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# National Agri-Environmental Standards Initiative (NAESI)

## Report No. 3-20

# Habitat and Population Analysis for Red-shouldered Hawk, American Bittern, and Pileated Woodpecker in the Eastern Ontario Pilot Region

Technical Series 2007

**Photos:**
Bottom Left- clockwise

Fraser Valley near Abbotsford, B.C.: Wayne Belzer, Pacific Yukon Region, Environment Canada
Crop spraying: Corel CD photo # 95C2840
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# NATIONAL AGRI-ENVIRONMENTAL STANDARDS INITIATIVE TECHNICAL SERIES

# HABITAT AND POPULATION ANALYSIS FOR RED-SHOULDERED HAWK, AMERICAN BITTERN, AND PILEATED WOODPECKER IN THE EASTERN ONTARIO PILOT REGION

## REPORT NO. 3-20

# NOTE TO READERS

The National Agri-Environmental Standards Initiative (NAESI) is a four-year (2004-2008) project between Environment Canada (EC) and Agriculture and Agri-Food Canada (AAFC) and is one of many initiatives under AAFC's Agriculture Policy Framework (APF). The goals of the National Agri-Environmental Standards Initiative include:

- Establishing non-regulatory national environmental performance standards (with regional application) that support common EC and AAFC goals for the environment
- Evaluating standards attainable by environmentally-beneficial agricultural production and management practices; and
- Increasing understanding of relationships between agriculture and the environment.

Under NAESI, agri-environmental performance standards (i.e., outcome-based standards) will be established that identify both desired levels of environmental condition and levels considered achievable based on available technology and practice. These standards will be integrated by AAFC into beneficial agricultural management systems and practices to help reduce environmental risks. Additionally, these will provide benefits to the health and supply of water, health of soils, health of air and the atmosphere; and ensure compatibility between biodiversity and agriculture. Standards are being developed in four thematic areas: Air, Biodiversity, Pesticides, and Water. Outcomes from NAESI will contribute to the APF goals of improved stewardship by agricultural producers of land, water, air and biodiversity and increased Canadian and international confidence that food from the Canadian agriculture and food sector is being produced in a safe and environmentally sound manner.

The development of agri-environmental performance standards involves science-based assessments of relative risk and the determination of desired environmental quality. As such, the National Agri-Environmental Standards Initiative (NAESI) Technical Series is dedicated to the consolidation and dissemination of the scientific knowledge, information, and tools produced through this program that will be used by Environment Canada as the scientific basis for the development and delivery of environmental performance standards. Reports in the Technical Series are available in the language (English or French) in which they were originally prepared and represent theme-specific deliverables. As the intention of this series is to provide an easily navigable and consolidated means of reporting on NAESI's yearly activities and progress, the detailed findings summarized in this series may, in fact, be published elsewhere, for example, as scientific papers in peer-reviewed journals.

This report provides scientific information to partially fulfill deliverables under the Biodiversity Theme of NAESI. This report was written by H.R. Akçakaya, J. Stanton, and E. Aalto of Applied Biomathematics. The report was edited and formatted by Denise Davy to meet the criteria of the NAESI Technical Series. The information in this document is current as of when the document was originally prepared. For additional information regarding this publication, please contact:


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# NOTE À L'INTENTION DES LECTEURS

L'Initiative nationale d'élaboration de normes agroenvironnementales (INENA) est un projet de quatre ans (2004-2008) mené conjointement par Environnement Canada (EC) et Agriculture et Agroalimentaire Canada (AAC) et l'une des nombreuses initiatives qui s'inscrit dans le Cadre stratégique pour l'agriculture (CSA) d'AAC. Elle a notamment comme objectifs :

- d'établir des normes nationales de rendement environnemental non réglementaires (applicables dans les régions) qui soutiennent les objectifs communs d'EC et d'AAC en ce qui concerne l'environnement;
- d'évaluer des normes qui sont réalisables par des pratiques de production et de gestion agricoles avantageuses pour l'environnement;
- de faire mieux comprendre les liens entre l'agriculture et l'environnement.

Dans le cadre de l'INENA, des normes de rendement agroenvironnementales (c.-à-d. des normes axées sur les résultats) seront établies pour déterminer les niveaux de qualité environnementale souhaités et les niveaux considérés comme réalisables au moyen des meilleures technologies et pratiques disponibles. AAC intégrera ces normes dans des systèmes et pratiques de gestion bénéfiques en agriculture afin d'aider à réduire les risques pour l'environnement. De plus, elles amélioreront l'approvisionnement en eau et la qualité de celle-ci, la qualité des sols et celle de l'air et de l'atmosphère, et assureront la compatibilité entre la biodiversité et l'agriculture. Des normes sont en voie d'être élaborées dans quatre domaines thématiques : l'air, la biodiversité, les pesticides et l'eau. Les résultats de l'INENA contribueront aux objectifs du CSA, soit d'améliorer la gérance des terres, de l'eau, de l'air et de la biodiversité par les producteurs agricoles et d'accroître la confiance du Canada et d'autres pays dans le fait que les aliments produits par les agriculteurs et le secteur de l'alimentation du Canada le sont d'une manière sécuritaire et soucieuse de l'environnement.

L'élaboration de normes de rendement agroenvironnementales comporte des évaluations scientifiques des risques relatifs et la détermination de la qualité environnementale souhaitée. Comme telle, la Série technique de l'INENA vise à regrouper et diffuser les connaissances, les informations et les outils scientifiques qui sont produits grâce à ce programme et dont Environnement Canada se servira comme fondement scientifique afin d'élaborer et de transmettre des normes de rendement environnemental. Les rapports compris dans la Série technique sont disponibles dans la langue (français ou anglais) dans laquelle ils ont été rédigés au départ et constituent des réalisations attendues propres à un thème en particulier. Comme cette série a pour objectif de fournir un moyen intégré et facile à consulter de faire rapport sur les activités et les progrès réalisés durant l'année dans le cadre de l'INENA, les conclusions détaillées qui sont résumées dans la série peuvent, en fait, être publiées ailleurs comme sous forme d'articles scientifiques de journaux soumis à l'évaluation par les pairs.

Le présent rapport fournit des données scientifiques afin de produire en partie les réalisations attendues pour le thème la biodiversité dans le cadre de l'INENA. Ce rapport a été rédigé par H.R. Akçakaya, J. Stanton, et E. Aalto d'Applied Biomathematics. De plus, il a été révisé et formaté par Denise Davy selon les critères établis pour la Série technique de l'INENA. L'information contenue dans ce document était à jour au moment de sa rédaction. Pour plus de renseignements sur cette publication, veuillez communiquer avec l'organisme suivant :

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# EXECUTIVE SUMMARY

This report describes the habitat and population modeling and viability analyses we conducted for three species in the in Eastern Ontario Pilot Region: Red-shouldered Hawk, American Bittern, and Pileated Woodpecker. This project was in support of the development of biodiversity performance standards under the National Agri-environmental Standards Initiative.

Our modeling approach is based on linking demographic and habitat models to estimate the viability, stability, and functionality of the metapopulation in the study area, based on the distribution, amount and quality of their habitat, and their demographic properties. The models were developed using RAMAS GIS, which links spatial data (such as habitat maps) to demographic data to simulate metapopulation dynamics with an age- or stage-structured model for each subpopulation. For each species, we describe the model in three sections: Demographic model, Habitat model, and Linking Habitat Model to Demography.

We identified and defined "measures", which the model outputs that are used to summarize the results of the simulations in terms of the performance criteria. In this report we used 2 measures for each performance criteria: viability, stability and functionality.

For each species, we performed two sets of simulations. One set was for sensitivity analysis and focused on identifying parameters to which the models results were most sensitive. The second set of simulations focused on the potential effects of future habitat loss scenarios on the viability, stability and functionality of the metapopulations in the study area. For the second set, we modeled two different habitat loss scenarios to explore how the spatial pattern of landscape change will effect the population. The first scenario ("small fragment loss") makes the assumption that smaller fragments of remnant habitat will be most vulnerable to conversion to

other land uses and will be lost before larger fragments. The second scenario ("edge erosion") assumes that habitat will be lost through a process of degradation from patch edges and openings.

Results showed some variability among the three species, and substantial uncertainty within each species, in terms of viability, stability and functionality. American Bittern seemed to be the least viable and least stable population, due to its small abundance in the study area, which in turn is because of its less abundant habitat. The most important parameters contributing to this uncertainty were neighborhood distance and carrying capacity. These parameters are based on two related variables, the home range size and density of nests. For both parameters, higher values resulted in higher viability, stability and functionality.

An interesting result is that the small fragment loss scenario resulted in a larger loss of total habitat suitability than the edge erosion scenario. This is likely because the edges were already less suitable than core areas, and even small fragments contained enough core areas that losing a given area of small fragments resulted in a greater decrease in suitable habitat than losing the same area of edges.

Both types of habitat loss resulted in more fragmented populations, but this effect was not uniform. For Red-shouldered Hawk and Pileated Woodpecker, the small fragment loss scenario resulted in more fragmentation than the edge erosion scenario. For American Bittern, the small fragment loss scenario also resulted in more fragmentation than the edge erosion scenario, but only for the best-case model.

Measures of viability, stability and functionality were in general sensitive to both types of habitat loss, except in worst-case models or high amounts of habitat loss. All measures are continuous variables, describing the level or degree of viability, stability, and functionality. We did not

define the border between viable and nonviable, between stable and unstable, or between functional and nonfunctional, as these are policy, not scientific, decisions. However, we give examples to illustrate how to answer questions such as "What level of habitat loss can be tolerated?" once these policy decisions are made.

An important question is the applicability of the methods and results of these case studies to other regions. We believe that in general all methods we used in these case studies, including the variables used to measure viability, stability and functionality, are applicable to other regions and other species. However, we believe only some of the results are applicable to populations of these three species in other regions. In particular, we believe the habitat models may be applicable to other regions with minor modifications, if the recommended improvements are implemented. In addition, we recommend reviewing local/regional differences in habitat use and preference of species before applying the habitat models to other regions.

We believe the habitat-based approach focusing on viability, stability and functionality of selected species is feasible and practical, and it will satisfy the requirements for the development of biodiversity performance standards. However, there are a number of shortcomings, which in our opinion limit the applicability of this approach within the overall project framework. Some of these are data shortcomings, which we believe can be addressed by implementing a set of specific recommendations, including

1. Increasing the study area

2. Increasing reliability of habitat maps by (i) collecting presence-absence (occurrence) data in the region on the target species, (ii) collating more layers of habitat maps, and (iii) using quantitative methods such as logistic regression or programs such as MaxEnt.

3. Decreasing model uncertainty by (i) creating more reliable habitat maps, (ii) collecting spatially comprehensive data (e.g., the location of all individuals or pairs in a few small study areas), (iii) collecting temporally comprehensive data (e.g., survey data on several consecutive years), and (iv) using statistical methods such as mark-recapture analysis, time series analysis and others to estimate demographic parameters.

We believe there is another, more fundamental, shortcoming, which relates to the way the model results are used to reach conclusions about the best management practices that would lead to the development of biodiversity performance standards. Tasks such as identifying "core and satellite population area requirements and structural elements (i.e., patch sizes, corridors, buffers, etc.)" represent a patter-oriented approach, as they aim to identify patterns of landscape structure and configuration that would meet certain policy goals (e.g., a certain level of species viability). Although generalizations based on identification of such patterns may be of academic interest, we maintain that in most practical cases, this is not possible.

Instead of this pattern-oriented approach, we recommend a far more practical management-oriented approach. This approach requires starting from a limited set of management practices, determined by experts, managers, and other stakeholders (in this case, including farmers), and taking into account issues of feasibility, cost, and social acceptability. Each management practice is then analyzed in detail to quantify its effects on habitat and demography, including the uncertainties in these effects. Each practice is likely to have several effects, some on habitat (quality, distribution), some on demography (survival, fecundity, dispersal). These effects are then combined into a single model simulating the effects of that management practice. After the initial simulation of each practice by itself, some practices can be selected for further analysis in

combinations. Compared to the pattern-oriented approach, this approach would not only substantially decrease the effort required to run all the necessary model simulations, it would also make it possible to obtain practical results and aid in the communication of those results.

# 1 INTRODUCTION

This report describes the habitat and population modeling and viability analyses we conducted for three species in the in Eastern Ontario Pilot Region: Red-shouldered Hawk, American Bittern, and Pileated Woodpecker. This project was in support of the development of biodiversity performance standards under the National Agri-Environmental Standards Initiative.

In this section, we describe our modeling approach, the parameter estimation methods, assumptions and other features common to all three models. The models were developed using RAMAS GIS (Akçakaya, 2005), which links spatial data (such as habitat maps) to demographic data to simulate metapopulation dynamics with an age- or stage-structured model for each subpopulation. For each species, we describe the model in three sections: Demographic model, Habitat model, and Linking Habitat Model to Demography. The methods used in each of these sections are described below.

Later in this section, we describe the "Measures" we identified. Measures are the model outputs that are used to summarize the results of the simulations in terms of the three performance criteria: viability, stability, and functionality of the metapopulation in the study area.

Finally, we describe in this section the simulations we set up, which included one set of simulations for sensitivity analysis, and another set for simulating habitat loss scenarios.

## 1.1 Demographic models

The demographic component of the population model refers to the stage matrix (which includes survival rates and fecundities for different age classes or stages), variability (standard deviations of survival rates and fecundities), and density dependence (how average values of survival rates

and fecundities change in relation to population size).

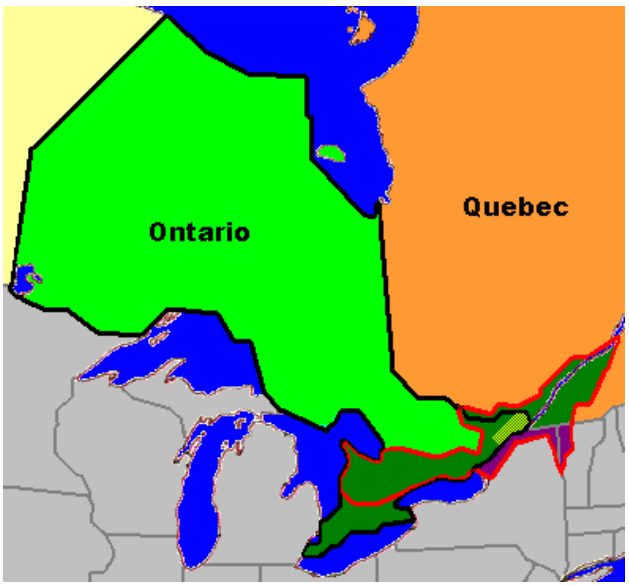
The best types of data for building demographic models include mark-recapture data, and census data (in which individuals in different age classes or stages are counted in several consecutive years). These types of data were not available for any of the three species from the study area. Actually, there were very few demographic studies of any kind on these three species in the study area or even in the region. As a result, we had to rely on studies in other regions, e.g., in the Midwestern USA. Studies in different regions often resulted in substantially different estimates of population parameters such as survival rate or fecundity. In order to make sure that the parameters we use in the models reflect the dynamics of the populations in the study area, we calibrated these parameters based on population trends observed in regions around the study area.

To estimate population trends, we used three sets of North American Breeding Bird Survey (BBS, Sauer et al., 2005) time-series data from regions which encompassed the pilot area: the Canadian Wildlife Service (CWS) indices for all of Ontario, the CWS indices for the Lower Great Lakes/St. Lawrence plain area, and the United States Geological Service (USGS) BBS population indices for the St. Lawrence plain (Figure 1). Both CWS and USGS used the BBS data for their analysis, but used different algorithms to calculate yearly population indices. These are indices of relative abundance, so they cannot be used (by themselves) to estimate or infer population levels. However, they can be used to estimate trends and levels of fluctuations.

In each case, we fist estimate the stage matrix based on available data on survival rates and fecundities. We then used RAMAS Metapop to calibrate this default matrix, by matching the observed parameters (rate of change of the population index, and the variability in the population index) from the three time series. The matrix was multiplied by a scaling factor and the CV of

the fecundity was increased until both the growth and variability targets were reached. Survival CV was kept constant at 0.1. The fecundity CV was chosen to manipulate because survival rates are bounded between 0 and 1, and consequently their CV is limited in range. Tuning for each time series produced three models, and low and high estimates for growth and variability. The mean of the three parameters was used as the medium value. In addition to environmental stochasticity modeled with the fitted CV, we also incorporated demographic stochasticity in the models. Because the trends are used to calibrate the stage matrix for future projections, there is a trade-off between using the most recent data that reflect the current trends, and using data with sufficient length (number of years) to allow a robust estimation. We used the maximum available number of years, unless there was a sharp change in observed variance or trend in the data, in which case, we used the time period following this change.

**Figure 1: Regions used to estimate population trends.**




*Ontario is outlined in black. The CWS Lower Great Lakes/St. Lawrence plain area is shown in dark green, and extends into Quebec but not the United States. The USGS St. Lawrence plain area is outlined in red. It overlaps with the CWS region, but extends into northern New York and Vermont and does not include the portion between Lake Huron, Lake Erie, and Lake Ontario. The pilot area is highlighted in yellow in eastern Ontario, and is included in all regions.*

An important factor in determining viability and stability of populations is density dependence (Ginzburg et al., 1990). Unfortunately, there is often very limited data to determine the type and strength of density dependence. In our models, we assumed Ceiling and Contest types of density dependence functions. Contest type requires an estimate of Rmax, which we based on the eigenvalue of the stage matrix that was modified as described above.

## 1.2 Habitat models

Habitat model refers to the functional relationship between land-cover or land-use variables and the suitability of the habitat for the species. This is the formula entered in RAMAS GIS as the "Habitat function" parameter in the "Habitat relationships" dialog box.

The preferred approach to developing habitat models is using occurrence data with statistical methods such as logistic regression or more recently developed methods such as MaxEnt (see a recent review by Elith et al., 2006). However, the available occurrence data (e.g., the BBS survey discussed above) have a very coarse spatial resolution compared to the relatively small spatial extent of the NAESI pilot area (and consequently limited numbers of species presence observation locations). Thus, it was not possible to construct a reliable independent habitat model for the study area. Therefore we had to rely on descriptions of nesting and foraging areas from available published sources, paired with the NAESI landcover descriptions and FRI database information to construct the habitat suitability models. Each habitat model was based on a 0 to 1 scale with 1 being most suitable.

The function for each species is then used in RAMAS GIS to create a habitat map, which becomes the basis of the metapopulation model.

## 1.3 Linking Habitat Model to Demography

This section describes the parameters that form a link between the habitat map and the full model.

### *1.3.1 Threshold Habitat Suitablity*

The "Threshold Habitat Suitability" parameter is the minimum habitat suitability (HS) value for the species modeled to reproduce. This value is used to define "suitable cells", which include any cell with an HS equal to or larger than this parameter. These are then connected according to the neighborhood distance parameter (see below) to form patches (Akçakaya, 2005). Thus, the value of this parameter represents a trade-off between including suitable areas in the habitat map and excluding unsuitable areas from the map. A lower value means more of the suitable habitat is included, and a higher value means more of the unsuitable habitat is excluded. When a habitat model is estimated by statistical methods based on presence-absence data, there are several decision-making techniques to determine the value of this threshold (see Liu et al., 2005 for a review). However, in our case, the models are based on mostly qualitative descriptions of habitat requirements (see above). Thus, we consider these habitat functions to be rather crude descriptions of the suitable habitat for each species. Consequently, we decided to set the thresholds rather low, in order not to miss any areas that may be highly suitable. We set the minimum, medium, and maximum values of the "Threshold Habitat Suitability" parameter to 0.1, 0.2, and 0.3.

### *1.3.2 Neighborhood distance*

Neighborhood distance is used to find patches in the HS map. It represents the spatial scale at which the population can be assumed to be panmictic (Akçakaya, 2005). Suitable cells (as defined above) that are separated by a distance less than or equal to the neighborhood distance are

regarded to be in the same habitat patch (i.e., in the same biological population). We based the "Neighborhood Distance" parameter on the size of the home range and density of nests for each species.

In many cases, the values for the "Threshold Habitat Suitability" and "Neighborhood Distance" parameters resulted in one large population and several smaller populations near the borders of the study area. We believe that these smaller populations may not be real biological populations; instead, they may be parts of larger populations which mostly are outside the study area. Thus, the spatial structures of the metapopulations reflect to some extent the artificial boundaries of the study area.

### *1.3.3 Carrying capacity (K)*

The carrying capacity of each patch is based on the total predicted HS in that patch, and data on the density of nests or pairs. The total HS is calculated by adding the HS value of all cells in the patch. Thus, it incorporates both the size of the patch and the quality of the habitat within the patch (Akçakaya, 2000).

In the formulae for carrying capacity, we also used a threshold function, so that patches that do not have at least 5 individuals are not considered a population. In our models, both sexes are modeled, so carrying capacities are in terms of males + females. Thus, a "population" of fewer than 5 individuals corresponds to 0 to 2 breeding pairs (depending on the sex ratio). We believe considering such a small fragment a population would overestimate carrying capacity of the metapopulation, so we set this threshold to exclude such small fragments.

### *1.3.4 Patches versus fragments*

An important aspect of the RAMAS GIS methodology (Akçakaya, 2005) is the precise definition

of a "patch" as a set of raster cells above a certain threshold of habitat suitability and within a certain neighborhood distance of each other, as well as the use of a patch to delineate the area of habitat used by one biological subpopulation of the modeled species. This definition is different from the usual (and usually arbitrary) definition of a patch as an area of a certain land cover (or vegetation) type that is surrounded by areas of different cover types, which does not incorporate species-specific biological characteristics such as mobility (dispersal ability and home range size) and the fact that habitat quality is often a continuum. Thus, for example, two areas of forest separated by a narrow gap may actually belong to the same patch as defined here, because they are used by the same biological population (even by the same breeding pair).

However, the effect of human activities on the habitats of many species is determined by, or is more easily understood and modeled in scales of, the human perception of a "patch". Thus, in order to model habitat loss scenarios (discussed below), we defined a *habitat fragment* as any single habitat pixel (i.e., a 1-ha raster cell with a suitability value of 0.0001 or greater), or any set of contiguous habitat pixels (i.e., cells sharing an edge or a corner). Thus, some fragments may not be part of any patch (because of low suitability and/or high isolation), or several fragments (that are separated by gaps smaller than the neighborhood distance) may form one patch, or, more rarely, a fragment may include multiple patches (separated by large gaps of low quality habitat).

### *1.3.5 Dispersal*

We used a dispersal-distance function to parameterize the dispersal rates, using the exponential model $M = a \exp(-D / b)$. In this model, $M$ is the dispersal rate, $D$ is the distance (km) between two populations, and $a$ and $b$ are model parameters. For distance, we used center-to-edge distances from source to target populations.

In addition, dispersal rates were linked to target carrying capacity, using the largest $K$ for all patches. This limited dispersal from large patches into small ones, which mediated the otherwise strong 'source-sink' effect.

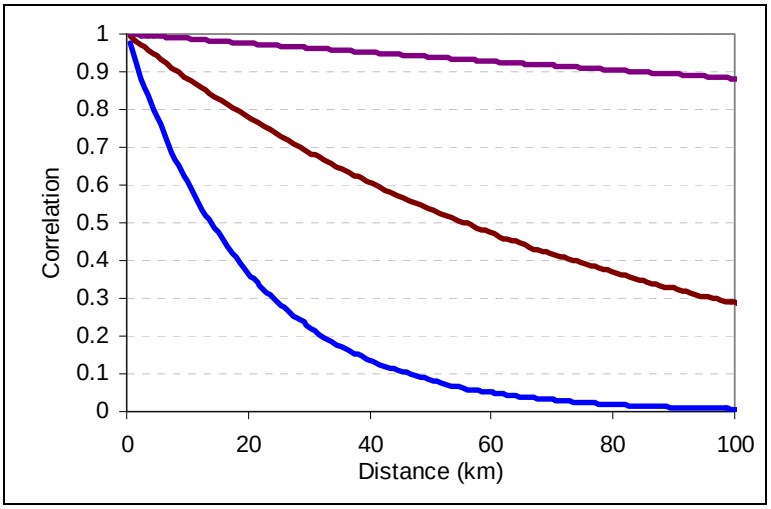
### *1.3.6 Correlation*

Estimating the magnitude of spatial correlation among the dynamics of population requires estimates of demographic variables (e.g., population size, population growth rate, vital rates) from multiple time steps and multiple locations. In the study area, the only relevant data are the population indices discussed above. However, the spatial resolution of these indices is extremely coarse compared to the relatively small area of the study area, and an analysis of these indices from different regions or provinces did not give consistent results.

The option of ignoring correlations (i.e., assuming independent fluctuations among the different populations) is unrealistic (because geographically close areas very often experience correlated environmental fluctuations), and would lead to underestimation of overall variability and hence risks. Instead, we modeled spatial correlation using a range of correlation-distance functions, using the model $C = \exp(-D / b)$, where $C$ is the correlation coefficient, $D$ is the distance (km) between two populations, and $b$ is a model parameter.

At the one extreme, we assumed that correlations would decline from 1 (full correlation) to almost 0 (independence), from a distance of zero to a distance equal to the length of the study area (about 100 km). At the other extreme, we assumed that correlations remain close to 1 even between two populations at different ends of the study area. Finally, we assumed an intermediate correlation distance function. These assumption resulted in the three correlation-distance functions with $b$=20, 80, and 800 (Figure 2).

**Figure 2: Correlation-distance functions, with parameters b=20 (bottom curve), b=80 (middle curve), and b=800 (top curve).**




## 1.4 Measures

"Measures" are the model outputs that are used to summarize the results of the simulations in terms of the performance criteria. In this section, we discuss how we used the model results to measure viability, stability and functionality of the metapopulation in the study area. For each of these three criteria, we defined two measures to capture different aspects what the criterion aims to assess. For consistency in the presentation and communication of results, we devised each measure in such a way that a higher value for the measure corresponds to higher viability, stability, or functionality. In many cases, this meant subtracting the risk result (given by RAMAS) from 1.0.

All the measures we defined depend on the time horizon over which the measurement is made (i.e., the duration of simulations). In all models we used a time horizon of 50 years, as a compromise between the need to base assessments on the long-term viability, stability and

functionality of the metapopulation, and the need to minimize prediction uncertainty due to the limited data the models are often based on. All models were run with 10,000 replications.

### *1.4.1 Viability*

Viability is the likelihood that the population will remain extant in the future.

1. **Persistence probability (One minus risk of quasi-extinction).** We defined persistence probability as the probability that the population will remain above a certain threshold for the entire duration of a simulation. We calculated this as one minus the risk of decline to or below that threshold anytime during the simulation, using the Interval Extinction Risk result.

In RAMAS, we calculated this measure by including only adult males and adult females in the population totals, and using the Interval Extinction Risk result to obtain an estimate for the risk of falling to or below thresholds of **0, 50, 250, or 1000 adults** anytime during the 50-year simulation. The threshold of zero is for measuring probability of being extant (one-extinction risk). We based the other threshold for this measure of viability on the IUCN Red List criterion D for the number of mature individuals: 50, 250, and 1000 mature individuals are the IUCN thresholds for the Critically Endangered, Endangered, and Vulnerable categories, respectively.

For most cases, we used a threshold of 250 mature individuals (based on Endangered). In some cases, this was not informative, because all scenarios resulted in persistence probabilities very close to 1.0 or 0.0. In such cases, we used lower or higher thresholds (as indicated) for all the scenarios being compared (we do not present results with different thresholds in the same table column or in the same figure).

For example, in the best-case and worst-case assumptions, a threshold of 250 may be

uninformative, because the risks are very close to 0 and 1, respectively. In such a case, the scenarios for habitat loss can be compared under each assumption, using thresholds of 1000 mature individuals for best-case assumption and 50 mature individuals for the worst-case assumption. Of course, in this case, the best-case and worst-case scenarios are not compared to each other, or even plotted in the same graph.

**2. Expected minimum number of adults (EMA).** This measure of viability is the minimum number of mature individuals (as defined above) in the metapopulation at any time during the simulated 50 years. The minimum values from all replication are averaged to estimate the average, or expected, minimum abundance. Thus, this measure is an estimate of the smallest number of mature individuals' that is expected to occur within the simulated time period. The expected minimum abundance is often used as an index of propensity to decline, especially when the population variability and risks of decline are low. In addition, expected minimum abundance can be used to compare results of two models: the area between two interval extinction risk curves is equal to the difference between the two expected minimum abundance estimates (McCarthy and Thompson, 2001).

### *1.4.2 Stability*

Stability is not well defined in the progress report and other related documents of the NAESI project. With respect to a single species dynamics, stability is often defined in terms the propensity of population size to return to equilibrium after the population size has been perturbed (increased or decreased by an external factor). Stability in this sense is directly related to (and is a function of) the type and strength of the density dependent regulation of the population. In the species we studied, there was no quantitative information on the strength of density dependence,

so stability in this sense would only reflect model assumptions, and would not be a practical measure. Another, less technical, meaning of population stability is remaining at the same size, or, more commonly, not declining. We devised two measures based on this definition of stability. Both measures we describe below are based on the probability distribution of final metapopulation sizes.

**1. Median growth rate (Ratio of median final to initial abundance).** This measure is calculated as the ratio of the median final metapopulation size to initial total metapopulation size (including all individuals). A value greater than 1.0 means a population that will likely increase, and a value less than 1.0 means a population that will likely decrease. Thus the lower this measure, the less stable the population is likely to be.

In several cases, the models predicted an initial decline followed by a more stable population trajectory in the later part of the simulated time period. In such cases, this stability measure was mostly determined by the initial decline. An alternative stability measure might focus only in the final X number of years of the simulated period, if the initial decline is judged to be either transitional or an artifact of the model assumptions. Although this may be a reasonable alternative measure of stability, it would require an additional (rather arbitrary) decision on the proportion of the total trajectory to consider. Thus, we decided to use the total trajectory, but would like to mention this alternative for possible use in future assessments.

**2. Robustness (One minus risk of 50% terminal decline).** This measure is intended to take into account the stochastic nature of the models. Even if the median population does not decline, or even increases, variability may cause a substantial risk that the final population size will be less than the initial population size. We calculated this measure as **one minus** the probability that

the final metapopulation size (including all individuals) is less than 50% of the initial total metapopulation size under medium parameter values. In RAMAS, we calculated this measure using the Terminal Percent Decline result to obtain an estimate for the risk that the final metapopulation size (at year 50) is less than 50% of the initial metapopulation size, and subtracting this from 1.0.

It is important to note two aspects of this measure. First, the threshold for this measure is relative to the initial abundance for the particular model (e.g., for a given scenario). This has important implications for comparing scenarios and simulations that differ in the assumed initial population size. Second, the measure is based on the probability distribution of final metapopulation sizes; thus it is a measure of "terminal" (as opposed to "interval") risk. In these two characteristics, this measure differs from the Functional Presence measure (defined below).

### *1.4.3 Functionality*

Functionality refers to population size being large enough for the population to fulfill its ecological functions. These functions may be related to a species' trophic role as prey or predator, or in terms of its effect on vegetation, species composition, or physical, chemical, or structural characteristics of the ecosystem. In the absence of a clear definition of the desired function, and the characteristics of the species' population (in terms of size, age composition, etc.) necessary to fulfill that function, it is not possible to use population models to measure functionality. As a result, we adopted two generic measures. One measure is related to the probability that the metapopulation will maintain a certain abundance in the future, and the other is related to the minimum size the metapopulation is likely to reach in the future.

1. **Functional Presence (One minus risk of interval decline).** We defined this measure as

the probability that, in any year during the simulation, the total metapopulation size (including all individuals) is more than a fixed threshold, which is set at 50% of the initial total metapopulation size under medium parameter values for each species. We calculated this measure as **one minus** the risk of decline to a fixed threshold, and used the Interval Extinction Risk result to obtain an estimate for the risk anytime during the 50-year simulation.

It is important to note that, unlike the Robustness (a measure of stability discussed above), the threshold for this measure is absolute (not relative to the initial abundance for each scenario). Also unlike the Robustness measure, this is an "interval" (as opposed to "terminal") measure; Functional Presence requires the metapopulation size to be above the threshold ***in all years***, not just the final year.

**2. Expected minimum total abundance (EMTA).** This measure of viability is the minimum total abundance in the metapopulation at any time during the simulated years. The minimum values from all replications are averaged to estimate the average, or expected, minimum abundance. Thus, this measure is an estimate of the smallest metapopulation size that is expected to occur within the simulated time period. This is similar to the "Expected minimum number of adults" measure discussed under viability, but it is based on the total population size. As discussed above, the expected minimum abundance is used especially when the population variability and risks of decline are low (McCarthy and Thompson, 2001). In such cases, risks of extinction are low, but the total population size may still decline below functional levels. In addition, expected minimum abundance makes it easier to compare scenarios with large differences in variability and risks of decline. Comparing such scenarios using risk of decline may be difficult when the risks are close to 0 or 1 for one or more scenarios regardless of where

the decline threshold is set.

### *1.4.4 Target population levels*

We did not use any measures related to target population levels, because we could not find any that were both relevant and specific enough. The only target population level mentioned for any of the three species in the Terms of Reference (or RFP) for this project involved the Red-shouldered Hawk. This target is to maintain current population of 13,000 birds in Ontario, based on a 2005 conservation plan by Partners in Flight. However, there are two problems with this target. First, it is not specific to the study area. Determining a target for the study area, based on this regional target requires additional assumptions. Second, the target is deterministically set at the current population size. However, natural populations are not deterministic; they fluctuate due to demographic and environmental factors. Thus, it is almost certain that the target will not be met (i.e., the population will decline below the current level in at least one year), unless the target is expressed in a more realistic way. For example, the target may be set at a low probability of falling below a certain level, which in turn can be based on the current population size. This is the approach we took in defining *functional presence*, one of the functionality measures (see above).

## 1.5 Simulations

For each species, we performed two sets of simulations. One set was for sensitivity analysis and focused on identifying parameters to which the models results were most sensitive. The second set of simulations focused on the potential effects of future habitat loss scenarios on the viability, stability and functionality of the metapopulations in the study area.

### *1.5.1 Sensitivity analysis*

The primary simulation used the medium value for each parameter. To test the sensitivity of the results, two additional models were created for each parameter.

The 'high' model used the maximum value for the parameter with all others remaining at their medium values, while the 'low' model used the minimum value similarly. The stage matrix scaling factor was an exception, using 'ceiling' density dependence instead of the medium 'contest 1.1' value. This is because 'contest' density dependence itself alters the stage matrix, and would render the stage matrix adjustments moot.

Results were evaluated using the same viability, stability, and functionality measures used for the primary simulation. Sensitivity to each parameter was determined by the range between minimum and maximum values for each measure. Once parameter effects were known, 'best case' and 'worst case' models were constructed by combining the 'increased viability' and 'decreased viability' values, respectively, for each parameter.

### *1.5.2 Habitat loss scenarios*

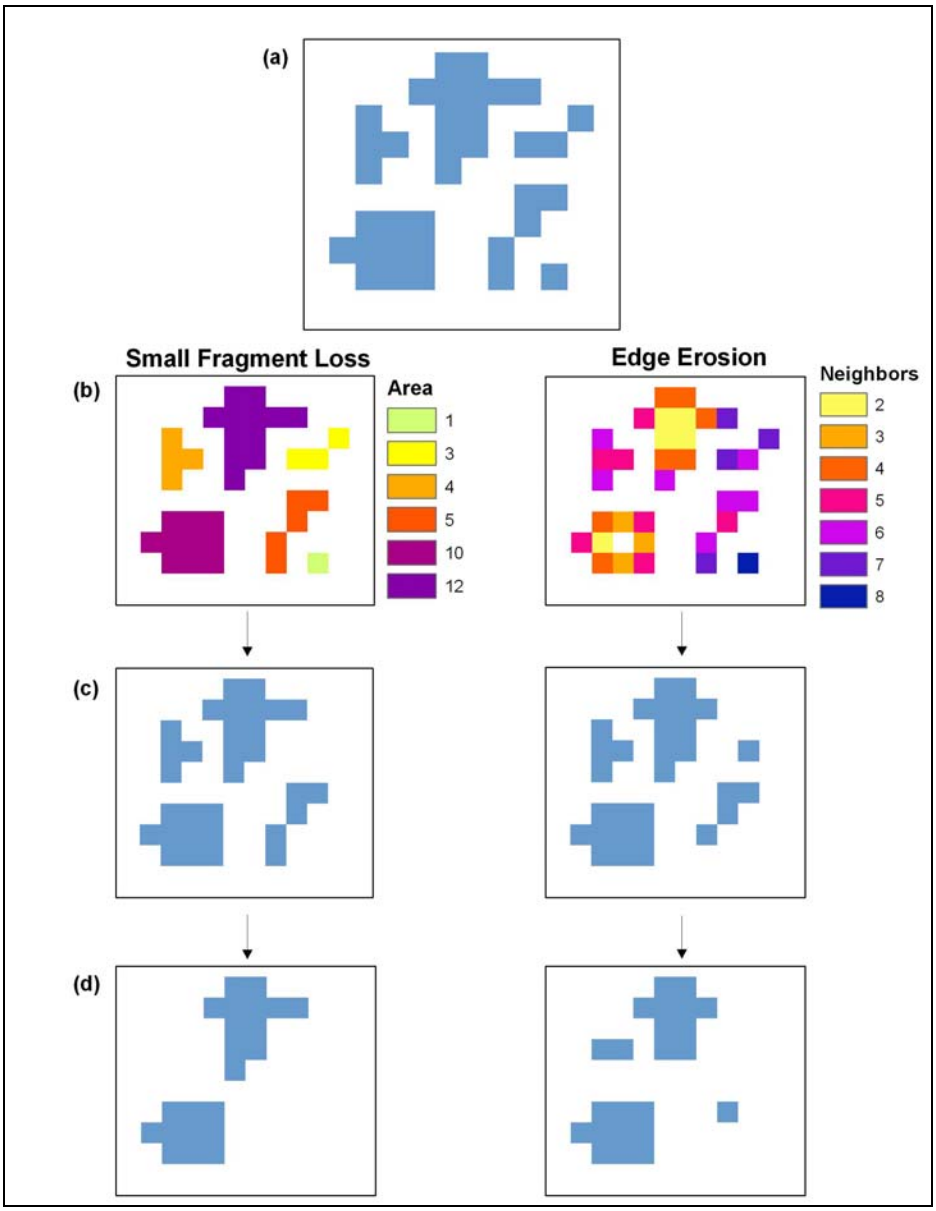
For each species, we modeled two different habitat loss scenarios to explore how the spatial pattern of landscape change will effect the population. In both scenarios, any single habitat pixel (i.e., a 1-ha raster cell with a suitability value of 0.0001 or greater), or any set of contiguous habitat pixels (i.e., cells sharing an edge or a corner), is considered a 'fragment'. The first scenario ("small fragment loss") makes the assumption that smaller fragments of remnant habitat will be most vulnerable to conversion to other land uses and will be lost before larger fragments. It represents an example of only the largest tracts of habitat being protected and managed for suitability for the species. We modeled this scenario by ranking fragments by total area and

removing entire fragments from the study area, from smallest to largest (see Figure 3).

The second scenario ("edge erosion") assumes that habitat will be lost through a process of degradation from patch edges and openings. This scenario simulates situations where non-habitat land use encroaches along the edges of habitat fragments due to intensification of agriculture (removal of hedges and natural borders), increased livestock grazing along edges, introduction of invasive species, widening roads, or incrementally increasing development. In this scenario, relatively small fragments will be lost before larger fragments due to the higher edge/interior ratio. We modeled this scenario by systematically setting to zero habitat pixels adjacent to non-habitat pixels, in general removing more exterior pixels before the more interior (see Figure 3).

In both scenarios, the current landscape is represented as 0% habitat loss. We ran both scenarios at five stages of habitat loss ranging from approximately 20 to 70% of the present total habitat area. Both scenarios were run with the population model under the medium parameter values, then again with both the population models representing the best and worst case for comparison.

**Figure 3: Simplified example of the two habitat loss scenarios. (a) The initial landscape, with each raster cell represented as habitat (blue) or not habitat (white). (b) The categorization of raster cells for modeling the two scenarios.**




*For the small fragment loss scenario, each contiguous (sharing an edge or corner) set of raster cells is identified as a 'fragment' and each fragment is identified with its area. For the edge erosion scenario, each raster cell is identified with the number of non-habitat neighbors (thus, a single habitat pixel with no others around it gets a value of 8). (c) First step of habitat loss. For the small fragment loss scenario, fragments with sizes (areas) less than or equal to 3 pixels are eliminated. For the edge erosion scenario, pixels with 7 or more non-habitat neighbors are eliminated. (d) Second step of habitat loss. For the small fragment loss scenario, fragments with sizes less than or equal to 5 pixels are eliminated. For the edge erosion scenario, pixels with 6 non-habitat neighbors are eliminated.*

# 2 RED-SHOULDERED HAWK

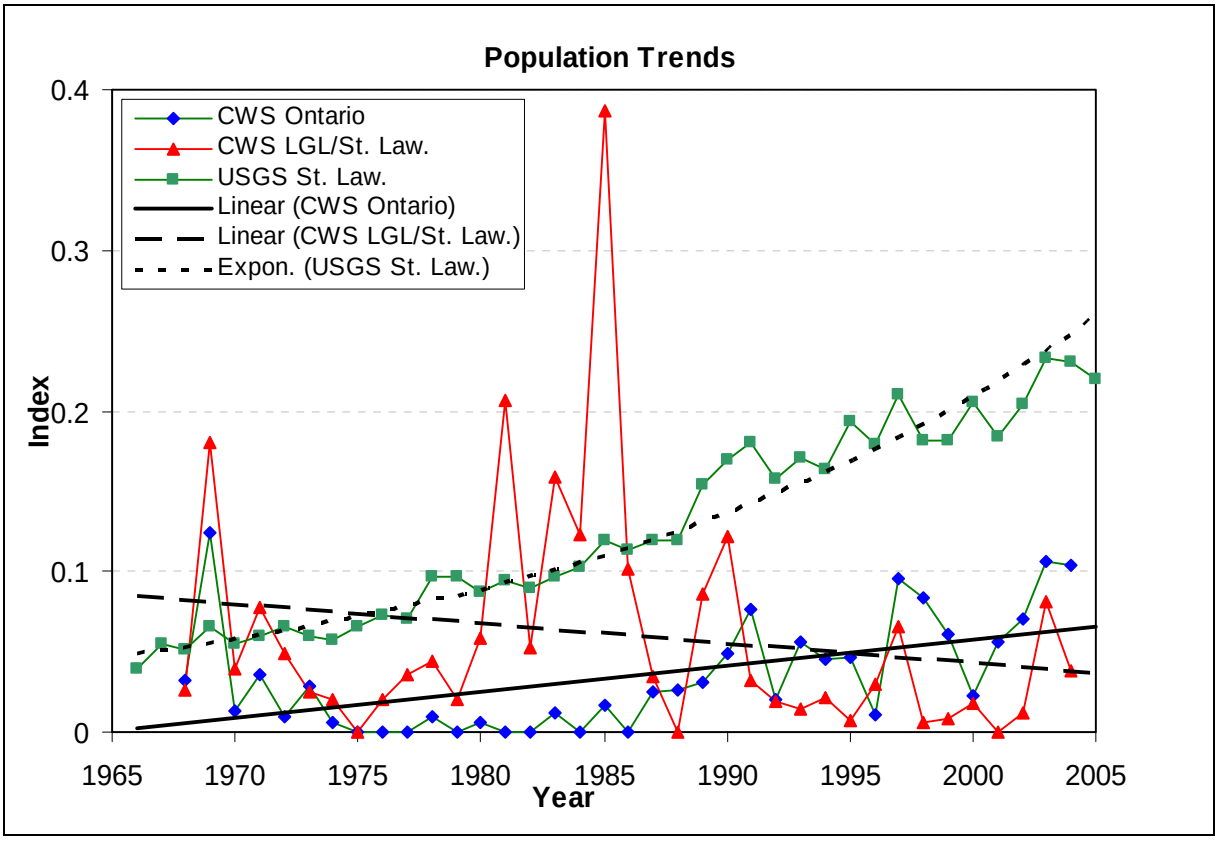
The Red-shouldered Hawk (*Buteo lineatus*) is a species that depends on multiple habitat types. It nests in mature forest stands, but depends on riparian areas, woody swamps, and wetland margins for forage. The Red-shouldered Hawk was selected as a surrogate for these habitat types due to its habitat area requirements, large home range, and dependence on forest interiors.

## 2.1 Demographic Model

### *2.1.1 Population trends*

The time periods covered were 1968-2004 and 1966-2005 for the CWS and USGS BBS series, respectively (Figure 4). These time series were used to estimate growth rate and population variance for Red-shouldered Hawk in the pilot area. The mean indices of the first and last 5 years were compared to determine overall population change. Our simulations were tuned using the final mean population and coefficient of variation as targets (see below).

**Figure 4: Population trends in regions of interest. Y-axis indicates a derived population index. The USGS series uses a different index algorithm than the two CWS series.**




### *2.1.2 Stage matrix*

The matrix consisted of only two stages, juvenile and adult (Table 1), and modeled a pre-breeding census. We derived all values from Jacobs and Jacobs (2002). First reproduction was reported as mainly in the second year, although 5.3% of females reproduced in the first year. Ninety-seven % of adults bred each year. Young fledged per nest was 1.607, based on a weighted average of the Minnesota, New York, and Ontario results (Wisconsin was excluded because Jacobs and Jacobs considered it to be non-representative). Mean survival rates were 47% for juveniles and 77.5% for adults.

Fecundity, based on pre-breeding census, was calculated as:

(percent breeding) * (average fledged /nest) * (juvenile survival) * 0.5.

The default stage matrix is in Table 1. The stable distribution is 26.2% juveniles, 73.8% adults.

**Table 1: Default stage matrix**

| | **Juvenile** | **Adult** |
|---|---|---|
| Juvenile | 0.020 | 0.366 |
| Adult | 0.775 | 0.775 |

We tuned the default matrix using RAMAS Metapop to match the observed parameters from the three time series. The matrix was multiplied by a scaling factor, and the CV of the fecundity was increased until the growth and variability targets were reached. Survival CV was kept constant at 0.1. Tuning for each time series produced three models and low and high estimates for growth and variability (Table 2). The mean of the three parameters was used as the medium value because the middle observed value was very close to the maximum. The mean scaling factor was 0.974 and the mean fecundity CV was 0.664.

**Table 2: Targets and tuning parameters for regional data series. (Target values were reached within +/- 2.5%)**

| **Series Info** | | **Targets** | | **Tuning Parameters** | | |
|---|---|---|---|---|---|---|
| **Region** | **Years** | **Final N** | **Pop. CV** | **Scaling fact.** | **Fec. CV** | **Surv. CV** |
| CWS Ontario | 37 | 501 | 1.012 | 0.984 | 0.871 | 0.1 |
| CWS LGL/St. Law. | 37 | 120 | 1.254 | 0.950 (Low) | 1.000 (High) | 0.1 |
| USGS St. Law. | 40 | 1203 | 0.469 | 0.988 (High) | 0.120 (Low) | 0.1 |
| Average (for Medium values) | | | | 0.974 | 0.664 | 0.1 |

After adjusting the stage matrix and the standard deviations matrix, we added sex structure to the model, by adding juvenile male and adult male stages, and assuming monogamous mating. The stage matrix and the standard deviation matrix with sex structure and medium values are given in Table 3.

**Table 3: Stage matrix (top) and standard deviations matrix (bottom) with medium values for vital rates and their variabilities.**

| | | **Females** | | **Males** | |
|---|---|---|---|---|---|
| | | **Juvenile F** | **Adult F** | **Juvenile M** | **Adult M** |
| Female | Juvenile F | 0.01948 | 0.35648 | 0 | 0 |
| | Adult F | 0.75485 | 0.75485 | 0 | 0 |
| Males | Juvenile M | 0.01948 | 0.35648 | 0 | 0 |
| | Adult M | 0 | 0 | 0.75485 | 0.75485 |
| Female | Juvenile F | 0.01294 | 0.2367 | 0 | 0 |
| | Adult F | 0.02451 | 0.02451 | 0 | 0 |
| Males | Juvenile M | 0.01294 | 0.2367 | 0 | 0 |
| | Adult M | 0 | 0 | 0.02451 | 0.02451 |

### *2.1.3 Density dependence*

We assumed Ceiling-type and Contest-type density dependence functions. Contest type also requires an estimate of Rmax. The eigenvalue of the medium matrix was 1.023.This is the average growth rate, and is likely lower than the maximum growth rate at low population sizes. Thus, we assumed Rmax=1.1 or 1.2. Only 5% of juveniles (one-year-olds) breed, thus, we assumed that density dependence (and carrying capacity) is based on the abundance of adult females and adult males.

## 2.2 Habitat Model

The habitat suitability in this model is based on a 0 to 1 scale with 1 being most suitable. Overall

habitat suitability is the product of three factors; 1) forest type, 2) proximity to water or wetlands, and 3) stand age.

### *2.2.1 Forest type*

Red-shouldered Hawks are most often associated with hardwood and mixed forest habitat including upland stands (Armstrong and Euler, 1982) as well as bottomland, riparian areas, and swamps (Crocoll, 1994, Jacobs and Jacobs, 2002). Some studies report associations with forest stands of specific tree species composition (Holloway et al., 2004). However, due to the fact that over 40 different species have been reported as Red-shouldered Hawk nesting trees (Jacobs and Jacobs, 2002) it is more likely that the physical structure and proximity to other landscape features such as good hunting grounds are more important than species composition.

All deciduous and mixed forests with dry-fresh and fresh-moist soils were selected as potential habitat. This includes the NAESI land cover classes 2002-2008, and 3001-3008. Deciduous and mixed swamp lands were also selected. These include the NAESI classes 4005-4017. Without more information on forest preference in the study region all forests within these classes were given an equal 'forest type' value of 1.0 in the habitat suitability equation.

### *2.2.2 Water and wetlands*

Proximity to water is considered an important landscape characteristic for Red-shouldered Hawk habitat suitability. This is believed to be due to the large portion of amphibians, reptiles, and small mammals dependent on standing water or moist ground in Red-shouldered Hawks' reported diets (Jacobs and Jacobs, 2002). Dykstra et al. (2000) and McLeod et al. (2000) found Red-shouldered Hawk nesting sites to be closer to water than paired random sites. Similarly, another study found Red-shouldered Hawks use wetland and riparian habitats more than their

proportional availability in the landscape (Dykstra et al., 2001).

The distance of nesting sites to water or wetland features is highly variable across studies, ranging from less than 50m to more than 300m (Jacobs and Jacobs, 2002). Since we wish to model suitable habitat for both nesting and foraging, when selecting distance to water boundaries we opted to be more inclusive of potential habitat by allowing the water feature to occur within the likely range of a nesting bird. Most reported home ranges are between 90 and 175 ha (Jacobs and Jacobs, 2002), with a core area only a fraction of the entire home range (Dykstra et al., 2001).

We set a primary buffer of 0.4km around all water, and non-forested wetland sites (NAESI classes 4019-4021, 4101, 4102, and 9001) with a 'proximity to water' value of 1.0. An additional buffer was also added for distances between 0.4 and 0.8km from water (NAESI class 9001) with a value of 0.5. Deciduous and mixed forested stands classified as 'swamp' (NAESI classes 4005-4017) were given a 'proximity to water' value of 1.0.

### *2.2.3 Stand age*

Red-shouldered Hawks generally prefer mature forests with closed canopies (Armstrong and Euler, 1982, Crocoll, 1994, Jacobs and Jacobs, 2002). McLeod et al. (2000) found that trees in nesting sites had higher DBH and basal areas than paired random plots in Minnesota with nest tree ages estimated at 50 to 89 years. Most studies that report age of nesting tree or stand give ages between 40 and 200 years old (Jacobs and Jacobs, 2002).

We gave stands with present age greater or equal to 40 but less than 80 years a value of 0.8. Stands greater than or equal to 80 years received a 'stand age' value of 1.0. Stands less than 40 years old were given a value of zero. Data used to calculate present stand age was taken from the NAESI linked FRI database from 1991, therefore, we adjusted stand age accordingly by adding

15 to the reported 1991 age. Where no stand age was reported in the FRI data, stands received a value of zero.

### *2.2.4 Habitat mapping*

The spatial extent of each of the above components of habitat suitability were initially mapped separately at 2m resolution (with the exception of the distance to water which was calculated at a 4m resolution to speed computing time) using the raster coverages of the pilot area and given their respective suitability values. The separate components were then each converted to a coarser resolution of 100m using the 'aggregate' function in ArcGIS Spatial Analyist (ArcView 8.1.2) which will assign a new value to each coarser resolution pixel based on the mean average of the values of the underlying finer resolution pixels. The separate components of the suitability measure were then combined to find overall habitat suitability at the coarser resolution (see Figure 5).

## 2.3 Linking Habitat Model to Demography

### *2.3.1 Threshold Habitat Suitability*

The method with which we modeled habitat necessitates setting a threshold value on habitat suitability (see discussion on this topic in the introduction). We set the "Threshold Habitat Suitability" parameter to 0.1, 0.2, and 0.3. At these thresholds, respectively, 68, 58, and 50% of all cells with non-zero habitat suitability are above the threshold totaling 19, 16, and 14% of the total land area of the pilot study (see Figure 6).

### *2.3.2 Neighborhood distance*

We based the "Neighborhood Distance" parameter on the size of the home range and density of nests. For a minimum value, we used the density of nests or pairs in 6 studies in WI, NY, MD,

and OH. The average density in these six studies was 0.85 nests/km$^2$, which corresponds to a distance of about 1.2 km between circular territories. For a maximum value of the "Neighborhood Distance" parameter, we used the maximum size of breeding home range, which is reported as 339 ha (Crocoll, 1994), and corresponds to a distance of about 2.1 km. For a medium estimate, we used the mid-point of this range. Thus, we used Neighborhood Distances of 12, 17, and 21 cells (1 cell==100 m).

### *2.3.3 Carrying capacity (K)*

We based our estimate of carrying capacity of a patch, on the total habitat suitability in that patch. Thus, both the size of the patch (number of cells) and the quality of habitat in the patch (HS value of each cell) contribute to the carrying capacity in the patch.

The function that links the carrying capacity of a patch (K) to the total habitat suitability in that patch is:

K = thr(0.036*ths,5).

In this formula, "thr" is the threshold function, so that patches that do not have at least 5 individuals are not considered a population. In our model, both sexes are modeled, so K is in terms of breeding males + breeding females. Thus, a "population" of fewer than 5 individuals corresponds to 0 to 2 breeding pairs (depending on the sex ratio). We believe considering such a small fragment a biological population would overestimate carrying capacity of the metapopulation, so we set this threshold to exclude such small fragments. This is consistent with the suggestion that this species prefers patches >100 ha. But, it is also consistent with the suggestion that it may utilize patches as small as 10 ha. The important point here is the definition of a patch. As discussed in the Introduction (see *Patches versus fragments*), a patch is defined as

a set of raster cells above a certain threshold of habitat suitability and within a certain neighborhood distance of each other, and used to delineate the area of habitat used by one biological subpopulation of the modeled species. Thus, RSH may use habitat *fragments* as small as 10 ha, but biological populations are not likely to exist in habitat *patches* that do not support at least 5 individuals.

In the above formula, "ths" is total habitat suitability, i.e., the sum of HS values of all cells in the patch. This number is multiplied by a constant (0.036) to calculate the carrying capacity. This constant has units of breeding individuals per cell (per ha). We calculated this constant based on the maximum density of nests observed. Jacobs and Jacobs (2002) estimated a density of 1.8 per $km^2$ in central Wisconsin, which corresponds to 3.6 breeding individuals per $km^2$, and 0.036 breeding individuals per ha (or per cell). For minimum and maximum values, we used ±20% (0.029 and 0.043).

The model with medium parameters for "Threshold Habitat Suitability", Neighborhood Distance and K function resulted in two habitat patches (see Figure 7).

### *2.3.4 Initial abundance*

We assumed that initially, all populations are at their carrying capacity. Because K is in terms of breeding stages, the function for initial abundance is the function for K, divided by the proportion of the population in breeding stages. For example, with the medium stage matrix, 73.8% of the population is in adult stages at the stable age distribution. Thus, the function for initial abundance is:

$$N_0 = (0.036/0.738)*ths = 0.0488*ths$$

Note that the "thr" function is not necessary here, because initial abundance is calculated only for patches that are identified as populations, based on the carrying capacity function.

### *2.3.5 Dispersal*

We used a dispersal-distance function to parameterize the dispersal rates, using the exponential model $M = a \exp(-D / b)$. In this model, $M$ is the dispersal rate, $D$ is the distance (km) between two populations, and $a$ and $b$ are model parameters. For distance, we used center-to-edge distances from source to target populations. In the model with medium parameters, the center-to-edge distances were 8.8 and 23.4 km, from small to large, and from large to small populations, respectively.

Red-shouldered Hawks are thought to occupy the same territory for life, often using the same nest tree (Crocoll, 1994). In one Wisconsin study (Jacobs and Jacobs, 1993), of 60 nests used in 1992, 50% were reoccupied the following year, and none of new nests were more than 400 m from their 1992 locations. Thus, we modeled dispersal only for the juvenile stages.

The dispersal rates of juveniles were based on data from individuals banded as nestlings or fledglings. In Wisconsin, 11 banded nestlings (six males, five females), later recaptured as breeding birds, dispersed an average distance of only 16.95 km (.38-80.5 km). Females moved farther than males. Five females averaged 26.6 km; six males averaged 8.9 km. (Jacobs and Jacobs, 1995; 2002). In southwestern Ohio, analysis of distance from natal nest at time of encounter indicated that 50% of Red-shouldered Hawks were found <15 km from their natal nest, 75% were <29 km away, and 95% were <62 km away (Dykstra et al., 2004).

Based on these data, we used an exponential dispersal-distance function with the distance-related parameter ($b$) set as 20, and the scaling parameter $a$ to a value of 0.34. The $b$ parameter was

fitted to 21.63 (using MS Excel goal-seek) based on Dykstra et al. (2004). Distance classes were assumed to be 8.5 to 20.5 (small to large) and 23.5 to 30.5 (large to small). At this *b*, the proportions of exponential distribution within these two distance classes are 25.1% and 9.1%, respectively. We adjusted the scaling parameter *a* to 0.34so that at the center-to-edge distances, the dispersal rates were similar to these.

### *2.3.6 Sensitivity analysis*

The minimum, medium and maximum values of the parameters used in the simulations are given in Table 4.

**Table 4: The values of model parameters used in the simulations**

| Parameter | Minimum | Medium | Maximum |
|---|---|---|---|
| Stage matrix (scaling factor for default matrix) | .950 | .974 | .988 |
| Variability in vital rates (fecundity CV) | .120 | .664 | 1.000 |
| Threshold Habitat Suitability | 0.1 | 0.2 | 0.3 |
| Neighborhood Distance (cells lengths, 100 m) | 12 | 17 | 21 |
| Density dependence (type, and Rmax if Contest) | Ceiling | Contest 1.1 | Contest 1.2 |
| Carrying capacity (K) function (adult males and female adults, as a multiple of total habitat suitability in the patch) | 0.029 | 0.036 | 0.043 |
| Initial abundance function (number of individuals as a multiple of total habitat suitability in the patch) (co-varies with K function) | 0.0393 | 0.0488 | 0.0583 |
| Dispersal, scaling parameter a | 0.17 | 0.34 | 0.51 |
| Dispersal, distance parameter b (co-varies with a) | 10 | 20 | 30 |
| Correlation-distance function parameter b | 20 | 80 | 800 |

## 2.4 Results

### *2.4.1 Habitat model*

The habitat model resulted in the map in Figure 5.

**Figure 5: Suitable habitat for Red-shouldered Hawk within study area**

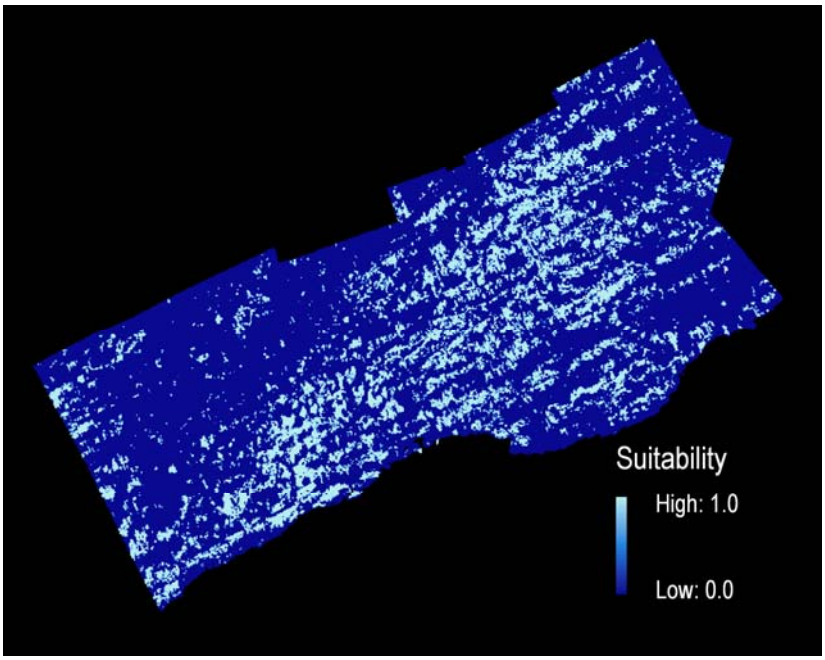



**Figure 6: Percentage of total study area with HS values greater than or equal to the values in the x-axis. For example, 12% of the study area has HS values of 0.4 or more.**

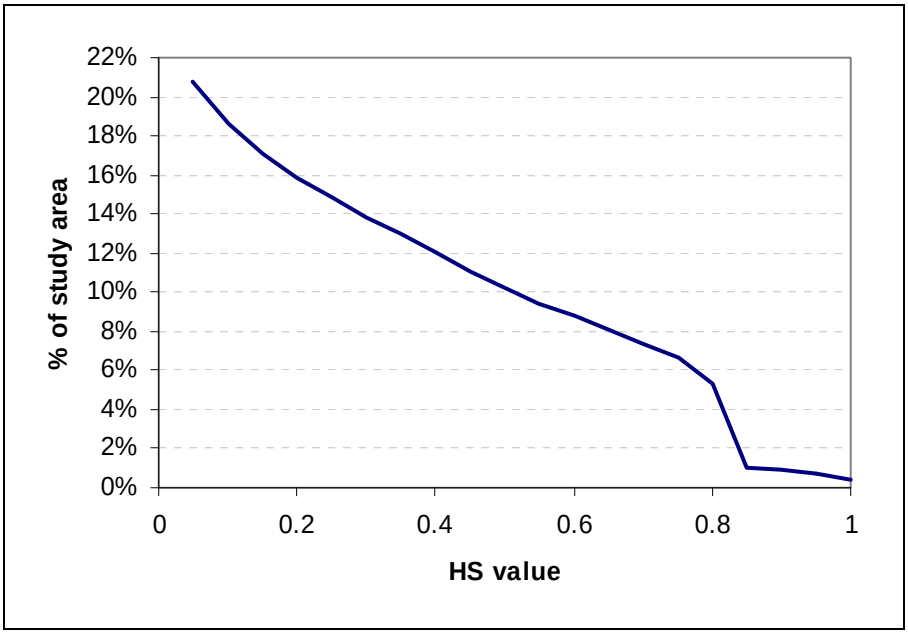
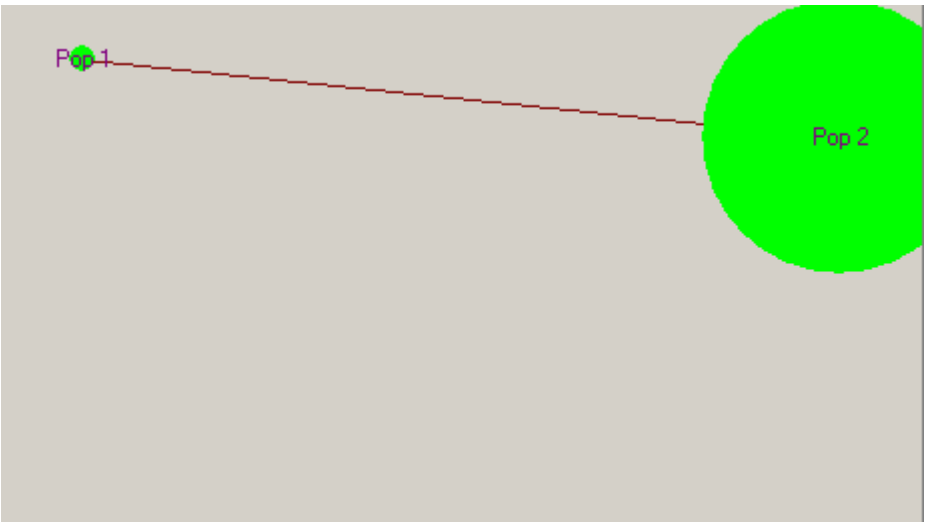


**Figure 7: Metapopulation structure of medium model. All populations are initially at carrying capacity with a stable stage distribution**




### *2.4.2 Simulation results with the Medium model*

The primary, or 'medium', population model used the medium values for all parameters. It had 2 patches (Figure 7) and a total initial abundance of 1549 individualsdivided into 406 juveniles and 1143 adults.

#### 2.4.2.1 Viability

For the medium model, persistence probability (measured as one minus risk of quasi-extinction) was 0.9861 for a threshold of 250 individuals.Expected minimum adult abundance was 538.6.

#### 2.4.2.2 Stability

Median growth rate (ratio of median final abundance to initial abundance) was 0.7224, indicating a decline from initial abundance.However, the decline appeared to be asymptotic (Figure 9). Mean yearly growth rate was 0.9953. Robustness (measured as one minus risk of 50% terminal decline) was 0.8050.

#### 2.4.2.3 Functionality

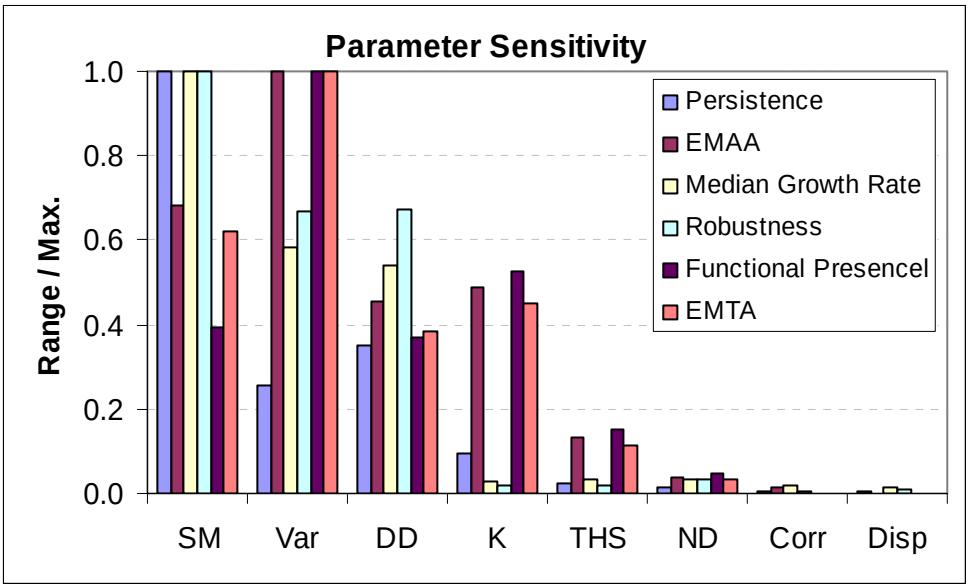
Functional presence (measured as one minus risk of interval decline to a threshold of 775 individuals) was 0.3031, and expected minimum total abundance (EMTA) was 683.5.

Overall, the medium model resulted in a declining population, albeit one which appears to be stabilizing eventually at approximately 80% of its initial abundance. According to the sensitivity analysis, the most important factor affecting the model is the amount of variability in vital rates and density dependence (see below).

### *2.4.3 Sensitivity analysis*

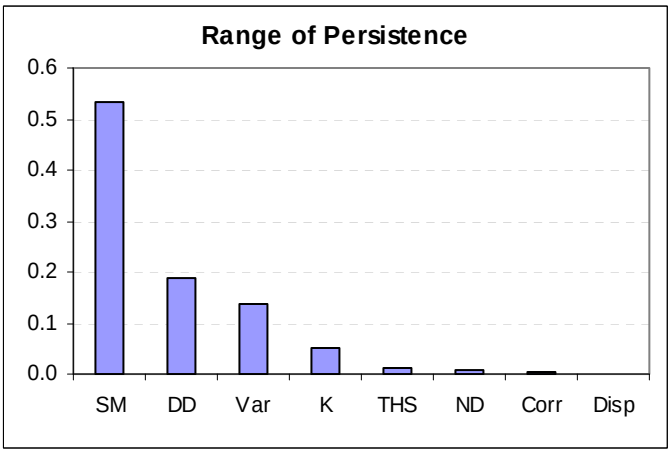
The sensitivity analysis identified the stage matrix (SM) and variability (Var) as the parameters to which the model was most sensitive. The measures were also sensitive to density dependence (DD) and the carrying capacity function (K). The threshold for habitat suitability (THS), neighborhood distance (ND), correlation (Corr), and dispersal (Disp) were relatively unimportant (Figure 8).

**Figure 8: Parameter sensitivity. Values are normalized ranges within each measure. Range for each parameter indicates maximum minus minimum from the 'high' and 'low' models. This value is then normalized by dividing by the maximum range across all parameters for the same population measure.**



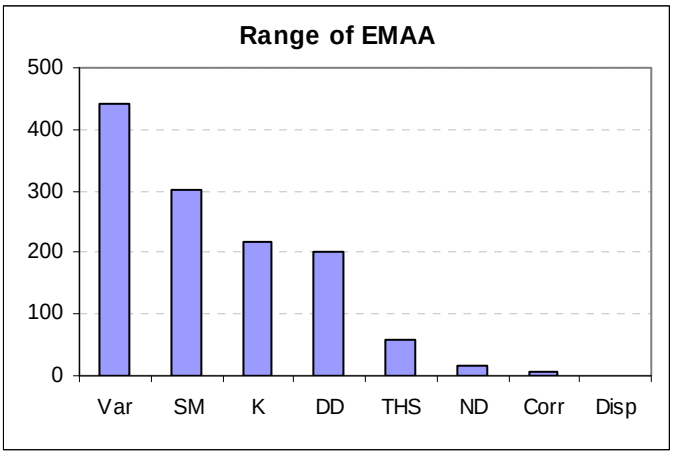

The parameters are sorted by mean normalized range across the six measures (A-F).

**A. Ranges for the risk of dropping below 250 adults. This measure is most sensitive to the stage matrix.**

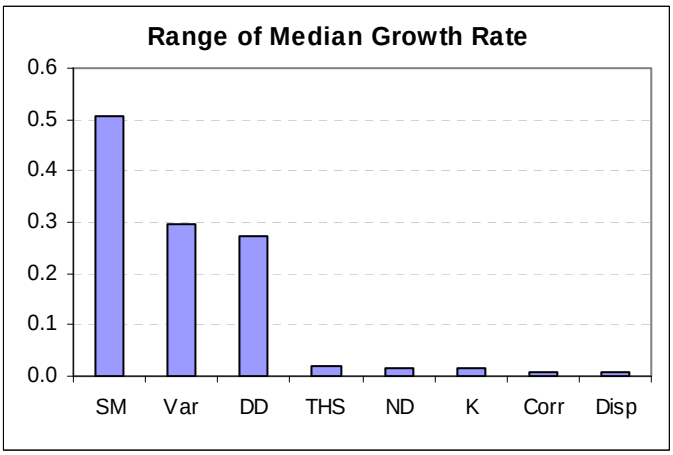



.

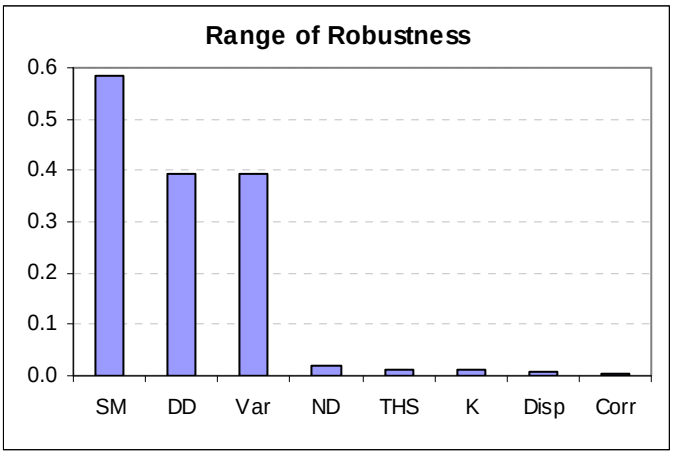
**B. Ranges for the minimum expected adult abundance (EMAA). This measure is most sensitive to variability and the stage matrix.**



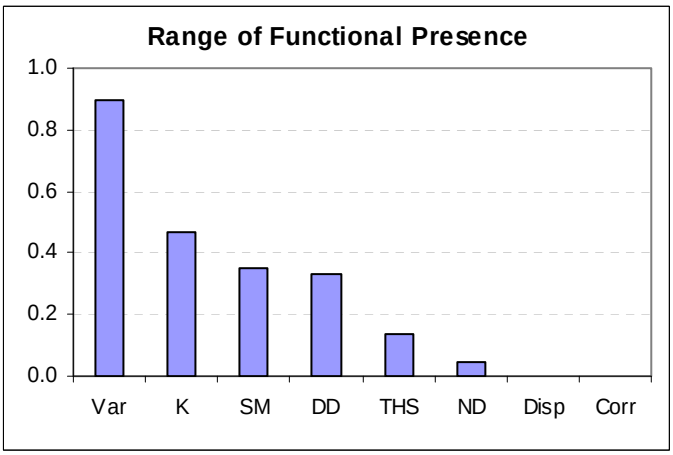

**C. Ranges for the proportion of median final abundance to initial abundance. This measure is most sensitive to the stage matrix, variability, and density dependence.**



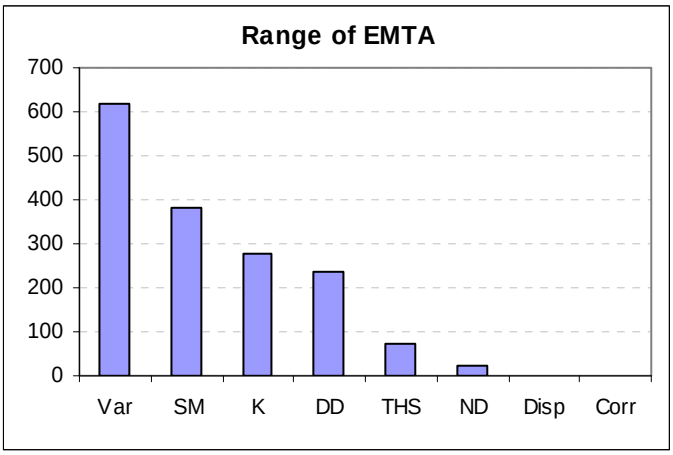
**D. Ranges for the risk of dropping below 50% of initial abundance for the final time step. This measure is most sensitive to the stage matrix, density dependence, and variability**




**E. Ranges for the risk of dropping below 50% of standard initial abundance for any time step. This measure is most sensitive to variability and carrying capacity**



**F. Ranges for the minimum expected total abundance. This measure is most sensitive to variability and the stage matrix.**




### *2.4.4 Best-case and worst-case models*

Using the sensitivity analysis, best-case and worst-case models were constructed by choosing each parameter value to maximize or minimize, respectively, the population measures. The model parameters are shown in Table 5, and the results are shown in Table 6. The best-case model showed very little decline, and stabilized around 1829 individuals, or approximately 94% of initial abundance. The medium model decreased by around 21%, while the worst-case model was continuing to decline at about 19% of initial abundance.

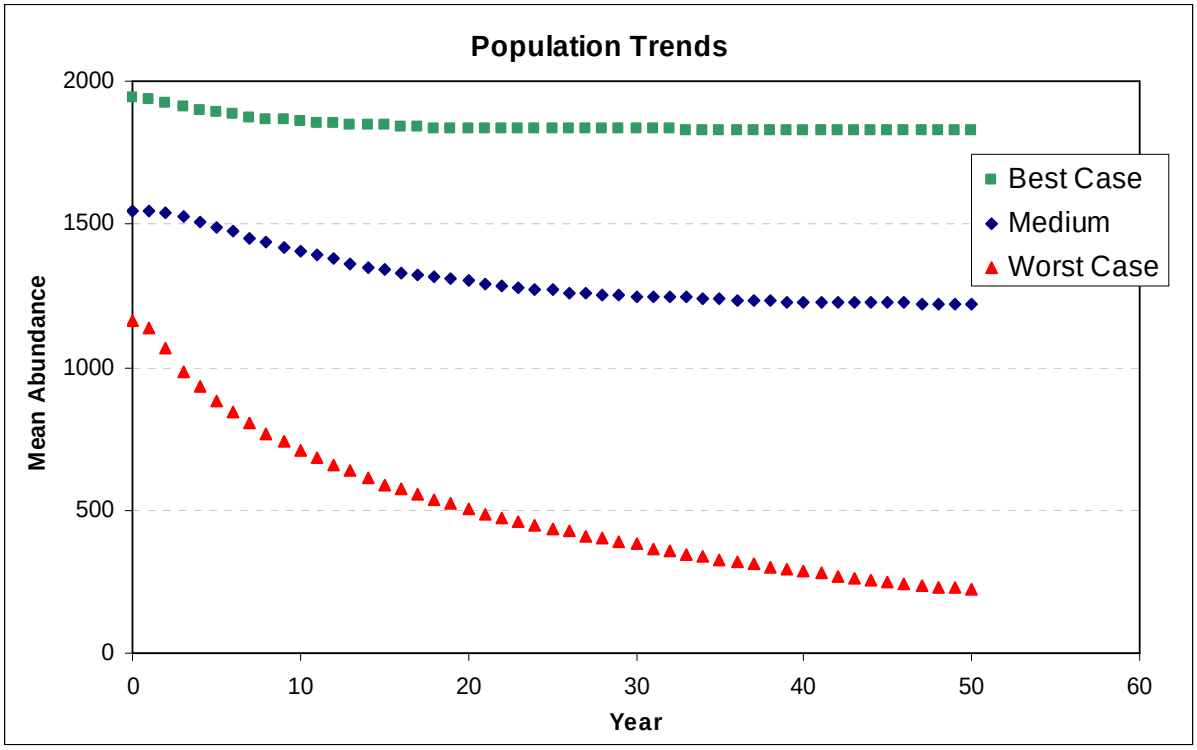
**Table 5: Best-case, medium, and worst-case model parameters.**

| Model | SM | F CVs | THS | ND | DD | K | Disp. (*a*/*b*) | Corr. |
|---|---|---|---|---|---|---|---|---|
| Best case | 0.9880 | 0.120 | 0.1 | 21 | Contest 1.2 | .043/.0583 | .34/20 | 20 |
| Medium | 0.9740 | 0.664 | 0.2 | 17 | Contest 1.1 | .036/.0488 | .34/20 | 80 |
| Worst case | 0.9500 | 1.000 | 0.3 | 12 | Ceiling | .029/.0393 | .17/10 | 800 |

**Table 6: Results for best-case, medium, and worst-case models.**

| Model | Patches | Initial Abundance | Persistence | EMA | Median Growth Rate | Robustness | Functional Presence | EMTA |
|---|---|---|---|---|---|---|---|---|
| Best case | 2 | 1944 | 1.0000 | 1154.2 | 0.9367 | 1.0000 | 1.0000 | 1519.8 |
| Medium | 2 | 1549 | 0.9861 | 538.6 | 0.7224 | 0.8050 | 0.3031 | 683.5 |
| Worst case | 3 | 1163 | 0.0890 | 102.1 | 0.1058 | 0.0960 | 0.0000 | 131.0 |

**Figure 9: Mean abundance for the best-case, medium, and worst-case models. Mean yearly growth rate ranges from 0.9674 to 0.9988.**




### *2.4.5 Habitat loss scenarios*

The habitat loss scenario where small fragments were removed as suitable habitat before larger fragments, in general had lower viability, stability and functionality for the Red-shouldered Hawk population in the pilot study area than the edge erosion scenario (see the Discussion section for

reasons). Number of patches, initial abundances, and expected minimum abundances for the two scenarios at five levels of habitat loss relative to present levels are presented in Table 7. Total habitat area is dependent on the corresponding HS threshold value under medium, best-case, and worst-case parameters (see Figure 6). Total habitat suitability of all patches declined more quickly with each level of habitat loss for the small fragment scenario than for the edge erosion scenario for the population under medium, best-case, and worst-case parameters (Figure 10).

Population viability measured in terms of persistence probability (Figure 11) declined more rapidly for the small fragment loss scenario than for the edge erosion scenario under all population models tested. Thresholds used for this measure were 250, 1,000, and 50 for the medium, best-case, and worst-case models, respectively. These thresholds were selected to best illustrate differences between the two habitat loss scenarios. Estimated minimum abundance (EMA) (Figure 12) of adults was lower, at all levels of habitat loss, in the small fragment loss than in the edge erosion scenario under all three population models.

Stability for the Red-shouldered Hawk measured as median growth rate (Figure 13) and robustness (Figure 14) declined more quickly for the small fragment loss scenario under the medium and best-case models. Under the worst-case model, both habitat loss scenarios had similarly low values for these two stability measures.

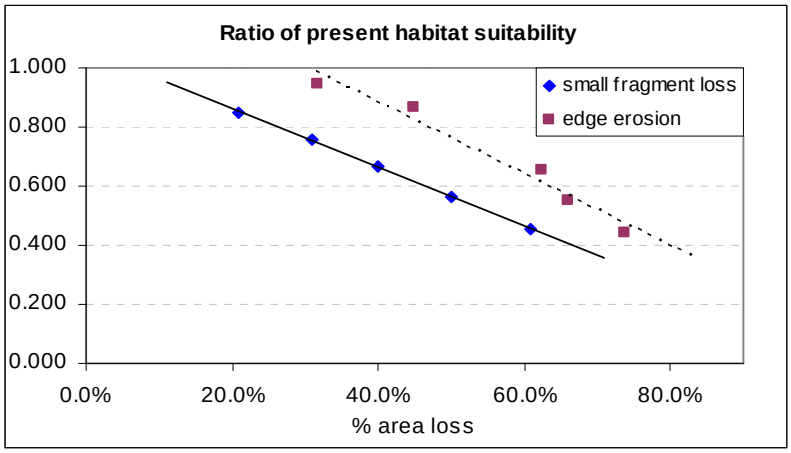
Functionality measured as the functional presence (Figure 15) was high for both scenarios under the best-case model until around 60% of present habitat area loss was reached at which point both scenarios drop very low. Functional presence for the small fragment loss scenario declined more rapidly than the edge erosion scenario under the medium population model, while both scenarios resulted in zero-value at all levels of habitat loss under the worst-case model. The small fragment

loss scenario resulted in a lower EMTA values (Figure 16) than the edge erosion scenario for the total population under all three models.

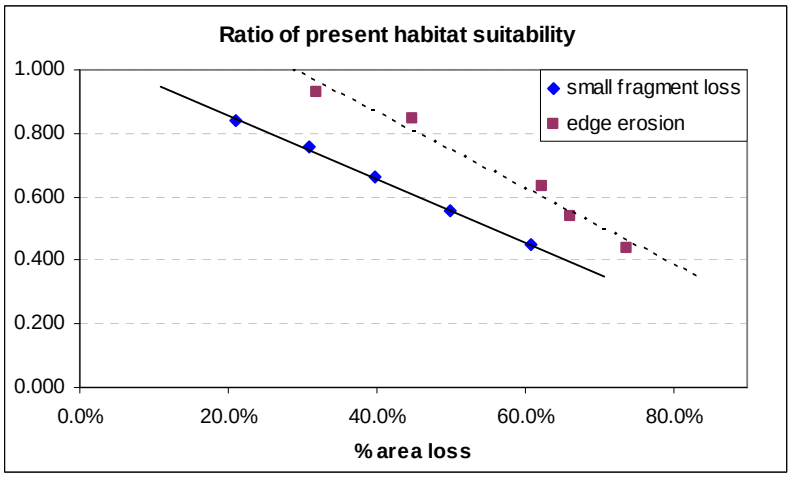
**Table 7: Habitat loss scenario patch number and population abundance.**

| Habitat scenario | % area loss | # patches | | | Initial abundance | | | Expected min. abundance | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | medium model | best case | worst case | medium model | best case | worst case | medium model | best case | worst case |
| **Present** | **0.0%** | **2** | **2** | **3** | **1549** | **1944** | **1163** | **685** | **1519** | **128** |
| Small fragment loss | 21.0% | 8 | 8 | 7 | 1311 | 1635 | 967 | 551 | 1241 | 93 |
| | 30.8% | 10 | 11 | 7 | 1177 | 1472 | 865 | 481 | 1094 | 78 |
| | 39.9% | 9 | 9 | 8 | 1037 | 1285 | 783 | 420 | 963 | 61 |
| | 50.1% | 4 | 4 | 4 | 871 | 1077 | 668 | 374 | 831 | 56 |
| | 60.8% | 3 | 3 | 3 | 700 | 865 | 539 | 296 | 663 | 43 |
| Edge erosion | 31.8% | 3 | 3 | 3 | 1461 | 1804 | 1098 | 635 | 1400 | 122 |
| | 45.0% | 3 | 3 | 3 | 1342 | 1635 | 1009 | 582 | 1268 | 110 |
| | 62.4% | 2 | 2 | 2 | 1010 | 1239 | 764 | 435 | 950 | 76 |
| | 66.1% | 6 | 6 | 4 | 854 | 1063 | 591 | 351 | 812 | 52 |
| | 73.7% | 4 | 7 | 2 | 681 | 860 | 452 | 281 | 649 | 40 |

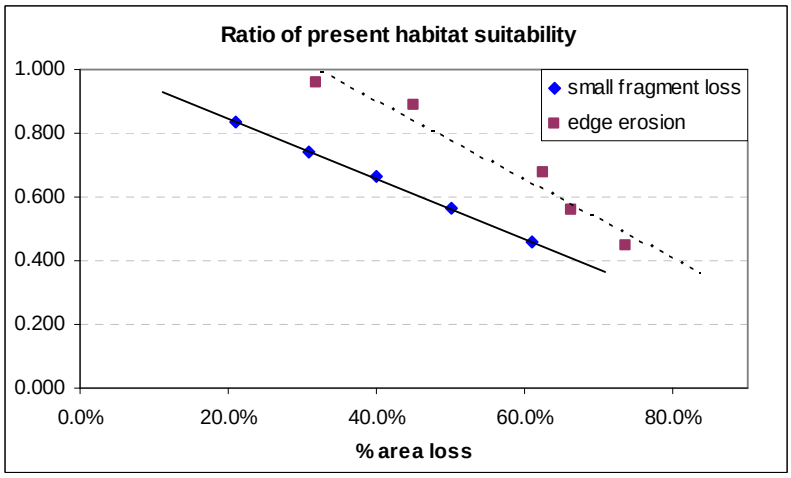
**Figure 10: Ratio of present total habitat suitability as a function of the percent of area lost under the two scenarios. Model under medium population parameters is shown in (a). The best-case and worst-case population models shown in (b) and (c), respectively.**




a.

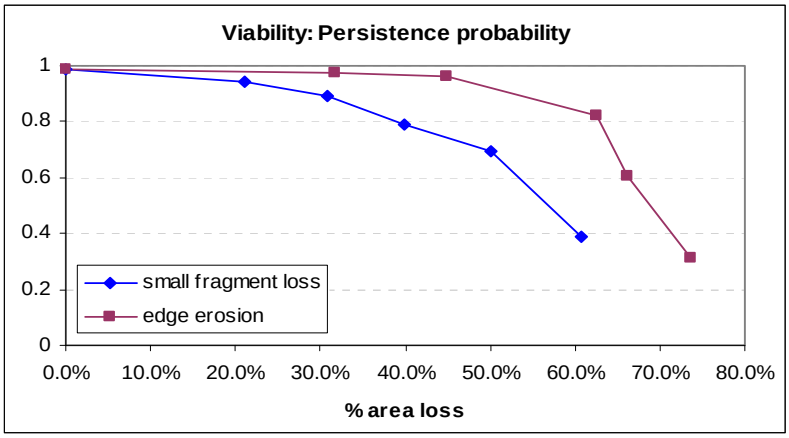



b.

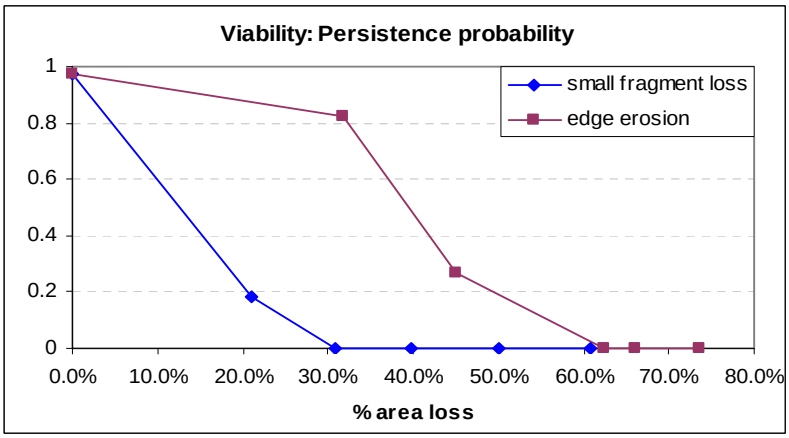



c.

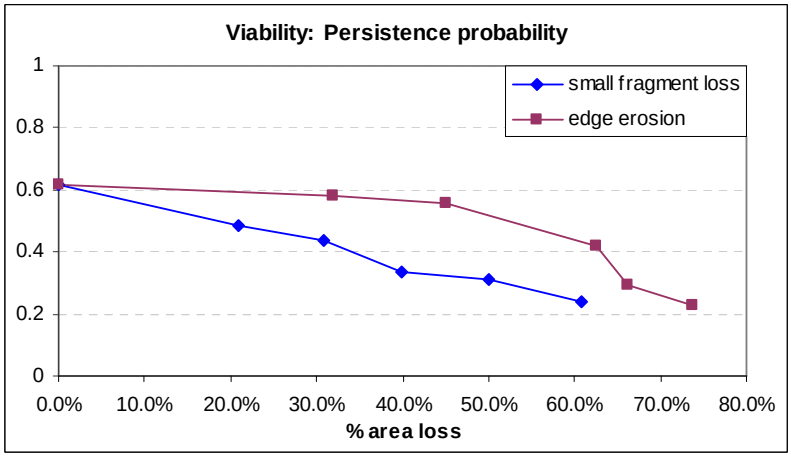
**Figure 11: Persistence probability (measured as one minus the risk of decline to a threshold abundance of adults at any time) for the two habitat loss scenarios under (a) the medium, (b) best-case, and (c) worst-case population parameters. The thresholds are 250 adults for (a), 1,000 for (b), and 50 for (c).**




a.

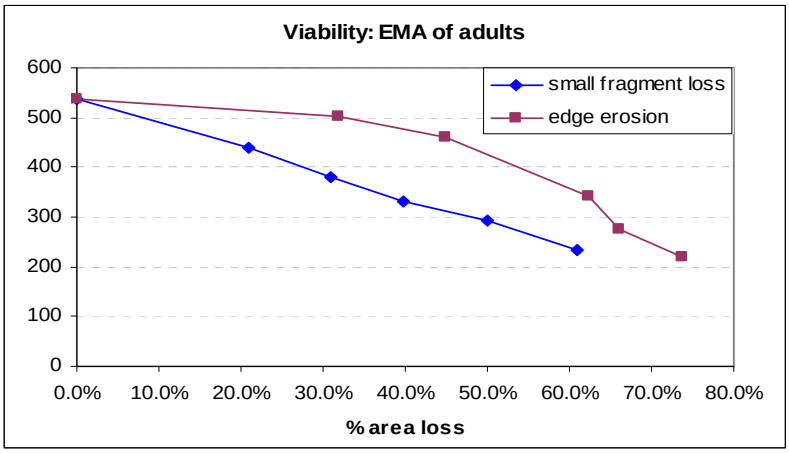



b.

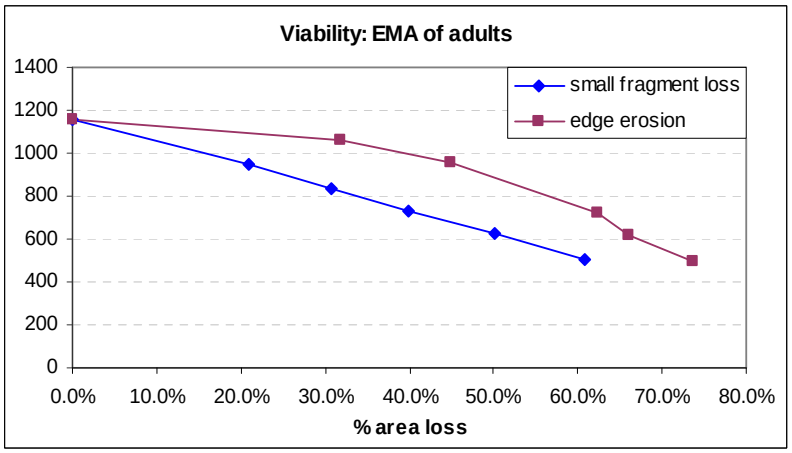



c.

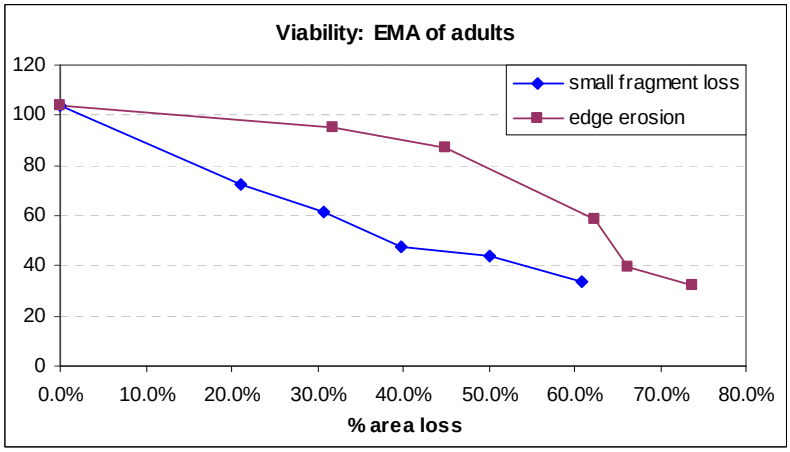
**Figure 12: Expected minimum abundance of adults for the two habitat loss scenarios under (a) the medium, (b) best-case, and (c) worst-case population parameters.**




a.

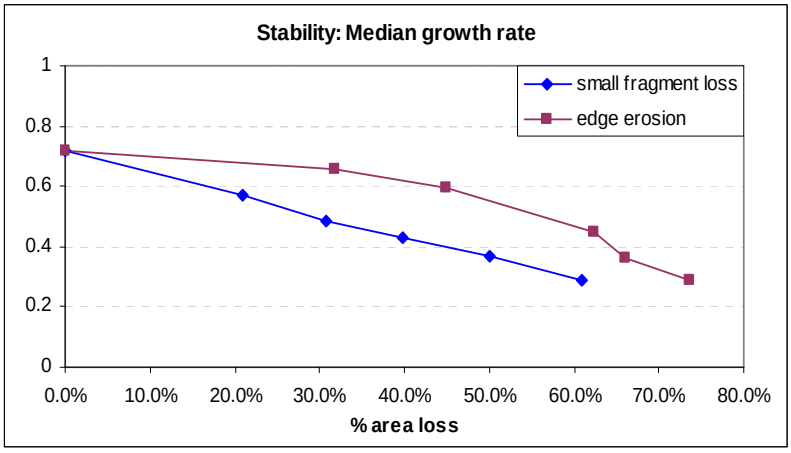



b.

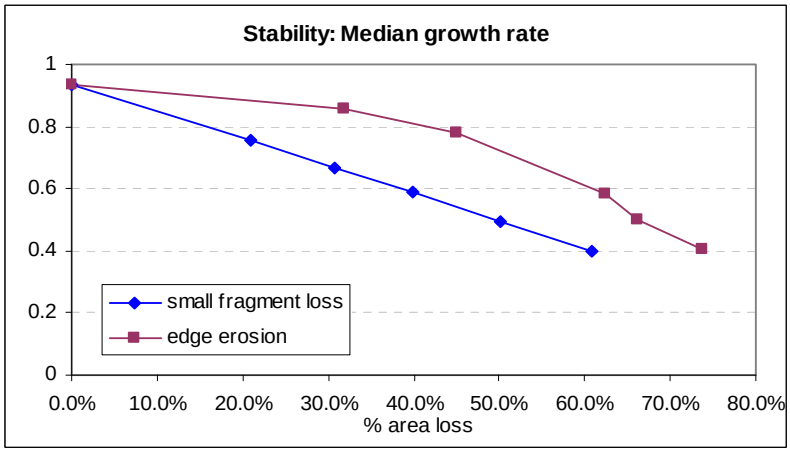



c.

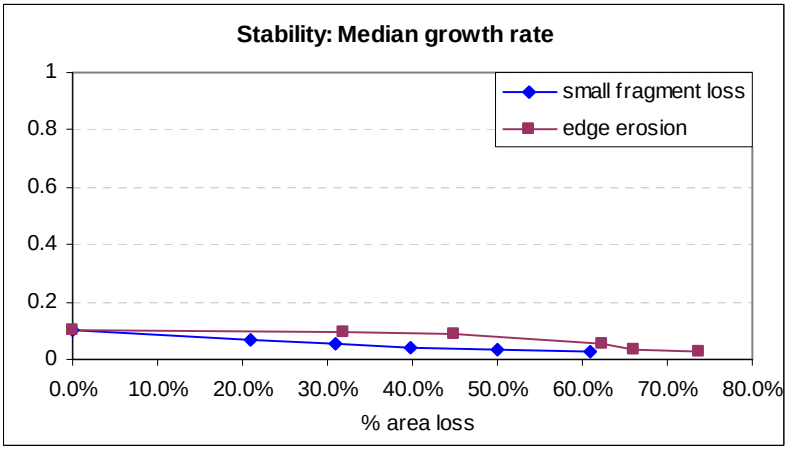
**Figure 13: Median growth rate (measured as the ratio of median final abundance to initial abundance) for the two habitat loss scenarios under (a) the medium, (b) best-case, and (c) worst-case population models.**




a.

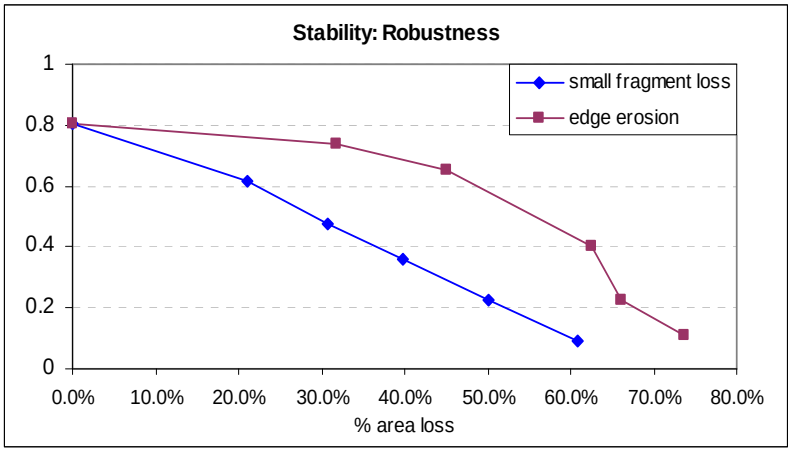



b.

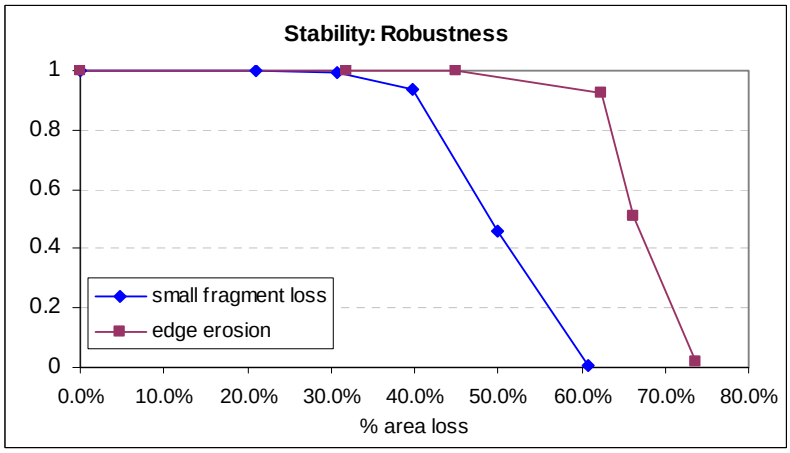



c.

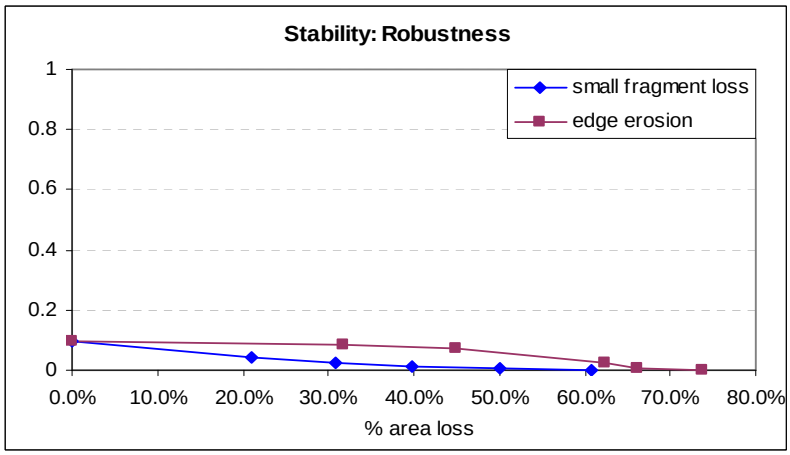
**Figure 14: Robustness (measured as one minus the risk of the final abundance falling below 50% of initial abundance at present habitat extent) for the two habitat loss scenarios under (a) the medium, (b) best-case, and (c) worst-case population models.**




a.

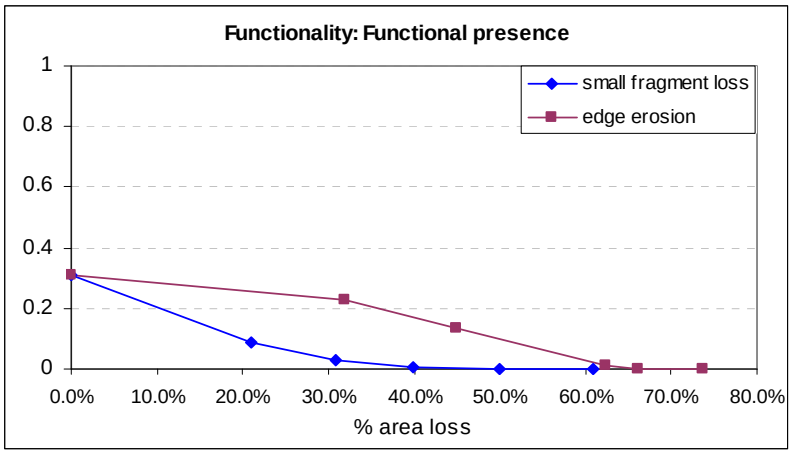



b.

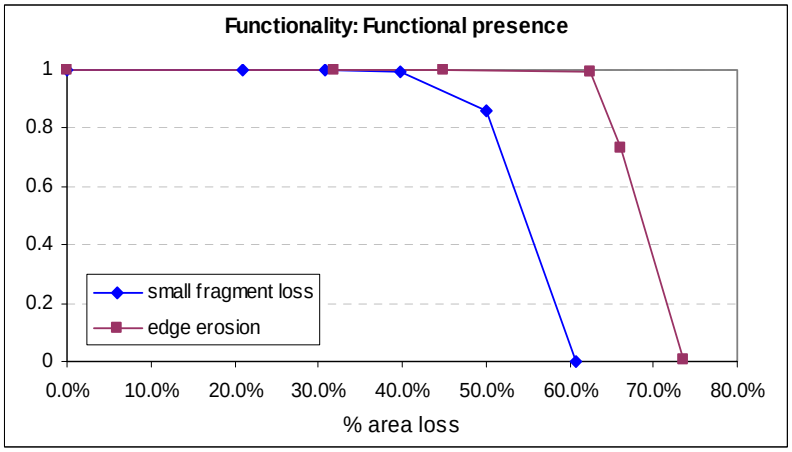



c.

**Figure 15: Functional presence (measured as one minus the risk of the population falling below 50% of initial abundance at present habitat extent and under medium population parameters) for the two habitat loss scenarios under (a) the medium, (b) best-case models. The worst-case model resulted in zero functional presence for all amounts of habitat loss.**



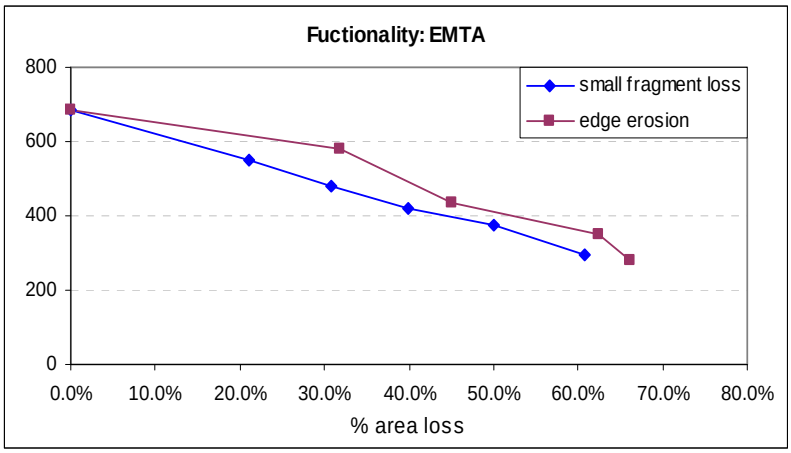

a.



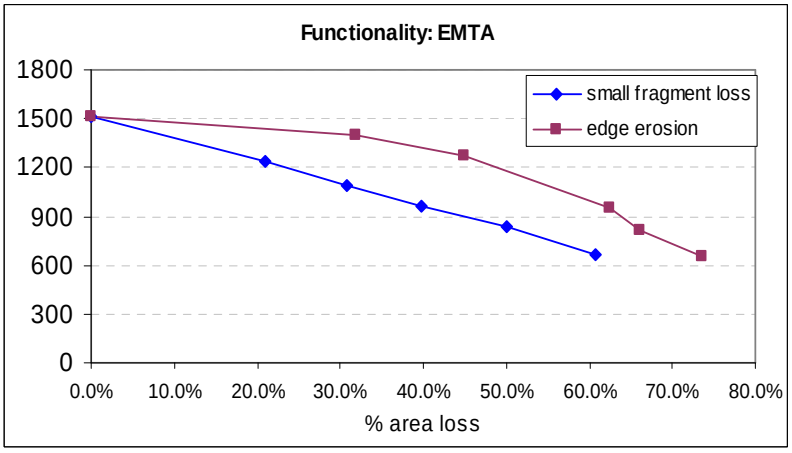

b.

**Figure 16: Expected minimum total abundance of metapopulation for the two habitat loss scenarios under the (a) medium, (b) best-case, and (c) worst-case models.**

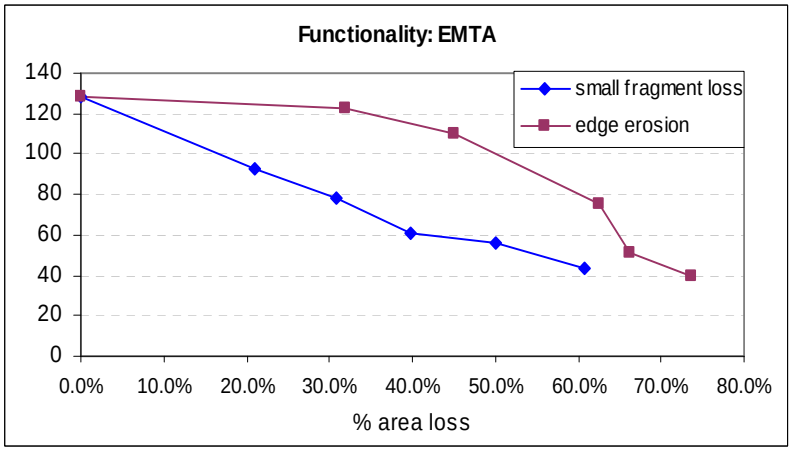
a.




b.




c.



# 3 AMERICAN BITTERN

The American Bittern (*Botaurus lentiginosus*) is a species of marshes, wet meadows, swamps, bogs, and riparian vegetation. It was chosen as a surrogate species for these habitat types due to its habitat area requirements, large home range, and sensitivity to human disturbance.

## 3.1 Demographic Model

We used data on the American Bittern to build the demographic model. When information on a particular parameter was not available for this species, we used information on the old-world species, the Great Bittern *B. stellaris.*

### *3.1.1 Population trends*

The time periods covered were 1968-2004 and 1966-2005 for the CWS and USGS series, respectively (Figure 17). These time series were used to estimate growth rate and population variance for American Bittern in the pilot area. The mean indices of the first and last 5 years were compared to determine overall population change. Our simulations were tuned using the final mean population and coefficient of variation as targets (see below).

### *3.1.2 Stage matrix*

The stage matrix consisted of only two stages, juveniles (<1 year old) and adults (1+ years old) (Table 8), and modeled a pre-breeding census. First reproduction was in the first year (Gibbs et al., 1992), and we assumed 100% of individuals bred (no data found). Young fledged per nest was 0.85 (Dechant et al., 2003). Mean survival rates were 48.8% for juveniles (survival until end of first year) and 64.8% for adults (mean value derived from Wiggins, 2006, Puglisi and Bretagnolle, 2005, and Brininger, 1996).

Fecundity, based on pre-breeding census, was calculated as:

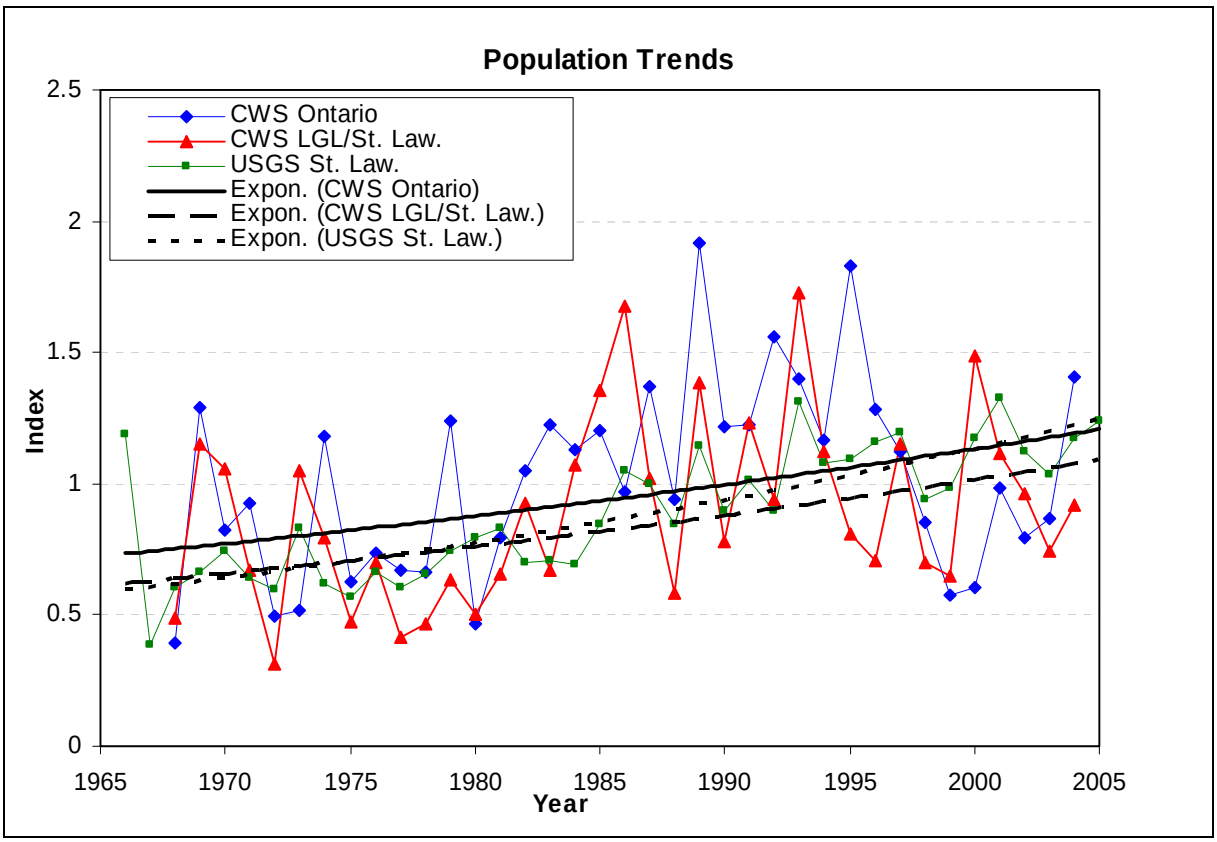
(percent breeding) * (average fledged /nest) * (juvenile survival) * 0.5.

The default stage matrix is in Table 8. Stable distribution is 24.3% juveniles, 75.7% adults

**Table 8: Default stage matrix**

| | **Juvenile** | **Adult** |
|---|---|---|
| Juvenile | 0.208 | 0.208 |
| Adult | 0.648 | 0.648 |

**Figure 17: Population trends in regions of interest. Y-axis indicates a derived population index. The USGS series uses a different index algorithm than the two CWS series**



The default matrix was then tuned using RAMAS Metapop to match the observed parameters from the three time series. The tuning model was sex-structured, with a small initial abundance of 100 to reflect the limited estimated numbers in the pilot region. The matrix was multiplied by a scaling factor and the CV of the fecundity was increased until both the growth and variability targets were reached. The fecundity CV was chosen to manipulate because survival rates are bounded between 0 and 1, and consequently their CV is limited in range. Survival CV was kept constant at 0.1, except for when tuning the USGS data, which had such low variability that even setting both CVs to zero couldn't equal it. This is due to the high demographic stochasticity from our small initial abundance. Tuning for each time series produced three models and low and high estimates for growth and variability (Table 9). The mean of the three parameters was used as the medium value because the middle observed value was very close to the maximum. The mean scaling factor was 1.212, the mean fecundity CV was 0.118, and mean survival CV was 0.067. The stage matrix and the standard deviation matrix with sex structure and medium values are given in Table 10.

**Table 9: Targets and tuning parameters for regional data series. (Target values were reached within +/- 2.5%).**

| **Series Info** | | **Targets** | | **Tuning Parameters** | | |
|---|---|---|---|---|---|---|
| **Region** | **Years** | **Final N** | **Pop. CV** | **Scaling fact.** | **Fec. CV** | **Surv. CV** |
| CWS Ontario | 37 | 59 | 0.362 | 1.209 (Low) | 0.176 | 0.1 |
| CWS LGL/St. Law. | 37 | 71 | 0.388 | 1.213 | 0.178 (High) | 0.1 |
| USGS St. Law. | 40 | 82 | 0.269 | 1.215 (High) | 0.0 (Low) | 0.0 |
| Average (for Medium values) | | | | 1.212 | 0.118 | 0.067 |

**Table 10: Stage matrix (top) and standard deviations matrix (bottom) with medium values for vital rates and their variabilities.**

| | | Females | | Males | |
|---|---|---|---|---|---|
| | | **Juvenile F** | **Adult F** | **Juvenile M** | **Adult M** |
| Female | Juvenile F | 0.252096 | 0.252096 | 0.0 | 0.0 |
| | Adult F | 0.785376 | 0.785376 | 0.0 | 0.0 |
| Males | Juvenile M | 0.252096 | 0.252096 | 0 | 0 |
| | Adult M | 0.0 | 0.0 | 0.75485 | 0.75485 |
| Female | Juvenile F | 0.029747 | 0.029747 | 0.0 | 0.0 |
| | Adult F | 0.01438 | 0.01438 | 0.0 | 0.0 |
| Males | Juvenile M | 0.029747 | 0.029747 | 0.0 | 0.0 |
| | Adult M | 0.0 | 0.0 | 0.01438 | 0.01438 |

### *3.1.3 Density dependence*

We assumed Ceiling-type and Contest-type density dependence functions. Contest type also requires an estimate of Rmax. The eigenvalue of the medium matrix is 1.038.This is the average growth rate, and is likely lower than the maximum growth rate at low population sizes. Thus, we assumed Rmax values of 1.1 or 1.2.

## 3.2 Habitat Model

The habitat suitability for the American Bittern in this model is based on a 0.0 to 1.0 scale with 1.0 being most suitable. Overall habitat suitability is the product of two factors: (1) land cover suitability and (2) disturbance.

### *3.2.1 Cover suitability*

American Bitterns are species of primarily freshwater wetlands with tall, emergent vegetation (Gibbs et al., 1992). Detailed descriptions of nesting and foraging habitats including vegetation type and density, interspersion, and management regimes are available (Dechant et al., 2003).

However, without further information about land cover and management conditions in the pilot study area we considered all marshes (WMrsh, # 4021), bogs (WBog, # 4020), fens (Wfen, # 4019), and thicket swamps (WetE1, #4101; WetE2, #4102) suitable cover and were given a suitability value of 1.0.

In parts of the Western United States American Bitterns have been observed nesting in upland pasture or hayfields adjacent to water when management practices exclude livestock grazing, mowing, and burning prior to and throughout nesting. However, this occurrence is rarely observed in eastern North America (Gibbs pers. comm.). Further, because information was not available regarding management practices in hayfields and pastures in the study area, we excluded as suitable habitat land cover classes classified as agriculture. Cultural meadows (CUmed, # 6101) within 100 meters of water (# 9001) were given a cover suitability of 0.5.

### *3.2.2 Disturbance*

Habitat disturbance and degradation is a concern for American Bitterns (Gibbs et al., 1992). Surveys in the North American Great Plains have found seemingly suitable habitat unoccupied, suggesting either low food availability or human disturbance may be effecting habitat quality (Wiggins, 2006). We gave suitable habitats more than 100m from rural development (RDev, # 9103) and urban areas (# 9003) a disturbance rating of 1.0. Within 100m of these land cover types, we gave a disturbance score of 0.5. In other words, the cover suitability score was halved if it was within 100m of urban or rural development, otherwise it was unaffected.

### *3.2.3 Habitat mapping*

We initially mapped the spatial extent and suitability values of land cover at the original 2m resolution using the raster coverage of the pilot area. We calculated distance to disturbance at a

4m resolution to speed computing time. The two components were each then converted to a coarser resolution of 100m using the ‘aggregate’ function in ArcGIS Spatial Analyst (ArcView 8.1.2) which will assign a new value to each coarser resolution pixel based on the mean average of the values of the underlying finer resolution pixels. We combined the separate components of the suitability measure at the coarser resolution to calculate overall habitat suitability (see Figure 18).

## 3.3 Linking Habitat Model to Demography

### *3.3.1 Threshold Habitat Suitability*

We set the "Threshold Habitat Suitability" parameter to 0.1, 0.2, and 0.3. At these thresholds, respectively, 71, 57, and 46% of all cells with non-zero habitat suitability are above the threshold totaling 4.3, 3.6, and 3.0% of the total study area (see Figure 19).

### *3.3.2 Neighborhood distance*

We based the "Neighborhood Distance" parameter on the size of the home range and density of nests.

For a minimum value, we used the density of calling males in Maine, where the density was 2.6 calling males per $km^2$ (Gibbs et al., 1992), which corresponds to a distance of about 0.7 km between circular territories.

For a maximum value of the "Neighborhood Distance" parameter, we used the maximum size of breeding home range, which is reported as 415 ha/male, and 337 ha/female in Minnesota (Brininger, 1996). The average of these two areas, is 376 ha, and corresponds to a distance of about 2.2 km.

Another study in Minnesota estimated average home range size as 127 ha (Wiggins, 2006), which corresponds to a distance of about 1.3 km, and is close to the midpoint between maximum and minimum estimates. Thus, we used Neighborhood Distances of 7, 13, and 22 cells (1 cell==100 m).

### *3.3.3 Carrying capacity (K)*

We based our estimate of carrying capacity of a patch, on the total habitat suitability in that patch. Thus, both the size of the patch (number of cells) and the quality of habitat in the patch (HS value of each cell) contribute to the carrying capacity in the patch.

The function that links the carrying capacity of a patch (K) to the total habitat suitability in that patch is:

K = thr(0.052*ths,5).

In this formula, "thr" is the threshold function, so that patches that do not have at least 5 individuals are not considered a population. In our model, both sexes are modeled, so K is in terms of males + females. Thus, a "population" of fewer than 5 individuals corresponds to 0 to 2 breeding pairs (depending on the sex ratio). We believe considering such a small fragment a population would overestimate carrying capacity of the metapopulation, so we set this threshold to exclude such small fragments.

In the above formula, "ths" is total habitat suitability, i.e., the sum of HS values of all cells in the patch. This number is multiplied by a constant (0.052) to calculate the carrying capacity. This constant has units of individuals per cell (per ha). We calculated this constant based on the density of calling males observed in Maine (see above), which corresponds to 5.2 breeding

individuals per $km^2$, and 0.052 breeding individuals per ha (or per cell). For minimum and maximum values, we used ±20% (0.042 and 0.062).

The model with medium parameters for "Threshold Habitat Suitability", Neighborhood Distance and K function resulted in 9 habitat patches (see Table 11).

### *3.3.4 Initial abundance*

We assumed that initially, all populations are at their carrying capacity, and thus used the same scaling as for carrying capacity. Thus, the function for initial abundance is:

$$N_0 = 0.052*ths$$

Note that the "thr" function is not necessary here, because initial abundance is calculated only for patches that are identified as populations, based on the carrying capacity function.

### *3.3.5 Dispersal*

Information about dispersal patterns of the American Bittern is scarce. Some studies focus on post-breeding dispersal (dispersal between breeding and wintering ranges), but this is not relevant to dispersal for a model with an annual time step. The studies on nest fidelity are more relevant, but most studies cannot differentiate between winter mortality and dispersal to outside the study area (thus return rates underestimate fidelity). In two studies in Minnesota, site fidelity was about 50-60%. Thus, we selected dispersal parameters so that total dispersal from a population was no more than 40%. Based on this assumption, we used an exponential dispersal-distance function with the distance-related parameter (*b*) set as 10, and the scaling parameter *a* set to a value of 0.2. For minimum and maximum values, we used ±50% of each parameter.

### *3.3.6 Sensitivity analysis*

The minimum, medium and maximum values of the parameters used in the simulations are given in Table 11.

**Table 11: The values of model parameters used in the simulations**

| **Parameter** | **Minimum** | **Medium** | **Maximum** |
|---|---|---|---|
| Stage Matrix (scaling factor for default matrix) | 1.209 | 1.212 | 1.215 |
| Variability in vital rates (fecundity/survival CVs) | 0.0/0.0 | 0.118/0.067 | 0.178/0.1 |
| Threshold Habitat Suitability | 0.1 | 0.2 | 0.3 |
| Neighborhood Distance (cells lengths, 100 m) | 7 | 13 | 22 |
| Density Dependence (type, and Rmax if Contest) | Ceiling | Contest 1.1 | Contest 1.2 |
| Carrying capacity (K), and Initial abundance functions (number of individuals as a multiple of total habitat suitability in the patch) *(co-varying)* | 0.042 | 0.052 | 0.062 |
| Dispersal, scaling parameter *a* | 0.1 | 0.2 | 0.3 |
| Dispersal, distance parameter *b (co-varies with a)* | 5 | 10 | 15 |
| Correlation-distance function parameter *b* | 20 | 80 | 800 |

## 3.4 Results

### *3.4.1 Habitat model and spatial structure*

The habitat model resulted in the map in Figure 18.

**Figure 18: Suitable habitat for American Bittern within study area.**

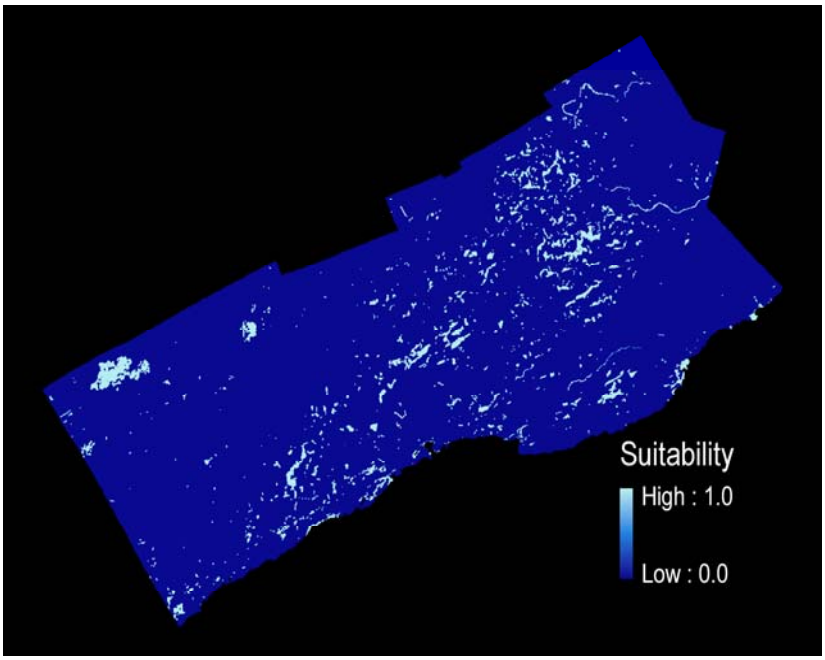



**Figure 19: Percentage of total study area with HS values greater than or equal to the values in the x-axis. For example, 2.5% of the study area has HS values of 0.4 or more.**

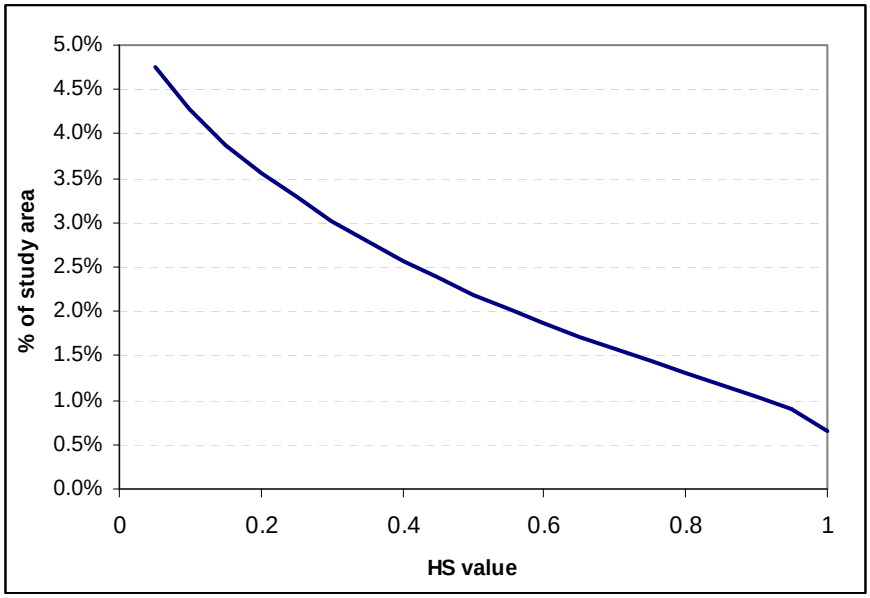
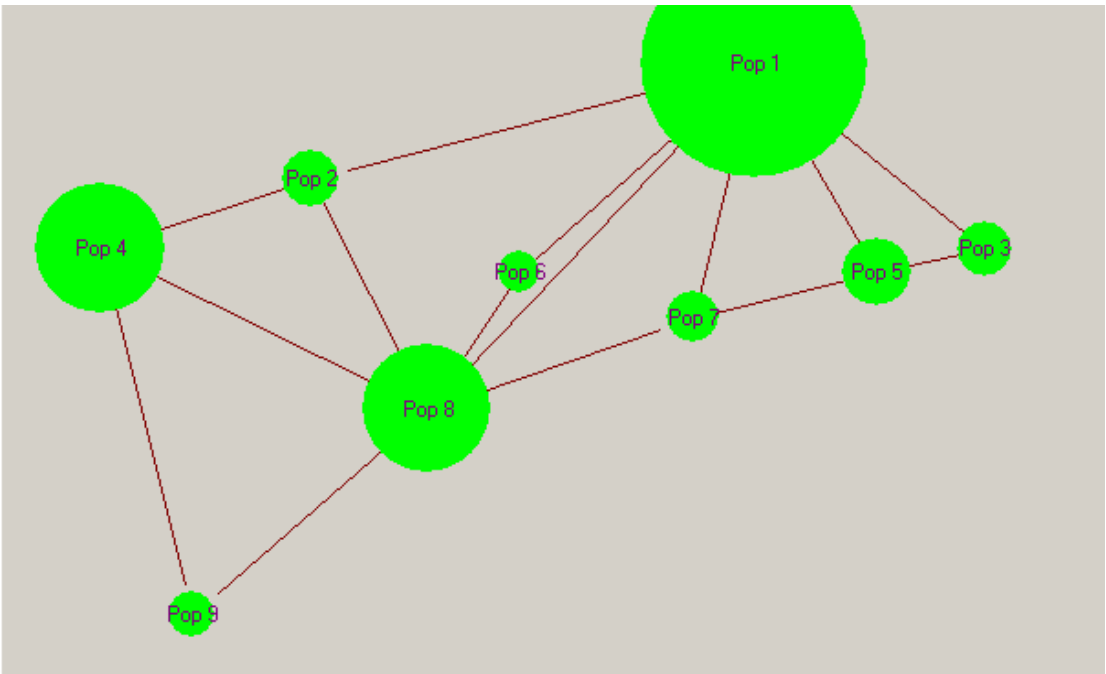


**Figure 20: Metapopulation structure of medium model. All populations are initially at carrying capacity with a stable stage distribution.**




### *3.4.2 Simulation results with the Medium model*

The primary, or 'medium', population model used the medium values for all parameters. It had 9 patches (Figure 20) and a total initial abundance of 333 individuals, divided into 80 juveniles and 253 adults.

#### 3.4.2.1 Viability

For the medium model, persistence probability (measured as one minus risk of quasi-extinction) was 0.9824 for a threshold of 100 individuals. Our default thresholds of 50 and 250 individuals were inappropriate as they resulted in universal persistence probabilities of 1.0 and 0.0, respectively. Since both stages are breeders (mature individuals), expected minimum adult abundance was the same as expected minimum total abundance (see below).

#### 3.4.2.2 Stability

Median growth rate (ratio of median final abundance to initial abundance) was 0.5556, indicating a substantial decline from initial abundance. However, the decline appeared to be asymptotic (Figure 22). Mean yearly growth rate was 0.9884.Robustness (measured as one minus risk of 50% terminal decline) was 0.6793.

#### 3.4.2.3 Functionality

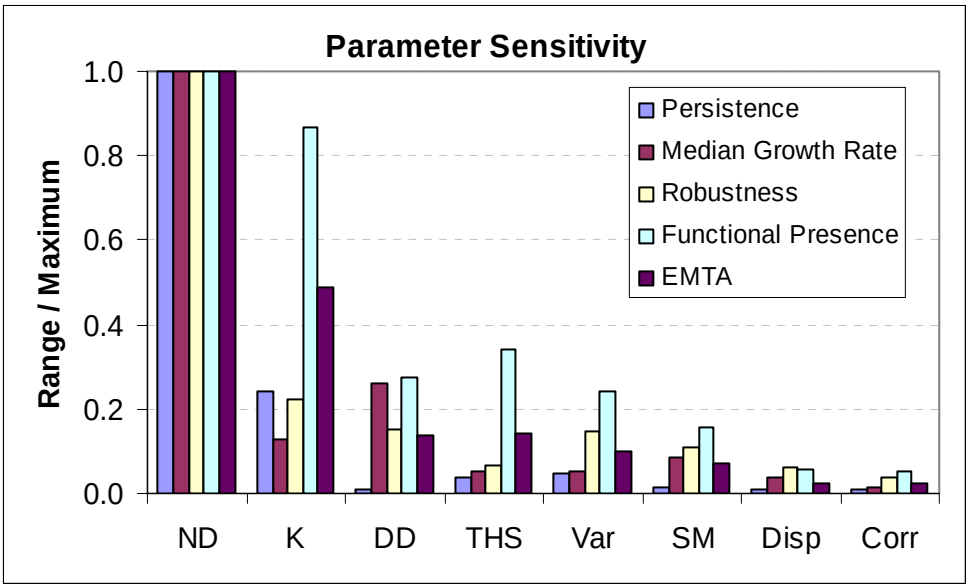
Functional presence (measured as one minus risk of interval decline to a threshold of 167 individuals) was 0.4201, and expected minimum total abundance (EMTA) was 161.7.

Overall, the medium model resulted in a declining population, albeit one which appears to be stabilizing eventually at approximately 50% of its initial abundance. According to the sensitivity analysis, the most important factor affecting the model is patch structure as determined by the neighborhood distance parameter (see below).

### *3.4.3 Sensitivity analysis*

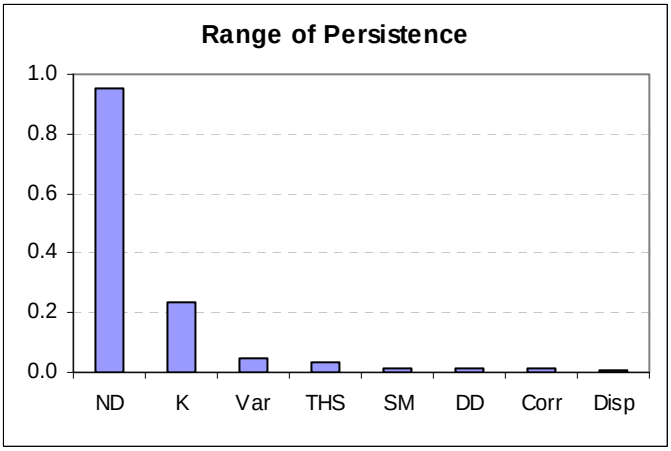
The sensitivity analysis identified neighborhood distance (ND) and carrying capacity function (K) as the parameters to which the model was most sensitive. Progressively less important were density dependence (DD), threshold for habitat suitability (THS), variability (V), stage matrix (SM), dispersal (Disp), and correlation (Corr).

**Figure 21: Parameter sensitivity. Values are normalized ranges within each measure. Range for each parameter indicates maximum minus minimum from the 'high' and 'low' models. This value is then normalized by dividing by the maximum range across all parameters for the same population measure.**

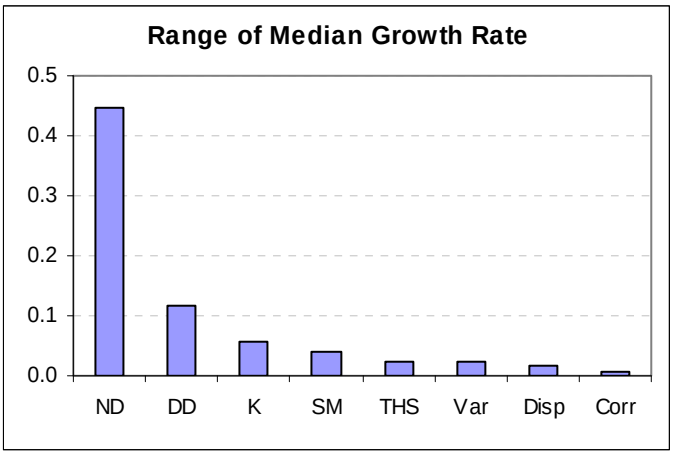



The parameters are sorted by mean normalized range across the five measures (A-E).

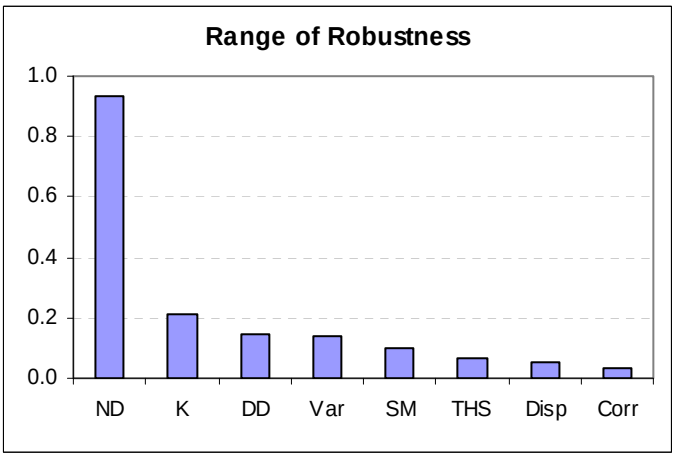
**A. Ranges for the risk of dropping below 100 adults. This measure is most sensitive to neighborhood distance and carrying capacity.**



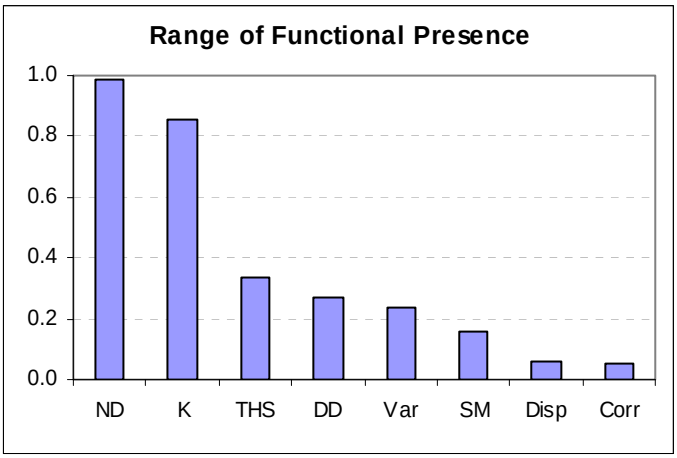
**B. Ranges for the proportion of median final abundance to initial abundance. This measure is most sensitive to neighborhood distance.**



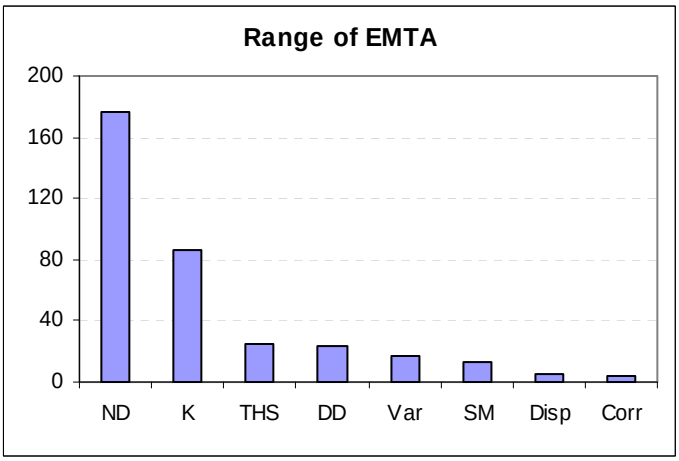

**C. Ranges for the risk of dropping below 50% of initial for the final time step. This measure is most sensitive to neighborhood distance.**



**D. Ranges for the risk of dropping below 50% of standard initial abundance for any time step. This measure is most sensitive to neighborhood distance and carrying capacity.**




**E. Ranges for the expected minimum total abundance (EMTA). This measure is most sensitive to neighborhood distance and carrying capacity.**




### *3.4.4 Best-case and worst-case models*

Using the sensitivity analysis, best-case and worst-case models were constructed by choosing each parameter value to maximize or minimize, respectively, the population measures. The model parameters are shown in Table 12, and the results are shown in Table 13. The best-case

model showed a small decline, but appeared to stabilize around 410 individuals, or approximately 85% of initial abundance. The medium model decreased by around 50%, while the worst-case model was close to extinction.

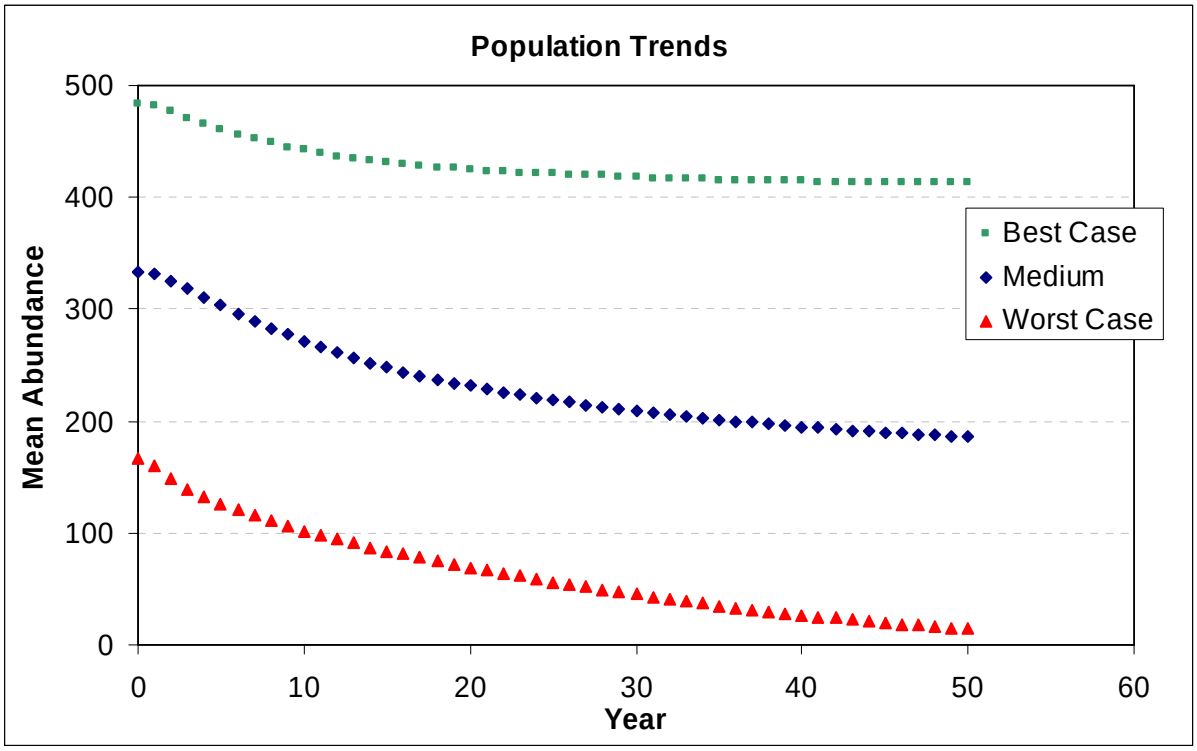
**Table 12: Best-case, medium, and worst-case model parameters.**

| Model | SM | Fec./Surv. CVs | THS | ND | DD | K | Disp. (*a*/*b*) | Corr. |
|---|---|---|---|---|---|---|---|---|
| Best case | 1.215 | 0.0/0.0 | 0.1 | 22 | Contest 1.2 | 0.062 | 0.1/5 | 20 |
| Medium | 1.212 | 0.118/0.067 | 0.2 | 13 | Contest 1.1 | 0.052 | 0.2/10 | 80 |
| Worst case | 1.209 | 0.178/0.100 | 0.3 | 7 | Ceiling | 0.042 | 0.3/15 | 800 |

**Table 13: Results for best-case, medium, and worst-case models.**

| Model | Patches | Initial Abundance | Persistence | Median Growth Rate | Robustness | Functional Presence | EMTA |
|---|---|---|---|---|---|---|---|
| Best case | 6 | 483 | 1.0000 | 0.8551 | 1.0000 | 1.0000 | 375.2 |
| Medium | 9 | 333 | 0.9824 | 0.5556 | 0.6793 | 0.4201 | 161.7 |
| Worst case | 11 | 167 | 0.0000 | 0.0479 | 0.0036 | 0.0000 | 13 |

**Figure 22: Mean abundance for the medium, best-case, and worst-case models. Mean yearly growth rate ranges from 0.9521 to 0.9969.**




### *3.4.5 Habitat loss scenarios*

The habitat loss scenario where small fragments were removed as suitable habitat before larger fragments, in general had lower viability, stability, and functionality for the American Bittern population in the pilot study area than the edge erosion scenario. Number of patches, initial abundances, and expected minimum abundances for the two scenarios are presented in Table 14. Total habitat suitability of all patches declined more quickly with each level of habitat loss for the small fragment scenario than for the edge erosion scenario for the populations under the medium and best-case models. There was no difference between the two scenarios for the decline in total habitat suitability under the worst-case model (Figure 23).

Population viability measured in terms of persistence probability (Figure 24) declined more rapidly under the small fragment loss scenario for both the medium and best-case models. There was no difference for this measure between the two habitat loss scenarios under the worst-case model as it was very low even at present habitat levels. Thresholds used for this measure were 50 for the medium and worst-case models, and 250 for the best-case model, respectively. These thresholds were selected to best illustrate differences between the two habitat loss scenarios. Estimated minimum abundance (EMA) (Figure 25) of adults was lower at all levels of habitat loss in the small fragment loss than in the edge erosion scenario under the medium and best-case models. Under the worst-case model the EMA's were closer for the two scenarios with the edge erosion slightly lower at moderate and high levels of habitat loss.

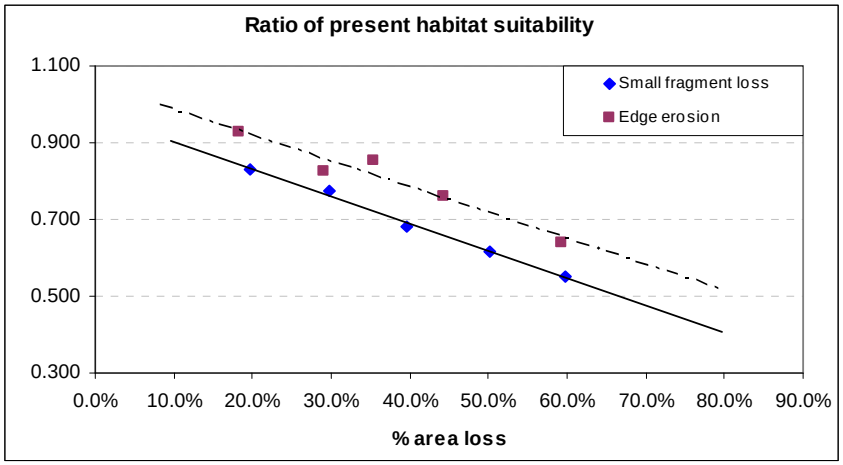
Stability for the American Bittern measured as median growth rate (Figure 26) and robustness (Figure 27) showed little differences between the two habitat loss scenarios under the worst-case model as both measures were very close to zero for all levels of habitat loss. Under the medium and best-case models the small fragment loss scenario declined more quickly for both stability measures, although only marginally so under medium parameters.

Functional presence (Figure 28) showed little difference between the two habitat loss scenarios under the medium model. Under the best-case model the small fragment loss scenario showed a rapid decline in the measure at moderate levels of habitat loss, whereas the edge erosion only began to show decline in functional presence at the highest levels of simulated area lost. The worst-case model resulted in functional presence values of zero at all levels of habitat loss under both scenarios.

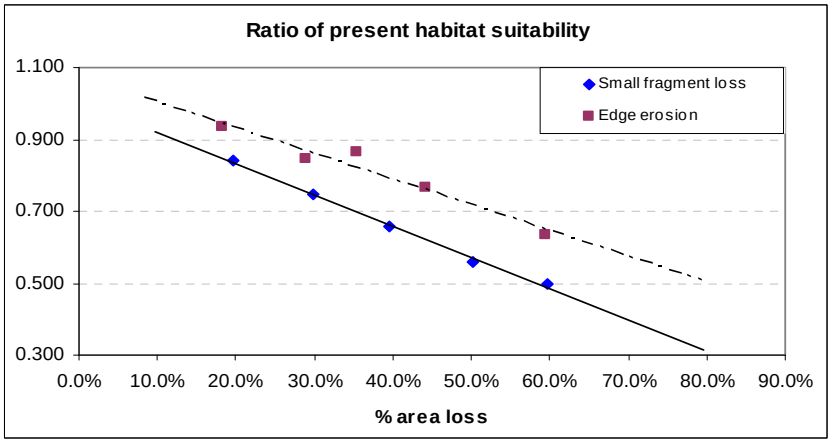
**Table 14: Habitat loss scenario patch number and population abundance.**

| Habitat scenario | % area loss | # patches | | | Initial abundance | | | Expected min. abundance | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | medium model | best case | worst case | medium model | best case | worst case | medium model | best case | worst case |
| Present | 0.0% | 9 | 6 | 11 | 333 | 483 | 167 | 161 | 376 | 13 |
| Small fragment loss | 19.7% | 12 | 12 | 11 | 277 | 407 | 161 | 98 | 256 | 12 |
| | 29.8% | 13 | 12 | 11 | 258 | 362 | 155 | 79 | 213 | 11 |
| | 39.7% | 13 | 12 | 10 | 226 | 315 | 147 | 54 | 174 | 11 |
| | 50.1% | 11 | 11 | 10 | 206 | 270 | 146 | 49 | 145 | 11 |
| | 59.7% | 11 | 11 | 10 | 184 | 242 | 134 | 36 | 117 | 9 |
| Edge erosion | 18.3% | 12 | 7 | 11 | 308 | 451 | 164 | 124 | 336 | 12 |
| | 29.0% | 13 | 9 | 11 | 276 | 410 | 155 | 95 | 285 | 10 |
| | 35.3% | 12 | 8 | 11 | 285 | 418 | 155 | 104 | 297 | 10 |
| | 44.2% | 14 | 10 | 10 | 253 | 372 | 143 | 66 | 244 | 11 |
| | 59.4% | 13 | 9 | 10 | 213 | 307 | 132 | 47 | 189 | 9 |

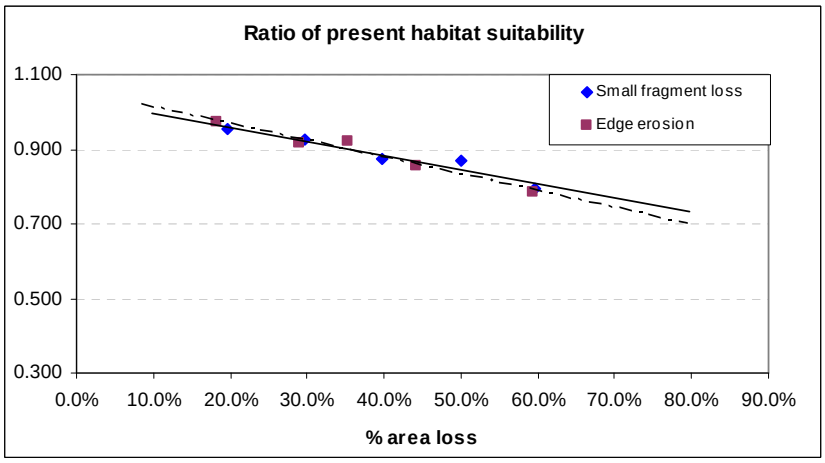
**Figure 23: Ratio of present total habitat suitability as a function of the percent of area lost under the two scenarios. Model under medium population parameters is shown in (a). The best-case and worst-case population models shown in (b) and (c), respectively.**




a.

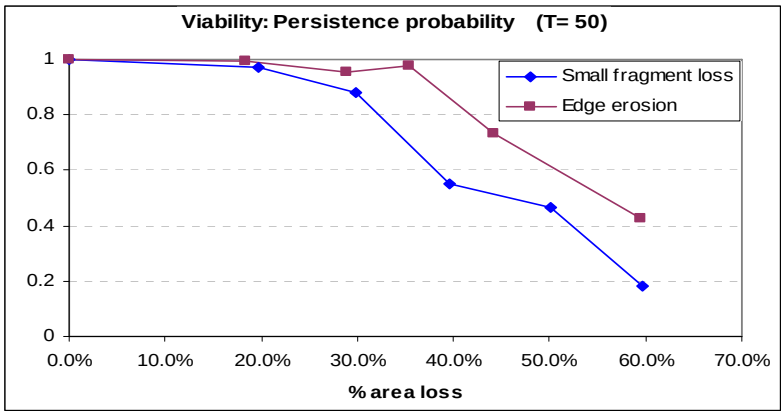



b.

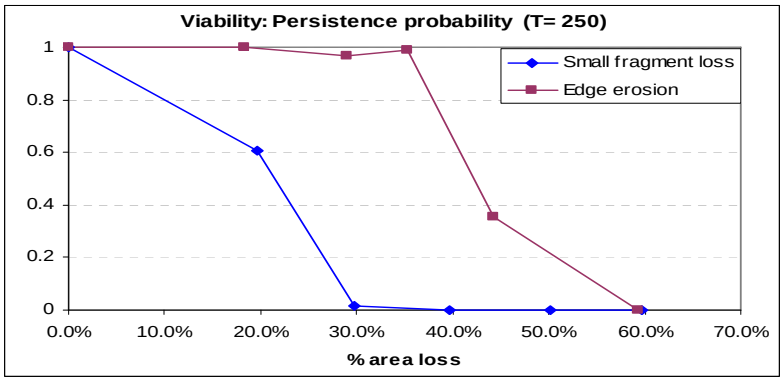



c.

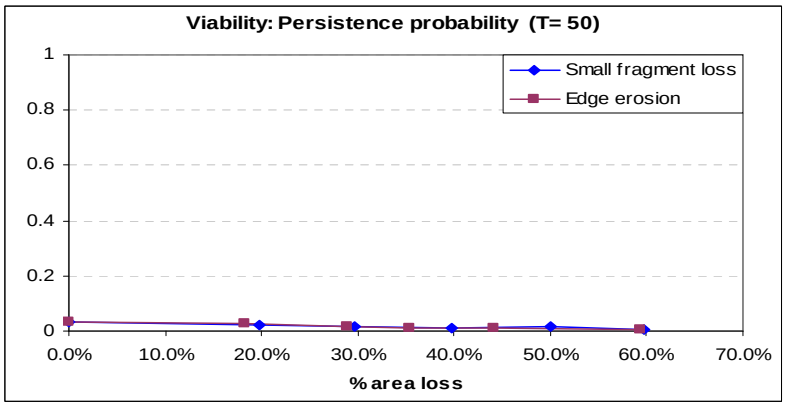
**Figure 24: Persistence probability (measured as one minus the risk of decline to a threshold abundance of adults at any time) for the two habitat loss scenarios under (a) the medium, (b) best-case, and (c) worst-case population parameters. The thresholds are 50 adults for both (a) and (c) and 250 for (b).**




a.

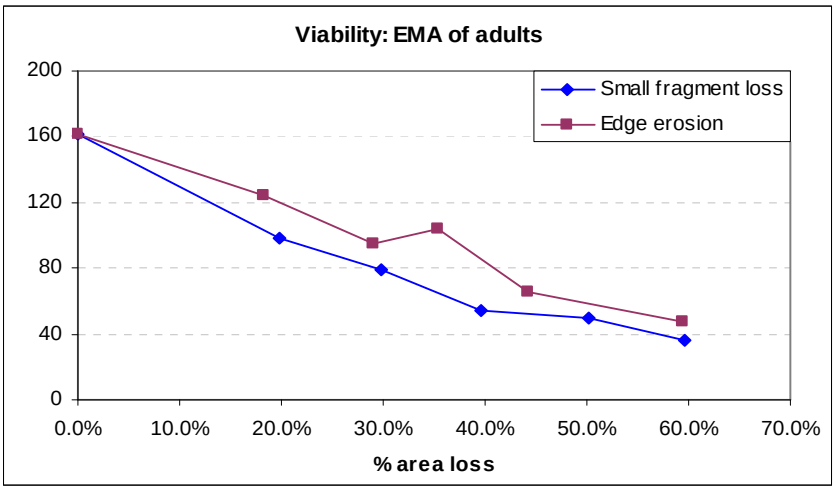



b.

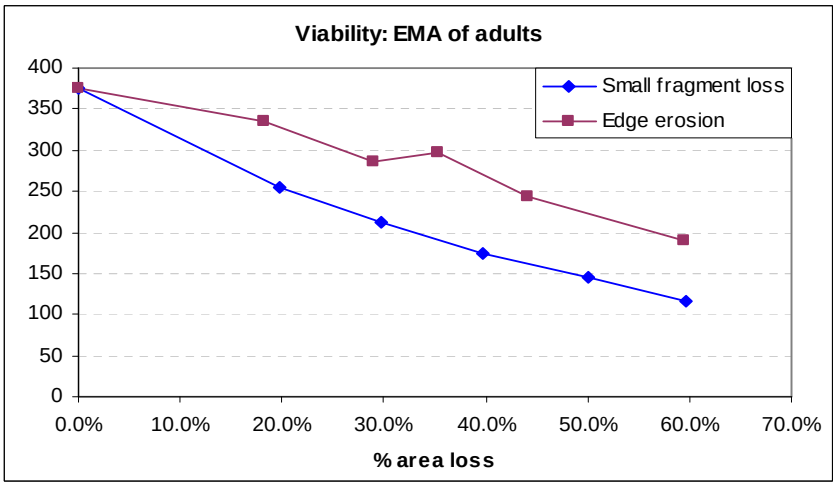



c.

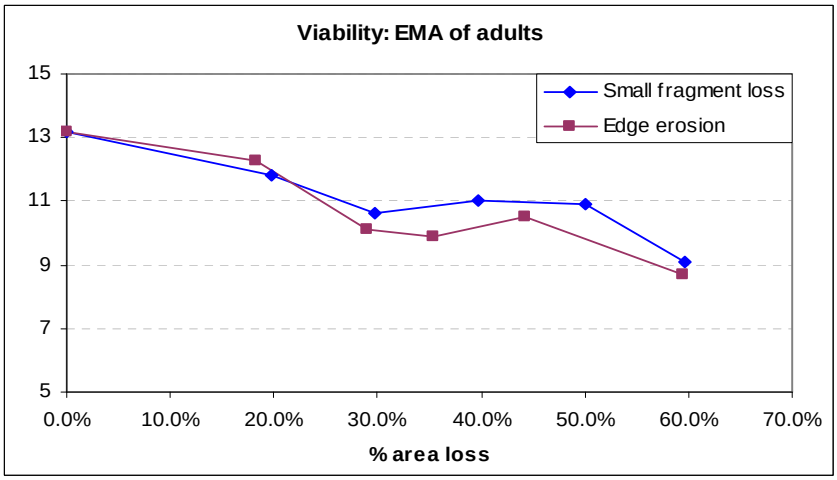
**Figure 25: Expected minimum abundance of adults for the two habitat loss scenarios under (a) the medium, (b) best-case, and (c) worst-case population parameters.**




a.

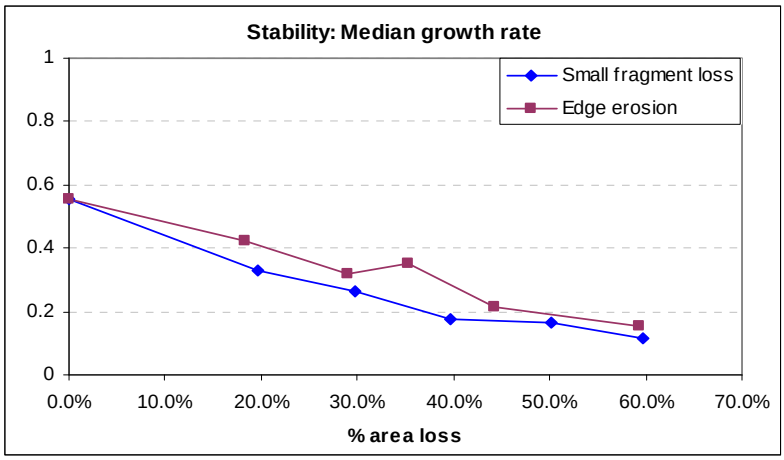



b.

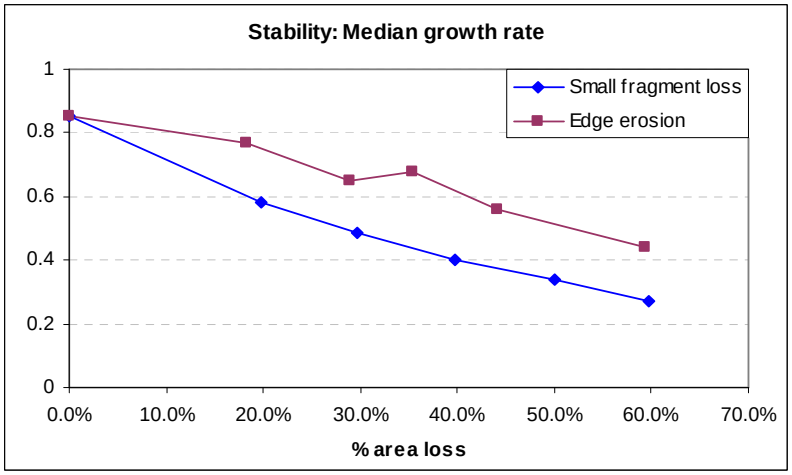



c.

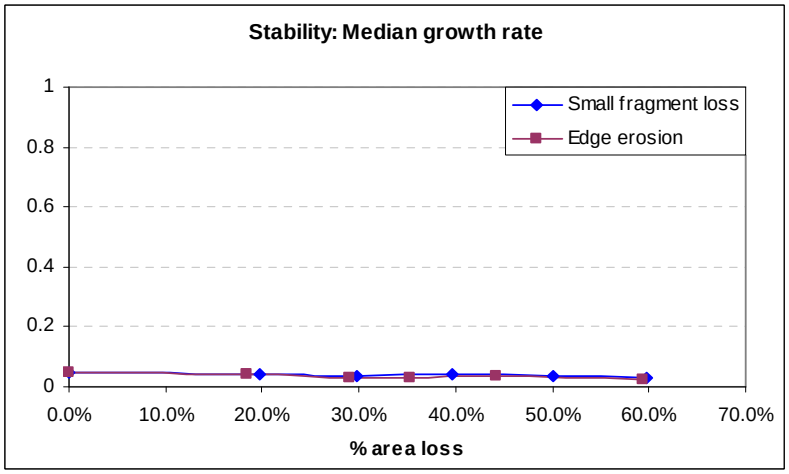
**Figure 26: Median growth rate (measured as the ratio of median final abundance to initial abundance) for the two habitat loss scenarios under (a) the medium, (b) best-case, and (c) worst-case population models.**




a.

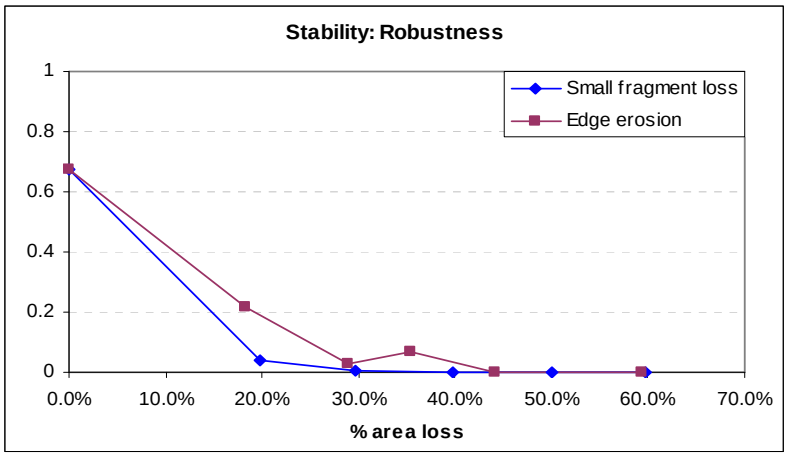



b.

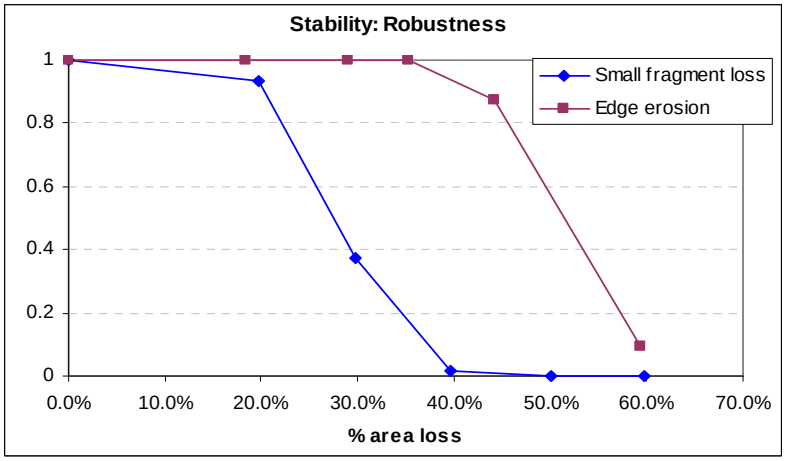



c.

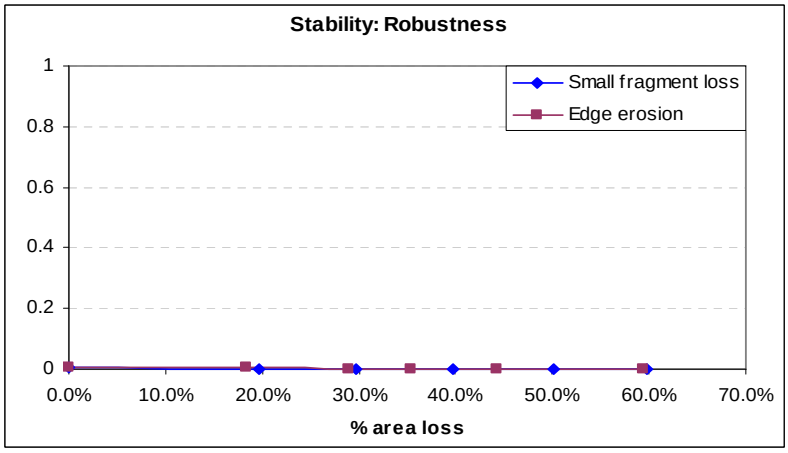
**Figure 27: Robustness (measured as one minus the risk of the final abundance falling below 50% of initial abundance at present habitat extent) for the two habitat loss scenarios under (a) the medium, (b) best-case, and (c) worst-case population models.**




a.

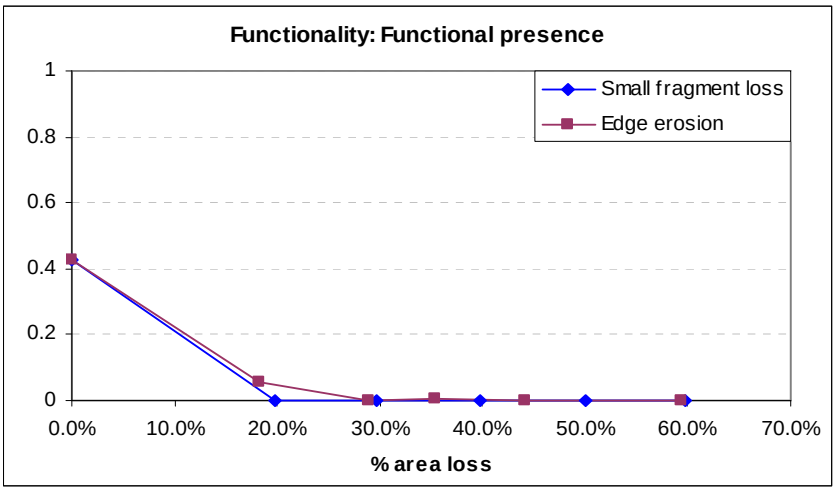



b.

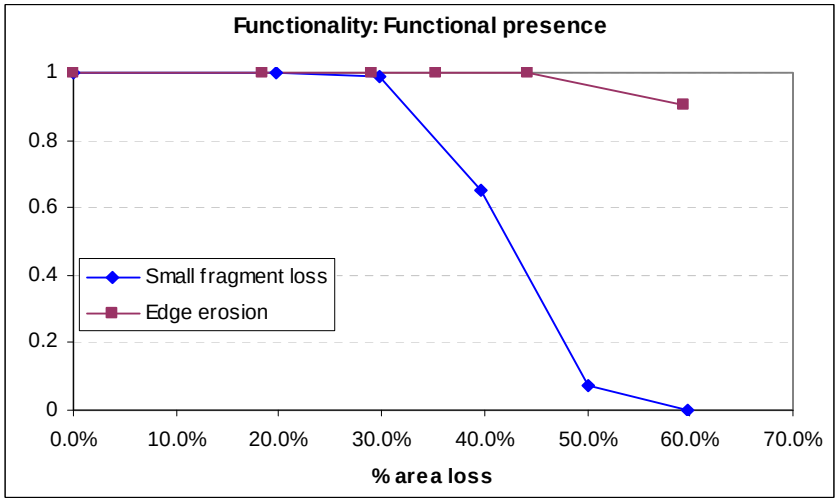



c.

**Figure 28: Functional presence (measured as one minus the risk of the population falling below 50% of initial abundance at present habitat extent and under medium population parameters) for the two habitat loss scenarios under (a) the medium, (b) best-case models. The worst-case model resulted in zero functional presence for all amounts of habitat loss.**




a.




b.

# 4 PILEATED WOODPECKER

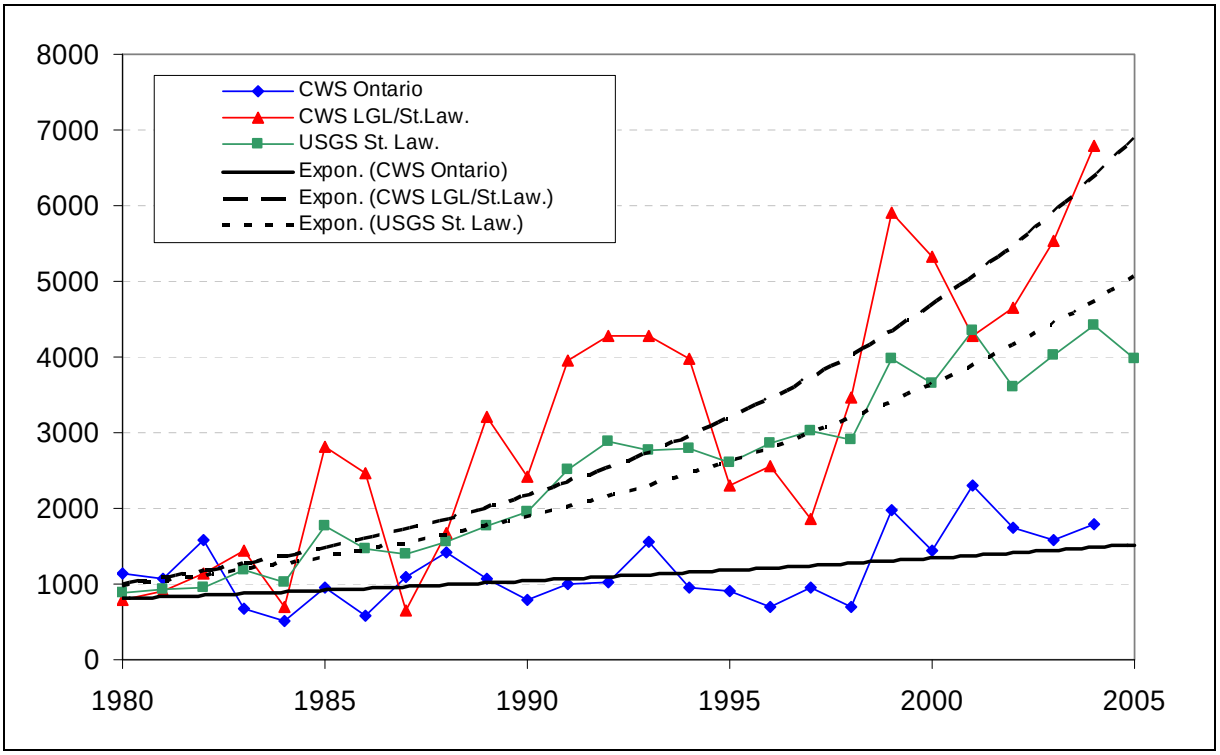
The Pileated Woodpecker (*Dryocopus pileatus)* is a species of deciduous and mixed forests. They have unique foraging and nesting requirements, and rely on forest stands with abundant snags and downed woody debris. It was selected as a surrogate species for mature deciduous and mixedwood forests due to its habitat area requirements, large home range, and dependence on forest interior.

## 4.1 Demographic Model

### *4.1.1 Population trends*

The time periods covered were 1968-2004 and 1966-2005 for the CWS and USGS series, respectively (Figure 29). These time series were used to estimate growth rate and population variance for the Pileated Woodpecker in the pilot area. However, there was a sharp change in observed variance and abundance after the first 15 years. Consequently, we limited the time periods to 1980-2004/2005. The mean indices of the first and last 5 years were compared to determine overall population change. Our simulations were tuned using the final mean population and coefficient of variation as targets (see below).

**Figure 29: Population trends in regions of interest from 1980 onwards. Y-axis indicates a derived population index. The USGS series uses a different index algorithm than the two CWS series.**




### *4.1.2 Stage matrix*

The matrix consisted of only two stages, juveniles (<1 year old) and adults (1+ years old) (Table 1), and modeled a pre-breeding census. First reproduction was in the first year (Bull and Jackson, 1995), and we assumed 100% of individuals bred (no data found). Young fledged per nest was 2.13 (Bull and Jackson, 1995). Mean survival rates were 47.0% for juveniles (survival until end of first year) and 69.1% for adults (mean value derived from Bull and Jackson, 1995, Martin, 1995, Bull, 2001, Bonar, 2001, and Wiebe, 2006).

Fecundity, based on pre-breeding census, was calculated as:

(percent breeding) * (average fledged /nest) * (juvenile survival) * 0.5.

The default stage matrix is in Table 15. Stable distribution is 42.0% juveniles, 58.0% adults.

**Table 15: Default stage matrix**

| | **Juvenile** | **Adult** |
|---|---|---|
| Juvenile | 0.501 | 0.501 |
| Adult | 0.691 | 0.691 |

The default matrix was then tuned using RAMAS Metapop to match the observed parameters from the three time series. The tuning model was sex-structured, with an initial abundance of 1000 to reflect the estimated numbers in the pilot region. The matrix was multiplied by a scaling factor and the CV of the fecundity was increased until both the growth and variability targets were reached. The fecundity CV was chosen to manipulate because survival rates are bounded between 0 and 1, and consequently their CV is limited in range. Survival CV was kept constant at 0.1. Tuning for each time series produced three models and low and high estimates for growth and variability (Table 16). The mean of the three parameters was used as the medium value because the middle observed value was very close to the maximum. The mean scaling factor was 0.8767 and the mean fecundity CV was 0.066. The stage matrix and the standard deviation matrix with sex structure and medium values are given in Table 3.

**Table 16: Targets and tuning parameters for regional data series. (Target values were reached within +/- 2.5%).**

| **Series Info** | | **Targets** | | **Tuning Parameters** | | |
|---|---|---|---|---|---|---|
| **Region** | **Years** | **Final N** | **Pop. CV** | **Scaling fact.** | **Fec. CV** | **Surv. CV** |
| CWS Ontario | 37 | 1773 | 0.392 | 0.8640 (Low) | 0.127 (High) | 0.1 |
| CWS LGL/St. Law. | 37 | 5315 | 0.569 | 0.8865 (High) | 0.055 | 0.1 |
| USGS St. Law. | 40 | 4009 | 0.458 | 0.8795 | 0.015 (Low) | 0.0 |
| Average (for Medium values) | | | | 0.8767 | 0.066 | 0.1 |

**Table 17: Stage matrix (top) and standard deviations matrix (bottom) with medium values for vital rates and their variabilities.**

| | | Females | | Males | |
|---|---|---|---|---|---|
| | | **Juvenile F** | **Adult F** | **Juvenile M** | **Adult M** |
| Female | Juvenile F | 0.439227 | 0.439227 | 0 | 0 |
| | Adult F | 0.6058 | 0.6058 | 0 | 0 |
| Males | Juvenile M | 0.439227 | 0.439227 | 0 | 0 |
| | Adult M | 0 | 0 | 0.6058 | 0.6058 |
| Female | Juvenile F | 0.028989 | 0.028989 | 0 | 0 |
| | Adult F | 0.03942 | 0.03942 | 0 | 0 |
| Males | Juvenile M | 0.028989 | 0.028989 | 0 | 0 |
| | Adult M | 0 | 0 | 0.03942 | 0.03942 |

### *4.1.3 Density dependence*

We assumed Ceiling-type and Contest-type density dependence functions. Contest type also requires an estimate of Rmax. The eigenvalue of the medium matrix is 1.045.This is the average growth rate, and is likely lower than the maximum growth rate at low population sizes. Thus, we assumed Rmax values of 1.1 or 1.2.

## 4.2 Habitat Model

Several habitat suitability models have been constructed for Pileated Woodpeckers in the region based on local empirical data. The habitat suitability index for this model is based on a 0.0 to 1.0 scale with 1.0 being most suitable.

Pileated Woodpeckers rely on dead, dying, or partially decayed trees for excavating nest and roost holes. In addition, a large portion of their diet consists of insects infesting dead or decaying trees (Bull and Jackson, 1995). Due to these nesting and foraging strategies, this species is most commonly associated with mature and old growth forests with standing snags well as downed

woody debris (James, 1984, Naylor et al., 1996, Samson, 2005). They are occasionally found in younger stands if there is some remnant structure providing sufficient numbers of snags (Samson, 2005). Pileated Woodpeckers will nest, roost, and forage in a wide variety of tree species (Higgelke and MacLeod, 2000), but are most often associated with the shade-intolerant to intermediate hardwoods such aspens, poplars, and oaks (Naylor et al., 1996, Higgelke and MacLeod, 2000). In Alberta, Canada Pileated Woodpeckers were not found to be sensitive to human activity in close proximity to suitable habitat (Higgelke and MacLeod, 2000).

We adapted our habitat suitability map for the Pileated Woodpecker for the pilot study region from the non-spatial habitat model described by Halloway et al. (2004) for the Great Lakes-St. Lawrence (GLSL) region forests. The model is based on defined forest ecosites which were translated to NAESI pilot land cover classes based primarily on the 'Draft Roll-up for Ecosites' (Baldwin et al., 2006). Suitability scores in Halloway et al (2004) rate forests as 'not-used', 'used', and 'preferred' based on the ecosite type and development stage. We transformed the model's suitability scores such that they would scale from 0.0 (not used) to 1.0 (preferred). Suitable ecosite development stages were translated to one of three minimum stand age classes (Table 18) based on the Forest Resource Inventory (FRI) data, which we converted to 2006 values by adding 15 years.

**Table 18: Minimum stand age and suitability for Pileated Woodpeckers in the NAESI Eastern Ontario pilot region.**

| NAESI Pilot VDDT Number | Minimum Stand Age | Suitability Score |
|---|---|---|
| 1001 | 80+ | 1 |
| 1002 | 70-79 | 1 |
| 1003 | 80+ | 0.5 |
| 1004 | 70-79 | 1 |
| 2001 | 70-79 | 1 |
| 2002 | 70-79 | 1 |

**Table 18: Minimum stand age and suitability for Pileated Woodpeckers in the NAESI Eastern Ontario pilot region.**

| NAESI Pilot VDDT Number | Minimum Stand Age | Suitability Score |
|---|---|---|
| 2003 | 80+ | 0.5 |
| 2004 | 70-79 | 1 |
| 2005 | 60-69 | 1 |
| 2006 | 80+ | 0.5 |
| 2007 | 70-79 | 1 |
| 2008 | 60-69 | 1 |
| 3001 | 70-79 | 1 |
| 3002 | 70-79 | 1 |
| 3003 | 60-69 | 1 |
| 3004 | 70-79 | 0.5 |
| 3005 | 70-79 | 0.5 |
| 3006 | 70-79 | 0.5 |
| 3007 | 70-79 | 0.5 |
| 3008 | 60-69 | 1 |
| 4001 | 70-79 | 1 |
| 4002 | 70-79 | 0.5 |
| 4003 | 70-79 | 1 |
| 4004 | | 0 |
| 4005 | 70-79 | 1 |
| 4006 | 70-79 | 0.5 |
| 4007 | 60-69 | 1 |
| 4008 | 70-79 | 1 |
| 4009 | 70-79 | 0.5 |
| 4010 | 60-69 | 1 |
| 4011 | 60-69 | 1 |
| 4012 | 70-79 | 0.5 |
| 4013 | 70-79 | 0.5 |
| 4014 | 60-69 | 1 |
| 4015 | 70-79 | 0.5 |
| 4016 | 70-79 | 0.5 |
| 4017 | 60-69 | 1 |

We averaged the ecosite development stages when more than one ecosite was defined by a single NAESI pilot land cover class. When the conversion of ecosites to NAESI pilot land cover classes

resulted in conflicting suitability scores we examined the species composition of the NAESI cover classes to determine which ecosite was most closely resembled. Resulting suitability scores are presented in Table 18.

The hardwood swamps were not defined in the Halloway et al. (2004) model, and therefore were not included in the draft roll-up. However, there is no evidence to suspect that these stands would not contain appropriate habitat, assuming the tree species composition is appropriate. We assigned minimum forest age and suitability scores based on the species composition for these stands.

We extracted the spatial extent for each NAESI pilot forest cover class and assigned suitability scores at the original 2m resolution from the raster coverage. We converted the resulting suitability map to a coarser 100m resolution using the 'aggregate' function in ArcGIS Spatial Analyist (ArcView 8.1.2) which will assign a new value to each coarser resolution pixel based on the mean average of the values of the underlying finer resolution pixels.

## 4.3 Linking Habitat Model to Demography

### *4.3.1 Threshold Habitat Suitability*

We set the "Threshold Habitat Suitability" parameter to 0.1, 0.2, and 0.3. At these thresholds, respectively, 74.3, 61.9, and 51.7% of all cells with non-zero habitat suitability are above the threshold totaling 12, 10, and 9 % of the study area (see Figure 31).

### *4.3.2 Neighborhood distance*

We based the "Neighborhood Distance" parameter on the size of the home range. In eastern North America, the home range size varies from 40 to 260 ha (Naylor et al., 1996), which corresponds to range of distances of 0.71 km to 1.82 km between circular territories. Thus, we

used Neighborhood Distances of 7 and 18 cells (1 cell==100 m) for minimum and maximum values, respectively, and the mid-point of 13 cells for the medium value.

### *4.3.3 Carrying capacity (K)*

We based our estimate of carrying capacity of a patch, on the total habitat suitability in that patch. Thus, both the size of the patch (number of cells) and the quality of habitat in the patch (HS value of each cell) contribute to the carrying capacity in the patch.

The function that links the carrying capacity of a patch (K) to the total habitat suitability in that patch is:

K = thr(0.06*ths,5).

In this formula, "thr" is the threshold function, so that patches that do not have at least 5 individuals are not considered a population. In our model, both sexes are modeled, so K is in terms of males + females. Thus, a "population" of fewer than 5 individuals corresponds to 0 to 2 breeding pairs (depending on the sex ratio). We believe considering such a small fragment a population would overestimate carrying capacity of the metapopulation, so we set this threshold to exclude such small fragments.

In the above formula, "ths" is total habitat suitability, i.e., the sum of HS values of all cells in the patch. This number is multiplied by a constant (0.06) to calculate the carrying capacity. This constant has units of individuals per cell (per ha). We calculated this constant based on the density of pairs in Ontario, which is estimated as 1-4 pairs per $km^2$. Because the multiplication with "ths" in the K function already takes into account habitat quality, we used the higher range of 2-4 pairs per $km^2$ or 4 to 8 breeding individuals per $km^2$, which corresponds to 0.04 to 0.08

breeding individuals per ha (or per cell). For medium value, we used the midpoint of this range (0.06).

The model with medium parameters for "Threshold Habitat Suitability", Neighborhood Distance and K function resulted in 6 habitat patches (see Figure 32).

### *4.3.4 Initial abundance*

We assumed that initially, all populations are at their carrying capacity, and thus used the same scaling as for carrying capacity. Thus, the function for initial abundance is:

$$N_0 = 0.06*\text{ths}$$

Note that the "thr" function is not necessary here, because initial abundance is calculated only for patches that are identified as populations, based on the carrying capacity function.

### *4.3.5 Dispersal*

We used a dispersal-distance function to parameterize the dispersal rates, using the exponential model $M = a \exp(-D / b)$. In this model, $M$ is the dispersal rate, $D$ is the distance (km) between two populations, and $a$ and $b$ are model parameters. For distance, we used center-to-edge distances from source to target populations.

The Pileated Woodpecker appears to have high site fidelity with pairs remaining on same territory year after year. The available information on dispersal is mostly from western US, where home ranges are much larger. In Oregon, 8 nestlings dispersed 0.7-8.7 km from natal nest after 1-7 yrs; in Alberta and New York, two adults have been killed 16 and 32 km from natal site after 9-10 yrs (Bull and Jackson, 1995). Although this information is not sufficient to estimate dispersal rates, it does indicate that dispersal is rather limited, especially for adults. Thus, we set dispersal rate for

the adult stages to half the value for juvenile dispersal, and used a wide range that includes (as minimum) zero dispersal for the juveniles. For maximum juvenile dispersal, we used an exponential dispersal-distance function with the distance-related parameter (*b*) set as 10, and the scaling parameter *a* to a value of 0.2. For medium values, we used midpoints (a=0.2, b=5).

### *3.4.6 Sensitivity analysis*

The minimum, medium and maximum values of the parameters used in the simulations are given in Table 19.

**Table 19: The values of model parameters used in the simulations**

| Parameter | Minimum | Medium | Maximum |
|---|---|---|---|
| Stage matrix (scaling factor for default matrix) | 0.8640 | 0.8767 | 0.8865 |
| Variability in vital rates (fecundity CV) | 0.015 | 0.066 | 0.127 |
| Threshold Habitat Suitability | 0.1 | 0.2 | 0.3 |
| Neighborhood Distance (cells lengths, 100 m) | 7 | 13 | 18 |
| Density dependence (type, and Rmax if Contest) | Ceiling | Contest 1.1 | Contest 1.2 |
| Carrying capacity (K), and Initial abundance functions (number of individuals as a multiple of total habitat suitability in the patch) *(co-varying)* | 0.04 | 0.06 | 0.08 |
| **Juvenile** Dispersal, scaling parameter *a* | 0 | 0.1 | 0.2 |
| **Juvenile** Dispersal, distance parameter *b (co-varies with a)* | 0 | 5 | 10 |
| Correlation-distance function parameter *b* | 20 | 80 | 800 |

## 4.4 Results

### *4.4.1 Habitat model*

The habitat model resulted in the map in Figure 30.

**Figure 30: Suitable habitat for Pileated Woodpecker within study area.**

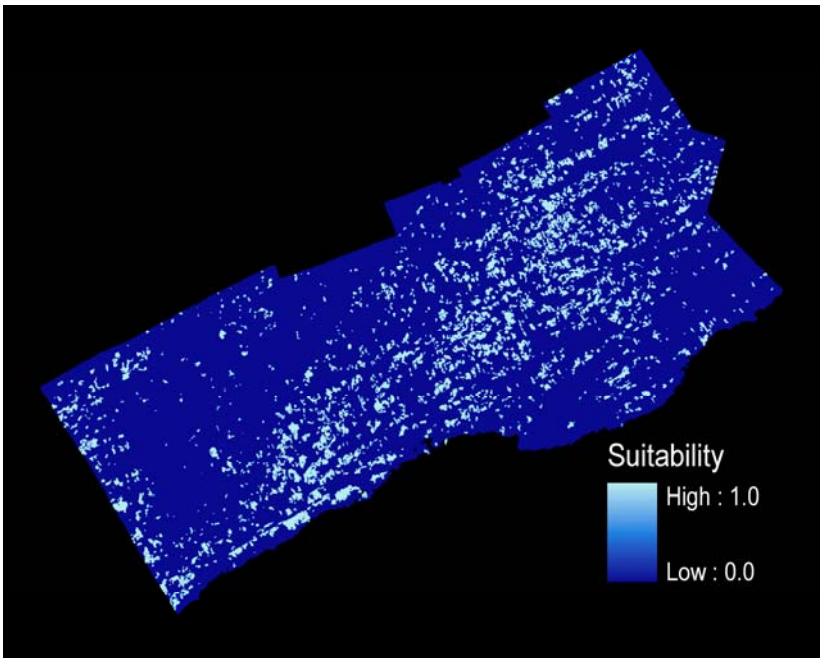



**Figure 31: Percentage of total study area with HS values greater than or equal to the values in the x-axis. For example, 10% of the study area has HS values of 0.2 or more.**

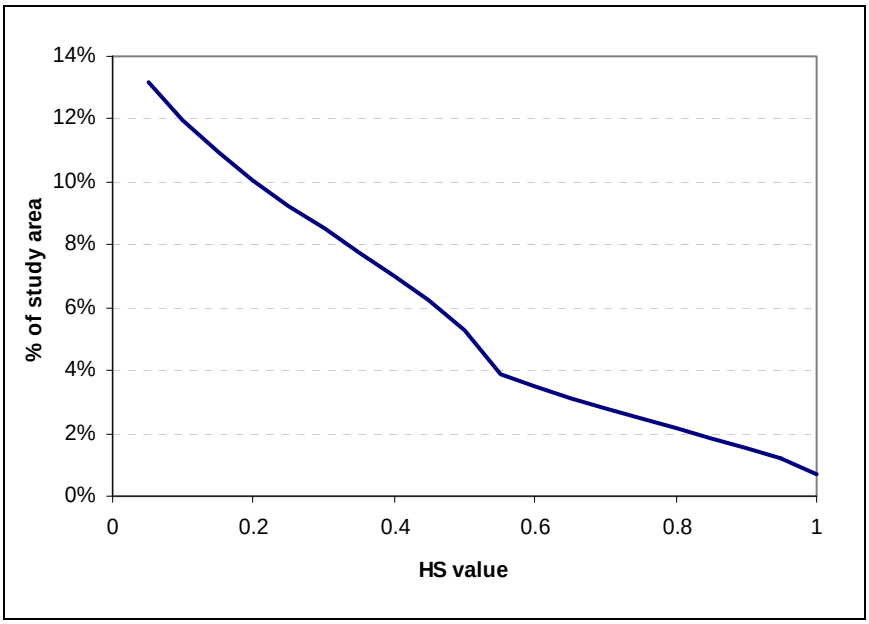
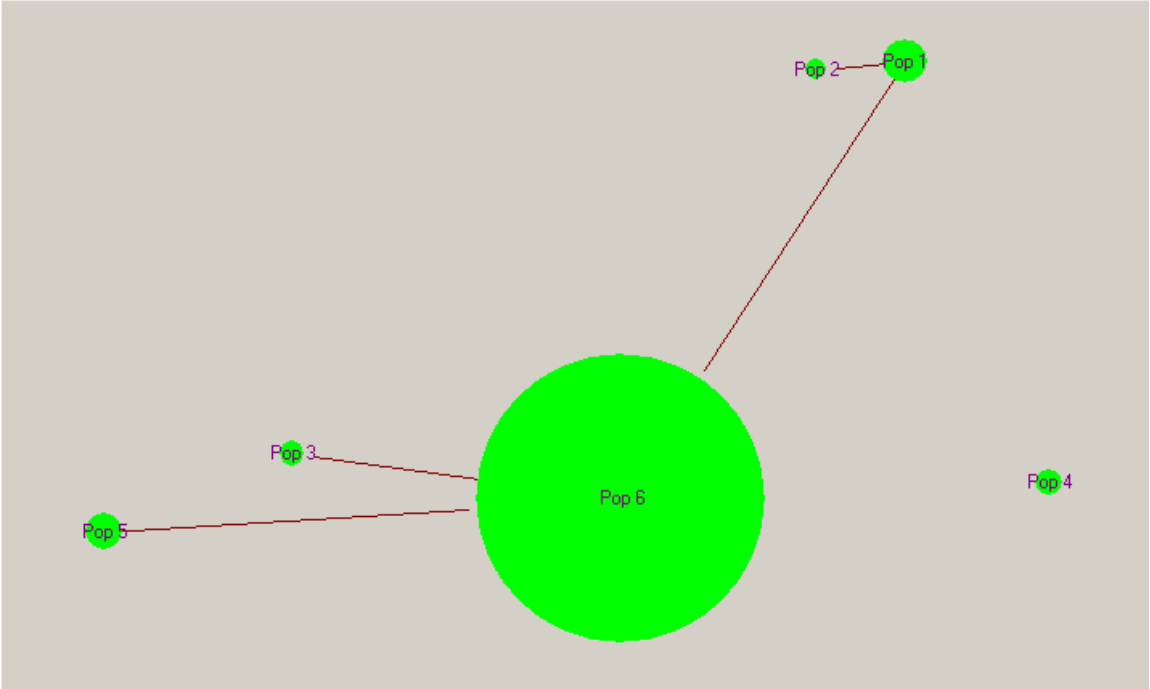


**Figure 32: Metapopulation structure of medium model. All populations are initially at carrying capacity with a stable stage distribution.**




### *4.4.2 Simulation results with the Medium model*

The primary, or 'medium', population model used the medium values for all parameters. It had 6 patches (Figure 32) and a total initial abundance of 1080 individuals, divided into 454 juveniles and 626 adults.

#### 4.4.2.1 Viability

For the medium model, persistence probability (measured as one minus risk of quasi-extinction) was 0.9999 for a threshold of 250 individuals. Since both stages are breeders (mature individuals), expected minimum adult abundance was the same as expected minimum total abundance (see below).

#### 4.4.2.2 Stability

Median growth rate (ratio of median final abundance to initial abundance) was 0.7907, indicating

a decline from initial abundance.However, the decline appeared to be asymptotic (Figure 34). Mean yearly growth rate was 0.9955. Robustness (measured as one minus risk of 50% terminal decline) was 0.9798.

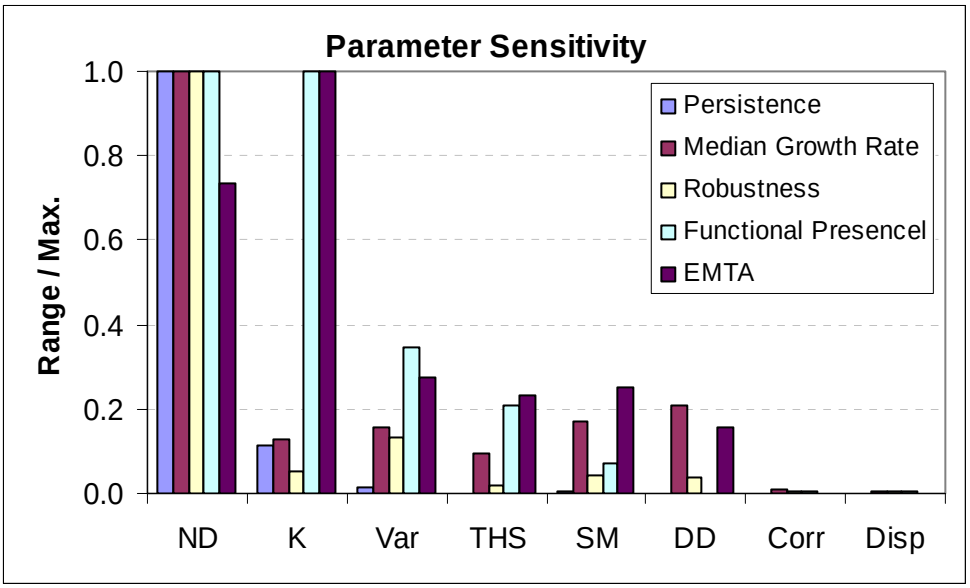
#### 4.4.2.3 Functionality

Functional presence (measured as one minus risk of interval decline to a threshold of 540 individuals) was 0.8859, and expected minimum total abundance (EMTA) was 668.1.Overall, the medium model resulted in a declining population, albeit one which appears to be stabilizing eventually at approximately 80% of its initial abundance. According to the sensitivity analysis, the most important factor affecting the model is patch structure as determined by the neighborhood distance parameter (see below), as well as carrying capacity estimation.

### *4.4.3 Sensitivity analysis*

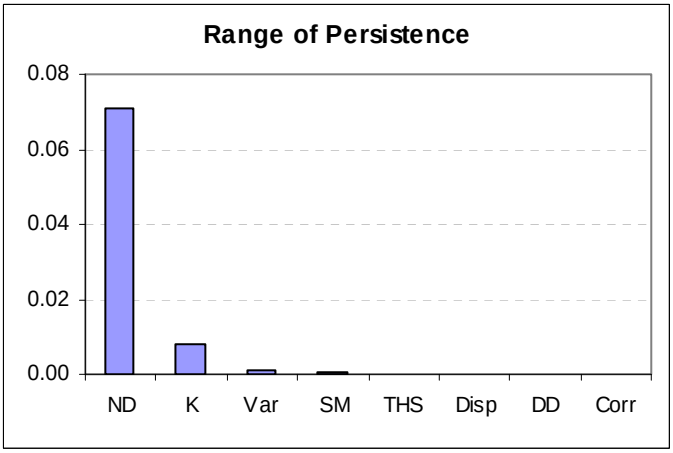
The sensitivity analysis identified neighborhood distance (ND) and carrying capacity function (K) as the parameters to which the model was most sensitive (Figure 33). Progressively less important were variability (V), threshold for habitat suitability (THS), stage matrix (SM), density dependence (DD), correlation (Corr), and dispersal (Disp).

**Figure 33: Parameter sensitivity. Values are normalized ranges within each measure. Range for each parameter indicates maximum minus minimum from the 'high' and 'low' models. This value is then normalized by dividing by the maximum range across all parameters for the same population measure.**

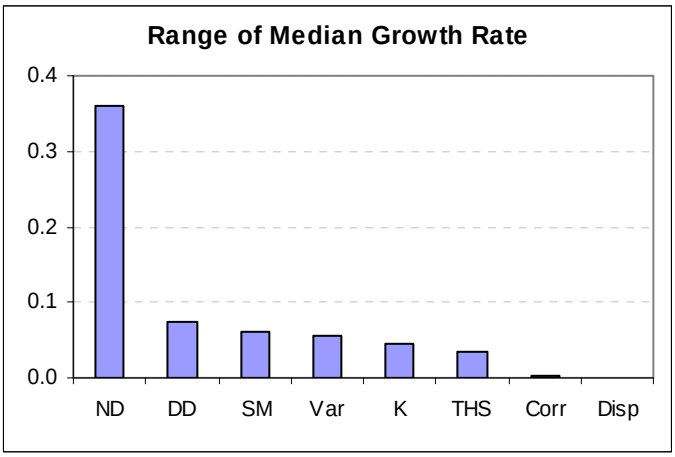



The parameters are sorted by mean normalized range across the five measures (A-E)

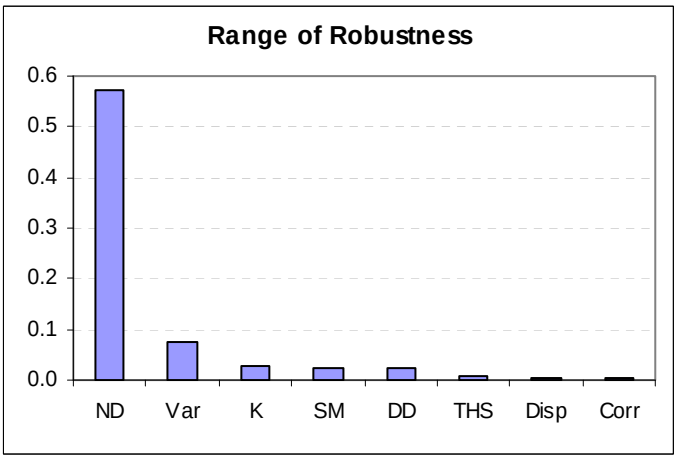
**A. Ranges for the risk of dropping below 250 adults. This measure is most sensitive to neighborhood distance.**



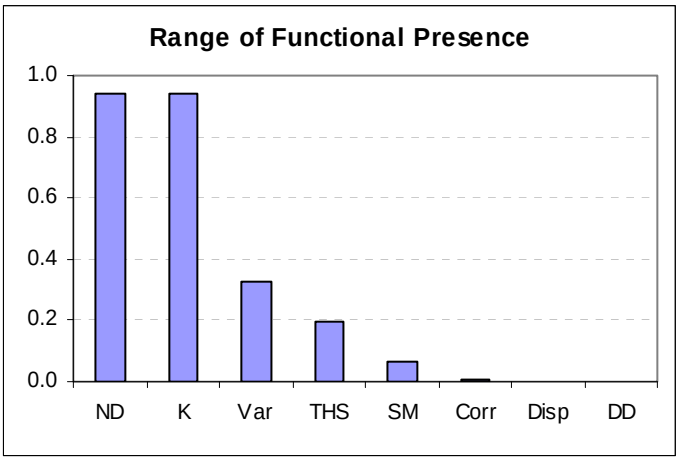
**B. Ranges for the proportion of median final abundance to initial abundance. This measure is most sensitive to neighborhood distance.**



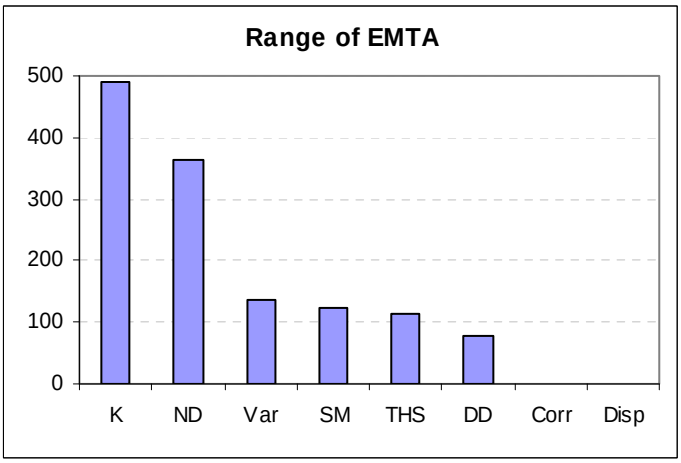

**C. Ranges for the risk of dropping below 50% of initial for the final time step. This measure is most sensitive to neighborhood distance**



**D. Ranges for the risk of dropping below 50% of standard initial abundance for any time step. This measure is most sensitive to neighborhood distance and carrying capacity.**




**E. Ranges for the expected minimum total abundance (EMTA). This measure is most sensitive to carrying capacity and neighborhood distance.**




### *4.4.4 Best-case and worst-case models*

Using the sensitivity analysis, best-case and worst-case models were constructed by choosing each parameter value to maximize or minimize, respectively, the population measures. The model parameters are shown in Table 20, and the results are shown in Table 21. The best-case

model showed very little decline, and stabilized around 1508 individuals, or approximately 98% of initial abundance. The medium model decreased by around 20%, while the worst-case model was leveling off at about 38% of initial abundance.

**Table 20: Best-case, medium, and worst-case model parameters.**

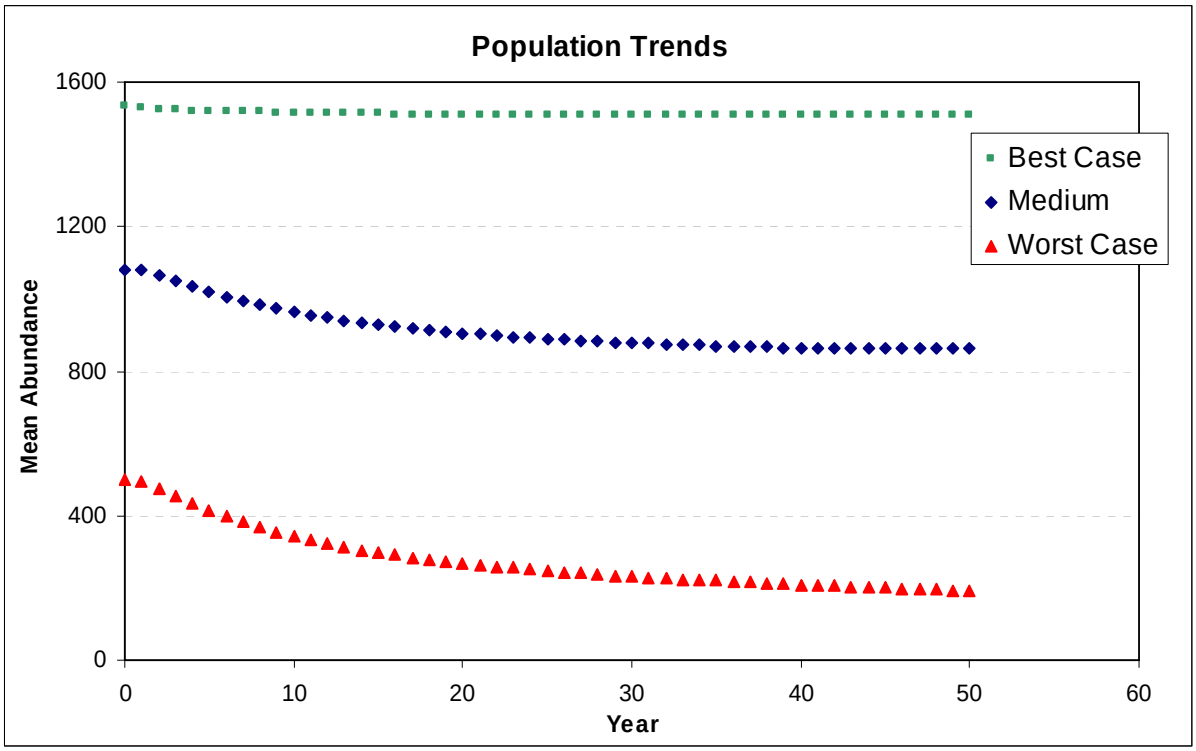
| Model | SM | F CVs | THS | ND | DD | K | Disp. (a/b) | Corr. |
|---|---|---|---|---|---|---|---|---|
| Best case | 0.8865 | 0.015 | 0.1 | 18 | Ceiling | 0.08 | 0/0 | 20 |
| Medium | 0.8767 | 0.066 | 0.2 | 13 | Contest 1.1 | 0.06 | 0.1/5 | 80 |
| Worst case | 0.8640 | 0.127 | 0.3 | 7 | Contest 1.1 | 0.04 | 0.2/10 | 800 |

**Table 21: Results for best-case, medium, and worst-case models.**

| Model | Patches | Initial Abundance | Persistence | Median Growth Rate | Robustness | Functional Presence | EMTA |
|---|---|---|---|---|---|---|---|
| Best case | 2 | 1536 | 1.0000 | 0.9896 | 1.0000 | 1.0000 | 1393.4 |
| Medium | 6 | 1080 | 0.9999 | 0.7903 | 0.9777 | 0.8814 | 668.2 |
| Worst case | 17 | 500 | 0.0264 | 0.3680 | 0.2155 | 0.0000 | 145.6 |

**Figure 34: Mean abundance for the medium, best-case, and worst-case models. Mean yearly growth rate ranges from 0.9811 to**

**0.9996.**




### *4.4.5 Habitat loss scenarios*

The habitat loss scenario where small fragments were removed as suitable habitat before larger fragments, in general had lower viability, stability and functionality for the Pileated Woodpecker population in the pilot study area than the edge erosion scenario. Total habitat suitability of all patches declined more quickly with each level of habitat loss for the small fragment scenario than for the edge erosion scenario for the population under medium, best-case, and worst-case parameters (Figure 35).

Population viability measured in terms of persistence probability (Figure 36) declined more

rapidly for the small fragment loss scenario than for the edge erosion scenario under all population models tested. Thresholds used for this measure were 250, 1,000, and 50 for the medium, best-case, and worst-case models, respectively. These thresholds were selected to best illustrate differences between the two habitat loss scenarios. The edge erosion scenario maintained relatively high persistence probability for their respective thresholds under the medium and best-case models until the highest amounts of habitat were lost. Estimated minimum abundance (EMA) (Figure 37) of adults was lower, at all levels of habitat loss, in the small fragment loss than in the edge erosion scenario under all three population models.

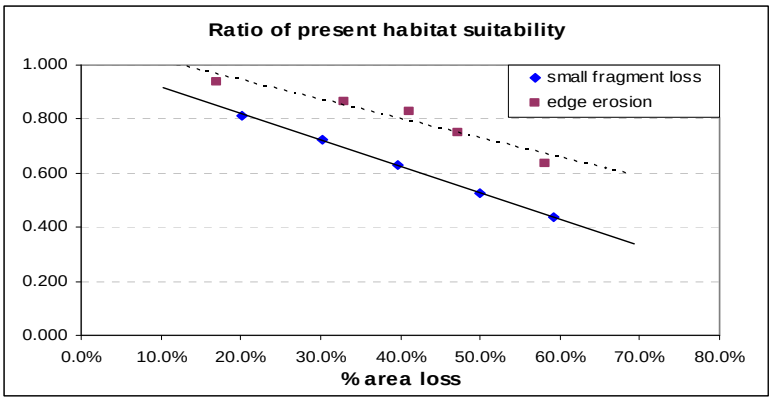
Stability for the Pileated Woodpecker measured as median growth rate (Figure 38) declined more quickly for the small fragment loss scenario under all three models. Whereas, when robustness was measured (Figure 39), the two scenarios diverged rapidly under the medium population parameters but were similar under the worst-case model. Under the best-case model, robustness remained high for both scenarios at the lowest levels of habitat loss then dropped precipitously for the small fragment loss scenario while the edge erosion scenario remained high.

Functionality measured as the functional presence (Figure 40) was high for both scenarios under the best-case model until around 60% area loss was reached where the small fragment loss scenario dropped lower. Functional presence for the small fragment loss scenario declined more rapidly than the edge erosion scenario under the medium population model, while both scenarios were equally low at all levels of habitat loss under the worst-case model.

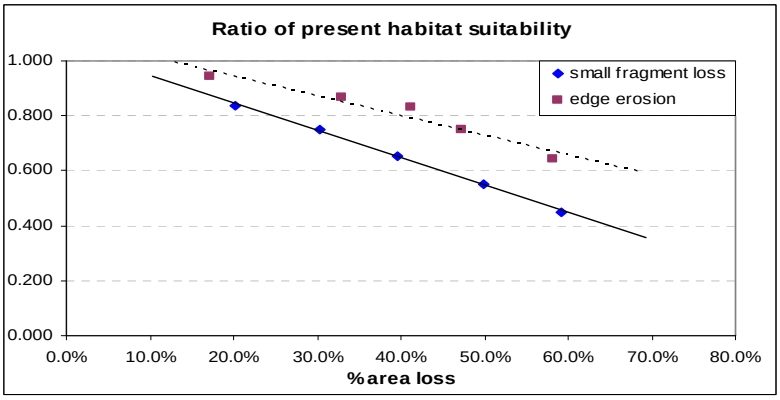
**Table 22: Habitat loss scenario patch number and population abundance.**

| Habitat scenario | % area loss | # patches | | | Initial abundance | | | Expected min. abundance | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | medium model | best case | worst case | medium model | best case | worst case | medium model | best case | worst case |
| Present | 0.0% | 6 | 2 | 17 | 1080 | 1536 | 500 | 667 | 1394 | 142 |
| Small fragment loss | 20.2% | 18 | 11 | 20 | 877 | 1289 | 389 | 411 | 1031 | 13 |
| | 30.3% | 21 | 17 | 19 | 784 | 1149 | 345 | 314 | 846 | 7 |
| | 39.6% | 18 | 19 | 18 | 685 | 1000 | 315 | 270 | 712 | 6 |
| | 50.0% | 19 | 18 | 16 | 571 | 847 | 264 | 199 | 601 | 5 |
| | 59.3% | 16 | 18 | 15 | 472 | 691 | 239 | 151 | 459 | 4 |
| Edge erosion | 17.1% | 7 | 3 | 16 | 1009 | 1446 | 452 | 615 | 1301 | 113 |
| | 32.9% | 10 | 4 | 15 | 935 | 1332 | 395 | 520 | 1189 | 69 |
| | 41.2% | 7 | 5 | 15 | 896 | 1274 | 386 | 516 | 1135 | 79 |
| | 47.3% | 11 | 4 | 15 | 813 | 1155 | 323 | 434 | 1029 | 24 |
| | 58.3% | 13 | 3 | 18 | 688 | 985 | 243 | 347 | 880 | 0 |

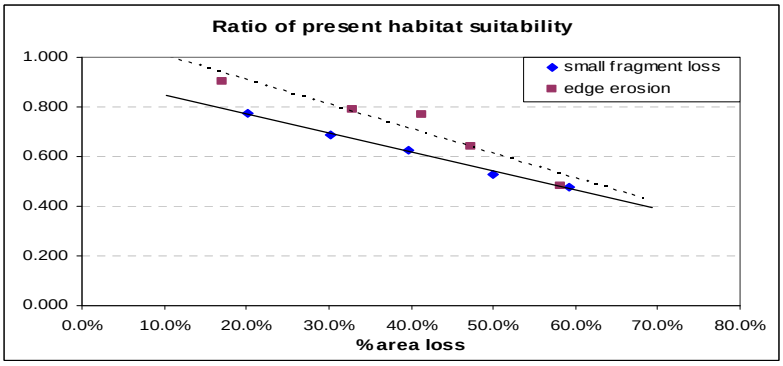
**Figure 35: Total habitat suitability as a function of the percent of area lost under the two scenarios. Model under medium population parameters is shown in (a). The best-case and worst-case population models are shown in (b) and (c), respectively. Habitat suitability index is the ratio of remaining habitat suitability over total habitat suitability at the present habitat extent.**




a.

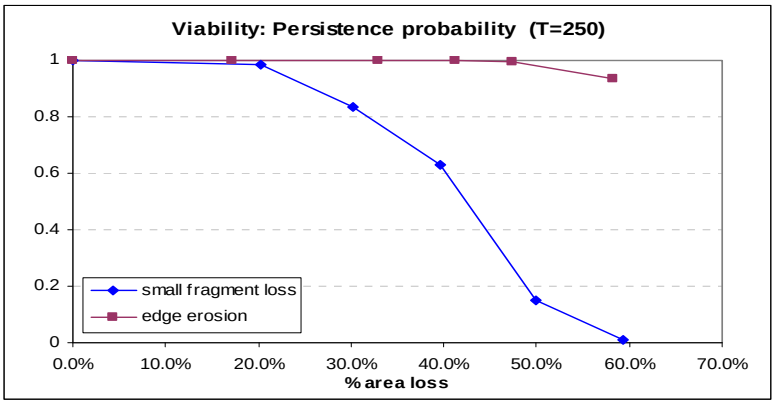



b.

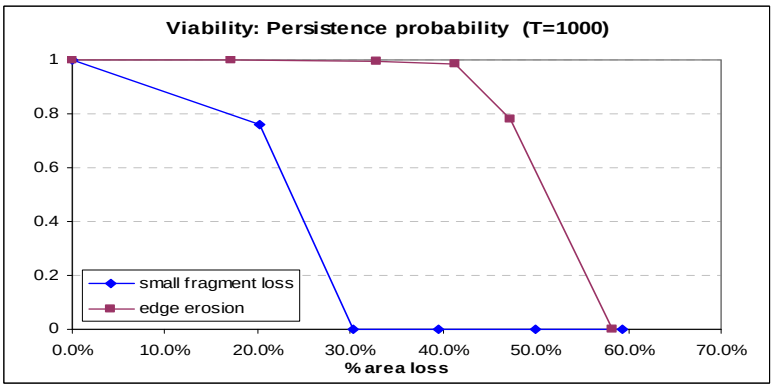



c.

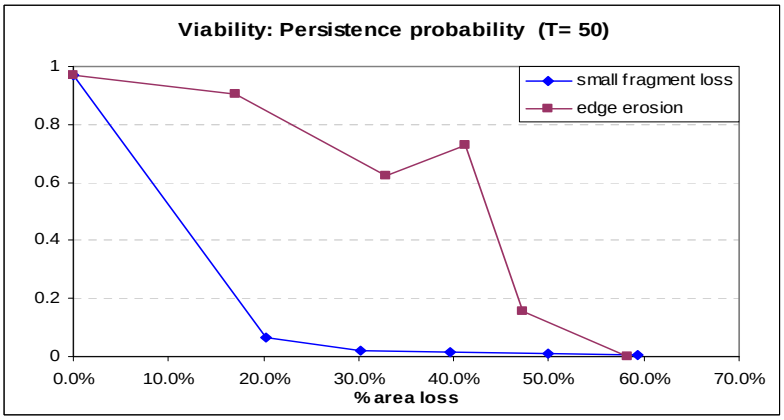
**Figure 36: Persistence probability (measured as one minus the risk of decline to a threshold abundance of adults at any time) for the two habitat loss scenarios under (a) the medium, (b) best-case, and (c) worst-case population parameters. The threshold is 250 adults for (a), 1000 for (b), and 50 for (c).**




a.



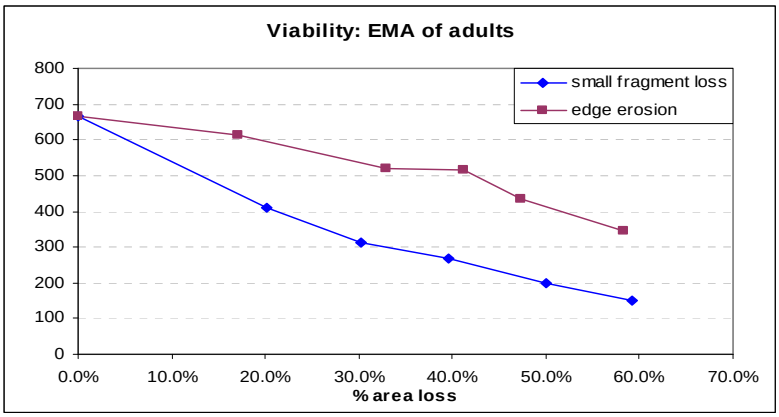

b.



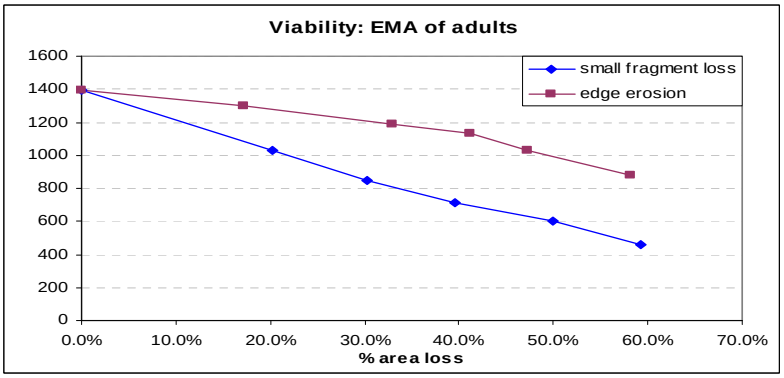

c.

**Figure 37: Expected minimum abundance of adults for the two habitat loss scenarios under (a) the medium, (b) best-case, and (c) worst-case population parameters.**

a.




b.




c.

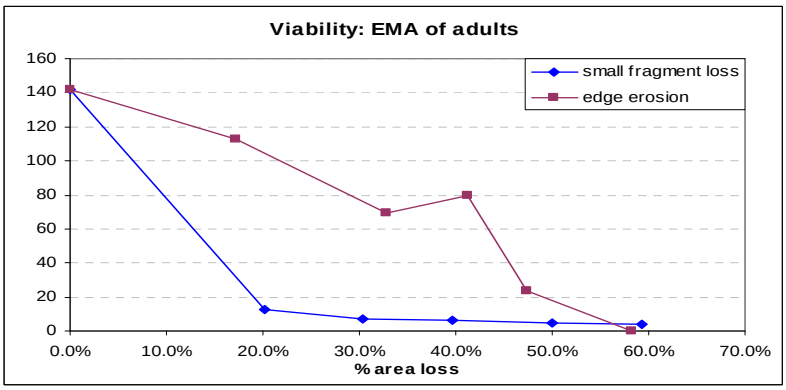
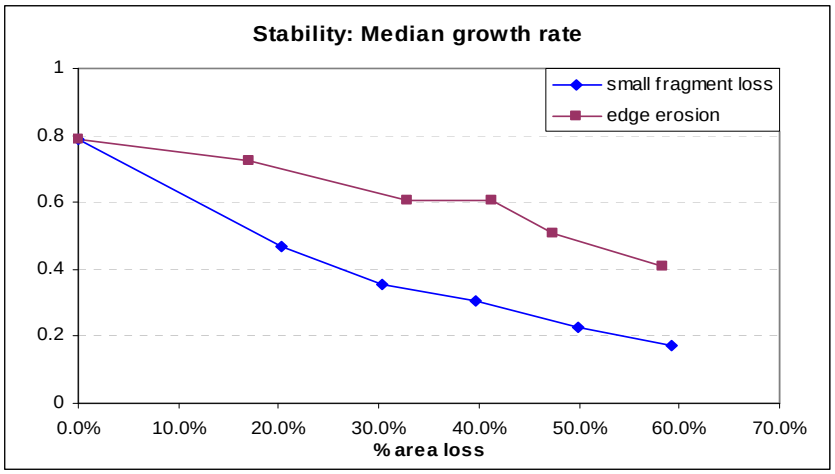
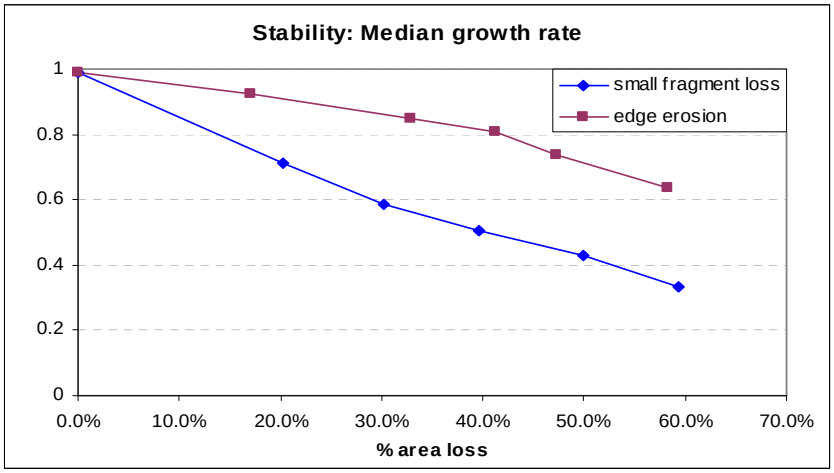


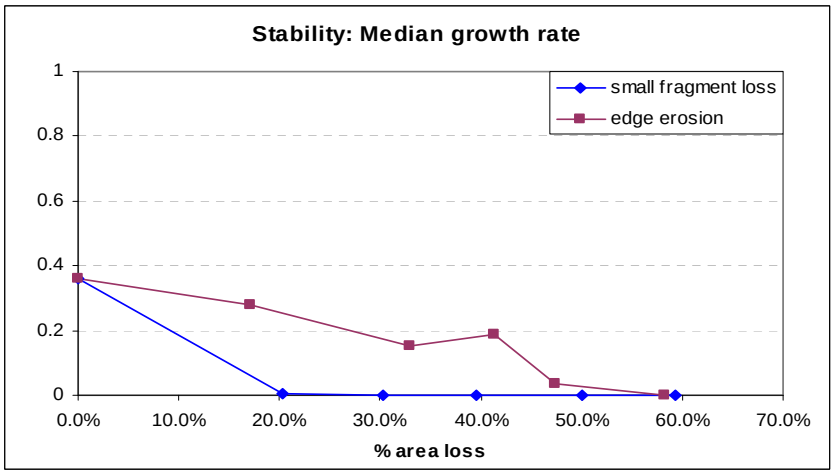
**Figure 38: Median growth rate (measured as the ratio of median final abundance to initial abundance) for the two habitat loss scenarios under (a the medium, (b best-case, and (c worst-case population models.**




a.



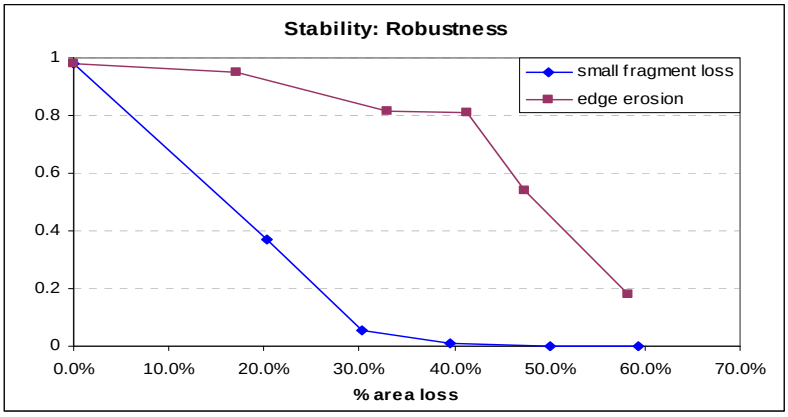

b.



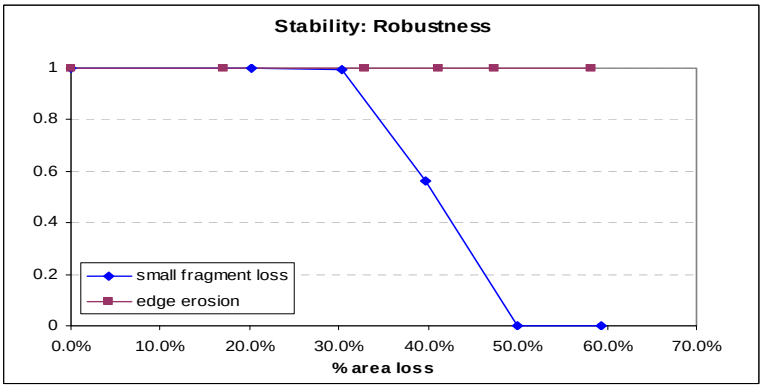

c.

**Figure 39: Robustness (measured as one minus the risk of the final abundance falling below 50% of initial abundance at present habitat extent) for the two habitat loss scenarios under (a the medium, (b best-case, and (c worst-case population models.**

a.




b.




c.

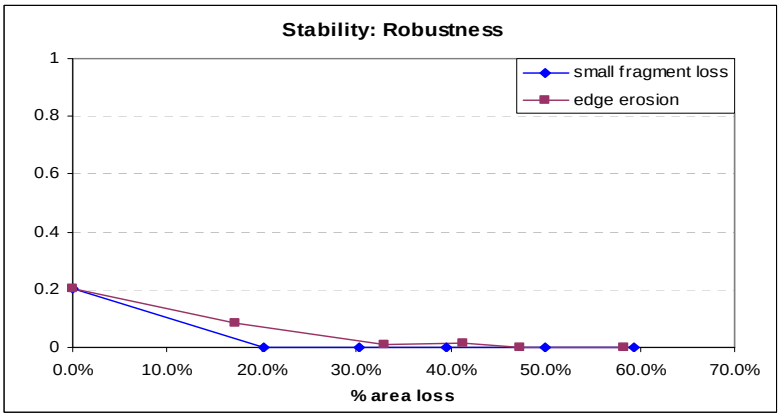
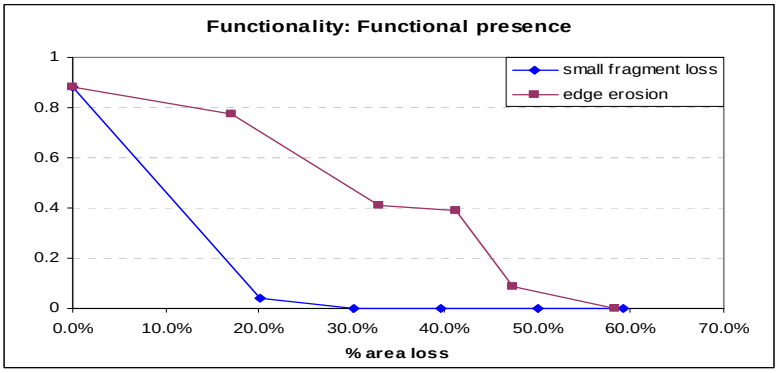
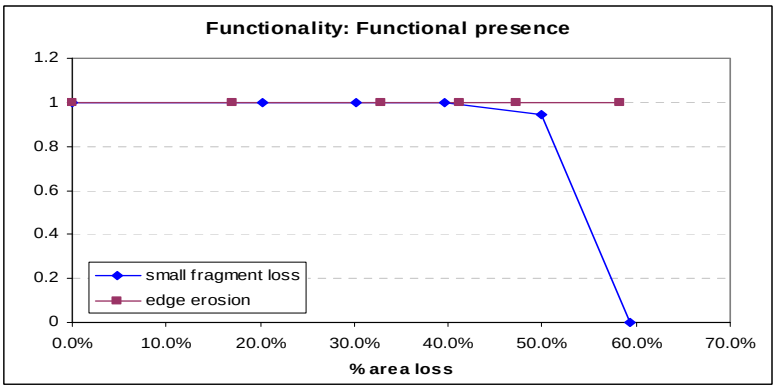


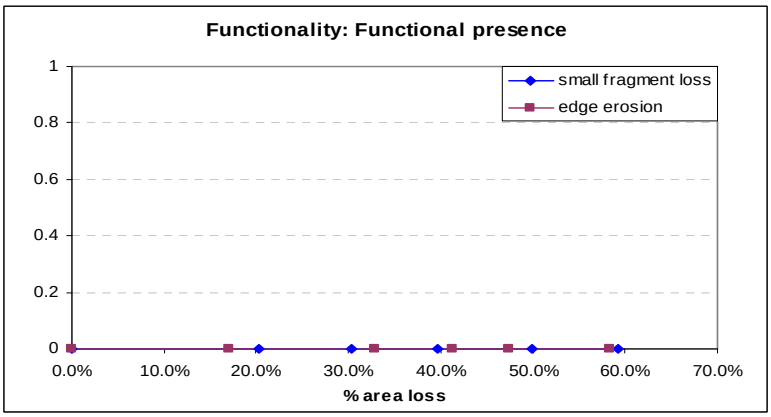
**Figure 40: Functional presence (measured as one minus the risk of the population falling below 50% of initial abundance at present habitat extent and under medium population parameters) for the two habitat loss scenarios under (a the medium, (b best-case, and (c worst-case population models**




a.




b.




c.

# 5 DISCUSSION

## 5.1 Interpretation of Results

Results showed some variability among the three species, and substantial uncertainty within each species, in terms of viability, stability and functionality. American Bittern seemed to be the least viable and least stable population, due to its small abundance in the study area, which in turn is because of its less abundant habitat.

### *5.1.1 Sensitivity of results to model parameters and assumptions*

The sensitivity analyses indicated that, the uncertainty of the results, as expressed in terms of the difference between best-case and worst-case models, was quite substantial. The most important parameters contributing to this uncertainty were neighborhood distance and carrying capacity. These parameters are based on two related variables, the home range size and density of nests. For both parameters, higher values resulted in higher viability, stability and functionality. A higher value of neighborhood distance means a more connected (or less fragmented) population structure, with fewer and larger populations, which are less affected by demographic stochasticity. A higher value of carrying capacity means higher population sizes.

Sensitivity to a parameter measures a combination of two related but independent factors: the inherent importance of the parameter to the viability, functionality and stability of the metapopulation, and the uncertainty with which the parameter is estimated. If a parameter is very uncertain, then there will be a large difference between the low and high values of that parameter, and as a result, results with the low and high values of that parameter will be substantially different from each other. High sensitivity to neighborhood distance points out to the importance of fragmentation as a factor in determining viability, functionality and stability. High sensitivity

to carrying capacity points out to the importance of habitat quality. For both parameters, high sensitivity indicates a high degree of uncertainty in the estimates of home range size and density of nests.

Other important parameters were variability, stage matrix and density dependence. These are based on the vital rates (survival and fecundity), including their temporal variation and their dependence on abundance. Higher variability leads to lower viability, stability and functionality, because more variable population sizes are more likely to reach lower values. Higher values for stage matrix (survival and fecundity) means higher growth rates, and less likelihood of reaching low population sizes, and thus higher viability, stability and functionality. The effect of the type of density dependence (Ceiling or Contest) is more complicated, and depends on the value of the stage matrix (if Ceiling) and Rmax (if Contest).

It is important to note that the sensitivity analyses did not include the habitat maps or habitat functions. This is because of two reasons. First, a simple sensitivity analysis based on high and low values would be conceptually identical to sensitivity to threshold habitat suitability. For example, *increasing* all values of the habitat map by 0.1 is conceptually identical to *decreasing* the Threshold HS parameter from 0.2 to 0.1 (although there would be some numerical difference in terms of total habitat suitability). Second, the fundamental uncertainties about the habitat function cannot be done by the simple high-and-low-values approach. These uncertainties relate to the information on habitat requirements of the species, the availability of maps for each variable that is relevant to a species, and the form of the function relating these variables to species' habitat preferences. Incorporating these types of uncertainties requires different types of data than were available (see Recommendations below).

### *5.1.2 Effects of habitat loss*

An interesting result is that the small fragment loss scenario resulted in a larger loss of total habitat suitability than the edge erosion scenario. This is likely because the edges were already less suitable than core areas, and even small fragments contained enough core areas that losing a given area of small fragments resulted in a greater decrease in suitable habitat than losing the same area of edges.

Another result of the comparison of the two scenarios with respect to decrease in total habitat suitability is that the small fragment loss resulted in a more-or-less linear decrease in total suitable habitat, whereas the change in total habitat as a function of edge erosion was nonlinear and more variable. This result may possibly be an artifact of the method used to simulate the levels of habitat loss in the edge erosion scenario. Edge erosion was simulated by running a center vs. neighbor (CVN) pattern function on the Boolean map of total habitat area. This results in a map where the value in each cell represents the number of non-same neighbors (after masking by habitat area). Removing the higher value cells is equivalent to removing the most exterior habitat edge. However, simply removing edge pixels from highest to lowest (exterior to interior) often resulted in increments of habitat loss that were either very small or very large, and not especially useful for comparison with the other habitat loss scenario. In order to remedy this, after an initial level of habitat was removed using the CVN function, we ran the pattern a second time on the new reduced habitat area map resulting in two CVN maps. Each subsequent level of habitat loss was selected from either of the two resulting CVN pattern maps in order to select incremental levels of total habitat loss. So although we attempted to always remove the most exterior before more interior edge pixels, in order to get incremental levels of total habitat loss comparable to the small fragment loss scenario, this rule was not strictly followed. This may have

resulted in the observed non-linear decline in total habitat suitability with increasing habitat area loss, which in turn resulted in non-linear declines in some of the viability, stability, and functionality measures. An alternate method of simulating edge-erosion would be to randomly select increasing numbers of pixels amongst all the identified 'edge' pixels.

#### 5.1.2.1 Effects on fragmentation

Both types of habitat loss resulted in more fragmented populations, but this effect was not uniform. For Red-shouldered Hawk and Pileated Woodpecker, the small fragment loss scenario resulted in more fragmentation than the edge erosion scenario (actually, there was no increase in the number of patches with edge erosion under the worst-case model). For American Bittern, the small fragment loss scenario also resulted in more fragmentation than the edge erosion scenario, but only for the best-case model (there was no difference between the two scenarios under the medium and worst-case models).

#### 5.1.2.2 Effects on viability

Both persistence probability (measured as one minus risk of quasi-extinction) and expected minimum abundance were sensitive to both types of habitat loss, except in worst-case models or high amounts of habitat loss. Expected minimum abundance was a better measure of viability for detecting effects of habitat loss, because the response was more consistent, and the measure does not depend on threshold settings.

#### 5.1.2.3 Effects on stability

Median growth rate (ratio of median final abundance to initial abundance) was a sensitive measure of habitat loss and its response was close to a linear function of the area of lost habitat, except under the worst-case model. Robustness (measured as one minus risk of 50% terminal

decline) was a very sensitive measure, but its response was nonlinear with a sharp decline at a certain amount of habitat loss (usually between 20% to 50%, depending on the model and the habitat loss scenario).

#### 5.1.2.4 Effects on functionality

Functional presence (measured as one minus risk of interval decline to a fixed threshold) was zero or practically zero for the worst-case models of all three species. This measure had a low starting value (e.g., for 0% loss) for two of the species, and showed a sharp decline at a certain amount of habitat loss (dependent on the model and the habitat loss scenario). Again the expected minimum total abundance was a more consistent measure in terms of its gradual response to amount of habitat lost.

#### 5.1.2.5 What level of habitat loss can be tolerated?

We did not make a decision about what level of persistence probability or expected minimum abundance marks the arbitrary border between viable and nonviable, because this is not a scientific decision but a policy decision. Similarly, we did not define the border between stable and unstable or between functional and nonfunctional. We strongly believe that it is the duty of scientists to avoid making policy recommendations (Lackey, 2007). Deciding, for example, whether an 80% risk of falling below the quasi-extinction threshold (of say, 250 birds) is an acceptable or unacceptable risk is not a scientific question. It is a policy decision. Without this decision, it is not possible to state what level of habitat loss can be tolerated. Depending on how these levels (e.g., of acceptable risk) are set, the populations in the study can be considered to become nonviable, unstable or nonfunctional after as little as 10% loss of their current habitat (or even to be currently nonviable, unstable or nonfunctional), or only after more than 60% of their habitat is lost.

However, in response to the comments on the first draft of this report, we give examples (Table 23) of how this question can be answered using the results presented in this report. We must emphasize, however, that these are only examples; actual determination of the level of habitat loss that can be tolerated depends on policy preferences and risk tolerance attitudes.

**Table 23: Amount of habitat loss (as percent of current habitat) that can be tolerated by each species and still meet certain criteria for viable, stable and functional populations.**

| Species | Criteria* | Type of habitat loss | |
|---|---|---|---|
| | | Small fragment loss | Edge erosion |
| Red-shouldered Hawk | Viability (Persistence>0.8 at T=250) | 40% | 62% |
| | Stability (Robustness>0.6) | 21% | 49% |
| | Functionality (Functional presence>0.4) | 0% | 0% |
| American Bittern | Viability (Persistence>0.8 at T=50) | 32% | 42% |
| | Stability (Robustness>0.6) | 0% | 0% |
| | Functionality (Functional presence>0.4) | 0% | 0% |
| Pileated Woodpecker | Viability (Persistence>0.8 at T=250) | 32% | 60% |
| | Stability (Robustness>0.6) | 12% | 46% |
| | Functionality (Functional presence>0.4) | 12% | 37% |

** These criteria are only examples. The setting of these criteria is a regulatory and policy matter, and not a scientific issue.*

### *5.1.3 Applicability to other regions*

An important question is the applicability of the methods and results of these case studies to other regions. We believe that in general all methods we used in these case studies, including the variables used to measure viability, stability and functionality, are applicable to other regions and other species. However, we believe only some of the results are applicable to populations of these three species in other regions. In particular, we believe the habitat models may be applicable to other regions with minor modifications, if the recommended improvements discussed in the next section are implemented. Many of these recommendations relate to

eliminating or reducing data shortcomings; these recommendations will also lead to the modification (and improvement) of the habitat models for this study area. In addition, we recommend reviewing local/regional differences in habitat use and preference of species before applying the habitat models to other regions.

In addition to habitat models, certain aspects of the demographic models are also applicable to other regions. This includes the general structure of the stage matrix and dispersal patterns. However, we recommend that the stage matrix and the standard deviations matrix are modified for each region based on observed trends and fluctuations in that region, as we did in these case studies.

Beyond these, we believe that the applicability of results to other regions is limited. For example, variables such as home range size and density of nests vary among regions, and these variables determine model parameters to which the results are sensitive (see above). Of course, the quality, quantity and spatial distribution of habitat also differs among regions; thus the simulation results in terms of the effects of habitat loss on viability, stability and functionality are region-specific.

## 5.2 Recommendations

We believe the habitat-based approach focusing on viability, stability and functionality of selected species is feasible and practical, and it will satisfy the requirements for the development of biodiversity performance standards. However, there are a number of shortcomings, which in our opinion limit the applicability of this approach within the overall project framework. Some of these are data shortcomings, which we believe can be addressed by implementing a set of specific recommendations we discuss in the following three sections. We believe there is another, more fundamental, shortcoming, which relates to the way the model results are used to reach

conclusions about the best management practices that would lead to the development of biodiversity performance standards. We discuss this issue in the final section.

### *5.2.1 Increasing the study area*

Although a small study area makes certain tasks (such as collating the GIS data) easier, and thus may be appropriate for a pilot study, it can also make other tasks harder for species with relatively large area requirements, such as the ones analyzed in this report. For example, finding the spatial structure of the metapopulation is made more difficult, and the results less realistic, when the study area is small compared to the size and spatial distribution of populations. It is possible, for instance, that the smaller habitat patches identified by the program, that are located close to the edges of the study area would be parts of larger patches when a larger area is studied. In other words, the small study area may artificially result in a more fragmented metapopulation than the actual metapopulation, which in turn may result in an artificially low prediction of viability or stability in the study area. Thus, we recommend that the size of the study area be increased. In addition to allowing a more realistic estimate of the spatial structure of the metapopulation, a larger size may also allow more reliable habitat maps (see below).

It is difficult to state how large the study area should be without seeing the range-wide distribution of habitat for each species. Thus, ideally, the first step would be to develop a low resolution, range-wide habitat map for each species with large area requirements. Then, if the total range is too large for practical reasons or irrelevant for social/regulatory reasons, then the study are should be based on a subset of the range selected to include complete biological populations, and even metapopulations that have little interaction (exchange) with other metapopulations. In any case, it is important to avoid having the borders of the study area cut

through populations, or leave out populations that are very close to (and presumably frequently exchange dispersers with) populations within the study area.

### *5.2.2 Increasing reliability of habitat maps*

As discussed above, our sensitivity analyses did not include the habitat maps or habitat functions, because the available, and mostly qualitative, data do not allow a method for systematically incorporating uncertainties. In addition, and independent of the issue of sensitivity analysis, the qualitative nature of the data also precludes using statistical methods of habitat modeling, which are more reliable approaches to estimating the habitat function necessary for habitat-based metapopulation modeling. To increase the reliability of habitat maps, we suggest the following:

1. Collect presence-absence (occurrence) data in the region on the target species. This need may be met to some extent by increasing the size of the study area, because a larger area may contain enough BBS routes and other survey locations. However, specifically collected presence-absence data will be needed both to increase the sample size for the rarer species, and for a more representative set of locations for all species (because the short observation period of the BBS protocol may not allow observers to record species that are present in suitable habitat, resulting in a relatively low detection probability).

2. Collate more layers for habitat maps. All three species' habitat requirements as described require specific site-level features or management. For example, the Pileated Woodpecker needs snags and woody debris, which may not be available under some timber harvest scenarios, and the American Bittern may utilize some upland agricultural sites adjacent to wetlands under certain mowing/grazing regimes. These types of habitat preference cannot be obtained from the available GIS layers. Including layers that are relevant to habitat preferences of selected species

would increase the reliability of the habitat maps. Examples of layers that may be useful for describing the habitat for these species include the following:

- Detailed wetland information (vegetation composition, average water depth)
- More recent forest information on canopy closure and tree age
- Layers related to timber management or other habitat management practices
- Layers with more detailed information on agricultural practices (including crops, pesticide use, etc.)
- More detailed road map (e.g., distinguishing roads with different amounts of traffic)
- Development/urban layers (with housing density, or human population density)
- Land ownership and use (public, private, conservation easement, etc.)

3. Use quantitative methods such as logistic regression or programs such as MaxEnt. Although these methods are more labor- and data-intensive and require more expertise, their results are more reliable than the qualitative approach we had to use due to lack of the above types of data. In addition, maps estimated with these methods can be validated using established metrics such as the area under the ROC curve and kappa.

### *5.2.3 Decreasing model uncertainty*

The most important parameters contributing to this uncertainty were neighborhood distance and carrying capacity. These parameters are based on two related variables, the home range size and density of nests, and thus require spatial data. Other important parameters were variability, stage matrix and density dependence, which relate to population dynamics and require temporal data.

To decrease the uncertainties in the model results, we suggest the following:

1. Create more reliable habitat maps (see above).

2. Collect spatially comprehensive data. These are data on the location of all individuals or pairs in a few small study areas, with the aim of estimating home range size and population (or breeding) density in different types of habitat.

3. Collect temporally comprehensive data. These are survey data on several consecutive years, designed to estimate population growth rate, variability, and other demographic parameters. The two most useful types of temporal data are mark-recapture studies, and age (or stage) specific surveys (e.g., a census of all juveniles and adults in a given habitat patch in several consecutive years).

4. Use statistical methods such as mark-recapture analysis, time series analysis and others to estimate demographic parameters (e.g., Brook and Bradshaw, 2006).

### *5.2.4 Getting the most out of models: pattern-oriented vs. management-oriented approaches*

One of the most important ways of making population viability analyses more useful is asking a set of specific questions (Akçakaya and Sjögren-Gulve, 2000). Generic questions are not easy to address using PVA because fully exploring such questions requires so many combinations of models that it becomes impossible to distill the required answer from the large amount of model output.

For example, one of the tasks of this pilot project is identifying "core and satellite population area requirements and structural elements (i.e., patch sizes, corridors, buffers, etc.)". This is related to

one of the objectives of this pilot project, to complete population analysis for selected species with the goal of quantifying the amount and configuration of suitable habitat required to support viable, stable, and functional populations. We call such questions pattern-oriented, as they aim to identify patterns of landscape structure and configuration that would meet certain policy goals (e.g., a certain level of species viability). Although generalizations based on identification of such patterns may be of academic interest, we maintain that in most practical cases, this is not possible. We contrast this pattern-oriented approach with a far more practical management-oriented approach.

#### 5.2.4.1 Pattern-oriented approach

Consider, for example, the question of the minimum area of habitat required for viability of the Red-shouldered Hawk. First, the specific viability criterion must be specified. As discussed above, this depends on policy preferences, and cannot be determined by scientists alone. Assuming that this has been determined, the next question is what the purpose of asking the question is. If the purpose is to develop generally applicable guidelines or policy, all assumptions and parameters of the models must be reevaluated for the general area where the policy will be applied. If this area is larger than the study area, the most important parameters to reconsider include the stage matrix (which should be modified for the region based on observed trends and fluctuations in that region), home range size, and density of nests (which vary among regions, and determine model parameters to which the results are sensitive). If these adjustments are done, then the minimum habitat required for the Red-shouldered Hawk depends on a minimum of 8 variables:

1. Forest type in the patch (determines habitat quality)

2. Average distance to water for each cell in the patch (determines habitat quality)

3. Stand age in the patch (determines habitat quality)

4. Number of patches (degree of fragmentation; determines the effect of demographic stochasticity)

5. Size distribution of patches (e.g., equal-sized patches vs. one-large-several-small)

6. Distances among the patches (determine dispersal rates)

7. Habitat in the "matrix" between the patches (may modify the dispersal function)

8. Correlation of fluctuations among the patches.

Any statement regarding the habitat the minimum habitat required for the Red-shouldered Hawk needs to specify the dependencies between all these variables. This can only be done by exhaustively exploring all the combinations of all these variables, some of which may have a very large number of possible values, depending on how general an answer is required. Systematically evaluating, or even randomly sampling from, these combinations would result in thousands or millions of models and would not lead to any practical answers. In other words, for all practical purposes, questions that focus on identifying patterns, such as "What is the quantity, quality and pattern of habitat, at multiple scales, required for these species?" are unanswerable. Any attempted answers to such pattern-oriented questions are likely to be incomplete and thus misleading.

#### 5.2.4.2 Management-oriented approach

Instead, we recommend a management-oriented approach that is based on "whole-model"

analyses of selected management practices. "Whole-model" analysis requires starting from a limited set of management practices, determined by experts, managers, and other stakeholders (in this case, including farmers), and taking into account issues of feasibility, cost, and social acceptability. Each management practice is then analyzed in detail to quantify its effects on habitat and demography, including the uncertainties in these effects. Each practice is likely to have several effects, some on habitat (quality, distribution), some on demography (survival, fecundity, dispersal). These effects are then combined into a single model simulating the effects of that management practice. After the initial simulation of each practice by itself, some practices can be selected for further analysis in combinations.

We do not want to imply that the management-oriented approach is quick and easy. Depending on the species, it could take considerable effort to determine the effect of different management practices on various model parameters. However, compared to the pattern-oriented approach, this approach would not only substantially decrease the effort required to run all the necessary model simulations, it would also make it possible to obtain practical results and aid in the communication of those results.

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