	Restore	Reserve
1 contiguous		0	0	0	0
2 gaps	75	2		26	15
3 patchy	20	40	20	60	50
4 isolated	4	38	39	13	27
5 scarce	0	20	40		8
Total score	100	100	100	100	100

* One hundred likelihood points are distributed across the five outcomes for each time period or alternative. The distribution of points reflects the certainty of a particular outcome.

opinion to assess land management alternatives.

Other more quantitative methods, such as demographic PVA models, are valuable tools to address some of those risk issues and should not be ruled out. They were not illustrated because their complexity demands information far more sophisticated than is available in the data matrixes, and that is nonexistent for the vast majority of species that the manager has to consider. Quantitative PVA models will be most appropriate when the focus of management is a single species suspected or known to be at risk, and when reliable data are available to model population and habitat dynamics under management alternatives.

It is first and foremost necessary to remember that the examples were meant simply to illustrate some of the ways information in the data matrixes can be used to determine factors that might contribute to risk levels of species, or to rank species in terms of risk. Further and more complete analyses, using these methods or others described in this chapter, are really needed to verify our initial findings on how life history or taxonomic categories could predispose some species to various risk levels. Those conclusions should be taken as tentative working hypotheses.

The following is an example of how one might draw conclusions from the example risk analyses. Conclusions from these types of analyses might differ if the focus of such analyses shifted to specific taxonomic or functional groups. That given, it could be significant that the best distinguishing features of the three species groups analyzed in the first three examples mostly refer to habitat selection, habitat breadth, and population distribution, and not as much to inherent life history attributes per se. At the start of this analysis, we expected at least some life history attributes, such as age at first reproduction, reproduction rates, site fidelity, and movement distances, to predict risk level. Life history attributes still may be important to distinguish risk levels among species within genera or families, which remains to be formally tested with an expanded analysis of the entire species dataset.

However, the importance of life history attributes for characterizing risk within taxonomic groups does not

seem to hold equally across the 4 taxonomic classes. That also was the general finding of Russell et al.,¹⁴⁵ who found that distributions of extinctions and threat classifications were clustered unevenly within certain genera and families, particularly in taxa that contain few species. Whether taxonomic affiliation and diversity alone predisposes species to certain risk levels, or patterns of habitat use and population distribution are themselves directed by life history characteristics, is unclear and needs further analysis.

The first three analyses were developed mostly as examples of the kinds of evaluations that could be done with data to test how life history attributes might contribute to risk levels. The rank model, the third example, also ranked species by potential risk. More specific and more thorough analyses can follow these examples by: (1) focusing on species within specific individual habitats, structural conditions, physiographic provinces, taxonomic groups, known risk categories, or geographic areas; (2) rerunning such analyses for all such species within the data matrixes; (3) better determining the mechanisms by which life history traits influence habitat selection and population distribution; and (4) better determining the influence of life history traits on risk levels among species within genera and families.

Following more complete analysis, the results can be integrated into a broader risk management framework. The risk analysis portion of a decision evaluation can include those life history traits and habitat selection behavior of species found to portend risk levels, and thereby determine how alternative management actions might influence the species' habitat use and population response. In the risk management phase, the decision-maker then would have explicit information on which species might be at greater risk.

The qualitative PVA example for the Columbia River Basin showed how information from the first three types of analyses could be melded with matrix data and expert opinion to assess and score the effects of different land management alternatives at a broad regional scale. That information, then, would inform decision makers on how

best to manage risk. The qualitative expert-opinion process used in the example could be developed further by formalizing the relationships between life history, habitat, and population status in a decision analysis or knowledge-based system. Then, the risk analysis process could be easily refined or repeated as management alternatives are modified from public input or changing agency priorities. Formalizing such expert models also has the advantage of explicitly stating the relationships between species attributes, habitat, and risk, thus, opening the scientific "black box" for review and agreement among interested parties that the best available science is being used for management.

Conclusions

Wildlife managers do risk analyses that vary in spatial scale, taxonomic scope, and complexity of information needs and methods—it is a daunting task. Moreover, the public is scrutinizing resource management actions that can affect wildlife viability, and is asking for the best available science to analyze the effects of those actions. Armed with a basic understanding of the theory and criteria for identifying species at risk, managers and scientists can use available datasets and analytical tools to meet that challenge at different levels of geographic and ecological scale.

Species are at risk from a combination of systematic and stochastic processes that affect population size and distribution. Systematic processes are usually the ultimate cause of extirpation, and occur when something essential is removed from the environment, such as habitat, or when something lethal is inserted into the environment, such as a new predator or poison. Stochastic, or random, processes are usually the proximate cause of extirpation in populations already made small by systematic pressures. The vulnerability, or risk, for species is a function of how systematic and stochastic processes interact with habitat selection behavior, and the demographic and life history attributes of the species. Habitat selection, habitat breadth, and population distribution likely are among the most important influences on risk level.

Understanding the processes underlying species risk allows managers to select the right analysis tools. While much of the conservation literature on wildlife risk analysis focuses on data-intensive quantitative PVA models, there are many situations for which that tool is unsuitable in terms of number of species to be analyzed, the data available for the analysis, or the time and money available to do it. Fortunately, there are datasets and analytical tools that can meet the risk analysis needs of managers for different levels of taxonomic and procedural complexity. The data matrixes included in this book are an important basic resource for risk analysis that can be linked with analytical methods in this chapter. Results of such risk assessments will provide the essential information for decision-makers about the alternatives for managing risk.

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