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Boundary, Costs and Trade-offs in Reserve Design Systems

Justus Hurd

Departmental Honors Thesis The University of Tennessee at Chattanooga Department of Mathematics

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Lakmali Weerasena Assistant Professor of Mathematics Thesis Director Sumith Gunasekera Associate Professor of Mathematics Department Examiner

Aniekan Ebiefung UC Foundation Professor Department Examiner

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Abstract

Due to limitations in funding and natural resources, it is infeasible to construct perfect reserve systems for large populations of critical species. For this project, our objective is to formulate a reserve design model that minimizes the distance between reserve sites meeting a threshold of biodiversity features subject to a species coverage constraints. Coupled with other spatial characteristics including reserve size and configuration, the boundary of a reserve system is of key importance. While positive area effects are gained when selecting additional sites, negative boundary length effects are also experienced. For example, it is costly to implement and maintain boundary sites, especially those fragmented from a main cluster of sites. Further, due to the difficulties in maintaining more site boundaries, species populations are now prone to negative boundary effects such as inability to remain in the site reserve and increased predator presence. However, it is frequently the case that the reserve boundary is expanded by introducing a boundary site containing an endangered species. Thus, we must consider the trade-offs that accompany selecting a new boundary reserve site and its cost. In this project, we perform numerical analysis on hypothetical test problems to study the efficient selection of boundary sites.

1 Introduction

The reserve site selection problem is to select reserve sites with the goal to maximize the number of the species contained in the reserves. It ensures the long term protection of the species. When species distributions are known, this corresponds to the maximal coverage problem or minimum cost coverage problem. The problem is generally known as the Reserve Site Selection Problem (RSSP). Mathematical modeling in RSSP has been received great attention in the literature. In addition to coverage constants, a budget constraint is also included in the mathematical model. The budget constant benefits to design a cost-effective reserve system. The maximal coverage problem work towards maximizing the number of distinct species given a predetermined amount of land or given a budget to be used for land acquisition (1). In addition to standard coverage constraints and a budget constraint additional constraints are introduced to maintain the contiguity, and the compactness of the reserve systems. Compactness of reserve systems have been considered by several papers in the recent literature (1; 13; 14). For example, in (1), the compactness of a reserve system is defined as the average Euclidean distance between any two parcels in a reserve proposal. Further, contiguity of reserve systems have been considered by several papers in the recent literature. In many studies, the contiguity is defined as the average number of reserved parcels that were adjacent to any other reserved parcel, were two parcels were defined to be adjacent if they share a common edge or corner. When the distance between any two parcels is minimized species will have to travel through the less unprotected area, thus leading to the increased chance of species survival. Contiguity is paramount to this study since minimizing the number of unprotected edges around a reserve allows for greater movement among some species inside the reserve. It should be noted that preservation of disjoint clusters of patches, patches not attached to the main reserve system, may help minimize the impact of the spread of both disease and natural disasters.

One of the main limitations of these problems is data about the presence of species may not be fully developed which renders the method only as good as the estimate on species presence. Also, these formulation processes are limited in the sense that they should be used only as an upper bound for the total number of species present (7). To account for both species presence and habitat fragmentation a new model, which is an extension of the RSSP, has been developed (6). This model differs from the traditional RSSP in two different ways. First, this model uses the coarse filter approach which has the main goal of representing habitat types instead of attempting maximum species coverage. Secondly, this model considers spatial constraints when examining and choosing potential reserves.

Patches and corridors are the key components to the composition of reserve habitats. Patches (also known as clusters or nodes) are defined as a collection of reserve sites. Corridors are designed to link patches and manage species migration between patches. The goal of reserve planning is to establish and maintain self-sustaining wildlife populations at levels of dynamic equilibrium with the ecological, social, and economic values of the human community (2). This goal is to be accomplished by making necessary changes to existing patches, designing and implementing new patches and corridors, and maximizing the positive attributes of the reserve systems while minimizing the negative impacts (8). Understanding the spatial and size relationships regarding patches and corridors can help land managers make informed decisions. In attempting to create design and plan reserves, it should be pertinent to preserve and connect nodes through linking corridors (4). A corridor can be thought of as an isthmus of type, a narrow body of land connecting two greater bodies of land, in this case patches. In the following sub-sections we briefly discuss some of the key design principles in reserve designing.

1.1 Large reserves and patches are better than small reserves and patches



Figure 1: Large Patch vs Small Patch

Compared to smaller reserve patches, larger reserve patches generally lead to better quality of habitats as well as increased species diversity. Smaller areas often lead to species inbreeding and genetic drift. Also, smaller areas are more prone to total species extinction due to natural disasters. Firstly, larger reserve patches positive area effects are increased. Greater reserve areas allow for larger population sizes and decreased competition for natural resources among species. Further, animal and plant species are more likely to achieve a dynamic equilibrium when they are given larger areas to grow and flourish. Secondly, the edge effects are reduced. Edge effects are a break in continuity between two adjacent habitats, leading to changes in the environmental and biological conditions (4). Interior species, which are normally those most susceptible to local extinction, benefit greatly from larger reserves since more area is comprised of interior habitat compared to smaller reserves. Finally, species diversity is increased. Bigger reserves allow for more habitat diversity, consequently more species diversity is possible.



Figure 2: Connected Patches vs Separated Patches

1.2 Connected reserves and patches are better than separated reserves and patches

When corridors are introduced to connect patches there an increase in the area of the habitat due to the connectivity. This increased area of habitat allows for additional species to grow and flourish. Connecting corridors often serve as transitional habitats for animals moving through them (?). Connecting corridors provide species populations safe travel between protected patch reserves. Moreover, corridors allow for movement of protected species in the event of sudden environmental change.

Without these corridors species could face extinction due to their lack of ability to move in response to natural disasters. Further, corridors can inhibit winds, pollutants, and undesirable species traveling orthogonal to the corridors. It is not to be overlooked that corridors can also be detrimental to the patches and reserves they connect; in the same way that corridors facilitate the movement of protected species, they may also facilitate the movement of species and diseases that are detrimental to the habitat. Lastly, reserves and patches that are connected by corridor channels have a higher probability of being a source for introduction of new individuals into populations when compared to non-connected reserves (5).

1.3 Unified reserves and patches are better than fragmented reserves and patches



Figure 3: Unified Patch vs Fragmented Patch

Consider two reserves of equal area, one whole and the other split into two parts. Even though the two reserves have the same total area, the reserve that is unified is of greater value. The reasons for its greater value are increased positive area effects, reduced edge effects and increased habitat diversity. Refer to "Large Reserve Patches Are Better Than Small Reserve Patches" for further discussion on these reasons (?).

1.4 Several reserves and patches are better than one single reserve or patch



Figure 4: Several Patches vs Single Patch

Species populations often depend on multiple patches in order to have their needs met. If only a single protected patch exists a natural disaster or disease outbreak has the potential to decimate all populations living in that patch. Conversely, if multiple protected patches exist then populations may be able to migrate to nearby patches in the event of natural disaster preventing total extinction of a population. Multiple patches may also contribute to larger total numbers of individuals, greater genetic diversity, viable metapopulations, and the increased probability of recolonization after local extinction in one patch (8).

1.5 Nearness is better than separation



Figure 5: Nearness vs Separation

It is the case that sometimes individuals or groups of individuals will roam outside of their natural habitat. When these individuals roam, it is more likely that they come across, and consequently use, a patch that is closer to their home patch as opposed to a distant patch. As the distance between any two patches increases, the chance that species from those two patches will interact with each other decreases. The opposite of this is also true, as the distance between any two patches decreases, the likelihood that the species from the two patches will interact with each other increases (8).

1.6 The SLOSS Problem: a single large patch or several small patches



Figure 6: SLOSS: Single Large or Several Small

Whether to create a single large or several small reserves, totaling the same area, is among ongoing debate among conservation biologists. The creation of several small reserve patches is argued to allow for the highest density of species, however, this should be contrasted with the notion that the smaller patch sizes may negatively impact area-sensitive species. To address this issue it has been suggested that it may be equally viable to create a system of patches connected by corridors as it is to create a single large patch of the same area. Diamond (1976) suggests, "The question is not which refuge system contains more total species, but which contains more species that would be doomed to extinction in the absence of refuges." If it is possible to achieve connectivity between patches via corridors then it is less likely for the entire system to be decimated by natural disaster or disease when compared to a single large patch system. If it is not possible to achieve connectivity between patches via corridors, it is generally accepted that a single large patch is superior.

1.7 Continuous corridors are better than fragmented corridors

Corridors are designed to direct movement between patches and serve as a home for some organisms. Gaps in corridors impede the movement of species. However, corridors with gaps are often better than having no corridors whatsoever. Wide corridors are generally better than narrow corridors. Corridors serve as a temporary habitat for species moving from one patch to another through the corridor. The longer that the species is present in the corridor, the more important it is for that corridor to serve as a temporary habitat for those species. Wider corridors make the corridor a more viable habitat because it reduces the edge effects within the corridor. Corridors that are too wide, however, may have adverse effects on the species that attempt to use it. For example, if corridors are too wide then it may cause an increase in the time spent wandering in the corridor, leading to an overall higher mortality rate. Further multiple corridors between patches are better than a single corridor. This is evident in that having multiple corridors allows for insurance if one of the two corridors was disrupted (8).

1.8 Applying principles

When planning a reserve system the project team should first research the natural composition of previous patches and corridors. Next, the team should scout to find a location where a potential reserve is not only prudent but also practical. Finally, the team should employ the principles previously discussed to create a reserve matrix that maximizes the benefit to the target species while minimizing the negative impact to the surrounding human population. The ideal mix of patch and corridor size, location, composition, and formation varies based on the project, however, the general principles discussed usually apply (8).

The goal of this study is to develop a cost-effective mathematical model to protect species by efficiently selecting the boundary sites of a reserve system. Here we use the reserve design concept 'Nearness is better than separation'. We define the objective function of our mathematical model is to minimize the sum of the Euclidean distances between sites within the reserve system. This formulation also incorporates the requirements to cover all target species at least once with a limited conservation budget. Then we introduce an additional constraint to include the boundary sites based on the available probabilities of species occurrences.

The thesis is organized as follows. In Section 2, we provide the mathematical model. In Section 3, we provide numerical examples to illustrate the performances of the mathematical model. Section 4 summarizes our work and discusses future research directions.

2 Mathematical Model: Efficiency and Trade-offs in Reserve Design

For a given reserve area, we are interested in protecting certain species occurring within the area. It is assumed that the prevalence of existing species does not change with time but prevalence of existing species is known as a probability. Further, we assume that the the entire reserve system is considered to be partitioned into a number of potentials reserve sites. For example, Figure 1 shows a 3×3 grid, containing 9 unit reserve sites named as x_1, x_2, \ldots, x_9 . For example, the ordered pair (1, 1) shows the site 1 while the ordered pair (2, 3) shows the site 6.

| X₁ | X₂ | X₃ |
|-----------------------|--------------------------|----------------|
| (1,1)● | (1,2)● | (1,3) |
| X₄ | X₅ | X ₆ |
| (2,1)● | (2,2)● | (2,3)● |
| X7 _(3,1) ● | X ₈ (3,2)● | X9 (3,3)● |

Figure 7: Sample Reserve system

Let M be the number of reserve sites and N be the number of species. In this model, we define decision variables to indicate which sites are included in the reserve and their allocation to clusters:

$$X_i = \begin{cases} 1 & \text{if site } i \text{ is selected for a conservation} \\ 0 & \text{otherwise.} \end{cases}$$

The mathematical model can be written as follows:

minimize
$$f(x) = \sum_{j=1}^{M} \sum_{j=1}^{M} d_{jk} x_j x_k$$
(1)

subject to

$$\sum_{j=1}^{M} p_{ij} x_j \ge t_i \sum_{j=1}^{M} p_{ij} \text{ for } i = 1, \dots, N$$
(2)

if
$$j \in D_b$$
 then $\sum_{i=1}^{N} p_{ij} x_j \ge \alpha N$ (3)

$$\sum_{j=1}^{M} c_j x_j \le B \tag{4}$$

$$x_j \in \{0, 1\}$$
 for $j = 1, \dots, M$ (5)

In this system x_j is the control variable which takes the value 1 if site j is included in the reserve system or the value 0 if site j is not included in the reserve system. Further, c_j is the cost to protect site j and d_{jk} is the euclidean distance between the centers of sites j and k. The information about the probability of a species being found at a site j is contained in a probability matrix, P, whose elements p_{ij} are the probabilities of finding species i in the site j. The α is the minimum target species fraction in boundary sites where $\alpha \in [0, 1]$. The summation in the objective function calculates the total of Euclidean distances between sites j and k (10). Constraint (2) is the species representation requirement which states that each conservation species will be represented at t_i % of their total distribution or abundance. The set D_b denotes the boundary sites of the reserve system. Constraint (4) guarantees that the total cost of selected sites cannot exceed the conservation budget B.

2.1 Boundary Sites

For each selected boundary site we must to ensure that it is a species rich site. The information about the probability of a species being found at a site j is contained in a probability matrix, P, whose elements p_{ij} are the probability of finding species i in the site j. The summation $\sum_{i \in N} p_{ij} x_j$ calculates the total probability of finding species in the boundary sites. We decide to include a boundary site in the reserve system if it is a species-rich site. We determine if a site is species-rich by comparing it to the term αN which calculates the minimum percentage of the total number of species per boundary site according to $\alpha \in [0, 1]$. If $x_j = 1$ for some $j \in D_b$, then $\sum_{i \in N} p_{ij} x_j \ge \alpha N$. We analyze the if-then conditions as follows:

We obtain the two conditions either $x_j = 1$ and $\sum_{i \in N} p_{ij} x_j \ge \alpha N$ or $x_j = 0$. We introduce a new auxiliary variable y_j such that $y_j \in \{0, 1\}$ for all $j \in D_b$.

$$x_{j} \leq Q(1 - y_{j})$$
$$-\sum_{i \in N} p_{ij} x_{j} + \alpha N \leq Q y_{j}$$
$$y_{j} \in \{0, 1\} \text{ for all } j \in D_{b}$$
(6)

Here Q is a large, arbitrary positive number. According to $x_j \leq Q(1-y_j)$ if $x_j = 1$ then, y_j must be zero; otherwise we obtain $1 \leq 0$ which is a contradiction. In this case where $y_j = 0$ we have $-\sum_{i \in N} p_{ij}x_j + \alpha N \leq 0$ or $\sum_{i \in N} p_{ij}x_j \geq \alpha N$. This confirms that we select a boundary site if it has species richness greater than or equal to αN . If $x_j = 0$ then $y_j = 1$ and it satisfies $-\sum_{i \in N} p_{ij}x_j + \alpha N \leq Qy_j$ since Q is a large, arbitrary positive number (11).

Further, inequalities in (6) can be rewritten as

$$x_{j} + Qy_{j} \leq Q$$

$$-\sum_{i \in N} p_{ij}x_{j} - Qy_{j} \leq -\alpha N$$

$$y_{j} \in \{0, 1\} \text{ for all } j \in D_{b}$$

$$(7)$$

Thus, the set of constraints given by (7) guarantees that if a boundary reserve site is selected for conservation then it contains at least $\alpha * 100\%$ of the total number of species. This mathematical model will be computationally expensive to solve as the size of the problem is reasonably large and thus solution by exact methods (e.g. branch and bound) can be troublesome. The complete mathematical model for our study can be written as follows:

minimize
$$f(x) = \sum_{j=1}^{M} \sum_{j=1}^{M} d_{jk} x_j x_k$$
(8)

subject to

$$\sum_{j=1}^{M} p_{ij} x_j \ge t_i \sum_{j=1}^{M} p_{ij} \text{ for } i = 1, \dots, N$$
(9)

$$x_j + Qy_j \le Q \tag{10}$$

$$-\sum_{i\in N} p_{ij}x_j - Qy_j \le -\alpha N \tag{11}$$

$$\sum_{j=1}^{M} c_j x_j \le B \tag{12}$$

$$x_j \in \{0, 1\}$$
 for $j = 1, \dots, M$, and $y_j \in \{0, 1\}$ for $j \in D_b$ (13)

In this study, we will vary the minimum target representation fraction, α , in (11) then analyze the effects on optimal boundary configuration. It is still a topic of debate among conservation biologists as to what level α is required for species to flourish (11; 12). Current estimates indicate this level is within the range 30-75 percent (11). We will vary this level and interpret the results.

3 Computational results

This section represents the computational results we obtained from the proposed mathematical model. In Section Section 3.1 we consider a small hypothetically generated test problems with 15 sites (Test Problem 1) and, in Section 3.2 we consider a large hypothetically generated test problem with 120 sites (Test Problem 2). We vary α value and analyze the trade-offs between the optimal cost and the boundary sites. We used The proposed mathematical model were implemented in MATLAB, version R2019a MathWorks (2019), using the GA routine. This routine finds a constrained minimum of a several variables function starting at an initial set of feasible solutions.

3.1 Test Problem 1

| | | S1 | | | | | <mark>S2</mark> | | | | | S3 | | |
|-------|-------|-------|-------|-------|-------|-------|-----------------|-------|-------|-------|-------|-------|-------|-------|
| 0.043 | 0.392 | 0.943 | 0.853 | 0.406 | 0.504 | 0.941 | 0.474 | 0.8 | 0.564 | 0.259 | 0.512 | 0.153 | 0.841 | 0.672 |
| 0.621 | 0.169 | 0.383 | 0.699 | 0.833 | 0.88 | 0.251 | 0.251 | 0.457 | 0.353 | 0.979 | 0.304 | 0.145 | 0.428 | 0.331 |
| 0.618 | 0.486 | 0.237 | 0.285 | 0.921 | 0.399 | 0.419 | 0.201 | 0.826 | 0.04 | 0.965 | 0.977 | 0.854 | 0.56 | 0.553 |

Figure 8: Probability Matrices for S_1 , S_2 , S_3

A species is said to be covered if the species is present in at least one site selected for the reserve system. It is assumed that the presence or absence of a species in a site is known with certainty. We illustrate the mathematical model using MATLAB generated 3×5 probability matrices to gain an understanding of the model. We assume that there are N = 3 types of species, S_1, S_2, S_3 , in the system. The matrices containing the probability of availability for each species S_1, S_2, S_3 is given in Figure 7. For this analysis we will fix $\beta = t_i = 0.2$ and vary α at levels $\alpha_1 = 0.7, \alpha_2 = 0.8$ and $\alpha = 0.9$. Three iterations of the mathematical model must be performed, one for each level of α . Once applied the model will output an initial solution indicating which sites from species matrices S_1, S_2, S_3 should be selected; these are highlighted yellow. Total species richness is computed by simple matrix addition of S_1, S_2, S_3 . Next, the corresponding cells chosen from the initial solution will be projected onto the total richness matrix; we highlight these selected cells in the richness matrix either light green or dark green. In the richness matrix cells highlighted light green indicate a boundary site that is selected for protection whereas cells highlighted dark green indicate a boundary site that will not be selected for protection. A boundary site is deemed suitable for protection if it corresponds to a cell from the initial solution and has a value in the richness matrix greater than or equal to $\alpha \times N$, where N is the number of species. In order to obtain a feasible solution at least one boundary site must be selected for protection.

| | | S1 | | | | | <mark>S</mark> 2 | | | | | S3 | | |
|-------|-------|-------|-------|-------|-------|-------|------------------|-------|-------|-------|-------|-------|-------|-------|
| 0.043 | 0.392 | 0.943 | 0.853 | 0.406 | 0.504 | 0.941 | 0.474 | 0.8 | 0.564 | 0.259 | 0.512 | 0.153 | 0.841 | 0.672 |
| 0.621 | 0.169 | 0.383 | 0.699 | 0.833 | 0.88 | 0.251 | 0.251 | 0.457 | 0.353 | 0.979 | 0.304 | 0.145 | 0.428 | 0.331 |
| 0.618 | 0.486 | 0.237 | 0.285 | 0.921 | 0.399 | 0.419 | 0.201 | 0.826 | 0.04 | 0.965 | 0.977 | 0.854 | 0.56 | 0.553 |

Figure 9: S_1 vs S_2 vs S_3 ; $\alpha_1 = 0.7$, $\beta = 0.2$

| 0.806 | 1.845 | 1.57 | 2.493 | 1.643 | 0.806 | 1.845 | 1.57 | 2.493 | 1.643 |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| 2.48 | 0.725 | 0.779 | 1.584 | 1.517 | 2.48 | 0.725 | 0.779 | 1.584 | 1.517 |
| 1.982 | 1.882 | 1.291 | 1.67 | 1.514 | 1.982 | 1.882 | 1.291 | 1.67 | 1.514 |

Figure 10: Richness and Solution $\alpha_1 = 0.7$, $\beta = 0.2$

We start the analysis by varying α in ascending order beginning with $\alpha_1 = 0.7$ as in above. $\beta = 0.2$ is fixed. The mathematical model is applied using the software MATLAB. The resulting initial solution output from MATLAB indicates 3 candidates, j = 4, 6, 8, for boundary sites. The corresponding values in the richness matrix are as follows: $\sum_{i \in N} p_{i4}x_4 = 2.493$, $\sum_{i \in N} p_{i6}x_6 = 2.4800$, and $\sum_{i \in N} p_{i8}x_8$ = 0.779. For a cell to be selected for boundary site protection it must satisfy (11). Therefore with N = 3 species at level $\alpha_1 = 0.7$ a site will be selected as a boundary site if $\sum_{i \in N} p_{ij}x_j \ge 2.1$. Thus since for j = 4, $6 \sum_{i \in N} p_{ij}x_j \ge 2.1$, these sites will be selected as protected boundary sites. Note that while j=8 was a potential boundary site, its richness value 0.779 is less than the required 2.1 so it will not be selected as a boundary site. We conclude that at level $\alpha_1 = 0.7$ we have a feasible solution with two boundary sites selected for protection.

| | | S1 | | | | | <mark>\$2</mark> | | | | | S3 | | |
|-------|-------|-------|-------|-------|-------|-------|------------------|-------|-------|-------|-------|-------|-------|-------|
| 0.043 | 0.392 | 0.943 | 0.853 | 0.406 | 0.504 | 0.941 | 0.474 | 0.8 | 0.564 | 0.259 | 0.512 | 0.153 | 0.841 | 0.672 |
| 0.621 | 0.169 | 0.383 | 0.699 | 0.833 | 0.88 | 0.251 | 0.251 | 0.457 | 0.353 | 0.979 | 0.304 | 0.145 | 0.428 | 0.331 |
| 0.618 | 0.486 | 0.237 | 0.285 | 0.921 | 0.399 | 0.419 | 0.201 | 0.826 | 0.04 | 0.965 | 0.977 | 0.854 | 0.56 | 0.553 |

Figure 11: S_1 vs S_2 vs S_3 ; $\alpha_2 = 0.8$, $\beta = 0.2$

| 0.806 | 0.1845 | 1.57 | 2.493 | 1.643 | 0.806 | 0.1845 | 1.57 | 2.493 | 1.64 |
|-------|--------|-------|-------|-------|-------|--------|-------|-------|------|
| 2.48 | 0.725 | 0.779 | 1.584 | 1.517 | 2.48 | 0.725 | 0.779 | 1.584 | 1.51 |
| 1.982 | 1.882 | 1.291 | 1.67 | 1.514 | 1.982 | 1.882 | 1.291 | 1.67 | 1.51 |

Figure 12: Richness and Solution $\alpha_2 = 0.8$, $\beta = 0.2$

We conduct our second analysis by increasing α to $\alpha_2 = 0.8$. $\beta = 0.2$ remains fixed as before. The resulting initial solution output from MATLAB indicates 4 candidates, j = 4, 7, 8, 9, for boundary sites. The corresponding values in the richness matrix are as follows: $x_4 = 2.493, x_7 = 0.725, x_8 = 0.779$, and $x_9 = 1.584$. Once again for a cell to be chosen as a boundary site it must satisfy $\sum_{i \in N} p_{ij}x_j \ge \alpha \times N$ where N = 3; now $\alpha_2 = 0.8$ so instead of 2.1 in the previous example, $\alpha_2 \times N = 2.4$. Therefore because $x_4 \ge 2.4$ is the only site which satisfies the necessary condition there will be only a single boundary site chosen. Similarly to the previous iteration x_7, x_8, x_9 are not chosen as boundary sites because all fail to meet the condition $\sum_{i \in N} p_{ij}x_j \ge \alpha \times N$. We conclude that at a level $\alpha_2 = 0.8$ we have a feasible solution with only one boundary site selected for protection. Note that as our α increased the number of boundary sites selected for protection has decreased.

| | | S1 | | | | | <mark>S</mark> 2 | | | | | <mark>S</mark> 3 | | |
|-------|-------|-----------|-------|-------|-------|-------|------------------|-------|-------|-------|-------|------------------|-------|-------|
| 0.043 | 0.392 | 0.943 | 0.853 | 0.406 | 0.504 | 0.941 | 0.474 | 0.8 | 0.564 | 0.259 | 0.512 | 0.153 | 0.841 | 0.672 |
| 0.621 | 0.169 | 0.383 | 0.699 | 0.833 | 0.88 | 0.251 | 0.251 | 0.457 | 0.353 | 0.979 | 0.304 | 0.145 | 0.428 | 0.331 |
| 0.618 | 0.486 | 0.237 | 0.285 | 0.921 | 0.399 | 0.419 | 0.201 | 0.826 | 0.04 | 0.965 | 0.977 | 0.854 | 0.56 | 0.553 |

Figure 13: S_1 vs S_2 vs $S_3 \alpha_3 = 0.9$; $\beta = 0.2$

| 0.806 | 1.845 | 1.57 | 2.493 | 1.643 | 0.806 | 1.845 | 1.57 | 2.493 | 1.643 |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| 2.48 | 0.725 | 0.779 | 1.584 | 1.517 | 2.48 | 0.725 | 0.779 | 1.584 | 1.517 |
| 1.982 | 1.882 | 1.291 | 1.67 | 1.514 | 1.982 | 1.882 | 1.291 | 1.67 | 1.514 |

Figure 14: Richness and Solution $\alpha_3 = 0.9$, $\beta = 0.2$

The final case analyzed is that of $\alpha_3 = 0.9$. Once again $\beta = 0.2$ is the same. As done previously MATLAB is used to apply the mathematical model. At this new α level MATLAB finds 3 potential candidates for boundary sites x_7, x_8, x_9 . The corresponding values in the richness tables are as follows $:x_7 = 0.725, x_8 = 0.779$, and $x_9 = 1.584$. Due to an increased α each potential cell must satisfy $\sum_{i \in N} p_{ij} x_j \geq 2.7$ to be selected as a boundary site. Notice how all potential boundary sites are less than 2.7 and therefore none are suitable for boundary site selection. Thus since no boundary site can be selected, we conclude at level $\alpha_3 = 0.9$ there is no feasible solution to our program.

Analyzing the results of just three iterations reveals that increasing the value of α seems to lead to fewer boundary sites selected. Here each time we increased α by 0.1, one less boundary site was selected. Thus as the minimum target species fraction α increases, the proportion of boundary sites selected to total sites selected decreases. With a heightened understanding of the mathematical model, we may now examine cases with more species and larger probability matrices.

3.2 Test Problem 2

With a thorough understanding of the model, we can extend the model to a larger, more realistic example. The computational time grows exponentially with the number of variables; due to this, we will consider a reserve system size 10×12 . That is the system contains 120 sites. We examine the case of N = 4 species, S_1 , S_2 , S_3 , S_4 , each having its own unique 10×12 species probability matrix. We fix $\beta = 0.05$. Notice β has decreased from the previous example since we have introduced an additional species and increased the sizes of the species probability matrices; that is to say as the number of species and size of species probability matrices increase, the choice of β must decrease to obtain a feasible solution. Values larger than $\beta = 0.05$ never return a feasible solution for this example.

Using the programming software MATLAB we conduct 50 iterations of the mathematical model at each step size of α . To comply with current estimates by conversational biologists we choose $\alpha \in [0.33, 0.75]$ with step size 0.07; the set $\alpha \in \{0.33, 0.40, 0.47, 0.54, 0.61, 0.67, 0.75\}$.

For 50 iterations each level α we compute:

- 1. average objective function value
- 2. average total number of sites given by the initial solution
- 3. average total number of boundary sites
- 4. ratio of the average total number of sites given by the initial solution to the average total number of boundary sites
- 5. frequency of obtaining a feasible solution

Item (4) is used to check the level of efficiency of selecting boundary sites for each α . Item (5) quantifies how many times out of 50 iterations at each α the mathematical model obtains a feasible solution. Recall a feasible solution is obtained if at least one boundary site is selected for conservation[6]. Below Table 1, Table 2, Table 3 and Table 4 represent the individual species presence probability matrices for S_1 , S_2 , S_3 and S_4 respectively.

| 0.4192 | 0.8007 | 0.0983 | 0.9889 | 0.0194 | 0.1023 | 0.9034 | 0.8833 | 0.1147 | 0.3266 | 0.1723 |
|--------|--|---|---|---|---|---|---|---|--|--|
| 0.6852 | 0.9683 | 0.4211 | 0.7482 | 0.6788 | 0.4141 | 0.1375 | 0.6237 | 0.9495 | 0.5271 | 0.1371 |
| 0.2045 | 0.3134 | 0.9579 | 0.2804 | 0.2116 | 0.6944 | 0.1393 | 0.7509 | 0.4499 | 0.8859 | 0.9326 |
| 0.8781 | 0.6923 | 0.5332 | 0.7893 | 0.2655 | 0.4142 | 0.8074 | 0.3489 | 0.5784 | 0.3573 | 0.6968 |
| 0.0274 | 0.8764 | 0.6919 | 0.1032 | 0.4916 | 0.0500 | 0.3977 | 0.2699 | 0.4081 | 0.9085 | 0.0660 |
| 0.6705 | 0.8946 | 0.3155 | 0.4479 | 0.0534 | 0.5359 | 0.1654 | 0.8959 | 0.2370 | 0.6234 | 0.7555 |
| 0.4173 | 0.0850 | 0.6865 | 0.9086 | 0.5741 | 0.6638 | 0.9275 | 0.4281 | 0.9034 | 0.0158 | 0.7539 |
| 0.5587 | 0.0391 | 0.8346 | 0.2936 | 0.1467 | 0.5149 | 0.3478 | 0.9648 | 0.5737 | 0.9294 | 0.9230 |
| 0.1404 | 0.1698 | 0.0183 | 0.2878 | 0.5893 | 0.9446 | 0.7508 | 0.6634 | 0.0029 | 0.6909 | 0.7115 |
| 0.1981 | 0.8781 | 0.7501 | 0.1300 | 0.6998 | 0.5866 | 0.7260 | 0.6217 | 0.6171 | 0.9973 | 0.1243 |
| | 0.4192 0.6852 0.2045 0.8781 0.0274 0.6705 0.4173 0.5587 0.1404 0.1981 | 0.4192 0.8007 0.6852 0.9683 0.2045 0.3134 0.8781 0.6923 0.0274 0.8764 0.6705 0.8946 0.4173 0.0850 0.5587 0.0391 0.1404 0.1698 0.1981 0.8781 | 0.4192 0.8007 0.0983 0.6852 0.9683 0.4211 0.2045 0.3134 0.9579 0.8781 0.6923 0.5332 0.0274 0.8764 0.6919 0.6705 0.8946 0.3155 0.4173 0.0850 0.6865 0.5587 0.0391 0.8346 0.1404 0.1698 0.0183 0.1981 0.8781 0.7501 | 0.4192 0.8007 0.0983 0.9889 0.6852 0.9683 0.4211 0.7482 0.2045 0.3134 0.9579 0.2804 0.8781 0.6923 0.5332 0.7893 0.0274 0.8764 0.6919 0.1032 0.6705 0.8946 0.3155 0.4479 0.4173 0.0850 0.6865 0.9086 0.5587 0.0391 0.8346 0.2936 0.1404 0.1698 0.0183 0.2878 0.1981 0.8781 0.7501 0.1300 | 0.4192 0.8007 0.0983 0.9889 0.0194 0.6852 0.9683 0.4211 0.7482 0.6788 0.2045 0.3134 0.9579 0.2804 0.2116 0.8781 0.6923 0.5332 0.7893 0.2655 0.0274 0.8764 0.6919 0.1032 0.4916 0.6705 0.8946 0.3155 0.4479 0.0534 0.4173 0.0850 0.6865 0.9086 0.5741 0.5587 0.0391 0.8346 0.2936 0.1467 0.1404 0.1698 0.0183 0.2878 0.5893 0.1981 0.8781 0.7501 0.1300 0.6998 | 0.4192 0.8007 0.0983 0.9889 0.0194 0.1023 0.6852 0.9683 0.4211 0.7482 0.6788 0.4141 0.2045 0.3134 0.9579 0.2804 0.2116 0.6944 0.8781 0.6923 0.5332 0.7893 0.2655 0.4142 0.0274 0.8764 0.6919 0.1032 0.4916 0.0500 0.6705 0.8946 0.3155 0.4479 0.0534 0.5359 0.4173 0.0850 0.6865 0.9086 0.5741 0.6638 0.5587 0.0391 0.8346 0.2936 0.1467 0.5149 0.1404 0.1698 0.0183 0.2878 0.5893 0.9446 0.1981 0.8781 0.7501 0.1300 0.6998 0.5866 | 0.4192 0.8007 0.0983 0.9889 0.0194 0.1023 0.9034 0.6852 0.9683 0.4211 0.7482 0.6788 0.4141 0.1375 0.2045 0.3134 0.9579 0.2804 0.2116 0.6944 0.1393 0.8781 0.6923 0.5332 0.7893 0.2655 0.4142 0.8074 0.0274 0.8764 0.6919 0.1032 0.4916 0.0500 0.3977 0.6705 0.8946 0.3155 0.4479 0.0534 0.5359 0.1654 0.4173 0.0850 0.6865 0.9086 0.5741 0.6638 0.9275 0.5587 0.0391 0.8346 0.2936 0.1467 0.5149 0.3478 0.1404 0.1698 0.0183 0.2878 0.5893 0.9446 0.7508 0.1981 0.8781 0.7501 0.1300 0.6998 0.5866 0.7260 | 0.4192 0.8007 0.0983 0.9889 0.0194 0.1023 0.9034 0.8833 0.6852 0.9683 0.4211 0.7482 0.6788 0.4141 0.1375 0.6237 0.2045 0.3134 0.9579 0.2804 0.2116 0.6944 0.1393 0.7509 0.8781 0.6923 0.5332 0.7893 0.2655 0.4142 0.8074 0.3489 0.0274 0.8764 0.6919 0.1032 0.4916 0.0500 0.3977 0.2699 0.6705 0.8946 0.3155 0.4479 0.0534 0.5359 0.1654 0.8959 0.4173 0.0850 0.6865 0.9086 0.5741 0.6638 0.9275 0.4281 0.5587 0.0391 0.8346 0.2936 0.1467 0.5149 0.3478 0.9648 0.1404 0.1698 0.0183 0.2878 0.5893 0.9446 0.7508 0.66341 0.1981 0.8781 0.7501 0.1300 0.6998 0.5 | 0.4192 0.8007 0.0983 0.9889 0.0194 0.1023 0.9034 0.8833 0.1147 0.6852 0.9683 0.4211 0.7482 0.6788 0.4141 0.1375 0.6237 0.9495 0.2045 0.3134 0.9579 0.2804 0.2116 0.6944 0.1393 0.7509 0.4499 0.8781 0.6923 0.5332 0.7893 0.2655 0.4142 0.8074 0.3489 0.5784 0.0274 0.8764 0.6919 0.1032 0.4916 0.0500 0.3977 0.2699 0.4081 0.6705 0.8946 0.3155 0.4479 0.0534 0.5359 0.1654 0.8959 0.2370 0.4173 0.0850 0.6865 0.9086 0.5741 0.6638 0.9275 0.4281 0.9034 0.5587 0.0391 0.8346 0.2936 0.1467 0.5149 0.3478 0.9648 0.5737 0.1404 0.1698 0.0183 0.2878 0.5893 0.9446 <td< th=""><th>0.4192 0.8007 0.0983 0.9889 0.0194 0.1023 0.9034 0.8833 0.1147 0.3266 0.6852 0.9683 0.4211 0.7482 0.6788 0.4141 0.1375 0.6237 0.9495 0.5271 0.2045 0.3134 0.9579 0.2804 0.2116 0.6944 0.1393 0.7509 0.4499 0.8859 0.8781 0.6923 0.5332 0.7893 0.2655 0.4142 0.8074 0.3489 0.5784 0.3573 0.0274 0.8764 0.6919 0.1032 0.4916 0.0500 0.3977 0.2699 0.4081 0.9085 0.6705 0.8946 0.3155 0.4479 0.0534 0.5359 0.1654 0.8959 0.2370 0.6234 0.4173 0.0850 0.6865 0.9086 0.5741 0.6638 0.9275 0.4281 0.9034 0.0158 0.5587 0.0391 0.8346 0.2936 0.1467 0.5149 0.3478 0.9648 0.5737</th></td<> | 0.4192 0.8007 0.0983 0.9889 0.0194 0.1023 0.9034 0.8833 0.1147 0.3266 0.6852 0.9683 0.4211 0.7482 0.6788 0.4141 0.1375 0.6237 0.9495 0.5271 0.2045 0.3134 0.9579 0.2804 0.2116 0.6944 0.1393 0.7509 0.4499 0.8859 0.8781 0.6923 0.5332 0.7893 0.2655 0.4142 0.8074 0.3489 0.5784 0.3573 0.0274 0.8764 0.6919 0.1032 0.4916 0.0500 0.3977 0.2699 0.4081 0.9085 0.6705 0.8946 0.3155 0.4479 0.0534 0.5359 0.1654 0.8959 0.2370 0.6234 0.4173 0.0850 0.6865 0.9086 0.5741 0.6638 0.9275 0.4281 0.9034 0.0158 0.5587 0.0391 0.8346 0.2936 0.1467 0.5149 0.3478 0.9648 0.5737 |

Table 1: S_1 Presence Probability Matrix 10×12

| 0.4360 | 0.6211 | 0.5052 | 0.4678 | 0.9646 | 0.5442 | 0.8003 | 0.5040 | 0.5827 | 0.3133 | 0.7780 | 0.2638 |
|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| 0.0259 | 0.5291 | 0.0653 | 0.2017 | 0.5000 | 0.0821 | 0.6018 | 0.3235 | 0.0256 | 0.0418 | 0.1340 | 0.9139 |
| 0.5497 | 0.1346 | 0.4281 | 0.6404 | 0.8895 | 0.3663 | 0.7650 | 0.2597 | 0.6622 | 0.7384 | 0.8689 | 0.4197 |
| 0.4353 | 0.5136 | 0.0965 | 0.4831 | 0.3416 | 0.8509 | 0.1692 | 0.3869 | 0.3875 | 0.6575 | 0.7488 | 0.5402 |
| 0.4204 | 0.1844 | 0.1272 | 0.5052 | 0.5671 | 0.4063 | 0.2930 | 0.8320 | 0.4971 | 0.2146 | 0.7986 | 0.6084 |
| 0.3303 | 0.7853 | 0.5967 | 0.3869 | 0.4275 | 0.0272 | 0.5241 | 0.7367 | 0.4149 | 0.4168 | 0.5433 | 0.8262 |
| 0.2046 | 0.8540 | 0.2260 | 0.7936 | 0.4367 | 0.2472 | 0.3566 | 0.3792 | 0.3509 | 0.6438 | 0.2208 | 0.6236 |
| 0.6193 | 0.4942 | 0.1069 | 0.5800 | 0.7766 | 0.0671 | 0.0457 | 0.0130 | 0.5510 | 0.6615 | 0.9185 | 0.1767 |
| 0.2997 | 0.8466 | 0.2203 | 0.1623 | 0.5356 | 0.9939 | 0.9832 | 0.7974 | 0.9729 | 0.1705 | 0.5921 | 0.5913 |
| 0.2668 | 0.0796 | 0.3498 | 0.7008 | 0.9537 | 0.9706 | 0.4414 | 0.2694 | 0.1128 | 0.8817 | 0.3462 | 0.4893 |

Table 2: S_2 Presence Probability Matrix 10×12

| 0.5508 | 0.0299 | 0.2835 | 0.9760 | 0.4065 | 0.2054 | 0.3736 | 0.6915 | 0.1293 | 0.7263 | 0.1921 | 0.4851 |
|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| 0.7081 | 0.4568 | 0.6931 | 0.6724 | 0.4689 | 0.2014 | 0.6681 | 0.6505 | 0.5533 | 0.4802 | 0.7257 | 0.4553 |
| 0.2909 | 0.6491 | 0.4405 | 0.9028 | 0.2692 | 0.5140 | 0.3398 | 0.7239 | 0.1878 | 0.8421 | 0.7849 | 0.2180 |
| 0.5108 | 0.2785 | 0.1569 | 0.8458 | 0.2918 | 0.0872 | 0.5728 | 0.4751 | 0.9521 | 0.7448 | 0.9721 | 0.1772 |
| 0.8929 | 0.6763 | 0.5446 | 0.3780 | 0.4577 | 0.4836 | 0.3258 | 0.5967 | 0.6816 | 0.6603 | 0.8510 | 0.0736 |
| 0.8963 | 0.5909 | 0.7803 | 0.0922 | 0.8605 | 0.3622 | 0.4451 | 0.0670 | 0.5410 | 0.9140 | 0.5436 | 0.8924 |
| 0.1256 | 0.0240 | 0.3064 | 0.6534 | 0.5863 | 0.7077 | 0.0615 | 0.0726 | 0.7072 | 0.6337 | 0.0898 | 0.6402 |
| 0.2072 | 0.5589 | 0.2220 | 0.5578 | 0.2835 | 0.7467 | 0.2427 | 0.1990 | 0.2639 | 0.3659 | 0.4889 | 0.1433 |
| 0.0515 | 0.2593 | 0.3880 | 0.3616 | 0.2780 | 0.6911 | 0.9716 | 0.1519 | 0.9267 | 0.5528 | 0.9279 | 0.4141 |
| 0.4408 | 0.4151 | 0.9364 | 0.2251 | 0.4546 | 0.6892 | 0.2306 | 0.1001 | 0.8392 | 0.1964 | 0.7876 | 0.0491 |

Table 3: S_3 Presence Probability Matrix 10×12

| 0.9670 | 0.7794 | 0.4361 | 0.5279 | 0.3969 | 0.8955 | 0.9047 | 0.7326 | 0.0485 | 0.6669 | 0.2609 | 0.3475 |
|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| 0.5472 | 0.1977 | 0.9490 | 0.9376 | 0.6239 | 0.3629 | 0.4048 | 0.8947 | 0.1098 | 0.1487 | 0.4125 | 0.0589 |
| 0.9727 | 0.8630 | 0.7863 | 0.5217 | 0.7674 | 0.6376 | 0.3312 | 0.5147 | 0.6840 | 0.3646 | 0.4190 | 0.6118 |
| 0.7148 | 0.9834 | 0.8663 | 0.1082 | 0.1790 | 0.1914 | 0.5721 | 0.6036 | 0.5147 | 0.8658 | 0.9024 | 0.1240 |
| 0.6977 | 0.1638 | 0.1732 | 0.1582 | 0.3756 | 0.4978 | 0.8454 | 0.0651 | 0.5716 | 0.3503 | 0.9796 | 0.7595 |
| 0.2161 | 0.5973 | 0.0749 | 0.5452 | 0.5025 | 0.1824 | 0.8610 | 0.5401 | 0.8437 | 0.1890 | 0.6236 | 0.7944 |
| 0.9763 | 0.0090 | 0.6007 | 0.5244 | 0.6867 | 0.9184 | 0.5957 | 0.1292 | 0.4877 | 0.4726 | 0.0832 | 0.4086 |
| 0.0062 | 0.3866 | 0.1680 | 0.6376 | 0.2537 | 0.4318 | 0.0847 | 0.6146 | 0.8101 | 0.3928 | 0.7330 | 0.9438 |
| 0.2530 | 0.0442 | 0.7334 | 0.4015 | 0.5547 | 0.8302 | 0.5973 | 0.3637 | 0.5102 | 0.6189 | 0.6787 | 0.1738 |
| 0.4348 | 0.9567 | 0.4084 | 0.6498 | 0.6249 | 0.4168 | 0.2455 | 0.7678 | 0.9267 | 0.4368 | 0.8260 | 0.9426 |

Table 4: S_4 Presence Probability Matrix 10×12

The calculation of total species richness in each site is identically to the previous example is Section 5. For thoroughness, total species richness in site j = 1 is calculated by summing the site j = 1 entries from the individual species probability matrices S_1 , S_2 , S_3 and S_4 :

$$p_{11} + p_{21} + p_{31} + p_{41} = 0.4170 + 0.4360 + 0.5508 + 0.9670 = 2.3708$$

Each entry of the total species richness matrix is calculated similarly. Table 5 displays the total species richness matrix of S_1 , S_2 , S_3 and S_4 .

| 2.3708 | 1.8496 | 2.0255 | 2.0700 | 2.7569 | 1.6645 | 2.1809 | 2.8315 | 1.6438 | 1.8212 | 1.5576 | 1.2687 |
|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| 2.0015 | 1.8688 | 2.6757 | 2.2328 | 2.3410 | 1.3252 | 2.0888 | 2.0062 | 1.3124 | 1.6202 | 1.7993 | 1.5652 |
| 1.8134 | 1.8512 | 1.9683 | 3.0228 | 2.2065 | 1.7295 | 2.1304 | 1.6376 | 2.2849 | 2.3950 | 2.9587 | 2.1821 |
| 1.9632 | 2.6536 | 1.8120 | 1.9703 | 1.6017 | 1.3950 | 1.7283 | 2.2730 | 2.2032 | 2.8465 | 2.9806 | 1.5382 |
| 2.1578 | 1.0519 | 1.7214 | 1.7333 | 1.5036 | 1.8793 | 1.5142 | 1.8915 | 2.0202 | 1.6333 | 3.5377 | 1.5075 |
| 1.5350 | 2.6440 | 2.3465 | 1.3398 | 2.2384 | 0.6252 | 2.3661 | 1.5092 | 2.6955 | 1.7568 | 2.3339 | 3.2685 |
| 1.4928 | 1.3043 | 1.2181 | 2.6579 | 2.6183 | 2.4474 | 1.6776 | 1.5085 | 1.9739 | 2.6535 | 0.4096 | 2.4263 |
| 1.1783 | 1.9984 | 0.5360 | 2.6100 | 1.6074 | 1.3923 | 0.8880 | 1.1744 | 2.5898 | 1.9939 | 3.0698 | 2.1868 |
| 1.0010 | 1.2905 | 1.5115 | 0.9437 | 1.6561 | 3.1045 | 3.4967 | 2.0638 | 3.0732 | 1.3451 | 2.8896 | 1.8907 |
| 1.6812 | 1.6495 | 2.5727 | 2.3258 | 2.1632 | 2.7764 | 1.5041 | 1.8633 | 2.5004 | 2.1320 | 2.9571 | 1.6053 |

Table 5: Total Species Richness $S_1,\,S_2,\,S_3,\,S_4$

With the total species richness matrix, we apply the fully developed mathematical model 50 times for each level α . The results are tabulated below in Table 6.

| α | Average $f(x)$ | Average Sites Selected | Average Boundary Sites Selected | Ratio | Feasibility Frequency |
|------|----------------|------------------------|---------------------------------|---------|-----------------------|
| 0.33 | 194.43 | 6.2 | 5.6 | 0.90322 | 50 |
| 0.40 | 205.28 | 6.4 | 4.8 | 0.75 | 50 |
| 0.47 | 188.076 | 7.8 | 4.8 | 0.61538 | 50 |
| 0.54 | 176.45 | 6.8 | 3.7 | 0.41176 | 50 |
| 0.61 | 258.51 | 7.6 | 3 | 0.39474 | 48 |
| 0.68 | 254.64 | 7.2 | 1.8 | 0.25 | 37 |
| 0.75 | 274.8 | 7.8 | 0.2 | 0.02564 | 2 |

Table 6: Mathematical Model Results: 50 Iterations

Now tabulated we can conduct analysis by comparing the results at each level α . Immediately recognize that as α increases the average number of boundary sites selected decreases. Thus, for any data set, increasing the minimum species target fraction for boundary sites lowers the probability of obtaining a feasible solution. This is expected due to $\alpha \times N$ increasing while the entries of the total species richness matrix remain the same. When the number of species N are added lower levels of α are required to obtain an optimal solution. We do not always obtain a feasible solution for $\alpha \in \{0.61, 0.67, 0.75\}$. We prefer to choose an α that guarantees a feasible solution for this data set, so we will not consider these levels of α . Recall from Background that when planning a reserve having multiple boundary sites selected for conservation benefits species in a multitude of ways. Therefore we want the average number of boundary sites selected to be greater than 1; this is the case for all α we consider. The level of α that achieves this with the smallest average

boundary length f(x) value is $\alpha = 0.54$ and thus it is the optimal solution for our purpose. If a minimum amount of boundary sites are required for a reserve system one can decrease α at the expense of increasing boundary length. For example, if a reserve planner added the condition of at least 4 boundary sites that must be selected, then we would choose $\alpha = 0.47$ since it meets the minimum requirement for average boundary sites selected with the smallest average boundary length f(x). Notice that this new constraint would add 11.626 to the average boundary length. Lower values of α result in more efficient boundary site selection. Therefore more efficient boundary site selection comes at the expense of lowering α .

4 Conclusions And Extensions

This paper focused on the development of a mathematical model to minimize the total distance between all pairs of sites included in a reserve system with respect to a minimum target species fraction for each boundary site. The model is an extension of the Reserve Site Selection Problem (RSSP) which maximizes the number of distinct species given a predetermined amount of land or given a budget to be used for land acquisition. We examined how various minimum target species requirements affect this distance. The mathematical model was developed following generally accepted reserve design principles to promote viability for practical data purposes. We considered how species representation and design targets are achieved with the least amount of individual sites and minimal boundary length.

In practice, individual species probabilities for each site in a species probability

matrix should be duly researched and estimated. To ensure species survival of each species richness matrix should be carefully constructed. Individual species should be studied to understand at what minimum threshold they must be represented at to repopulate and survive as desired by the reserve planners. Those reserve planners should be cautious when attempting to protect large numbers of species in a single reserve since doing so would require smaller values of α to obtain a feasible solution. The level of α that produces a feasible solution, minimizes the total distance between sites included in the system, and coincide with the specific goal of a reserve design team is chosen. Preliminary findings suggest the mathematical model is successful and should be further studied with practical data.

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