ABSTRACT: Prioritizing sites as potential research natural areas (RNAs) to represent a set of target vegetation types can be a complex planning problem in which competing objectives, such as suitability and efficiency, must be satisfied simultaneously. The current U.S. Forest Service manual contains guidelines on the desired qualities of RNAs but provides little in the way of a structured methodology for selection. We propose an explicit and repeatable generic process for selecting target vegetation types and potential RNAs to represent them. The process is based on a systematic description of vegetation and environmental variation in an ecoregion, analysis of patterns of vegetation and land ownership and management, and optimization of site selection based on both vegetation and environmental criteria. Detailed ground survey and administrative review as currently practiced are integrated into the process. An application to site RNAs representing four forest types on Los Padres National Forest on the central coast of California demonstrates key aspects of the process. This reserve selection process could also be readily adapted to similar regional conservation planning programs.

Index terms: geographic information system, research natural area, reserve selection algorithm, weighted-benefits maximal covering location model

INTRODUCTION

The U.S. Forest Service Research Natural Area (RNA) Program was established in 1927 to identify, protect, and manage a representative sample of pristine areas of forest, shrubland, grassland, alpine vegetation, aquatic systems, and geologic types as well as other special features of scientific interest and importance (U.S. Forest Service 1994). RNAs also serve to

- preserve and maintain genetic diversity,
- protect against serious environmental disruptions,
- serve as reference areas for the study of succession,
- provide on-site and extension educational activities,
- serve as baseline areas for measuring long-term ecological changes,
- serve as control areas for comparing results from manipulative research,
- monitor effects of resource management techniques and practices (U.S. Forest Service 1994).

The Forest Service has not specified a formal process for identifying target vegetation types and selecting sites for establishment as RNAs, nor are there measurable criteria for determining whether the existing network of RNAs adequately represents regional ecosystem diversity. Rather, the nationwide program provides only general guidelines regarding the characteristics of good candidate sites. Forest Service guidelines recommend that new RNAs "best represent the ecological conditions needed to complete the natural area system in areas where conflicting uses are minimal. Whenever possible, select proposed areas that show no evidence of major disturbances by humans, such as livestock grazing or timber cutting, for the past 50 years" (U.S. Forest Service 1994). Guidelines for the minimum size of new RNAs state that they must be large enough to provide essentially unmodified conditions within their interiors. In the western United States, this guideline translates into a minimum area of 120 ha (300 acres) (U.S. Forest Service 1994). Also, to maintain interrelationships among terrestrial and aquatic systems, new RNAs should consist of entire small drainages, which also are easier to identify and manage on the ground.

The Forest Service Manual (U.S. Forest Service 1994) does not specify measurable criteria, however, by which to evaluate the adequacy of the RNA network or the relative quality of sites for representing ecosystems. For instance, there is no fixed number of sites or ecological types to be represented in the RNA system. Belbin (1995) distinguished between two in-
interpretations of the term "representativeness" as a conservation objective. One interpretation refers to capturing the full range of variation in conditions in an ecoregion, both among and within ecosystem types. This meaning is perhaps most relevant for purposes of ecological monitoring or conservation of biodiversity. A second meaning favors typicalness, which appears to be the major intent in the RNA guidelines. Establishing long-term research and monitoring sites in typical environmental settings means that findings from these control sites can be extrapolated more widely than is possible from unique or uncommon sites.

Selection of sites for a regional RNA system can be approached as a specific case of the reserve selection problem, which has been widely discussed in the scientific literature in recent years (Kirkpatrick 1983, Margules et al. 1988, Pressey et al. 1993, Church et al. 1996). Reserve selection is a complex planning problem in which competing objectives must be satisfied simultaneously. A number of analytical approaches have been developed to identify efficient, representative reserve systems based on principles of complementarity, flexibility, and irreplaceability (summarized in Pressey et al. 1993). These location/allocation methods rely on iterative heuristic algorithms (e.g., Kirkpatrick 1983, Margules et al. 1988) or integer programming methods (Cocks and Baird 1989, Church et al. 1996) to identify a minimum set of sites that meet stated objectives, or conversely, the maximum number of target elements represented by a given number of sites. The emphasis in these models has been on efficiency; suitability or representativeness of sites is seldom considered. Despite the wealth of publications on reserve selection modeling, we have seen no evidence that these methods have been utilized in selecting RNA sites.

Finding sites for individual target types one at a time can be inefficient in terms of the area required to represent all types. If good examples of different target types co-occur in a watershed, it may be more efficient and practical to select that watershed for both types than to designate and manage a separate watershed for each type.

Also, effective monitoring of environmental change may depend on a well-designed ensemble of RNA sites that efficiently capture floristic and environmental variation both within and among plant community types. This requires planning over entire biogeographic or administrative regions rather than piecemeal planning for individual national forests.

To provide an explicit, repeatable process and measurable evaluation criteria, we developed a systematic approach to identify and prioritize sites within an ecoregion as potential RNAs. The approach features measures of representativeness of individual sites (in relation to the target types) and of the representativeness of all targets. It makes use of geographic information systems (GIS) and optimization techniques as part of a general process that is based on (1) a systematic description of vegetation and environmental variation in a whole ecoregion, (2) analysis of patterns of vegetation and land ownership and management, and (3) site selection based on both vegetational and environmental criteria. We are thus able to formally evaluate the relative trade-offs between two objectives in RNA selection: efficiency of proposed sites at representing target types, and favoring of higher quality sites.

In this paper we first describe the current U.S. Forest Service RNA Program and then propose a generic process for selecting target types and prioritizing sites. We then demonstrate application of the process in a case study in which the goal was to represent four forest types on Los Padres National Forest (LPNF) on the central coast of California. The case study is a slightly simplified example of the generic process so that readers can follow the steps. Nevertheless, it is sufficiently complex to demonstrate the salient features and key analytical decision points of the process.

THE RESEARCH NATURAL AREA PROGRAM

The current Forest Service Manual (U.S. Forest Service 1994) does not specify a procedure for selecting a comprehensive set of sites that efficiently represents all target vegetation types. Committees in each Forest Service administrative region decide what the target types should be and allow individual national forests to provide the most representative sites. The search for potential sites on a national forest is often done by a process of elimination, using map layers in a GIS to identify lands that do not meet one or more criteria listed above. Lands containing the target type that remain after this screening step are evaluated further. The most promising sites are then scrutinized on the ground by Forest Service personnel and other scientists and, if recommended, are proposed through the regular Forest Service land management planning process and associated environmental analyses required by the National Environmental Policy Act (NEPA). The regional forester of the Forest Service region in which the site is located is ultimately responsible for establishing new RNAs. The process may be repeated independently for each target type.

This screening approach may be adequate in some circumstances, such as where the screening removes all but a few sites and the choices between them are relatively straightforward. We suggest that in complex situations, a more formal basis is desirable for identifying a set of alternative sites and systematically choosing among those sites based on the degree to which they meet the goals of representativeness, pristine condition, size, and configuration. It is not generally feasible to subject all occurrences of a type in a large region to detailed ground survey. We hypothesize, however, that mapped information on vegetation, environmental factors, and land management can be used to select target types and then reduce and prioritize the set of candidate sites to a few alternatives that can be analyzed in detail. Ideally, any map-guided procedure for initial screening and prioritization should be explicit, repeatable, and successful at locating a smaller set of the best candidate sites.

The Forest Service RNA Program in California began in 1931, but it was not until 1977 that a formal process was formulated to select RNAs from the rich array of vegetation types represented on California's national forest lands (Keeler-Wolf 1990).
The state was divided into eleven geomorphic provinces, and target elements were assigned to each province. Target elements included 40 major vegetation types with extensive geographic distribution and 15 minor types of limited distribution. In 1990, following the publication of a natural community classification system by the state’s Natural Heritage Division (Holland 1986), a number of nonforested, riparian, and aquatic types were added to the original target elements. The current selection process has been very effective in identifying areas that contain occurrences of types that are noteworthy for their condition and structural and floristic properties. However, it is not possible using the current approach to measure the degree to which a site typifies floristic and environmental properties of the type within a region. Therefore, the process could be strengthened by a more systematic and repeatable method for identifying and selecting target types and alternative sites.

THE PROPOSED PROCESS

Six steps are proposed in our generic process for identifying and establishing potential RNA sites.

1. Selection of Target Types: identify the set of plant communities to be represented in RNAs.
2. Quantification of Environmental Variation: characterize regional environmental variation within the target types.
3. Calculation of Site Suitability: characterize the suitability of sites to represent each target type.
4. Preliminary Site Selection: apply a reserve selection model to identify alternative sets of the most efficient and/or suitable sites to represent target types.
5. Validation: evaluate the best sites in the field.

Note that selecting sites (step 4) is just one of the six steps. It is first necessary to systematically review the pool of community types in an ecoregion to determine which should be represented in RNAs, then to examine which environments best represent the target types and where these occur. Below, we elaborate briefly on the six steps.

Selection of Target Vegetation Types

We suggest that the classification of types conform to the proposed National Vegetation Classification System (Federal Geographic Data Committee 1996) at the alliance level, which is defined by dominant canopy species within structural formations. Targets should ideally be set within ecoregions (e.g., sections in the ECOMAP classification; Bailey 1995). Not all types occurring in an ecoregion should necessarily be represented in Forest Service RNAs, however. Types that only marginally occur on National Forest System lands perhaps should be the responsibility of other land managers. The purpose of this step is to determine which types the Forest Service should be responsible for representing in RNAs. The current Forest Service Manual (U.S. Forest Service 1994) offers little guidance on how this should be done. We recommend that a measurable criterion be used. For instance, one possible criterion could be that target types have greater than 50% of their current distribution in an ecoregion on National Forest System lands. Exceptions could be made for special cases.

Quantification of Environmental Variation

Because designation of an RNA involves long-term land allocation, one must consider the probability that a site will ensure persistence of a community at that location. By quantifying the amount of environmental variability that is exhibited for each vegetation type across a region, one can formally describe the “typical” environmental characteristics for each type. In taking this approach, one hopes that the relatively small amount of land in reserves adequately represents the full range of variation exhibited across a given ecoregion (e.g., Mackey et al. 1988, Cumming et al. 1996). Having research sites that are typical or representative implies that scientific knowledge gained there can be applied across the greatest geographical extent.

What is needed is a quantitative criterion, such as the central tendency, by which to measure representativeness and to compare sites (Bellin 1995). As is well documented, the distributions of many plant species and communities exhibit unimodal patterns of frequency or abundance along environmental gradients (e.g., Whittaker 1975). For instance, Engelking et al. (1994) found that although Gambel oak (Quercus gambelii Nutt.) occurs at Gray Ranch in southern New Mexico, that site is outside the range of highest probability of occurrence as measured from climatic and geologic variables. Thus Gray Ranch would not be a very good choice as the sole representative site for this species. (It might be appropriate as one of a series of sites to represent the variation of environments in which Gambel oak occurs, but this level of representation is beyond the scope of the RNA mission). Sites near the margins of the environmental gradients for a community or species would generally be the most sensitive to changes in conditions that may alter community composition, structure, and functioning. Occasionally, these sites might follow entirely different successional trajectories following disturbance or extreme conditions. The variation in environmental characteristics and identification of typical environments should be quantified so that site suitability can be evaluated and down-weighted if a site is considered atypical for the vegetation type in question. Ideally, the variables used (e.g., elevation or mean weather conditions) should be relatively stable over the relevant time scales.

Calculation of Site Suitability

The selection of candidate sites presupposes we have a set of sites in mind from which to select. Because the RNA guidelines suggest watershed units as the appropriate management boundaries in most circumstances, some division of the national forest into hydrologic units is desirable. This step then relates the characteristics of the target types to the pool of candidate sites. Some Forest Service staff use a GIS screening process to eliminate lands that have been heavily modified by past land uses or that would potentially conflict with current resource management
objectives. The binary (in or out) screening process runs the risk of eliminating from consideration all lands for a given target type. We propose instead that site condition or resource conflicts be incorporated into the suitability rating process rather than simply deleting sites below some threshold. Other potential factors for site suitability include patch size and site representativeness.

**Preliminary Site Selection**

Some situations may not be so complex as to need a formal selection model. If target types are rare and only occur in a few locations, or if most sites with a target type are clearly unsuitable because of past or current land uses, the selection may be obvious by inspection. Similarly, if the planning problem were merely to select the most suitable site for each type, simply ranking sites by their suitability index would be sufficient. In real land allocation decisions, however, the problem is often so complex that a computer algorithm is required to evaluate the large number of potential combinations of sites. In this step, the “best” site or sites to represent one or more of the target types for potential RNA designation are identified. This selection can involve trade-offs between picking the most efficient set of sites (i.e., least number of sites with the most types present) and picking the most suitable sites. The trade-offs between efficiency (least number of sites) and suitability (best sites) become difficult to evaluate without the aid of mathematical models. These models can sort through the potentially complex data sets and select optimal, multi-objective solutions more reliably than human analysts. No single solution may provide an unequivocal selection, but by modifying model parameters (e.g., weights for suitability levels, number of sites to be selected), planners can quickly explore the “decision space” of reasonable alternatives. Sites that are repeatedly selected in various alternatives will become apparent as likely choices in any final network of sites.

**Validation**

There will always be a need to conduct field ecological surveys of the most promising sites to confirm biotic composition, determine site condition, and collect other site-specific data not available in the regional GIS database. Although this step is critical in practice, we do not discuss it further in this paper.

**Nomination and Establishment**

The last steps in the process are clearly prescribed by the National Environmental Policy Act and by U.S. Forest Service land management planning regulations. We mention them here only for completeness.

**THE CASE STUDY**

**Study Area**

We selected the Central Western biogeographic region of California, as described in Hickman (1993) (Figure 1), for applying our RNA selection process because data had already been compiled for this region by the California Gap Analysis Project (CA-GAP; Davis et al. 1998). This region is geographically similar to the combination of two ECOMAP sections (261A, Central California Coast and M262A, Central California Coast Ranges; Bailey 1995), but the required spatial data were not available for these ECOMAP sections.

The Central Western California region contains the Central Coast Ranges and the valleys between the Russian River north of San Francisco Bay and the Santa Ynez Mountains near Santa Barbara on the south. The region extends inland from the Pacific Ocean to the edge of California’s Great
Central Valley. Whereas half of California is publicly owned, only 25% of the Central Western region is public (Davis et al. 1998). The U.S. Forest Service is the principal public land steward, and LPNF is the only national forest within this region. Other public agencies manage very small percentages of the total public land area.

LPNF (Figure 1) is divided geographically into two segments, the Monterey Ranger District (MRD) in the north and the Main Division in the south. The portion of the Main Division outside the Central Western region (Figure 1) did not contain the target vegetation types and was not analyzed in this study. The MRD covers 122,786 ha in the rugged Santa Lucia Mountains. At various locations along the coast, mountains rise from sea level to elevations of more than 1,500 m within a distance of 4 km and form a series of steep, closely set northwesterly-southwesterly trending mountain ridges and deeply dissected drainages that continue inland for 25 km before descending into the Salinas Valley.

**Target Vegetation Type Selection**

The Forest Service had expressed interest in exploring representation of mixed evergreen forest in our pilot study. However, this plant community is very heterogeneous, consisting of many combinations of dominant tree species, possibly requiring several sites to represent the full range of variation. Therefore, we used quantitative methods to identify specific types of mixed evergreen forest and then select appropriate target types for LPNF from that set.

Mixed evergreen forest occurs throughout much of the area of California's coastal mountains and is the dominant forest type at middle elevations where the Mediterranean climate is not ameliorated by summer fog (Barbour and Major 1977). This forest type ranges from 10 to 30 m in height and is composed of various mixtures of two or more mostly broad-leaved evergreen tree species such as tan-oak (Li-thocarpus densiflorus [Hook. & Arn.]] Rehd.), madrone (Arbutus menziesii Pursh), coast live oak (Quercus agrifolia Nee), canyon live oak (Q. chrysolepis Liebm.), interior live oak (Q. wislizenii A.DC.), and California bay (Umbellularia californica [Hook. & Arn.]] Nutt.). Winter-deciduous species like bigleaf maple (Acer macrophyllum Pursh) and California black oak (Q. kelloggii Newb.) may also be components of this forest (Sawyer et al. 1977, Holland 1986, Hunter 1995).

Mixed evergreen forest is divided into two provinces based on the importance of Douglas-fir (Pseudotsuga menziesii [Mirbel] Franco). Pseudotsuga menziesii is lacking or is but a minor component in the study area but is common in mixed evergreen forest north of the Central Western region of California.

There are many phases of this forest in which one or more species change dominance depending on latitude, aspect, elevation, soil type, and distance inland from the coast. For example, the Quercus wislizenii phase occupies coastal canyon bottoms and north-facing slopes below 700 m. The Quercus agrifolia phase extends inland along lower slopes and canyons, while the extensive Quercus chrysolepis phase inhabits more inland sheltered slopes and ravines (Talley 1974).

We decided to subdivide mixed evergreen forest into more homogeneous types and then, from among these, to select which ones should be represented in RNAs. To subdivide the mixed evergreen forest community, as described in Holland (1986), we used a vegetation map and associated data on dominant overstory species prepared for the entire Central Western California region by the CA-GAP using methods described by Davis et al. (1995, 1998). This regional vegetation map delineated 3,595 landscape (or map) units with an average size of 1,037 ha, and documented the distribution of 152 dominant plant species, 76 community types, and 15 land use/land cover types. Each map unit was described by up to three upland community types. For each type, up to three dominant overstory species were recorded. The CA-GAP land-cover map contained 425 map units with dominant species data for 13 trees and 4 shrubs associated with mixed evergreen forest.

We classified these species combinations using two-way indicator species analysis (TWINSPAN; Hill 1979). TWINSPAN uses reciprocal averaging to ordinate the matrix of species by map units and then to hierarchically subdivide the species combinations into classes. Uncommon species combinations occurring in less than three map units remained assigned to a general mixed evergreen forest class. Based on the TWINSPAN analysis, 23 widespread types of mixed evergreen forest were recognized. The appropriate map units in the original CA-GAP vegetation map were reassigned to these 23 types. This revised land-cover map was overlaid with the CA-GAP map of land ownership to determine the share of each type represented on LPNF.

Table 1. Percentage ownership and mapped distribution of the four mixed evergreen forest target types in the Central Western region of California. Species codes, following U.S. Natural Resources Conservation Service (1997), are: ARME = Arbutus menziesii (madrone); LIDE3 = Lithocarpus densiflorus (tan-oak); QUAG = Quercus agrifolia (coast live oak); QUCH2 = Q. chrysolepis (canyon live oak). LPNF = Los Padres National Forest, CW = Central Western.

<table>
<thead>
<tr>
<th>Type Code</th>
<th>Dominant Species</th>
<th>% Land on LPNF</th>
<th>% Land on Other Public</th>
<th>% Land on Private</th>
<th>Mapped Area (km²) in CW Region</th>
</tr>
</thead>
<tbody>
<tr>
<td>81112</td>
<td>QUAG</td>
<td>75.5</td>
<td>2.4</td>
<td>22.1</td>
<td>53.9</td>
</tr>
<tr>
<td>81113</td>
<td>QUAG</td>
<td>59.4</td>
<td>9.0</td>
<td>31.6</td>
<td>26.0</td>
</tr>
<tr>
<td>81117</td>
<td>QUAG</td>
<td>51.3</td>
<td>17.6</td>
<td>31.1</td>
<td>32.0</td>
</tr>
<tr>
<td>81119</td>
<td>ARME</td>
<td>80.1</td>
<td>7.1</td>
<td>12.8</td>
<td>190.8</td>
</tr>
</tbody>
</table>
related with elevation, which can be used as a surrogate for climatic variables such as temperature and precipitation. A modified measure for elevation was chosen as the environmental characteristic to use in determining whether a specific site was typical for a vegetation type for this case study. Variation due to changes in both elevation and latitude is captured through data representing “equivalent elevation” of an area, which is the actual elevation derived from a digital elevation model that was adjusted to account for distance from the equator (Schoenherr 1992). As such, equivalent elevation is useful only in comparing sites and is higher than actual elevations for central California (e.g., mixed evergreen sites for this case study have an average equivalent elevation of approximately 3,500 m). The latitudinal adjustment used was 0.625 m of elevation per km of northness and has been added to a digital elevation model with a 100-m cell size. Boxplots of the variation in equivalent elevation of the four target vegetation types (Figure 3) show that types with 

Quantification of Environmental Variation

The topographic moisture gradient, based on slope and aspect, also strongly controls vegetation patterns (Whittaker 1975). The elevation data with 100-m resolution are too coarse to use for computing meaningful slope angle and aspect values. Other factors such as distance from the coastline or mean annual precipitation did not appear to explain much of the variation within the habitats of the target types. Notice for example in Figure 2 how the four vegetation types tend to occur in relatively narrow bands of roughly equal distance from the coast (left edge of the maps). We therefore elected to use a single variable, equivalent elevation, to characterize environmental variation.

The spatial units for characterizing environmental variation are the polygons that result from GIS overlay of the CA-GAP vegetation map (Davis et al. 1995) and planning watersheds delineated by the California Department of Forestry and Fire Protection (Menning et al. 1997). Each vegetation-watershed map unit was then
Figure 3. Boxplots for regional distributions of equivalent elevation for target vegetation types in the Central Western California region. The notched line in the center of a box indicates median value, and the size of the notch indicates approximate 5% confidence intervals. The size of boxes indicates the quartiles, and the outermost whiskers indicate 1.5 times the interquartile range; individual values outside the whiskers are shown as hollow circles.

characterized by overlaying a grid representing environmental variation. For each target type, we calculated statistics characterizing environmental variation across its entire range in the ecoregion. These statistics allowed us to compare the environmental characteristics of each site with those of all sites in the ecoregion in which target types occur.

Calculation of Site Suitability

Based on the RNA Program's guideline recommending selection of entire small drainages for RNA status, we adopted Calwater planning watersheds (Menning et al. 1997) as the set of sites to which to apply our analysis and selection process. These watersheds were delineated by an interagency committee on 1:24,000-scale topographic maps and are used by the California Department of Forestry and Fire Protection to evaluate cumulative watershed effects of timber harvest plans. In the study area, they averaged 2,750 ha in size and are thus considerably larger than the RNA Program's recommended 120-ha minimum area for the western United States. We are not presuming that the entire planning watershed would necessarily be designated as an RNA, although this is certainly possible. However, this scale of analysis is compatible with the resolution of available digital biological and environmental data, and is consistent with our overall goal of screening and prioritizing areas for more detailed analyses. Furthermore, the larger planning watersheds usefully define the landscape-level context of sites where the target types occur. Ultimately the relative merit of different sites for representing a type in an RNA depends not only on local factors but also on the broader spatial context that influences disturbance regime, responses to environmental change, management strategies, and so forth.

We based site (watershed) suitability for preliminary selection as an RNA on three factors: (1) the spatial extent of all mixed evergreen forest types (target and nontarget) in the watershed, (2) the spatial extent of the target types in the watershed, and (3) the degree to which environmental conditions in the watershed typify conditions within which the target types are found in the region. A suitability index was calculated for each target type in each site in which it occurs. Because the Monterey Ranger District occupies steep, inaccessible terrain, there has been little impact from land uses and few conflicts between research and resource management. It was unnecessary, therefore, in this case study to incorporate these factors into the suitability scoring.

To determine the first factor, we assumed that a small, isolated patch of a target community surrounded by distinctly different types is more vulnerable to destruction by a disturbance event than a large patch would be. Accordingly, we computed the proportion of the planning watersheds in all mixed evergreen forest types combined (i.e., both target and nontarget types). Watersheds with less than 15% coverage by mixed evergreen types and less than 300 ha of the combination of the four target types on Los Padres National Forest were deleted from the set of candidate sites. Consequently, some watersheds appear to contain a target type in Figure 2 but are classified as "Not Suitable" in Figure 4. After the screening step based on extent of mixed evergreen forest in the planning watershed, 24 sites remained that could potentially represent one or more target types. Types 81112, 81113, and 81117 each occur in 5 watersheds (although they are not the same 5 watersheds for all three target types), while type 81119 occurs in 18 (Table 2).

Our second premise is that larger contiguous areas of the target vegetation type are more suitable for RNA selection than smaller areas because they are more likely to experience biophysical conditions and disturbance regimes characteristic of that type. An area suitability index was computed for each map unit. The area index was set to 0.0 if the area in a single vegetation map unit was less than 75 ha, while areas greater than 300 ha were assigned an index.
value of 1.0. All intermediate sizes were scaled linearly between 0.0 and 1.0.

Suitability based on environmental factors was calculated independently for each of the four target types. The absolute value of the difference between regional median equivalent elevation for the type and the map unit’s median elevation was linearly scaled from the minimum to maximum values, with 1.0 assigned to the smallest difference and 0.0 for the largest or least typical elevation.

Three steps were required to determine the suitability of each site to represent each target vegetation type. First, an overall suitability for each target type in each vegetation map unit was calculated simply as the product of the area suitability and environmental suitability, again resulting in potential values between 0.0 and 1.0. (The products were not rescaled from 0.0 to 1.0, however.) Second, for each target type, the maximum suitability index value of all map units in a watershed was selected as the site (watershed) suitability for that type. Third, the numerical suitability index of a watershed for each type was converted into ordinal scores with low (between 0.0 and 0.50), medium (0.51 to 0.75), and high (0.76 to 1.0) categories.

To make this scoring method clearer, let us work through a specific example. The Blue Creek watershed contains several landscape units containing vegetation type 81119. The largest area of this type in any of the landscape units is 429 ha, which (being greater than 300 ha) is given an area suitability score of 1.0. The deviation of the median equivalent elevation of this landscape unit from the median of the type in the ecoregion is 157 m. The environmental suitability score is given by -0.001692 x deviation + 1.0050761, or in this case, 0.739. The total suitability index is the product of the area and environmental suitability scores, or 1.0 x 0.739 = 0.739. This score is just below the threshold for a high rating, and Blue Creek watershed is therefore rated as medium suitability for type 81119.

The site suitability ratings for each target vegetation type are listed by watershed in Table 2 and depicted graphically in Figure 4. No watershed had high suitability for more than a single type. All four target types had high, medium, and low ratings in at least one watershed, except for 81117 for which no watershed site was rated higher than medium suitability.

**Preliminary Site Selection**

The site selection problem was formulated as an optimization model that can be used to explore trade-offs between efficiency and suitability. The basis of the model is a maximal covering location problem (MCLP) model, which involves maximizing the number of types represented, or “covered,” while selecting a fixed number of sites (Church et al. 1996). Standard operations research techniques can be used to find an optimal (i.e., most efficient) solution to such a model. It is possible that multiple solutions that are optimal might exist (i.e., that cover the same number of target types with the same number of sites). We modified the original model (Church et al. 1996), which treated all sites with a target element as equally suitable, to accommodate variations in site suitability. Such a formulation is technically referred to as a weighted-benefits MCLP model (Church and Roberts 1983).

The model’s objective function maximizes a weighted sum of the number of target types represented. If a target type is represented at
Table 2. Suitability ratings of watersheds in the Monterey Ranger District and results of the alternative RNA selection model runs. A blank in the suitability ratings indicates the watershed is unsuited to be a representative of the vegetation type. H = high, M = medium, L = low; X indicates watershed was selected in the alternative, * indicates a tie between equally optimal single sites in alternative 1b. See Table 1 for explanation of vegetation types.

<table>
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<th>Watershed</th>
<th>Suitability Ratings by Type</th>
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<td></td>
<td>81112 81113 81117 81119</td>
<td>1a 1b 2a 2b 2c 3 4</td>
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<tr>
<td>Big Creek</td>
<td>H</td>
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<tr>
<td>Blackrock Creek</td>
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<td></td>
</tr>
<tr>
<td>Blue Creek</td>
<td>L</td>
<td></td>
</tr>
<tr>
<td>Bruce Fork</td>
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<td>Carrals Spring</td>
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<tr>
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<td>M</td>
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</tr>
<tr>
<td>N. Fork Big Sur R.</td>
<td>M H</td>
<td>*</td>
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<tr>
<td>S. Fork Big Sur R.</td>
<td>H</td>
<td></td>
</tr>
<tr>
<td>S. Fork Little Sur R.</td>
<td>H</td>
<td></td>
</tr>
<tr>
<td>Salsipuedes Creek</td>
<td>H</td>
<td></td>
</tr>
<tr>
<td>Upper Tassajara Ck.</td>
<td>M L</td>
<td>X</td>
</tr>
<tr>
<td>Upper Little Sur R.</td>
<td>L H</td>
<td></td>
</tr>
<tr>
<td>Ventana Creek</td>
<td>L</td>
<td></td>
</tr>
<tr>
<td>Vicente Creek</td>
<td>L</td>
<td></td>
</tr>
<tr>
<td>Willow Creek</td>
<td>L</td>
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</tr>
</tbody>
</table>

Our intent was to demonstrate the site identification, evaluation, and selection process as a case study, not to recommend any specific sites for RNA establishment. Nevertheless, an examination of the pattern of selected sites in the various alternatives can provide some insight into the functioning of the selection model and particularly the trade-offs between efficiency and suitability (Table 2). Lion Creek was selected as the most efficient site in Alternative 1a, being the only watershed with three target types in it. In fact, this site was identified by inspection, rather than by running the model. However, Lion Creek was rated as a low suitability site for types 81113 and 81119, so this site would be relatively poor for representing them. In contrast, if high suitability is valued as in alternative 1b, then the North Fork Big Sur River or Lower or Upper Tassajara Creek would be the best site, although each includes only two vegetation types, one with high and one with medium suitability. The types covered at these three sites are not the same, however, so there would be a trade-off between types, which could be resolved by giving more preference to one of the target types.

All four target vegetation types can be covered in any of several combinations of just two watersheds (e.g., Lower Tassajara Creek and Carrals Springs). Alternatives 2a, 2b, 2c, and 3a each covered at least one target type in a low suitability site. The only way to ensure that only sites with at least medium and high suitability are selected is to increase their relative weights as in alternative 4.

Lower Tassajara Creek was selected in five of the seven alternatives and Carrals Spring in four. These two watersheds, therefore,
Table 3. Parameters of the alternative RNA selection model runs. See text.

<table>
<thead>
<tr>
<th>Alternative</th>
<th>Number of Sites to Select</th>
<th>Weight for High Suitability</th>
<th>Weight for Medium Suitability</th>
<th>Weight for Low Suitability</th>
</tr>
</thead>
<tbody>
<tr>
<td>1a</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>1b</td>
<td>1</td>
<td>4</td>
<td>3</td>
<td>1</td>
</tr>
<tr>
<td>2a</td>
<td>2</td>
<td>3</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>2b</td>
<td>2</td>
<td>4</td>
<td>3</td>
<td>1</td>
</tr>
<tr>
<td>2c</td>
<td>2</td>
<td>3</td>
<td>3</td>
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</tr>
<tr>
<td>3</td>
<td>3</td>
<td>3</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>4</td>
<td>4</td>
<td>10</td>
<td>4</td>
<td>1</td>
</tr>
</tbody>
</table>

appear to be robust candidates for RNA status, regardless of the set of weights applied to the model. Rocky Creek best complements these two sites in alternatives 3 and 4 since it is the only site with high suitability for type 81112. Most other watersheds were only selected in one alternative each, suggesting that they are contenders but are more sensitive to the model parameters.

CONCLUSIONS

We have proposed a planning process for an explicit and repeatable method of identifying target types and selecting sites worthy of further study as possible research natural areas. The process encourages an ecoregional perspective in selecting both types and sites, so its implementation might include more than one national forest. Within this regional context, target types can be chosen that are primarily the responsibility of U.S. Forest Service managers, and the most representative sites for each type can be identified. The process includes a series of decision points regarding which target elements to represent, which environmental (and spatial extent) factors determine site suitability and how they should be calculated, and what weights on suitability levels to use in the selection algorithm. Throughout this process there is latitude in the choices made and criteria used, to allow the flexibility to respond to particular circumstances of decision-making style, other resource management issues, and ecological differences among geographic regions. Different alternatives can be generated by varying these criteria, weights, or number of sites to be selected. These alternatives could then be used as input into the national forest land management planning process to evaluate the effects of RNA establishment on other resources and socioeconomic factors.

Prioritizing sites as potential RNAs to represent a set of target vegetation types is a complex planning problem in which competing objectives must be satisfied simultaneously. The two most important objectives are that the most representative, or suitable, site for each type should be selected and that the least amount of area be withdrawn from resource utilization. In practice, these suitability and efficiency objectives may conflict, so that some level of compromise will be required. For instance, in this case study the most efficient site covered three target types that were relatively lower quality, while the most suitable site covered only two. Thus the relative importance of efficiency and suitability to a particular decision maker must be recognized in the planning process. The advantage of the proposed process is that such trade-offs in benefits can be explicitly stated and quickly explored.

In cases involving a single plant community type and a small number of sites, evaluating the set of sites and selecting the most suitable can be done with simple tools. Problems with many target types and sites, covering the full range of vegetation on a national forest, become increasingly complex. The approach described in this paper combines the spatial analysis capability of a geographic information system with optimization modeling to prioritize sites. Multivariate environmental factors and spatial relationships can be modeled more objectively and effectively than polling a panel of local experts for their thoughts about good sites. This statement by no means implies experts are replaced by a computer model. On the contrary, expert knowledge is essential throughout this process, from identifying target types, to defining what factors make a site suitable, reviewing the selection model results, and surveying and evaluating the set of potential sites. The proposed process only makes the thought processes of the experts more visible and repeatable and provides geographical tools for sorting through a complex array of data.

The approach was developed to prioritize sites as potential U.S. Forest Service research natural areas, but it could be readily adapted to similar programs involved in identifying representative sites for conservation or long-term ecological research. The spatial and statistical analyses are performed using widely available commercial software packages. The weighted-benefits covering modeling was conducted with a commercial optimization software system, but even it could be modeled in a geographic information system (Gerrard et al. 1997). Suitability can be derived from any number of environmental factors deemed relevant. For example, we are currently investigating variation in fire regime within the target communities as an additional suitability criterion. Human impacts and management issues can also be incorporated (Davis et al. 1996). The RNA guidelines encourage selection of sites that show little evidence of past human disturbance. Site condition was not used in this case study because the rugged terrain has pre-empted intensive land uses. Finding comprehensive data on land use history may, however, pose a serious obstacle to evaluating site condition.
in other regions. Despite endless permutations of suitability factors, the basic framework outlined here provides a systematic and repeatable planning process by which to reduce the number of sites in a large region to a smaller set upon which to focus field inventory for potential designation of good representative occurrences of target elements.

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LITERATURE CITED


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