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An Assessment of Methods for Testing the Reliability of Wildlife Occurrence Models Used in Gap Analysis

Sandra M. Schaefer

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AN ASSESSMENT OF METHODS FOR TESTING THE

RELIABILITY OF WILDLIFE OCCURRENCE

MODELS USED IN GAP ANALYSIS

BY

Sandra M. Schaefer

B.S. West Virginia University, **1996**

A THESIS

Submitted in Partial Fulfillment of the

Requirements for the Degree of

Master of Science

(in Wildlife Ecology)

The Graduate School

The University of Maine

August, 2002

Advisory Committee:

المعاملة الأسلامية.
معاملة الأسلامية

William B. Krohn, Professor of Wildlife Ecology and Zoology and Leader, Maine Cooperative Fish and Wildlife Research Unit - Advisor

Daniel J. Harrison, Professor of Wildlife Ecology

Steven A. Sader, Professor of Forest Resources and Cooperative Professor of Wildlife Ecology

Randall B. Boone, Scientist, Natural Resource Ecology Laboratory, Colorado State University (ad *hoc* member)

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An Abstract of the Thesis Presented in Partial Fulfillment of the Requirements for the Degree of Master of Science (in Wildlife Ecology) August, 2002

Habitat association models designed to predict species occurrence are often tested by comparing predictions to field observations. Two types of error are then reported, omission (Yo of species not predicted but present on a site) and commission (% of species predicted but not present on a site). The purpose of this research was to assess the Maine Gap Analysis vertebrate predictions using the traditional site-specific approach and to determine what factors influence the amounts of error reported. I also developed a species-specific approach for testing the accuracy of the vertebrate predictions and compared these results to the site-specific method.

When tested with the site-specific approach, the Maine Gap habitat models were found to have'low omission errors (medians across all sites: 0.0% for both amphibians and birds, 10.0% for reptiles, and 5.4% for mammals) and higher commission errors (medians across all sites: 0.0% for amphibians, 5.0% for reptiles, 18.9% for manimals, and 91.9% for birds). Error rates were influenced by factors such as test site size and survey length, how species are defined as present, and how likely a species is to be

observed during a field survey. Using a liberal definition of avian occurrence on a site increased omission error with a corresponding decreased in commission error. Test site size and inventory length also influenced commission error. As test site size and field survey length increased, the commission error decreased $(p > 0.003)$. How likely a species is to be observed during a field survey also influenced commission error. Using an *a priori* ranking system called Likelihood Of Occurrence Ranks (LOORs) the commission error for birds decreased as the species' LOOR increased ($p = -0.87$ to -1.0).

To date, testing of multiple-species predictions has focused on calculating sitespecific error rates. Omission and commission errors are reported by taxonomic class for each site and across the entire state. An alternative approach would be to use the same data to look at the discrepancies for each species across all of the test sites. This approach would compare the predictions to field records of presence or absence for each species on sites within their range limit. Assumptions of data completeness were used to calculate error ranges that indicated model performance and variability of the error for each species. Commission *error range* was significantly correlated with species distribution ($\rho = -0.583$, P < 0.000), as well as with the likelihood of detecting a species in the field ($\rho = -0.657$, $P < 0.000$). In cases where high *error range* is reported for a species with a high LOOR the most likely cause for the over prediction is in the model. However, if a species has a low LOOR and a high *error range,* the over prediction error is likely caused by incompleteness in the test data. Site-specific and species-specific approaches to testing predicted occurrences are calculated from the same data, but provide different information. Therefore, I recommend that both approaches be used when testing predicted occurrences of multiple vertebrate species.

ACKNOWLEDGMENTS

Many thanks go out to all the people who have helped make this thesis a reality. Financial support was provided the Gap Analysis Program of the U.S. Geological Survey, Biological Resources Division (BRD) through Cooperative Agreement No. 14- 16,009- 1557, Research Work Order Number 39 to the Maine Cooperative Fish and Wildlife Research Unit. The Maine Unit is supported by the BRD, The University of Maine (UM), The Maine Department of Inland Fisheries and Wildlife, and The Wildlife Management Institute. Thanks to Dr. William B. Krohn for being my advisor and for entrusting this project to me. For believing in me and for being continually supportive, energetic, and always ready to give a pep-talk when it was greatly needed. I would also like to thank my committee members Dr. Randall B. Boone, Dr. Daniel J. Harrison, and Dr. Steven A. Sader for their mentoring, insights, and manuscript reviews. I am grateful to Raymond 07Connor who was vital to the development of a species-specific approach to testing knowledge-based wildlife-habitat models. Finally, I would like to thank Dr. William Halteman for his statistical guidance, a method of thinking that I had a hard time comprehending until being taught by Bill.

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INTRODUCTION

A commonly asked question in wildlife conservation studies is: Why do wildlife species occur where they do? Wildlife occupy areas that satisfy their behavioral and physical requirements needed for reproduction and survival (Morrison *et al.* 1992, Patton 1992). This physical area, or habitat (as defined by Morrison and Hall 2002), varies depending on the life stages of the animal or ecological scale. It has long been known that we can use the functional relationship between a species and its habitat to predict occurrences in a given area (Morrison *et al.* 1992). The recent advances in computer technology has increased the ability of biologists to create spatially explicit models to predict species occurrences over broader areas and a variety of scales Werner *et al.* 1986, Scott *et al.* 2002).

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There are two different categories of models that can be used to predict species present or absence: statistical and knowledge-based. Statistical models take occurrence data gathered at a given location and correlate the presences with environmental variables to predict where the species is likely to occur. Regression analysis, classification regression tree analysis, and Bayesian statistics, are a few examples of the more commonly used statistical models for predicting species occurrence (Fielding and Bell 1997, Scott *et al.* 2002). These models are generally complex as well as specific to a particular area and scale.

In contrast, knowledge-based models are much simpler and incorporate data fiom research which describes the associations between the occurrence of a species and environmental (biotic and abiotic) variables. In this type of model the environmental data is queried to determine if the conditions needed for a given species are present. Predicted occurrences are based on the presence or absence of habitat types that are needed by the species. Habitat Suitability Index models (Terrell and Carpenter 1997), Wildlife and Fish Habitat Relationship models of the United States Department of Agriculture (Thomas *et al.* l988), and the predictive models generated for the Gap Analysis Program (GAP) (Scott *et al.* 1993), are a few major examples where knowledge-based models are used.

Regardless of the type of predictive model, the reliability of the predictions must be assessed prior to using them in management (Fielding and Bell 1997). When assessing the accuracy of a species habitat model, carehl consideration must be given to the purpose of the model and the testing methods and metrics used (Fielding and Bell 1997). For example, if a species occurrence model is to intended to identify the habitat for a common and widely distributed game species, then the desired outcome may be realized (i-e., actual) habitat. A concern for this type of model lies in committing Type I, or false positive errors. In contrast, if the focus of the model is mapping endangered species habitat, then one may not want to be too restrictive in identifying potential locations that could be occupied. Because endangered species usually occur at depressed populations and often do not occupy all available habitat, the concern lies in committing a Type **IT,** or false negative statistical error (Fielding and Bell 1997). In the case of GAP, a national program of the United States Geological Survey (USGS) Biological Resources Division **(BRD)**, the predictive model goal is to identify where species that breed in the state may potentially occur (Scott *et al.* 1993). Because GAP deals with endangered and commonly occurring species, both false positives and negatives are common predictive errors.

As a course scale biodiversity assessment, GAP attempts to capture a complete picture in time and space of the terrestrial vertebrate community. GAP relies on knowledge-based models, integrating data fiom many locations where wildlife are studied under a wide range of environmental and population conditions. Because data fiom various sources are integrated, the habitat models used in GAP tend to over-predict rather L' than under-predict vertebrate occurrences (Edwards *et al.* 1996, Krohn *et al.* 1998, Hepinstall 2000). Currently, the level of error is estimated by comparing the GAP predictions to actual species occurrence lists (test data), obtained fiom conservation lands with long-term field inventory data (Scott et *al.* 1993, Edwards *et al.* 1996, Krohn *et al.* 1998). Error is reported for each site as commission error (percentage of species predicted by GAP that are not in the test data), and omission error (percentage of species in the test data but not predicted by GAP) for each taxonomic class. Error is then averaged across the entire state for all taxonomic classes (Csuti and Crist 1998).

Determining the cause of omission error is a fairly straightforward process (e.g., in a GAP model, omission means failure to predict a species in a location where it is known to occur). A close examination of which species were missed on each site will give insight into the cause of the error and indicate if the correction should be made to the habitat map, species range limit, or the species-habitat model. In contrast, commission is more difficult to interpret because not all of the error reported may be real. Errors are either: (1) actual errors, the species does not occur on the area where it is predicted to be; or (2) apparent errors, the species does occur there but the field surveys have failed to detect its presence. Because recommendations of Gap Analysis studies rely so heavily on

the predicted distributions of terrestrial vertebrates, it is essential that factors influencing the level of error be understood. For example, mechanical factors in the testing process, such as the size of the test sites chosen, or the length of the field inventory, may increase or decrease the commission and omission errors (Edwards et *al.* 1996, Krohn et al. 1998). Understanding which factors influence the error rates may give insight as to why some predictive models appear to be more accurate than others.

The purpose of this research was to assess the vertebrate predictions generated for Maine Gap Analysis using a site-specific (Chapter 1) versus a species-specific (Chapter 2) approach to testing accuracy. Within the site-specific method I looked at how selected factors (i.e., test site size and field inventory length, and how species are defined as present on an area) influence the omission and commission error rates. Understanding the influences of these factors will give guidance for researchers selecting test sites to be used in similar assessments. I also looked at how a species' detectability influenced commission error to determine if levels of apparent versus actual error could be assessed (Chapter 3).

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CHAPTER 1

A SITE-SPECIFIC APPROACH TO ASSESSING THE ACCURACY OF PREDICTED VERTEBRATE OCCURRENCES FROM MAINE GAP ANALYSIS

INTRODUCTION

Wildlife occurrence models that are designed to predict species presence or absence have several potential uses. Uses include but are not limited to generating maps that identify potential occurrence locations for individual species, or when analyzed in a Geographic Information System (GIs), can help to estimate the number of species in an area (i.e., species richness). Predicted occurrences can also be used to identify sites that are potentially being used by rare or endangered species. Before the habitat models are applied the quality of the predictions should be tested (Salwasser and Krohn 1982, Fielding and Bell 1997).

Habitat-relationship models, which use the functional relationship between a species and its habitat to predict occurrence in a given area (Morrison *et al.* 1992), can be tested using a variety of methods (Krohn 1996, Fielding and Bell 1997). Care must be taken when choosing a testing method so that it reflects the purpose of the original model (e.g., predicting **occurrencelnon-occurrence** of a species). For example, the Gap Analysis Program (GAP) of the United State Geological Survey, Biological Resources Division (USGS, BRD) uses knowledge-based models of wildlife-habitat associations, with other appropriate data layers (e.g., vegetation map, and species range limits) in a GIs, to predict the potential occurrence of vertebrate species known to breed regularly in a state (Scott *et al.* 1993).

Knowledge-based habitat models, such as in GAP, use data that are gathered from research spanning many years and locations. However, the predictions are snapshots of potential occurrence at one particular point in time. Ideally, the data used in testing should be for that time period. In Gap Analysis, the standard of truth comes from comparing the predicted occurrences to species lists obtained from conservation lands with long-term field inventory data (such lists are also known as checklists) (e.g., Scott *et al.* 1993, Edwards *et al.* 1996, Krohn *et al.* 1998). Error is reported by taxonomic class for multiple test sites and across the entire state in terms of commission error (percentage of species predicted by that are not on site lists) and omission error (percentage of species on site lists but not predicted) (Csuti and Crist 1998). However, there are several key factors in the testing methodology that may influence the errors reported.

One factor effecting commission and omission error is how species of interest are defined. The Gap handbook specifies that, at a minimum, wildlife habitat models should be built for all species that are non-accidental breeders in the study area (i.e., the state) (Butterfield *et al.* 1994, Csuti and Crist 1998). If the state chooses to liberally define regular breeders (e-g., species are present in the state at least once during the ten-year period of interest) then the accuracy assessment would be expected to report low commission errors with relatively high omission error. If a more conservative approach is taken when defining residency (e.g., modeling those species present during at least five of the 10 years), then interpreting the field observations to be used as test data becomes more complicated.

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Data used in model assessment should reflect the both the purpose of the model and specified time period. Test sites however, will have varying levels of available information. Some sites may have information regarding breeding regularity as well general occurrence during the breeding season. Whereas other sites may only record presence and absence of species. Because the predictions are designed to capture presence and absence on an area without any indication of use (Csuti and Crist 1998) choosing which species count as regularly occurring on a site can become complicated if frequency is not considered.

The effects of site size and survey length on predictive error rates is generally unknown. To ensure that there is some consistency in the methods, the GAP handbook established guidelines for considering test sites (Csuti and Crist 1998). Test sites should be greater than 1,000 ha and have long-term field inventory data that are independent of the data used for model building (Custi and Crist 1998). Small test sites are generally considered undesirable for use in GAP model testing because the models are not intended to capture accuracy at fine resolutions. Therefore, high levels of commission may result (Custi and Crist 1998).

Boone and Krohn (1 999) reported that sites with a short history of field inventory had higher commission errors. They suspected that the increase was likely caused by rare and reclusive species that were present on a site but were not observed during field inventory. Therefore, it can be assumed that longer surveys are more likely to have more complete species inventories. Although intuitive, this assumption has not been throughly tested.

The purpose of this study was to calculate the reliability of terrestrial (i.e., nonfish) vertebrate occurrences from Maine Gap Analysis, and to explore factors affecting the errors. More specifically, my objectives are to: (1) calculate rates of omission and commission error for each test site and over all test sites (i.e., site-specific rates); (2) assess the effect of liberal versus conservative definition of breeding species on these error rates; and (3) to examine the effect of test site characteristics on error rates.

METHODS

ACCURACY ASSESSMENT

Predicted vertebrate occurrences generated for Maine Gap Analysis (Boone and Krohn 1998a,b) were assessed using a site-specific testing approach. Test sites available for use included, one national park, one state park (Oliveri 1993), one national forest (D. Capen, Univ. of Vermont, pers. comm.), four national wildlife refuges (NWR), and two privately managed forestlands (Hagan *et al.* 1997, *J.* Witham, pers. comm.) (Figure 1.1). All nine sites had field inventories for birds. Three of the nine sites had data for herptiles and four of the nine had data for mammals (Table 1.1).

The Maine Gap Analysis models were designed to predict the presence or absence of species breeding in inland Maine during at least five years of the 10 year period studied, 1984 - 1993 (Krohn *et al.* 1998). To mirror this conservative definition for avian species, the test data used in the assessment were limited to records of species known to frequently occur on each site (usually denoted by breeding on the site). Three test sites (numbers 1,2, and 3) were included to improved the geographic distribution of sites, but did not have frequency information or breeding status for species. For these

Figure 1.1. Geographic distribution of test sites used for testing the accuracy of the predicted terrestrial vertebrate occurrences fiom Maine Gap Analysis.

Table 1.1. Test sites with available field inventory data used to assess the accuracy of vertebrate predictions fiom Maine Gap Analysis. Sites are listed according to the number of years surveyed.

^a - The field survey has records indicating frequency of occurrence or known breeding status.

presence was assumed to indicate regular occurrence (Table **1. I).** A two-way cross tabulation table was used to compare the predicted occurrences with the test **data.** These data were then used to calculate the omission error and commission error with the following equations:

 $O =$ Number of species present on a site that are not predicted Total number of species present on the site,

 $C =$ Number of species predicted on a site that are not present Total number species present on the site;

where $Q = O$ mission error and $C =$ commission error

The percentage of species matched for each site was calculated using the following equation:

 $PM =$ Number of species present and predicted on a site Total number of species present on the site.

The errors were summarized by taxonomic class with medians and ranges reported across all sites.

BREEDING STATUS

Only records of regularly occurring species were included in the original accuracy assessment. However, six of the test sites **(Sunkhaze NWR,** Holt Research Forest, Petit Manan NWR, Rachel Carson NWR, Moosehorn NWR, Mount Desert Island/ Acadia National Park) had records for species that were simply present during the breeding season (June, July and August) with no confirmation of breeding. These records were not used in the original assessment process. To determine if using liberal guidelines for defining species presence influenced omission and commission error rates, the test data

used in the original assessment were broadened to include these records of unconfirmed breeders. The revised occurrence lists were then compared with the predictions using a two-way cross tabulation table. Omission error, commission error, and percent matched were recalculated for each site and across all sites. A Wilcoxon Sign **Rank** test was used to determine if there was a significant difference between the errors reported by the two methods.

SURVEY LENGTH AND **TEST** SITE SIZE

The null hypothesis that a test site's size and the length of its field inventory has no effect on the errors reported by Maine Gap Analysis was tested using a linear regression model, alpha 0.05. Because there is a visible relationship between site size and survey length for the available test data, separate models evaluating each of these factors could not be created. A log transformation on the two independent variables was performed prior to conducting the regression to meet the assumptions of normality.

Ideally, it would have been nice to know the exact length of each inventory. In some cases, especially with the older test sites, like Moosehom NWR and Acadia National Park, this data does not exist. If the actual number of years of inventory was unavailable, the number of years in existence was used as a surrogate for inventory length. This may over estimate the length of surveys for some taxonomic classes (i.e., amphibians and reptiles) so the inventory length should be viewed as only a coarse measure of relative effort.

RESULTS

Test sites used in the accuracy assessment had field data ranging in length from one to 79 years, and a median area of 993 ha (range: 172 - 28,033 ha) (Table 1.1). For all test sites the percentage of species correctly predicted to occur in each taxonomic class was high (Table 1.2). This, along with the low median omission errors (0.0% for amphibians, 10.0% for reptiles, 5.4% for mammals, and 0.0% for birds) suggests that the predictive models missed very few species (Table 1.3). Commission error on each site (Table 1.2) tended to be higher then omission error with overall medians of 0.0% for amphibians, 5.0% reptiles, and 18.9% for mammals (Table 1.3). Commission error was especially high for birds, with an overall median of 91.9% (Table 1.3).

Broadening the definitions of species presence on six of the nine test sites **had** a significant effect on both commission and omission error rates. Mean omission error for the six sites with a liberal definition was 6.2% (\pm 2.3), significantly higher then the mean of 1.8% (\pm 2.0) reported for the same six sites when a narrower definition was used (p = 0.003) (Table 1.4). The increase in omission was observed across all sites with no apparent relationship to the test site size or survey length (Figure 1.2a). Commission error, on the other hand, significantly declined on the six sites when a liberal definition was used, mean of 18.9% (\pm 12.6). In contrast to a mean of 61.3% (\pm 47.0) for the six sites using the narrow definition ($p = 0.003$) (Table 1.4). The decline in commission error was observed across all test sites with the smaller sites with shorter field inventories showing the greatest decline in error rates (Figure 1.2b).

Table 1.2. Site-specific results of the accuracy assessment of vertebrate species predictions fiom Maine Gap Analysis.

Continued

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Table 1.2 **cont.**

a - Individual species results for each site can be found in Appendix A.

Table 1.3. Overall results of the accuracy assessment of vertebrate species predictions from Maine Gap Analysis. Medians and ranges for accuracy were calculated within taxonomic group across all sites.

 \overline{a}

Table 1.4. Effects of using a conservative versus a liberal criteria to define species presence on omission and commission errors calculated for the Maine Gap predicted occurrence models [percentage mean \pm standard deviation (range)].^a

^a - Individual species results for using a liberal definition of breeding can be found in Appendix B.

Figure 1.2. Differences in (a) omission error, $p = 0.003$, and (b) commission error, $p =$ **0.003, when a liberal versus a conservative definition of avian species presence is used. Sites arranged fiom smallest to largest (left to right).**

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On the nine sites used in the accuracy assessment, site size increased as the number of years surveyed increased (Figure 1.3). For this reason both variables were used as independents in the linear regression analysis. There was no correlation between omission error and the logs of test site size and survey length $(p < 0.63)$ (Figure 1.4a). A correlation was detected between commission error and site size and survey length ($p <$ 0.003) (Figure 1.4b).

DISCUSSION

This, and previous studies, have shown that wildlife-habitat modelscan be used to predict species presence and absence (e.g., Scott *et al.* 1993, Edwards *et al.* 1996). Scott (1 993) and Edwards (1 996) reported relatively low omission error rates with higher rates of commission. This same trend was observed with the predicted occurrences fiom Maine Gap Analysis. The low omission errors and high percentage of species matched indicates that the models can be used to predict species presence on a statewide scale (Table 1.3). The high levels of commission error indicate that more species **are** being predicted then might actually occur on the sites.

Definitions of species presence were found to have a significant effect on omission and commission error. To be included in the Maine Gap modeling process a species had to be known to breed in the state at least five of the ten years being analyzed. This rule was used to eliminate over predicting those species that only migrate through or have accidental occurrences in Maine (Boone and Krohn 1999, Krohn *et al.* 1998). The conservative definition used for the modeling process was also applied to testing the model accuracy. For birds an explicit rule was applied where only species having

Figure 1.3. Relationship of the log of site area, in hectares, and log of the number of years inventoried on nine sites with known occurrence data for terrestrial vertebrates in Maine. Numbers refer to locations of individual test sites as shown on Figure 1.1.

Figure 1.4. Relationship between the log of test site size, number of years surveyed and the percentage of avian (a) omission error $(p < 0.63)$, and (b) commission error $(p <$ **0.003).**
confirmed breeding and/or high frequency of observation were included. This conservative nature reported low omission errors and higher commission errors (Table 1.3). When the species lists were broadened to include all the species on the test data, omission error increased significantly with a matching decrease in commission error (Figure 1.2). Because Gap is a landscape level project designed to help with the conservation of biodiversity, it is felt that omission error is much more significant than commission error. If species are omitted by the predictive process then the possibility of them being omitted fiom conservation plans **are** high (Edwards et *al.* 1996). This is in contrast to commission error where conservative plans could be made that might benefit a few rare individuals or provide a place for population establishment in the **future.**

Whichever definition is used, conservative or liberal, it is important that the same definition be applicable to the data being used to test the predictions. Without this consistency error rates **are** difficult to interpret. Furthermore, if one wants to compare test results fiom individual Gap Projects the breeding definitions need to be consistent not only between species data being used develop and test the occurrence models, but across all the states.

Incorrectly defined range limits used in the Maine Gap modeling process are a probable explanation of the increase in omission error fiom using a liberal definition of breeding (Appendix C). Observations of the omitted species on the site probably do not indicate a stable breeding population and thus lends to continued support of the predictive abilities of the models. The decrease in commission error on larger test sites with longer survey lengths supports this hypothesis (Figure 1.4a). This decline indicates that the

surveys have not been conducted over a sufficient duration of time on the smaller sites to capture the presence of all species on the site. If Gap data are to be integrated for national and regional analysis, more consistent definitions of species to include in the modeling process needs to be established.

Test site size and survey effort had a significant effect on commission error. Ideally, a study needs to be done where the individual effects of these variables on error rates can be assessed. This is critical because, even though the Gap Handbook establishes a size threshold for test sites, no guidance is currently available for how long a site must be surveyed to be completely sampled for all breeding terrestrial vertebrates. The minimum size recommended for use by GAP is 1,000 hectares. Following this standard was problematic not only for Maine, but also for some of the Gap projects in the western U.S.A. (Thompson *et al.* 1996, Cassidy *et al.* 1997). *In* Maine only two sites larger than 1,000 ha had available survey data for all taxonomic classes. A third site had records for mammals and birds only, and a fourth site had data for birds only (Table 1.1). Including the smaller test sites allowed for an additional site for testing the amphibian, reptile, and mammal predictions and five additional sites for testing the avian predictions.

I found that the larger sites with longer surveys reported lower commission errors than smaller sites with shorter surveys (Table 1.2 vs Table 1.4). Because omission error was not influenced by site size or survey length (Figure 1.3) much of the commission error came fiom incomplete test data (see also Chapter 3). Longer surveys have a higher potential for capturing hard to detect species, thus decreasing the amount of commission error on a site (Boone and Krohn 1999, Chapter 3). Because test sites in each state will

vary in size and survey effort, so too will the overall accuracy results. States with the same quality habitat models, but differing test site histories would get differing results.

CONCLUSIONS

My results are consistent with earlier research (Scott *et al.* 993; Edwards *et al.* 1996) and supports the use of wildlife-habitat models for predicting the occurrence of regularly breeding terrestrial vertebrates in an area. To date, there hasn't been research that indicates what contributed to the amount of error reported. Interpretations of test metrics such as commission and omission error have been limited. This study indicates that the reliability of errors reported are influenced by factors such as test site size and survey length, and how species are defined as present. Care must be taken in selecting test sites (longer surveys and larger sizes are better) and in defining species presence (e.g., a species regularly breeds on the site if there are records of it breeding on the site 8 out of the ten year period) to ensure that the predictions can accurately be used in conservation studies.

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CHAPTER 2

A SPECIES-SPECIFIC APPROACH TO ASSESSING THE RELIABILITY OF PREDICTED VERTEBRATE OCCURRENCES FROM SPECIES-HABITAT MODELS

INTRODUCTION

In many wildlife and conservation studies it is necessary to predict where wildlife species occur. Vertebrate occurrences can be predicted by several different model types. For example, a statistical relationship between the animal's presencelabsence and environmental variables can be used to create the model. **Or** a thorough review of the literature can be used to determine what environmental variables constitute habitat for the species in question (Scott *et al.* 2002). The predicted distributions can then be mapped based on the location of the habitat variables (Morrison *et al.* 1992, Scott *et al.* 1993). Regardless of the prediction method, the occurrences are only a prediction, and the output of the habitat model should be tested against an independent measure of presence or absence (Krohn 1996, Fielding and Bell 1997).

The complexity of species-habitat relationships, incomplete habitat data, and limited availability of complete field inventories, makes the process of testing predicted occurrences difficult (Edwards *et al.* 1996; Krohn 1996, Fielding and Bell 1997, Schaefer and Krohn 2002). These complexities are greatly increased when the distributions of multiple species are predicted and mapped, as in the Wildlife and Fish Habitat Relationships Program (Nelson and Salwasser 1982; Block *et al.* 1994) or the Gap Analysis Program (GAP) (Scott *et al.* 1993). Factors that were problematic with just one

species are now multiplied across many species and taxonomic classes (i.e., amphibians, reptiles, mammals, and birds).

To date, testing of wildlife-habitat models that predict the occurrence of multiple species has focused on calculating site-specific error rates. With this method the species predictions are compared against field survey data on multiple sites within the study area. For example, the testing method used in GAP, a nationwide program of the U.S. Geological Survey (USGS), Biological Resources Division (BRD) (Scott *et al.* 1993), compares the predictions against pre-existing presence and absence data obtained fiom management areas such as state or federal wildlife areas (Scott *et al.* 1993, Edwards *et al.* 1996, Krohn *et al.* 1998). The assumption is made that the survey lists represent all species breeding on a site during a specified time period. The predicted occurrences are compared to these lists and discrepancies (i.e., "errors") are recorded for each site.

Omission error (species present on a site but not predicted) is calculated for the site using the total number of species in a taxonomic class that were missed. In the same way commission error (species predicted but not recorded as present on a site) is calculated using the total number of species in a taxonomic class that were over predicted. The resulting errors for each site are then used to obtain a statewide accuracy (Csuti and Crist 1998). An alternative approach to this would be to use the same data to look at the discrepancies for each species across all of the test sites. This alternative species-specific approach would compare the predictions to field records of presence or absence, for each species on sites within their range limit. Commission and omission errors could then be calculated for individual species.

With the species-specific approach one could also calculate the highest and lowest levels of commission and omission error for each species. This is possible using different assumptions regarding the quality of the test data (i.e., field inventories and/ or checklists). First, we can assume that the test data is completely accurate (i.e., all species present on the site are properly identified and recorded). With this assumption one has to keep in mind that species that are harder to detect in the field (rare or reclusive in nature) are more likely to be the primary source of the estimated commission error rate on a'site (Boone and Krohn 1999; Schaefer and Krohn 2002). Also, it has been shown, in Maine, that small sites with shorter-term test data had greater levels of commission error than the larger sites where the test data had been collected longer (Chapter 1). Thus, assuming the surveys are complete may result in artificially higher levels of commission error. The contrasting assumption would be that the field surveys are incomplete (i.e., not all species present on the site have been recorded). Although the truth is generally somewhere between the two assumptions, calculations based on these extremes provides the upper and lower bound of error.

The purpose of this study is to develop a species-specific approach to testing predicted avian occurrences generated by the Maine Gap Analysis Project. For this method I will also use contrasting assumptions of test data quality to determine the upper and lower bounds of error. My specific objectives are to: 1) calculate species-specific error rates for avian species known to breed regularly in Maine, using two different assumptions of data completeness; 2) determine if the estimation of error is correlated with the extent of a species distribution; 3) for birds with statewide distribution,

determine if the estimation of error is correlated with the likelihood of a species being observed in a field survey; and 4) using groups based upon primary breeding habitat, compare estimated error rates reported by the site-specific and the species-specific approaches.

METHODS

CALCULATING SPECIES-SPECIFIC ERROR RATES

The presence of breeding species was determined from species lists from sites having test data that were collected as checklists or field inventories. Data were gathered from nine sites consisting of one national park, one state park (Oliveri 1993), one national forest (D. Capen, Univ. of Vermont, pers. comm.), four National Wildlife Refuges (NWR), and two privately owned areas (Hagan *et al.* 1997, *J.* Witham, Univ of Maine, pers. comm.) (Figure 2.1). Occurrence information used in creating the predictive models were not used in the testing process. Due to the limited amount of data available for other taxa only birds were considered in this analysis.

Species-specific error rates were calculated using presence and absence records fiom the sites on which each species could potentially occur. Potential occurrence was determined based upon the geographic range limit of the species, as defined by Maine Gap Analysis (Krohn *et al.* 1998), and site-specific occurrence information. The test data was included in determining potential occurrence because the habitat models used in Gap Analysis will only predict species occurrence on sites within the species range. If a site outside of the range indicates the species is present, then failure to include this information in the accuracy assessment would underestimate omission error for that

species. For each species an occurrence tables was developed showing the sites where the species could potentially occur, the Gap range limit, the field survey results, and the prediction results fiom Maine Gap Analysis (Appendix D).

Upper and lower error bounds were calculated using two different assumptions of test data completeness. First, I assumed that the test data were complete (i.e., all species recorded on the site as present were present, and no species were missed). In this case, all absences are true absences and not the result of missed sightings due to incomplete test data. The equations used for estimating omission and commission error under the assumption of complete test data were:

- $O =$ Number of sites where the species was detected on survey but not predicted Total number sites where the species was detected;
- $C =$ Number of sites where the species was predicted but not detected on a survey Total number sites where the species could potentially occur;

where $O =$ Omission error and $C =$ commission error (Equations A).

The second assumption was that the test data were incomplete. Specifically under this assumption I assumed that all absences in the test data were a result of species being missed during the inventory (i.e., species present but not detected). To reflect this assumption in the data all recorded absences of a species on a potential occurrence site were changed to presences. The modified survey data were then compared to the predictions and error was estimated using Equations A above.

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Figure 2.1. Geographic distribution of test sites used in testing the accuracy of the predicted terrestrial vertebrate occurrences fiom Maine Gap Analysis.

Once omission and commission error bounds were calculated for each species an *error range* was calculated. The *error range* in this analysis was the difference between the highest and lowest possible errors obtained fiom the assumptions of complete and incomplete test data.

DATA ANALYSIS

A frequency distribution was generated to visually determine if species could be placed into separate distribution categories (limited, moderate, and broad). The distribution was based upon the maximum number of sites a on which a species could potentially occur (Figure 2.2). A Spearman's Rho was used to test for a correlation between species distribution and the error range. The test was conducted for all species and was not separated by distribution class.

The next analysis was to determine if commission error range was related to how likely a species was to be seen during a field survey. Observability was defined using Likelihood of Occurrence Ranks (LOORs), which ranks species based upon how likely they are to be recorded during a standard field inventory (Boone and Krohn 1999). LOORs were developed using occurrence data fiom the Maine Breeding Bird Atlas (MBBA) (Adamus 1987) and the Breeding Bird Survey (BBS). Boone and Krohn (1999) first calculated a spatial incidence fiom MBBA occurrence data by dividing the number of MBBA blocks having confirmed or potential breeding occurrences for a species, by the number of MBBA blocks within the species range. Because the MBBA for Maine was greater than 15 years old, Boone and Krohn (1999) updated the spatial incidences using a logistic regression to model a suite of avian species-specific variables, including data

Figure 2.2. Frequency distribution of the maximum number of test sites on which each bird species could potentially occur based on range limits in Maine. A= species with limited distribution, B= species that are moderately distributed, and *C=* **species that essentially occur statewide.**

taken from the USGS, BRD's BBS. The incidences were then sorted and assigned a rank from one to "n," becoming the statewide LOORs for each species. Species with an inadequate amount of data available to assign spatial incidences were given a rank of zero (see Boone and Krohn 1999). High LOOR ranks indicate species that are very likely to be observed during a field survey, whereas the low ranks indicate species that are difficult to detect. **A** Spearman's Rho test was used to see if a correlation existed between a species LOOR and the commission error range (α = 0.05). This analysis was limited to only those species that could potentially occur on all nine test sites, consistent with the assumptions of using the LOORs as a ranking tool (see Boone and Krohn 1999 for details). 37

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Finally, the test results of the species-specific approach were directly compared to the site-specific method used in Maine Gap Analysis (Krohn et *al.* 1998). *In* the sitespecific method, error matrices were used to determine the total number of species over predicted and under predicted on each site, for each taxonomic class. Commission and omission error in Maine Gap Analysis (Krohn et *al.* 1998) were estimated using the following equations :

- Total number of species detected on the site;
- $C =$ Number of species predicted on a site that are not detected Total number species detected on the site;

where $O = \text{Omission error and } C = \text{ commission error (Equations B)}$.

A statewide error is obtained by averaging error across all sites for each taxonomic group (see Chapter 1).

To ensure comparability only those species found to occur on all nine test sites in the species-specific approach were tested with the site-specific method. Site-specific errors were calculated by first assigning all species to a habitat classification based upon primary breeding habitats (i.e., barren [little or no vegetation], early successional, forest coniferous, forest deciduous, forest generalists, and wetland species) (Gawler et al. 1986). The error equations used in Maine Gap Analysis (above) were then used to calculate a site-specific error for each habitat group. Mean commission error for each habitat class in the site-specific approach were plotted against the mean commission error in the speciesspecific method. A two-way ANOVA was then used to determine if a significant difference existed between the two methods. Method and habitat were included in the ANOVA as factors in the model and commission error was the dependant variable.

RESULTS

Of the 183 species determined by Maine Gap Analysis to regularly breed in Maine (Krohn et al. 1998), 179 species were used in this analysis. Three species could not be included [Black Tern (Chlidonias niger), American Wigeon (Anas americana), and American Pipit (Anthus rubescens)] because their ranges do not fall on or within any of the nine test sites. A fourth species, the Nelson's Sharp-tailed Sparrow (Ammodramus nelsoni), was not included in the analysis because its taxonomic split from the Salt-Marsh Sharp-tailed sparrow (Ammodramus caudacutus) was believed to be too recent to have reliable field records. Occurrence records for each site and the corresponding Maine Gap predictions for each species are found in Appendix D.

Under the assumption of complete field inventories, 170 species were never omitted (omission error $= 0.0$, out of a possible range of 0.0-1.0). Three species, the American Black Duck (Anas rubripes), Golden Eagle (Aquila chrysaetos), and Ring-neck Duck (*Aythya collaris*), were missed entirely by the predictive models (omission = 1.0). The remaining species errors ranged fiom 0.0 to 1 .O, with a trend toward low omission error (Figure 2.3B, Appendix E). Omission error was slightly higher under the assumption of incomplete test data. With this assumption only 151 species were correctly predicted (omission $= 0.0$) (Figure 2.3D, Appendix E). Despite the slight increase in omission error there were not enough species missed by the models to calculate error ranges to be used in further analysis. Thus, all following analyses **are** limited to commission error ranges.

Under the assumption of complete test data commission error was much higher than omission error (Figure 2.3). Only 25 were never over-predicted, reporting a commission error of zero (possible range of 0.0 to 1.0). Twenty-one species reported commission errors of zero, indicating they were over-predicted 100% (Figure 2.3A, Appendix E). The assumption that the field surveys were incomplete returned commission errors of zero for all species (Figure 2.3C). As a result the commission error range had the same value as the estimated commission error obtained from the assumption of complete test data.

The frequency distribution of potential occurrence revealed natural breaks between in species distribution. Narrowly distributed species are those potentially occurring on one to four sites, moderately distributed species can potentially be

Figure 2-3. Frequency distribution omission and commission errors from predicted avian occurrences with the assumption of complete (A and B) and incomplete (C and D) test data. 40

found on five to eight sites, and broadly distributed species can potentially be found on all nine sites (Figure 2.2). Species with small geographic distributions had large commission error ranges. Those most broadly distributed tended to have small commission error ranges (Figure 2.4). Species potential distribution was significantly correlated with a decrease in commission error (Rho = -0.583 , P < 0.001).

Commission error range was also correlated with how likely a species is to be observed during field inventories. For those species that could potentially occur on all nine sites a negative correlation was found between commission error range and the species LOORs $(Rho = -0.657, P < 0.000)$ (Figure 2.5).

In comparing results of the site-specific to the species-specific method the mean commission error in each habitat group tended to be higher (Figure 2.6). The two-way **ANOVA** reported that the commission error reported by the species-specific method is significantly lower in each habitat category then the error reported by the site-specific approach (F ratio 20.6, $P < 0.000$). It also showed that there is also an overall effect of habitat on commission error rate (F ratio = 4.41, $P < 0.001$). Finally there was no interaction reported between the primary breeding habitat and testing method (Table 2.2).

Number of potential occurrence sites for each species.

Figure 2.4. Commission Error Range for all avian species across all test sites used in assessing model accuracy.

Likelihood of occurrence ranks.

Figure 2.5. Relationship between commission error range and a species likelihood of occurrence rank, which is the relative likelihood of a species being recorded in a field inventory (Boone and Krohn 1999).

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Figure 2.6. Mean commission error by major habitat association for the site-specific (light bars) and the species-specific (dark bars) approach to testing predicted avian occurrences.

Table 2.1. Analysis of variance results reporting the difference between the site-specific and species-specific approach to testing species-habitat models.

DISCUSSION

As in the site-specific testing method, commission error in the species-specific method was higher then omission error (Scott *et* al. 1993, Edwards *et* al. 1996, Krohn *et* al. 1998). Given that GAP is a course scale biodiversity assessment project, there is a greater concern for missing species. Species that are consistently missed by the predictive models could potentially be neglected when establishing new conservation lands and practices (Morrison et al. 1992). With only nine species reporting errors of omission I am confident that the habitat models used in Maine Gap Analysis are not missing species that **are** present in the state.

In contrast to the omission error, the habitat models did have higher levels of commission. Approximately half of the species (80 out of 179) reported commission error ranges greater then 50%. The highest possible commission error for each species was obtained fiom the assumption that the test data were complete (i.e., all species present on the site were recorded). Errors observed under this assumption ranged fiom zero to one (Appendix D). For example, the Mourning Dove (Zenaida macroura), a fairly common bird had an upper bound of 0.0, whereas the less common Tufted Titmouse (Parus bicolor) had an upper bound of 0.8 (Appendix E). The variability in estimated commission error across species comes from our inability to understand and model every aspect of species habitat needs to determine with complete accuracy where it will occur.

The lower bound for commission error range was obtained from the pessimistic assumption that the test data were incomplete. Under this assumption absences in the

field surveys on sites within the species range limit were considered missed occurrences and were changed to presences. With this change commission error for all species became zero (Appendix E). This finding is theoretically consistent, if we know all there is to know about a species and all the factors of habitat use can be equally mapped, then the lowest possible over-prediction possible is zero. With this finding the species commission error range was always numerically equal to the upper error bound. For example, the upper bound of the Tufted Titmouse was 0.8 and the lower bound was 0.0, the error range is 0.8 (the absolute value of the difference between the two values).

Despite the importance of not omitting species presence it is important that the models **are** not designed to excessively over-predict occurrence. Where commission error does occur it is important that the cause be investigated and understood (Krohn 1996). This analysis indicated that commission error can be influenced by species distribution in the state. In Maine species that were narrowly distributed, such as the Grasshopper Sparrow (Ammodramus savannarum) whose range barely enters the state, or species that have very specific habitat requirements like the Purple Martin (*Progne subis*) (Boone and Krohn 1998b), had high commission error ranges $(1.0 \text{ and } 0.667 \text{ respectively})$ (Appendix E). In contrast, species that were broadly distributed such as the American Crow (Corvus brachyrhynchos) tended to have lower levels of commission error (0.22) (Figure 2.4c). The correlation between distribution and commission error may be related to habitat variability, availability, or both. Species that are broadly distributed may have a wider variety of habitats that **are** suitable for breeding, or there may be a larger amount of habitat available. For those species creating predictive models is less restrictive then for

species with very narrow distributions and a low range of habitat varieties. Species that breed in very specific habitat conditions, such as cavity nesters, are much harder to predict because mapping such specific locations on a broad-scale is problematic (Edwards et *al.* 1996).

The extent of a species distribution in Maine was only part of the explanation for the high predictive errors because commission error was still reported for broadly distributed species (e.g., occuring on all nine sites). In such cases, LOORs were useful in determining the potential cause of the error. For example, the Mourning Dove is a highly visible and abundant species, with a LOORs of 157 (out of 182) and was not over predicted. The Tufted Titmouse, in contrast, occurs less fiequently in Maine (LOORs of 68) and was over predicted 80% of the time (Appendix E). By definition, species that are more likely to occur across the landscape are less likely to generate absences in survey data and therefore will have lower commission error ranges. This analysis supported the former definition, as a species LOORs increased the commission error range decreased $(Rho = -0.657, P < 0.000)$. Therefore, it is likely that the error reported for the Titmouse is apparent and not true (i.e., the results of incomplete field surveys; Chapter 3). However, additional field surveys should be conducted to see if the Titmouse is actually occurring in areas where it was predicted but had not been reported.

When compared to the site-specific method commission error in the speciesspecific approach was significantly lower in all primary breeding categories (Figure 2.6, Table 2.1). This result can possibly be explained by looking at the definition of commission error occurrence in each method, holding constant the assumption that the

ranges and habitat mapping are correct. Commission error in the site-specific approach occurs when at least one species (out of a possible 179 species in this analysis) is over predicted on a test site. For the species-specific method to report commission error the species in question has to be over predicted on at least one of the test sites on which it can potentially occur (for a statewide species in this study it would have to be over-predicted on one of nine sites). Because the former is more likely to occur then the latter, sitespecific mean commission error will tend to be higher then species-specific error rates.

There are a number of advantages in using a species-specific approach to testing predicted occurrences. It permits the evaluation of commission error ranges for each species and determine if the model needs to be improved or if the test data used in testing was not possibly complete. If a high error range is reported for a species that has a high likelihood of occurrence then the most likely cause for the over-prediction in the model. However, if the species has a low LOORs, (i.e., it tends to be rare in the state and or reclusive in nature) and a high commission error, one wants to obtain more field survey data to ensure the species did not go undetected. If the error is in the models, the speciesspecific approach allows you to see which species are being poorly predicted and changes can be made directly to how those species are modeled. Or if necessary, changes can be made to how the habitat and range maps are created.

As with any approach to testing, difficulties with the species-specific approach arise when there is a limited amount of field occurrence information. Nine test sites were used to test the predicted distributions of species for Maine Gap Analysis. Of those nine sites only 3 had information for amphibians and reptiles, and 4 had data for mammals.

The sites with data for all taxonomic classes were not evenly distributed across the state and did not provide a large enough base of comparison to test the species predictions on a per species basis. Similar problems were encountered in the Gap Analysis projects for Idaho (Scott et al. 1993) and Utah (Edwards et *al.* 1996). In Idaho, four sites were used in the testing process. Eight sites were used in the Utah Gap Analysis, but all eight were located in the south-eastem comer of Utah. The fewer sites used in testing and the more concentrated their locations the greater the possibility that error could be mis-represented.

Both the site-specific and the species-specific approach to testing predictive occurrence models for multiple wildlife species indicate model performance. The sitespecific approach will provide a generalized idea of how well the models are capturing species presence and absence across the entire state. Whereas, the species-specific approach gives a more detailed description of which species are reporting the highest levels of error and helps to answer the question of why. For example, if you have two sites with similar habitat types and high quality long term survey information (e.g., Rachel Carson and Mount Desert Island/Acadia National Park) the site-specific testing method will not clearly state why over prediction is being reported. The species-specific approach will tell exactly which species are being over predicted, and how much. By taking into account species distribution and how likely it is to occur on a test site during a standard field survey, one can start to see where the cause for the error lies. Is the model correctly stated, is there an error in the mapping of habitat or range, or is it that the survey not capturing the species presence? For example, if the ranges are too broadly mapped errors of commission will increase as sites where the species does not occur are included

in the prediction process. Errors of omission would result when ranges are too narrowly defined and sites where the species is known to occur are missed.

CONCLUSIONS

Traditionally, commission and omission error from predictive wildlife occurrence models are calculated not for individual species but across taxonomic class by test sites. This site-specific of testing habitat models makes it difficult to determining if the error is due to model quality, or if it is related to the completeness of the field surveys. By using assumptions of data completeness in a species-specific approach to testing model predictions, error ranges were calculated that indicated model performance as well as the variability of the commission error for each species. Commission error range was significantly correlated with species distribution, as well as with the likelihood of detecting a species in the field. If a **high** error range is reported for a species that has a **high** likelihood of occurrence in a field survey then the most likely cause for the over prediction is in the model. However, if a species has a low likelihood of occurrence, and a **high** error range, then the over prediction error is likely due to having an incomplete test data for that species. Because the site-specific approach to testing predictive occurrences provides different information then the species-specific approach, I recommend using both approaches when testing predicted occurrences of multiple species of wildlife.

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CHAPTER 3

PREDICTING VERTEBRATE OCCURRENCES FROM SPECIES HABITAT ASSOCIATIONS: IMPROVING THE INTERPRETATION OF COMMISSION ERROR RATES

INTRODUCTION

A crucial step in conservation is determining where animal and plant species occur. However, conducting intensive field inventories of vertebrate occurrences is generally infeasible. So wildlife-habitat relationship models are used to predict species presencelabsence, and relative or true abundance. Since our knowledge of species habitat use is limited, validation of these models is essential (Morrison *et a1.* 1992, Csuti 1996, Krohn 1996). One common testing method is to compare the predicted occurrences to species lists obtained from test sites having long-term field inventories. Omission error (percent of species present but not predicted), commission error (percent of species predicted but not present), and the percentage of species matched (percent of species present that are predicted) can then be used to evaluate model reliability (e.g., Scott *et al.* 1993, Edwards *et al.* 1996, Fielding and Bell 1997).

Problems with this validation method are often encountered in the interpretion stage (Krohn 1996). There are many biological and methodology factors which can influence errors and can complicate their interpretation, including the presence of species that go unsurveyed (Nichols *et al.* 1998, Boone and Krohn 1999, Karl *et al.* 2002). Futher, size of test sites and definitions of species presence on a site can influence commission and omission errors (Chapter 1). Generally, a close examination of the species being omitted and the data layers used in the prediction process will often identify the actual cause of the omission error. In contrast, commission error is more troublesome, with a key issue being the need to assess if the error reported is an *achral* error (the species actually is not present on the site) or if it is an *apparent* error (the species is present but has not been recorded as a result of incomplete field inventories). For example, since the publication of the predicted distributions fiom the Idaho Gap Analysis Project, the Sharp-tailed Grouse (Tympanuchus phasianellus) has been confirmed to be present in areas where it had never before been recorded (Scott *et al.* 1993). *In* this case commission error could be viewed as an apparent error of the prediction and not an actual error.

Rare and reclusive species can be difficult to detect during standard field surveys designed to inventory a wide variety of species. Thus, these species are likely to have higher estimates of commission error when predicted occurrences are compared to known field observations. Boone and Krohn (1999) recognized that biological characteristics of species can influence detectability, and proposed that an *a priori* ranking system based upon the likelihood of detection could be related to commission error. Using avian occurrences fiom the Maine Breeding Bird Atlas (Adamus 1987) they established a ranking system called Likelihood of Occurrence Ranks (LOORs), which ranked all of the birds known to breed in Maine based upon how frequently they occurred in towns within their range limit (see below). In a gap-like analysis they observed a strong correlation between LOORs and commission error on five of six test sites $(\rho = 0.86 - 0.93, P \le 0.002;$ Boone and Krohn 1999).

The purpose of this analysis was to determine if the *a priori* ranking system of Boone and Krohn (1999) improves the interpretation of the commission errors resulting fiom species-habitat models designed to predict presence or absence for Gap Analysis. The Gap Analysis Program (GAP) is a nationwide effort of the U.S. Geological Survey, Biological Resources Division (USGS, BRD) designed to assess some elements of biodiversity (Scott *et al.* 1993, Scott *et al.* 1996). GAP uses models primarily based on species-habitat associations, along with other data, such as range limits and vegetation, in a geographic information system (GIs), to predict the presence of terrestrial vertebrates that breed in a state (Scott *et al.* 1993). Data for this analysis came fiom the Maine Gap Analysis Project (Maine Gap) (Krohn *et al.* 1998), and my objective was to determine if LOORs and commission error were correlated. If rates of commission are constant across LOORs, then over-prediction by the habitat models would be suggested (i.e., actual errors).

METHODS

ASSIGNING LIKELIHOOD OF OCCURRENCE RANKS

For this study avian LOORs were calculated by Boone and Krohn (1999) and herptile LOORs were tabulated by Krohn *et al.* (1998). In both studies atlas occurrence information was used to generate a spatial incidence for all species. Mammals were not included in this analysis because no unbiased surveys of incidence existed for Maine. To calculate the avian LOORs, Boone and Krohn (1 999) used occurrence data fiom the Maine Breeding Bird Atlas (ME-BBA) (Adamus 1987). The spatial incidence was calculated by dividing the number of ME-BBA blocks having confirmed or potential breeding occurrences by the number of ME-BBA blocks within the species range. Because the ME-BBA for Maine was more than fifteen years old, they updated the spatial incidences using logistic regression to model a suite of avian species-specific variables,

including data taken fiom the USGS BRD's Breeding Bird Survey (BBS) during the period of the ME-BBA. The outdated ME-BBA data was then replaced with the new information, giving updated incidences. These incidences were sorted and assigned a rank which became the species LOORs. Low ranks indicate the species has low detectability, conversely high ranking species are those which are easier to detect. Species with an inadequate amount of data available to assign spatial incidences were given a rank of zero and excluded fiom the correlation analysis (Boone and Krohn 1999).

Krohn *et al.* (1998) used occurrence information from Maine Amphibian and Reptiles (Hunter *et al.* 1999) to calculate herptile LOORs. Since the information in the amphibian and reptile atlas was recent there was no need to conduct additional modeling to update the data, as was done for avian species. Incidences for amphibians and reptiles were combined into one list of herptiles, sorted, and then ranked giving the LOORs for each species. The combining of the two taxonomic classes was done to increase the sample size used in the correlation analysis.

CORRELATION ANALYSIS

Predicted occurrences from Maine Gap Analysis (Boone and Krohn 1998a,b) were compared to records fiom nine sites in Maine having field surveys. Amphibian, reptile, and bird occurrences came fiom checklists complied by National Park Service (National Park Service 1990, 1996) and the U.S. Fish and Wildlife Service (U.S. Fish and Wildlife Service 1989, 1994a,b, 1995, 1996; Table 3.1, Figure 3.1). Additional avian occurrences were also obtained fiom field inventory and research records fiom the White Mountains

Table 3.1. Test site names, data **type** and available information used in testing the accuracy of the vertebrate predictions fiom Maine Gap Analysis.

^a - Number of years the area has been surveyed.

^b - Actual number of survey years unknown so the number of years in existence is reported.

Figure 3.1. Locations of test sites used in the accuracy assessment of predicted distributions of terrestrial vertebrates fiom Maine Gap Analysis.
National Forest (D. Capen, pers. comm.), Baxter State Park (Oliveri 1993), and two privately owned areas (Hagan *et al.* 1997, J. Witham, pers. comm.; Table 3.1, Figure 3.1).

For each site the number of species correctly predicted and the number in commission were tabulated and compared to five groups of species for birds and three groups of species for herptiles. Species were assigned to groups based upon LOORs (ranging fiom low to high) with equal number of species per group (as much as possible). This was done to remove any possibility of bias which might have occurred by including species that do not occur on a particular site due to range limits in the state. Spearman's Rho (alpha $= 0.05$) was used to quantify the relationship between species counts and the LOORs group for each taxonomic class on each site.

RESULTS

Overall the mean commission error for amphibians and reptiles was low $(\bar{x} =$ 12.3%, range 0 to 36.8%) and the mean percentage of species matched was high $(\bar{x} =$ 97.3%, range 92 to 100%; Table 3.2). No trend was apparent when combined amphibian and reptile errors were plotted for each LOOR group (Figure 3.2). A valid Spearman's Rho analysis on commission error could only be conducted for the Holt Research Forest, because on Rachel Carson National Wildlife Refuge there was no commission error, and Mount Desert Island had too many ties in the number of species matched to conduct a **rank** correlation test (Table 3.3). The Spearman's rho for the Holt Research Forest indicated that there was not a significant relationship between commission error and the LOOR groups ($\rho = -0.5$, $P \le 0.704$; Table 3.3). The correlation between the number of

Table 3.2. Percentage and number of species matched and in commission for test sites used in the predicted vertebrate accuracy assessment, sites are ordered by length of field inventory.

 $^{\circ}$ percent matched = [number of species predicted present that were present / number of species present] $*$ 100.

 α commission error = [number of species in predicted but not present / number of species present] * 100.

Figure 3.2. For each test site with amphibian and reptile data, the number of species correctly modeled (denoted by a circle and solid line) and the number of species in commission (denoted by a dashed line and a square). Sites are ordered fiom smallest to largest : (a) Holt Research Forest, (b) Rachel Carson National Wildlife Refuge, and (c) Mount Desert Island/ Acadia National Park.

Table 3.3. Results of tests of Likelihood of Occurrence Ranks^a for each test site having amphibian and reptile surveys in Maine. Number of years site potentially surveyed shown in parenthesis.

^a - LOORs, defined by Boone and Krohn (1999).

species matched and LOORs was also not significant ($\rho = 0.5$, $P \le 0.704$; Table 3.3).

Commission error was much higher for birds than it was for herptiles (\bar{x} = 76.8%) \pm 45.8, compared to 12.3% \pm 21.2; Table 3.2). The number of bird species matched and the LOOR groups were positively correlated ($\rho = 0.6$ to 1.0) on all sites ($n = 9$; Figure 3.3). Relationships were significant $(P \le 0.05)$ for all sites except for the White Mountains National Forest ($P \le 0.291$) and Acadia National Park ($P \le 0.059$) (Table 3.4). An inverse relationship was observed between commission error and the LOORs ($\rho = -$ 0.87 to -1 .O) (Figure 3.3). The Spearman's rho tests confirmed the significance of this relationship on all sites except Acadia National Park (P **s** 0.059; Table 3.4).

DISCUSSION

It is well known that field surveys are often incomplete censuses of the species present in a given area (e.g. Nichols *et* al. 1998). Factors such as species detectability, the number of years a survey has been conducted, and the amount of effort placed in searching for species, influences which species will be recorded and which will be missed during a survey (Boone and Krohn 1999; Karl *et* al., In Press; Fielding, In Press). I found that *a priori* ranking species based upon how likely they are to be observed during a field inventory helps to detect the effects of incomplete field surveys on model validation.

An initial interpretation of the commission errors reported for Maine Gap, without correcting for incompleteness of the inventories, would indicate that the models are overpredicting about 76% (Table 3.2) of the bird species in the state. Block *et* al. (1994) faced a similar problem with their predictive models. They reported commission errors ranging from 29 to 44% and felt that this level was unacceptable. In both studies these

Figure 33. For each test site with avian data, the number of species correctly modeled (denoted by a circle and solid line) and the number of species in commission (denoted by a dashed line and a square). Sites are ordered fiom smallest to largest : (a) North Maine Forestlands, Moosehead Lake Area; (b) Nesowadnehunk Field, Baxter State Park; (c) White Mountains National Park; (d) Sunkhaze National Wildlife Refuge; (e) Holt Research Forest; **(f)** Petit Manan National Wildlife Refbge; (g) Rachel Carson National Wildlife Refuge; (h) Moosehorn National Wildlife Refuge; (i) Mount desert Island Acadia National Park

Table 3.4. Results of tests of Likelihood of Occurrence Ranks^a for each test site having bird surveys in Maine. Number of years site potentially surveyed shown in parenthesis.

(continued)

(Table 4 cont.)

(Continued)

(Table 4 cont.)

a - **LOORs,** defined by Boone and Krohn (1999).

findings could lead researchers to believe that the species-habitat association models have not been correctly constructed. However, the inverse correlation we observed between commission error and LOO& indicates much of the errors reported in the Maine Gap predictions are related to the species detectability. Thus, by examining the models within an *a priori* ecological context of species detectability we were able to determine that much of our commission was due to apparent rather than actual errors in the models. Thus, we suggest that the models are adequately predicting the presence of species in Maine. However, additional effort needs to be put into surveying for those with low LOORs to be fully confident of this conclusion.

The highest correlation were found on smaller sites with shorter surveys, which also indicates that the errors are apparent rather then actual. Surveys such as those for the North Maine Forestlands and White Mountains National Park (conducted one year and five years, respectively) have not been established for a period of time long enough to capture the presence of the more uncommon and reclusive species (Chapter 1). Also, these surveys came from research projects having a specific objective of surveying forest songbirds (Hagan *et al.* 1997; D. Capen, pers. comm.). These factors in an *a posterior* evaluation of error may lead researchers to incorrectly conclude that actual errors are present in the models (Edwards *et al.* 1996) when it is more likely that much of the errors are related to incomplete field surveys.

A more or less constant rate of commission error over LOORs on test sites with long histories of field inventories, would indicate real over-predictions are being reported on the site (Boone and Krohn 1999). This can be seen in the number of species in commission on Moosehorn NWR and Acadia National Park (Figure 3.3). The moderate

correlation for these sites (rho $=$ -0.89 and -0.87) suggests that the species lists for these areas are relatively complete. Given that these sites have been surveyed for extended periods of time (61 and 79 years respectively; Table 3.1) it is reasonable to conclude that the species occurring on the sites have been well documented. However, even with a constant rate of error, care in the interpretation process must still be taken. The lack of correlation might be due to having too small of a sample size, or by having too many LOORs groups (data spread too thinly). Too small of a sample size was problematic in this analysis with the herptile data. On all sites these predictions were relatively accurate, having a high percentage of species matched $(\bar{x} = 97.3\%)$ and relatively little commission error $(\bar{x} = 12.3\%;$ Table 3.2). On the site where a significant amount of commission was reported (36.8%) the number of species separated into the LOORs groups in the rank correlation test was extremely small, and thus our ability to detect a significant correlation between LOORs and commission was weak (Table 3.2 and 3.3).

Because of similarities between this analysis and that of Boone and Krohn (1999) further investigations still need to be made into the use of a *priori* ranking of species detectability to separate apparent fiom actual error in species predictions. There are major differences between these two studies, however, worthy of mention. First, the predictions of vertebrate occurrences we used were based upon an operational gap analysis, meaning that a statewide vegetation and land cover map created with remotely sensed data (Hepinstall **er** al. 1999) was the main data layer underlying species predictions (Boone and Krohn 1998a,b). In contrast, the vertebrate predictions reported in Boone and Krohn (1999) were not based on a statewide vegetation map, but instead relied on the data available for each site, which in some cases included lists of vegetation cover (Boone and Krohn 1999). Unlike Boone and Krohn (1 999), I wanted to study amphibians and reptiles as well as birds. Because there are few herptiles breeding in Maine, the number of LOOR groups was reduced to three. The number of LOOR groups identified by Boone and Krohn (1999) for birds was reduced fiom ten to five. This change tended to smooth some of the graphs of the number of species correctly modeled verses LOO& (e.g., note Moosehorn **NWR** in Fig. 3b of Boone and Krohn [I9991 vs. my Fig. 3.3h), but did not change the overall patterns. Finally this study reports data fiom nine test sites, three more then was used by Boone and Krohn (1999).

CONCLUSIONS

Having an ecological context in which to evaluate commission error is important and will help investigators to have greater confidence in their predictive models (Fielding and Bell 1997). The ideal situation in validating habitat-association models designed to predict the presencelabsence of terrestrial vertebrates would be to have standardized field censuses capturing the presence of all species on test sites to compare to the predicted distributions. However, until such detailed surveys are available an a *priori* ranking system, such as LOORs, will permit fuller interpretation of rates of commission but helping to distinguish commission errors that are actual verses those resulting from incomplete field data. An ability to distinguish actual errors of over-prediction from incomplete test data is critical to understanding the level of confidence model users should have in their findings.

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APPENDICES

APPENDIX A.

Comparisons between predicted occurrences of individual species and known observations from sites with field inventories.

					Mt. Desert Is. &			
	Holt Forest			Rachel Carson NWR	Acadia NP			
Common Name	results	range	results	range	results	range		
American Toad	M		M		M			
Blue-spotted Salamander	M		M		M			
Bullfrog	M		M		M			
Dusky Salamander	M		M		M			
Eastern Newt	M		M		M			
Four-toed Salamander	M		M		M			
Gray Treefrog	M		M		M			
Green Frog	M		M		M			
Mink Frog	NP	0	NP	0	NP	0		
Northern Leopard Frog	M		M		M			
Northern Two-lined								
Salamander	M		M		M			
Pickerel Frog	M		M		M			
Redback Salamander	M		M		M			
Spotted Salamander	M		M		M			
Spring Peeper	M		M		M			
Spring Salamander	NP	0	M		NP			
Wood Frog	M		M		M			

TABLE A.1. Comparison of Maine Gap predictions with available test data for amphibians. "M" indicates match, "C" is commission error, "O" is omission error, and "NP" is for not present/not predicted. Range information has also been incorporated $(0 = \text{test site outside of range}, 1 = \text{within range}).$

Common Name					Mt. Desert Is. &		
	Holt Forest		Rachel Carson NWR		Acadia NP		
	results	range	results	range	results	range	
Blanding's Turtle	NP	0	M		O		
Brown Snake	M		M		NP	0	
Common Garter Snake	M		M		M		
Common Musk Turtle	NP	0	M		Ω		
Eastern Box Turtle	NP	0	M		NP		
Eastern Ribbon Snake	C		M		NP		
Milk Snake	M		M		M		
Northern Water Snake	С		M		$\mathbf C$	0	
Painted Turtle	C		M		M		
Racer	NP		M		NP		
Redbelly Snake	M		M		M		
Ringneck Snake	M		M		M		
Smooth Green Snake	M		M		M		
Snapping Turtle	M		M		M		
Spotted Turtle	NP		M		NP		
Wood Turtle	C		M		M		

TABLE **A.2.** Comparison of Maine Gap predictions with available test data for reptiles. "M" indicates match, "C" is commission error, "O" is omission error, and "NP" is for not present/not predicted. Range information has also been incorporated $(0 = \text{test site outside of range}, 1 = \text{within range}).$

MAMMALS Common Name	Holt Forest		Rachel Carson NWR		Moosehorn NWR		Mt. Desert Is. & Acadia NP		
	results	range	results	range	results	range	results	range	
American Beaver	M		M		M		M		
American Marten	NP	0	NP	0	$\mathbf C$	0	NP		
Big Brown Bat	$\mathbf C$		M		$\mathbf C$		M		
Black Bear	NP	0	Ω	0	M		M		
Bobcat	NP	0	\mathbf{O}	0	M		Ω	0	
Common Gray Fox	$\mathbf C$		M		NP	0	NP	0	
Common Porcupine	M		M		M		M		
Common Raccoon	M		M		M		M		
Coyote	M		M		M		M		
Deer Mouse	NP	0	\mathbf{O}	0	M		M		
E. Small-footed Myotis	NP	0	Ω	0	NP	0	NP		
Eastern Chipmunk	M		M		M		M		
Eastern Gray Squirrel	M		M		M		M		
Eastern Pipistrelle	С		M		$\mathbf C$		$\mathbf C$		
Eastern Red Bat	$\mathbf C$		M		$\mathbf C$		$\mathbf C$		
Ermine	M		M		M		M		
Fisher	M		M		M		$\mathbf C$		
Hairy-tailed Mole	M		M		M		M		
Hoary Bat	$\mathbf C$		M		$\mathbf C$		$\mathbf C$		
Little Brown Myotis	C		M		M		M		
Long-tailed Shrew	NP	0	NP	0	NP	0	NP	0	

TABLE A.3. Comparison of Maine Gap predictions with available test data for mammals. Range information has also been incorporated ($0 =$ test site outside of range, $1 =$ within range).

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Range information has also been incorporated ($0 =$ test site outside of range, $1 =$ within range).										
	N.Maine Forest Moosehead Lake		Nesowadnehunk Field, Baxter State		White Mountains National Forest		Sunkhaze Meadows NWR		Holt Research Forest	
Common Name	results	range	results	range	results	range	results	range	results	range
Alder Flycatcher	M		$\mathbf C$		M		M		M	
American Bittern	M				С		M		M	
American Black Duck	C		$\mathbf C$		$\mathbf C$		M		М	
American Coot	NP		NP	0	NP	0	NP	0	NP	
American Crow	C		С		M		M		М	
American Goldfinch	M		C		M		M		M	
American Kestrel	C		$\mathbf C$		С		$\mathbf C$		C	
American Pipit	NP		NP	0	NP	0	NP	0	NP	
American Redstart	M		M		M		M		M	
American Robin	M		M		M		M		M	
American Wigeon	NP		NP	0	NP	0	2	0	NP	
American Woodcock	C		$\mathbf C$		$\mathbf C$		M		M	
Bald Eagle	NP		NP		NP		NP		NP	
Baltimore Oriole	C		С		M		M		M	
Bank Swallow	С		C		С		$\mathbf C$		C	
Barn Swallow			С		C		$\mathbf C$		C	
Barred Owl	C		C		M		M		M	
Bay-breasted Warbler	M		$\mathbf C$		M		M		М	
Belted Kingfisher	C		M		M		M		М	
Bicknell's Thrush	NP		NP		NP		NP	0	ΝP	
Black Tern	NP	0	NP	0	NP	0	NP	0	NP	0

TABLE A.4. Comparison of Maine Gap predictions with available test data for birds on sites 1-5. "M" indicates match, "C" is commission error, "O" is omission error, and "NP" is for not present/not predicted. Range information has also been incorporated $(0 = \text{test site outside of range}, 1 = \text{within range}).$

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TABLE A.5. Comparison of Maine Gap predictions with available test data for birds on sites 6-9.

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APPENDIX B.

Comparisons between predicted occurrences of individual bird species and known observations from sites with field inventories when a liberal definition of species presence is used.

TABLE **B.1.** Comparison of Maine Gap predictions with available test data for birds using a liberal definition of species presence. "M" indicates match, "C" is commission error, "O" is omission error, and "NP" is for not present/not predicted. Range information has also been incorporated $(0 = \text{test site outside of range}, 1 = \text{within range}).$

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APPENDIX **C.**

A closer look at the species omitted by the Maine Gap Analysis predictive models.

Table **C.1.** Shortest distance to range edge and potential error source for species omitted by Maine Gap Analysis using a conservative definition of species presence.

Figure C.1. Incidences of omission reported for Sunkhaze National Wildlife Refuge. The light grey denotes the study area of Maine, which includes some coastal areas and islands off the coast. The darker grey is the predicted distribution and the open polygons are the test sites.

Figure C.2. Incidences of omission reported for Holt Research Forest. The light grey denotes the study area of Maine, which includes some coastal areas and islands off the coast. The darker grey is the predicted distribution and the open polygons are the test sites.

Figure C.3. Incidences of omission reported for Rachel Carson National Wildlife Refuge. The light grey denotes the study area of **Maine, which includes some coastal areas and islands off the coast. The darker grey is the predicted distribution and the open polygons are the test sites.**

Figure C.4. Incidences of omission reported for Moosehorn National Wildlife Refuge. The light grey denotes the study area of Maine, which includes some coastal areas and islands off the coast. The darker grey is the predicted distribution and the open polygons are
the test sites.

Figure C.5. Incidences of omission reported for Mount Desert Island/Acadia National Park. The light grey denotes the study area of Maine, which includes some coastal areas and islands off the coast. The darker grey is the predicted distribution and the open polygons are the test sites. **Example 19** and 19 and 19 and 19 and 19 and 19 and 19 and produced distribution data the open.

APPENDIX D.

Species potential occurrence tables.

Table D.1. Individual species site occurrence records, on site range extent (as determined by ME-GAP), and ME-GAP predictions for the sites on which each species could potentially occur. A "1" indicates presence, a "0" absence, and dashed line indicates the species could not potentially occur on the site. Site codes are: 1 = North Maine Forestlands, $2 =$ Nesowandehunk Field, $3 =$ White Mountains National Forest, $4 =$ Sunkhaze Meadows Natioanl Wildlife Rehge (NWR), **5** = Holt Research Forest, 6 = Petit Manan NWR, 7 = Rachel

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Table D.1. (cont)										
Chimney swift								Ruby-throated hummingbird		
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APPENDIX E. Species-specific accuracy assessment results.

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Table E.1. Commission and Omission error rates for each species using two different assumptions of data quality with the corresponding error range. Assumption 1 : the survey data are complete, Assumption 2: the survey data are incomplete. Error Range = | complete - incomplete |

 $\label{eq:2.1} \frac{1}{\sqrt{2}}\int_{\mathbb{R}^3}\frac{1}{\sqrt{2}}\left(\frac{1}{\sqrt{2}}\right)^2\frac{1}{\sqrt{2}}\left(\frac{1}{\sqrt{2}}\right)^2\frac{1}{\sqrt{2}}\left(\frac{1}{\sqrt{2}}\right)^2\frac{1}{\sqrt{2}}\left(\frac{1}{\sqrt{2}}\right)^2\frac{1}{\sqrt{2}}\left(\frac{1}{\sqrt{2}}\right)^2\frac{1}{\sqrt{2}}\frac{1}{\sqrt{2}}\frac{1}{\sqrt{2}}\frac{1}{\sqrt{2}}\frac{1}{\sqrt{2}}\frac{1}{\sqrt{2}}$

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Habitat Group Definitions : WET = wetlands, EAR = Early Sucessional, BAR = Barren, FG = Forest Generalists, FCS = Forest Coniferous Specialist, FDS = Forest Deciduous Specialists

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BIOGRAPHY OF THE AUTHOR

Sandra Michelle Schaefer was born in Vista, California, on August 19, 1974. Being the daughter of a Marine Corps Officer she moved several times as a child with a final stationing in Stafford, Virginia where she spent the majority of her middle and high school years. She graduated with honors fiom North Stafford High School in June of 1992.

Sandi completed her Bachelor of Science degree in Wildlife and Fisheries Management at West Virginia University (WVU), Morgantown, West Virginina, in May of 1996. While attending **WVU,** Sandi worked as a technician on the West Virginia Gap Analysis Project. She graduated fiom **WVU** cum laude and secured a Geographic Information Systems (GIs) internship with the West Virginia Division of Natural Resources. Towards the end of her internship she began looking for a graduate research position where she could expand on her GIs and wildlife skills. In the summer of 1998 she moved to Maine to begin her graduate studies as a student in the Department of Wildlife Ecology. Sandra is a candidate for Master of Science degree in Wildlife Ecology from the University of Maine in August, 2002.