# AN INVENTORY SYSTEM FOR ASSESSING WILDLIFE HABITAT RELATIONSHIPS IN FORESTS

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ABSTRACT.

A wildlife and wildlife habitat survey system has been designed to efficiently collect data on the abundance of terrestrial vertebrate wildlife species and multivariate habitat charateristics for a large number of relatively small survey plots. Five standardizing sampling methods are used to sample amphibians, reptiles, birds, small mammals, ungulates, and carnivores. Plant species, vegetation physiognomy, and physiographic characteristics are also sampled. The data are coded on forms designed to facilitate computerization, then stored in a data base management system. This survey system could form a state or regionwide data base of standard wildlife and habitat information, thus providing a common basis from which independent researchers could develop second generation wildlife habitat relationship models.

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## INTRODUCTION

This report describes the design and some applications of a wildlife and wildlife habitat survey system designed to efficiently sample wildlife species and multivariate habitat characteristics for a large number of survey plots. One of the key features of its design is the collection of wildlife and plant species information, and physiographic characteristics, all on the same relatively small plot.

The survey system can be used for a variety of purposes, such as: (1) determining the association between wildlife species and habitat characteristics, (2) ground-truthing existing habitat models, (3) monitoring the effects of habitat manipulation on wildlife, and (4) providing a comparison of the flora and fauna in different habitats.

Much of the survey system's development has occurred within the application of monitoring the effects of habitat manipulation--specifically the removal of hardwoods from mixed conifer forests--and in describing the flora and fauna of 2 oak forest habitats. Examples from the latter study are used here to illustrate some of the survey's capabilities.

We acknowledge the support of this work by the California Agricultural Experiment Station (Project 3501MS) and the USDA Forest Service, Region 5. We are grateful to the many students who have contributed to this project over the past 4 years.

## SAMPLING DESIGN

### PLOT STRUCTURE AND LAYOUT

The basic sampling unit of the survey system is a small (0.25-ha) plot (Fig. 1). Wildlife (terrestrial vertebrates), plant species and other habitat characteristics are observed in a systematic fashion on the same plot. Centered in a 50 by 50-m grid cell of the Universal Transverse Mercator (UTM) land location system, the circular design of the plot facilitates its layout in the field. With a radius of 30 m, the area of the plot is a function of the minimum home range size of the wildlife species to be sampled and the need to keep the sampling area small enough to highlight important habitat characteristics. Elements (0.001 ha) within the plot are used for sub-sampling certain habitat variables and for the systematic detection of small mammals and ungulates. The elements are arranged in a radial design which focuses the sampling effort toward the center of the plot, the point of primary interest.

A number of plots are positioned over the survey area, the layout being dictated by the design of the study. To date, our use of the system has primarily been for gathering information over relatively homogeneous areas of habitat. We have found that the most efficient layout for this application is an even distribution of the plots over the survey area using a "random start, systematic" sampling scheme over the UTM grid.

A crew of 2 people can sample 40 plots in about 3 months, providing enough effort to adequately sample up to 1,000 ha of relatively homogeneous habitat. In the comparison of 2 oak forest habitats, 2 crews of 2 persons per crew conducted the survey on 80 plots: 40 in a black-oak forest on Hogback Mountain at 1,100 m elevation in the Shasta-Trinity National Forest, and 40 in a tan oak-mixed confer forest at 850 m elevation in the Plumas National Forest. While this report focuses on the comparison of the 2 areas, the plots were distributed to achieve both pretreatment and control section on each area thus providing baseline data for an experimental analysis of the effects of hardwood removal on wildlife.

### DATA COLLECTION

Once the plots are located and marked in the field, data collection can begin. There are 4 general kinds of information collected on each plot: (1) physiographic characteristics (such as basal area, canopy closure, slope, aspect, etc.), (2) vegetation physiognomy (sometimes referred to as foliage height profiles), (3) plant species, and (4) wildlife species.

Each of these categories of information are recorded on field data sheets which provide brief instructions for each of the variables to be recorded. The data sheets are also designed to be submitted directly for keypunching, reducing the possibility of mistakes in data transference as well as cutting the work load of the field crew.

Physiographic and Physiognomic Characteristics -- On each plot, 29 variables are used to describe various physiographic, positional, and environmental features. In addition to these data, 47 variables are recorded to describe the vegetation physiognomy. On each of the 20 even-numbered elements in the plot, the physiognomy is expressed as the percentage of the element's area covered by a vegetation or ground cover category for each of 8 strata (0-40 m) above the forest floor (Fig. 1). The cover categories include live wood, dead wood, conifer foliage, broad-leaved evergreen foliage, and broad-leaved deciduous foliage. We have found that an estimate of percent cover of a cover category for a given stratum is more accurately obtained as a consensus of both crew members. After several days of training, independent estimates of cover are usually within 10 percentage points of each other. The strata heights are initially found using a range finder, but crews soon become proficient at estimating these levels. For each cover category at each stratum, a mean and coefficient of variation summarize the physiognomy over the 20 elements sampled on each plot.

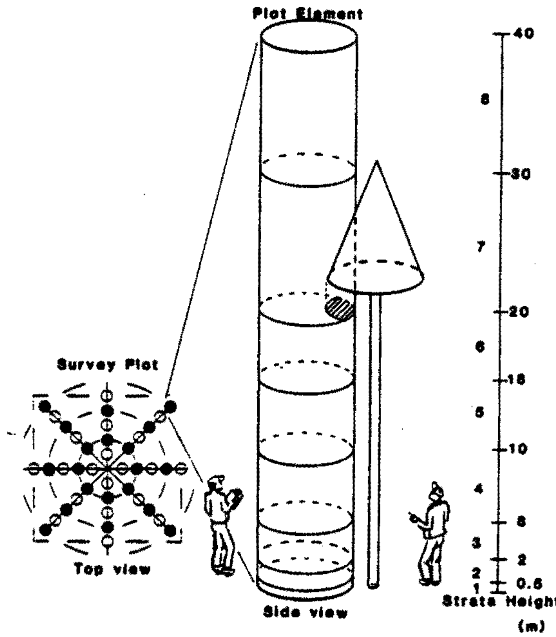


Figure 1. Illustration of the procedure for estimating vegetation physiognomy on a 50 by 50-m survey plot. See text for details.

Species Composition -- All species information is recorded in a standard format. This format is designed to guide field workers in the desired method of data collection as well as to facilitate subsequent data analysis. Each species detected, plant or animal, is recorded with: (1) a "Species code" which labels the species, (2) an "observation note" which indicates the method in which it was detected, (3) the date of detection, and (4) 2 variables which indicate the frequency or abundance of the species.

Plant Species -- All plant species are recorded on the same 20 elements sampled for vegetation physiognomy. The frequency represents the percentage of elements in which a species was detected, and the abundance is its mean percent cover over the 20 elements.

Wildlife Species -- For the wildlife species, 5 standardized sampling methods are used. Each method is designed to efficiently sample certain types of animals, including amphibians, reptiles, birds, small mammals, ungulates, and carnivores.

The birds and certain mammals (such as squirrels), are most effectively sampled with a "time-area count". This is done during the breeding season while the birds' territories are stationary and their detection is facilitated by territorial displays. The count begins 30 minutes after sunrise, and within each of the next 20 10-minute intervals the observer sits quietly in the plot and tallies the number of individuals of each bird species detected. The 2 summary variables reflect the proportion of 10-minute intervals that a species was found on the plot, as well as its relative abundance.

Pit trapping is employed to sample the herps and shrews. A 5-gallon container is sunk to ground level somewhere within the plot boundaries but outside any element. Species captured are recorded daily for 6 days. For each species captured, the summary variables record the number of individuals and their frequency of capture over the 6 days.

Small mammals are sampled with Sherman live traps and/or Museum Special kill traps. A trap is positioned within each of the 40 plot elements and run for 3 consecutive nights. The traps are baited with a mixture of peanut butter and oatmeal and checked each morning. The total trapping effort is thus 120 trap-nights per plot which is usually adequate to detect most of the resident small mammal species using the plot. The recorded values for a species caught with this method are the number of individuals captured per trap-night and the proportion of traps catching them.

Carnivores and omnivores are detected by their tracks left on the surface of 1-$M^2$ aluminum sheets blackened by a kerosene flame (Barrett, in press). A can of tuna, its top punctured by small holes, is placed in the center of the sheet. The sheets are checked every 2 days for a total of 6 consecutive days. The frequency variable for this method is the percentage of sample periods that a new track was observed, and the abundance variable is the total number of individuals of a species as evidenced by the size and shape of the tracks.

For the ungulates we count accumulated pellet groups found in the 20 even-numbered elements and record this value along with the proportion of elements containing them.

Finally, if a wildlife species or its sign is observed anywhere within the plot and it has not been detected by other methods, it is recorded as present along with the appropriate "observation note" to show how it was detected.

Timing of Sampling -- To date, most field work has focussed on the spring-summer reproductive season, however, sampling could occur at any time of year. The plots are most efficiently sampled by a crew of 2 persons with the following schedule (Fig. 2). The bird survey is the most constrained activity -- limited by the duration of the breeding season. Since the bird work is completed in the morning, the afternoons are left to continue establishing the locations of remaining plots, or, when that's completed, to conduct the pit-trapping procedure. Subsequent to a month of bird sampling, the vegetation and mammal sampling can be performed together, requiring about another 2 months of work.

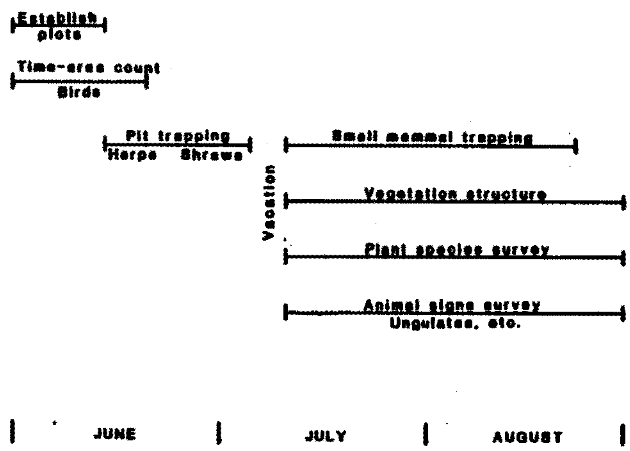


Figure 2. Sampling schedule for the spring-summer season.

## DATA STORAGE

Because a voluminous amount of data is collected in the survey, the use of a computer data base system is essential for storing, retrieving and analyzing the data efficiently. We use the Scientific Information Retrieval (SIR) data base management system (Robinson, et al. 1980), which provides compatability with most major statistical programs on the UC Berkeley IBM 4341 computer. This system has the added capability of checking data for valid values, thus contributing to the integrity of the data base.

## DATA APPLICATIONS

As an illustration of some of the many uses of information from this survey, we provide some results of a comparison between 2 forest habitats. The simplest output would be a summary list of species, both plants and wildlife, for each of the 2 areas. This would include means and standard errors of the summary variables. But because the data are in a computer usable form, more sophisticated analyses are relatively simple to perform and can provide greater insight than simple species lists. For a first look at multivariate habitat data, cluster analysis is useful in viewing the similarities of the plots based on the species sampled on them (Gauch 1982). A dendrogram reveals the similarity of survey plots based on the sampled mammal species composition. As expected, the plots sampled in the tan oak-mixed conifer habitat show a greater similarity to each other than they do to plots in the black oak habitat (Fig. 3.) This dendrogram also shows that the plots in the tan oak-mixed conifer habitat have a more homogeneous composition of mammal species than do the plots in the black oak habitat.

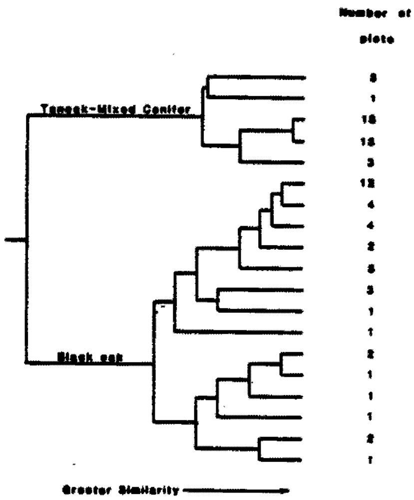

Figure 3. Dendrogram of plot relationships in 2 habitats based on the presence of 17 mammal species. Unweighted pair-group arithmetic average clustering (Sneath and Sokal 1973:230) was performed on a matching resemblance function data matrix (Ochiai 1957).

An extension of cluster analysis is a two-way coincidence table of the original data (Fig. 4). Cluster analysis was used to determine the plot order based on species composition, and to order the species based on their occurrences over the plots. Once the data are arranged in this fashion, it is easier to answer questions such as which species tend to occur together on plots, or which species are confined to one area.

## CONCLUSION

We believe that an important use of this comprehensive survey system is in the validation of models such as the Wildlife Habitat Relationship models currently being developed by the Forest Service, Region 5, in cooperation with the California Department of Fish and Game (Salwasser 1982). Such models predict the suitability of habitats for wildlife species but have not generally been "ground-truthed" to determine their accuracy.

On a state or region-wide basis, a survey system such as this would be useful for establishing a common data base of wildlife species and habitat characteristics (Myers and Shelton 1980). The information would be in a standardized form that researchers could then tap to produce second generation wildlife habitat relationship models. By incorporating such a system into a multi-resource inventory program, with appropriate sampling schemes involving multi-stage sampling, the cost would be minimal relative to the benefits provided.

## Survey Plots

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|         Black oak         |     Tanoak-Mixed Conifer     |

4744455677744555565574456667667775674466 2  12132233 313 223111812233433  121 12   Species
19431678716857324901572864983322500594162443489019276921526856001573604579738830

----------------------------------------------------**----**-------*--*----*---- Didelphis virginiana
----------------------------------------**--------*****-*****------------******- Neotoma fuscipes
----------------------------------------**********************--**************** Peromyscus boylei
----------------------------------------****************--*-*------****------**- Sorex trowbridgei
----------------------------------------------******------***---------*--------- Spilogale putorius
***-***********----************************************************----***-**--- Odocoileus hemionus
**-*******************************----****************************************** Scapanus latimanus
------------------*---***************--**********-*-----**********-***---------- Peromyscus maniculatus
************---*****-*********----*------**---*-------------**---------***------ Thomomys sp.
-*-******************-*******-***-******---------------------------------------- Urocyon cinereoargenteus
****------------------**-------------******-----****----------**-**-*---****-*** Sciurus griseus
-------------------------------------------------**---------**------**-----*---- Reithrodontomys megalotis
-----------------------------------------*-**-------*-------***----------*--*--- Tamiasciurus douglasi
----------------------------------------------------------*--------**--*------** Felis domesticus
---------------------------**-----------------------------------------------***- Procyon lotor
--*-----------------------------------------------------*---------------*-*----- Mephitis mephitis
-------------------****--------------------------------------------------------- Sorex ornatus
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Figure 4. A two-way coincidence table of the distribution of mammals in 2 habitats. The sampled presence of a mammal on a plot is indicated by an asterick (*), and its absence by a dash (-).

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