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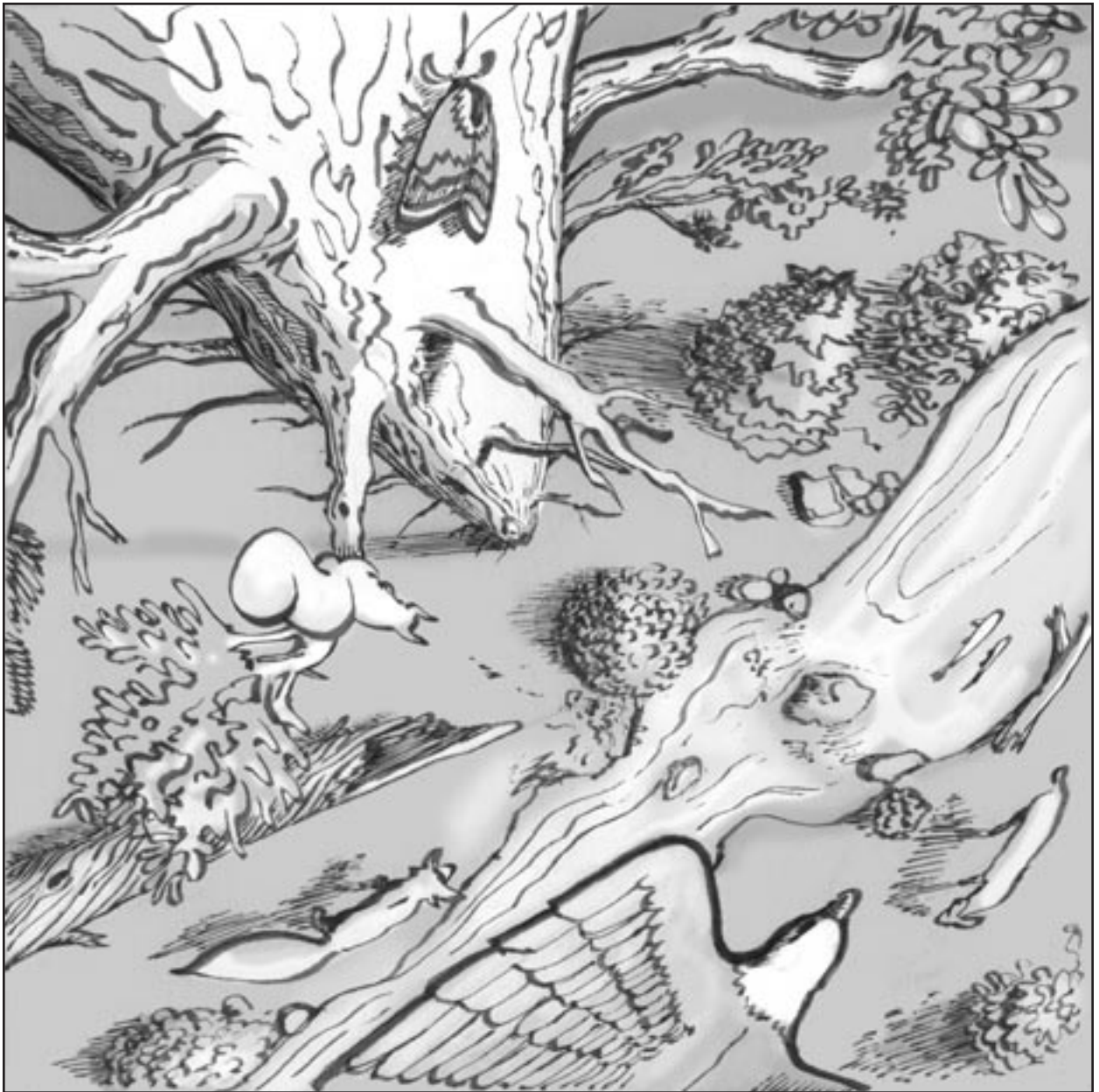
**Forest Service**

Pacific Northwest  
Research Station

General Technical  
Report  
PNW-GTR-443  
March 1999

# Monitoring Biodiversity: Quantification and Interpretation

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## Abstract

**Gaines, William L.; Harrod, Richy J.; Lehmkuhl, John F. 1999.** Monitoring biodiversity: quantification and interpretation. Gen. Tech. Rep. PNW-GTR-443. Portland, OR: U.S. Department of Agriculture, Forest Service, Pacific Northwest Research Station. 27 p.

Monitoring is necessary for an adaptive management approach and the successful implementation of ecosystem management. In this document, we present an approach to monitoring biological diversity at different levels of ecological organization: landscape, community or ecosystem, population or species, and genetic. Our approach involves identifying monitoring questions derived from regional, provincial, or watershed assessments; identifying monitoring methods; and analyzing and interpreting data to integrate into management strategies. Examples of monitoring methods, data analysis, and interpretation are provided for each level of ecological organization, beginning with the most inclusive level, the landscape. Our objective is to provide land managers with an approach and examples to develop biodiversity monitoring strategies.

Keywords: Biodiversity, monitoring, genetic diversity, landscape diversity, species diversity, ecosystem diversity.

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## **Introduction**

The conservation of biodiversity has become an important issue receiving national and international attention (Noss 1991, Noss and Cooperrider 1994, Wilson 1992). The word biodiversity, however, has little meaning to many people (Brussard and others 1992) and can have many interpretations for those who study it. Because of this, there are various definitions of biological diversity (Harrod and others 1996). For example, Volland (1980) and Gast and others (1991) define biodiversity as “the variety, distribution, and structure of plant and animal communities, including all vegetative stages, arranged in space over time that support self-sustaining populations of all natural and desirable naturalized plants and wild animals.” On the other hand, Wilcox (1984) used biodiversity to describe the variety of life forms, the ecological roles they perform, and the genetic diversity they contain.

The biodiversity hierarchy theory suggests that what happens at the higher levels of ecological organization, such as the landscape or ecosystem level, will constrain the lower levels, such as the species or genetic level (Allen and Star 1982, Noss 1990). The biodiversity hierarchy is composed of the genetic, species-population, community-ecosystem, and landscape or regional levels (Grumbine 1992, Harrod and others 1996). Although these levels are convenient for the sake of discussion, they present only one perspective of biodiversity. In addition to these levels, biodiversity can be influenced by scale, both temporal and spatial.

A decision to commit resources to monitor biodiversity could be based on legal mandates such as the National Forest Management Act (NFMA 1976) or the Endangered Species Act (ESA 1973 as amended: Harrod and others 1996). In addition, Everett and others (1994) and Noss and Cooperrider (1994) pointed out that monitoring is an important element of ecosystem management and an adaptive management approach. We hope that by providing some “real world” examples of how biodiversity can be monitored, we will encourage land management agencies to develop comprehensive and scientifically credible monitoring programs.

## **Biodiversity Monitoring Approach**

The initial phase in biodiversity surveys is estimating diversity at one point in time and location (in other words, knowing what species or communities are present). The second phase, monitoring biodiversity, is estimating diversity at the same location at more than one time period for drawing inference about change (Wilson and others 1996).

Wilson and others (1996) identified attributes of biodiversity that can be assessed at each level of ecological organization. At the landscape level, attributes that could be monitored include the identity, distribution, and proportions of each type of habitat, and the distribution of species within those habitats. At the ecosystem level, richness, evenness, and diversity of species, guilds, and communities are important. At the species level, abundance, density, and biomass of each population may be of interest. And, at the genetic level, genetic diversity of individual organisms within a population is important. It is best to assess and interpret biodiversity across all these levels of organization by using various approaches at several spatial and temporal scales (Noss 1990, Noss and Cooperrider 1994).

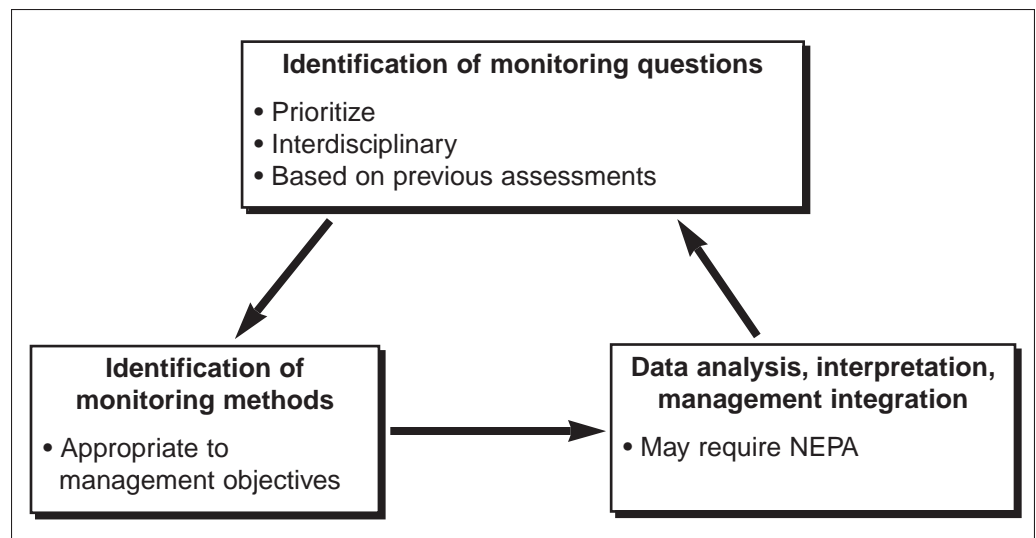


Figure 1—Three phases of biodiversity monitoring.

We propose a three-phase approach to monitoring biodiversity: identifying monitoring questions; identifying monitoring methods; and analysis and interpretation of information for integration into management strategies (fig. 1). Each of these phases are described in greater detail below.

### Identifying Monitoring Questions

This phase includes identifying and refining biodiversity monitoring questions, determining data needs to address the questions, and prioritizing monitoring questions and data needs. Examples of monitoring questions appropriate to each biodiversity level are shown in figure 2. Prioritizing monitoring questions is important because the resources available to accomplish monitoring are likely to be limited.

Identifying monitoring questions is a critical and difficult step. It could be accomplished through an interdisciplinary process with experts knowledgeable of the issues at the appropriate level (e.g., landscape, ecosystem, species, genetic, etc.) and should be considered an iterative process that is adapted as new information becomes available.

Monitoring questions could be derived from information available in watershed analysis, late-successional reserve (LSR) assessments, or regional assessments. For example, in the Wenatchee National Forest LSR assessment (USDA Forest Service 1997), the assessment team developed monitoring questions, proposed data collection methods, and identified appropriate expertise needed to accomplish the monitoring. The monitoring questions were ranked as low, moderate, and high priority. Ultimately, management must determine which monitoring questions should be addressed.

### Monitoring Methods

Methods selected for monitoring biodiversity depend on management objectives. A management objective of maintaining species viability would involve different monitoring methods than an objective of restoring inherent disturbance regimes.

Monitoring scale	Monitoring questions	Monitoring methods
Landscape level	A. Trends in landscape diversity	<ul style="list-style-type: none"> <li>A. Indices of landscape patterns</li> <li>B. Historic reference conditions</li> <li>C. Remote sensing and GIS</li> </ul>
	B. Trends in habitat availability and distribution	<ul style="list-style-type: none"> <li>A. Indices of landscape patterns</li> <li>B. Historic reference conditions</li> <li>C. Remote sensing and GIS</li> </ul>
	C. Trends in landscape elements (e.g., edge fragmentation, interior forest)	<ul style="list-style-type: none"> <li>A. Indices of landscape patterns</li> <li>B. Historic reference conditions</li> <li>C. Remote sensing and GIS</li> </ul>
Community or ecosystem level	A. Management actions or natural disturbance affects on species diversity	A. Species diversity indices
	B. Function—role of species in community or ecosystems	A. Functional group and guild analysis
	C. Level of protection of areas with high species richness	<ul style="list-style-type: none"> <li>A. Rapid assessment</li> <li>B. Gap analysis</li> </ul>
Species or population level	A. Species—population trends	<ul style="list-style-type: none"> <li>A. Abundance indices</li> <li>B. Population estimates</li> </ul>
	B. Affect of management actions or natural disturbance on a species—population	<ul style="list-style-type: none"> <li>A. Abundance indices</li> <li>B. Population estimates</li> </ul>
	C. Probability of species or population persistence	<ul style="list-style-type: none"> <li>A. Qualitative population viability analysis</li> <li>B. Quantitative population viability analysis</li> </ul>
Genetic level	A. Genetic diversity within a population—species	<ul style="list-style-type: none"> <li>A. Morphological variation</li> <li>B. Allozyme analysis</li> <li>C. DNA analysis</li> </ul>
	B. Genetic diversity among populations	<ul style="list-style-type: none"> <li>A. Morphological variation</li> <li>B. Allozyme analysis</li> <li>C. DNA analysis</li> </ul>
	C. Effects of management activities or habitat fragmentation on species diversity	<ul style="list-style-type: none"> <li>A. Morphological variation</li> <li>B. Allozyme analysis</li> <li>C. DNA analysis</li> </ul>

Figure 2—Example of monitoring questions and methods for each level of ecological organization.

Selecting the appropriate biodiversity monitoring approach includes identifying methods that will provide answers to specific monitoring questions (fig. 2). A wide range of methods are available, and selection of methods would be made based on costs, available resources, and statistical constraints. It might be helpful, if not absolutely necessary, to consult a statistician at this stage to determine sampling sizes, strategies, and statistical power.

### **Data Analysis, Interpretation, and Management Integration**

Periodically, data collected from monitoring would be analyzed and integrated into management strategies based on the knowledge gained. If monitoring reveals that adjustments need to be made in management strategies, then this becomes a decision step requiring National Environmental Policy Act (NEPA 1969) documentation and plan revisions.

### **Examples of Monitoring at Each Biodiversity Level**

Presented below are several examples of monitoring biological diversity at each level of ecological organization, beginning with the landscape level. For each level, we provide definitions and background on the relevance of monitoring to land managers; examples of monitoring questions; a summary of available monitoring methods and references to determine appropriate methods; and case studies of the actual application of these methods, the results they can produce, and interpretations of these results. Some methods have not been adequately developed due to our limited understanding of certain aspects of biodiversity (Harrod and others 1996). Other methods have serious limitations, which we attempt to point out.

### **Landscape Monitoring**

A landscape has been defined as a land area with groups of plant communities or ecosystems forming an ecological unit with distinguishable structure, function, geomorphology, and disturbance regimes (Forman and Godron 1986, Noss 1983, Romme and Knight 1982). Landscape diversity is the number of ecosystems, or combinations of ecosystems, and types of interactions and disturbances present within a given landscape.

The relevance of landscape structure to biodiversity has been established in the scientific literature (e.g., Forman and Godron 1986). Landscape features such as patch size, heterogeneity, connectivity, etc., have major implications to species composition, distribution, and viability (Noss and Harris 1986). Because of this, it may be important that managers monitor elements of biodiversity at the landscape scale to meet species viability requirements of the NFMA and ESA.

**Monitoring questions**—Examples of monitoring questions at this level could include, What is the current level of landscape diversity and how does it compare with historic or sustainable levels? What are the trends in habitats or populations of a particular species? and What are the trends in landscape features such as the amount of edge, patch size, forest interior, etc.?

**Monitoring methods**—Presented below are several approaches to assessing biological diversity at a landscape scale. Each of these approaches relies on the use of geographic information systems (GISs) and requires mapped vegetation and other layers that can be analyzed with GIS technologies.



## Indices of Landscape Patterns

Landscape pattern measurements, or metrics, can be classified into three categories: patch, class, and landscape (McGarigal and Marks 1993). Examples of commonly used metrics can be found in the appendix. Patch metrics describe the attributes of individual patches of vegetation. The size, shape, edge, or nearest-neighbor relations of individual patches are measured. Class metrics describe those same patch attributes as the mean, minimum, maximum, or variance for a class of mapped landscape attributes (e.g., late-successional forest). Landscape pattern metrics describe these and other attributes for all landscape classes combined without distinction between different classes. For example, mean patch size might be measured for all patches in a landscape, instead of for just one vegetation type (class). In addition to the diversity and evenness indices that will be discussed later, there are other landscape metrics available to index specific aspects of landscape spatial pattern. Some of these attributes also can be used to measure class attributes (McGarigal and Marks 1993).

O'Neill and others (1988) and Turner (1990) proposed indices of dominance, contagion, fractal complexity, and disturbance as standard measures of landscape pattern. Dominance is an index of vegetation type composition and equitability. Contagion measures the extent to which a single class of vegetation or all types combined are clumped (high contagion) or patterned in a fine-scale (low-contagion) mosaic. Fractal indices describe patch shape and boundary (edge) complexity. The perimeter-area fractal is the most commonly used fractal index, and the one described by O'Neill and others (1988); however, other forms of the fractal index have been developed. For example, Korcak's fractal incorporates the number-area relation of vegetation patches to describe patch-size variability and fragmentation (Burrough 1986, Milne 1988). Most fractal indices can be easily calculated with simple regression methods (Burrough 1986). A disturbance index is calculated as a ratio of the area of disturbed vegetation to that of undisturbed vegetation.

Other class or landscape pattern indices have been developed by landscape ecologists and can be found in the literature. For example, Lehmkuhl and others (1991) and Lehmkuhl and Raphael (1993) used a form of the contagion index, as suggested by Turner and others (1989), to measure fragmentation of late-successional forest. Ripple and others (1991) and Lehmkuhl and Raphael (1993) calculated an index of late-successional forest isolation that incorporates information on both the total area and spatial distribution of late-successional forest patches by using a standard GIS proximity function.

An application of these indices to forest landscapes in western Washington can be found in Lehmkuhl and others (1991). They found that forest patch shape is not complex as measured by the fractal index (maximum value of 1.27 within a possible range of 1 to 2). The dominance indices showed that no one vegetation type was dominant in most landscapes (mean value of 0.93 compared to a maximum value of 3). Their landscapes showed high vegetation type contagion (mean of 1.7 out of a possible 20). The disturbance index showed a relatively low level of logging disturbance on the landscape (mean of 20 percent disturbed).

Lehmkuhl and others (1991) found that contagion of all vegetation types proved to be a variable closely associated with differences among vertebrate assemblages in forests of western Washington and Oregon. O'Neill and others (1988) and Turner (1990) caution users, however, that the index can be sensitive to the number of types in the landscape so that comparisons of different areas with different numbers of vegetation types could be misleading if the index is not normalized to the number of types. Lehmkuhl and others (1991) also found their isolation index is another attribute of late-successional forest pattern associated with differences in vertebrate assemblages. The isolation index, however, is correlated with the total area of late-successional forest, which would indicate that simply measuring late-successional forest area might be an effective and simple method. Lehmkuhl and Raphael (1993) also concluded that simply measuring the area of habitat is the single best indicator of habitat pattern distinguishing northern spotted owl (*Strix occidentalis caurina*) areas on the Olympic Peninsula of Washington. Measures of patch size and shape are other important attributes of spotted owl habitat.

Landscape edge complexity measured by the perimeter-area fractal and Korcak's fractal also is associated with differences in vertebrate occurrence in western Washington and Oregon (Lehmkuhl and others 1991). Turner and Ruscher (1988) and Mladenoff and others (1993) found that the perimeter-area fractal is a good indicator of landscape disturbance, indicating the conversion of complex wild landscapes to the simple geometry of human-dominated landscapes. Lehmkuhl and others (1994), however, found that fractal indices are poorly correlated with logging disturbance measured as the area of clearcut in the landscape. Others have questioned the accuracy of the fractal and other indices of landscape pattern (Cale and Hobbs 1994, Groom and Schumaker 1996, Schumaker 1996).

There are caveats for using landscape pattern metrics. Not all metrics may be useful in describing the attributes of all landscapes or in answering specific questions about landscapes relative to the ecology or management of a particular plant or animal community. Spatial analysis software packages, such as FRAGSTATS (McGarigal and Marks 1993), generate much data on landscape metrics, and sorting through those results can be confusing and wasteful unless careful thought is given to the questions to be answered and what metrics can answer those questions. Moreover, attention should be paid to the differences in scale and dimension of maps when comparing indices of pattern between locations. Turner (1989, 1990) and Lehmkuhl and Raphael (1993) found that several indices of pattern differ simply because the map dimensions differ.

## **Historic Reference Conditions**

Swanson and others (1994) and Morgan and others (1994) described the application of the range of natural variability as a reference to compare the current condition of landscapes. They stressed that the use of natural variability as a reference condition is not an attempt to turn managed landscapes into wilderness areas or return them to a single preexisting condition. Instead, it is an approach to meet ecological objectives by bringing the range of existing conditions in a landscape within the natural range.

Caraher and others (1992) applied the range of natural variability concept to the Blue Mountains landscape in eastern Oregon. They estimated the range of natural variability for several ecosystem components (i.e., distribution of several stages, stream

shrub cover, streambank stability, etc.). They found that several ecosystem elements are currently outside the range of natural variability because of activities such as fire exclusion, tree planting, and fish restocking (Caraher and others 1992, Harrod and others 1996). Lehmkuhl and others (1994) compared the historical and current condition of several landscape variables and indices for forests of eastern Oregon and Washington. They used the standard error of the mean to estimate the range of variability (Lehmkuhl and others 1994). Gaines and Harrod (1994) presented a process that could be used during watershed analysis to assess the condition of wildlife habitats and identify potential restoration projects. By using GIS, they mapped the current and projected historic distribution of habitats and by comparing the differences in these maps, identified areas on which to focus habitat restoration.

### **Community-Ecosystem Monitoring**

A community comprises the populations of some or all species coexisting at a site. An ecosystem includes the abiotic aspects of the environment and the biotic community.

Monitoring at this level is important to the maintenance of ecosystem functions and integrity that have been identified as a main theme of ecosystem management (Haynes and others 1996, Marcot and others 1994). Land managers may be interested in monitoring communities or ecosystems to determine if current management strategies meet legal and social obligations to sustain the health, diversity, and productivity of ecosystems (Haynes and others 1996).

**Monitoring questions**—Example monitoring questions could include, How have management activities or natural disturbances affected species diversity in a particular community? What is the function of a species in the community or ecosystem? and Where are the areas of high species richness, endemism, or rarity and how well are they protected?

**Monitoring methods**—A common way of assessing biodiversity is by measuring the number and relative abundance of species in a community or ecosystem, often referred to as species diversity. Species diversity is a function of the number of species present (richness) and the evenness or equitability (relative abundance) of each (Hurlbert 1971). Hurlbert (1971) pointed out that although species diversity and species richness are often positively correlated, situations do exist in which increases in species diversity are accompanied by decreases in species richness. Care should be taken therefore, when only species richness (counts of the number of species) is used to evaluate biodiversity. On the other hand, species diversity indices also should be carefully used because it may be hard to interpret differences in species composition at different sites. For example, two sites may have similar indices of diversity but have entirely different species composition. One site may be primarily exotic species, whereas the other mainly native or endemic species.

### **Diversity Indices**

Various indices and models have been developed to measure diversity within a community (Magurran 1988). In general, three main categories of measures are used to assess species diversity: (1) species richness indices, which measure the number of species in a sampling unit, (2) species abundance models, which have been developed to describe the distribution of species abundances, and (3) indices that are based on the proportional abundances of species such as the Shannon and Simpson indices (Magurran 1988). Examples of commonly used indices are provided in the appendix.

Selecting the appropriate index in which to assess community level diversity can be difficult as there are many to choose from and each has advantages and disadvantages. Magurran (1988) suggested that important criteria for selection include the ability to discriminate between sites, dependence on sample size, what component of diversity is being measured, and whether the index is widely used and understood. The most commonly used indices include the log series, species richness, Shannon index, and the Simpson index (Magurran 1988).

To quantify community level biodiversity, an inventory or sample of the species present and their relative abundance must be completed. Various methods have been used to inventory plant, wildlife, and fish species. Summaries of the techniques can be found in Cooperrider and others (1986), Barbour and others (1987), and Kent and Coker (1992).

Many examples of the application of indices to assess diversity of species within a community are in the literature. For example, Thiollay (1992) used species richness, the Shannon index, an evenness index, and the Simpson index to assess the influence of selective logging on bird species diversity. He used a point-count method in which 937, 0.25-hectare sample quadrants were inventoried for 20 minutes each. He discovered an overall 27- to 33-percent decrease of species richness, frequency, and abundance following logging, with a less marked decline of species diversity and evenness.

Cushing and Gaines (1989) used the species richness, the Shannon index, and an equitability or evenness index to compare diversity of aquatic insects in three cold-desert streams and to evaluate the affects of winter spates on diversity. They collected quantitative macroinvertebrate samples at monthly intervals from each stream. They discovered that species diversity increased with increasing stream size and substratum diversity but declined following winter spates.

## **Functional Groups or Guilds**

Some investigators have taken a different viewpoint by lumping species into functional groups or guilds. Many approaches for grouping species based on habitat or behavioral similarities and their potential problems have been discussed in the literature (Landres and others 1988, Morrison and others 1992, Noss and Cooperrider 1994). Walker (1992) suggests an approach in which species are grouped into guilds based on their function in the ecosystem, and then the relative importance of each guild is considered based on how a change in their abundance affects ecosystem and community processes. Gaines and others (1989) grouped aquatic insects into trophic levels and functional groups and then used density and biomass as indicators of numerical and biomass dominance to assess community diversity in three cold-desert streams. They found that detritivores are the dominant (both numerically and as biomass) function in their study streams and that collecting (gathering and filtering) is the major feeding strategy used. From this information, they inferred that detritus in the form of fine particulate organic matter is the major food source for benthic invertebrates in small, headwater cold-desert streams. Thus, managing for stream-side vegetation is important in maintaining the function of aquatic insect communities.

## **Rapid Assessment Techniques**

Another approach using groups of invertebrates and nonflowering plants as surrogates of biodiversity was presented by Oliver and Beattie (1993). They estimated species richness of spiders, ants, polychaetes, and mosses and divided them into recognizable taxonomic units (RTUs). These RTUs are taxa that are readily separated by morphological differences that are obvious to individuals with less training than professional taxonomists. They found that by using RTUs, there is little difference between classifications made by a biodiversity technician and those made by a taxonomy specialist. This could result in a considerable savings of time and money to complete the inventories needed to assess this one facet of biological diversity.

## **Gap Analysis**

Scott and others (1993) presented a method to assess biological diversity at the community level, applied at the landscape or regional scale. This approach, called gap analysis, provides a framework in which to obtain an overview of the distribution and conservation status of several components of biodiversity. The approach involves mapping, digitizing, and ground-truthing vegetation and species distribution data; digitizing biodiversity management areas and landownership maps; adding location data on all species and high-interest habitats such as wetlands and streams; and mapping, delineating, and ranking areas of high community diversity and species richness. These data are then used to identify “gaps” in protection of vegetation types and species-rich areas and provide land managers with information to make decisions about reserve selection and design, land management policy, and other conservation actions.

## **Population-Species Monitoring**

A population is defined as all individuals of one species occupying a defined area and usually isolated to some degree from other similar groups. A species is generally defined as a group of organisms formally recognized as distinct from other groups.

Monitoring at this level may have the most relevance to meeting the species or population viability objectives of the NFMA and ESA. For example, land managers may decide to monitor a species or population in order to measure trends. This would be important to determine if management strategies maintain population viability.

**Monitoring questions**—Monitoring questions at the species or population level could include, What is the trend in the species or population? How is species or population abundance affected by land management activities or natural disturbances? What is the probability of population or species persistence over a period of time in a specified area?

**Monitoring methods**—Most monitoring of biodiversity has occurred at the population-species level. Deciding which species or population to monitor has received considerable discussion, and no single approach is without pitfalls. Noss (1990) suggests five categories of species that may be selected for monitoring. These include (1) ecological indicators—species that signal the effects of perturbations on a number of other species with similar habitat requirements; (2) keystones—species on which the diversity of a large part of a community depends; (3) umbrellas—species with large area requirements, which if conserved, many other species also would be conserved; (4) flagships—popular, charismatic species; and (5) vulnerables—species that

are rare, genetically impoverished, or for some reason prone to extinction. When determining which species are best to monitor as bioindicators, it is appropriate to consider species of invertebrates, fungi, lichens, and amphibians, as well as vertebrates and vascular plants (Marcot and others 1997, Marcot and others 1998).

Monitoring a species or population may include counting of individuals but most often involves the monitoring of habitat that is used by or is important to a species (Cooperrider and others 1986, Noss 1990). Noss (1990) pointed out that monitoring habitat variables does not alleviate the need to monitor populations because the presence of habitat is no guarantee that the species is present. Conversely, monitoring only population variables could be misleading because some individuals may occur in areas of marginal habitat (Van Horne 1983). The most reliable approach would include monitoring both habitat and population variables (Noss 1990).

Various methods are available to monitor and inventory populations and species, and their habitats. Cooperrider and others (1986) provide a comprehensive reference of the available methods for monitoring and inventorying fish and wildlife habitat and populations, Wilson and others (1996) provide an overview of standard methods to measure and monitor mammals, and Heyer and others (1994) summarize standard methods for amphibians. Several methods are available for plants but are not discussed in great detail here. Where appropriate, we have discussed some common methods and provide references where discussions of these techniques in greater detail can be found.

## Abundance Indices

An index is usually a count statistic that is obtained in the field and carries information about a population (Wilson and others 1996). An index is usually used when individuals of the species in question are difficult to observe and count, or capture and tag, or when a formal abundance estimate is too expensive or time-consuming. Abundance indices are divided into direct indices and indirect indices. Direct indices are based on direct observation of animals, either visually or through capture or harvest (Seber 1982). These include incomplete counts such as obtained from aerial surveys, capture indices based on the number of individual animals captured per unit of time or effort, and harvest indices based on the number of animals harvested over a specific period of time or effort (Wilson and others 1996). Indirect indices are based on indirect evidence of an animal's presence (Seber 1982): for example, track counts, scent station surveys, auditory indices (based on counts of animal sounds), structure surveys (numbers of nests, lodges, food caches, etc.), scat and other sign counts, and home range size estimates (use of home range as an index of population density) (Wilson and others 1996).

Gaines and others (1995) provide an example of an indirect index using auditory responses of coyotes (*Canis latrans*) and gray wolves (*Canis lupus*) to simulated howling. They conducted a total of 2,137 howling sessions resulting in 215 responses by canids and an overall response rate-howling session (RR-S) of 10 percent. Two responses had the vocal characteristics of wolves for a RR-S of 0.1 percent, and 213 responses were of coyotes for a RR-S of 9.9 percent. It remains unknown at this time how well RR-S relates to actual population size or density, requiring caution in its use as an abundance index.

The advantages of using abundance indices are that they are less expensive and less time-consuming than more formal population estimates. If appropriate indices are available, and if their relations to abundance are known to be invariant over time and survey conditions, then there is no need to estimate an absolute density (Wilson and others 1996). Such ideal conditions, however, almost never exist and often present potentially misleading conclusions regarding population size or density.

### **Population Estimates**

Estimates of population size and density usually require significant investments of time and money. They are divided into complete counts, or a census, and estimates when complete counts are not possible (Wilson and others 1996). In a complete count, the population size can be determined in a survey area from the number of individuals counted, with no correction for sampling observation probability (e.g., observability, sightability, visibility, and detectability). In most situations, counts of organisms in an area are incomplete and represent unknown portions of the total population. Thus it is important to determine the probability of detecting an individual in a given survey area in order to estimate the population size or density.

Miller and others (1997) provide an example of the use of radiotelemetry and replicated mark-resight techniques to estimate brown bear (*Ursus arctos*) and black bear (*Ursus americanus*) density. They estimated a mean probability of sighting a marked individual by experienced pilot-observer teams to be 0.323 for brown bears and 0.321 for black bears. Brown bear densities ranged from 10 to 551 bears per 1000 square kilometers of habitat from 15 different study areas. Black bear density ranged from 89 to 290 bears per 1000 square kilometers from three study areas. These estimates were used to track changes in bear abundance that may result from environmental disturbances or human impacts, to estimate the total number of bears in the state, and as one component of determining sustainable harvest quotas.

### **Population Viability Analysis**

Population viability analysis (PVA) estimates what conditions are necessary for a population to persist for a given period of time in a given place (Soulé 1987). The PVA allows for a prediction of the possible trend of a population and can provide insights into why a population may be decreasing. One of the disadvantages of a quantitative PVA is the rigorous data set that is needed to complete the analysis. These data are often expensive to obtain and require several years or decades of study. Because of the need to have such a rigorous and extensive data set, PVA may be too cumbersome to use to monitor biodiversity. When such data are available, however, PVA may be useful in establishing baseline population information to predict how management actions might effect viability. Recently, a new approach has been used to develop a qualitative PVA relying on the professional judgement of scientists familiar with a species or group of species (Thomas and others 1993, Lehmkuhl and others 1997). This qualitative approach has the advantage of not requiring such a rigorous data set, yet still meets the essential criterion of a PVA, to provide an estimate of the likelihood that a population will persist over a given time period.

Beier (1993) conducted a quantitative PVA for cougars (*Felis concolor*), which exist at low density and require large areas. Beier (1993) used population parameters that included mean litter size, juvenile survival rates, adult survival rates, and carrying capacity in his PVA model. These data were obtained from an extensive study of a cougar population in the Santa Ana Mountains of southern California. Beier also factored into his PVA model different sizes of habitat areas, levels of immigration, and some degree of environmental stochasticity. He found that there was a high likelihood of extinction if the amount of habitat that is currently available is reduced and if an important movement corridor is further degraded by land development activities.

There are several studies that use PVA for rare plant species, and each takes a slightly different approach. We suggest reviewing these studies (e.g., Burgman and Lamont 1992, Harper 1977, Koopowitz and others 1994, Manasse 1993, Menges 1990, Possingham and others 1992) and selecting an approach that best fits the specific situation while considering the following points. When carrying out such analysis for plants, consider the mode of reproduction of the species under study. Plants that are autogamous (self-fertilizing) or agamospermic (seed production without fertilization) may persist indefinitely regardless of numbers, assuming that their fixed genomes provide the ability to exist in a given environment. Small populations of plants that are obligate out-crossers may be subject to loss of genetic diversity, such as from genetic drift. Given (1994) stated that 64 percent of the neutral genetic variation of a population will be lost through genetic drift in 100 generations (see Lesica and Allendorf 1992, however). It follows that the rate of seedling recruitment into the adult population is an important aspect in determining how long small populations will persist.

Thomas and others (1993) used a qualitative approach to PVA to assess different forest management alternatives in the Forest Ecosystem Management Assessment and Lehmkuhl and others (1997) for the Interior Columbia Basin Ecosystem Management Project. This approach allowed for an assessment of many species at a regional or multiregional scale. However, although a qualitative approach allows for a rapid viability assessment without the commitment of resources to gain extensive life history data, it is not without some drawbacks. Qualitative assessments could be used as interim PVAs until resources become available to obtain the data necessary to test the many assumptions that interim PVAs are based on (Shaffer 1990).

## **Genetic Monitoring**

Genetic diversity refers to the breadth of genetic variation within and among individual populations and species. Frankel (1970) postulated that genetic variation is essential for the long-term survival of endangered species, especially those that occur in fast-changing or harsh environments. Genetic diversity is a necessary prerequisite for future adaptive change or evolution, and presumably, populations and species that lack genetic variation are at greater risk of extinction (Hamrick and others 1991, Schaal and others 1991). Land managers may decide to monitor genetic diversity to determine if management strategies are providing for species viability as required under NFMA and ESA.



**Monitoring questions**—Examples of monitoring questions that could be asked include, What is the genetic diversity within a population or among populations? How has habitat fragmentation affected the genetic structure of a population or species?

**Monitoring methods**—Determining which population or species should be monitored for genetic diversity would be identified when specific monitoring questions are developed. Most of the time, however, the resources available in which to conduct genetic diversity studies will be the limiting factor in their application. We therefore recommend the following criteria in the selection of populations or species for this level of monitoring: (1) species or populations that are limited in their numbers and distribution (e.g., endangered, threatened, and candidate species), (2) populations that are naturally fragmented or have become fragmented as a result of human activities and the likelihood of genetic interchange among component populations is low, (3) populations that are on the edge of a species range, and (4) species that naturally occur at low densities but may have wide distribution (e.g., large carnivores).

Lande and Barrowclough (1987) recommend that long-term population management programs should involve some form of direct monitoring of genetic variation. Three major types of characters have been used to estimate the level of genetic diversity: morphological, allozyme, and DNA sequences (Schaal and others 1991).

## Morphological Variation

The measurement of morphological variation is the most easily obtained indicator of genetic diversity. Morphological measurements often can be obtained in the field or from field specimens, not requiring laboratory studies. Another advantage is that morphological characters may be ecologically adaptive (Schaal and others 1991), meaning they are good indicators of genetic variation, local differentiation, or ecotypes. This method is often the most realistic when the biochemical analysis discussed below are impractical. Perhaps the greatest disadvantage is the assumption that morphological variation is a reliable indicator of underlying genetic variation. This assumption can be difficult to validate unless it is done in conjunction with allozyme or DNA analysis.

Several examples of the use of morphological measurements are available in the published literature. Rausch (1963) compared skull measurements of grizzly bears and brown bears from 26 different regions and found geographic variation among populations. Erickson (1945) found a hierarchical distribution of leaf-shape variation within and among groups of *Clematis fremontii* ssp. *reihlii* in the limestone glades of the Missouri Ozarks. Taylor and others (1994) used needle and cone characteristics to determine patterns of similarity of spruce (*Picea* spp.) in western North America.

Analysis of morphological variation is also commonly presented in papers dealing with biosystematics. For example, Anderson and Taylor (1983) analyzed morphological variation within a large (50-hectare) population of mixed species of *Castilleja* to determine patterns of relationships. They measured 98 characters of 100 selected plants and subjected the data to various taximetric analysis including cluster, discriminant, and principal components.

## Allozyme Variation

Allozyme electrophoresis has been the most common method used to assess genetic diversity. Allozyme analysis provides an estimate of gene and genotypic frequencies within populations (Schaal and others 1991). Such data can be used to measure population subdivision (Weir and Cockerham 1984), genetic diversity (Nei 1973), gene flow (Slatkin and Barton 1989), genetic structure of species, and comparisons among species (Taylor 1991). In general, allozyme variation does seem to be a good indicator of the overall level of variation within a genome (Hamrick 1989). However, because this analysis includes only a single class of genes, those encoding soluble enzymes, these genes may not always be representative of the variation within the genome (Schaal and others 1991).

Analysis of allozyme variation has been used to describe the genetic structure of populations of bull trout (*Salvelinus confluentus*) in the Columbia and Klamath River drainages (Leary and others 1993). Leary and others (1993) discovered that the two populations had little genetic variation within the populations, but significant genetic differences between populations, thereby indicating substantial genetic divergence. In fact, these populations would qualify as separate "species" under the ESA according to criteria established for anadromous salmonid species (Leary and others 1993).

Stangel and others (1992) used allozyme variation analysis to survey genetic variation and examine population structure among 26 populations of the endangered red-cockaded woodpecker (*Picoides borealis*). They found a large among-population component of genetic variation when compared to other bird species (Stangel and others 1992). Genetic variation was reduced in some small populations, but these small populations were important as reservoirs of unique genetic combinations (Stangel and others 1992).

## Variation in DNA

The development of recombinant DNA technologies allows the direct measurement of genetic variation as opposed to being estimated from a phenotype. There are, however, some significant drawbacks to DNA analysis. For example, the laboratory techniques are complicated, time-consuming, and costly. In addition, because only a small segment of the genome is analyzed at one time, there is a potential danger of misinterpreting conclusions about genetic variation in one type of sequence to the entire genome (Schaal and others 1991).

Restriction-site analysis of mitochondrial DNA has been used to deduce population structure (Avice and others 1987). Populations within species often have unique mitochondrial DNA genotypes that reflect the distance between populations or the presence of geographic barriers to genetic interchange (Wayne and others 1992).

There are many examples of the application of DNA technology to the study of wildlife, fish, and plant species. Leary and others (1993) used mitochondrial DNA restriction fragments in combination with allozyme analysis to study genetic variation in populations of bull trout. Wayne and others (1992) used mitochondrial DNA to measure the variability of gray wolf populations from 26 locations across their worldwide range. They discovered 18 mitochondrial DNA phenotypes in gray wolves: seven derived from hybridization with coyotes, four only in the New World, six found only in

the Old World, and one found in both areas (Wayne and others 1992). They hypothesized that genetic differences among the wolf populations may be a result of population declines and habitat fragmentation rather than a long history of genetic isolation (Wayne and others 1992).

## Conclusion

In this document, we have presented an approach to the large effort required to monitor biological diversity. We suggest a three-phase approach that includes the identification of monitoring questions; identification of monitoring methods; and the analysis, interpretation, and integration of the data into management strategies. The identification of monitoring questions and methods could be accomplished through an interdisciplinary approach, building on baseline information provided in watershed analysis, LSR assessments, and other provincial or regional assessments. We have provided several examples of methods available for land managers to use to monitor biodiversity that allow the quantification and interpretation of monitoring data.

Because monitoring biodiversity is a potentially large effort, we suggest it is better to monitor a few elements well than to spread resources too thin. In addition, monitoring should focus on elements that have relevance to key management issues. In order to accomplish biodiversity, monitoring at a variety of temporal and spatial scales, and interagency effort that is based on cooperation and collaboration will be needed. Collaboration between researchers and managers will be especially important. Managers with skills in the quantitative sciences will be needed in order to quantify and interpret monitoring information. Monitoring biological diversity is important for land managers to determine if management strategies meet the legal mandates of the ESA and NFMA, and to implement an adaptive approach to ecosystem management.

## Acknowledgments

We thank the Blue Mountains Natural Resources Institute for the impetus to produce this synthesis document to address this important issue. We also thank Bruce Marcot, Susan Piper, Lynn Starr, and Peter Morrison for their thorough review and thoughtful suggestions to improve this manuscript.

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## Appendix 1

Examples of monitoring questions and methods for each level of ecological organization (numerical and letter codes refer to steps in fig. 2, e.g., 1,B,C):

Example 1: (1) landscape level, (B) trends in habitat availability and distribution, (C) remote sensing and GIS.

Monitoring question: Is a functional interacting, late-successional ecosystem maintained where adequate, and restored where inadequate?

Monitoring method: The use of remote sensing and GIS technologies could be used to map the size, location, spatial distribution, species composition, and development of late-successional habitats over time.

Example 2: (2) community-ecosystem level, (A) management actions or natural disturbance affects on species diversity, (A) species diversity indices.

Monitoring questions: How would the implementation of the Dry Site Strategy affect species diversity of bird and small-mammal communities? Do the Dry Site treatments restore habitats for fire-climax associated bird and small-mammal communities?

Monitoring methods: The relative abundances of species within this community were sampled by using fixed-radius circular plot point counts for birds and pitfall grids for small mammals. Species diversity was estimated by using the Shannon-Weiner, Simpson and evenness indices before treatment, immediately after treatments, and at 3-year intervals posttreatment.

This monitoring protocol would address the question of how communities of species respond to restoration treatments. In addition, it allows for monitoring of community composition after the restoration activities and the vegetation responds to the treatments.

Example 3: (3) species-population level, (B) effects of management actions or natural disturbances on a species-population, (B) population estimates.

Monitoring questions: Does fire stimulate, decrease, or not affect vegetative growth and vigor of four rare plant species? Does fire affect species' density? How does fire affect reproductive potential?

Monitoring methods: Fixed-radius plots were used to gather biological and ecological information for each species. Data collected were morphological characters, such as height, leaf size, number of flowers-fruits, and clump size, and population attributes including density, percentage of cover, and population structure. Plots were placed in both burned and unburned sites, and data were collected over several years.

Data were analyzed by using analysis of variance. Results of the analysis were used to determine how certain rare plants respond to fire and subsequent changes in habitat. This information is critically important when designing restoration activities that include prescribed fire within habitats occupied by these plants.

Example 4: (4) genetic level, (B) genetic diversity among populations, (A) morphological variation and (B) allozyme analysis.

Monitoring questions: How morphologically and genetically distinct are populations of showy stickseed (*Hackelia venusta*)?

Monitoring methods: Several morphological characters were measured on plants from three of the four extant populations of showy stickseed and three other more common taxa. Morphological variables were analyzed by using multivariate analysis to determine patterns of relation among high- and low-elevation populations of showy stickseed and comparative taxa. Results of these analysis were used to show that populations of showy stickseed do not belong to the same taxon nor do they affiliate with more common taxa.

Fresh leaf material was collected from showy stickseed plants from two populations and several populations of other *Hackelia* species. Leaf samples were ground to extract isozymes, which are compared in starch gel electrophoresis. Different migration patterns of isozymes within gels can be quantified and determine genetic variation within taxa.

## Appendix 2

Commonly used landscape metrics:

### **Dominance (D)**

Equation:

$$D = H(\max) + \sum^s P(k) \times \ln P(k) ,$$

where

s = the number of habitats observed,

P(k) = the proportion of the landscape in habitat (k), and

H(max) =  $\ln(s)$ , the maximum diversity when habitats occur in equal proportions.

### **Nearest Neighbor Probabilities (q)**

Equation:

$$q(i,j) = n(i,j)/n(i) ,$$

where

n(i,j) = the number of cells of type i adjacent to type j, and

n(i) = the number of cells of type i.

### **Contagion (C)**

Equation:

$$C = 2 s \log s = \sum^m \sum^n q(i,j) \log q(i,j) ,$$

where

q(i,j) = the probability of habitat i being adjacent to habitat j, and

s = number of habitats observed.

### **Edges (E)**

Equation:

$$E(i,j) = \sum e(i,j) \times l ,$$

where

e(i,j) = the number of horizontal and vertical interfaces between cells of types i and j, and

l = the length of the edge of a cell.

## Appendix 3

Commonly used diversity indices:

### Species Richness (S)

Equation:

$$\sum n ,$$

where

n = number of species.

### Shannon Index (H')

Equation:

$$H' = -\sum p(i) \ln p(i) ,$$

where

p(i) = the proportion of individuals found in the ith species.

In a sample, the true value of p(i) is unknown but is estimated as n(i)/N.

The value of H' usually falls between 1.5 and 3.5 and only rarely surpasses 4.5.

### Simpson's Index (D)

Equation:

$$D = \sum \left( \frac{n(i) (n(i) - 1)}{N (N - 1)} \right) ,$$

where

n(i) = the number of individuals in the ith species, and

N = the total number of individuals.

Simpson's index is usually expressed as 1-D or 1/D.

## Glossary

- Abundance indices**—A count statistic that is obtained in the field and carries information about the abundance of a population of organisms. It is usually used when individuals of the species in question are difficult to observe and count or difficult to capture and mark, or when a formal estimate is too expensive or time-consuming.
- Adaptive management**—Implementing policy decisions as science-driven management experiments that test assumptions and predictions in management plans. Future management actions could then be modified based on the results of monitoring.
- Agamospermic**—Reproduction without fertilization in which embryos and seeds are formed asexually but not including vegetative reproduction.
- Allozyme variation**—A measure used to describe the patterns of genetic diversity using allozyme loci. The technique is most often carried out by using electrophoresis, by using a single class of genes, those encoding soluble enzymes.
- Autogamous**—The process of self-fertilization or self-pollination.
- Biological diversity or biodiversity**—(1) The variety, distribution, and structure of plant and animal communities, including vegetative stages, arranged in space over time that support self-sustaining populations of all natural and desirable naturalized plants and wild animals. (2) The term used to describe the various life forms, the ecological roles they perform, and the genetic diversity they contain.
- Class metrics**—Describes patch attributes such as the mean, minimum, maximum, or variance for a class of named landscape attributes (e.g., late-successional forest).
- Community**—Any group of organisms comprising a number of different species that co-occur in the same habitat or area and interact through trophic and spatial relations.
- Contagion**—A landscape pattern measurement of the extent to which a single class of vegetation or all vegetation types combined are clumped (high contagion) or patterned in a fine-scale mosaic (low contagion).
- Disturbance index**—The ratio of the area of disturbed vegetation to that of undisturbed vegetation.
- Diversity indices**—A single statistic (sometimes two or three statistics) derived from information about species richness and the abundance of individuals within a species.
- DNA variation**—The variability in DNA sequences can be measured to determine the degree of genetic variation within an organism. This method allows genetic variation to be measured directly, instead of being estimated from a phenotype.
- Dominance index**—A measure of landscape pattern that describes vegetation type composition and equitability.
- Ecosystem**—A community of organisms and their physical environment interacting as an ecological unit.
- Ecosystem function**—The flow of mineral nutrients, water, energy, or species within an ecosystem.
- Ecosystem management**—Conservation and use of natural resources that serve to maintain biological diversity, long-term site productivity, and sustainability of resource production and use.

**Ecosystem sustainability**—The ability to sustain diversity, productivity, resiliency to stress, health, renewability, yields of desired values, resource uses, products, or services from an ecosystem while maintaining the integrity of the ecosystem over time.

**Equitability or species evenness**—The degree to which relative abundances of individuals among the different species are similar.

**Fractal indices**—Describes patch shape and edge complexity.

**Functional group**—A categorization of species based on their feeding mechanism.

**Genetic**—Pertaining to genes. Genes are the basic unit of inheritance, comprising a specific sequence of nucleotides on a DNA molecule that has a specific function and occupies a specific locus on a chromosome.

**Genetic diversity**—The breadth of genetic variation within and among individuals, populations, and species.

**Genetic drift**—The occurrence of random changes in the gene frequencies of small isolated populations, not due to selection, mutation, or immigration.

**Guild**—A group of species having similar ecological resource requirements and foraging strategies, and therefore having similar roles in the community.

**Landscape**—A land area with groups of plant communities or ecosystems forming an ecological unit with distinguishable structure, function, geomorphology, and disturbance regimes.

**Landscape diversity**—The number of ecosystems, or combinations of ecosystems, and types of interactions and disturbances present within a given landscape.

**Landscape pattern metrics**—Describes attributes for all landscape classes such as mean patch size for all patches in a landscape.

**Monitoring biodiversity**—The estimation of diversity at the same location at more than one time period for the purpose of drawing inference about change.

**Morphological variation**—The degree of variation in the form and structure of an organism, with special emphasis on external features.

**Natural variability**—The range of spatial, structural, compositional, and temporal characteristics of ecosystem elements during a period specified to represent “natural” conditions.

**Patch metrics**—The attributes of individual patches of vegetation such as size, shape, edge, or nearest-neighbor relations.

**Population**—All individuals of one species occupying a defined area and usually isolated to some degree from other similar groups.

**Population viability analysis**—A process used to estimate what conditions are necessary or a population to persist for a given period of time in a given place.

**Species**—A group of organisms formally recognized as distinct from other groups.

**Species diversity**—The number of species present and the evenness or equitability (relative abundance) of each.

**Species richness**—The number of species in an assemblage or community.

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**Gaines, William L.; Harrod, Richy J.; Lehmkuhl, John F. 1999.** Monitoring biodiversity: quantification and interpretation. Gen. Tech. Rep. PNW-GTR-443. Portland, OR: U.S. Department of Agriculture, Forest Service, Pacific Northwest Research Station. 27 p.

Monitoring is necessary for an adaptive management approach and the successful implementation of ecosystem management. In this document, we present an approach to monitoring biological diversity at different levels of ecological organization: landscape, community or ecosystem, population or species, and genetic. Our approach involves identifying monitoring questions derived from regional, provincial, or watershed assessments; identifying monitoring methods; and analyzing and interpreting data to integrate into management strategies. Examples of monitoring methods, data analysis, and interpretation are provided for each level of ecological organization, beginning with the most inclusive level, the landscape. Our objective is to provide land managers with an approach and examples to develop biodiversity monitoring strategies.

Keywords: Biodiversity, monitoring, genetic diversity, landscape diversity, species diversity, ecosystem diversity.

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