

DISSERTATION

LANDSCAPE CONSERVATION DESIGN FROM THE PERSPECTIVE OF THE
OBLIGATE SPECIES: EXAMPLE FOR THE SAGEBRUSH STEPPE BIOME

Submitted by

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ABSTRACT

LANDSCAPE CONSERVATION DESIGN FROM THE PERSPECTIVE OF THE OBLIGATE SPECIES: EXAMPLE FOR THE SAGEBRUSH STEPPE BIOME

Conservation strategies in use today are not keeping up with the speed and scale of threats to the natural world. They are not effectively curbing the current wave of species extinctions. There is a critical need to conserve and manage whole landscapes, preserving their ecological integrity, to head off species imperilment. Habitat loss and fragmentation are significant causes of species imperilment, and both habitat amount and contiguity (inverse of fragmentation) must be addressed for effective conservation planning.

This study is focused on identifying the location, configuration, and contiguity of environmental and abiotic factors required to sustain the populations of species that are reliant on a particular landscape for some portion of their life histories. I used the sagebrush steppe biome in the western United States to demonstrate how this can be done. Several major issues have heretofore inhibited identifying habitats able to sustain the populations of a wide array of taxa: 1) insufficient data for many species; 2) bias issues with using publicly collected “big data”; 3) inadequate computing capacity for large-extent high-resolution habitat models, and; 4) no explicit way for habitat models to include species-specific habitat connectivity, important for population viability. Some of these issues can be addressed now because of the increasing availability of species location data, increased computational capacities, and better optimization algorithms, and some I propose ways to address. Surmounting these impediments allowed me to identify the fundamental habitats most likely to sustain populations of native species, and use these models as

inputs in a systematic conservation planning procedure to identify areas of the sagebrush steppe biome most likely to support the persistence of the obligate taxa using the least amount of land.

I compared this approach to using an umbrella species to protect habitats of sympatric species, assessing whether protecting habitats for sage-grouse species, greater sage-grouse (*Centrocercus urophasianus*) and Gunnison sage-grouse (*C. minimus*), would protect the other taxa reliant upon the sagebrush steppe landscape. I found that using sage-grouse habitat as an umbrella left many sympatric species with inadequate habitat protection. Determining whether sufficient habitat of sympatric species is protected requires knowing the habitat requirements of these taxa. If the habitat requirements of these taxa are determined, as done in this study, each species' required habitat can be included in a conservation plan, instead of relying on the assumption that conserving an umbrella species' habitat will provide sympatric species protection adequate to secure their persistence.

The approach developed here has additional advantages. Namely, as new information becomes available, the fundamental habitat models for species can be updated and included in the conservation plans. Also, the amount of species fundamental habitat required or supplemental goals (e.g., including core sagebrush, threats, or sage-grouse protection areas) can be easily added to the optimization routine to produce new optimal multi-species habitat configurations. This gives conservation planners the means to explore explicit effects and tradeoffs of pursuing different conservation objectives, while assuring the resulting plans can support the persistence of the obligate taxa of a biome.

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INTRODUCTION

Species are becoming imperiled at rates faster than we can evaluate their conditions, gather information about their needs, and devise conservation strategies (Ceballos et al. 2017, DeFries and Nagendra 2017, Ceballos and Ehrlich 2018, Díaz et al. 2019, Bryan and Archibald 2020, Ceballos et al. 2020). There is a critical need to conserve and manage whole biomes, preserving their ecological integrity, to head off species imperilment (Díaz et al. 2019, Kennedy et al. 2019, Leclère et al. 2020, Maheshwari and Bhatnagar 2021, Noss et al. 2021a). These extensive, complex conservation challenges require comprehensive, strategic conservation planning that match the scales and complexity of the threats (DeFries and Nagendra 2017, Pimm et al. 2018, Díaz et al. 2019, Woodley et al. 2019, Leclère et al. 2020).

There have been many whole-ecosystem, multi-species conservation approaches proposed to forestall species extirpations. The approach proffered here identifies the habitat requirements of individual species with the goal that all the obligate species in a landscape can persist. The intent of this approach is to identify the areas of a landscape, that if managed appropriately, would support viable populations of all obligate species using the least amount (or cost) of land, proactively keeping these species from becoming endangered. Habitat is delineated by the perception and behavioral responses of a species, so independent habitat models are required to ascertain the habitat needs of different species (Cushman et al. 2013). For a conservation approach to accomplish this, requires methods and the requisite data to develop spatially explicit landscape conservation plans that identify the type, amount, and configuration of habitat important for sustaining the populations of each species in a landscape (Moilanen et al. 2005, Reed et al. 2006, Early et al. 2008, Pimm et al. 2018).

Protected areas approaches

Existing protected areas (Venter et al. 2014, USGS Gap Analysis Program 2018) were not necessarily selected for and often fall short of preserving the taxa within their boundaries (Brooks et al. 2004, Craigie et al. 2010, Cantu-Salazar et al. 2013, Kendall et al. 2015, Venter et al. 2018, Mogg et al. 2019, El-Gabbas et al. 2020, Kshetry et al. 2020, Maheshwari and Bhatnagar 2021, Plumptre et al. 2021, Wauchope et al. 2022).

Some strategies propose conserving species richness “hotspots” (e.g., Myers et al. 2000) where multiple species are known to coexist. A problem with this approach is that if only hotspots are conserved, other habitats or ecosystems outside of hotspots are overlooked, leaving species found in “cold spots” potentially without protection, which could result in their extirpation (Araújo and Williams 2001, Kareiva and Marvier 2003, Orme et al. 2005, Ceballos and Ehrlich 2006, Fattorini et al. 2011).

To more comprehensively include species and ecosystems, some schemes propose a method of conserving protected areas that are representative of different habitat types to guide conservation toward an “ecologically representative” sample of biodiversity (e.g., Belote et al. 2017, Chauvenet et al. 2017). Some planners have proposed targeting conservation to areas with the fewest human impacts and most connectivity in order to maintain biodiversity and ecosystem function (e.g., Belote et al. 2017, Kennedy et al. 2019), or focus on protecting intact and functioning ecosystems (ecological “cores”) and then working to improve the management and restoration of more degraded surrounding landscapes (e.g., Meinke et al. 2009, Brown and Williams 2016, NRCS 2021, Plumptre et al. 2021, Doherty et al. 2022, Doherty et al. 2024). A similar approach proposes focusing on different “land facets” that provide abiotic and environmental conditions that could support different biotic communities (Brost and Beier 2012), intended to identify and protect representative samples of different ecological areas.

These approaches that focus on areas of species richness, ecosystem intactness, “integrity”, “quality”, uniqueness, or least human disturbance, may identify important areas to conserve, but they lack the means to determine the type, amount, location and configuration of required habitat for individual species’ persistence and therefore may allow extirpation of species (Noss 1996, Poiani et al. 2000, Carroll et al. 2004, Moilanen et al. 2005, Williams et al. 2005, Nicholson et al. 2006, Reed et al. 2006, MacNally 2007, Early et al. 2008).

Some planners have proposed combining coarse (e.g., landscape) and fine (e.g., endangered species) scale conservation approaches together to create comprehensive conservation plans (e.g., Poiani et al. 2000, Groves et al. 2002, Carroll et al. 2009, Noon et al. 2009, Noss et al. 2021a). In theory, these approaches would protect some of each unique ecosystem type (coarse-scale) and cover any missed habitats by using threatened species to identify habitats left out of landscape-scale planning, adding those to the planning. However, these approaches still do not have intrinsic methods to identify how much land should be protected and what configuration the protected areas need to be in to support the persistence of obligate species in these landscapes.

Species habitats instead of biodiverse areas

To ensure that species have a high likelihood of long-term persistence under conservation planning approaches, they should be based upon species’ habitat requirements instead of biodiversity proxies (Early et al. 2008).

One approach proposed to protect species in a landscape based upon their habitats, is the umbrella species approach (Wilcox 1984, Lambeck 1997, Carroll et al. 2001). This approach is popular because it offers a method to do large landscape multi-species conservation planning when there is a paucity of data about the habitat requirements of sympatric species (Copeland et al. 2014, Thornton et al. 2016, Barlow et al. 2020, Ward et al. 2020). However, conserving the land required to sustain the umbrella species may not be sufficient to sustain populations of other

species with different habitat needs (Carroll et al. 2010, Carlisle et al. 2018b, Dinkins and Beck 2019, Runge et al. 2019, Barlow et al. 2020, Ward et al. 2020, Wang et al. 2021). To assess whether conserving habitat for an umbrella species will effectively conserve populations of other species, the habitat requirements of the sympatric species must be known (Andelman and Fagan 2000, Bichet et al. 2016, Carlisle et al. 2018a, Timmer et al. 2019, Wang et al. 2021). If the habitat requirements of sympatric species can be individually determined, then their specific habitat needs can be targeted, instead of relying on an unknown amount of protection given by protecting an umbrella species' habitat.

The umbrella species approach is recommended when there is a paucity of data on sympatric species (Caro 2015). If there is a dearth of time and capacity to compile and model the newly available data on species, as is promoted here, the umbrella approach may still be useful to provide assurance that some sympatric species will receive some protection when umbrella species habitat is protected. This approach has the added advantage, that if the umbrella species was listed as threatened or endangered and critical habitat identified for protection, it would extend legal protection to the sympatric species' habitats which it overlaps. Whereas the approach I propose identifies areas that can protect species viability, it does not address the means to assure these areas are protected or managed appropriately.

Single species approaches

In the U.S., the Endangered Species Act is the primary tool used to prevent species from going extinct, however, this approach of focusing all our attention and resources on rescuing individual species from the brink of extinction, cannot keep up with the number of species that are becoming threatened or endangered and does not address the underlying causes of more species becoming imperiled (DeFries and Nagendra 2017, Díaz et al. 2019, Bryan and Archibald 2020). Methods are still needed that can determine which components and what spatial

configurations of landscapes are vital to protect the habitats and functions that will sustain populations of native species to keep them from becoming imperiled in the first place.

Spatially explicit population modeling

An approach that can determine the habitat configurations required to sustain viable populations of species, is to develop spatially explicit population models (SEPMs) (Lawler and Schumaker 2004, Heinrichs et al. 2010, Heinrichs et al. 2017). However, demographic information related to habitat use is required to build these models (Aldridge and Boyce 2007), which is difficult to attain and lacking for most species (Heinrichs et al. 2010). There are also high levels of uncertainty with these models, even with ample data (Minor et al. 2008).

There have also been attempts to link metapopulation dynamics (Hanski 1998) to habitat patch metrics (Nicholson et al. 2006), however, these models also require estimates of dispersal ability and extinction risks tied to habitat quality, patch sizes and configurations. Again, this information is rarely available. Even with much of these data for ten species, in a landscape with distinct habitat patches, Nicholson et al. (2006) had very high uncertainty and found the results sensitive to small variations in parameter estimates. Metapopulation models are also unlikely to be useful for landscapes with more continuous habitats, species with more uniform distributions, and species with unknown dispersal abilities and extinction risks (Noon and McKelvey 1996).

In the absence of demographic data, conservation planning strategies can integrate individual species habitat connectivity, based upon understandings of how habitat contiguity is related to population persistence (Saunders et al. 1991, Collinge 1996, Noss et al. 1997, Dale et al. 2000, Cabeza and Moilanen 2001, Kennedy et al. 2003, Moilanen et al. 2005, Wisdom et al. 2005, Reed et al. 2006, Fischer and Lindenmayer 2007, Early et al. 2008, Wilson et al. 2016, Crooks et al. 2017, Fletcher et al. 2018, Althagafi and Petrovskii 2021). To accomplish this, I devised a method to combine habitat contiguity (the inverse of fragmentation) at multiple scales

with habitat suitability probabilities to create spatially explicit results representing the highest habitat values in areas with highest suitability and contiguity.

Importance of configuration to habitat value

Habitat loss and fragmentation are significant causes of species imperilment (Andrén 1997, Wilcove et al. 1998, Sala et al. 2000, Haddad et al. 2015, Newbold et al. 2015, Díaz et al. 2019, IPBES 2019, Chase et al. 2020, Saura 2021, Teixido et al. 2021). There is a long and ongoing debate about whether habitat loss and fragmentation are distinct processes, or whether they are different manifestations of the single process of habitat loss (Andrén 1994, Jackson and Fahrig 2012, Fahrig 2013, Martin 2018, Saura 2020;2021). Regardless of whether the processes are coupled, manifest fragmentation has a discernable effect on species persistence (Andrén 1997, Crooks and Sanjayan 2006, Schmiegelow 2007, Haddad et al. 2015, Wilson et al. 2016, Crooks et al. 2017, Chase et al. 2020, Herse et al. 2020, Teixido et al. 2021, With and Payne 2021). The effects of this habitat degradation may not be readily apparent, but can have reached levels that will eventually cause species extirpations. This “extinction debt” response lag (Carroll et al. 2004, Kuussaari et al. 2009), where the deleterious effects of habitat fragmentation on species populations don’t show until it is too late, is another reason to proactively protect habitat connectivity. Therefore, both habitat amount and multi-scale, species-specific contiguity (inverse of fragmentation) must be addressed in effective conservation planning (Saura 2020).

Habitat suitability models identify habitats that are suitable for species, but if all suitable habitat cannot be protected, traditional models do not identify the subset of habitat that provide the essential connectivity important for species persistence (Dale et al. 2000, Stanton and Akçakaya 2013). Traditional habitat models are not designed to identify the spatial configurations important to species persistence (Noss 1991;1996, Margules and Pressey 2000, Poiani et al. 2000, Williams and Araújo 2000, Araújo et al. 2002, Groves et al. 2002, Reed et al. 2006, Moilanen and

Wintle 2007, Benito et al. 2009, Noon et al. 2009, Moilanen et al. 2011, Wiens and Hobbs 2015, Tilman et al. 2017, Pimm et al. 2018, Díaz et al. 2019, Bryan and Archibald 2020, Leclère et al. 2020, Noss et al. 2021b). For habitat models to predict configurations that support species persistence, they must incorporate habitat connectivity (Hanski and Ovaskainen 2000, Moilanen et al. 2005, Wisdom et al. 2005, Moilanen and Wintle 2006, Rayfield et al. 2009, Önal et al. 2016, Wang and Önal 2016, Hasui et al. 2017, Ortner and Wallentin 2020, Grimm et al. 2021).

Approaches to account for habitat connectivity

Determining habitat connectivity has often relied upon identifying patches of habitat and non-habitat (Moilanen and Wintle 2006;2007, Schmiegelow 2007, Arponen et al. 2012, Önal et al. 2016, Wang and Önal 2016, Ahmadi et al. 2017, Hasui et al. 2017, Ortner and Wallentin 2020, Rodrigues et al. 2021, Youngquist and Boone 2021). Connectivity analyses estimate the resistance or permeability of a landscape in allowing animals to traverse the matrix (non-habitat) between habitat patches. Such approaches are species-specific and use procedures to identify connecting pathways between habitat patches (e.g., corridors) (Beier and Noss 1998), generated via least cost paths (Parks et al. 2013), circuit theory (McRae et al. 2008, Dickson et al. 2019), network theory (Rayfield et al. 2011), or graph theory (Dilts et al. 2016). These assessments of spatial habitat structure require defining patches of habitat by demarcating their boundaries and quantifying the traversability of the “matrix” between patches.

The natural world, however, predominantly consists of environmental gradients, and the mix of environmental and geographic factors that constitute species’ habitats are usually messy, with islands of habitat and nonhabitat intertwined along patch “boundaries” (Rapport 1989, Noss 2000, Baker et al. 2002). Delineating patch boundaries and estimating matrix traversability costs are difficult to do in an objective, data-driven way and can have a large influence on analyses and associated connectivity planning (Rapport 1989, Beier and Noss 1998, Morrison and Boyce 2009,

Bowman et al. 2020). Connectivity is also species specific and even corridors specifically designed for a particular species are not guaranteed to be used by that species, which can result in ineffective planning for habitat connectivity (Beier and Noss 1998, Schmiegelow 2007, Morrison and Boyce 2009, Bowman et al. 2020) and may have potentially negative ecological effects (Haddad et al. 2014). There are examples of habitat corridors that improved connectivity for plants (Damschen et al. 2019), seed dispersal by birds (Levey et al. 2005), and insect pollinators (Townsend and Levey 2005), however, the effectiveness of corridors as a conservation strategy remains an open question (Robbins 2011). Also, delineating habitat patches, quantifying matrix cost surfaces, and identifying potential corridors requires detailed data for each species, which is not available for most species.

To avoid the uncertainty in defining patch boundaries, estimating the costs of movement through inhospitable matrices, and attempting to identify corridors to connect habitat patches for each species, I instead identified the least fragmented and scattered (most contiguous) habitat across the landscape at multiple scales for 164 obligate taxa of the sagebrush biome, including plants, invertebrates and vertebrates ([Appendix B](#)). This multi-species and multi-scale approach guards against fragmentation thresholds and demarcates more contiguous habitats, including natural corridors, that are important for species persistence (Hanski and Ovaskainen 2000, Gaston et al. 2002, Wiens 2006, Gilbert-Norton et al. 2010, Hilty et al. 2020). Combining habitat suitability and contiguity has been done, but only for species with sufficient data to understand their connectivity needs (Moilanen et al. 2005, Early et al. 2008, Ahmadi et al. 2017, Hasui et al. 2017, Ortner and Wallentin 2020, Rodrigues et al. 2021, Youngquist and Boone 2021). To create habitat models able to identify areas most likely to support species persistence for a wide range of taxa, I combined multi-scale habitat contiguity with habitat suitability for individual species, including species with sparse data.

The outputs of these models are hierarchical habitat value maps which spatially depict what I call “fundamental habitat”: the habitat types and configurations required as foundations for species persistence. I selected this term to describe the minimum amount and configuration of habitat required to sustain a species’ population, as a foundation – it is necessary but not sufficient to ensure species viability. The identified areas provide the necessary stage on which to implement conservation measures (e.g. protection from land use change, disturbances, degradation, invasive species, disease, etc). This term is consistent with how others have used it, incorporating the concepts of minimum or basic habitat requirements (Worthington et al. 2018, Bean et al. 2024), being essential (Viddi and Lescrauwaet 2005, Worthington et al. 2018, Liu et al. 2024), and providing underlying conditions to support species viability (Calcinai et al. 2024). Selecting an adequate amount of a species’ highest value fundamental habitat, produces spatially configured maps that include the most suitable and connected habitat, which is the most likely to support their persistence.

Conservation planners can estimate and easily adjust how much fundamental habitat is adequate and that amount of the highest value, spatially-explicit, fundamental habitat can then be included in multi-species spatially-optimized conservation plans. Planners only need specify a percentage of habitat they think is adequate and the model will produce spatially configured maps of the highest value fundamental habitat of that percentage. This differs from considering just suitable habitat, because protecting some portion of suitable habitat, without accounting for its configuration, does not address habitat connectivity, a critical component of species persistence.

Multi-species systematic conservation planning

Systematic conservation planning (SCP) has been proposed as a way to spatially prioritize conservation reserves to protect habitats of multiple species (Margules and Pressey 2000, Cabeza and Moilanen 2001). This approach uses an optimization process to include occurrences or some

amount of habitat of all species in a study area in a spatial conservation plan, for the least cost, e.g., amount of area. Several variations of multi-species prioritization procedures have been developed, e.g., Marxan (Ball et al. 2009), Zonation (Moilanen et al. 2009), prioritizr (Hanson et al. 2020). These typically use species habitats, ranges, or vegetation maps as inputs to identify optimal areas to focus multi-species conservation.

These methods typically assume that all identified habitats (e.g., from habitat suitability or resource selection models) are able to support species survival and reproduction (the definition of habitat; Hall et al. 1997), which also requires inter-population connectivity. In an SCP approach, areas are weighted using conservation criteria to produce optimized “solutions” identifying areas that meet multi-species conservation targets within the least area (or cost). The resulting solutions can identify places and ecosystems to focus conservation for multiple species, and some have optional constraints that can increase the compactness of the overall conservation solution, but they typically do not identify species-specific habitat configurations required to ensure the habitat connectivity required by each species. Without including the habitat connectivity needs of each species, the habitats included in these conservation designs may not insure species persistence (Araújo and Williams 2001, Cabeza and Moilanen 2001, Kareiva and Marvier 2003, Lawler et al. 2003, Orme et al. 2005, Moilanen and Wintle 2006, Taylor et al. 2006, Moilanen and Wintle 2007, Early et al. 2008). For this approach to be effective, information about the habitat type, amount, and configuration required to sustain populations of each species is required.

Research goals

This study is focused on identifying the location, configuration, and contiguity of environmental and abiotic factors required to sustain a broad array of species populations. There are several major issues that have heretofore inhibited identifying habitats able to sustain the

populations of a wide array of taxa. Five issues in particular have hindered predicting habitats capable of supporting persistence:

- Planning was not done at extents to encompass whole populations for a given species, thus may not have included enough habitat or population to ensure species persistence (Unnasch and Karl 2013, Pe'er et al. 2014, Runge et al. 2016);
- Plans made at population extents were done at a coarse granularity and lacked the specificity necessary to distinguish environmental conditions at the resolutions at which most species discern suitable habitat (Di Marco et al. 2017, Connor et al. 2018, Critchlow et al. 2022);
- Plans used species ranges or indices like species richness as conservation targets, instead of requisite habitats for individual species (Wiersma and Sleep 2016);
- Plans primarily or only included well-studied taxa, most often vertebrate species (Wiersma and Sleep 2016, Duchardt et al. 2021); and
- Habitat configuration planning for multiple species did not assess habitat contiguity for each species; if they incorporated habitat configuration, they only considered the overall compactness of the multi-species configuration, not individual species' habitat contiguity (Williams et al. 2005, McIntosh et al. 2017, McIntosh et al. 2018, Sinclair et al. 2018).

I developed solutions for these problems to derive habitat modeling procedures able to identify habitats most likely to sustain a wide range of obligate taxa populations at biome scales.

The ultimate goal of this research was to advance habitat suitability modeling by developing methods to overcome the barriers to producing these type of biome-scale fundamental habitat models for a wide-range of taxa and incorporate habitat connectivity, to develop multi-species conservation plans that support the persistence of the obligate species of a biome. To accomplish this, I completed 3 stages of the study:

1. Development of single-species biome-scale habitat models, using publicly available data, that combine habitat suitability and contiguity into fundamental habitat value maps for 164 obligate taxa of the sagebrush steppe biome, including all obligate vertebrates, invertebrates that there were data for, and obligate plant species listed by NatureServe as nationally or globally endangered (Chapter 1).
2. Development of multi-species habitat optimizations for the 164 obligate taxa that contained specific amounts of the highest value fundamental habitats of each species. I explored different conservation scenarios, such as maximizing existing protected areas in the solution, maximizing sage-grouse habitat, maximizing sagebrush landcover, and different combinations of these. I also evaluated the effects of including different amounts of each species fundamental habitat in the optimization procedure (Chapter 2).
3. Comparing this approach of multi-species landscape conservation planning to the umbrella species approach (Chapter 3).

The methods developed here can be incorporated into decision support tools that can be applied to the obligate taxa of any biome to support multi-species conservation planning by land management and species protection agencies, to identify multi-species habitat configurations that are most likely to support native species persistence.

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CHAPTER 1: HIGH-RESOLUTION, BIOME-EXTENT HABITAT SUITABILITY AND CONTIGUITY MODELS FOR SAGEBRUSH STEPPE OBLIGATE TAXA USING PUBLICLY COLLECTED SPECIES OBSERVATION DATA

Habitat loss, fragmentation, and degradation resulting from human activities are causing the extinction of many plant and wildlife species (Haddad et al. 2015, Crooks et al. 2017, Kuipers et al. 2021, Cowie et al. 2022). The combined effects of land use and exploitation of natural resources, exacerbated by climate change, pollution, and invasive species are having devastating impacts on the natural world (DeFries and Nagendra 2017, Ceballos et al. 2020, Román-Palacios and Wiens 2020). Consequently, many native species are facing extinction (Díaz et al. 2019, IPBES 2019, Ceballos et al. 2020).

Curtailling this mass species extinction (Ceballos et al. 2020) will require, at a minimum, providing the habitat needs of all species, as the foundation for efforts to assure their viability. Instead of putting all our resources into trying save each species from extinction as we notice their imperilment, which is not keeping up with the crises (Leclère et al. 2020), we need to conserve and manage the species in a landscape collectively, to prevent species from becoming imperiled in the first place - being proactive rather than reactive (DeFries and Nagendra 2017, Pimm et al. 2018, Díaz et al. 2019, Kennedy et al. 2019, Leclère et al. 2020, Noss et al. 2021).

Providing the fundamental habitat needs for every species in a landscape requires identifying the type, amount, and configuration of habitat within the landscape essential for sustaining the populations of each species (Moilanen et al. 2005, Reed et al. 2006, Early et al. 2008, Grimmett et al. 2021). To accomplish this, I propose methods to identify the areas of a landscape, that if managed appropriately, would support viable populations of obligate species, using the least amount (or cost) of land, to proactively keep them from becoming endangered.

Systematic conservation planning (SCP) has been proposed as a method to identify land configurations that can sustain populations of native species (Margules and Pressey 2000, Cabeza and Moilanen 2001). For SCP to successfully identify the habitats that can support multi-species persistence in a landscape, the habitat requirements that can sustain each species persistence must be used as inputs in the optimization routine (Grimmett et al. 2021). For habitat to support viable populations of species, it must be of a sufficient amount, configuration, and provide the conditions (e.g., micro-climate, food, shelter, safe movement) required by each species (Morrison et al. 1992, Hall et al. 1997, Lawler and Schumaker 2004, Crooks and Sanjayan 2006, Jackson and Fahrig 2012). If these fundamental habitat attributes are not provided for each species, their populations ultimately will not persist.

Conserving the required amount and configuration of land is the underpinning for any effort to keep species from becoming imperiled (Araújo and Williams 2000, Araújo et al. 2002, Crooks and Sanjayan 2006). This principle is analogous to the land facet approach to conserving land parcels to preserve “the arena” on which to perform biodiversity conservation (Beier and Brost 2010). The difference is that the approach described here relies on species habitat use to distinguish the fundamental habitats that species require. However, protecting these areas alone is often not sufficient to assure the species persistence. Managing the land for habitat quality, compatible land uses, elimination of detrimental disturbances, invasive species, pollution, etc. is also required (Heinrichs et al. 2010, Pocewicz et al. 2014).

The approach developed here places higher values on more contiguous habitats with the highest probabilities of being suitable; what I call “fundamental habitat”. The amount of fundamental habitat selected for conservation can subsequently be adjusted based upon planning objectives. Selecting increasing percentages of the highest value fundamental habitats will result

in increasingly comprehensive spatially-configured maps of the most suitable and (multi-scaled) contiguous areas of species habitats, which are more likely to support their persistence.

Study objectives

The goal of this study was to develop methods to produce large-extent, high resolution fundamental habitat maps, incorporating habitat suitability and contiguity, which are more likely to support population persistence, for a wide range of taxa, including data-poor species. This has not been done previously because of several intractable obstacles. I developed new methods to surmount these obstacles and generated fundamental habitat maps for 164 obligate species of the sagebrush steppe. Beyond the sagebrush steppe, these methods can be used to develop improved inputs for systematic conservation planning to support the persistence of the obligate species of a biome.

The five major issues that have heretofore impeded predicting habitats capable of supporting species persistence for a wide array of taxa are: 1) unavailability of data for many taxa; 2) sampling bias inherent in publicly collected data; 3) habitat models not encompassing all populations of a species; 4) coarse resolution models that miss fine-grained habitat distinctions; and 5) not accounting for habitat contiguity. I developed methods to address each of these.

Unavailability of data for many taxa

The occurrence data needed to create habitat models for a wide array of taxa had not been available until recently (Constable et al. 2010). Habitat models could only be developed for well-studied species that had sufficient data about their habitat use. Now, with the proliferation of publicly-collected species observations, along with accurate locations (e.g., via phones with built-in GPS location), these data are available for many more (albeit not all) taxa (Figure 1.1).

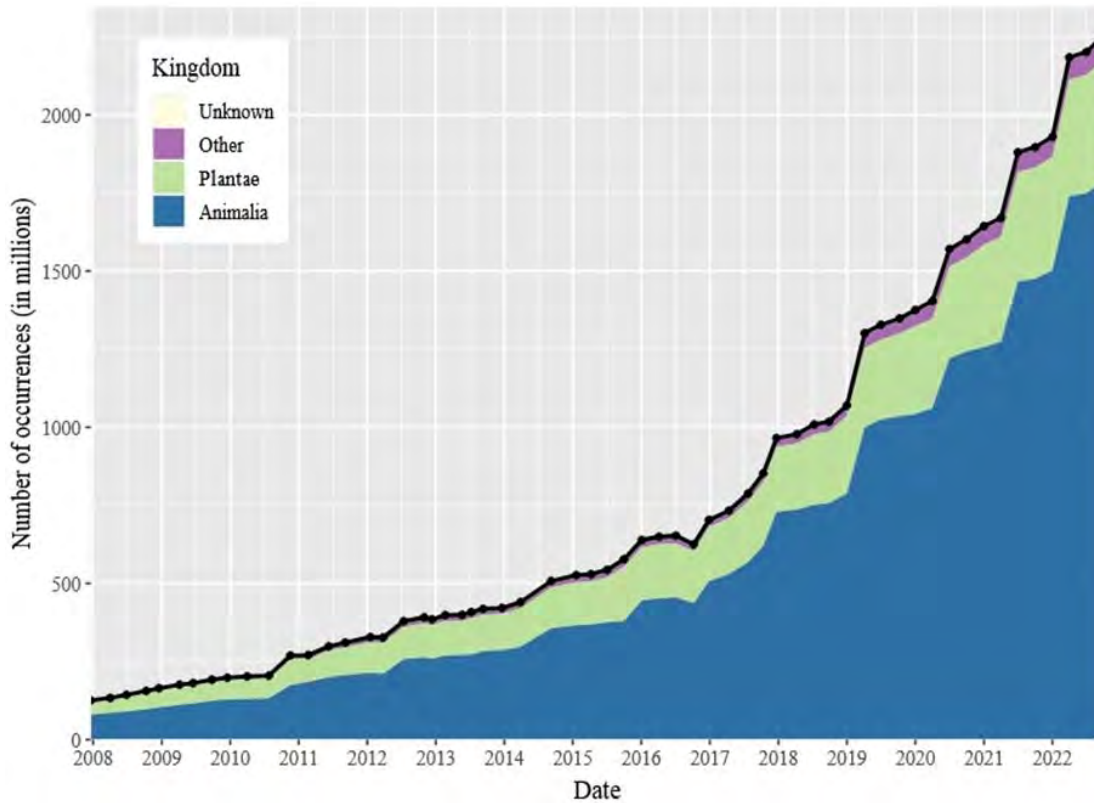


Figure 1.1. Species occurrence records compiled by the Global Biodiversity Information Facility over time (GBIF 2022).

There are many databases that accumulate data for many taxa (e.g., eBird (eBird 2012), Avian Knowledge Network (AKN 2009), Discover Life (Pickering 1999), iNaturalist (iNaturalist 2018), State Natural History Programs (NatureServe 2017), Xerces Society (Xerces Society 2018), etc.), acquired from many different sources, including species observations reported by the public. There are also databases that compile these data from the myriad of regional databases into a single searchable repository, e.g., the Global Biodiversity Information Facility (GBIF 2022), resulting in species location data now being available for a wide range of taxa across the globe. This availability of publicly collected data provides new opportunity to construct habitat models for data-limited species.

Sampling bias of publicly collected data

Publicly-collected data have sampling bias that must be addressed, e.g., species observations tend to be clustered in areas where people concentrate (Hughes et al. 2021). However, when addressed, these data can be used to create habitat models for taxa that had previously not been possible. I used two separate procedures to mitigate the bias in these data. Because publicly collected data are often collected along roads, roads were selected as a preferred habitat type in most model test runs and projected across the landscape as preferred habitat. When I removed roads from the land cover data layer, used as a covariate in the habitat models, the habitat types adjacent to the roads were selected as suitable habitat instead of roads. This was one way I ameliorated the bias in publicly-collected data. Another way to deal with the bias was to produce environmental background points that approximate the spatial sampling bias in the species observations, that allowed Maxent to differentiate preferred habitat based on differences in “sampled” background versus used habitat, further ameliorating bias in the data.

Spatial scale of habitat models

The spatial scales at which the models are developed is important in identifying habitats that can support species persistence. Habitat models are ideally developed at scales (extent, grain and thematic classification) that are relevant to species, populations, and ecological processes that affect species populations (Reed et al. 2006, Viña et al. 2010, Wiens and Bachelet 2010).

Population extents

To account for the biome-wide extent at which ecological processes and populations function, models used for species-level conservation planning also need to be developed at spatial extents that encompass species populations (Unnasch and Karl 2013, Matthiopoulos et al. 2019, Grimmett et al. 2021). Habitat models based on wide-ranging observations, even with less precision, have been shown to outperform models with systematically collected data with fewer

observations, from a smaller portion of a species range, and collected over shorter time periods (Heglund 2002, Braunisch and Suchant 2010). Computational limitations have, in the past, prohibited running models with high resolutions and large spatial extents (Arponen et al. 2012), however, advances in computational capacity have made this possible now.

Increased granularity

Because habitat conditions important for some species can vary at fine scales, habitat models developed for systematic conservation planning with higher spatial resolution (smaller grain size) and more thematic class distinctions are more likely to provide a more accurate representation of species' habitat associations (Early et al. 2008, Keller and Smith 2014, Nezer et al. 2017, Connor et al. 2018).

Habitat contiguity

Connectivity is an essential attribute of habitat, effecting the persistence of species populations (With and King 1999, Taylor et al. 2006, Poniowski et al. 2018) because habitat fragmentation can decrease species persistence (Wilson et al. 2016, Crooks et al. 2017, Herse et al. 2020, With and Payne 2021). Ideally, to identify areas important for conservation of species persistence, demographic data linking species fitness to environmental factors and habitat contiguity would be used to select essential habitats. However, since such data are not available for most taxa, models developed here were based upon the best understanding of how habitat suitability and connectivity relate to persistence (Saunders et al. 1991, Kennedy et al. 2003, Early et al. 2008, Wilson et al. 2016, Crooks et al. 2017, Herse et al. 2020, Althagafi and Petrovskii 2021, With and Payne 2021).

I developed a novel way to combine habitat contiguity (the inverse of fragmentation) at multiple spatial scales with models of habitat suitability for each species to identify the habitats most likely to support species persistence (Ahmadi et al. 2017, Rodrigues et al. 2021, Youngquist

and Boone 2021). Because I was modeling habitat for many different taxa without information on what constitutes connected habitat for each, and considering that species use habitat at several scales (Wiens et al. 1987, Hayward and Suring 2013, Stiver et al. 2015), I calculated contiguity at scales from local to landscape for each species.

Conservation planners can vary the percentage of each species spatially-configured fundamental habitat to include in systematic conservation plans to produce multi-species habitat configurations optimized for species persistence using the least amount of land. This differs from considering just suitable habitat, because protecting some portion of suitable habitat, without accounting for its configuration, does not address habitat connectivity, a critical component of species persistence.

METHODS

To create habitat models for sagebrush-obligate taxa, I identified obligate species in the sagebrush steppe and acquired available observation data for each species. I used these data and environmental covariate data layers that spanned the biome to model habitat for each species using a maximum entropy modeling approach (Phillips et al. 2006). I restricted the output that predicted suitable habitat to species' geographic ranges (NatureServe and IUCN 2018), to focus on important, currently occupied habitat. Finally, I incorporated multi-scale habitat contiguity into the habitat suitability models for each species, which produced spatially-explicit, hierarchical, "fundamental" habitat value maps, intended to better predict habitat configurations likely to support species persistence.

Study area

I demonstrated the application of these methods in a case study with the obligate taxa of the sagebrush steppe biome. I chose this landscape because it is under threat of increased habitat loss and degradation with high risk of extirpation of several obligate taxa (Hanser 2018). The

spatial extent for this study is based on the past and current ranges of sage-grouse species – the greater sage-grouse (*Centrocercus urophasianus*) and the Gunnison sage-grouse (*C. minimus*), because they require large areas within the biome for their conservation (Schroeder et al. 2004, USFWS Wyoming Ecological Services 2014); and the extent of sagebrush landcover of the western U.S. and southwestern Canada (Figures 1.2 and 1.3). The Gap Analysis Program (GAP) national land cover map (USGS Gap Analysis Program 2011) was used to locate sagebrush landcover in the U.S. portion of the study area and the Land Cover Database of North America (NALCMS 2010) was used to locate sagebrush landcover in the Canadian portions.

The extent of the study area is 177 million ha (685,000 sq mi) and includes portions of 14 states and 3 Canadian provinces and includes 8 major ecoregions (The Nature Conservancy 2009), including the Columbia, Modoc and Okanagan Plateaus, the Great Basin, the Colorado Plateau, Wyoming Basins, Black Hills, and Northern Great Plains Steppe, and is bisected by three Rocky Mountain ecoregions (Figure 1.4).

Species selection

I used publicly available data on species occurrences from the Global Biodiversity Information Facility (GBIF 2022). This database includes data compiled from many regional species occurrence databases (e.g., BISON (USGS 2013), eBird (eBird 2012), Avian Knowledge Network (AKN 2009), Discover Life (Pickering 1999), iNaturalist (iNaturalist 2018), State Natural History Programs (NatureServe 2017), Xerces Society (Xerces Society 2018)). I added observation records from the Butterflies and Moths of North America (BAMONA) database (Lotts and Naberhaus 2018), because these records were not included in GBIF at the time. I downloaded observations of these species in the study area for the years corresponding to the span of the landcover classification (1990-2011) from GBIF and BAMONA ([Appendix A](#)).

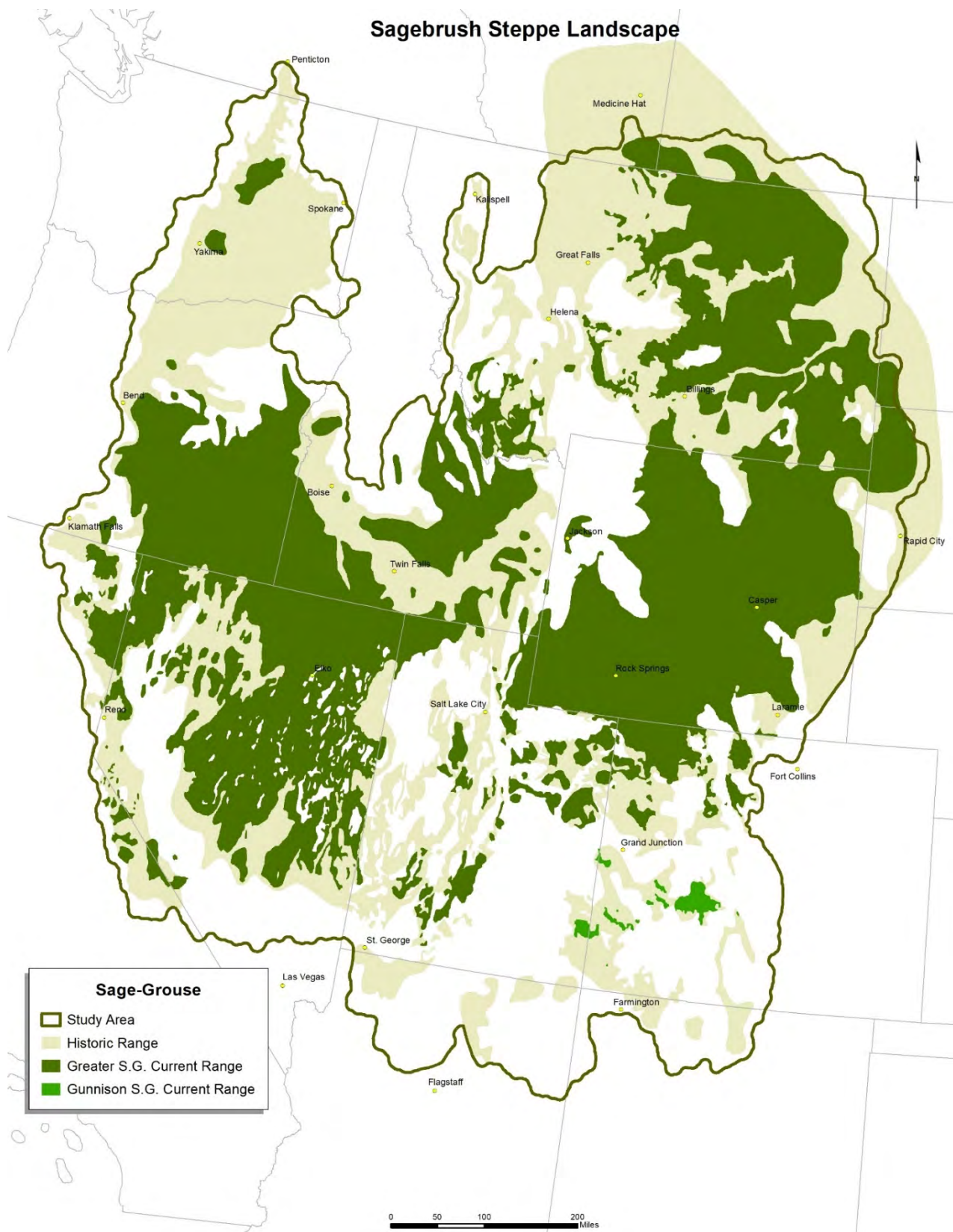


Figure 1.2. The current and historic ranges of sage-grouse species: greater sage-grouse (*Centrocercus urophasianus*) and Gunnison sage-grouse (*Centrocercus minimus*) (Schroeder et al. 2004).

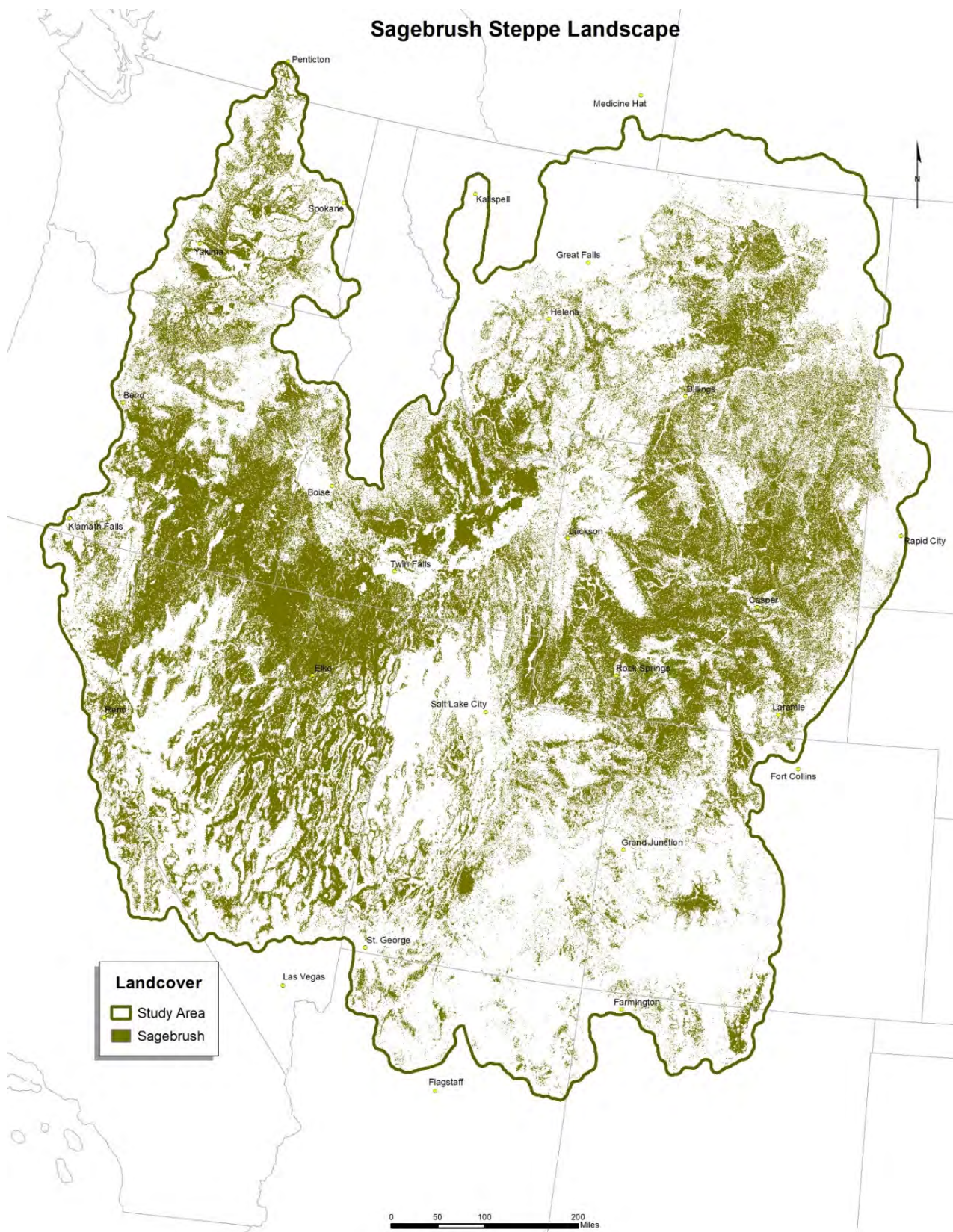


Figure 1.3. Spatial extent of the sagebrush steppe landscape and sagebrush landcover types from the GAP landcover classification (USGS Gap Analysis Program 2011) and the Land Cover Database of North America (NALCMS 2010).

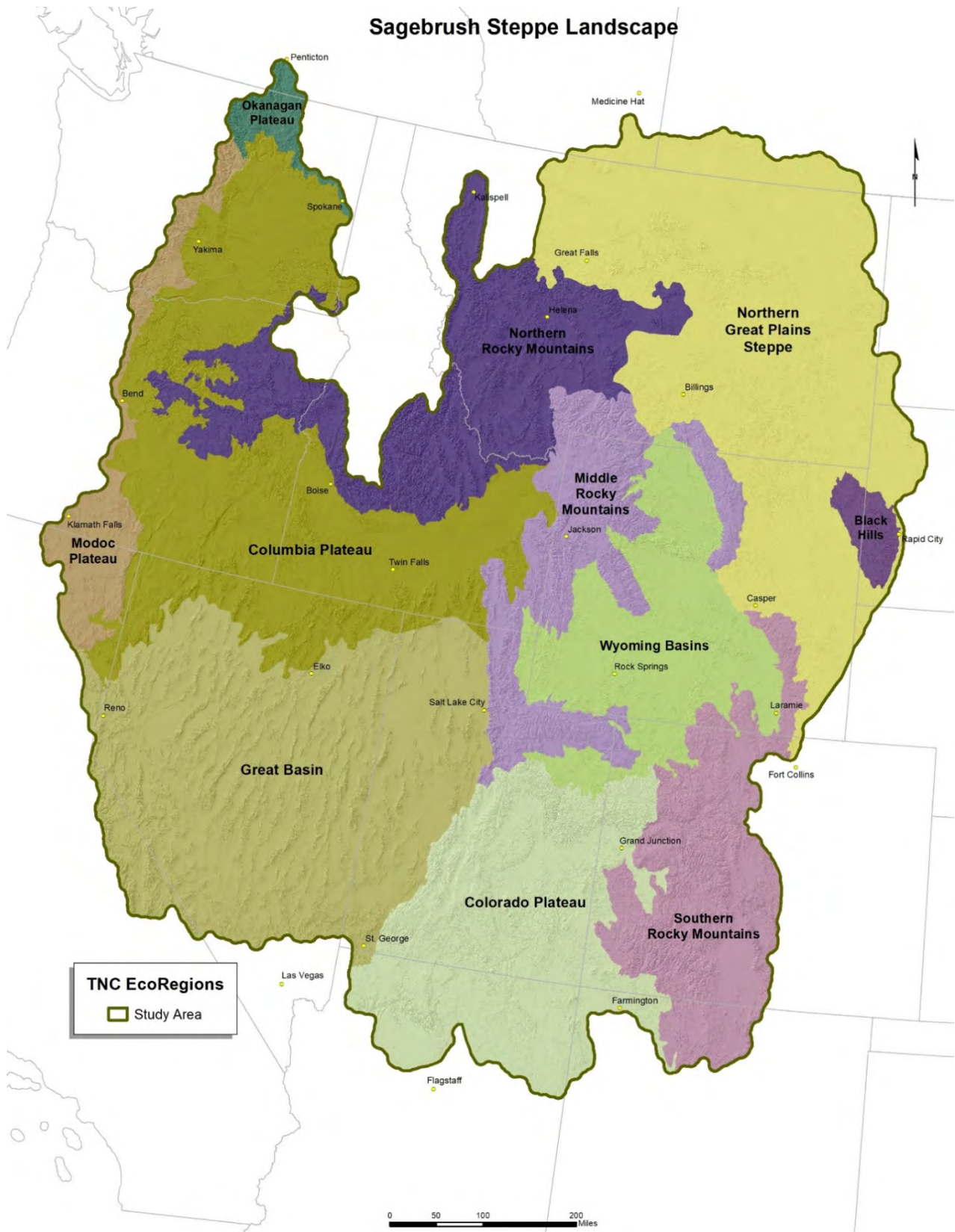


Figure 1.4. TNC EcoRegions (The Nature Conservancy 2009) within the study area.

I created a list of 446 terrestrial plant and animal species identified as “obligate species”, which are dependent on the sagebrush landscape for some part of their life histories, determined by independent analyses (Fautin 1946, Braun et al. 1976, Dobkin 1995, Paige and Ritter 1999, Knick et al. 2003, McAdoo et al. 2003, Gilbert and Chalfoun 2011, Rowland et al. 2011, Earnst and Holmes 2012, Holmes et al. 2015).

To achieve feasible processing times, of the 324 plant species on the original list, only plants with observation records in GBIF, and with NatureServe global imperilment rankings (Master et al. 2012) of “G1 - Critically Imperiled” or “G2 - Imperiled” (“T1” & “T2” for subspecies) were included ([Appendix A](#)). Habitat models were not done for the four raptor species found in this landscape because the observations for raptors tended to be “flyovers” and not necessarily indicative of used habitat. Mapping the habitats of the prey species of these raptors was a better spatial representation of the raptors’ habitat use (foraging) in this biome. The final list of sagebrush obligate species used for the study included: 1 amphibian, 19 reptiles, 23 birds, 43 mammals, 27 invertebrates and 51 plants ([Appendix B](#)).

I did not model sage-grouse (*C. urophasianus* and *C. minimus*) habitat because there are several pre-existing models of sage-grouse habitat (Aldridge 2005, Aldridge and Boyce 2008, Doherty et al. 2010, Heinrichs et al. 2017) and these sage-grouse habitat models and proposed conservation areas were used to compare this biome conservation approach to the umbrella species approach in Chapter 3. I also did not develop models for aquatic species, since they require a different modeling approach and I did not have access to important aquatic covariate data (e.g., water temperature, hydrology), which are key determinants of aquatic species habitat suitability. However, there have been some uses of proxy data (i.e., air temperature and precipitation) to model aquatic species habitat (McGarvey et al. 2017), which could be included in future applications.

Omitting some obligate species from the conservation plan for this biome resulted in selecting multi-species conservation areas that will not necessarily protect the species left out of the planning. The goal of this study was to develop the methods that can identify areas most likely to protect the persistence of the obligate taxa of a landscape. As more occurrence data become available, more species can be added into the planning process to eventually include all the identified obligate species and produce a comprehensive conservation plan.

HABITAT MODELING

I used the maximum entropy model Maxent (Phillips et al. 2004) to derive probabilities of species' habitat suitability, because it performs better than other models in producing accurate results using presence-only data (Giovanelli et al. 2010, Stryszowska et al. 2016). Maxent is also one of the best performing models using species occurrence data with location errors (Graham et al. 2008), and using small sample sizes (Elith et al. 2006, Hernandez et al. 2006, Wisz et al. 2008), which is all that was available for several of the species in this study. Halvorsen et al. (2016) also found that the predictive performance of Maxent models were unaffected by spatial autocorrelation, even with spatial autocorrelation in the residuals, because the spatial structure of the response variables came from topographic features, and was accounted for in the models.

Maxent compares the values of environmental or habitat covariates (e.g., temperature, precipitation, vegetation, topography) of species locations to the distributions of those values available in the study area. To compare the spatial distributions of habitat covariates (continuous surfaces) with species locations (points), a large number of background points are selected across the study area and the value of each covariate at each point is used to create a distribution of the covariate values for the area. Covariate values associated with species locations are compared to the distributions of the background values to determine whether the values for species locations diverge from the distribution of random (maximum entropy) samples of the background, which

indicates that species occurrences are associated with a particular environmental or habitat condition out of proportion to its occurrence in the background.

Although the outputs of Maxent models are often described as species distributions, or probabilities of presence (Phillips et al. 2006, Phillips et al. 2017), actual species distribution (or presence) depends on many factors in addition to environmental/habitat conditions (e.g., territoriality, migration, geographic barriers, competitive exclusion, disturbances, etc.). What Maxent models essentially predict is not species presence or distribution, but the probability that certain environmental/habitat conditions are suitable for a species. These conditions are located on a map and assigned a probability of suitability based upon how close the mix of conditions is to the model-estimated ideal for that species. Thus, Maxent outputs should be interpreted as the probability that habitat is suitable for a species at a particular location.

I used the same model settings (described below) for each species to produce model results that were comparable instead of finding assorted “best” models for each species. This ensured that species models were analogous when combined in landscape optimization models and allows for this method to be repeated in other landscapes. To ensure best results, I followed published recommendations for model inputs and settings for these data types (Elith et al. 2011, Merow et al. 2013, Radosavljevic and Anderson 2014).

I did not model habitat suitability for species with fewer than five observations in the study area. Instead, I created a polygon with concentric fading buffers around the observations to demarcate suitable habitat (this was done for 2 of 27 invertebrates, 28 of 51 plants, and 7 of 43 mammals; see Appendix A).

Covariate data layers

I compiled 19 environmental data layers for the study area that were potential determinants of species’ habitat suitability (Table 1.1). I did not include data layers with

inconsistent geographic coverage (e.g., soils, croplands, aerial imagery, high resolution climate data). I only included datasets as model covariates that had nationally seamless data, so that model results were not affected by regional data variations.

Since some covariate data layers had lower resolutions (larger cell sizes), they were all subdivided to match the highest resolution (10m x 10m) elevation data, resulting in cells with uniform values being divided into variants (e.g., a single 30m x 30m grid cell of sagebrush landcover was divided into 9 sagebrush cells of 10m x 10m each and combined with 9 cells of potentially different slopes and 9 potentially different aspects, etc. creating unique habitat values for each of the 10m x 10m cells).

I used the Gap Analysis Program (GAP) national landcover map (USGS Gap Analysis Program 2011) as a covariate layer because the GAP map had relatively high spatial resolution (30x30m) and the highest thematic resolution of national data sets: 584 landcover classes across the U.S., compared to the National Land Cover Database (NLCD) (Jin et al. 2019) which has 95 landcover classes for the entire U.S. Since this landcover map did not include Canada, for the Canadian portion of the study area, I used the Land Cover Database of North America (NALCMS 2010), with a 250x250m cell size and a coarser thematic classification, having only 19 classes for all of Canada. I resampled cells to 30x30m, cross-walked the classes to GAP types and mosaicked it to the GAP map (Figures 1.5 & 1.6). As a result, predictions of habitat suitability in Canada likely include more model uncertainty than those in the United States.

The data used for the GAP landcover classification were collected between 1990 and 2011. Therefore, I restricted all the datasets I used, including species location data, to this same timeframe so that all data represent conditions during the same time period.

Table 1.1. Covariate data layers used in the Maxent habitat suitability models.

Data Layer	Original Cell Size	Data Source
Landcover - U.S. portion - Canadian portion	30m 250m	GAP (USGS Gap Analysis Program 2011) Land Cover Database of N.A. (NALCMS 2010)
Patch sizes of sagebrush patches	30m	GAP (USGS Gap Analysis Program 2011)
Patch sizes of (other) shrub patches	30m	GAP (USGS Gap Analysis Program 2011)
Patch sizes of grass patches	30m	GAP (USGS Gap Analysis Program 2011)
Fragmentation of sagebrush patches	30m	GAP (USGS Gap Analysis Program 2011)
Fragmentation of (other) shrub patches	30m	GAP (USGS Gap Analysis Program 2011)
Fragmentation of grass patches	30m	GAP (USGS Gap Analysis Program 2011)
Elevation (m)	10m	USGS NED (USGS 2018)
Aspect (8 directions + flat)	10m	USGS NED (USGS 2018)
Slope (degrees)	10m	USGS NED (USGS 2018)
Average spring NDVI 1990-2011	30m	Landsat-7 TM (Landsat 1990-2011)
Average summer NDVI 1990-2011	30m	Landsat-7 TM (Landsat 1990-2011)
Average fall NDVI 1990-2011	30m	Landsat-7 TM (Landsat 1990-2011)
Average winter NDVI 1990-2011	30m	Landsat-7 TM (Landsat 1990-2011)
Summer-Winter difference NDVI 1990-2011	30m	Landsat-7 TM (Landsat 1990-2011)
Average precipitation 1990-2011 (mm/day)	1km	NASA Daymet (Thornton et al. 2018)
Average minimum temp 1990-2011 (°C)	1km	NASA Daymet (Thornton et al. 2018)
Average maximum temp 1990-2011 (°C)	1km	NASA Daymet (Thornton et al. 2018)
Distance from water (km) - U.S. portion - Canadian	vector vector	USGS Hydrography Dataset (USGS 2010) CanVec (Natural Resources Canada 2018)

Roads were removed from the landcover map because the species location data were primarily collected via the public and exhibited sampling bias, with observations tending to be clustered around roads and towns. I dealt with this bias in two ways (see the Background Data section for a description of the second). The first method, removing roads from the landcover map, was based on the premise that species were found near roads because of the habitats around the road, not the road itself. When habitat models were run with roads included, most selected roads as a preferred habitat type. When roads were removed, species were associated with the adjacent covariate data layers. However, if roads were associated more with certain landcover types (e.g., riparian areas or flat areas), removing roads could potentially create a biased positive association with those adjacent landcover types, affecting the habitat preferences selected by the

models. Also, some species may be attracted to or avoid roads and those preferences could have been obscured by removing roads. I decided that the bias observed by having roads in the models had a more deleterious effect on the models than the potential of introducing these other biases.

To remove roads from the landcover map, I used the ArcGIS (ESRI 2020) utilities Shrink and Expand to dissolve the roads in the landcover data layer. There are four “Developed” categories in the GAP landcover classification: High Intensity, Medium Intensity, Low Intensity and Open Space. Roads were classified as any of these 4 classes, so I used the Shrink process on the four classes combined, via four single-cell iterations. This caused the outer edges of roads to be replaced by the landcover class with the majority of cells adjacent to the road, and with each iteration the process was repeated, working towards the center of the road until the road was removed and replaced by the landcover types around it. Four single-cell iterations were sufficient to remove all the roads (i.e., none were larger than 8 cells wide), and did not significantly alter the boundaries of other developed areas (e.g., cities and towns). I then Expanded the developed areas by four cells, which restored them to their original sizes, except for the roads which had been removed and had no “Developed” cells from which to grow back (Figure 1.7).

Other covariate layers included in the habitat models were the patch sizes of sagebrush, (other) shrubs, and grass patches, to accommodate different preferences of species associated with this landscape. To delineate contiguous patches of these classes, I used the ArcGIS process Region Group with an 8-neighbor rule, then calculated the size of the patch (in hectares), and assigned the size of the patch to each cell in the patch. The patch size layer for sagebrush is shown in Figure 1.8.

I also calculated a multi-scale measure of fragmentation for these three vegetation types (sagebrush, shrubs, and grasslands) at multiple scales using ArcGIS to replicate a method used by the European Union to measure landcover fragmentation (Vogt 2018). I used the ArcGIS utility

Focal Statistics to sum the cell values within a moving window with different size square windows (7, 13, 27, 81 & 243 cells per side) around a central cell. Specifically, the procedure summed the number of cells of that landcover type found within the window, placing the total in the center cell, then moving to the next cell and repeating the process. This produced five grids each with cell values indicating the intactness of that landcover type around each cell at the five different scales (approx. 0.5 ha, 1.7 ha, 7.3 ha, 65.6 ha and 590.5 ha). Because the values at different scales were not directly comparable (larger windows produce larger sums), I standardized each scale so that habitat quality scores were integers ranging from 0 to 10. The five grids were then averaged together for a per cell multi-scale indication of fragmentation for these three landcover types. The fragmentation layer for sagebrush is shown in Figure 1.9.

For elevation and derivatives of elevation, I used 10m x 10m cell size elevation grids from the USGS National Elevation Dataset (NED) (USGS 2018). There were 160 NED raster grids required to span the study area. The grids were downloaded, mosaicked together, and then clipped to the study boundary. Slope and aspect layers were created from the elevation grid and used as additional covariate layers in the habitat models. Slope and aspect vary separately from each other and from elevation, so there was not a worry of spatial-autocorrelation between the data layers. The aspect layer is shown in Figure 1.10.

I created Normalized Difference Vegetation Index (NDVI) layers using 30m x 30m pixel Landsat-7 TM satellite images averaged across the years corresponding to the landcover classification (1990-2011), using Google Earth Engine. NDVI is an index of plant photosynthetic activity or productivity and is commonly used as an index of vegetation vigor. It is calculated using spectral reflectance from red and near-infrared frequencies, scaled so that the resultant value is between -1 and 1. I created layers for spring, summer, fall and winter NDVI averaged across the years 1990-2011, and created a fifth layer by subtracting the winter averages from the

summer averages to produce a layer that spatially represents the magnitude of changes between vegetation peak vigor and dormancy (Figure 1.11).

For climate layers to use in the habitat models, I used 1 km x 1 km cell size Daymet data collected by NASA (Thornton et al. 2018) clipped to the study area. I used Google Earth Engine to compile and average: precipitation (mm/day), minimum temp (°C), and maximum temp (°C) across the years 1990-2011, and divided the cells to 10m x10m (average maximum temperature is shown in Figure 1.12). I also created a distance (km) from open water (lakes and streams) data layer for the study area using the USGS North American Atlas hydrography dataset (USGS 2010) for the U.S. and the CanVec Series: Hydrographic Features (Natural Resources Canada 2018) for the Canadian portions, both vector datasets (Figure 1.13).

Maxent models

Maxent uses maximum likelihood to produce probability distributions, starting with a uniform probability distribution (maximum entropy) and using a sequential-update algorithm (Dudík et al. 2004) to assign and adjust weights to minimize regularized log loss (Phillips et al. 2006). The algorithm is deterministic and is guaranteed to converge on a probability distribution. It stops when the change in log loss in an iteration falls below a user-specified value or when a user-specified number of iterations has been performed, whichever comes first (Phillips et al. 2006). Regularization protects against overfitting by adding penalties for each term included in the model and for higher weights given to terms (Phillips et al. 2006, Anderson and Gonzalez 2011, Radosavljevic and Anderson 2014). Maxent adjusts the amount of regularization estimated to be appropriate for the sample size and the type of feature it attempts to fit (Dudík et al. 2007).

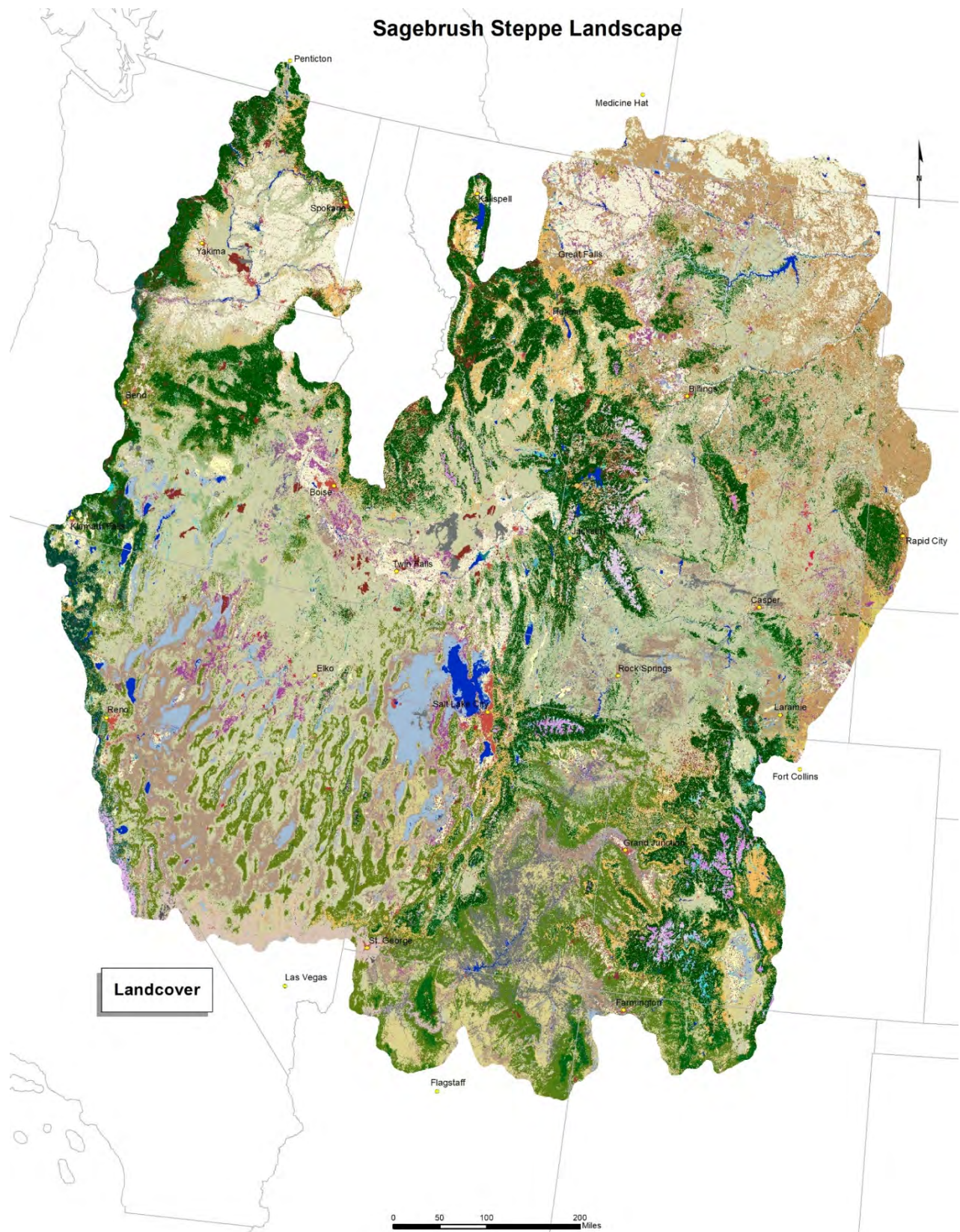


Figure 1.5. Landcover map for study area. GAP national landcover map for the U.S. (USGS Gap Analysis Program 2011) and the Land Cover Database of North America (NALCMS 2010) for Canada.

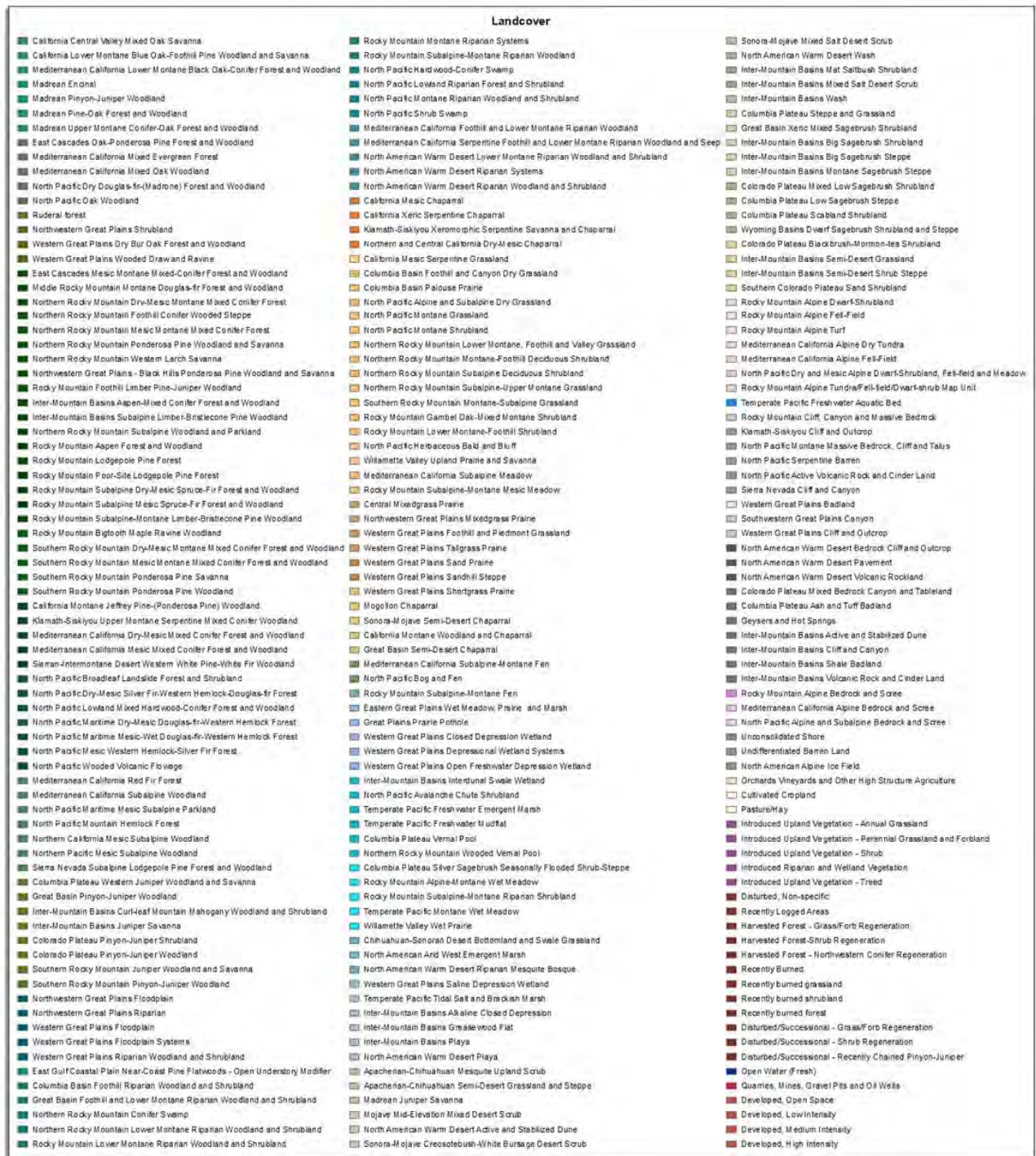


Figure 1.6. Legend for landcover map (above) with 231 classes in the study area.

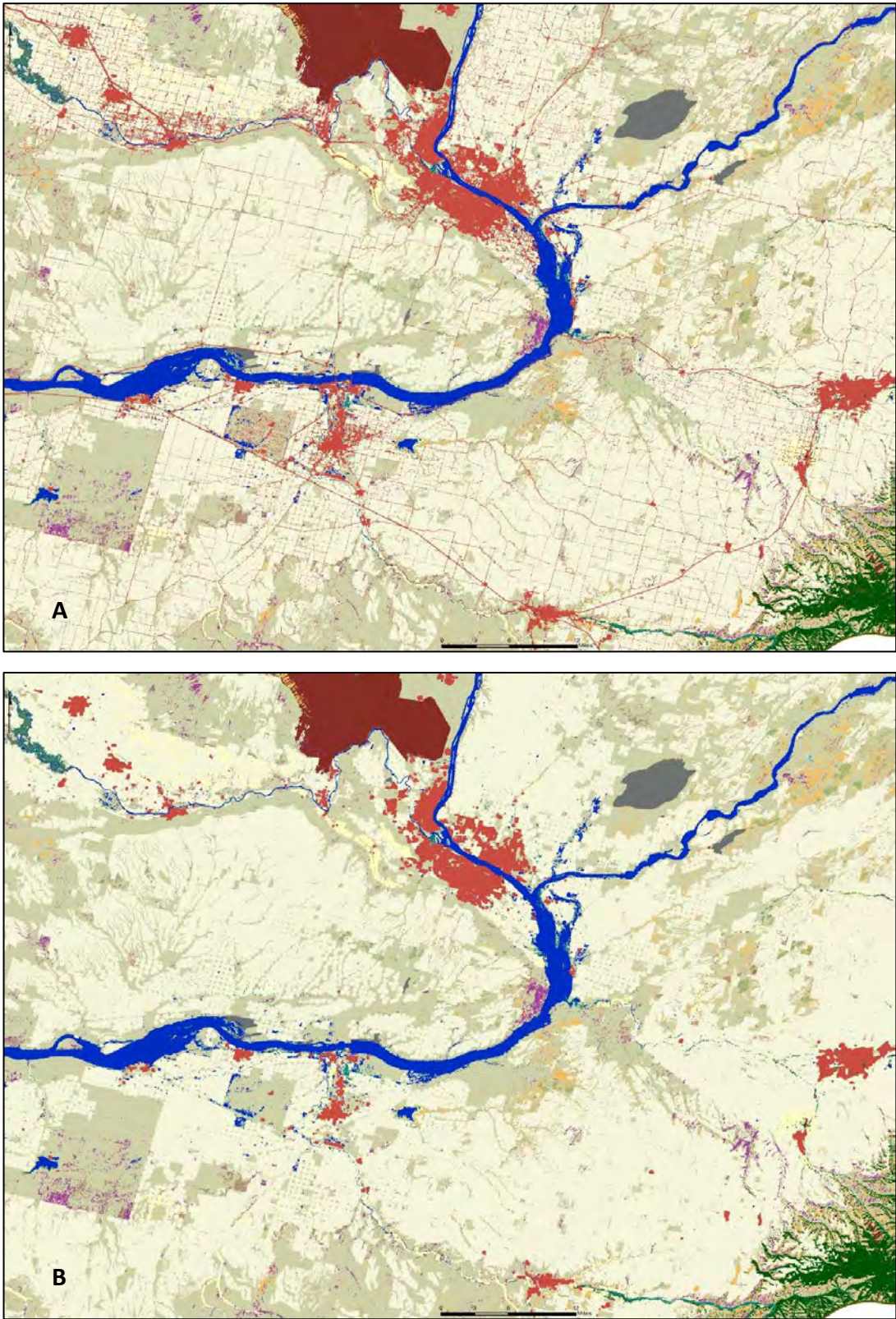


Figure 1.7. The GAP landcover map (USGS Gap Analysis Program 2011) showing the map (A) before and (B) after roads were removed (roads and developed areas are depicted by the lighter red-clay color).

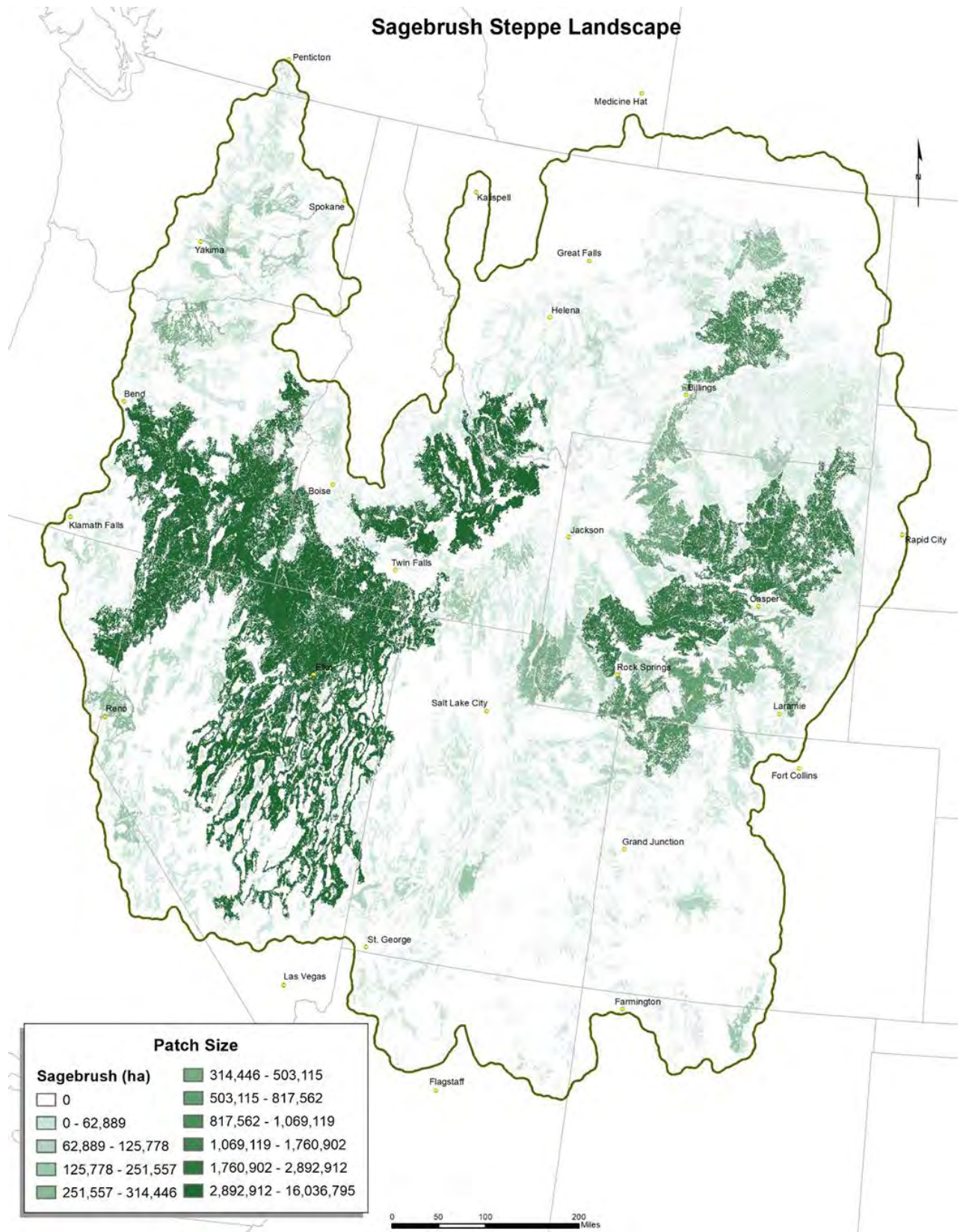


Figure 1.8. Patch size of sagebrush patches using 8-neighbor rule and assigning patch size (ha) to each cell. Similar layers were created for shrub and grassland landcover classes identified in the landcover map to be used as covariate data layers in the habitat models.

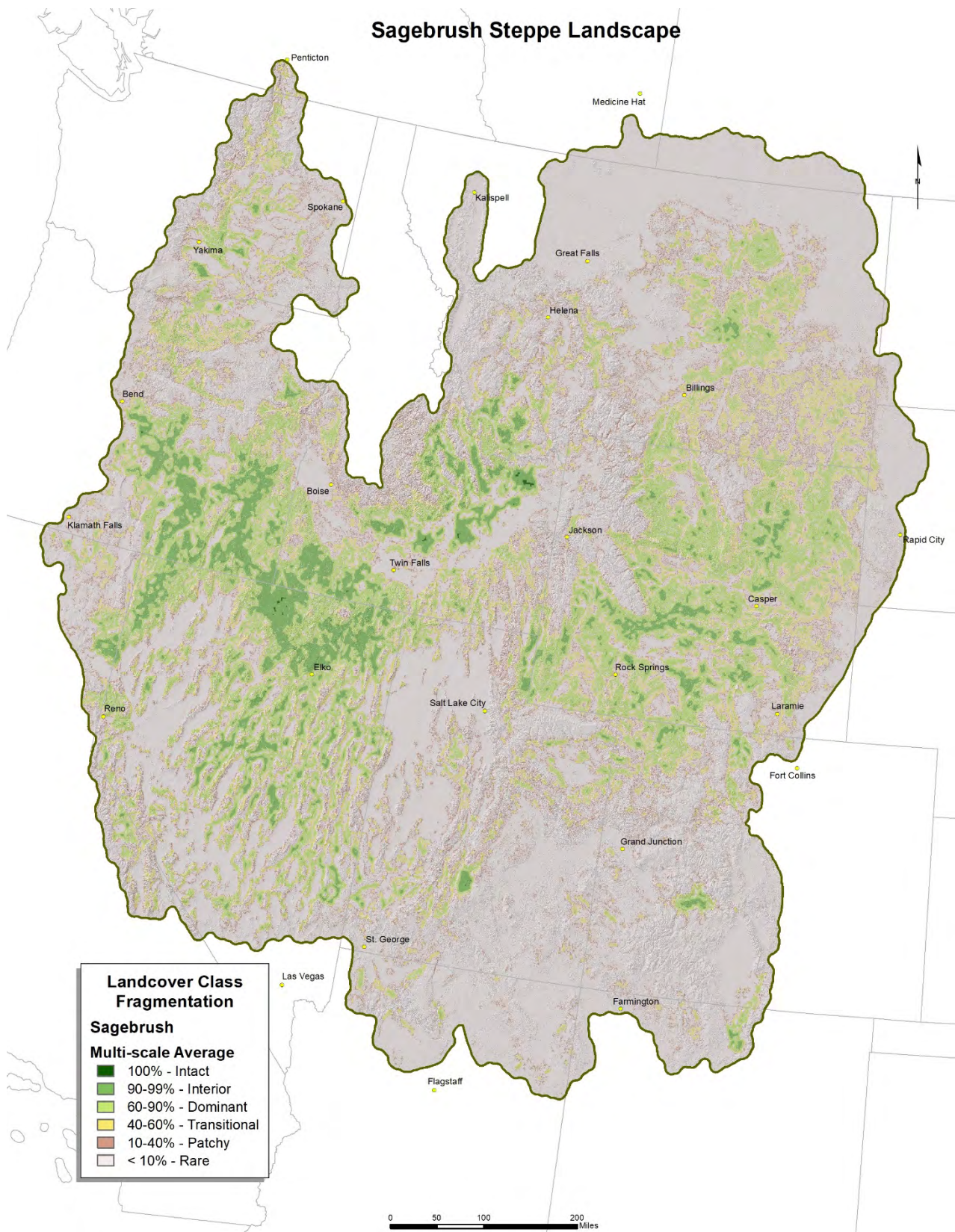


Figure 1.9. Multi-scale average fragmentation of sagebrush landcover around each cell across the landscape sensu Vogt (2018). Similar layers were created for shrub and grassland landcover classes identified in the landcover map to be used as covariate data layers in the habitat models.

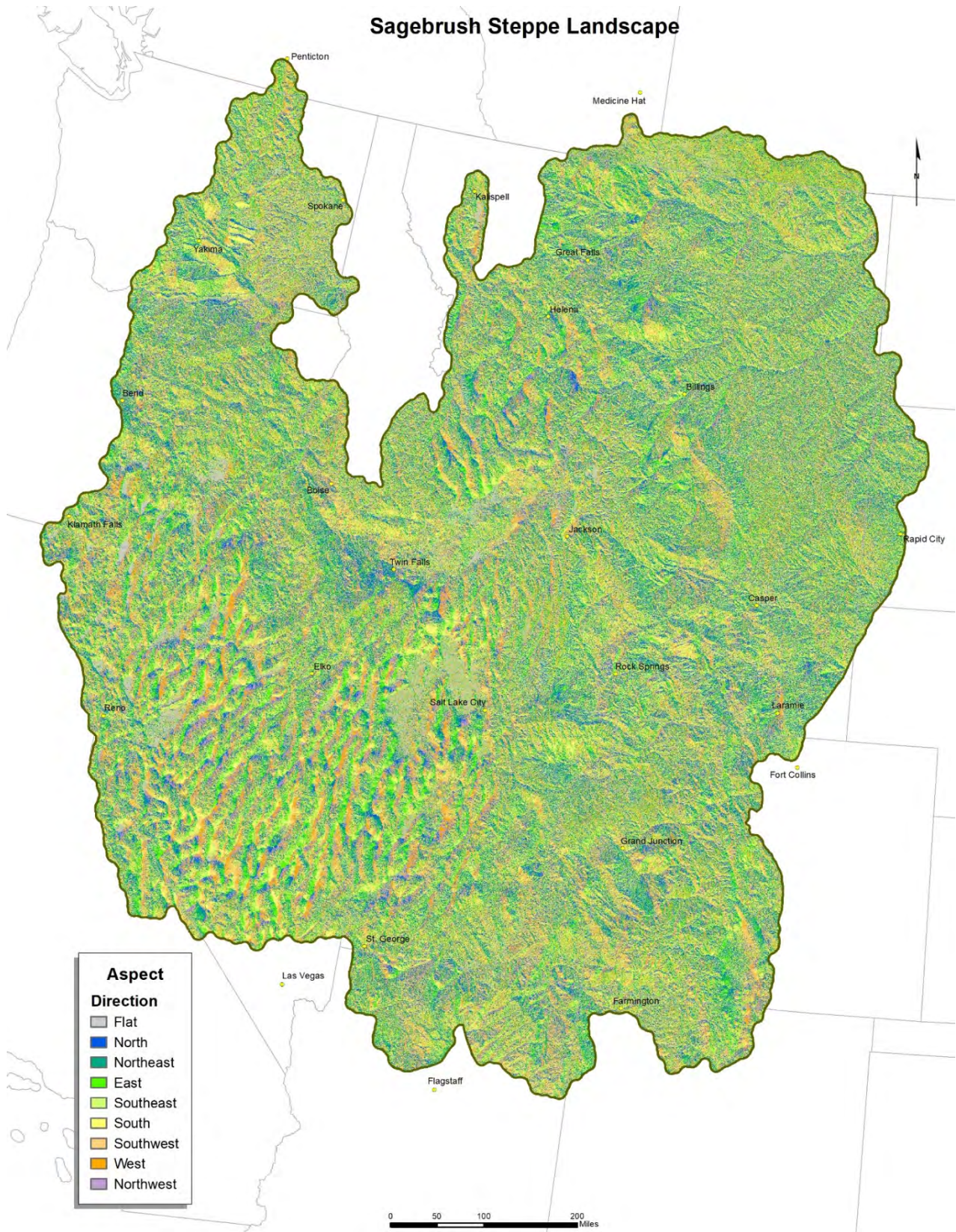


Figure 1.10. Aspect data layer (10m x 10m cell size) derived from the USGS NED elevation dataset (USGS 2018).

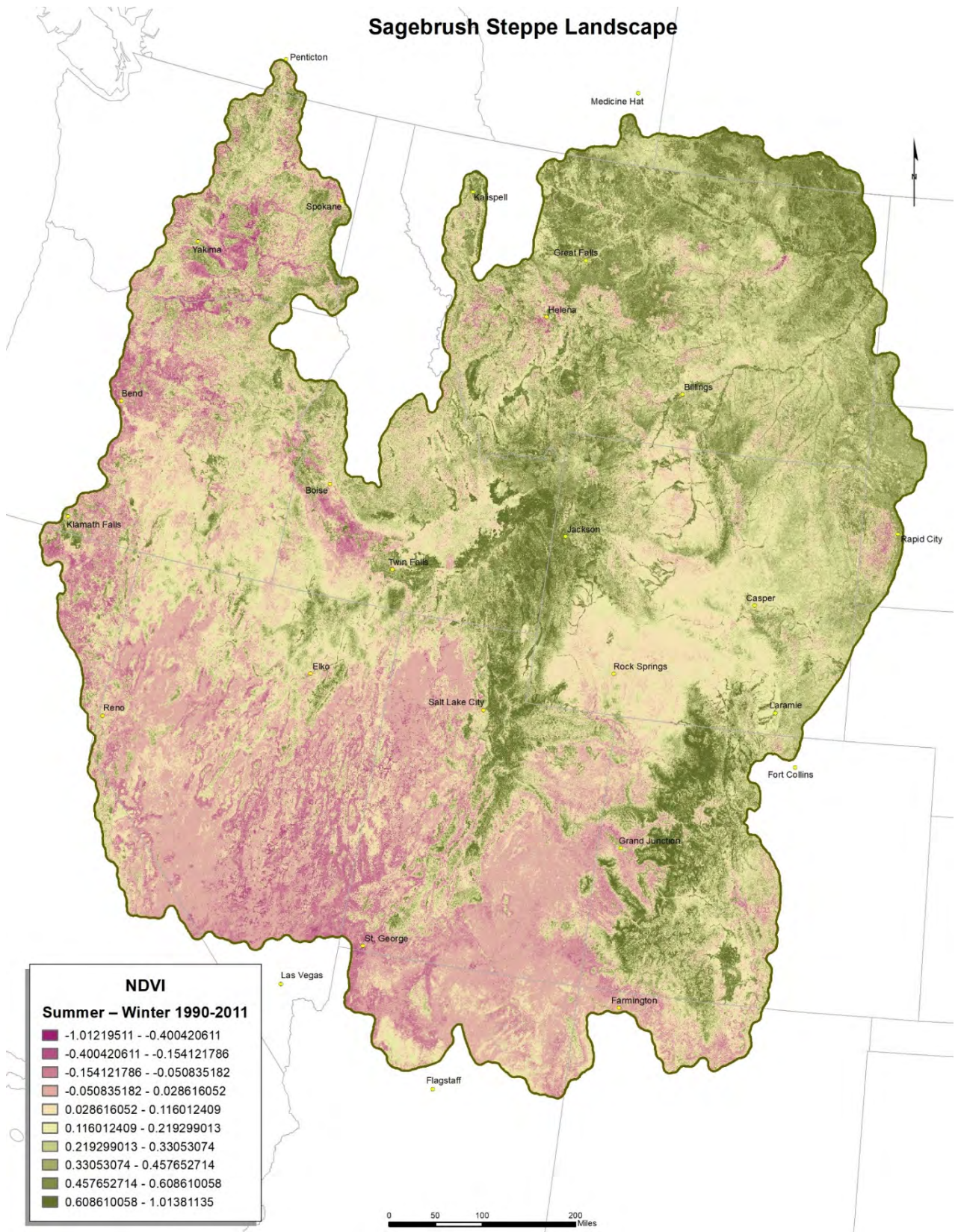


Figure 1.11. Average summer minus average winter NDVI for 1990-2011. Darker colors indicate a higher magnitude of change, with reds indicating more green-up in winter vs. summer, greens indicating more green-up in summer vs. winter, and light-pink to yellow indicating not much change in summer vs. winter.

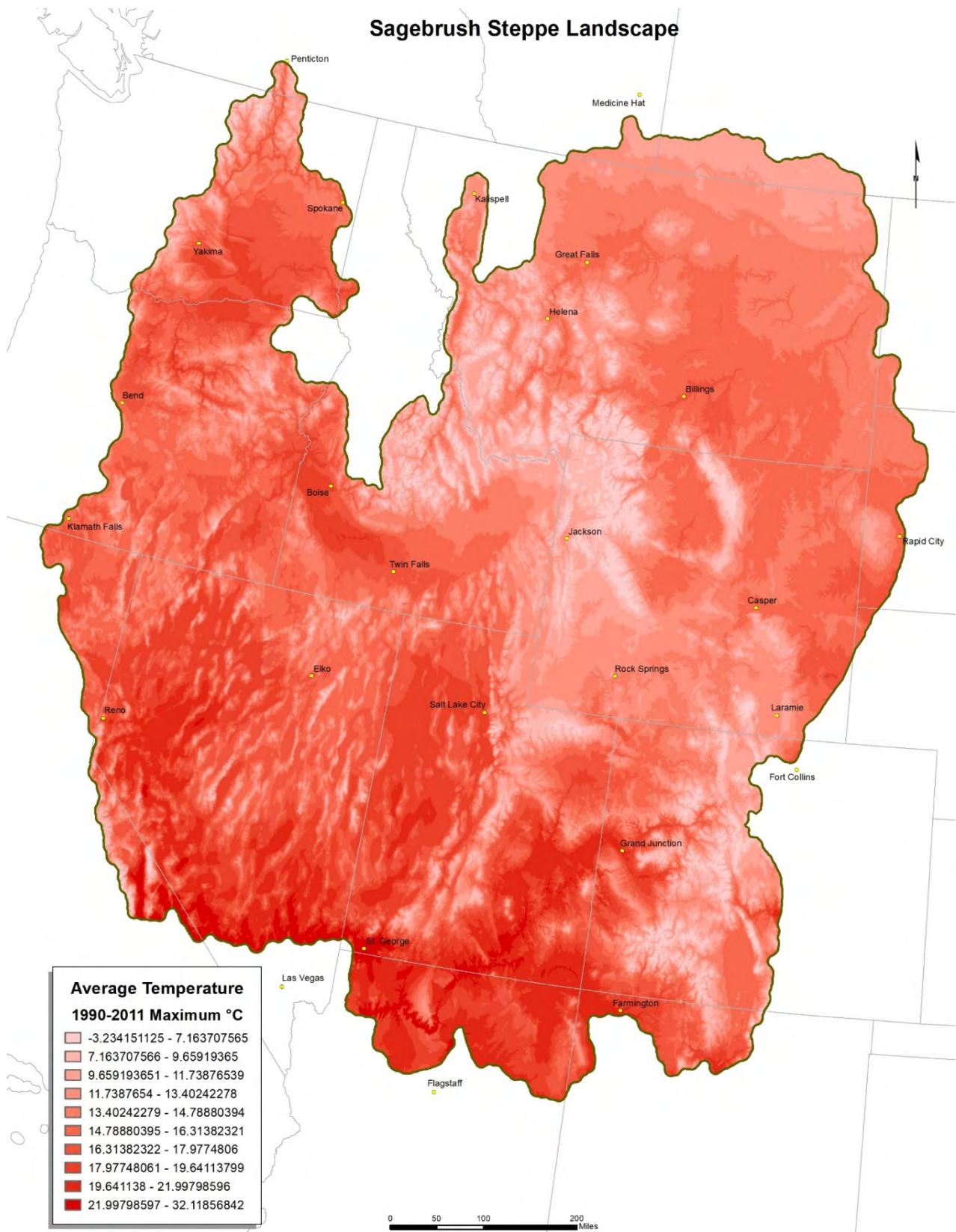


Figure 1.12. Average maximum temperatures for years 1990-2011 calculated using NASA Daymet data (Thornton et al. 2018).

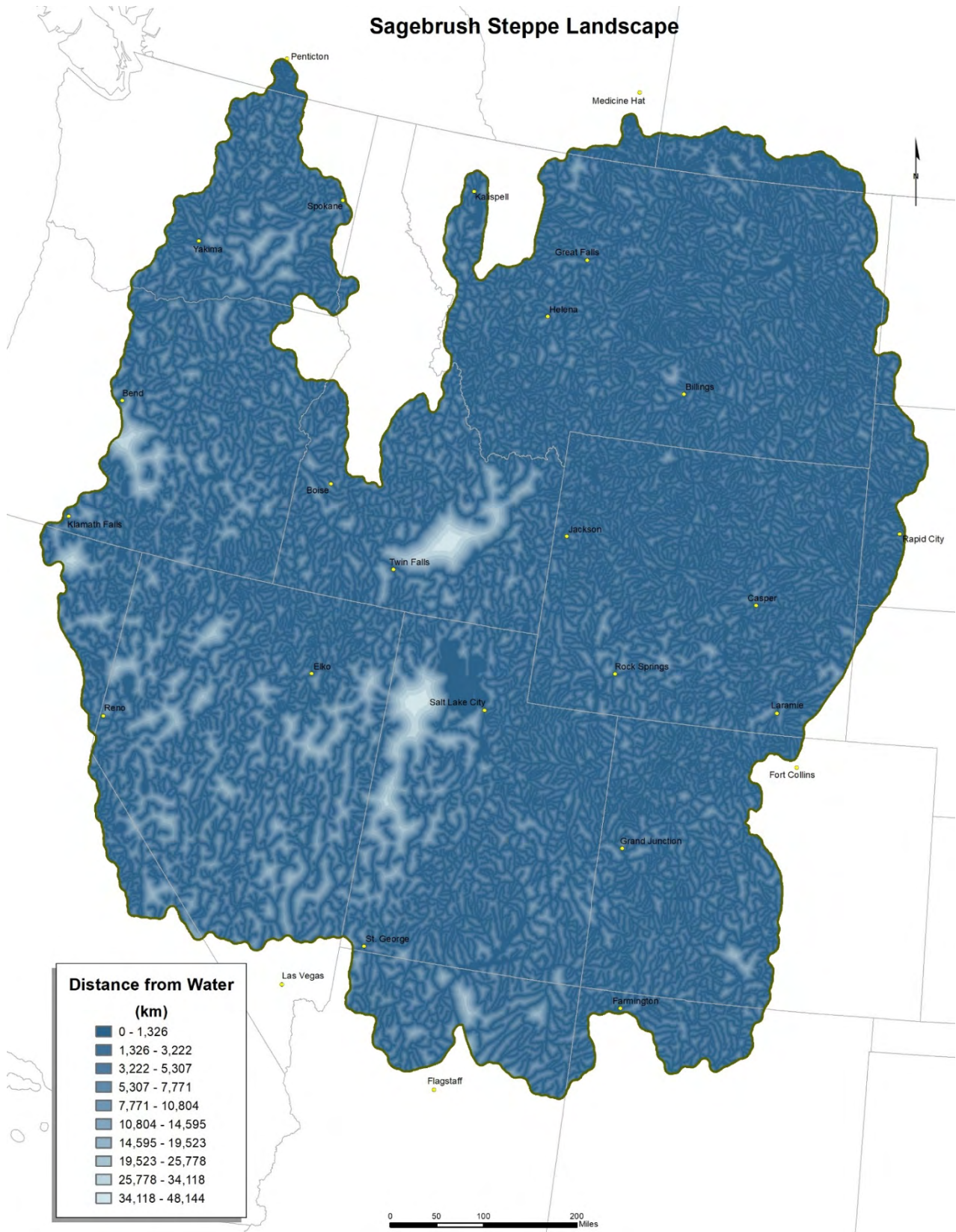


Figure 1.13. Distance (km) from open water calculated from USGS hydrography dataset (USGS 2010) for the U.S. and from CanVec Hydrographic Features (Natural Resources Canada 2018) for the Canadian portions.

This is a very large study area with high-resolution raster grids (10m x10m cell sizes), which resulted in approximately 13.2 billion grid cells per data layer. With so many data points for which to generate values, Maxent had difficulty building models with these datasets. To address this size limitation, I pre-processed the data outside of Maxent. Using QGIS (QGIS Development Team 2020), I overlaid the species observations and background points on the 19 covariate data grids and extracted the values from each covariate layer for each point, along with the coordinates of the points and saved these in comma-delimited (CSV) files. Creating these “samples with data” (SWD) files outside of Maxent kept it from freezing.

The results of running the Maxent models are spatially explicit models of the probability of habitat suitability for each species. Maxent outputs these raster grids as ASCII files, which, for this large area at 10m resolution, were extremely large (file sizes of many tens of gigabytes) and unreadable. I converted the ASCII rasters to .tif files, which reduced their sizes by about half and was a suitable format for subsequent steps.

Background data for Maxent models

Maxent requires background points from the area where species occurrences were sampled, to be able to tease apart species preferences for specific covariate values from those available in the background. If the background includes areas that were not sampled for species occurrences, the model will assume that the covariate values in those areas were being selected against because there were no recorded presence locations there, which can confound model predictions (Phillips et al. 2009). This problem arises when using publicly-collected species occurrence (GBIF) data because there was no sampling design and there tends to be spatial bias in the areas “sampled”. The majority of observations were opportunistically gathered (e.g., the observations tend to be near roads, cities, on public lands, and where the public expects to find species; (Reddy and D'avalos 2003, Boakes et al. 2010, Anderson 2012)). Also, different taxa

may be biased in different ways (Anderson 2003), e.g., song bird locations may primarily be reported by “birders” using public natural areas (Figure 1.14), whereas reptiles may primarily be reported on roads, having been observed or runover by drivers.

To be able to attribute the spatial distribution of species occurrences to habitat covariates instead of to sampling bias, the sampling bias needs to be accounted for in the models (Phillips et al. 2009, Elith et al. 2011). It has been shown that presence-only models are robust to sampling bias when the background points have the same bias as the occurrence points (Yackulic et al. 2013). The problem is that there is no reliable way to determine the sampling bias in the presence locations, because we cannot know whether the distribution of species observations is attributable to species habitat preferences or to observer sampling biases (Anderson 2003, Merow et al. 2014, El-Gabbas 2018). There is no definitive method to ensure that background points have the same spatial bias as the observation data (El-Gabbas 2018).

There are several methods proposed in the literature to deal with the sampling bias inherent in publicly-collected observation data (Zaniewski et al. 2002, Phillips et al. 2009, Mateo et al. 2010, Anderson and Gonzalez 2011, Kramer-Schadt et al. 2013, Syfert et al. 2013, Warton et al. 2013, Boria et al. 2014, Fourcade et al. 2014, Hertzog et al. 2014, Thibaud et al. 2014, Varela et al. 2014, Kiedrzyński et al. 2017, Vollerling et al. 2019). However, these methods vary in effectiveness across taxa (Ranc et al. 2017) or with the number of occurrence records (Anderson and Gonzalez 2011, Morales et al. 2017), and some researchers claim these methods are ineffective (Royle et al. 2012) or worsen model performance (Fourcade et al. 2014). The assessments of these methods are inconsistent and wide-ranging recommendations as to which methods might be best for different taxa, small sample sizes, or highly biased vs. slightly biased data (El-Gabbas 2018).

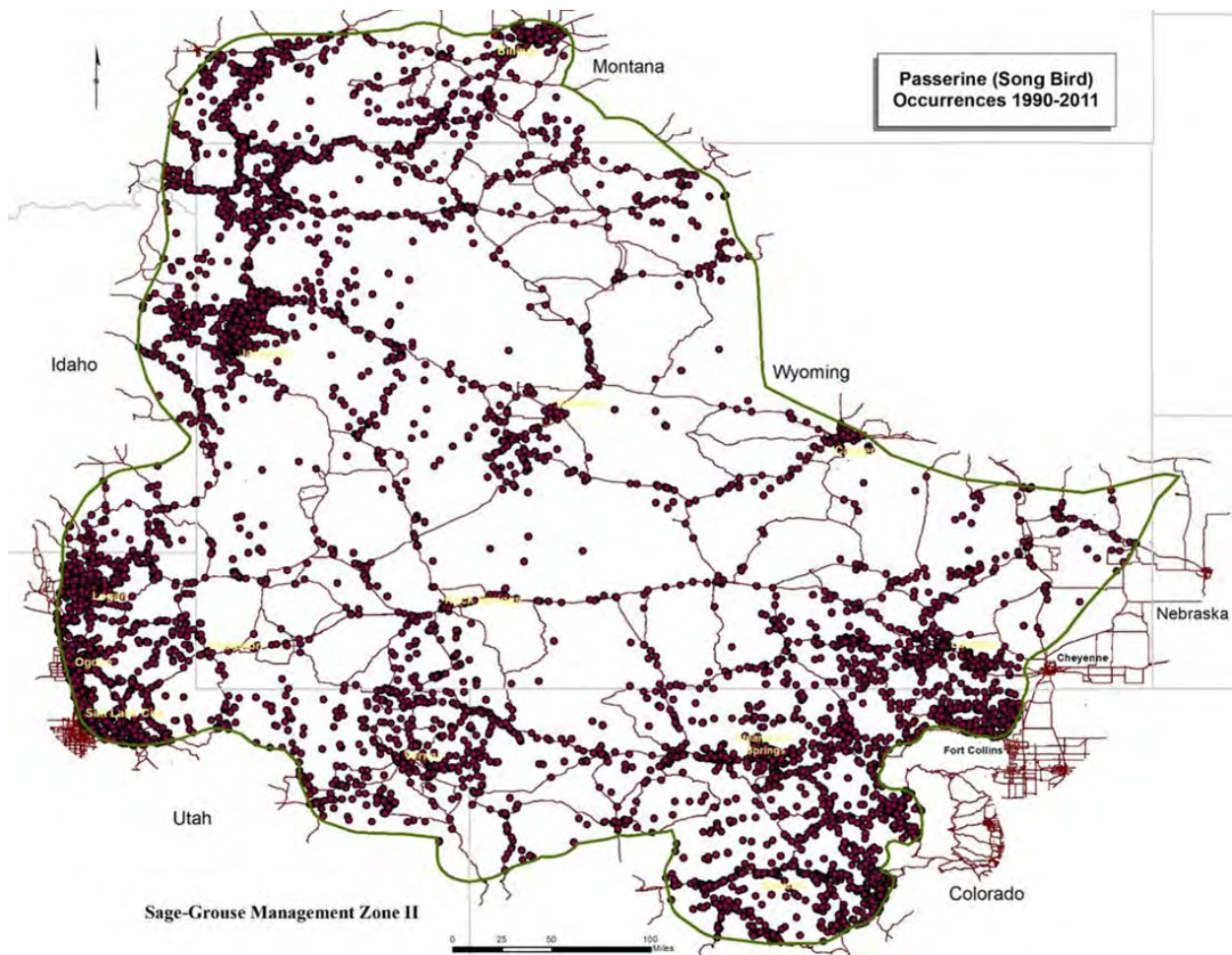


Figure 1.14. GBIF 1990-2011 observation records for song birds (GBIF 2022) in Sage-Grouse Management Zone II (USFWS 2015), showing sampling bias in the data, tending to be along roads and clustered near cities and parks.

I considered several potential methods of correcting for sampling bias. The target group method (Phillips et al. 2009, Syfert et al. 2013), which has shown positive results (Barber et al. 2022), uses observations of taxa that are similar to the target species as background points, assuming that people who report observations of similar taxa are revealing the areas “sampled” for the target species, since they would have reported the target species if they had observed it in these areas, as they did for similar taxa. Therefore, the observations of similar taxa should have the same spatial sampling bias as the target species, satisfying the criteria that background points have the same spatial bias. The problem with using observations of similar taxa as background

points is that there may not be enough of these observations for a good representation of the available covariate values in the background environment. Also, since these observations have the same spatial bias, they may be clustered (around cities, parks and roads), which can skew the distributions of background covariate values (Vollering et al. 2019).

A method proposed to deal with the problem of clustered observations is spatial filtering or thinning (Kramer-Schadt et al. 2013, Fourcade et al. 2014, Kiedrzyński et al. 2017). This method uses a grid laid over the study area to identify grid cells that have similar-taxa observations in them, then one observation location is randomly selected from each identified grid cell, which thins the clusters of observations (how much thinning depends on the size of the grid cells used). Another way this is done is to just randomly remove some of the observations that are within a certain distance of each other (Kramer-Schadt et al. 2013). A problem with this approach is that observations with information about species preferences are being removed from predicting suitable habitat. This is particularly a problem if there are not many observations spread across the study area, leaving only a few observations from a few areas, which may not provide a representative sample of preferred habitat values.

Another method proposed to deal with spatial sampling bias in the observation data is to model the sampling bias based on an assumed suite of accessibility “observer bias variables”, e.g., distance to main roads or cities, and to include these as potential predictor variables in the models (Warton et al. 2013). The issue with this approach is that these assumed barriers to accessibility of sampling sites may not be accurate predictors of observer bias - there may be other factors that bias sampling (e.g., species detectability, spatial auto-correlation) and, as stated, they may differ by taxa (e.g., observers may go farther afield to seek rare plants than birds).

Another proposed method to deal with sampling bias is to use a restricted background (Zaniewski et al. 2002) and have Maxent select background points only from these restricted

backgrounds. A suite of tools designed for ArcGIS, SDMtoolbox (Brown et al. 2017), create “bias files” to use in Maxent that restrict and weight areas of the background, which influences where and how Maxent selects background points. These tools use different methods (e.g., Gaussian kernel density of sampling, buffered local adaptive convex-hull) to demarcate boundaries around similar-taxa observations (weighted, if desired), and identifies restricted background areas. The problem with this approach is that there is no objective basis on which to determine which parameters are appropriate to use to demarcate background boundaries. This approach may also arbitrarily remove areas of the background that were actually sampled, adversely effecting model results (Jarnevich et al. 2016). Also, when bias files were attempted to be used within Maxent, with these very large extent data layers, it stalled and was unable to select background points.

Given the issues with these different approaches, I created a hybrid approach using a geographic information system (ESRI 2020), that attempts to address all these issues: identifying and restricting the background to areas “sampled”, ameliorating clumped observations and spatial auto-correlation, while providing a sufficient number of background points to provide a comprehensive representation of the covariate values across the sampled background area.

I used observations of similar taxa as target species to demarcate the area sampled ([Appendix A - Group Column](#)) and downloaded all observations within the study area for 21 taxa groups from GBIF for the same years (1990-2011) as the target species. The taxa groups were:

- Cacti
- Grasses
- Vines
- Forbs/herbs
- Subshrubs/dwarf shrubs
- Shrubs
- Mollusks
- Insects
- Spiders
- Amphibians
- Reptiles
- Galliformes
- Owls
- Song birds
- Wading birds
- Bats
- Small mammals
- Meso-mammals
- Ungulates

I created a buffer around these locations in ArcGIS. After experimenting with different buffer sizes, I chose 45 km because this distance tended to connect observations along roads, which reduced dividing these likely sampled areas. I then calculated the area of each of these polygons and filled each with randomly placed points so that they averaged 1 point per km², which was enough to adequately represent small and linear features in the landscape, while spaced at least 30m apart - the cell size of the landcover map, to avoid spatial autocorrelation of background points, using the ArcGIS tool Generate Random Points (Figures 1.15-1.17). If this procedure resulted in more than 100,000 points for the background, I subsampled them, selecting a random subset of 100,000 points. This was a sufficient number of points to use in Maxent to represent the background area, while not overwhelming the program.

Restricting habitat to species' ranges

While prediction beyond current species ranges may be useful for inferring potential habitat suitability (e.g., for invasive species or climate change-related range shifts), I restricted predictions to known species ranges because my interest was to inform conservation design for the current period (Figure 1.18 - example for Great Basin spadefoot toad). I used range maps for amphibians, reptiles, birds, and mammals created by NatureServe and maintained by the International Union for the Conservation of Nature (NatureServe and IUCN 2018) to restrict the distributions of predicted habitats. I used the ArcGIS Multi-Ring Buffer tool to create nine concentric 25 km buffers around the species ranges, weighted them from closest to farthest: 0.9, 0.8, 0.7... 0.1, with 0 outside the last buffer to account for uncertainty in the precise boundaries of species' ranges. I then converted the polygon layer to a raster and multiplied the predicted suitable habitat layer by this range-restricting layer (Figure 1.19 - example for Great Basin spadefoot toad). This resulted in maps with the original suitable habitat probabilities within the

species ranges and values decaying to 0 at 225 km outside their ranges (Figure 1.20 - example for Great Basin spadefoot toad).

Digital range maps were not available for plants, so for plant species that were not widespread, I created ranges using observation locations. I generated convex hull boundaries around the observation and added small (10km) concentric buffers around the boundaries to allow for uncertainty in the boundaries (Figures 1.21 and 1.22 - example for the tufted globemallow). I then multiplied the Maxent habitat models (Figure 1.23 - example for the tufted globemallow) by the restricted range layers (Figure 1.24 - example for the tufted globemallow).

There were nine species (seven mammals, one snail, and one spider) with too few observations with which to derive habitat suitability models (see [Appendix A](#)), so I used the same procedure for plants to create range-restricted predicted suitable habitat layers for these species.

One rattlesnake was a special case. This taxon is currently classified as 2 separate species, *Crotalus viridis* and *C. oreganus*, with *C. oreganus* divided into 3 subspecies, all having non-overlapping ranges (Figure 1.25). In this case, with ranges adjacent to each other, I used smaller (5 km) concentric decaying buffers around each range (Figure 1.26). The buffers were added to allow for some range overlap and for uncertainty in species/subspecies designations in the boundary areas, not to demarcate the extent of their overall range. I then multiplied the Maxent models (Figure 1.27) by the restricted range layers to produce habitat models specific to each subspecies (Figure 1.28).

Model fit

For a check on model fit, I ran 10 replicates of the models with bootstrapping (sampling 10% of the data with replacement) to produce an average ‘Test AUC’ (area under the receiver operating characteristic curve) score for the 10 replicates. For models with less than 10 location points, I used leave-one-out cross-validation to produce the Test AUC values, since bootstrapping

could not be done with so few points. The area under the receiver operating characteristic (ROC) curve, or AUC metric, is used to provide an assessment of how well the models fit a proportion of withheld data (Raes and ter Steege 2007, Lobo et al. 2008, Jiménez-Valverde 2012, Aguirre-Gutiérrez et al. 2013). Although the AUC metric is not reliable with presence-only data (Jiménez-Valverde 2012, Fourcade et al. 2018, Vollerling et al. 2019, Jiménez and Soberón 2020), it was useful for identifying models that significantly diverged from their input data.

Incorporating habitat contiguity

The Maxent model outputs depict spatially explicit probability of suitable habitat for each species, but they do not include factors such as habitat aggregation or connectivity in their computations. Species select preferred habitat at a gradient of scales, from landscapes (e.g., sagebrush steppe) to local (e.g., a sagebrush patch with a certain cover density at a specific distance from grass and water) to precise (e.g., a particular shrub to nest under) (Johnson 1980, Wiens and Rotenberry 1981, Wiens et al. 1987, Wiens 1989), therefore suitable habitat has to be considered across this gradient of scales. Moreover, it has been shown that aggregation of habitat increases species probability of persistence (Saunders et al. 1991, Collinge 1996, Noss et al. 1997, Dale et al. 2000, Cabeza and Moilanen 2001, Kennedy et al. 2003, Reed et al. 2006, Fischer and Lindenmayer 2007, Wilson et al. 2016, Crooks et al. 2017, Ofori et al. 2017, Fletcher et al. 2018a, Schivo et al. 2020, Althagafi and Petrovskii 2021, Grimmett et al. 2021).

Patch sizes and fragmentation of sagebrush, shrub, and grass vegetation classes were available as model covariates and may have been selected in some models as partial determinants of suitable habitat. Once suitable habitat was predicted for each species, from a combination of environmental variables, I derived spatially explicit, multi-scale measures of each species' habitat contiguity (the inverse of fragmentation) using the probabilities of habitat suitability generated by Maxent. Since the effects of contiguity/fragmentation on species populations is species and scale

dependent (Fletcher et al. 2018b), I modified the procedures of the fragmentation assessment of Vogt (2018), used on the 3 vegetation classes mentioned above, to calculate habitat contiguity for each species, at scales from local to landscape. The resulting maps spatially depict habitat values generated from a combination of habitat contiguity and (the probability of) suitability, which I call fundamental habitat, that identify areas more likely to support population persistence.

Since the Maxent output raster grids were very large, even after converting them from ASCII to tiff formats, I used ArcPy, Python language (Python Software Foundation 2020) scripts written to execute ArcGIS procedures on a high performance computing (HPC) system (USGS Advanced Research Computing 2020) with terabytes of RAM available to execute the following procedures. The habitat suitability layers produced by the Maxent models are raster grids with continuous probability values ranging from 0 to 1. To make the layers usable for successive operations, I used Reclass to reclassify the values to integers 0, 1, 2, 3... 10 (Table 1.2).

Table 1.2. Ranges of continuous Maxent model probability of suitability values reclassified to integers.

Non-Habitat	
0.0 – 0.0 = 0	
Habitat Values	
> 0.0 – 0.1 = 1	> 0.5 – 0.6 = 6
> 0.1 – 0.2 = 2	> 0.6 – 0.7 = 7
> 0.2 – 0.3 = 3	> 0.7 – 0.8 = 8
> 0.3 – 0.4 = 4	> 0.8 – 0.9 = 9
> 0.4 – 0.5 = 5	> 0.9 – 1.0 = 10

I incorporated contiguity into the habitat values by modifying an approach used by the European Union to evaluate land cover fragmentation (Vogt 2018). This approach is preferable to other methods because it does not require species-specific delineations of patches vs. matrix, nor assumptions about species use or scale of use of habitat or corridors. To evaluate the amount of suitable habitat around each cell at multiple scales, I ran four different size moving-windows

(81x81 cells, 321x321 cells, 1001x1001 cells and 3163x3163 cells, which were roughly 0.66 km², 10 km², 100 km² and 1,000 km², respectively) over the habitat suitability maps of each species. The 1,000 km² size window was included to encompass landscape-scale connectivity. The “landscape-scale” was determined based upon reports in the literature as the estimated size of habitat patches required to sustain sage-grouse populations, the species considered to require the largest areas in this biome (Connelly et al. 2004, Connelly et al. 2011, Stiver et al. 2015). The moving-windows at the four different scales summed the values of habitat suitability (converted to integers 0-10) within the window and placed the sum in the center cell, then moved to the next cell. The result was four layers for each species with the value of each cell containing the sum of habitat suitability values from the different sized windows (spatial scales) around the cell.

For example, if a target cell in the 10 km² scale analysis was in the middle of a completely intact patch of perfectly suitable habitat (values of 10), it would have a value of 1,030,410 (103,041 cells with habitat suitability values of 10). The value indicates both how intact and how suitable the habitat is around the center cell. Small habitat patches or scattered habitat will have non-habitat (0s) in many of the cells in the window, producing a lower value in the center cell. Also, if the habitat suitability around the target cell has smaller probabilities of being suitable (< 10), that also reduces the value of the cell in the center. Habitat values then reflect combined habitat suitability and contiguity at that scale. I averaged the standardized values from the four scales together along with the original Maxent suitable habitat layer for a multi-scale density of suitable habitat around each cell. I standardized these values as integers ranging from 0 to 100 to create maps of continuous habitat values reflecting the combined habitat suitability and multi-scale contiguity for each species (Figure 1.29 - examples for four species).

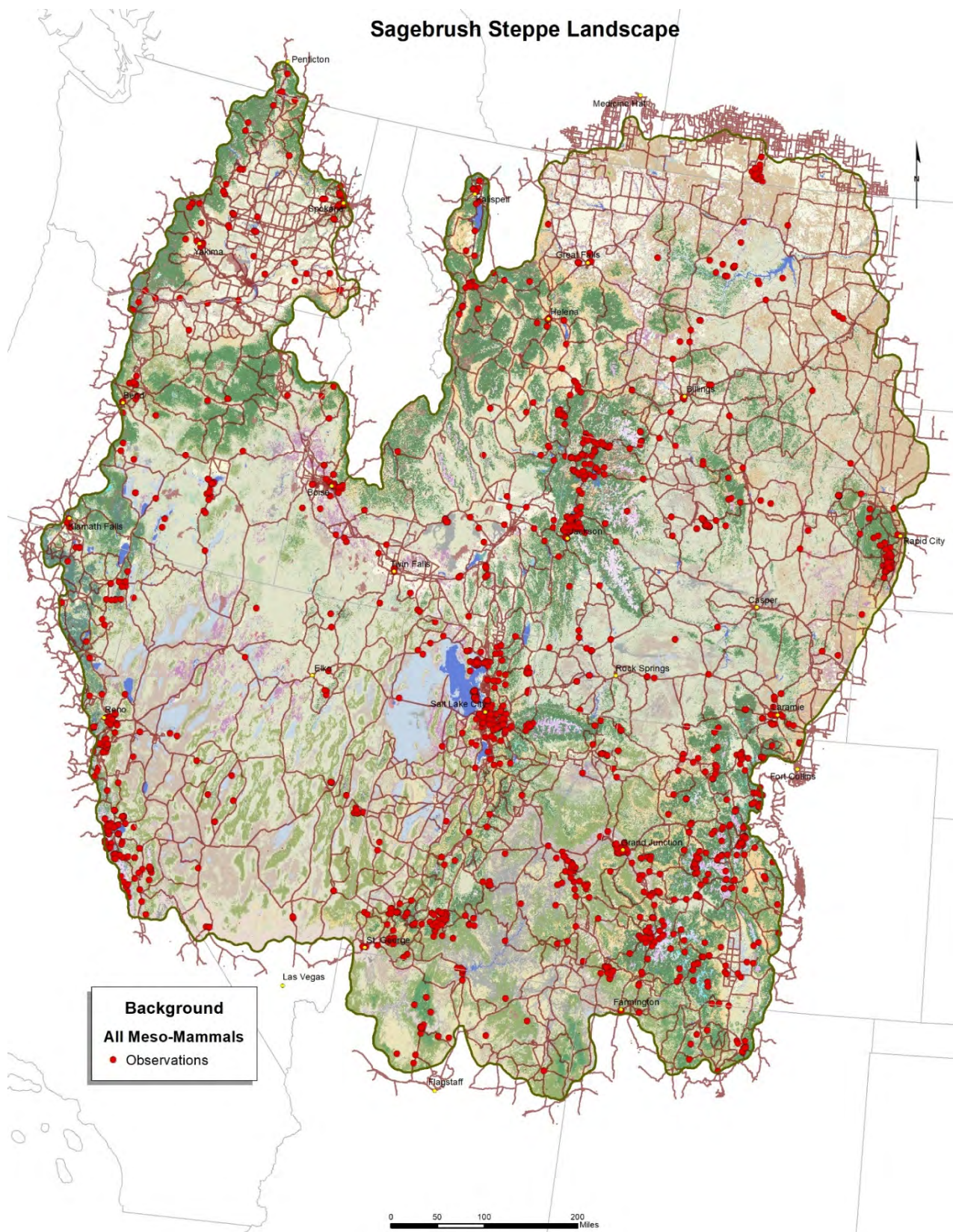


Figure 1.15. GBIF records (GBIF 2022) for all meso-sized mammals that were observed in years 1990-2011 (Appendix B) used to delineate the area “sampled” for this group of species.

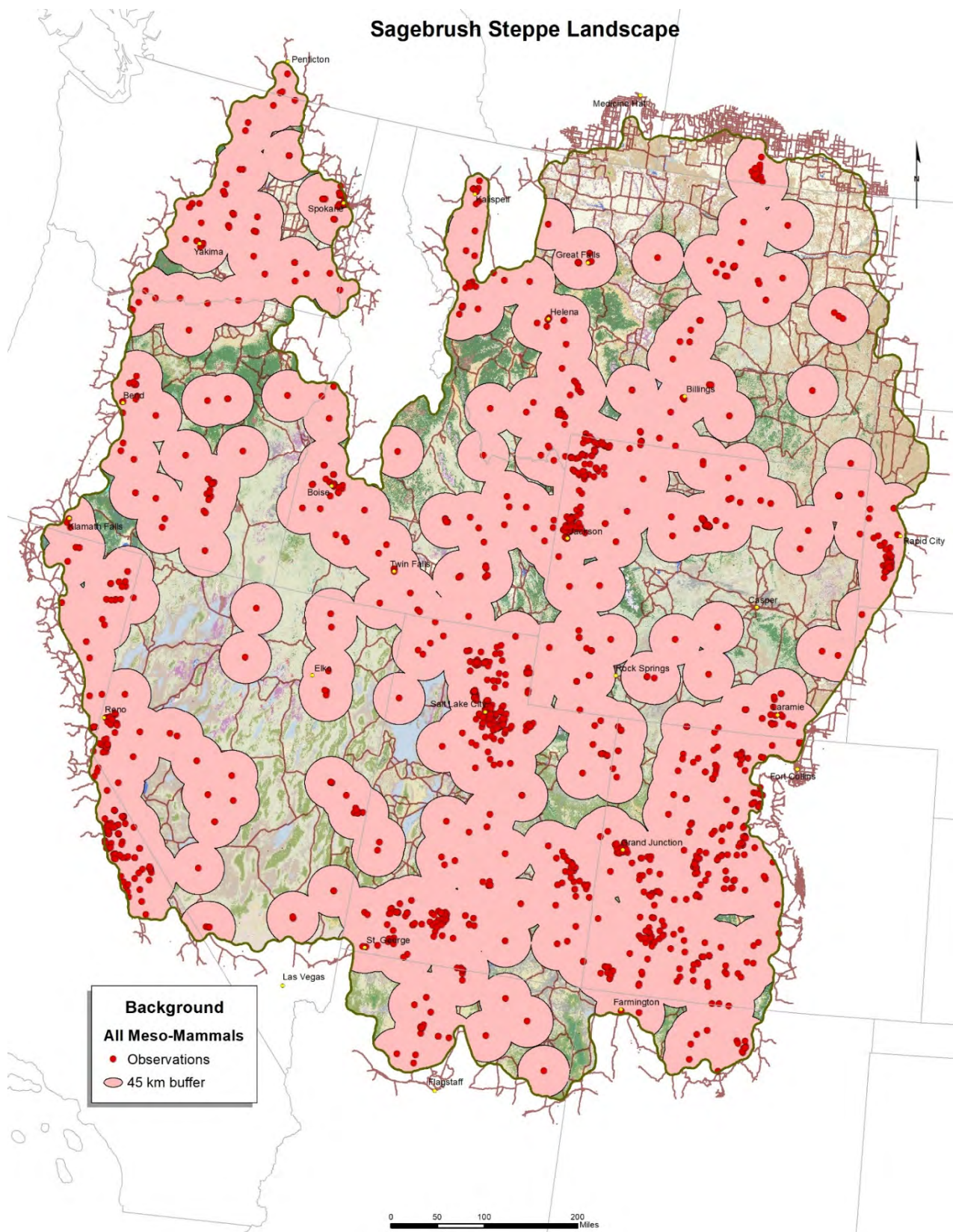


Figure 1.16. GBIF records (GBIF 2022) for all meso-sized mammals that were observed in years 1990-2011 with 45km buffers used to delineate the area “sampled” for this group of species.

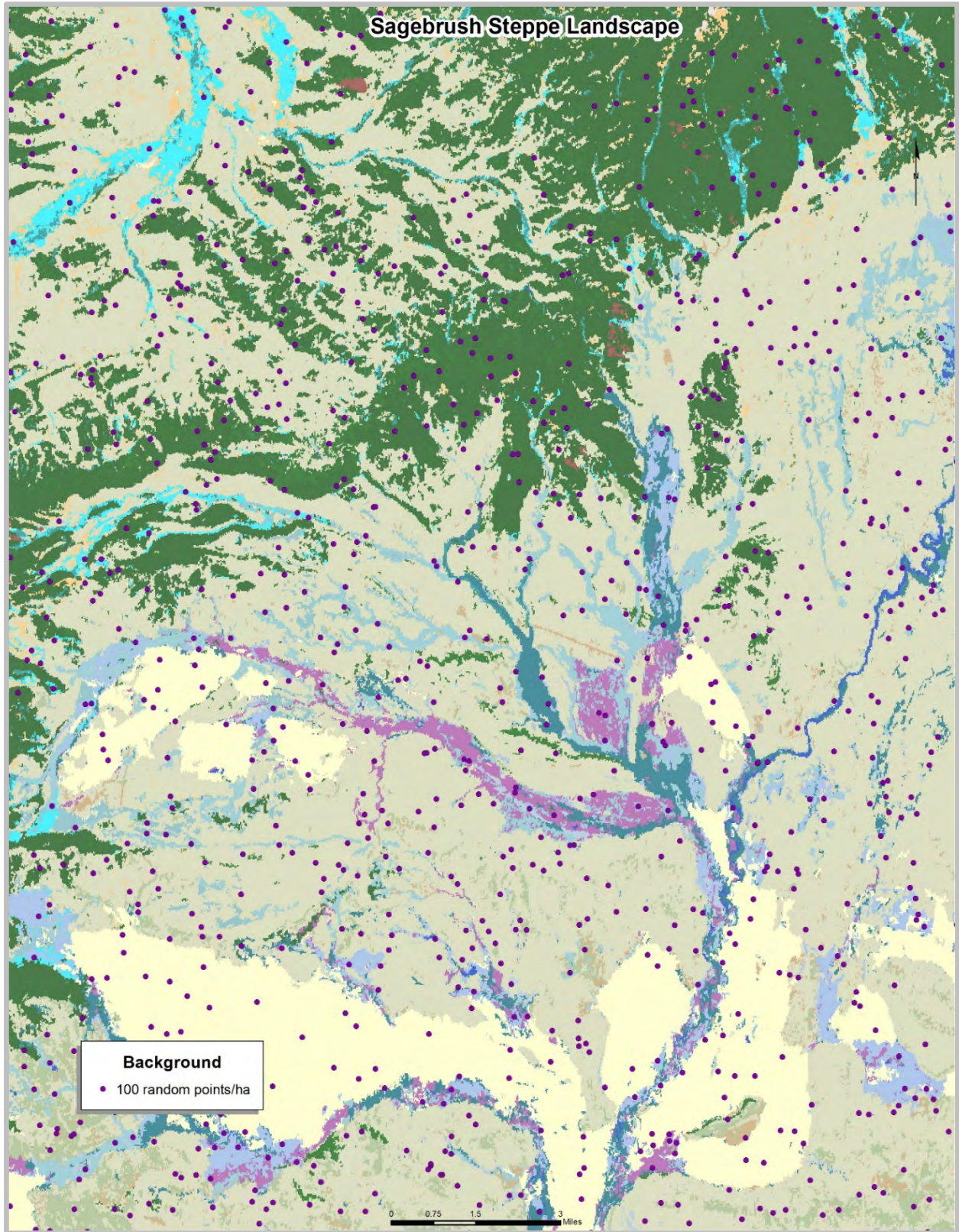


Figure 1.17. Background points used in Maxent models for meso-sized mammals, randomly placed at an average density of about a point/km² (at least 30m apart) were sufficient to capture small and linear features.

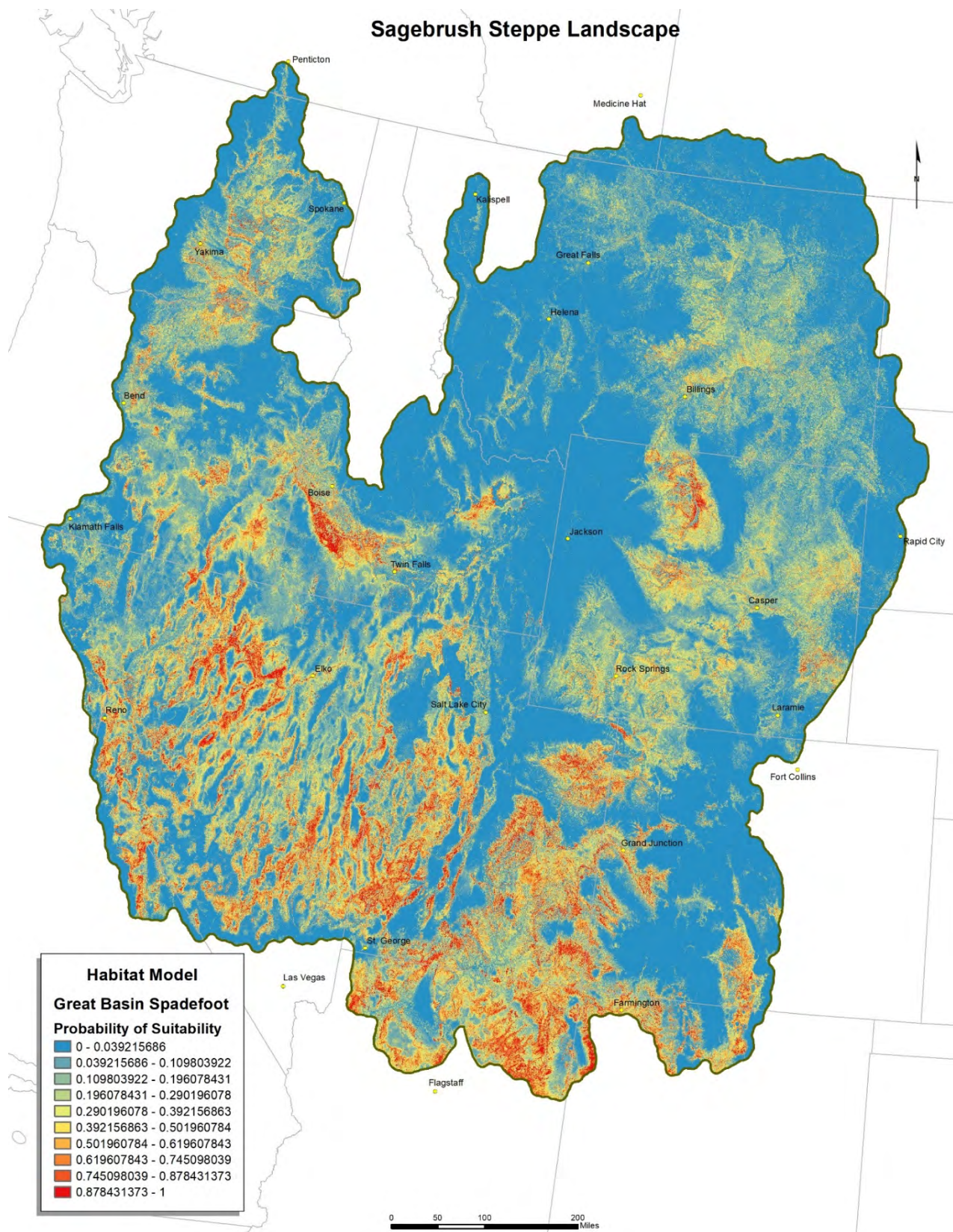


Figure 1.18. Maxent model output showing probability of habitat suitability for the Great Basin spadefoot toad (*Spea intermontana*).

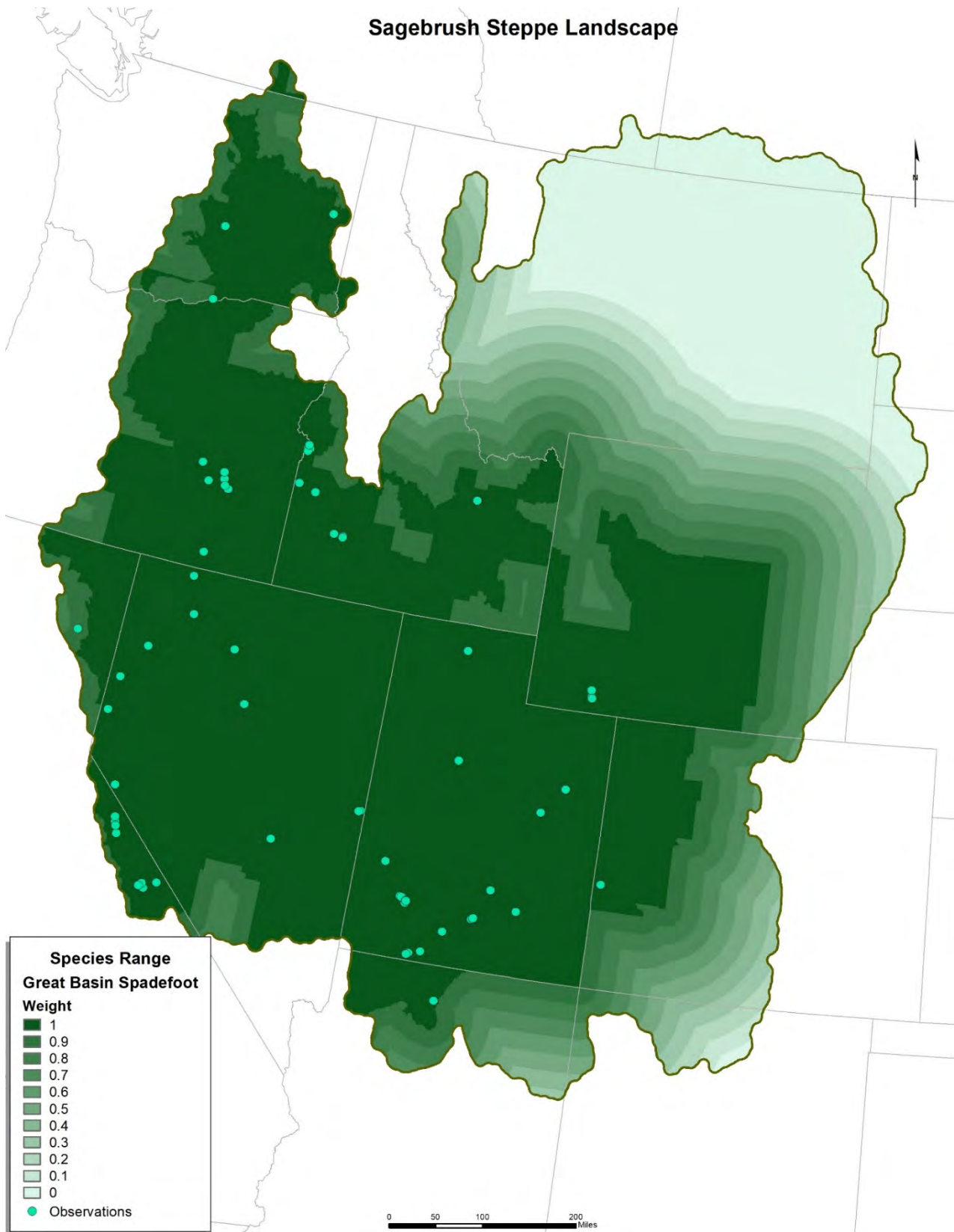


Figure 1.19. Observations (GBIF 2022) and range (NatureServe and IUCN 2018) of the Great Basin spadefoot toad (*Spea intermontana*) with concentric decaying 25km buffers weighted from 1 (within) to 0 (outside) their range.

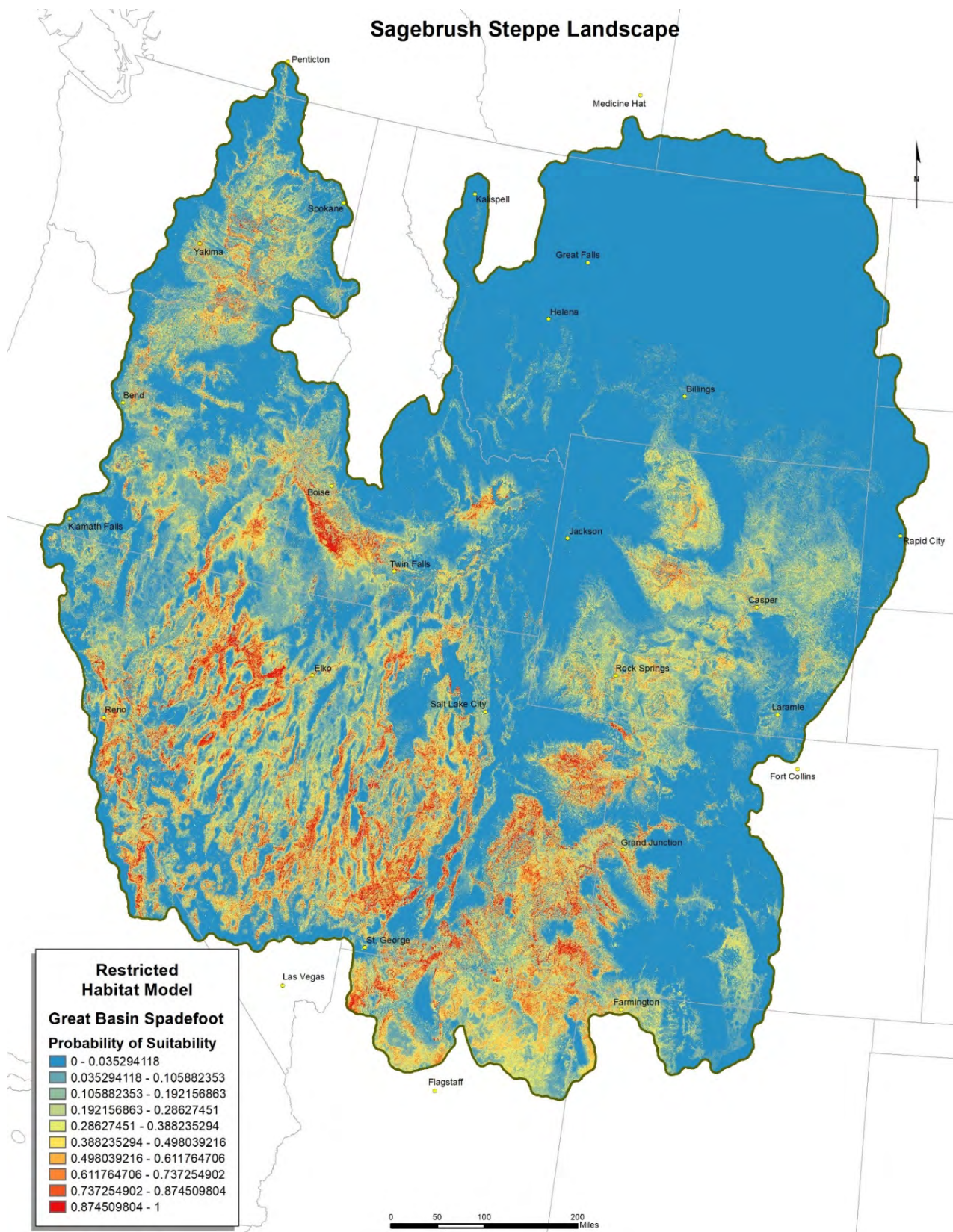


Figure 1.20. Maxent habitat suitability model for Great Basin spadefoot toad (*Spea intermontana*) multiplied by range map weights to restrict predicted suitable habitat to the approximate range of the species.

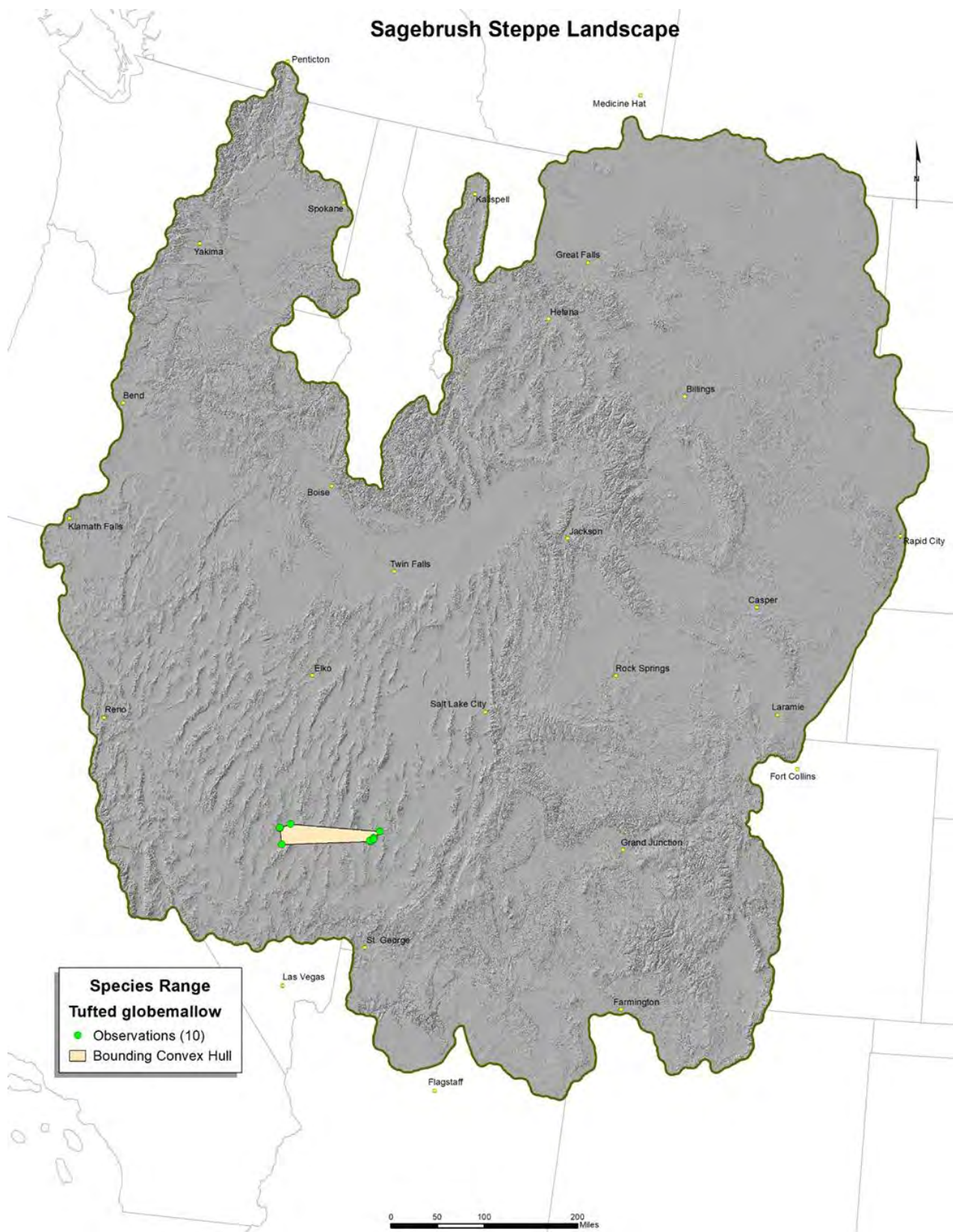


Figure 1.21. Locations (GBIF 2022) of the tufted globemallow plant (*Sphaeralcea caespitosa*) with convex hull drawn around observations to demarcate current known range of species.

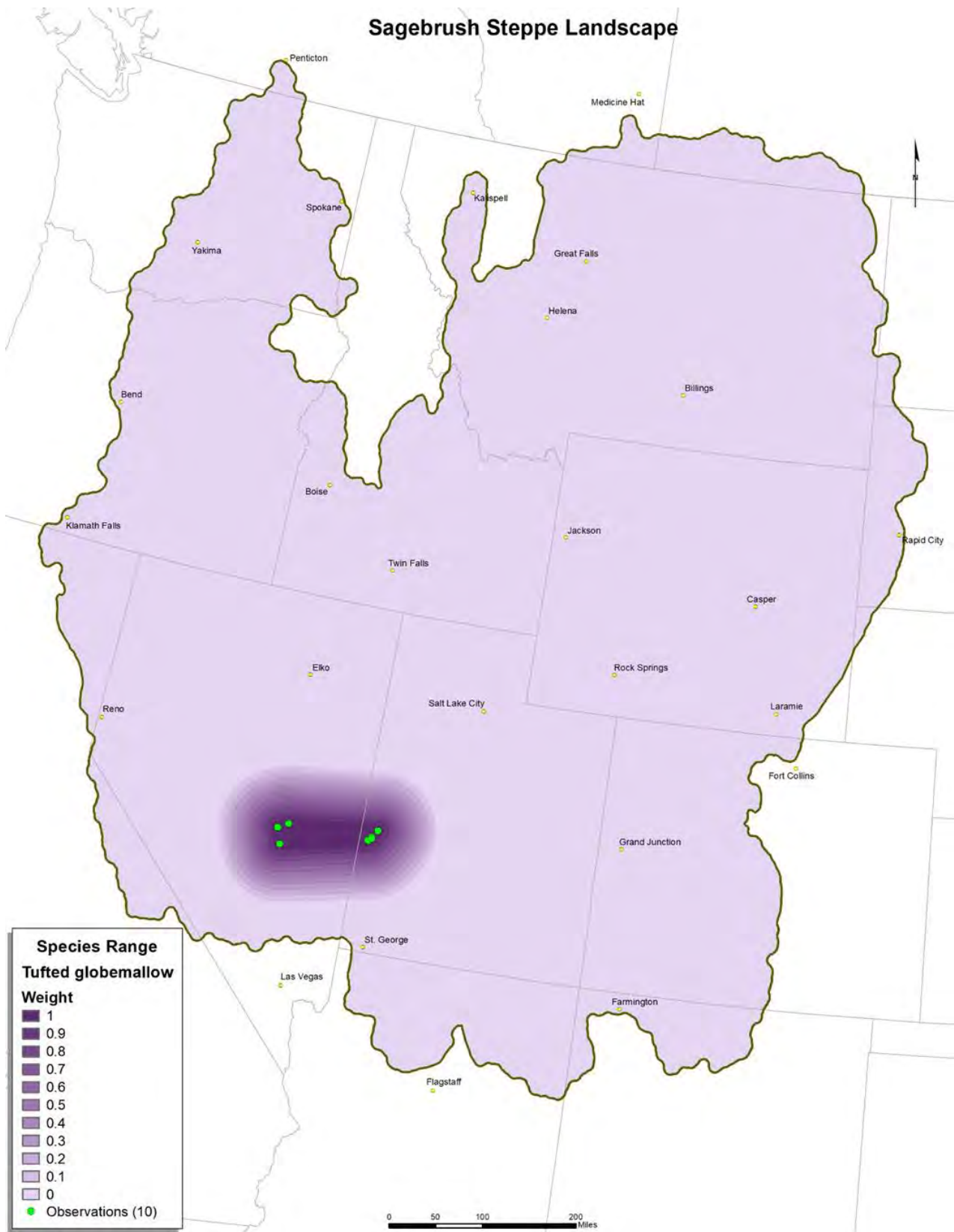


Figure 1.22. Locations (GBIF 2022) of the tufted globemallow plant (*Sphaeralcea caespitosa*) with concentric decaying 10km buffers weighted from 1 to 0.

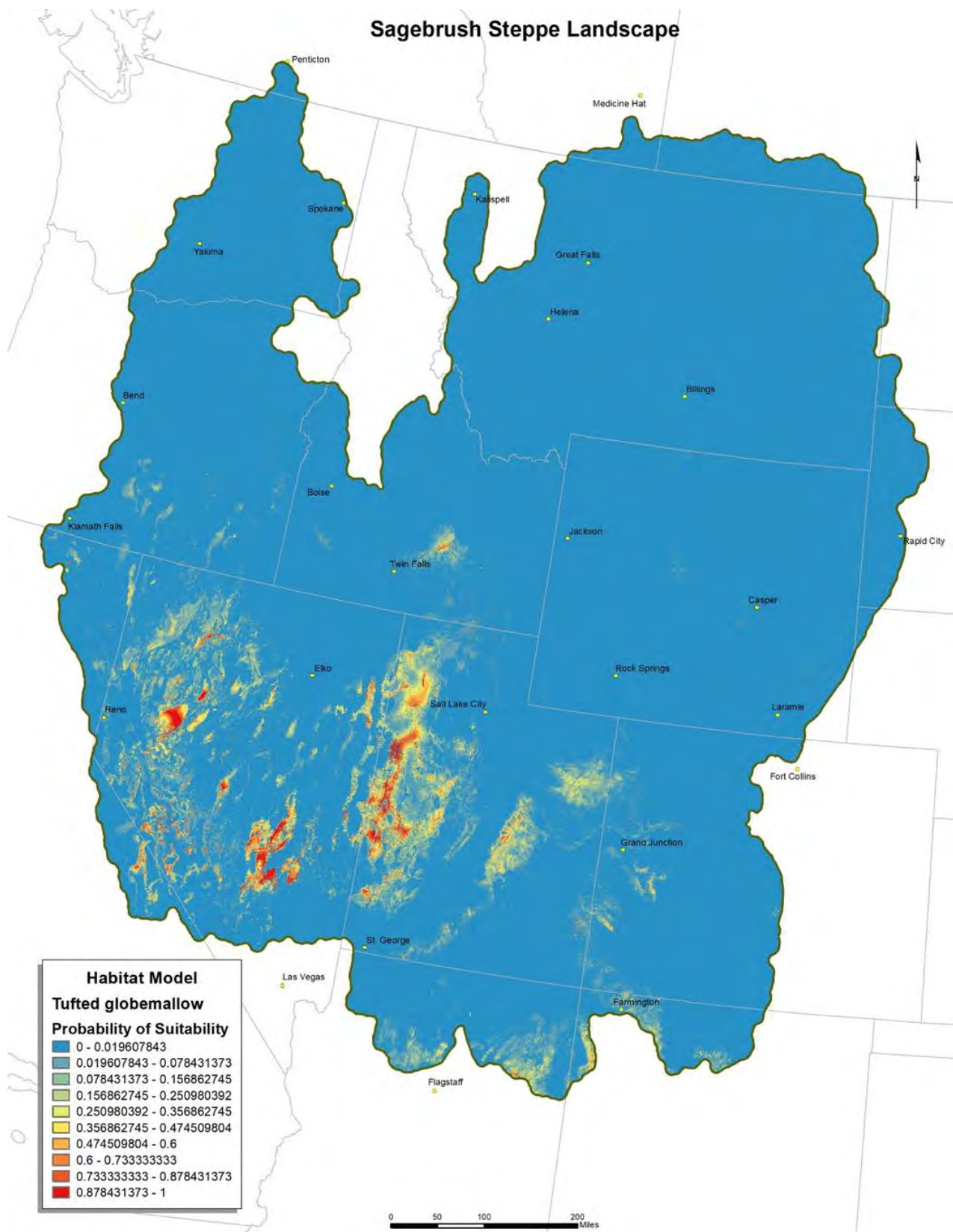


Figure 1.23. Maxent habitat suitability model for tufted globemallow plant (*Sphaeralcea caespitosa*).

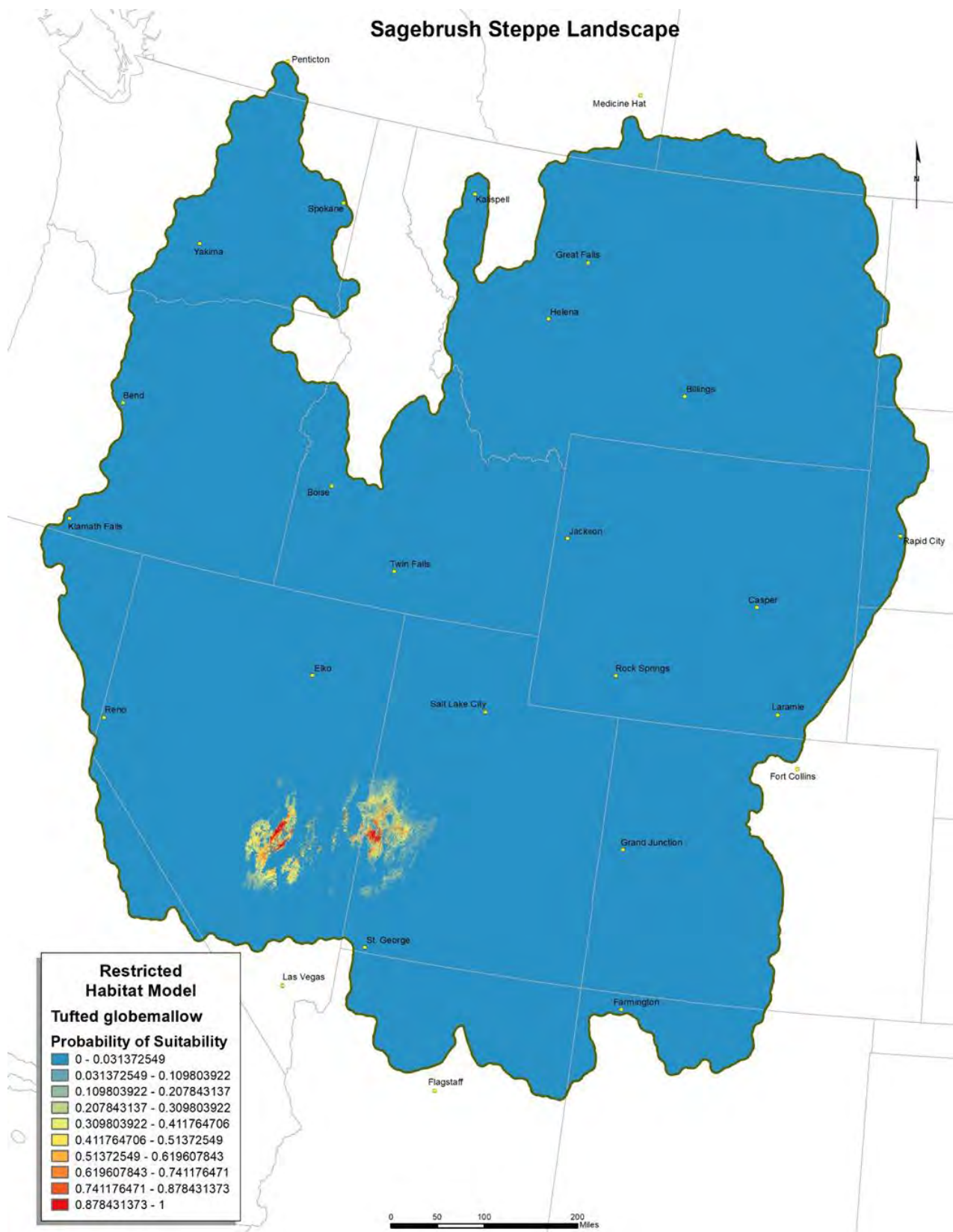


Figure 1.24. Maxent habitat suitability model for tufted globemallow plant (*Sphaeralcea caespitosa*) multiplied by range map weights to restrict predicted suitable habitat to the approximate range of the species.

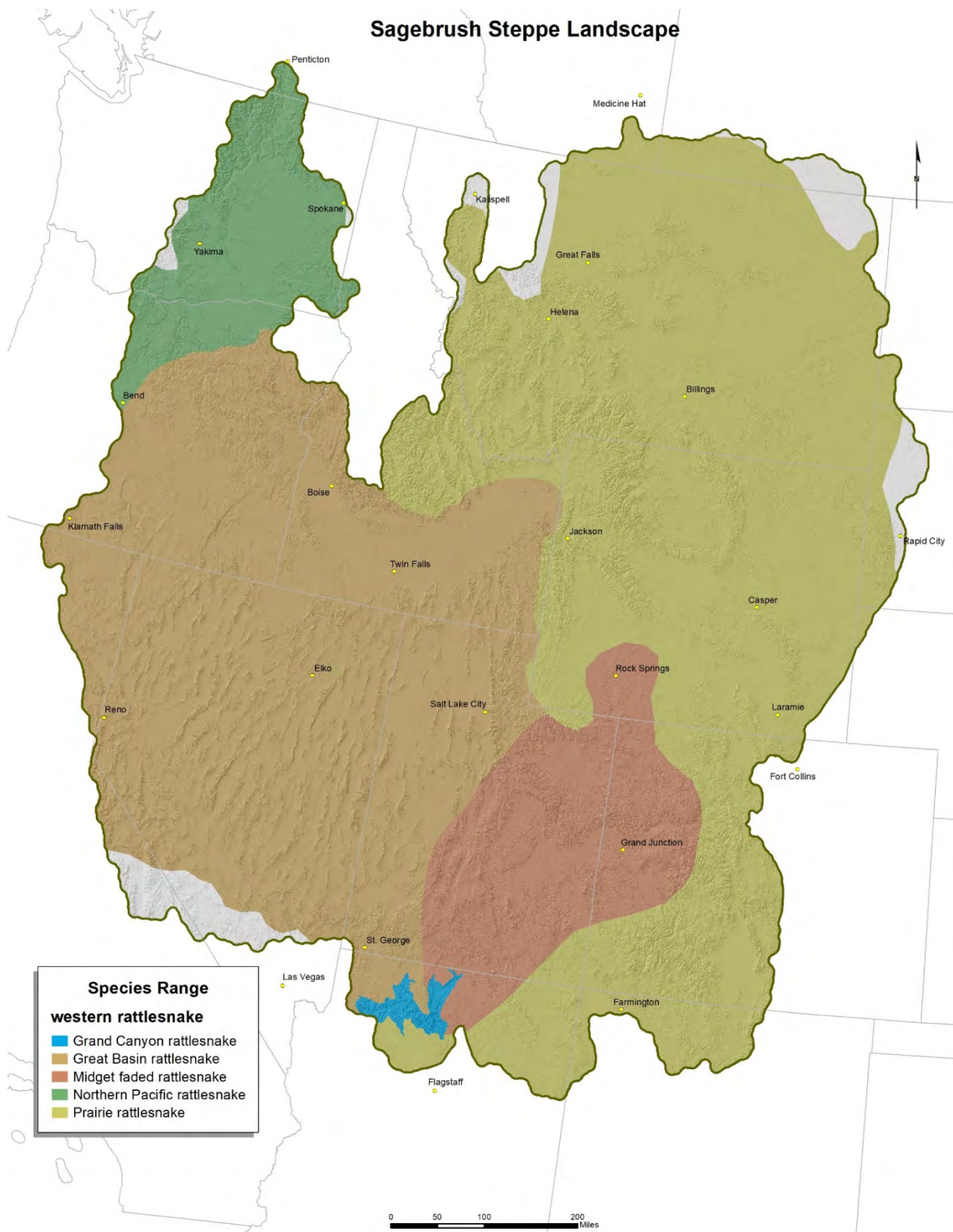


Figure 1.25. Non-overlapping ranges (NatureServe and IUCN 2018) of the western rattlesnake *Crotalus viridis* and *Crotalus oreganus* subspecies.

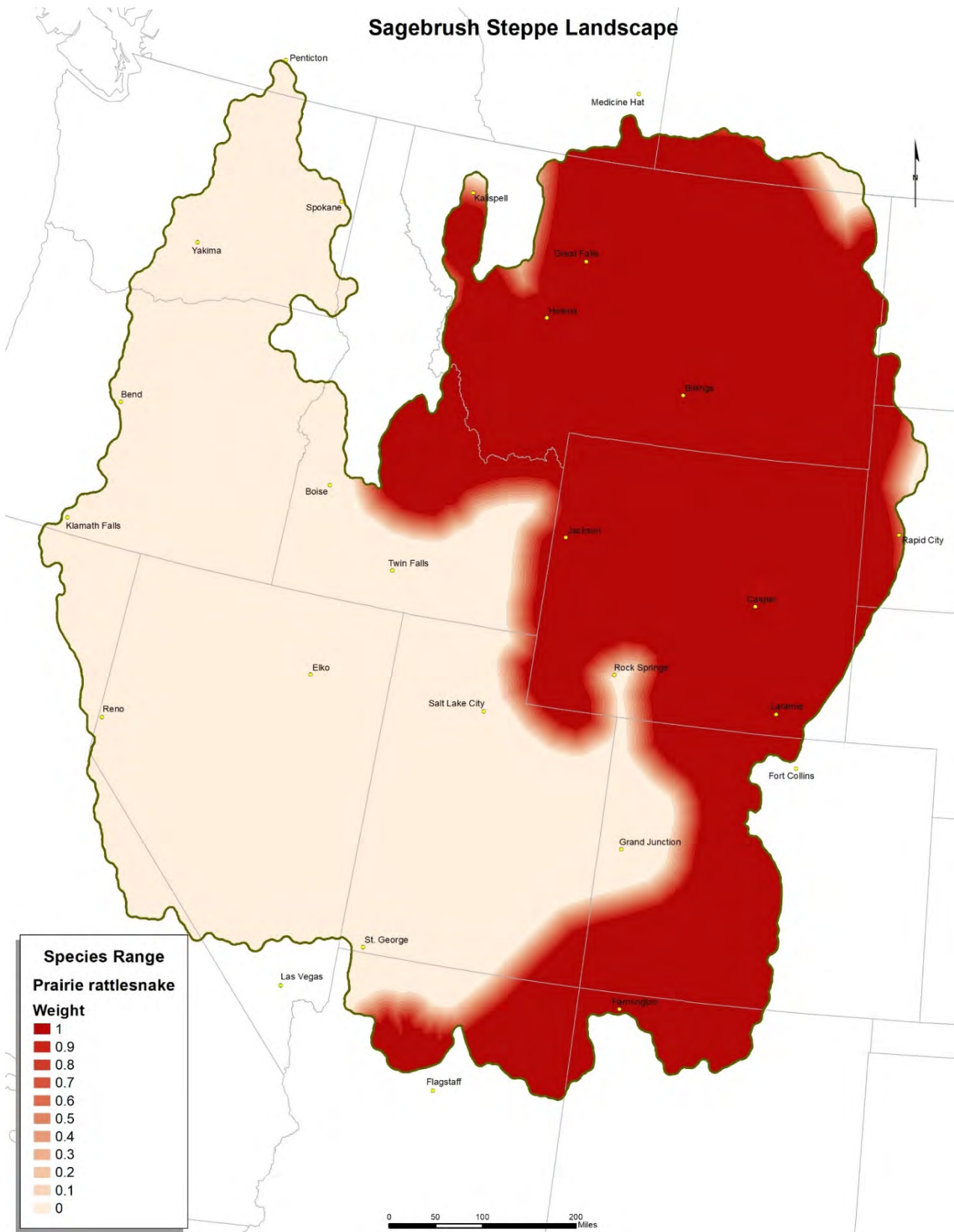


Figure 1.26. Prairie rattlesnake (*Crotalus viridis*) range with concentric decaying 5km buffers weighted from 1 to 0.

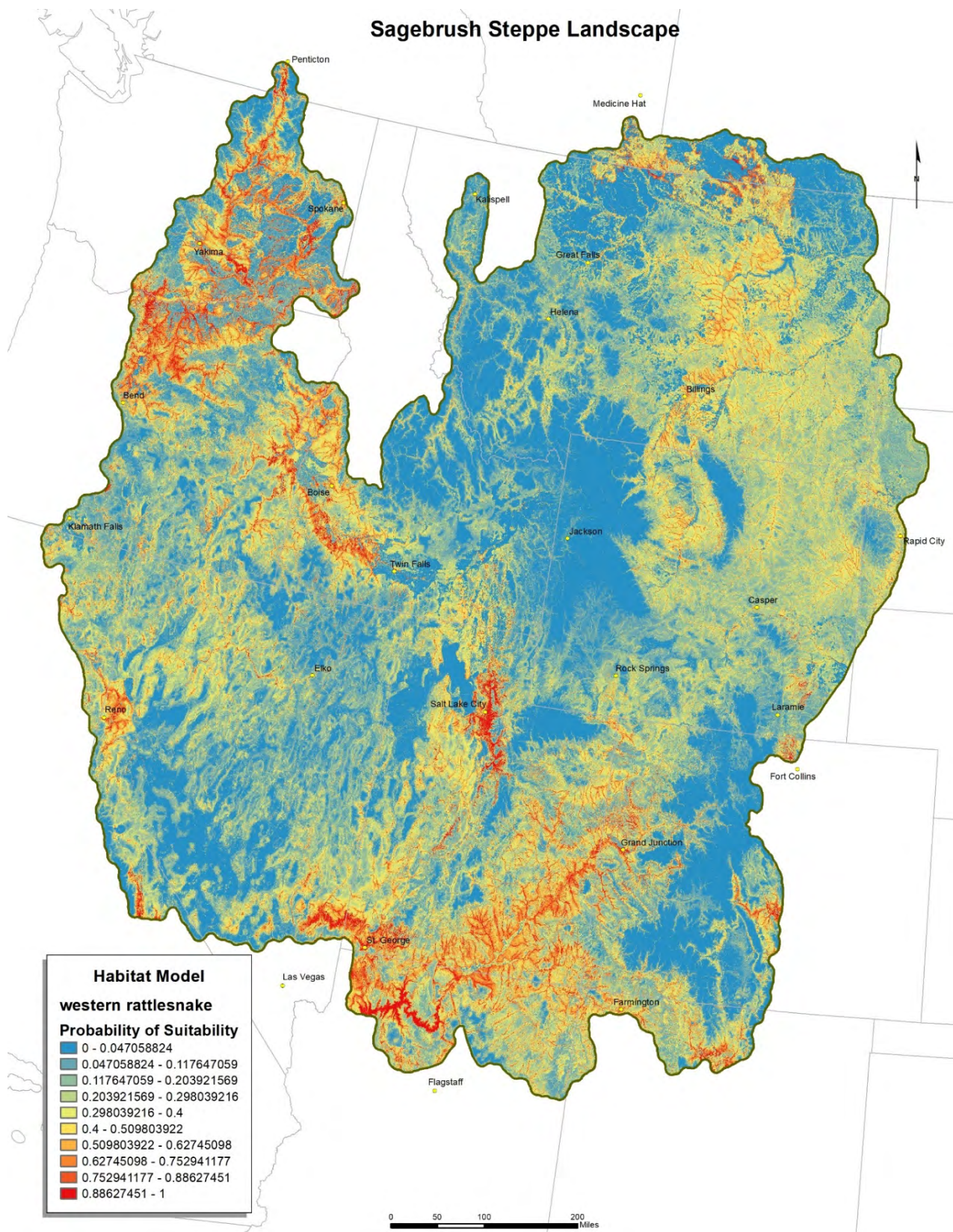


Figure 1.27. Maxent model output showing probability of habitat suitability for western rattlesnake *Crotalus viridis* and *Crotalus oreganus* subspecies.

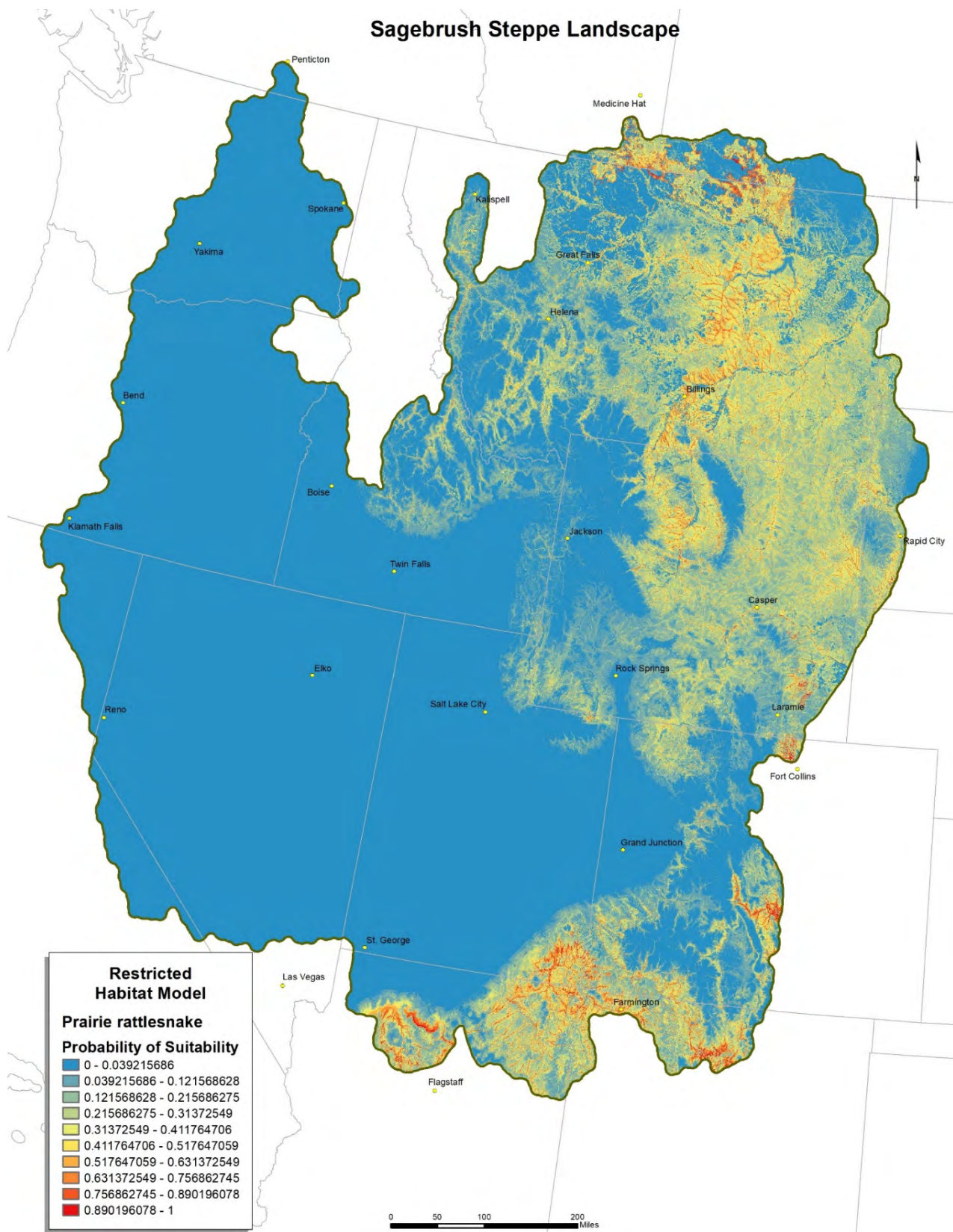


Figure 1.28. Maxent habitat suitability model for prairie rattlesnake (*Crotalus viridis*) multiplied by range map weights to restrict predicted suitable habitat to the species range.

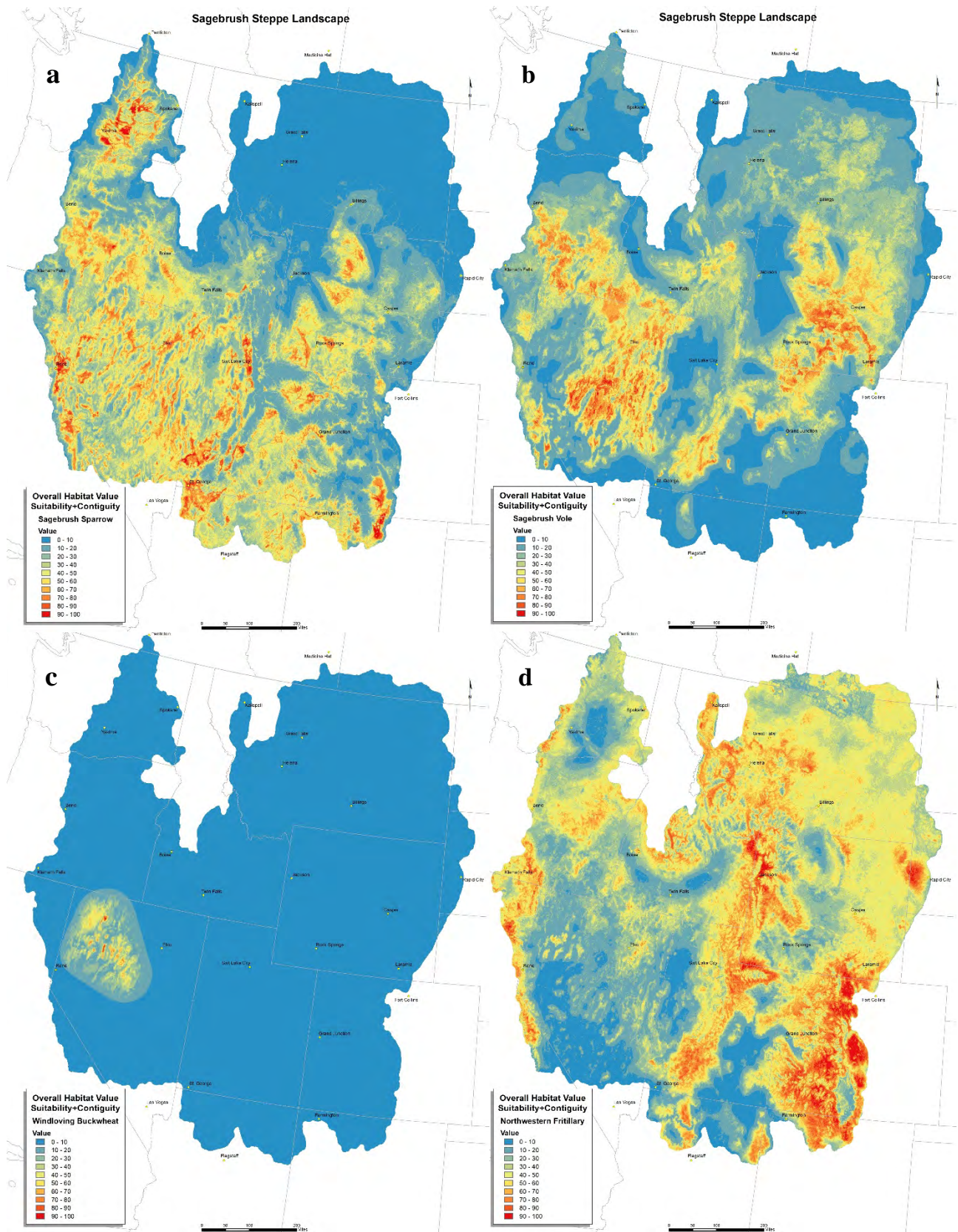


Figure 1.29. Example fundamental habitat maps for a) Sagebrush sparrow (*Artemisiospiza nevadensis*), b) Sagebrush vole (*Lemmyscus curtatus*), c) Windloving buckwheat (*Eriogonum anemophilum*) and d) Northwestern fritillary (*Speyeria hesperis*). These fundamental habitat maps were developed for 164 obligate sagebrush steppe species.

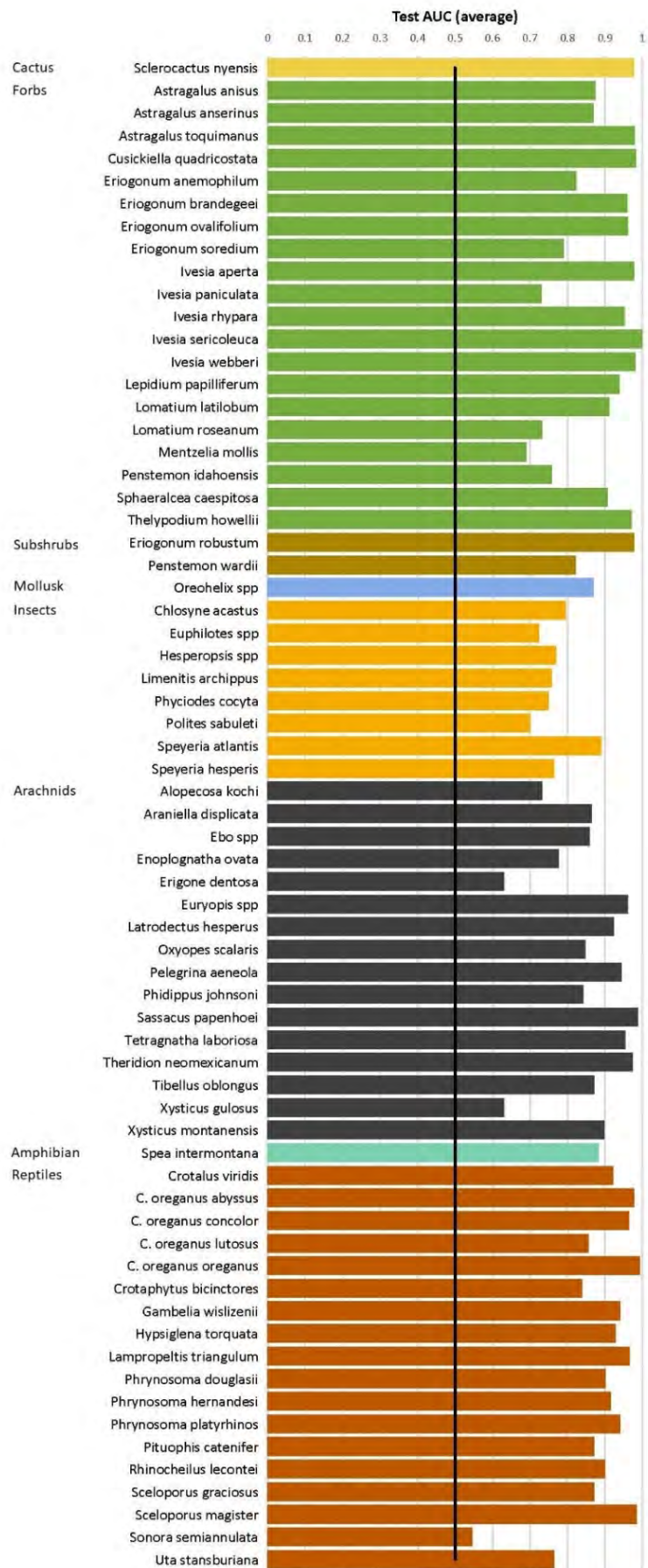
RESULTS

I developed methods to successfully overcome the impediments to creating large-scale, high-resolution habitat models for a wide range of taxa, including data-poor species, incorporating contiguity into fundamental habitat maps for 164 obligate taxa of the sagebrush steppe biome.

Nearly all species models performed well in bootstrapping and cross-validation tests of model fit (Figure 1.30). All but the model for the Idaho pocket gopher (*Thomomys idahoensis*), had Test-AUC averages above the threshold of 0.5 (better than expected by chance), which is the appropriate threshold for presence only models (Jiménez-Valverde 2012). The model fit was poor for *T. idahoensis* because only two recorded observations recorded were at unique locations.

Habitat valuation with and without contiguity

Adding species-specific habitat contiguity to habitat suitability models altered the mapped value of species habitats. Maps based on suitability alone frequently had widely dispersed, functionally fragmented habitat, spread across the biome. By contrast, maps incorporating multi-scale contiguity, identified and placed a higher value on more contiguous habitats. For example, comparing the distributions of habitat values of the Great Basin spadefoot (Figure 1.31) shows that isolated habitats with high probability of suitability (small, isolated areas of red in Map A) had reduced value when contiguity was considered (Map B), and areas that had lower predicted suitability but were near habitats with high predicted suitability (areas of yellow near areas of red in Map A), had increased value in the map including contiguity (Map B). Selecting the highest values within these spatially-explicit, hierarchical, habitat value maps, produces spatially configured areas, with the highest probabilities of suitability and greatest multi-scale contiguity, (which I call fundamental habitat) predicted to most likely support species persistence (Figure 1.32 - example of selecting 30% of highest value fundamental habitat for Great Basin spadefoot).



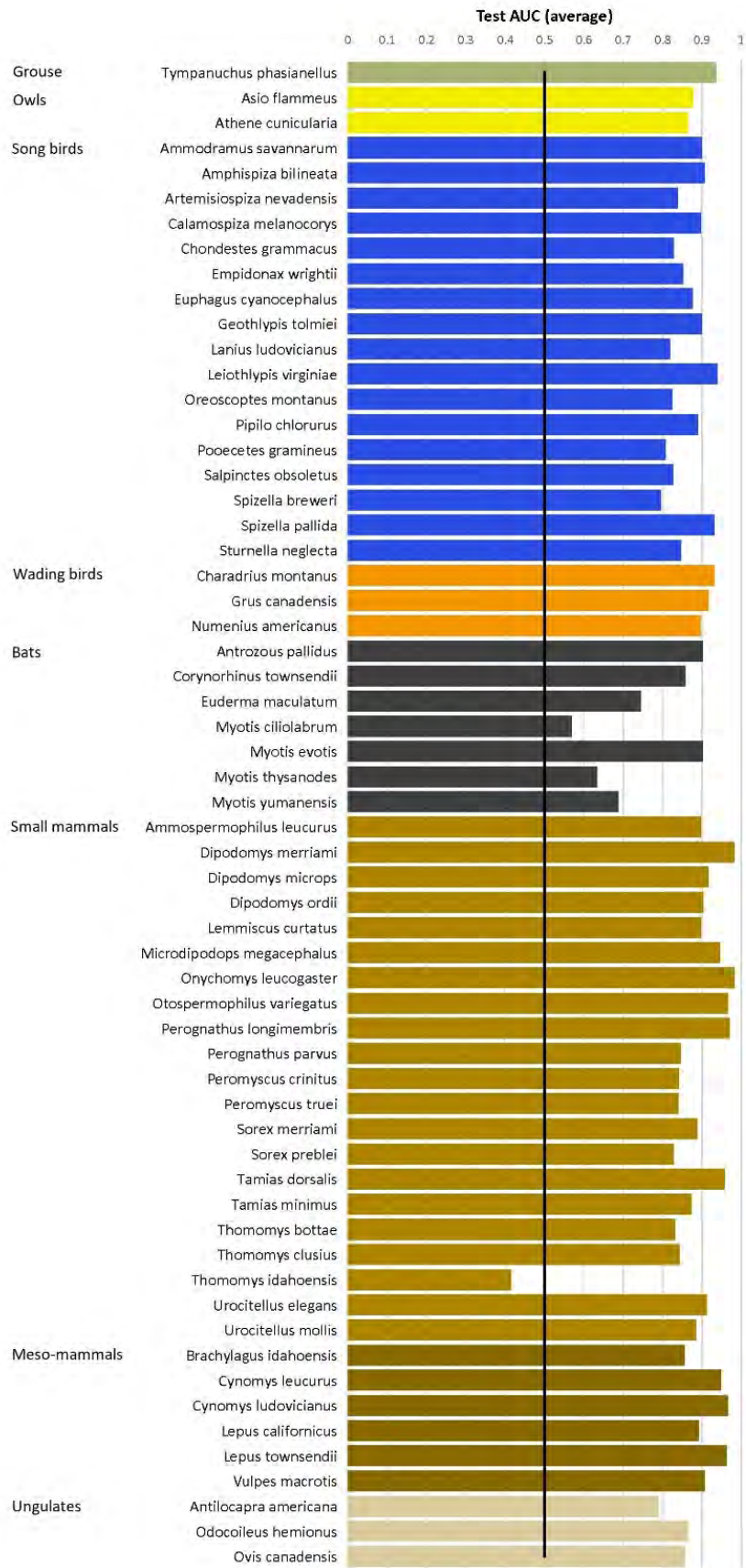


Figure 1.30. Average Test AUC values for habitat models [> 0.5 is better than expected by chance].

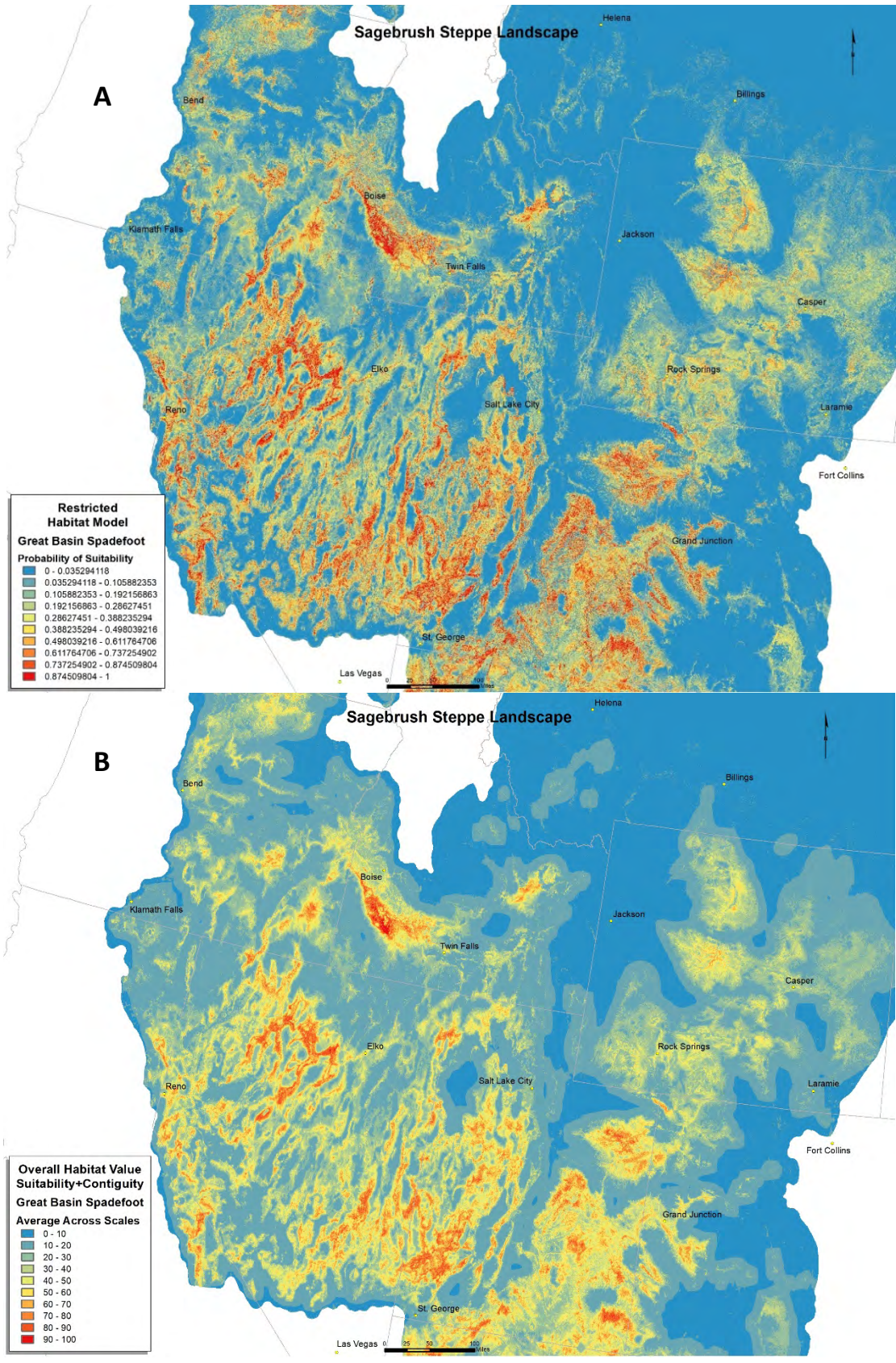


Figure 1.31. Range-restricted habitat suitability map (A) and the fundamental habitat map combining habitat suitability and multi-scale habitat contiguity (B) for the Great Basin spadefoot toad (*Spea intermontana*).

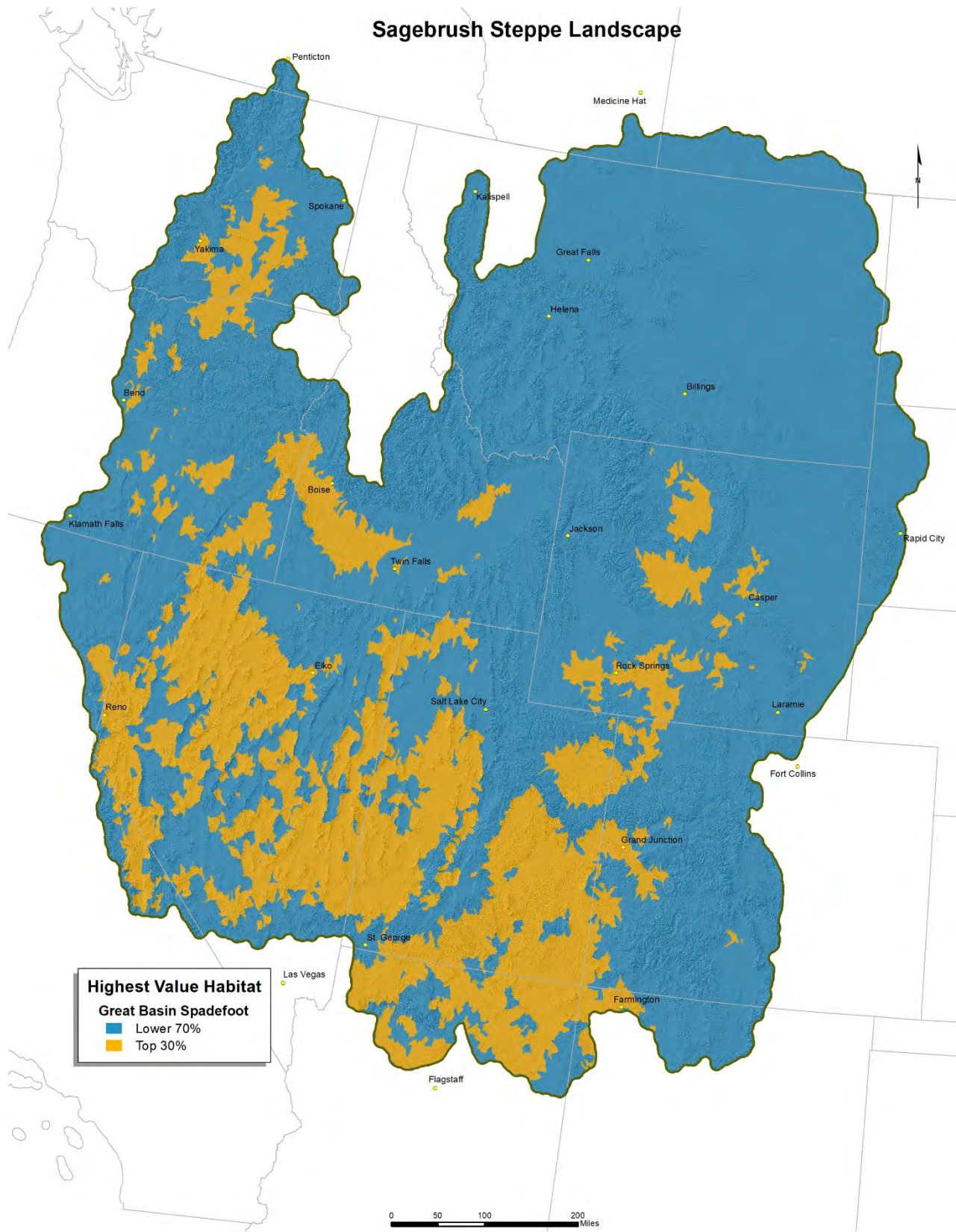


Figure 1.32. Selecting a percentage of the highest value habitat for a species, in this example the top 30% of Great Basin spadefoot toad (*Spea intermontana*) habitat values, produces a spatially-explicit and configured map of the “fundamental habitat” for the species, predicted to best support the species persistence.

DISCUSSION

The primary objective of this work was to develop methods to produce consistent biome-scale, high-resolution (10m x10m cell size) maps that identify areas with combined high probability of suitability and contiguity for 164 terrestrial obligate taxa of the sagebrush biome, including vertebrates, invertebrates and plant species. This approach overcame the impediments to creating large-scale, high-resolution models for a wide range of taxa that kept this from being done previously. Using “big” public datasets of species observation data, which included species that previously had a paucity of data, allowed the creation of habitat suitability models for the majority of obligate taxa of a biome. A hybrid of methods was utilized to account for the sampling bias in these data within the presence-only Maxent modeling procedure, allowing for more accurate estimation of species’ habitat selections. With increased computing capacity, I was able to run large extent models that encompassed species’ populations, at resolutions that were ecologically meaningful.

Removing roads from the landcover data layer avoided false selection of roads as a preferred habitat type because of the prevalence of publicly reported observations of species along roads. However, this may have introduced bias, if roads were primarily found in certain habitats (e.g., flat lands or along riparian areas), potentially creating apparent associations between species seen along roads with these habitat types. And it is possible that, in some cases, roads were a preferred habitat type (e.g., as a source of salt or warmth). It may be possible to account for this potential bias by modeling and removing the effects of roads or treating observations along roads as a detectability issue and modeling the likeliness of observing species as a function of the distance from roads. These approaches could be explored in subsequent studies.

The method developed to combine habitat suitability and contiguity was successful in creating maps of ‘fundamental habitat’ for each species. Higher habitat values represent higher contiguity and probability of habitat suitability. The contiguous, high value habitats are more likely to support species persistence (Crooks and Sanjayan 2006) and therefore will likely be more effective for multi-species systematic conservation planning. This had the desired result of identifying higher value habitats that were more contiguous over habitats that had high probabilities of being suitable but were scattered and isolated.

The fundamental habitat maps developed with these methods can be used by land management agencies for large-scale conservation planning for a wide range of taxa, including data-poor species, at resolutions relevant to species, for multi-species landscape conservation planning. This modeling approach can be repeated in any biome for most species because it makes use of now readily available publicly-collected species observation data and procedures to utilize these.

Which species are considered “obligate” in a landscape, and those included or omitted, obviously have a substantial effect on multi-species conservation plans. In the timeframe for this example, there were not occurrence data for many obligate invertebrate species and some plant species, so those were not included in this example application for the sagebrush steppe landscape. Conservation planners need to determine which species should be included in a plan, and that plans will be incomprehensive until data for missing obligate taxa are available.

Model fit was acceptable for all models except one, the model for the Idaho pocket gopher (*T. idahoensis*). The modeled results were within the restricted range of this species, so keeping the results of this model for inclusion in the multi-species conservation plan was justified, however, creating habitat models with fewer than five observations is not recommended.

I did not perform an accuracy evaluation of these models, because these evaluations do not necessarily indicate how well the models will perform for their intended use (Jiménez-Valverde et al. 2008, Aguirre-Gutiérrez et al. 2013, Fourcade et al. 2018). Assessing model fit or how well predictions match withheld or independent data, only shows how well the models work with these (usually similarly biased) data, they do not assess the accuracy of model predictions (Jiménez-Valverde 2012, Aguirre-Gutiérrez et al. 2013). Ultimately, the only way to assess how useful models are for their intended purpose, is to test their predictions (Langford et al. 2011). To accomplish this, model outputs should be treated as hypotheses (Jarnevich et al. 2015) and applied via experimental design using an adaptive management approach and monitoring population responses (Barrows et al. 2005).

The model outputs of complementary log-log (cloglog) transformed probabilities counter possible spatial dependency in the input data, and Halvorsen et al. (2016) found that spatial autocorrelation in data, if it occurs in the real world, did not affect the predictive performance of Maxent models. However, this was not tested in this study and there may be an effect on the model predictions due to spatial autocorrelation of sampling, this would need to be ascertained by further studies.

The models developed here provide a way to identify which areas of a biome are most likely to sustain native species populations, without having demographic data for the species. To effectively address the threats to the persistence of sagebrush steppe obligate taxa, minimally, the types, amounts and configurations of habitats that each species requires must be identified to assure that management prescriptions are done in places adequate to ensure species persistence.

Whether conserving these lands will actually be successful in sustain species' populations is another question. There are many factors that impact species persistence, e.g., land use change, climate change, invasive species, resource extraction, development, disturbance, livestock

grazing, disease, pollution (Pocewicz et al. 2014, Hanser 2018, Remington et al. 2021).

Determining how to manage habitats on these identified lands to sustain populations of sagebrush steppe obligate taxa, is the next step and beyond the scope of this study.

Using these maps in multi-species systematic conservation plans and selecting adequate amounts, as determined by planners, of the highest value fundamental habitat for conservation action, results in selecting spatially configured areas that include the most probably suitable and functionally connected habitat, which is most likely to support species persistence. I used these models next to find optimized configurations of combined fundamental habitats predicted to protect the obligate taxa of this biome.

Issues and recommended further work

There are many potential sources of uncertainty in these models, e.g., whether locations of observations are accurate (although this is less of concern since most observers these days have phones with built-in GPS); whether environmental/habitat variables (covariate data layers) were the factors that species used to determine their habitat preferences; whether environmental/habitat data layers accurately represent actual conditions; whether modeling procedures identified the correct relationships between species occurrences and suitable habitats; whether species observations were in marginal habitats (i.e., that species were just traversing through) or sink habitats that would not support species populations; whether species were identified correctly; sampling bias; observer bias; proper scale; and ultimately, whether the identified habitats can actually support these species. I attempted to mitigate many of these issues by following recommended procedures, however, the models surely include uncertainty.

There is uncertainty in all model predictions. To paraphrase Box (1976): all models are wrong - some models are useful. To develop useful models, it is important to follow best procedures (Elith et al. 2011, Merow et al. 2013, Radosavljevic and Anderson 2014) and

understand what the models are predicting and can and should not be used for. Also, covariate data and species location data should be from the same time period, to reliably associate species occurrences to habitat conditions. Once the habitat associations are made, then the models can be applied to different conditions (e.g., with climate or land use change).

Ultimately, the only way to assess how useful models are for their intended purpose, is to test their predictions. To accomplish this, model outputs should be treated as hypotheses (Jarnevich et al. 2015) and applied via experimental design using an adaptive management approach (Atkinson et al. 2004) while monitoring population responses (Barrows et al. 2005). In this case, to assess whether the identified habitat types, amounts and configurations can actually sustain species populations, as predicted. To accomplish this, the identified habitats would need to be appropriately managed, and the responses of species populations monitored, along with any other unforeseen stressors that may affect the populations (Cabeza and Moilanen 2001). A feasible way to implement this would be design an adaptive management application (Atkinson et al. 2004, Barrows et al. 2005, Williams et al. 2009, Fleishman et al. 2021), and use focal species to monitor population responses (Lambeck 1997, O'Connell et al. 2000).

Another factor that could influence the results of these models is the number of observations for each species. Even though Maxent has been shown to produce reliable results with small sample sizes (Elith et al. 2006, Hernandez et al. 2006, Wisz et al. 2008), models for species with very few observations may not comprehensively represent their suitable habitat. An area for possible further study could be to test the sensitivity of the models to the number of observations for each species. This might be done by subsampling the observations for species with many observations and determining whether the models are altered with fewer observations.

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CHAPTER 2: SYSTEMATIC CONSERVATION PLANNING FOR SAGEBRUSH STEPPE OBLIGATE TAXA USING FUNDAMENTAL HABITAT MODELS

INTRODUCTION

We are in the midst of a human-caused mass extinction of the Earth's biota (McCallum 2015, Ceballos et al. 2020, Cowie et al. 2022). Many species are facing extinction because of habitat loss, fragmentation, and degradation resulting from human activities (Haddad et al. 2015, Crooks et al. 2017, Díaz et al. 2019, IPBES 2019, Kuipers et al. 2021, Cowie et al. 2022). Putting all our resources into trying save each species from extinction as we notice their imperilment is not keeping up with the crises (Leclère et al. 2020), instead we need to conserve and manage the species in a landscape as a whole to prevent species from becoming imperiled in the first place (DeFries and Nagendra 2017, Pimm et al. 2018, Díaz et al. 2019, Kennedy et al. 2019, Leclère et al. 2020, Noss et al. 2021). Providing the fundamental habitat needs for every species in a landscape requires identifying the type, amount, and configuration of habitat withing the landscape essential for sustaining the populations of each species (Moilanen et al. 2005, Reed et al. 2006, Early et al. 2008, Grimmett et al. 2021).

Systematic conservation planning (SCP) has been proposed as a method to identify land configurations that can sustain populations of native species (Margules and Pressey 2000, Cabeza and Moilanen 2001). For systematic conservation planning to effectively identify habitats that can support multi-species persistence in a landscape, the habitat requirements that can sustain each species must be used as inputs (Grimmett et al. 2021). I adapted an SCP approach using an optimization algorithm and the fundamental habitat maps derived in the previous chapter to identify multi-species habitat configurations that are the best places to focus conservation management to sustain native species persistence (Watson et al. 2011).

Systematic conservation planning uses information on single species, such as range, occupancy, or habitat maps, with some sort of optimization procedure to identify areas that have the highest concentrations of species ranges or habitats with the least cost (or area) (Williams and Araújo 2000, Cabeza and Moilanen 2001). The optimization process “selects some of everything, for the lowest cost” or area (Ball et al. 2009). The procedure results in optimized spatial “solutions” that identify areas that meet species’ habitat needs, along with other specified conservation goals, using the least amount, or least costly (e.g., already protected) land.

Early optimization routines generated only heuristic solutions, e.g. Marxan (Ball et al. 2009), because exact solutions were computationally prohibitive. Heuristic solutions approach, but can fail to find, an optimum solution (Williams et al. 2004, Billionnet 2013, Beyer et al. 2016, Schuster et al. 2020). More recent exact integer linear programming (EILP) algorithms can find exact optimum solutions as quickly and efficiently as heuristic optimizers once found a suit of near optimum solutions (Rodrigues et al. 2000, Beyer et al. 2016, Schuster et al. 2020).

These optimization approaches, however, do not necessarily identify the configurations and amounts of habitat required to sustain populations (Araújo and Williams 2000, Cabeza and Moilanen 2001), though see Williams and Araújo (2000) and Early et al. (2008) for proposed alternative approaches that attempt to accomplish this. Without knowing the habitat each species requires for their populations to persist, the areas included in these conservation designs may not ensure their persistence (Araújo and Williams 2001, Cabeza and Moilanen 2001, Lawler et al. 2003, Early et al. 2008). Multi-species conservation plans can only identify areas likely to sustain populations of all the included species if the data used into the optimization routine include the habitat types, amounts, and configurations likely to sustain each individual species.

Habitat maps used in optimization algorithms for systematic conservation planning are generally assumed to support species’ survival and reproduction (i.e., the definition of habitat;

Hall et al. 1997). However, these habitat/range maps rarely, if ever, incorporate species-specific habitat connectivity; an essential factor in planning to sustain populations across a landscape (Crooks and Sanjayan 2006, Reed et al. 2006). Some SCP methods allow constraints that can increase the compactness of the overall conservation solution (Moilanen et al. 2022). However, this does not necessarily produce solutions that optimize species-specific habitat connectivity that is required for each species' persistence (Moilanen and Wintle 2007). The omission of species-specific habitat connectivity, can result in conservation plans that may be less suitable for species that rely upon dispersal for regional persistence (Cabeza and Moilanen 2001, Moilanen and Wintle 2006;2007, Early et al. 2008).

To overcome the limitations to creating effective multi-species, biome-scale conservation plans, I used fundamental habitat maps (Chapter 1) for native taxa as inputs into optimization calculations. These maps encompass the entire biome, had 10m spatial grain to differentiate the habitat at a fine scale, used species-specific habitat suitability maps rather than coarse occupancy or distribution records, included a wide range of taxa, and incorporated multi-scale contiguity in the valuation of habitat for each species, to better select areas of the landscape that will assure the persistence of each species.

METHODS

I selected the sagebrush steppe biome for this study because this ecosystem and many of its obligate species are threatened by habitat loss and degradation due to invasive plant species, altered fire regimes, conifer expansion, and human land uses including energy and infrastructure development, cropland conversion, and livestock grazing, all exacerbated by climate change (Hanser et al. 2011, Svejcar et al. 2017, Remington et al. 2021, Doherty et al. 2022). Further, there are several proposed conservation approaches (Runge et al. 2019, NRCS 2021, Doherty et al. 2024) for this biome, that allow a direct compare and contrast with this SCP approach.

I used fundamental habitat maps (Chapter 1) for 164 plant, invertebrate and vertebrate obligate taxa of this biome ([Appendix B](#)) as inputs to the optimization routine used to identify the configuration of species habitats that are most likely to sustain populations of these species. I used the R package `prioritizr` (Hanson et al. 2020) with the exact integer linear programming optimizer Gurobi (Gurobi Optimization LLC 2020), because they allowed for easily adjusting conservation goals and quickly reaching optimized solutions. I constructed six different scenarios as examples of what conservation planners might pursue, compared the optimization results, and assessed their potential usefulness for conservation planning. Scenarios can be easily adapted to target different conservation goals, the optimization routine run again, and the solutions compared. I compared the geographic distributions of the different solutions and the overall amount of land required to meet the habitat needs of all obligate taxa. The six conservation-goal scenarios entered into the optimization routine were:

1. **Minimum Area:** Identified the multi-species habitat configuration that included the specified percentage of each species' habitat using the least amount of land.
2. **Maximum Sagebrush:** This scenario modified the minimum area scenario by targeting the solution to include as much sagebrush as possible, since sagebrush is the dominant vegetation of this biome and many of the obligate taxa rely upon sagebrush.
3. **Protected Areas:** This scenario modified the minimum area scenario by targeting the solution to select areas within currently protected lands as much as possible.

Theoretically, incorporating existing protected areas where they contribute to the optimum solution, should reduce the amount of unprotected land required to meet the conservation needs of native species (Strassburg et al. 2019, Strassburg et al. 2020).

4. **Sage-Grouse PACs:** This scenario modified the minimum area scenario by targeting the solution to select priority areas for conservation (PACs) for sage-grouse (USFWS

Wyoming Ecological Services 2014), which are areas identified as important for the conservation of imperiled sage-grouse species (*Centrocercus urophasianus* and *C. minimus*). This scenario is based on the premise that other species' habitats may be protected if PACs are protected, potentially reducing the amount of unprotecting land required to protect all obligate species.

5. PAs and PACs: Sage-grouse PACS are not included in the U.S. protected areas database (USGS Gap Analysis Program 2018). Adding PACs to protected areas as conservation targets, potentially further reduces the unprotected lands required to protect habitats of the obligate species of this biome.
6. Sagebrush, PAs and PACs: Targeting places with the most sagebrush in already protected areas, including Sage-grouse PACs, encompasses all of the most likely conservation objectives planners may have for this landscape.

Multi-species habitat maps

I compared three methods of combining individual species' fundamental habitat maps. First, I simply added together the fundamental habitat maps of the 164 sagebrush steppe obligate species included in the study ([Appendix B](#)) to reveal where the highest quality habitat overlapped for a majority of species. Second, to determine the number of different species represented in areas where species' habitats overlapped, I used a thresholding procedure to categorize per pixel habitat quality values (scaled 0 to 100) as habitat or non-habitat. For each species, each pixel with a habitat value >10 was assigned 1, indicating "habitat," and each pixel with a habitat value <=10 was assigned 0, for "non-habitat." I added the raster layers of 1's and 0's for the 164 species together to produce counts of the number of species that had habitat in each cell. These two methods provided a view of the spatial overlap of species habitats, but did not yield a solution to identifying habitats that can meet conservation criteria for the species.

To identify the minimum amount and configuration of habitats most likely to collectively sustain these native taxa, I employed a systematic conservation planning approach to find optimum configuration solutions, which included a specified percentage of each species highest value habitats, using the least amount of area. I compared the habitat amounts and configurations for the six different conservation objectives described above. I used R and the *prioritizr* package (Hanson et al. 2020), which handles input and output of data layers, allows different scenario settings, and offers a choice of different optimization algorithms. I used the EILP optimizer Gurobi (Gurobi Optimization LLC 2020) to find optimal solutions for each of the conservation scenarios. The R code used to specify the different scenarios is available in [Appendix E](#).

Input data

The inputs to the optimization procedure were 10m x 10m grain, biome extent, maps of species' fundamental habitats ranked by predicted habitat suitability and multi-scale contiguity for 164 obligate taxa of the sagebrush steppe biome (Chapter 1, examples for 4 species: Figure 1.29). I also used other data layers, including the U.S. protected areas database (USGS Gap Analysis Program 2018), priority areas for sage-grouse conservation (USFWS Wyoming Ecological Services 2014), sagebrush distribution (USGS Gap Analysis Program 2011) to compare the inclusion of different conservation targets on the solution.

Planning units

Conservation optimization routines use “planning units” to construct optimized solutions to conservation problems. For this study, I used the highest resolution (Level-12) hydro-units that were consistent across the U.S. and Canada (Lehner et al. 2008). The units are geographically-based, delineated by the boundaries of small watersheds, and are small enough (~120 km²) that land managers can manage individual units, or clusters of units (Figure 2.1). The maps of fundamental habitats for each species (Figure 2.2; example for the Great Basin spadefoot toad

(*Spea intermontana*), were averaged per each hydro-unit to produce hydro-unit maps of hierarchical fundamental habitat values for each species (Figure 2.3). A specified percentage of each species' highest value planning units were then selected as input into the multi-species optimization routine. For on-the-ground conservation planning, once the planning units have been identified as part of a conservation solution, the 10m x10m grain fundamental habitat maps for individual species (Chapter 1), can be used instead of the planning units to demarcate fine-scale variations in each species' habitat.

Percentages of species' habitats included

I evaluated the effect of using different habitat percentages during the optimization process on the selected amount or configuration of land included in the solution. The amount of habitat included can be different for different taxa or set to be the same for all taxa. Many conservation plans recommend protecting a minimum of 30% of species overall habitat to safeguard their persistence (Convention on Biological Diversity 2021, USDOJ 2021) . However, because different taxa had widely varying amounts of habitat within this biome (from 23,000 ha to over 175,000,000 ha), targeting an equal percentage of habitat for all taxa would likely not provide sufficient protection for all species, especially species with small amounts of overall habitat. Using the rationale that species with small amounts of habitat need most of it protected to ensure their persistence (whereas species with a lot of available habitat could persist with smaller percentages of their most suitable and contiguous habitat protected), I based the percentages of each species habitat to include in the optimization routine on the amount of overall habitat each species had available ([Appendix C](#)). I compared using different percentages at the ends of the spectrum (20-30% at the low end and 90-95% at the high end) to see how sensitive the results were to using these different percentages.

I calculated how much habitat each species had in the study area, by summing habitat pixels within the study extent. I first resampled the fundamental habitat value maps for each species from 10m² to 30m², using a bilinear function (averaging cells around a center cell, weighted by the distance from center). This reduced the number of calculations needed for each species map from ~13 billion cells to ~2 billion cells, reducing the time and computational capacity required. I then converted the averaged habitat values to integers ranging from 0 to 100 and reclassified the values $\leq 10 = 0$ (nonhabitat) and values $>10 = 1$ (habitat), and counted the number of these 30m x 30m cells of habitat for each species, and sorted the species by available habitat from the smallest to largest amounts ([Appendix C](#)). I used these rankings to test 4 different ranges of habitat percentages to include in the optimization procedure, based on the amount of habitat each had available: 1) 20-90% of available habitat, 2) 30-90% of available habitat, 3) 20-95% of available habitat, and 4) 30-95% of available habitat, to assess what effects the percentage of habitat per species included in the optimization procedure had on the amount and configuration of the multi-species solution. I also ran the optimization using 30% of each species' habitat for all species, for comparison.

Conservation objectives

To assess the effects of different conservation objectives on the amount and configuration of land in the multi-species optimization solutions, I first ran the different target habitat percentage scenarios above to see what effect they had on the solution. Finding negligible differences in the outcomes, I ran all subsequent conservation scenarios using 30-95% of each species' habitat, based upon the amount of habitat each had available ([Appendix C](#)).

To weight certain lands as more desirable in the solutions (e.g., protected areas, sage-grouse PACs, sagebrush landcover), I used the "Cost" function in the optimization routine. Assigning higher costs to some planning units (e.g., private lands) caused the algorithm to select

units that meet the given criteria (e.g., include specified percentages of each species highest value habitat) for the least cost. This resulted in having more targeted lands (e.g., public, protected areas) in the solutions. It did not eliminate all less desirable lands (e.g., private lands) because to satisfy the overall criteria, some of those lands were required. For the baseline scenario, I set the costs for each unit the same (i.e., all had Cost = 1) to find the minimum amount and the configuration of land that would meet the criteria of including the specified percentages of each species highest value habitat, regardless of the land's distinction. This allowed the algorithm to pick the specified amounts of the highest value habitat for each species regardless of where a planning unit occurred. Habitat contiguity was implicit in the habitat values for each species, so using highest value habitats ensured that those were the most contiguous habitats for each species, so compactness or contiguity of the multi-species solution was not consequential. In alternatives that emphasized solutions targeted to particular areas, such as protected lands, I set the costs higher for units outside those areas. For example, to favor protected areas, I reversed the protected area category numbers (Figure 2.4) to use as costs, so that the most protected units (Category 4) had a cost of 0, while the least protected units (Category 0) had a cost of 4, with the other categories similarly re-ranked. These cost values are used as examples of how different objectives can be incorporated. They can be easily adjusted by planners with different objectives.

To assess the sensitivity of the optimized solutions to the magnitudes of the cost values input into the routine, I tested different variations of costs values (e.g., multiplying 0, 1, 2, 3, 4 cost values by 10, 100 and 1000, adding costs together vs. averaging when combining goals, weighting goals differently, etc.) and observed the effects on the resulting spatial solutions.

To run the six different conservation scenarios in prioritizr using the cost function, I set the costs for different categories of planning units as follows:

- 1) Minimum Area: All planning unit costs were set to 1 (e.g., there was equal cost to selecting any unit to arrive at the optimum solution).
- 2) Maximum Sagebrush: To accomplish this, costs were set to 0 for units within sagebrush landcover and to 1 for units outside, using the sagebrush landcover map (Figure 2.4).
- 3) Protected Areas: To favor areas with the most protection, costs were set from 0 to 4 in reverse order of the protected area map (USGS Gap Analysis Program 2018) categories (Figure 2.5), resulting in higher costs for progressively less protected lands.
- 4) Sage-Grouse PACs: To favor units within Sage-grouse PACs (Figure 2.6), I set the costs within PACs to 0, while setting costs outside PACs to 1.
- 5) PAs and PACs: To favor units within protected areas and sage-grouse PACs, I averaged the costs of the previous two scenarios together, resulting in the highest costs being in areas with the least protection and outside of PACs, and the costs diminishing with increasing levels of protection inside PACs and protected areas.
- 6) Sagebrush, PAs and PACs: I averaged the costs for these three target goals together to favor (with less cost) planning units that fell within all three.

Another important conservation objective in this landscape is to protect the migration routes of ungulate populations. Protecting pronghorn (*Antilocapra americana*), mule deer (*Odocoileus hemionus*), and elk (*Cervus canadensis*) migration routes has been identified as vital to preserving the only populations of these species that migrate long distances (Kauffman et al. 2020). Because it is necessary to keep entire migration routes intact for them to be viable (Copeland et al. 2014), I overlaid the routes over these optimal habitat configurations to ascertain what land would need to be added to multi-species solutions to protect these routes.



Figure 2.1. Level 12 Hydro-Units (Lehner et al. 2008) used as planning units for the optimization procedure.

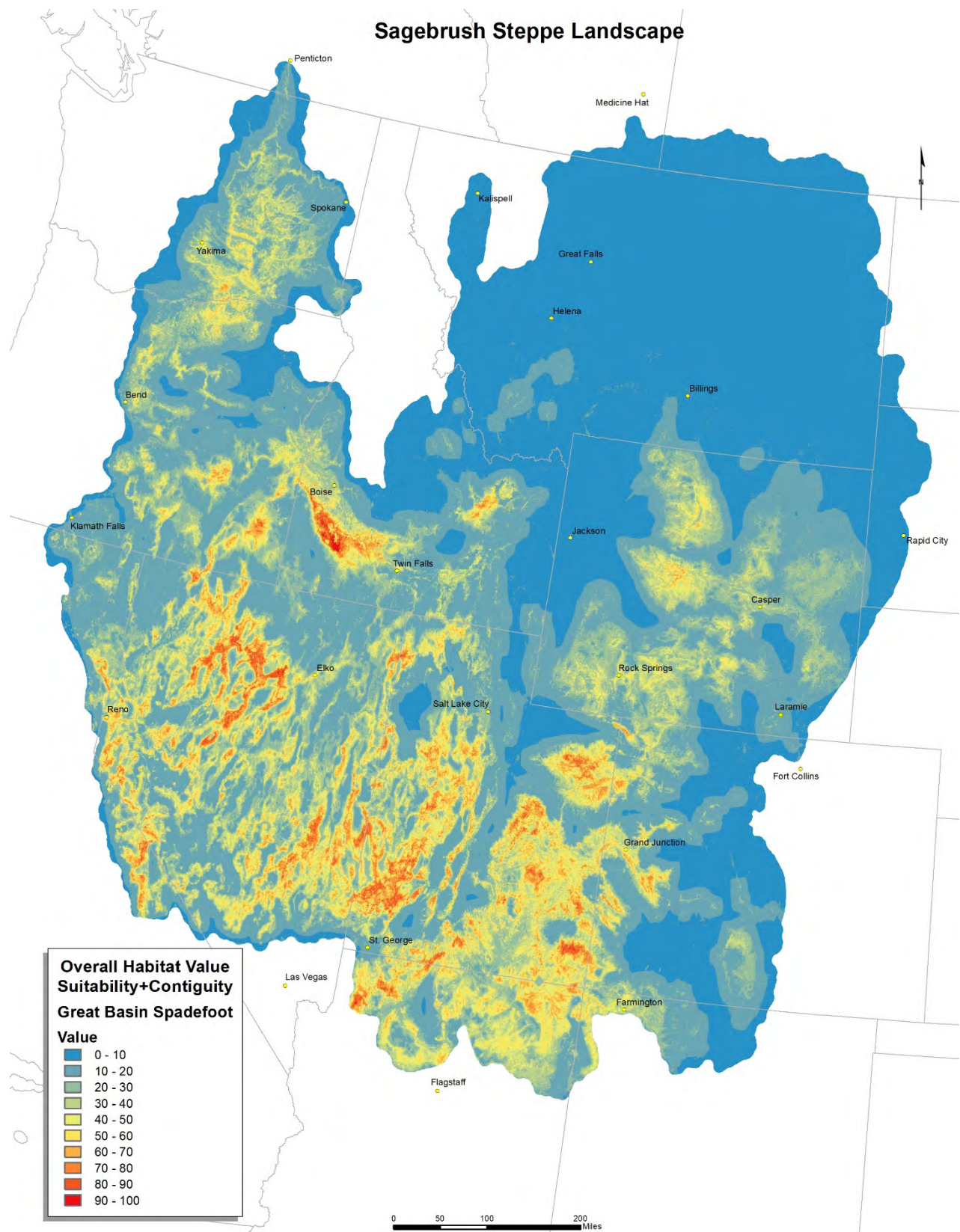


Figure 2.2. Fundamental habitat map for Great Basin spadefoot toad (*Spea intermontana*), incorporating habitat suitability and multi-scale contiguity to rank habitat values.

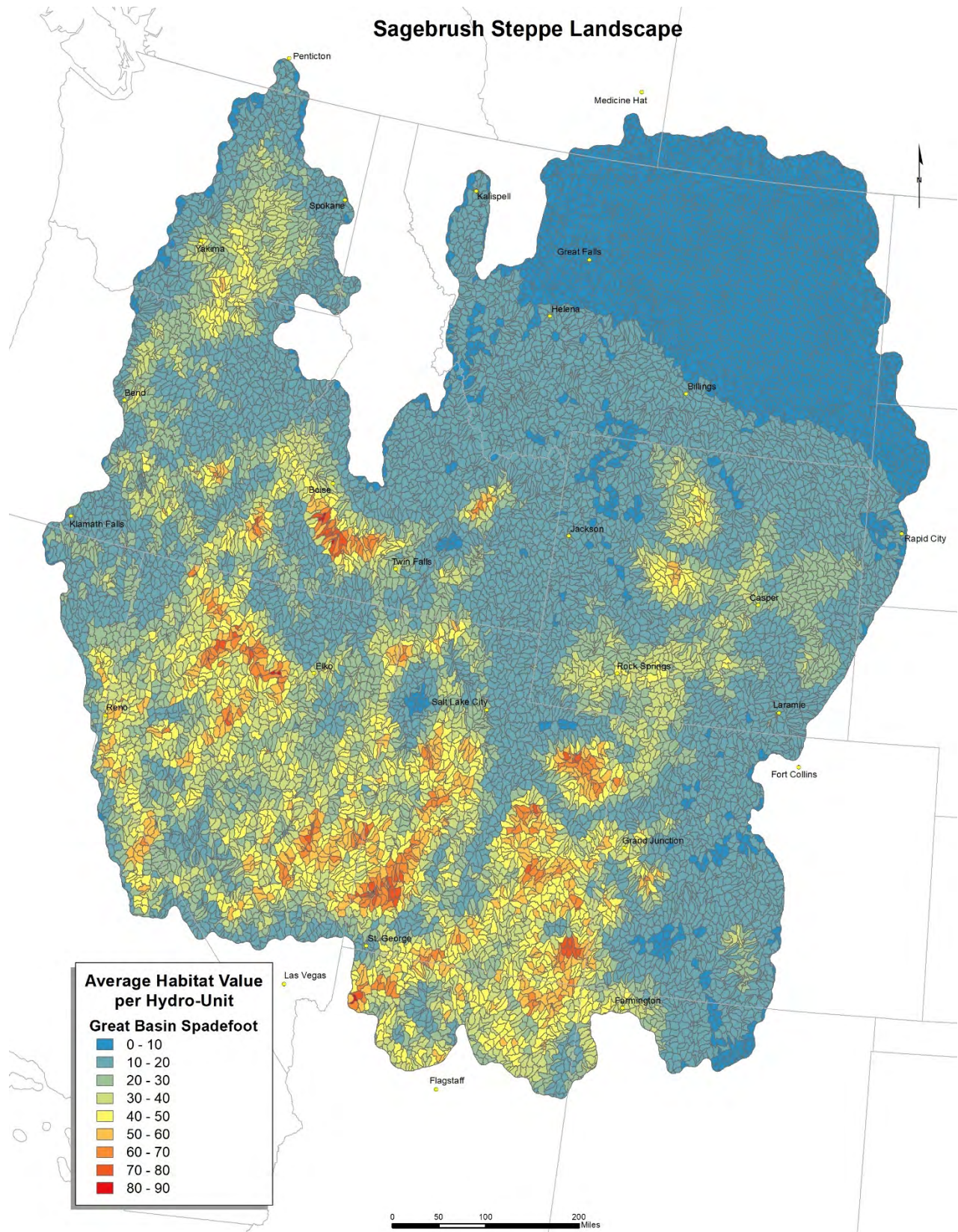


Figure 2.3. Habitat values for Great Basin spadefoot toad (*Spea intermontana*) averaged per Level-12 hydro-unit (Lehner et al. 2008). This was done for 164 sagebrush steppe obligate taxa to use as fundamental habitat planning units for multi-species optimization planning.

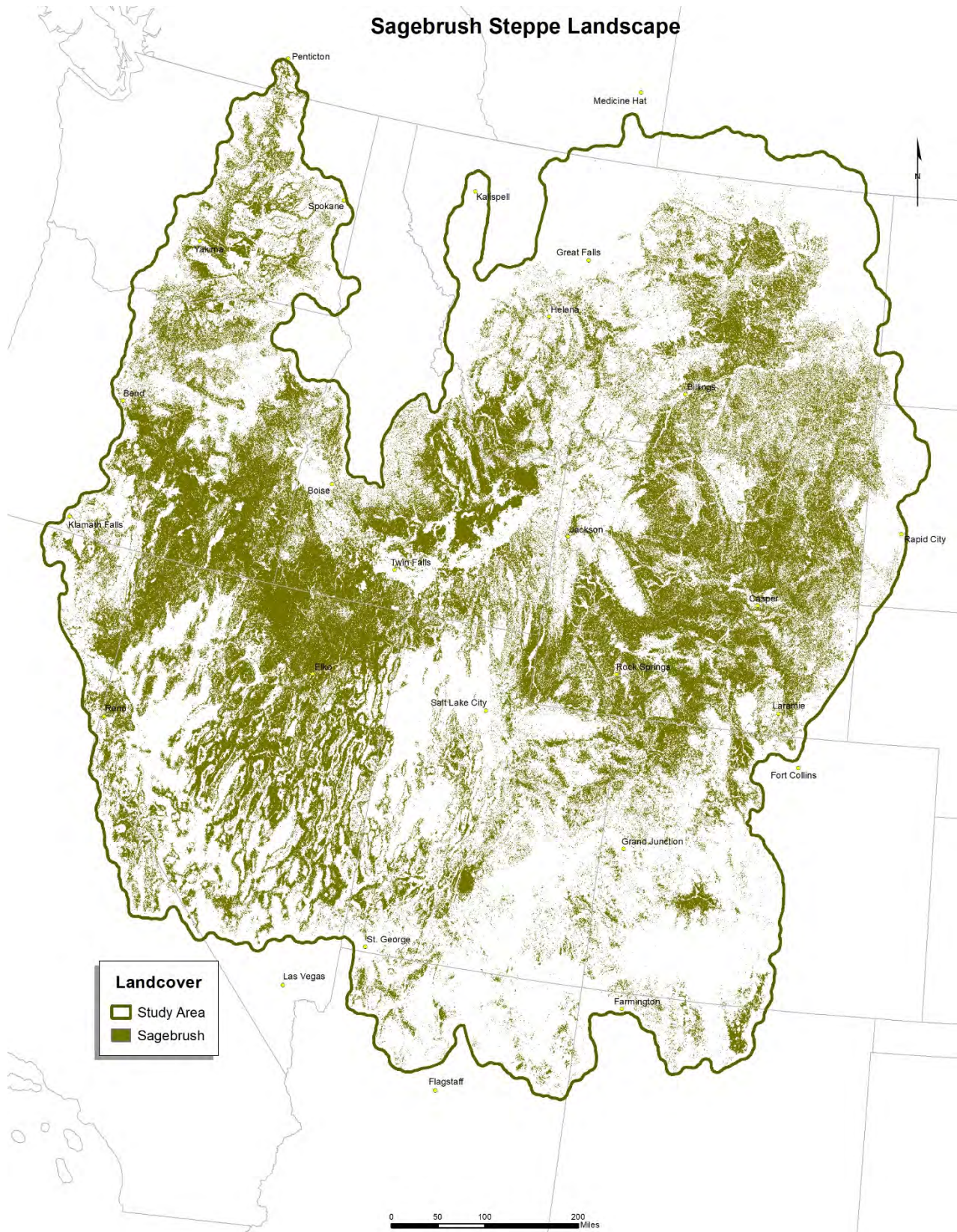


Figure 2.4. Sagebrush landcover types from the GAP landcover classification (USGS Gap Analysis Program 2011) and the Land Cover Database of North America (NALCMS 2010).

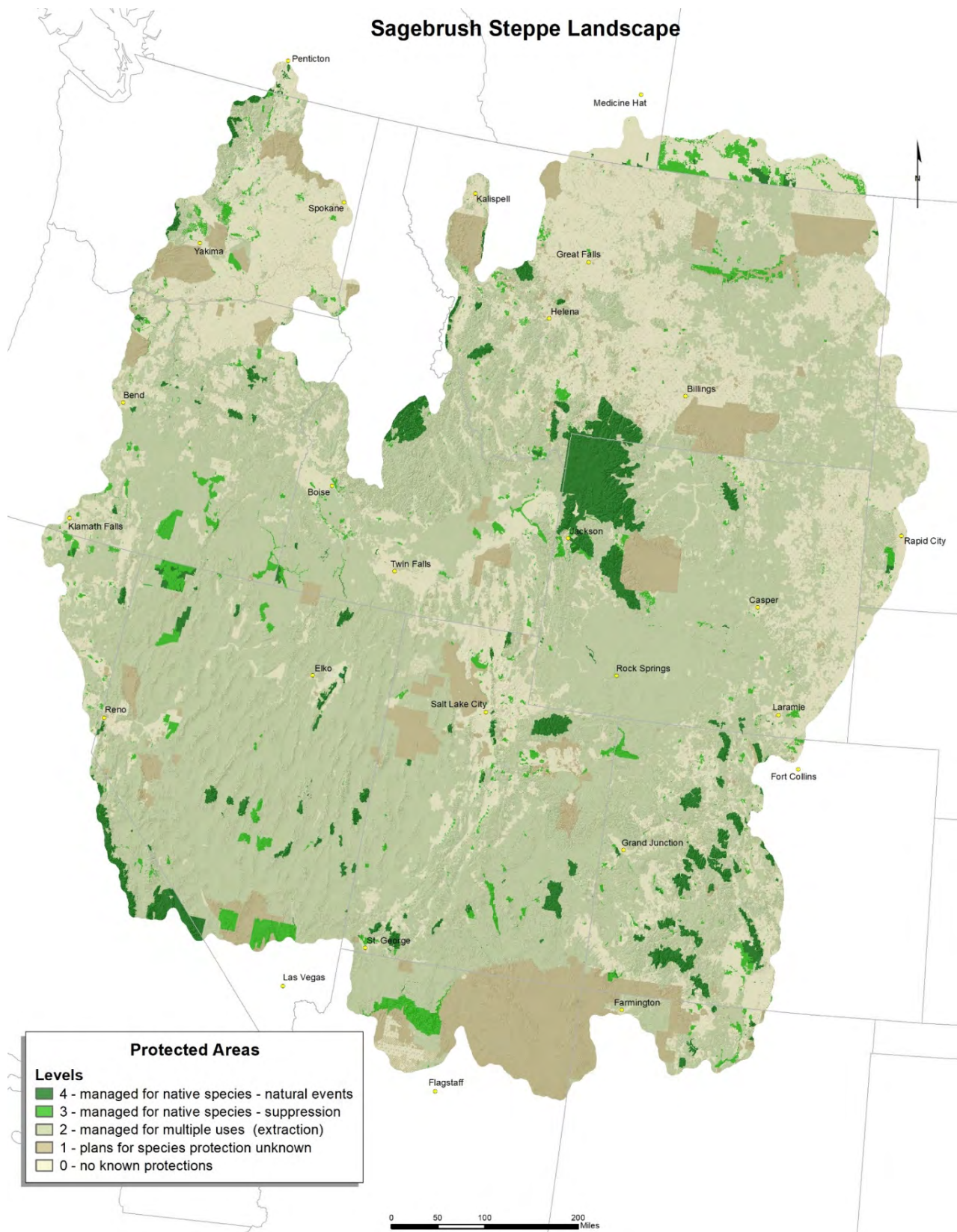


Figure 2.5. Map of protected areas (USGS Gap Analysis Program 2018) showing levels of native species protections. [Note: Native American lands are shown from the previous Protected Areas Database, with protection Level 1].



Figure 2.6. Sage-grouse Priority Areas for Conservation (PACs) (USFWS Wyoming Ecological Services 2014) [Note: the units in the SE are ranges of Gunnison sage-grouse >5,000 ha, not part of the original PACs].

RESULTS

The results of adding the 164 fundamental habitat layers of the species in this biome together highlighted areas important for multiple species (Figure 2.7). However, mapping the number of species represented (Figure 2.8), revealed that the areas with the highest number of species with overlapping habitats, consisted only of 94 of the 164 species. There were no areas that contained all species habitats together.

The optimization procedure produced biome-scale, high-resolution habitat configuration maps for a combination of specified percentages of the highest value fundamental habitats of 164 obligate taxa of the sagebrush steppe biome, using the least amount of land (Figure 2.9). These multi-species habitat configurations represent the areas most likely to support these obligate species' persistence, along with meeting other specified conservation objectives.

Percentages of species habitat included in solution

Setting the input percentage of habitat to protect to 30% for all species, resulted in substantially less area included in the multi-species solution (Table 2.1) and the configuration of the areas included was quite different (Figure 2.10) from the solution with included habitats ranging from 30-95% (Figure 2.9), however, only protecting 30% of the habitat of species with very little habitat available, is likely to leave these species vulnerable to extirpation.

Comparing the results of setting percentages of each species habitat to protect based upon their available habitat, revealed that changing the percentage of species with abundant available habitat, from protecting 20% to protecting 30%, had no effect on the optimal solution, either geographically or in the total amount of land required (Table 2.2). Changing the percentage of habitat to protect of the species with little available (< 160,000 ha) habitat, from 90% to 95%, slightly increased the overall amount of land required to protect all species, from 55.1% to 55.2%. (Table 2.1) but had very little effect on the geographic configuration for protecting a portion of all

species' habitats, swapping just a few planning units on the edges of the optimal configurations (Figure 2.11). Tests using 99% of species habitats instead of 95% did not change outcomes, but slowed processing considerably, and tests including 100% of species habitats were computationally prohibitive.

Table 2.1. The overall land area required for different levels of individual species habitat protection.

	<u>90-20%</u>	<u>90-30%</u>	<u>95-20%</u>	<u>95-30%</u>	<u>30%</u>
Solution Area (km²):	976,828	976,828	977,915	977,915	637,468
Total Area (km²):	1,772,161	1,772,161	1,772,161	1,772,161	1,772,161
% of Biome:	55.1%	55.1%	55.2%	55.2%	36%

Since the habitat percentages used, based upon available habitat on the extremes of the spectrum, had negligible effect on the solutions, I used habitat protections of 30% for species with large amounts of available habitat to 95% for species with small amounts of available habitat to run the optimization scenarios (Figure 2.9). These habitat percentages are examples and are not based on the biology of the species. For example, some species with large amounts of suitable habitat require large amounts (i.e., more than 30%) of habitat to sustain their populations (e.g., sage-grouse, grizzly bears, wolverines). In practice, the required habitat percentages should be determined by species experts. The percentages selected for this application were used to demonstrate the method, but can easily and should be modified by conservation planners and species experts.

Sensitivity of the optimization routine to cost values

Multiplying the costs (0, 1, 2, 3, 4) used in the Protected Areas optimization routine by 10 or 100 to produce cost values of 0, 10, 20, 30 and 40, or 0, 100, 200, 300 and 400 to increase the magnitude of difference between classes, had no effect on the resulting spatial solutions, they were identical. Multiplying the costs used in the Sage-Grouse PAC scenario by 10, 100 or 1000, resulted in a very few planning units on the edges switching with different cost levels, but the

area and overall configurations of the solutions remained the same. Changing the magnitude of the values when combining different scenarios resulted in the scenario with lower costs being favored. For example, multiplying the Protected Area costs by 10 and the Sage-Grouse Pac costs by 100 and combining them, compared to multiplying the Protected Area costs by 100 and the Sage-Grouse PAC costs by 10, resulted in favoring areas with the lower costs, which is consistent with expectations.

Comparing conservation scenarios

I compared the results of the different scenarios by comparing the geographic configuration of the optimal solutions required to protect the specified amount of each species’ habitats, and the percentages of the biome’s land area required to meet the scenario objectives. I assessed the consistency and differences between four different habitat protection combination amounts ([Appendix C](#)) and six different land conservation scenarios, to assess the effects on geographic configuration of habitats and the amount of land needed to meet the conservation objectives (Table 2.2).

Attempting to include as much sagebrush landcover in the optimal configuration to protect the specified amounts of habitat for each species (Figure 2.12), increased the amount of land in the biome needing protection from ~55% to ~59% (Table 2.2).

Table 2.2. The land area required for different optimal solutions.

	<u>95-30%</u>	<u>+ Sage</u>	<u>+ PA</u>	<u>+ PACs</u>	<u>+ PA/PACs</u>	<u>+ PA/PACs/Sage</u>
Solution Area (km²):	977,915	1,049,547	1,062,120	1,119,513	1,025,237	1,146,651
Total Area (km²):	1,772,161	1,772,161	1,772,161	1,772,161	1,772,161	1,772,161
% of Biome:	55.2%	59.2%	59.9%	63.2%	57.9%	64.7%
% Change from Min:		6.8%	7.9%	12.6%	4.6%	14.7%

Targeting protected lands in the optimization (Figure 2.13) increased the overall amount of land required to protect all species from ~55% to ~60% (Table 2.2), but since some of this land is already protected, this solution may result in a lower overall cost to conserve the land needed. The costs of managing different land parcels for conservation of native species would need to be calculated to determine which approach would be less costly overall.

Targeting sage-grouse priority areas for conservation (PACs) in the optimization procedure (Figures 2.14 & 2.15) increased the amount of land needed to protect all species from ~55% to ~63% (Table 2.2). Again, since some of this land is or will be protected, this solution may result in a lower overall cost to conserve the land needed. The costs of managing different land parcels for conservation of native species would need to be calculated to determine which approach would be less costly overall.

Targeting protected areas and sage grouse PACs resulted in a lesser increase in the land required to protect all species, increasing from ~55% to ~58% (Table 2.2). This is due to the optimization routine having more land to choose from to fulfill the requirement to protect all species with the least amount of land. However, this solution does not do a very good job of selecting protected areas or sage-grouse priority areas to include in the optimal solution, selecting only some of each - to reach the goal of protecting specified percentages of each species habitat (Figure 2.16).

Targeting protected areas, sage grouse PACs, and areas of sagebrush landcover (Figure 2.17) increased the overall amount of land required to protect all species from ~55% to ~65%, the most of any of the conservation scenarios (Table 2.2). This was likely due to the optimization routine attempting to get as much of all 3 property types into the solution as possible, while protecting the specified amount of each species' habitats.

Adding important pronghorn, mule deer and elk migration routes (Kauffman et al. 2020) to the different optimized landscapes (Figure 2.18), resulted in varying amounts of additional land required to protect all species and the migration routes. The additional land required per optimal habitat solution ranged from 2,291 km² for the solution targeting sage-grouse PACs to 7,714 km² for the minimum area solution, which required the least amount of land overall (Table 2.3).

Table 2.3. The land area required for different optimal solutions, adding important migration routes.

	<u>95-30%</u>	<u>+ Sage</u>	<u>+ PA</u>	<u>+ PACs</u>	<u>+ PA/PACs</u>	<u>+ PA/PACs/Sage</u>
Solution Area (km²):	977,915	1,049,547	1,062,120	1,119,513	1,025,237	1,146,651
+ Migration Areas (km²):	985,089	1,054,075	1,068,417	1,121,804	1,031,167	1,150,191
Additional Land (km²):	7,174	4,528	6,297	2,291	5,930	3,540
% Change:	0.7%	0.4%	0.6%	0.2%	0.6%	0.3%
% of Biome:	55.6%	59.5%	60.3%	63.3%	58.2%	64.9%
% Change from Min:		6.5%	7.8%	12.2%	4.5%	14.4%

The resulting multi-species habitat configurations represent the most efficient solutions (least amount of land required) to protect the 164 obligate taxa of the sagebrush steppe included in the study, for each conservation scenarios. The areas identified include the specified percentage of the highest value (most likely suitable and contiguous) habitats for each species. These percentages and the other conservation or efficiency objectives can easily be changed and the optimization routine rerun. The resulting GIS polygon layers of selected planning units for each solution, have stored within them: the costs that were used per each unit, and the fundamental habitat value for each of the 164 species for each unit.

One recommendation for prioritizing lands for conservation that I did not consider, is the threat level that different areas face. Some conservation approaches include anticipated threat levels to land parcels to prioritize their conservation (Noss et al. 1995, Orme et al. 2005, Doherty et al. 2022, Hamilton et al. 2022). A map of potential threats to this biome (Doherty et al. 2024) could easily be incorporated into the optimization routine as a cost layer by planners.

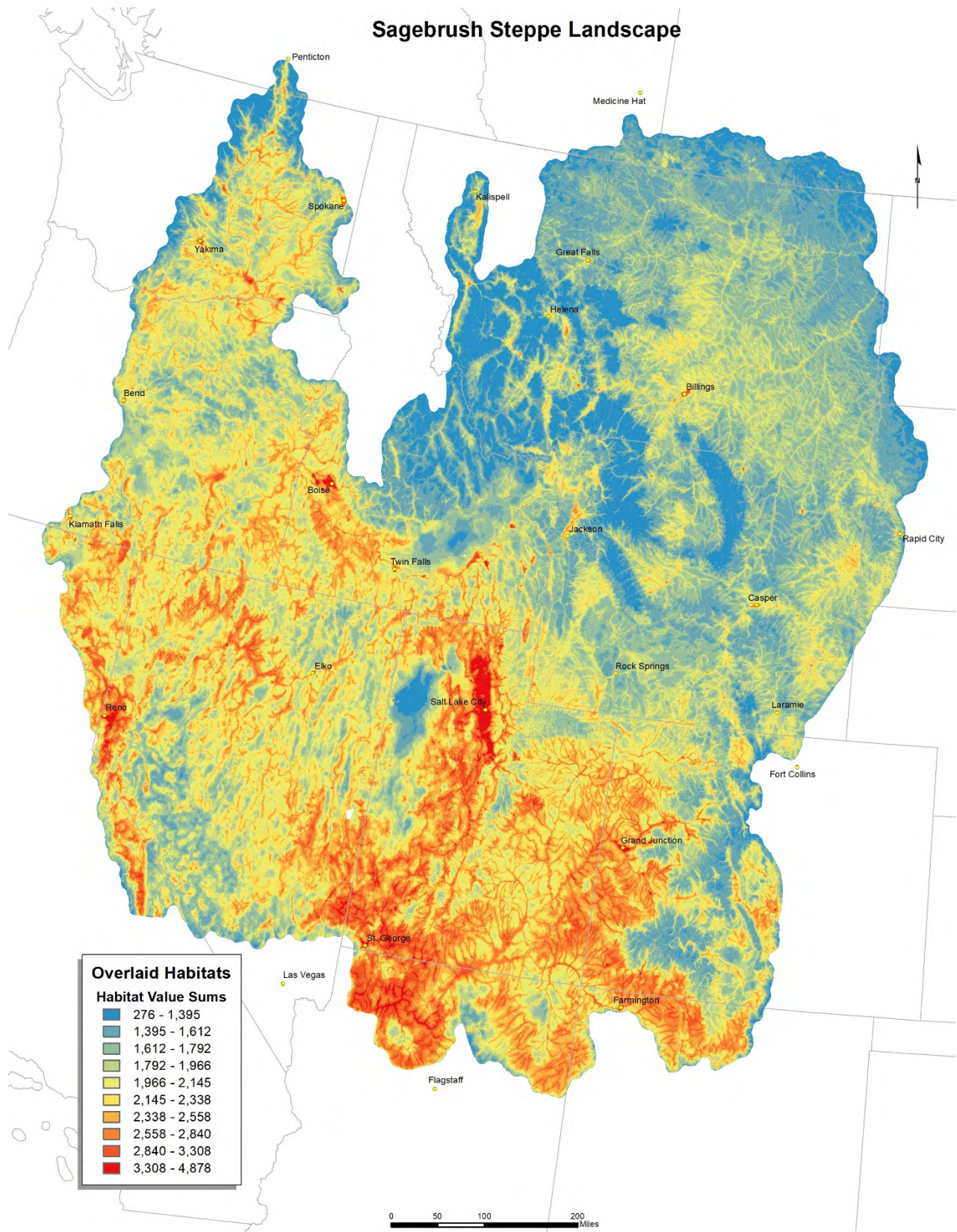


Figure 2.7. Fundamental habitats of 164 sagebrush steppe obligate species summed together to show areas of multi-species highest ranked habitats.

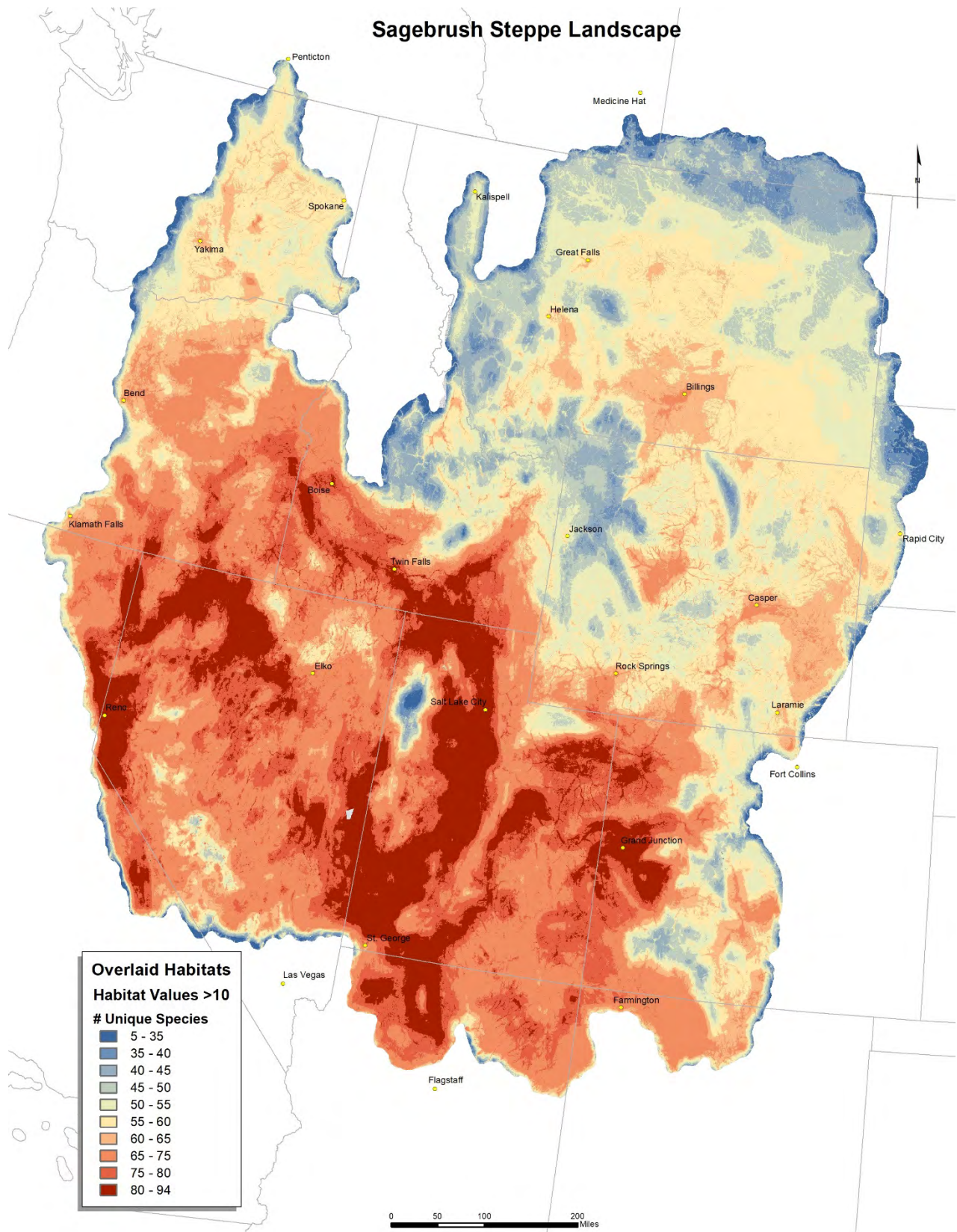


Figure 2.8. Overlays of 164 sagebrush steppe obligate species fundamental habitat values (values >10). Note that areas with the most habitat overlap consists of habitat for only 94 of the 164 species.

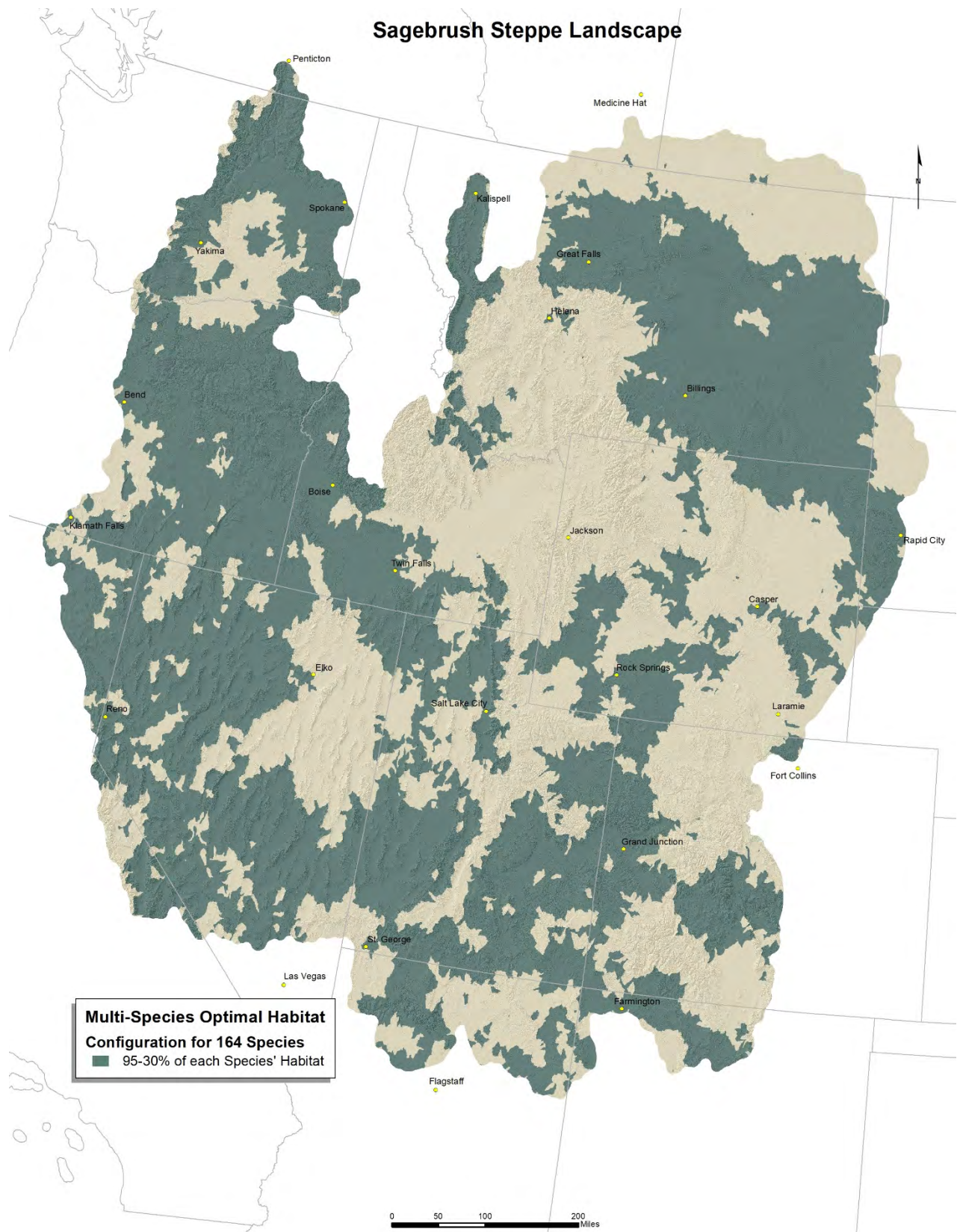


Figure 2.9. Optimal configuration of habitats of 164 sagebrush steppe obligate species, with 95% of their habitat included for species with small amounts of habitat available, ranging to 30% of habitat for species with large amounts of habitat available.

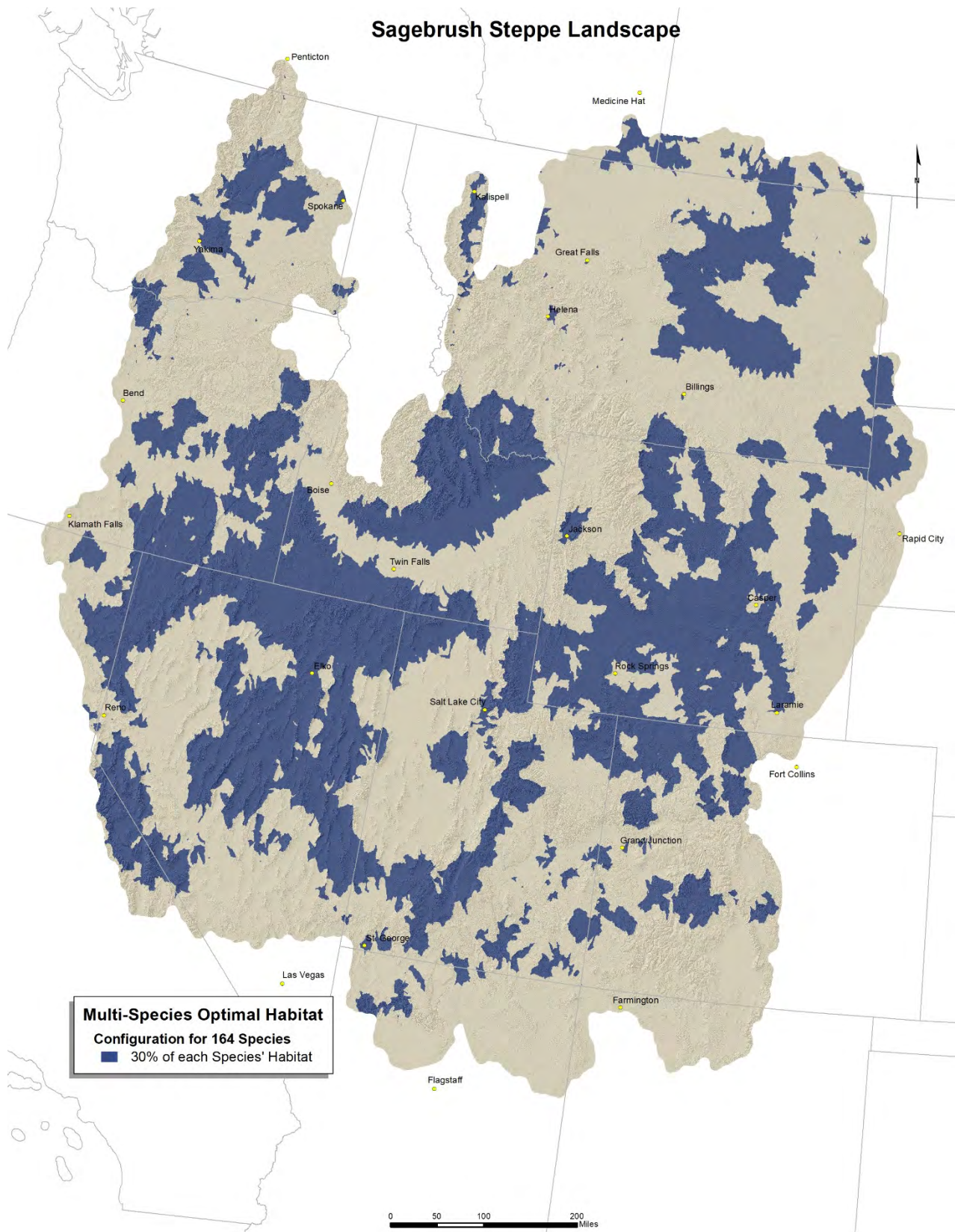


Figure 2.10. Optimal configuration of habitats of 164 sagebrush steppe obligate species, with 30% of their habitat included for all species.

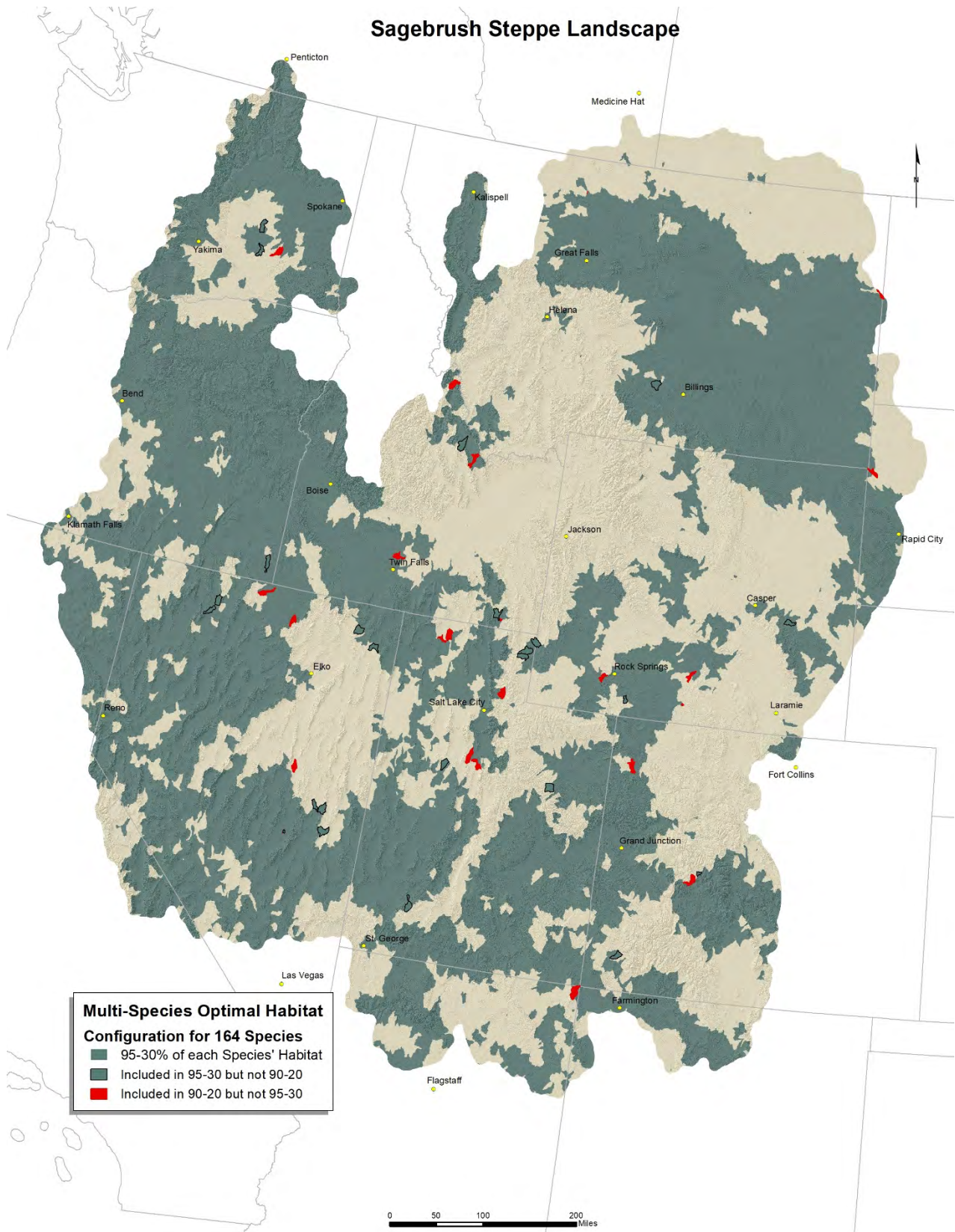


Figure 2.11. Comparison of optimization solutions using a range of included species habitats from 95% to 30% vs. 90% to 20%. The optimal habitat configurations are nearly identical except for a few watersheds on the edges that switch from being included or not depending on the ranges of habitats targeted in the solutions.

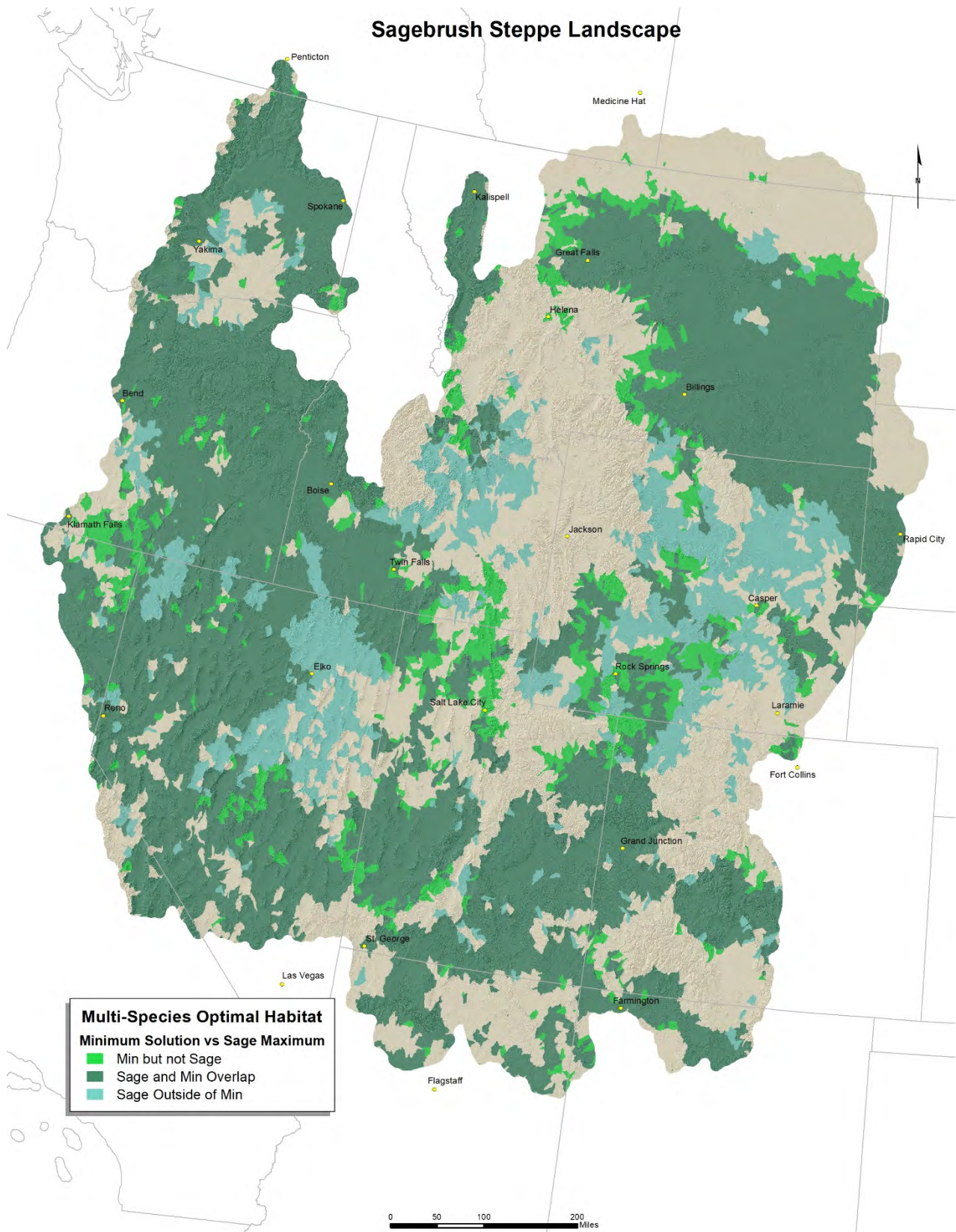


Figure 2.12. Comparison of optimization solutions: Minimum Area to the Maximum Sagebrush, targeting sagebrush landcover (USGS Gap Analysis Program 2011).

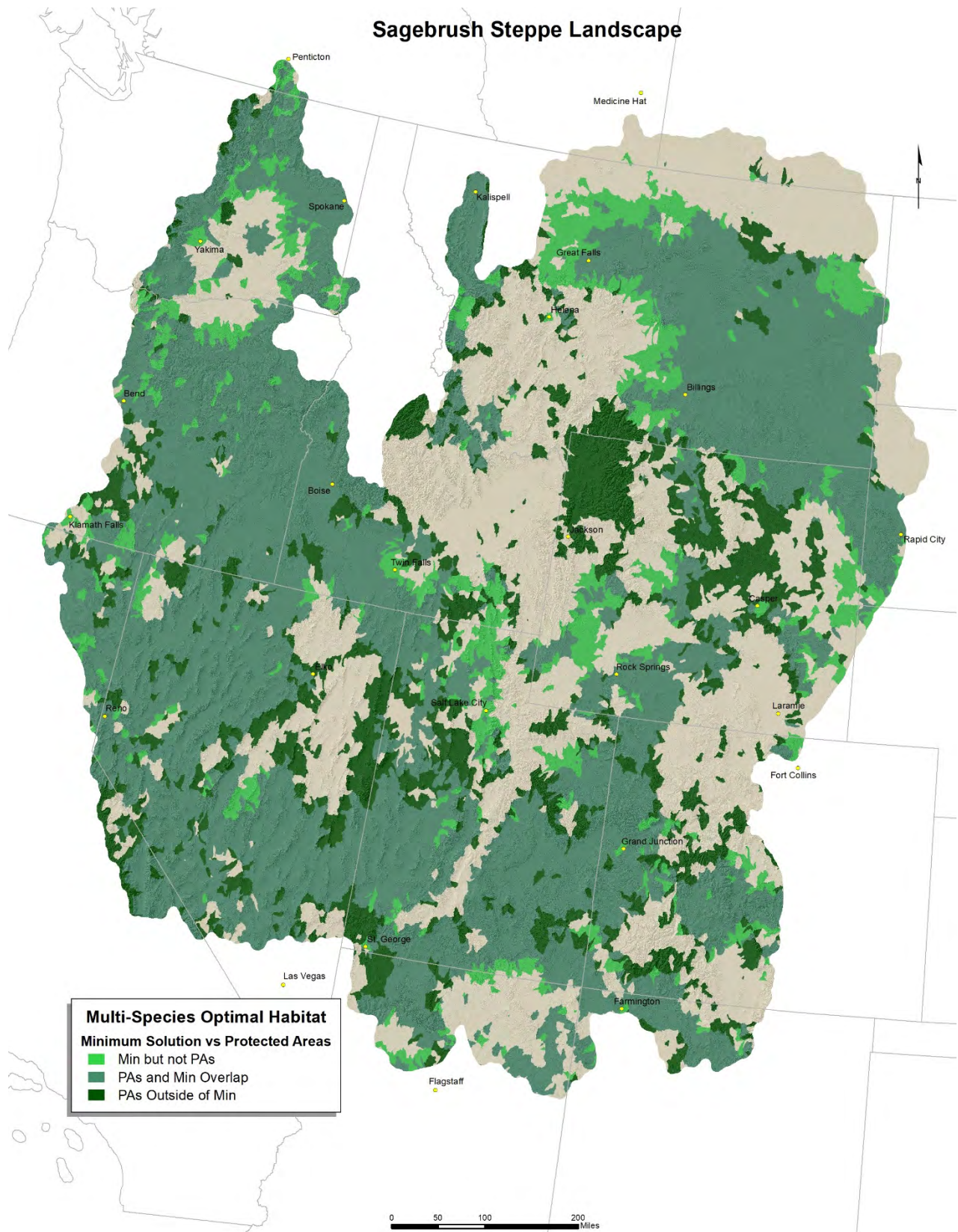


Figure 2.13. Comparison of optimization solutions: Minimum Area to the Protected Areas, targeting already protected areas (USGS Gap Analysis Program 2018), with more weight given to protected areas Levels 3 and 4.

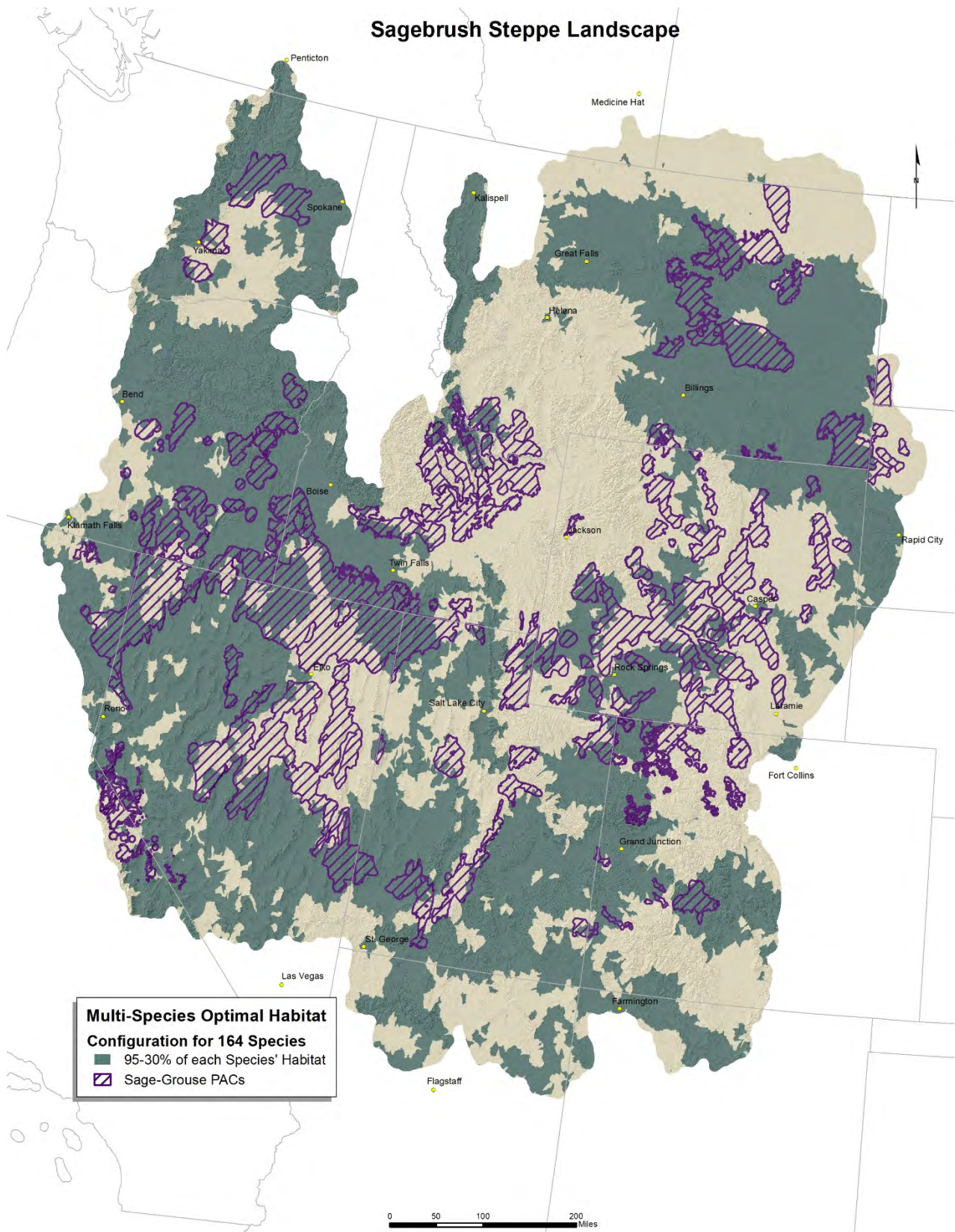


Figure 2.14. Sage-grouse Priority Areas for Conservation (PACs) (USFWS Wyoming Ecological Services 2014) overlaid on optimal multi-species habitat including 95% to 30% of species individual habitats. [Note: the units in the SE are ranges of Gunnison sage-grouse >5,000 ha, not part of the original PACs].

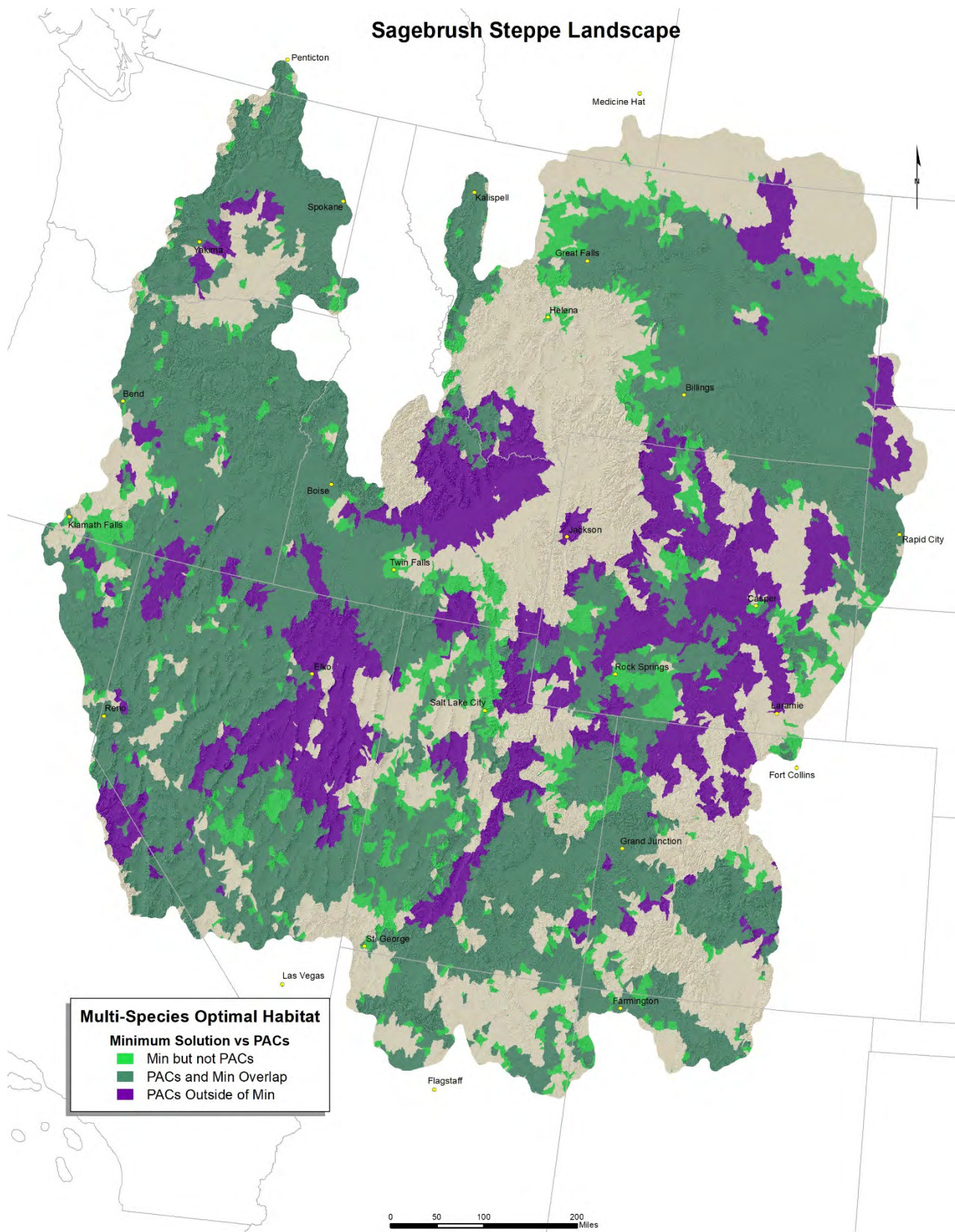


Figure 2.15. Comparison of optimization solutions: Minimum Area to the Sage-Grouse PACs optimization solutions, targeting sage-grouse Priority Areas for Conservation (USFWS Wyoming Ecological Services 2014).

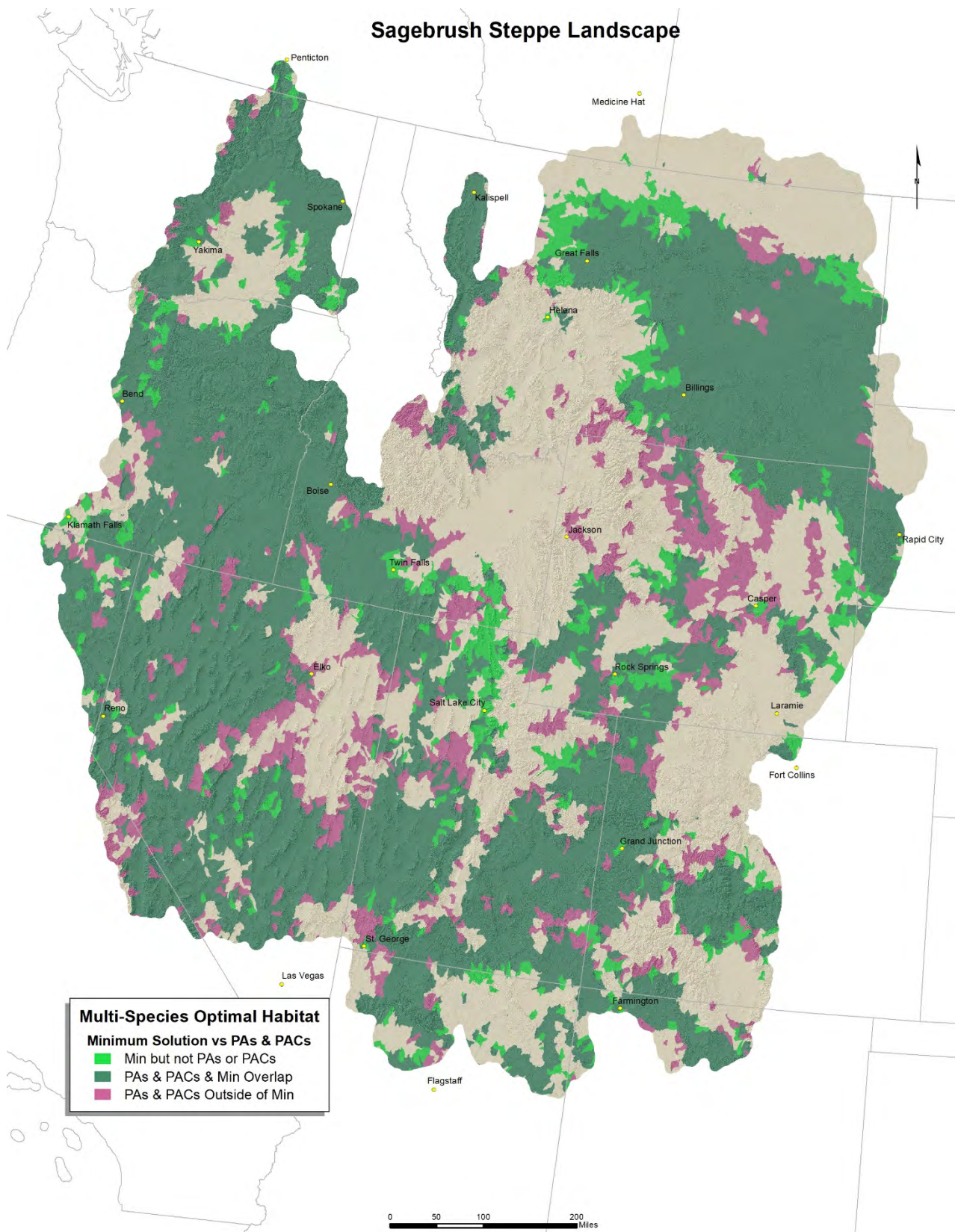


Figure 2.16. Comparison of optimization solutions: Minimum Area to the PA and PACs optimization solutions, targeting combined protected areas (USGS Gap Analysis Program 2018) and sage-grouse Priority Areas for Conservation (USFWS Wyoming Ecological Services 2014).

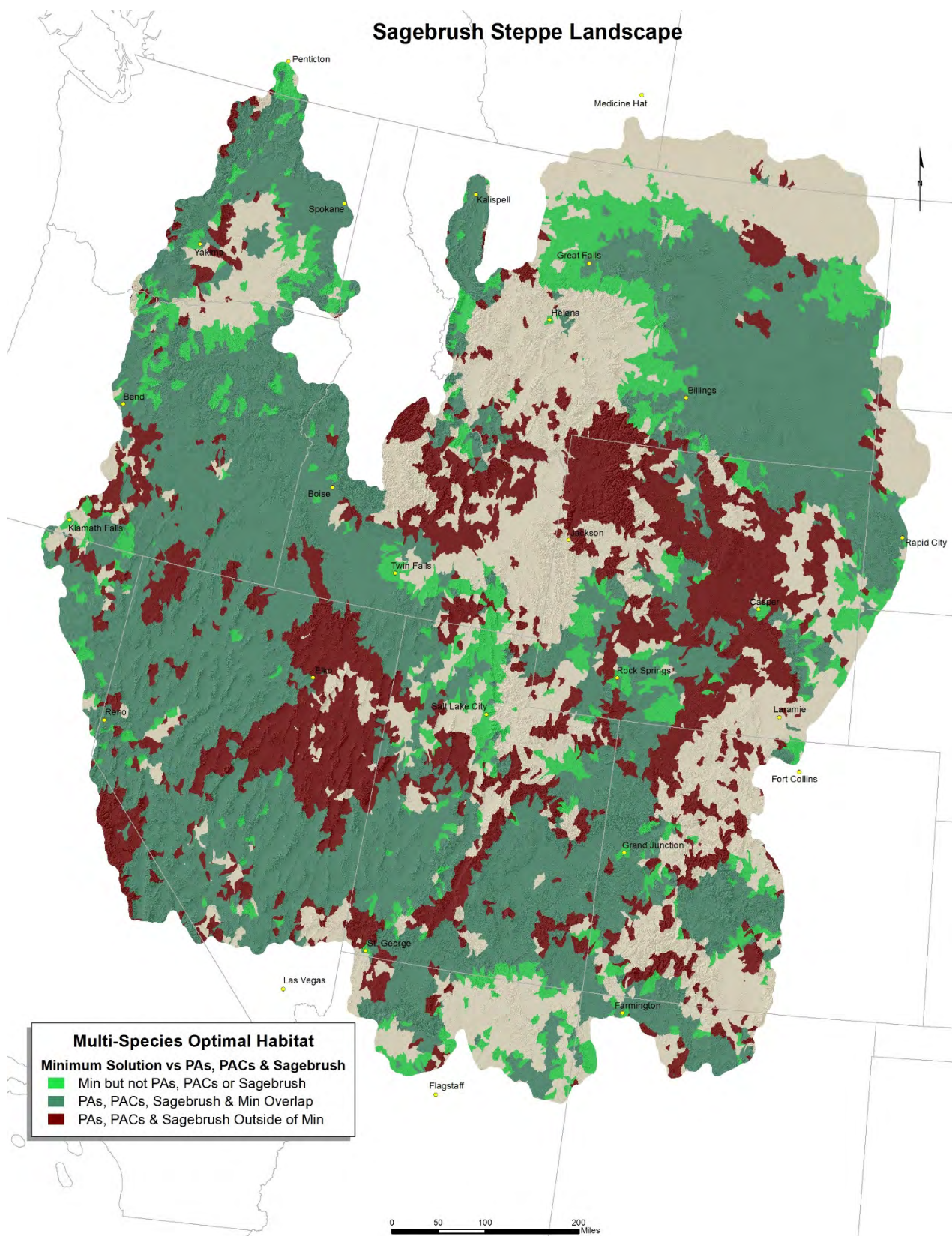


Figure 2.17. Comparison of optimization solutions: Minimum Area to the Sagebrush, PAs and PACs optimization solutions, targeting combined sagebrush landcover, combined protected areas (USGS Gap Analysis Program 2018) and sage-grouse Priority Areas for Conservation (USFWS Wyoming Ecological Services 2014).

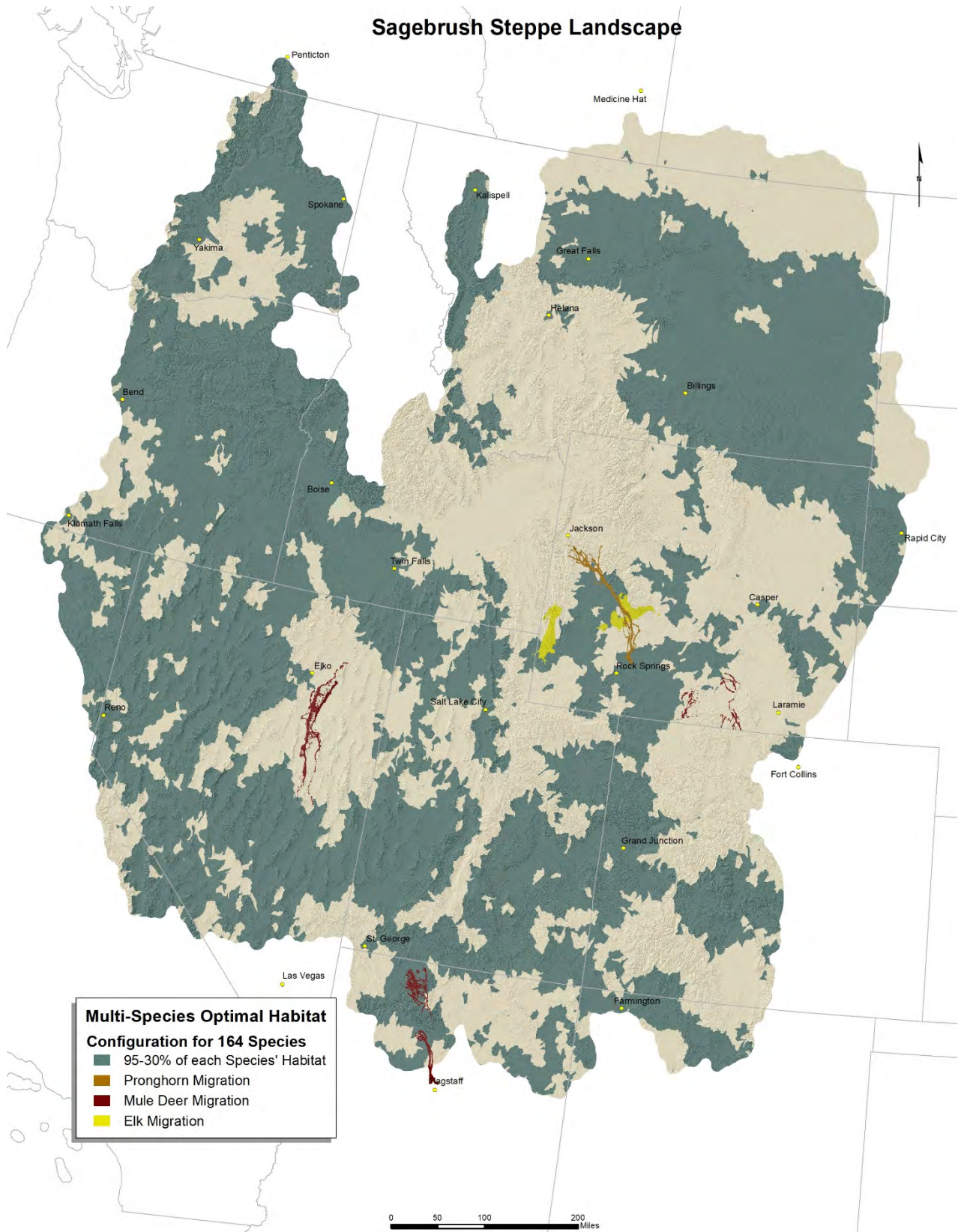


Figure 2.18. Optimal habitat configuration overlaid with important routes of 3 migratory species (Kauffman et al. 2020), showing the portions of the migration routes inside and outside of the 95-30% optimal habitat solution.

DISCUSSION

The results of adding the 164 fundamental habitat layers of the species in this biome together highlighted areas important for multiple species (Figure 2.10). However, mapping the number of species with overlapping habitats (Figure 2.11), revealed that the areas with the highest number of species with overlapping habitats, consisted of only 94 of the 164 species. There were no areas that contained all species habitats together. Targeting just these (specie-rich) areas, where many but not all species habitats overlap for conservation, would neglect protecting many species' fundamental habitats.

The land configuration estimates from this systematic conservation planning (SCP) approach are the most likely to ensure the persistence of all 164 species, given that it encompasses whole populations, is based upon fine-scale habitat distinctions, and includes the highest value fundamental habitats based upon suitability and contiguity for each species. These multi-species habitat configurations include taxa that have not been included in these types of conservation planning efforts before, due to the previous paucity of data about them.

The multi-species optimization solutions produced for different conservation objectives and different percentages of the 164 species' habitats, resulted in land configurations amounting to 36% to 65% of the biome's area. Setting the percentages of each species habitat to include in the optimization procedure to 30% for all species, resulted in 36% of the biome required for the multi-species solution. 30% is the minimum amount of land area recommended by conservation planners to preserve biodiversity. For example, the "30 x 30 Goal" to conserve, connect, and restore 30 percent of U.S. lands and waters by 2030 (USDOJ 2021), or the recently proposed global goal by the Convention on Biological Diversity (2021), which states "...that at least 30 percent globally of land areas and of sea areas, especially areas of particular importance for biodiversity and its contributions to people, are conserved through effectively and equitably

managed, ecologically representative and well-connected systems of protected areas and other effective area-based conservation measures, and integrated into the wider landscapes and seascapes.”

Many conservation planners claim, however, that 30% protection is inadequate, especially for species where small amounts of habitat are available to start with (Dinerstein et al. 2017, Mogg et al. 2019, Woodley et al. 2019). Allan et al. (2022) determined the minimum amount of land needed to be managed to protect biodiversity is 44% of terrestrial lands, on average across the globe. Others argue that goal is inadequate (Mogg et al. 2019, MacKinnon et al. 2021) and that the amount of required habitat for species depends upon the ecosystem, the conditions and the species. Given that the species in this biome had widely differing amounts of habitat available to them, the judicious conservative approach to protecting their persistence seemed to be to protect large percentages of habitats of species with smallest amounts of overall habitat available, while sequentially protecting smaller percentages of the highest value species’ habitats, of species with more fundamental habitat available (still resulting in more habitat included for these species).

The percentages of each species’ fundamental habitat used in the optimization routine is just one estimate of the amount of highest value fundamental habitat that might be required for each species’ persistence, used to illustrate how a multi-species biome-scale conservation plan can be developed with these fundamental habitat models. These habitat amounts can and should be updated with other criteria, such as range size and natural population density, or more precise demographic-viability information, when available, including via viability analyses that estimate the population sizes and habitat amounts needed to persist in changing landscapes and climate. Re-running the optimization routine with new habitat percentages and conservation objectives takes 10-15 minutes, so many different conservation objectives can easily be compared.

Comparing these areas, optimized to include the highest value fundamental habitats of the obligate taxa of this biome to already protected areas within the biome, revealed that existing protected areas will not provide sufficient habitat for these species on their own. Protected areas were not necessarily selected for protecting biodiversity and even those that were, are not usually sufficient to sustain populations of native species (Cantu-Salazar et al. 2013, Wauchope et al. 2022). Instead, this SCP approach can be used to identify the highest value habitats for native taxa and used to find a balance between utilizing protected lands (including PACs identified for sage-grouse conservation) and the overall amount of land required to protect all these taxa.

The least amount of land required for the multi-species optimized solution using a sliding scale of habitat inclusion was with the Minimum Area scenario, which required ~55% of the land area of the biome. Adding additional conservation objectives to the optimization procedure increased the amount of land required to meet the additional goals. The actual cost to meet these goals, however, might be less than the Minimum Area scenario even though they require more land, because some of these scenarios targeted areas that already have some level of protection for wildlife and therefore would not need as much additional land to acquire or manage. The resulting percentages of the amount of land required to protect the native taxa of this biome, are in line with recent estimates of what is required (Pimm et al. 2018, Mogg et al. 2019, MacKinnon et al. 2021).

Protecting 55-65% of the biome for native taxa may seem infeasible, but it is not suggested to set aside these lands for biodiversity conservation, rather it is to manage this land in such a way as to reduce the threats to species persistence. Planners promoting protecting lands for biodiversity acknowledge that protection must be accomplished while accommodating land uses that humans depend upon (Díaz et al. 2019, IPBES 2019, Almond et al. 2020, Leclère et al. 2020). Simply setting aside areas as off-limits to human activity for the protection of native taxa

is infeasible because of human needs, and ineffective because conditions are rapidly changing (Moilanen et al. 2005, Mora and Sale 2011, Mace 2014, Wauchope et al. 2022). Human activity already affects most of the lands and waters of Earth and will continue to do so (Steffen et al. 2018, Ellis 2021, Folke et al. 2021). The only option available now to protect native taxa is to work with private land owners, tribes, farmers, ranchers, developers, and other stakeholders to manage land in such a way as to provide for human needs, while at the same time attempting to preserve the ecological integrity of landscapes (Noss 2000, Coad et al. 2019, Díaz et al. 2019, Leclère et al. 2020).

This approach has advantages over other landscape-scale conservation planning approaches based on species richness “hotspots” (Ceballos and Ehrlich 2006), protected areas (Chauvenet et al. 2017), land facets (Beier and Brost 2010), umbrella species (Carlisle et al. 2018, Runge et al. 2019), undisturbed areas (Kennedy et al. 2019), ecosystem intactness (Plumptre et al. 2021), or ecological integrity (Meinke et al. 2009, Brown and Williams 2016, Doherty et al. 2022, Doherty et al. 2024). The SCP method developed here differs from these other methods by incorporating specified amounts of obligate species’ highest value fundamental habitats (based upon suitability and contiguity; Chapter 1) for a wide range of taxa, to produce optimal multi-species habitat configurations that require the least amount of land, while incorporating any of these other conservation objectives. The objectives, species-specific habitat amounts, and unit costs can be easily changed and the effects of different inputs and objectives explored.

The procedures developed here can be used as a decision support process for conservation planners attempting to conserve the native taxa of the sagebrush steppe biome. As more data become available for more taxa in more places (GBIF 2022, Mesaglio et al. 2023), this planning can be done in other biomes of the U.S. and Canada, using existing uniform biotic and abiotic data layers as covariate data, and in other places in the world with adequate covariate datasets.

If applying to different biomes (e.g. grasslands, wetlands), more appropriate covariate data layers may be required to identify the habitat associates that the obligate species of that biome are relying upon. For example, if you were to use this approach in the Everglades (Flooded Grassland) Biome in Florida, it would be beneficial to have a detailed map of wetland types to use as a covariate data layer for habitat modeling. Local conservation planners would be the best source of information to determine what habitat variables might be most important for local native species.

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CHAPTER 3: IS THE UMBRELLA SPECIES APPROACH EFFECTIVE IN PROTECTING THE FUNDAMENTAL HABITATS OF SYMPATRIC TAXA?

INTRODUCTION

Conservation of the sagebrush steppe biome has relied, in large part, on protecting and restoring habitat for the greater sage-grouse (*Centrocercus urophasianus*) and the Gunnison sage-grouse (*C. minimus*) (Dobkin 1995, Wisdom et al. 2005, Hanser and Knick 2011, Boyd et al. 2014, Remington et al. 2021). Sage-grouse are dependent upon vast, undisturbed tracts of sagebrush landcover to survive (Aldridge et al. 2008, Connelly et al. 2011, Manier et al. 2013) and are imperiled because this habitat has been converted, fragmented, disturbed, developed, invaded by conifers and nonnative species, and stressed by changing climate and increasing fire intensities (Wisdom et al. 2011). There are several rigorous, detailed models of sage-grouse habitat (Aldridge 2005, Aldridge and Boyce 2008, Doherty et al. 2010a, Heinrichs et al. 2010, Crist et al. 2015, Dumroese et al. 2015, Coates et al. 2016, Heinrichs et al. 2017), and considerable work has gone into determining what actions need to be taken to protect sage-grouse and what areas need to be protected (Knick and Connelly 2011, Knick et al. 2013, Manier et al. 2013, USFWS 2013, Arkle et al. 2014, Fedy et al. 2014, Stiver et al. 2015, Doherty et al. 2016, Heinrichs et al. 2017, Hanser 2018).

A common conservation strategy for this biome is based upon the idea that protecting sage-grouse habitat will protect the other taxa reliant upon the sagebrush steppe landscape; that is, that sage-grouse will serve as an umbrella species for sympatric species (Dobkin 1995, Rich and Altman 2001, Rowland et al. 2006, Hanser and Knick 2011, Gamo et al. 2013, Copeland et al. 2014, Holmes et al. 2015, Pilliod et al. 2020). The original concept of an umbrella species approach to conservation, is: "...if minimum area requirements are met for selected species which

fulfil certain criteria, adequate survival conditions can be simultaneously assured for many other species in a biota” (Wilcox 1984). “Minimum area requirements” for the umbrella species are those that will support population viability (Noss 1991, Berger 1997, Caro and O'Doherty 1999). This approach assumes that if the areas required to maintain viable populations of the umbrella species are sufficiently protected (this must be ascertained), then “adequate survival conditions” for some sympatric species will also be provided (Caro 2003, Roberge and Angelstam 2004).

To test the efficacy of the umbrella species approach, as originally conceived (Wilcox 1984, Noss 1991, Caro and O'Doherty 1999), the efficacy of potential protected areas to sustain populations of sympatric taxa must be assessed (Berger 1997, Caro and O'Doherty 1999, Roberge and Angelstam 2004). Merely determining the percentages of sympatric species habitats or ranges covered by an umbrella area does not establish how well the umbrella supports those species' persistence (Remington et al. 2021). For an umbrella to protect sympatric species persistence, it must encompass a sufficient amount and configuration of each species' essential habitat (Remington et al. 2021).

Only a few studies consider whether conserving sage-grouse habitat is sufficient to sustain populations of sympatric taxa (Rich et al. 2005, Hanser and Knick 2011, Dinkins and Beck 2019, Remington et al. 2021, Smith et al. 2021). These studies find that the level of protection afforded is species-specific, with some species potentially being negatively impacted by management for sage-grouse, if they have dissimilar habitat needs (Remington et al. 2021). None of these assessments found comprehensive protection for sympatric species (Dinkins and Beck 2019, Barlow et al. 2020, Remington et al. 2021, Smith et al. 2021). For example, Runge et al. (2019) evaluated the use of sage-grouse as an umbrella species for 81 sympatric vertebrate species “strongly associated with sagebrush habitat”. They used available habitat models, or ranges for the sympatric species, at 270 m grain resolution and overlaid these with sage-grouse Priority

Areas for Conservation (PACs) (USFWS Wyoming Ecological Services 2014). They found the average overlap of species' ranges with sage-grouse PACs was 25%, and estimated risks to sympatric species were lower within the boundaries of PACs. They concluded that the sage-grouse umbrella benefitted many sage-associated species, but that not all species benefitted equally, and that some species would not be adequately protected under the umbrella. They concurred with Carlisle et al. (2018) and ultimately did not recommend sage-grouse as an umbrella species for this biome, and instead suggested that multi-scale approaches, or different focal species, should be explored as the targets of conservation planning (Runge et al. 2019).

The objective of this chapter is to compare a systematic conservation planning (SCP) approach to support sustaining populations of the obligate taxa of a biome, to the umbrella species approach. I compared the comprehensiveness of covering a wide range of obligate taxa, the amount of species habitat protections, the adaptability of the approaches to addressing different conservation objectives, and the confidence in the different approaches abilities to ensure the persistence of sympatric species.

METHODS

To compare the umbrella species approach to the SCP approach, I first developed models of fundamental habitat for a wide range of sympatric species, estimating the habitats most likely to support species persistence based upon suitability and multiscale contiguity (Chapter 1, Figure 1.29, examples for four species). I then estimated the minimum amount of each species habitat expected to be required to support species population persistence, including large percentages of the highest value fundamental habitat for species with small amounts of available habitat, and smaller percentages of highest value fundamental habitat for species with large amounts of available habitat, ranging from 30%-95% of species available habitats (Chapter 2). I used an optimization procedure to select areas of the biome that included the designated percentages of

the highest value habitats for each species using the least amount of overall land. The resulting multi-species habitat configurations used for these comparisons estimate the fundamental habitat required to provide the minimum foundation for ensuring the persistence of these 164 obligate species (Chapter 2, Figure 2.9). Any portion of these multi-species optimal configurations left unprotected, increase the likelihood that some obligate species populations would not persist.

I compared two different optimized habitat configurations to three different sage-grouse umbrellas, using proposed protected areas and two different habitat characterizations, to assess the amount of coverage a sage-grouse umbrellas had over the optimal habitat configurations for sympatric species. If sympatric species' fundamental habitats are located outside of an umbrella, then the umbrella would likely not ensure those species' persistence. I identified the species and amounts of habitat left unprotected by the umbrellas.

Sage-grouse habitat/conservation areas

I used three different spatial characterizations to represent the sage-grouse umbrellas, to determine what effects the selection of the umbrella had upon the results. I used sage-grouse Priority Areas for Conservation (PACs) (USFWS Wyoming Ecological Services 2014) for one umbrella that represented the lands prioritized for sage-grouse conservation (Figure 3.1). However, since, protecting PACs alone may not be sufficient to maintain sage-grouse viability (USFWS 2013, Crist et al. 2015, Crist et al. 2017, Remington et al. 2021), a criterion for defining the umbrella of an umbrella species, I also used two more extensive representations of sage-grouse habitat as umbrellas:

- 1) PAC Umbrella - represents a subset of sage-grouse habitat adopted by the sage-grouse conservation community (USFWS 2015) as priority areas for conservation (318,236 km²).
- 2) Priority Habitat Umbrella - developed by combining published sage-grouse priority habitat models together to create a composite map of priority habitat (654,192 km²).

- 3) General Habitat Umbrella - developed by combining all identified published sage-grouse habitat models together to create a composite map of all habitat (1,054,597 km²).

For the sage-grouse habitat maps, I used the habitat similarity index (HSI) models (Figure 3.2), which predict sage-grouse habitat suitability (or “similarity”) based on landcover and anthropogenic, topographic, soil, and climate variables (Crist et al. 2017). The core areas of this map align with the PACs, but include areas of habitat outside the PACs and identify more connected habitats than do the PACs. I also used maps of breeding population densities of greater sage-grouse (Doherty et al. 2010b) (Figure 3.3), and Bureau of Land Management/U.S. Forest Service sage-grouse habitat maps (Figure 3.4) *sensu* Makela and Major (2012) and the USDA Forest Service (2015). I divided these maps into priority (core) and general (comprehensive) habitat maps and combined the priority habitats together to make a comprehensive map of priority (core) sage-grouse habitat, and combined all the modeled habitats together for a comprehensive map of all (general) sage-grouse habitat (Figure 3.5).

An issue with all conservation approaches is that just identifying these areas as habitats or conservation areas does not ensure that these areas will be protected. There are different land use restrictions applied to the different areas, which won’t necessarily protect sage-grouse or the sympatric species found in these areas (Remington et al. 2021). For this assessment of whether sage-grouse can serve as an effective umbrella species, I treated the identified sage-grouse habitats/conservation areas as if they would be protected, realizing this may not be the case.

I used the general habitat map to determine whether sage-grouse habitat, under the broadest interpretation, would serve as an umbrella for sympatric species, under the best-case scenario that all identified sage-grouse habitat would be protected/managed for sage-grouse persistence. I compared the results of using the PACs and the two habitat maps to determine the effects of using different characterizations of the sage-grouse umbrella.



Figure 3.1. Sage-grouse Priority Areas for Conservation (PACs) (USFWS Wyoming Ecological Services 2014) [Note: the units in the SE are ranges of Gunnison sage-grouse >5,000 ha, not part of the original PACs].

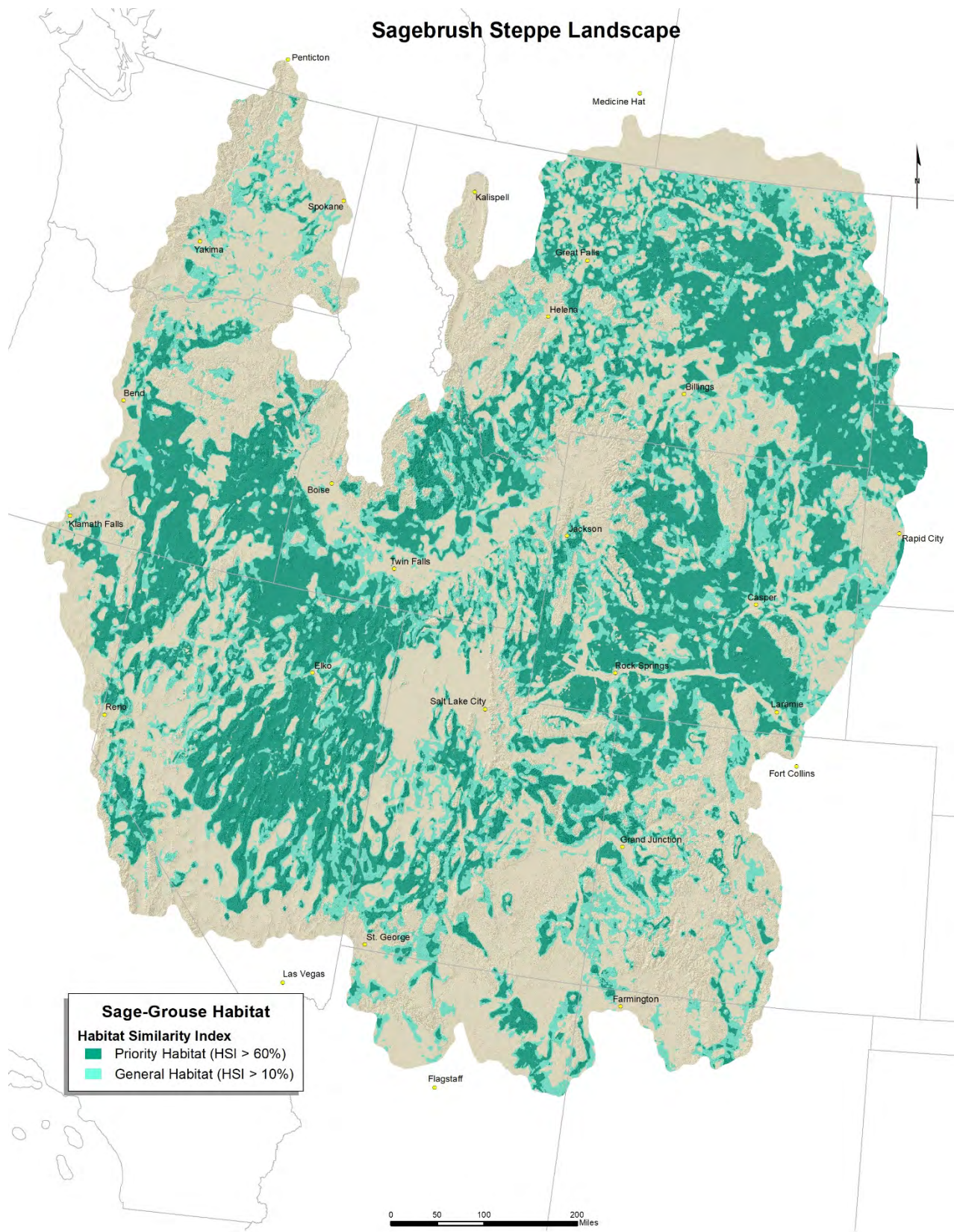


Figure 3.2. Habitat Similarity Index (HSI) for greater sage-grouse showing priority (HSI \geq 60%) and general (HSI \geq 10%) habitat areas. HSI is modeled from land cover, anthropogenic, soil, topography, and climate variables (Crist et al. 2015).

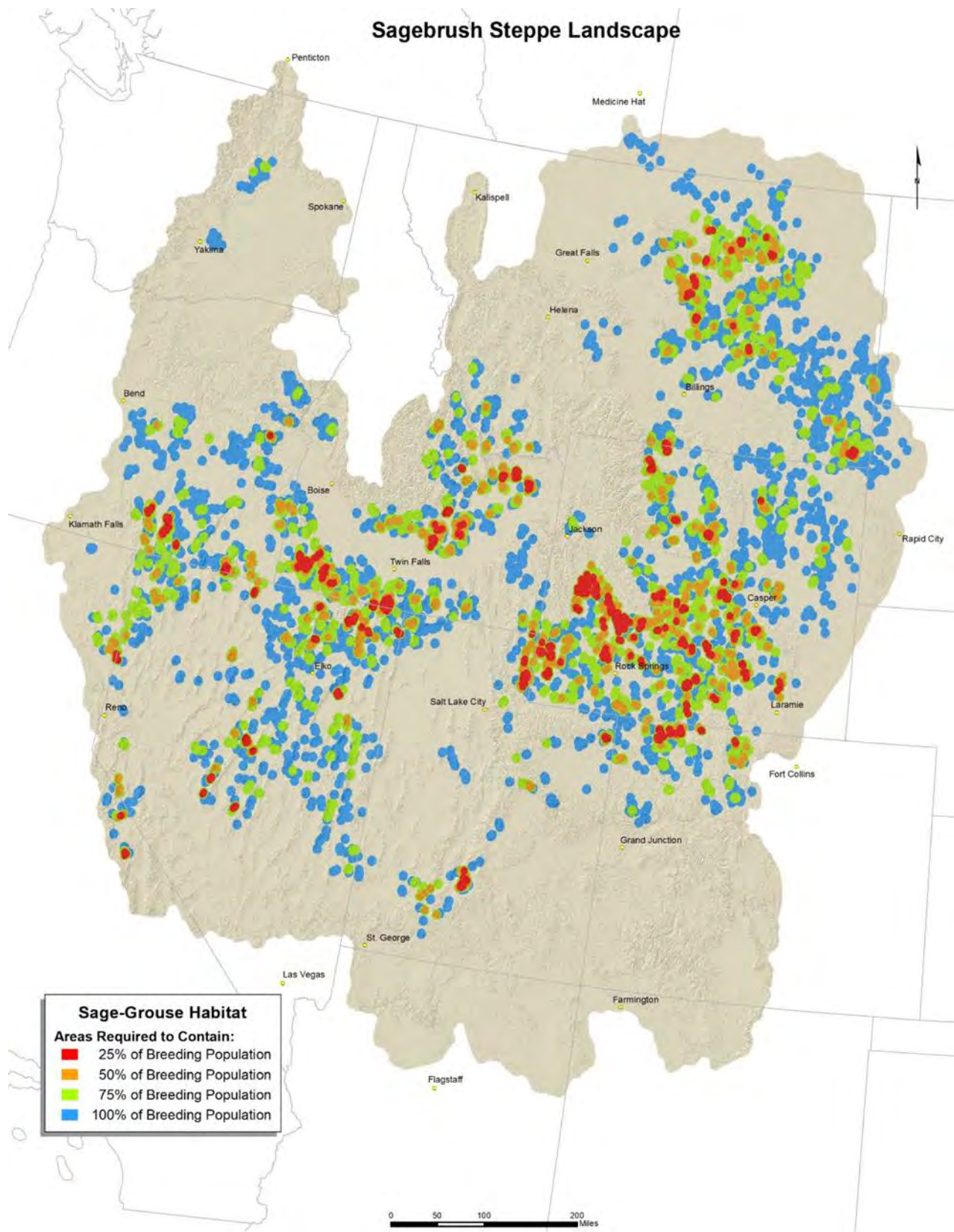


Figure 3.3. Areas required to contain 25%, 50%, 75% and 100% of greater sage-grouse breeding populations (Doherty et al. 2010b).

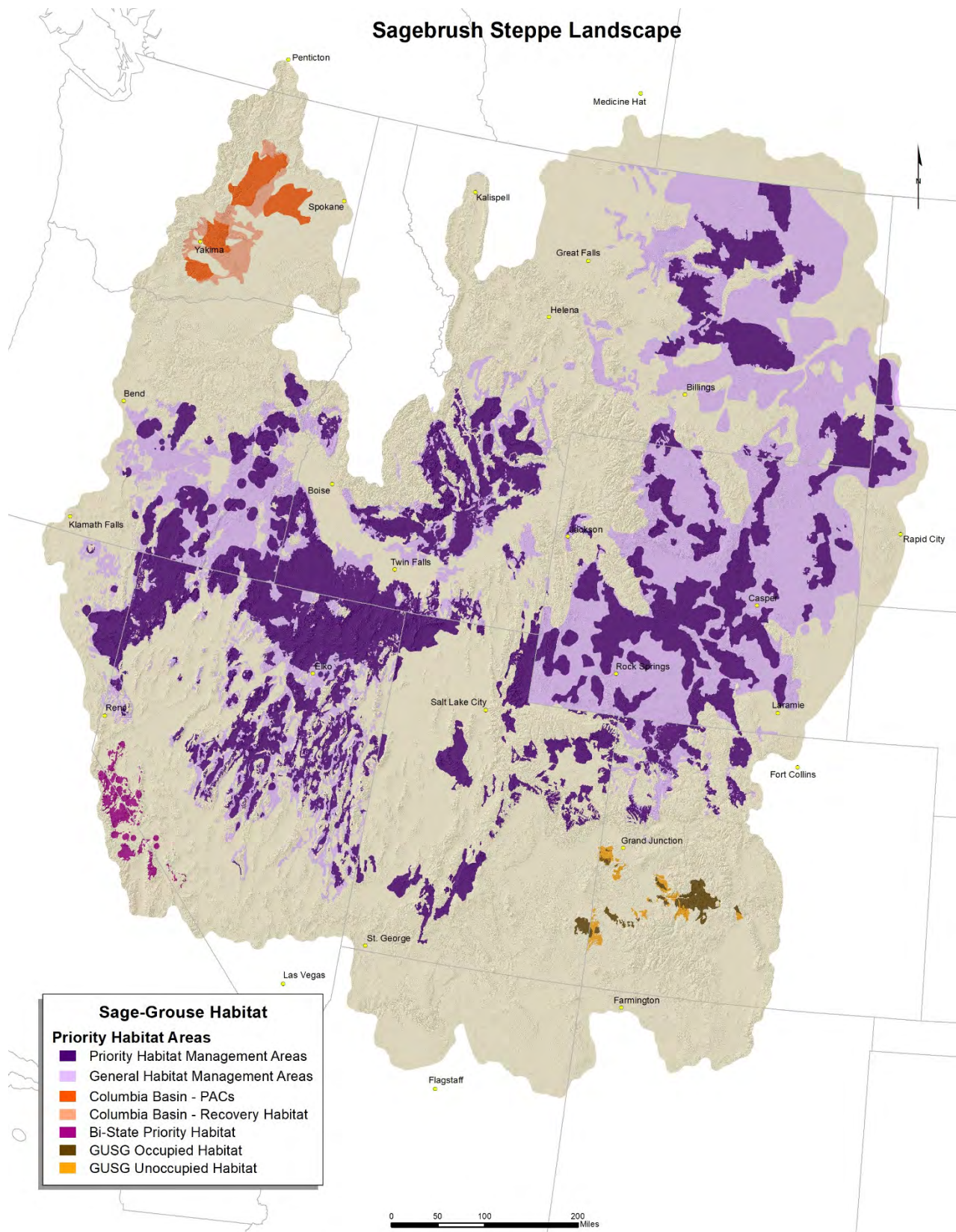


Figure 3.4. Priority and general sage-grouse habitat, compiled from different BLM and Forest Service state-wide assessments *sensu* Makela and Major (2012) and USDA Forest Service (2015), including PACs, PPAs & PPMAs, PHMAs & GHMAs, recovery habitat, and Gunnison sage-grouse habitat.

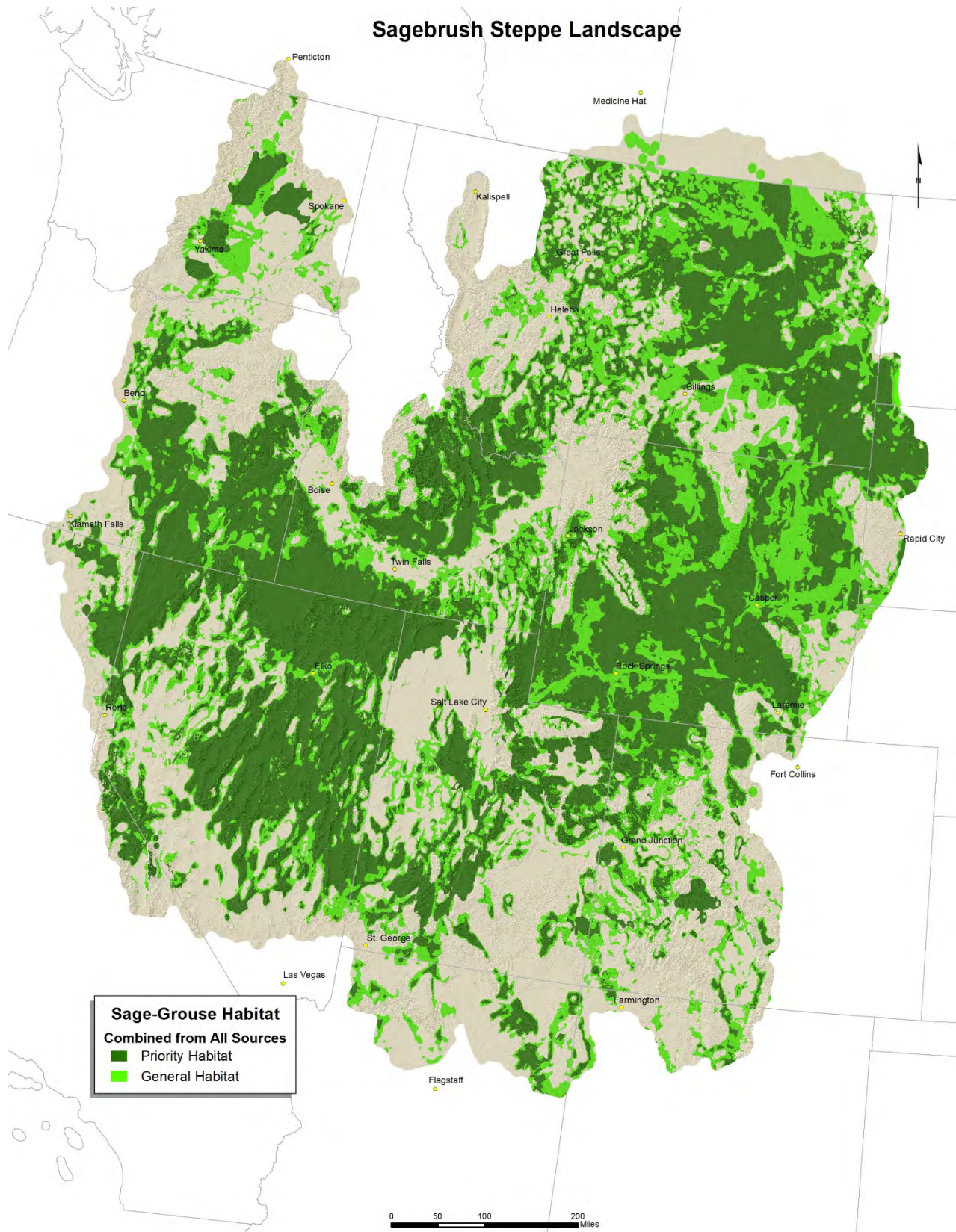


Figure 3.5. Combined predicted sage-grouse habitat from different sources, including PACs (USFWS Wyoming Ecological Services 2014), HSI (Crist et al. 2015), BLM state-wide assessments *sensu* Makela and Major (2012), and breeding population densities (Doherty et al. 2010b). Note that most did not include habitats in Canada.

Multispecies optimal habitat configurations of obligate species

I used two different multi-species habitat configurations for 30-95% of the highest value fundamental habitats of 164 sympatric species of the sage-steppe biome (Chapter 2): the Minimum Area solution, using the least amount of land (Figure 2.9); and the Sage-Grouse PACs solution, targeting sage-grouse PACs while still protecting the specified amount of each species highest value habitat (Figure 2.15).

Comparing umbrella species to systematic conservation approaches

To assess the effects that different land configurations had on the results, I overlaid the two different multi-species habitat configurations with the three different sage-grouse habitat/conservation maps using ArcGIS (ESRI 2020) for a total of six different umbrella - SCP comparisons. I recorded the amount of the multi-species optimized habitat solutions left outside the sage-grouse umbrellas for each of these six combinations, to reveal for each combination which species and how much of their optimal fundamental habitat would not be protected by a sage-grouse umbrella.

I also identified how much of each species overall fundamental habitat was left out of coverage under the umbrellas for the six different scenarios. I grouped species by the available habitat included in the multi-species solutions (which was based on the overall amount of fundamental habitat they had available), which was estimated to be the minimum amount of the highest value fundamental habitat required to support their persistence (Chapter 2). I partitioned species into three groups based on their overall available fundamental habitat:

- 1) Limited Habitat Species: with < 10 million ha of fundamental habitat (59 species)
- 2) Intermediate Habitat Species: with 10-55 million ha of fundamental habitat (17 species)
- 3) Abundant Habitat Species: with >55 million ha of fundamental habitat (88 species)

I quantified the amount of habitat covered by each of the three umbrellas for each of these groups of species to ascertain whether the umbrellas would include the estimated required percentages of each species fundamental habitat, based on the assumption made in Chapter 2 that these amounts of fundamental habitat are required to sustain each species population viability.

RESULTS

I calculated the amount of habitat in two different multi-species optimized habitat configurations (Minimum Area and Minimum Area Targeting PACs) that coincided with three different sage-grouse umbrella maps (PACS, Priority Habitat, and General Habitat). Assessing the amount of spatial overlap, I found that protecting habitats based on sage-grouse umbrella maps (habitats or conservation areas) left approximately a third to over three-quarters of sympatric species habitats unprotected (Figures 3.6 - 3.11); i.e., the umbrellas did not fully cover the multi-species solutions. The amount of sympatric species habitat left unprotected ranged from 33% (PAC solution, with general (comprehensive) sage-grouse habitats), to nearly 84% (minimum area solution, with sage-grouse umbrella represented by PACs; Table 3.1).

Table 3.1. Area of multi-species habitat solutions unprotected by sage-grouse habitat umbrellas

Multi-species Solutions:	<u>Minimum Area</u>		<u>Minimum Area + PACs</u>	
Area (km²):	977,915		1,119,513	
	<u>Sage-Grouse Umbrellas</u>		<u>Area Not Covered by Umbrellas</u>	
Sage-grouse PACs (318,236 km²):	818,188	83.7%	801,277	71.6%
Priority Habitat (654,192 km²):	624,260	63.8%	588,932	52.6%
General Habitat (1,054,597 km²):	410,661	42.0%	372,293	33.3%

All umbrellas left some species with no habitat protected, regardless of the multi-species habitat solution examined. This ranged from 1 species left unprotected in the scenario comparing the general (comprehensive) sage-grouse habitat umbrella to the multi-species solution targeting

PACs, to 6 species left unprotected in the scenario comparing the sage-grouse PAC umbrella to the minimum area multi-species solution (Table 3.2).

The number (and identities: Appendix D) of species from the three categories of species (based upon based upon their overall available habitat) with less than 40% (for species with abundant habitat available) and < 50% (for species with limited-intermediate amounts of available habitat) - left under protected in the six different comparisons of multi-species solutions to sage-grouse umbrellas are listed in Table 3.2. Species with limited habitat (n = 59), had a range of 40-52 species (67.8-91.5%) with less than 50% of their habitats protected under the umbrellas. Species with intermediate available habitat (n = 17), had a range of 2-17 species (29.4-100%) with less than 50% of their habitats protected by the umbrellas. And species with abundant available habitat (n = 88), had 1-5 species (1.1-5.7%) with less than 40% of their habitats protected by the umbrellas (Table 3.2). A 40% threshold was used for this group because they had abundant fundamental habitat available and 40% still left them with large amounts of habitat.

Table 3.2. Number of sympatric species with habitat left unprotected by sage-grouse umbrellas

Multi-Species Solutions Compared to Different Sage-Grouse Umbrella	Number of Species with Percentages of Habitat Not Covered by Umbrellas				
	0%	Limited Habitat Species < 50% Covered	Intermediate Habitat Species < 50% Covered	Abundant Habitat Species < 40% Covered	Total # Species Unprotected
Minimum Area Solution and Sage-Grouse PACs	6	51 (86.4%)	15 (88.2%)	2 (2.3%)	74 (45.1%)
Minimum Area Solution and Priority Habitat	4	51 (86.4%)	11 (64.7%)	1 (1.1%)	67 (40.9%)
Minimum Area Solution and General Habitat	2	41 (69.5%)	2 (29.4%)	1 (1.1%)	46 (28.0%)
Targeting PACs Solution and Sage-Grouse PACs	3	54 (91.5%)	17 (100%)	5 (5.7%)	79 (48.2%)
Targeting PACs Solution and Priority Habitat	2	52 (88.1%)	15 (88.2%)	2 (2.3%)	71 (43.3%)
Targeting PACs Solution and General Habitat	1	40 (67.8%)	2 (12.5%)	2 (2.3%)	45 (27.4%)

The number of species for which the sage-grouse umbrellas did not match the percentage of habitat estimated to be required to support species persistence (Chapter 2) ranged from 45 species for the general sage-grouse habitat umbrella overlaid on the multi-species optimum solution targeting PACs, to 79 species for the PAC umbrella overlaid on the multi-species optimum solution targeting PACs. If the amounts of habitat estimated to be required to sustain species' persistence (Chapter 2) is accurate, then these species would be insufficiently protected by the sage-grouse umbrellas. For example, 40% of its highest value fundamental habitat was estimated to be necessary to protect the persistence of the black-tailed prairie dog (*Cynomys ludovicianus*), but only 30-34% of its habitat was covered by the 3 different sage-grouse umbrellas, which may be inadequate to assure its persistence.

All three of the umbrellas left some sympatric species habitats entirely uncovered. The comparison between the general sage-grouse habitat umbrella, the most comprehensive, including all estimates of sage-grouse habitat combined into one map, left only one species' fundamental habitat entirely unprotected when compared to the Sage-Grouse PAC targeted multi-species solution. The other comparisons left 2-6 species completely outside the umbrellas. These results make sense because the general sage-grouse habitat umbrella was the largest umbrella compared to a multi-species solution targeted to sage-grouse habitat, and the sage-grouse PAC umbrella was the smallest umbrella compared to the multi-species solution with the smallest area.

The general habitat umbrella compared to the multi-species solution targeting PACs also had the fewest number of species with amounts of unprotected habitat larger than the amount estimated to support persistence. However, this number was 45 species out of 164, leaving over 27% of species not fully protected, under the largest, broadest definition of sage-grouse habitat, umbrella. The other two sage-grouse umbrellas left more species (up to 79) fundamental habitats unprotected (Table 3.2).

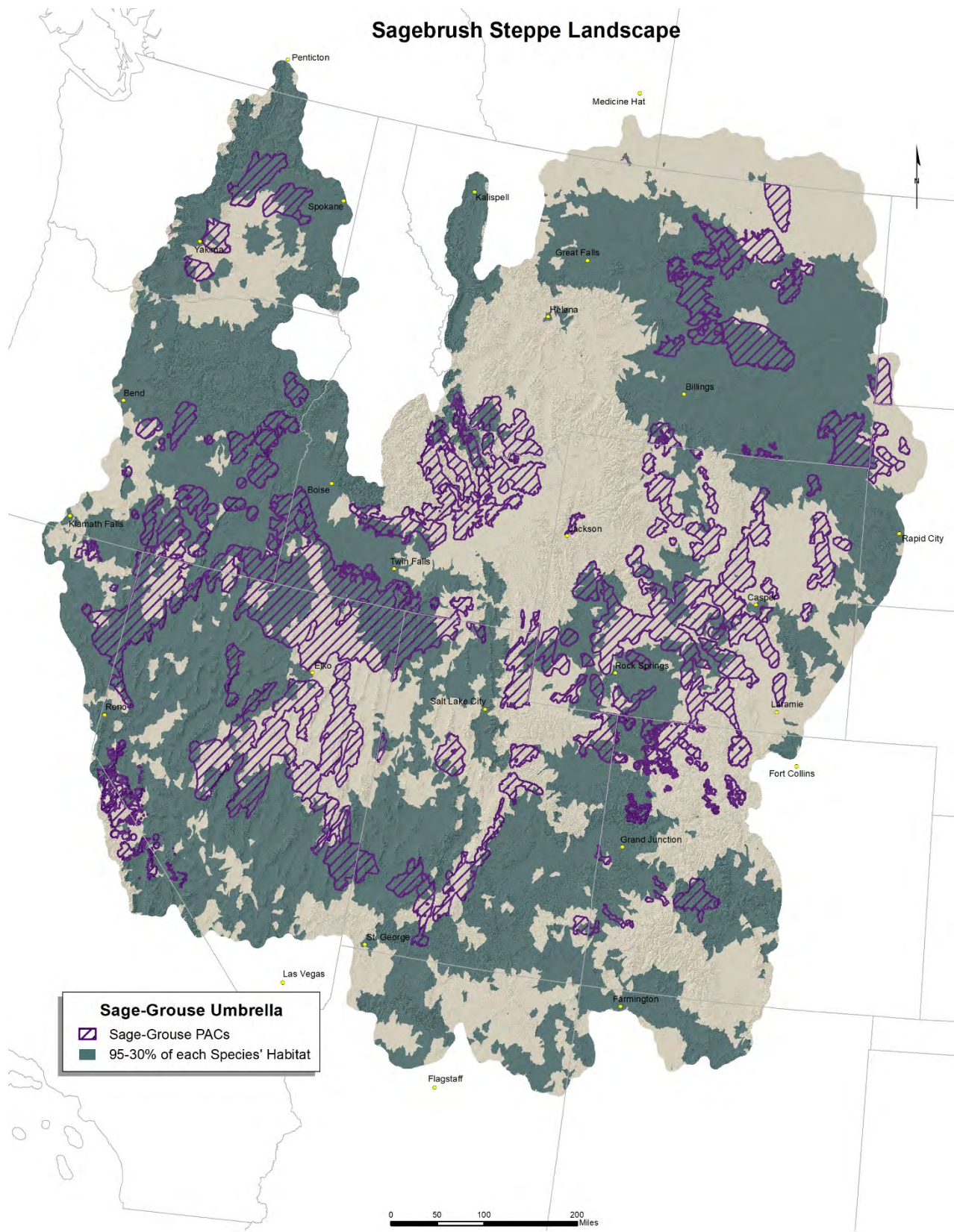


Figure 3.6. Sage-grouse Priority Areas for Conservation (PACs) umbrella (hatched) overlaid on the Minimum Area optimal multi-species configuration (including 95% to 30% of species fundamental habitats) showing areas of multi-species habitat configuration outside of sage-grouse umbrella.

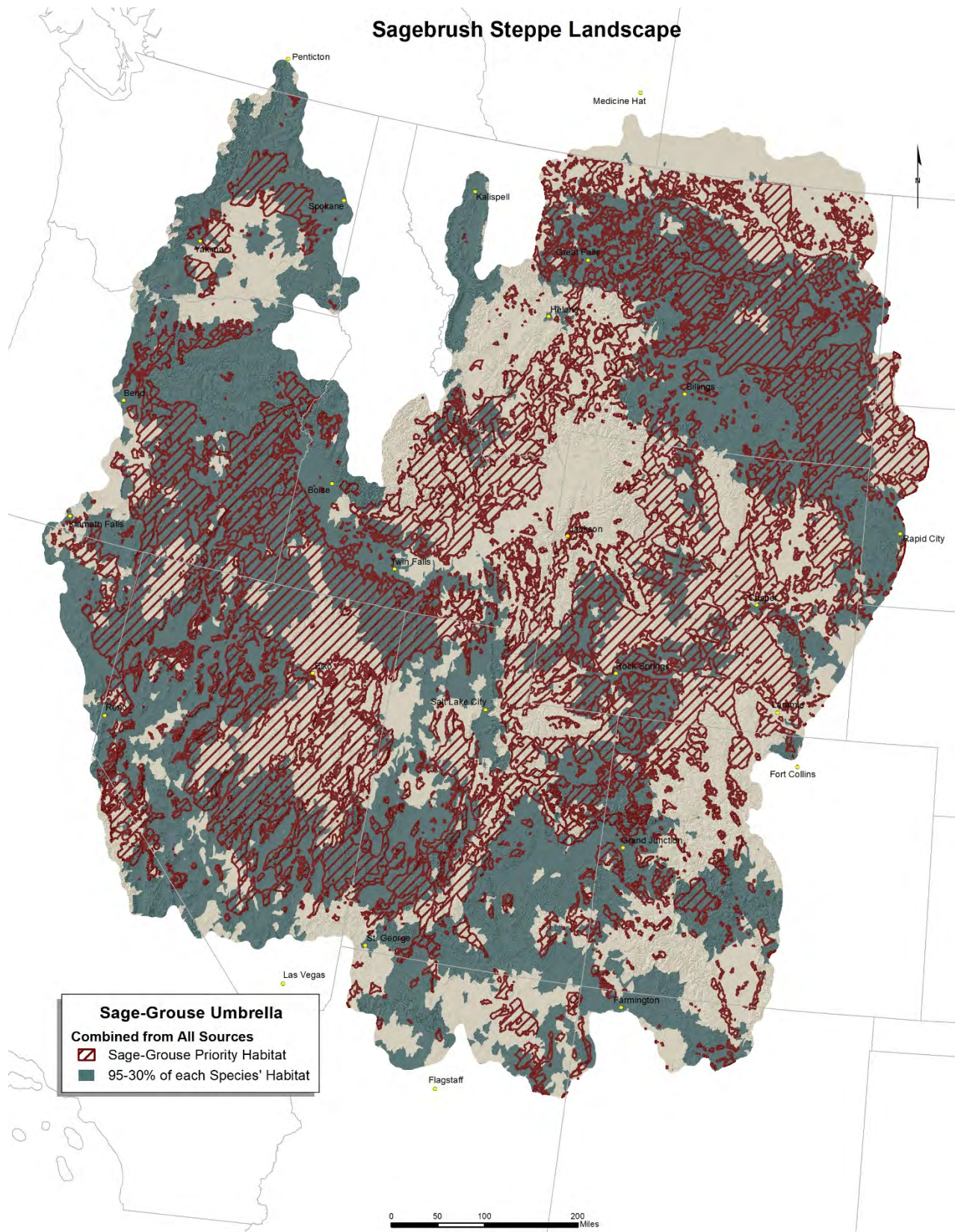


Figure 3.7. Priority sage-grouse habitat umbrella (hatched) overlaid on the Minimum Area optimal multi-species configuration (including 95% to 30% of species fundamental habitats) showing areas of multi-species habitat configuration outside of sage-grouse umbrella.

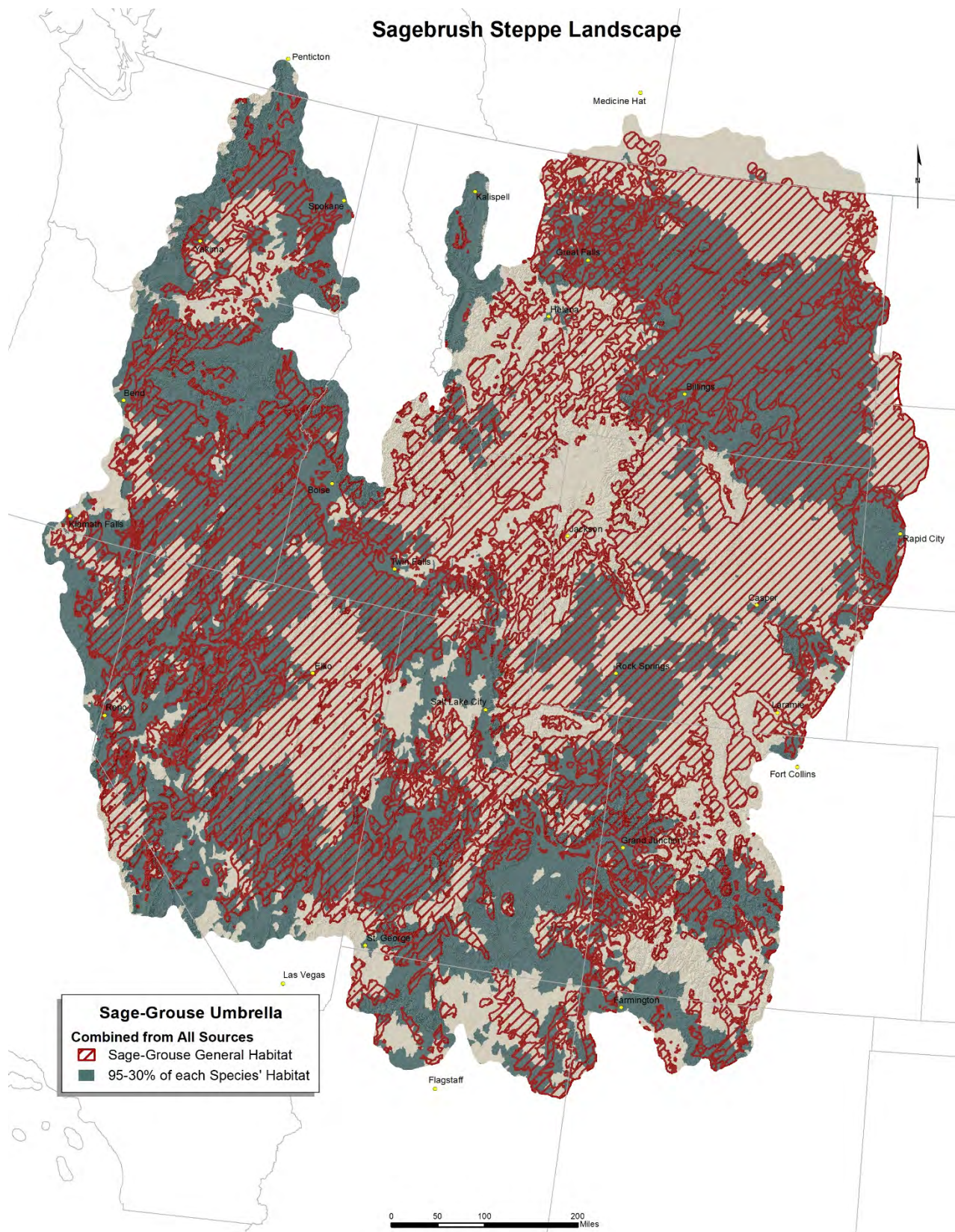


Figure 3.8. General sage-grouse habitat umbrella (hatched) overlaid on the Minimum Area optimal multi-species configuration (including 95% to 30% of species fundamental habitats) showing areas of multi-species habitat configuration outside of sage-grouse umbrella.

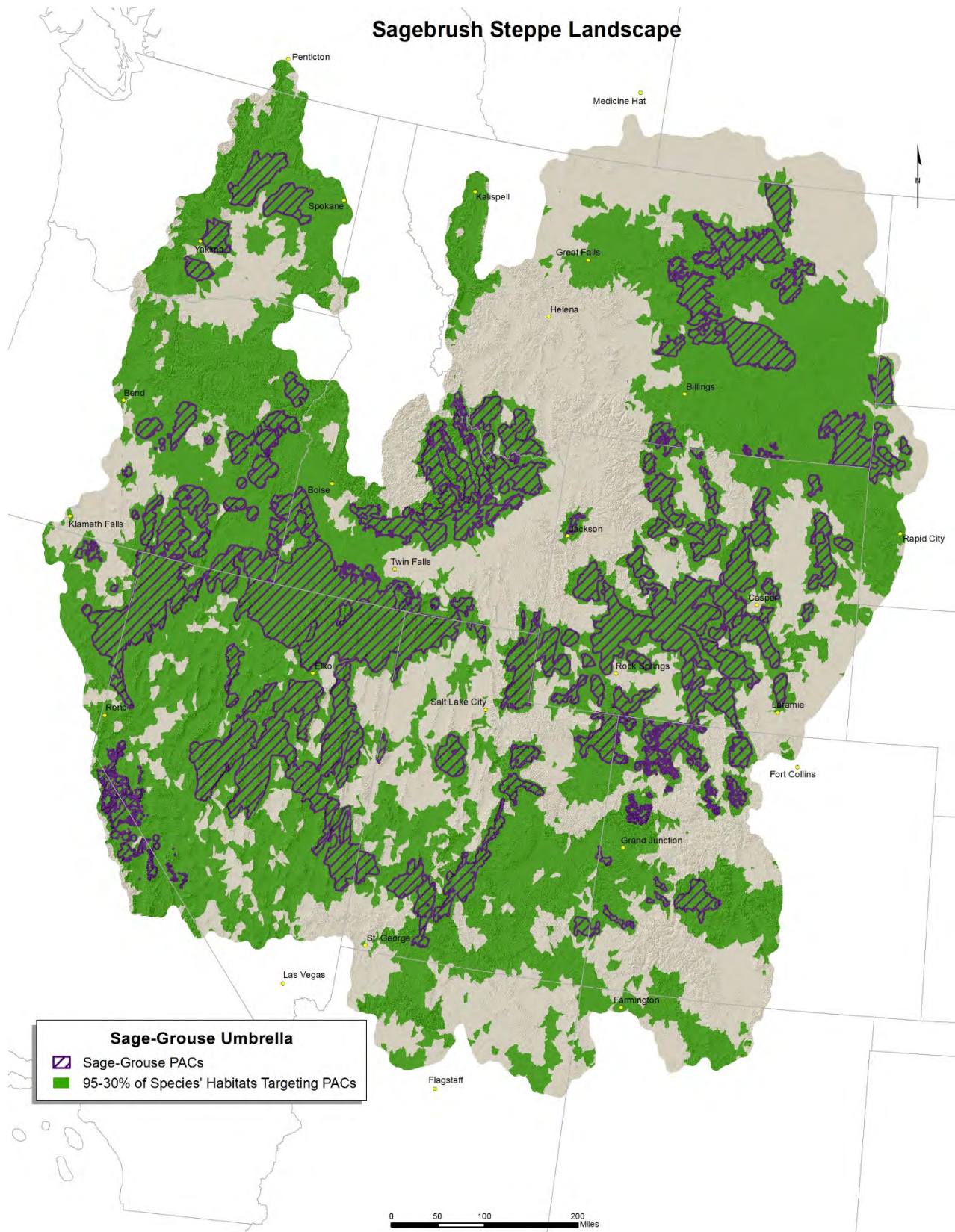


Figure 3.9. Sage-grouse Priority Areas for Conservation (PACs) umbrella (hatched) overlaid on the Sage-Grouse PACs targeted optimal multi-species configuration (including 95% to 30% of species fundamental habitats) showing areas of multi-species habitat configuration outside of sage-grouse umbrella.

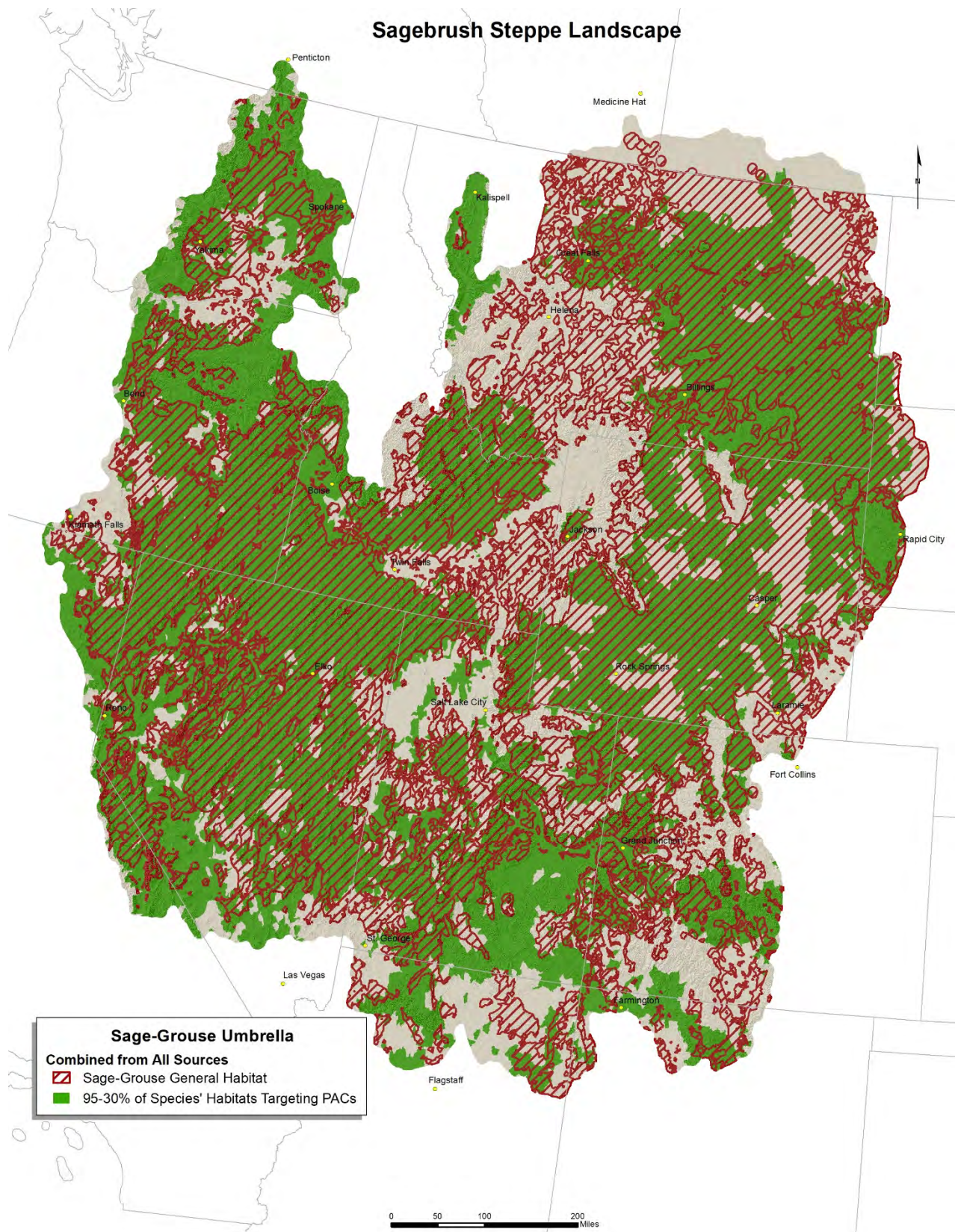


Figure 3.11. General sage-grouse habitat umbrella (hatched) overlaid on the Sage-Grouse PACs targeted optimal multi-species configuration (including 95% to 30% of species fundamental habitats) showing areas of multi-species habitat configuration outside of sage-grouse umbrella.

DISCUSSION

This comparison of approaches to multi-species biome-scale conservation revealed that using sage-grouse as an umbrella species and protecting even the broadest definition of sage-grouse habitat, would leave many sympatric species with insufficient protection or in some cases fully unprotected. The umbrella species approach is recommended to provide some level of general protection when there is little information about the other native species in a biome. This analysis showed that protecting a sage-grouse umbrella does protect the fundamental habitats of some sympatric species. However, if you just relied on the umbrella species approach, there would be some species habitats left entirely outside the umbrella (1-6 species in this analysis) and quite a few other species with significant portions of their habitats left unprotected (Table 3.2).

This analysis differed from others in that others overlay the umbrellas on sympatric species ranges or modeled habitats and postulate a level of protection for sympatric species based on how much of their habitat is covered by the umbrella (i.e., 50% of a species range or habitat offers some measure of protection to the species). This does not account for the importance of the habitats, covered by the umbrella, in sustaining species persistence. Protecting 50% of a species range or modeled habitat, for instance, may leave the most important, fundamental (most suitable, most contiguous) habitats unprotected, and the species' persistence may not be protected. Therefore, protecting some percentage of a species range or overall habitat does not equate to ensuring that level of protection of the species persistence, unless the coverage is very high, i.e., if 90% of a species habitat is protected by the umbrella, it is likely there is a high probability that that species persistence would be protected. However, quantifying that correlation can only be crudely done with species-area estimations, which are confounded by connectivity considerations (Fahrig 2002, Ovaskainen 2002).

The habitat models used in this study are significantly different than other habitat models in that they rank the importance of habitats based on the probabilities of habitat suitability and multi-scale contiguity, identifying areas that are most likely to support species persistence (Chapter 1). I call the outputs of these models “fundamental habitat”, because selecting an adequate amount of the highest value of this habitat for conservation action, results in spatially configured areas that include the most suitable and contiguous habitat, which is an essential foundation for conservation of species persistence.

I selected a percentage of the highest value fundamental habitat for each species to include in the conservation plans, based upon the overall amount of habitat each species had available (Chapter 2). These percentages are intended to represent the minimum amount of fundamental habitat that must be protected to support each species persistence. These percentages can be easily updated if new information becomes available about the amount of fundamental habitat required to support each species persistence.

Using fundamental habitat differs from comparisons of umbrellas to overall habitat, in that the amount, configuration, and location of the habitat is predicted to be required to support species persistence. Any portion of this habitat estimated as required to support the protection of species persistence, left unprotected, increases the risk of species not being able to persist. Without knowing the fundamental habitats required to protect species persistence, the effectiveness of an umbrella species approach to provide “adequate survival conditions” for sympatric species cannot be adequately ascertained. Protecting just some portion of a species’ suitable habitat does not provide enough information to assess their likelihood of persistence.

This analysis revealed that 1-6 species’ fundamental habitats were not covered by any of the umbrellas, depending upon the umbrella and multi-species configuration used, and overall 45-79 (27-48% of sympatric species) had portions of their habitat below the threshold estimated to be

required to support persistence, outside of a sage-grouse umbrella (Table 3.2). This indicates that a sage-grouse umbrella, however defined, would not adequately protect all sympatric species. Without these models of fundamental habitats and the amounts and configurations estimated to support species persistence, the essential habitats left outside the umbrella would not be known, therefore the amount of protection provided to sympatric species persistence is not known. Therefore, using an umbrella species approach leaves any unknown number of sympatric species with inadequate protection to support their persistence.

The larger amounts of habitat identified for protection by either the multi-species habitat solutions or the general sage-grouse habitat umbrella would protect more sympatric species, as expected. If we could protect the whole biome, we would not need to select any areas to prioritize for protection. Since we cannot protect the whole biome, a method is required to select the portions of the biome that are most likely to protect the native species which rely on it. The methods proposed in this systematic conservation planning approach attempt to identify the least amount of land that is most likely to ensure the persistence of all native species (and meet other conservation objectives). Obviously, the more land that is selected for protection, the easier it is to satisfy these objectives, so the largest interpretation of the sage-grouse umbrella would protect the most sympatric species. Acknowledging that the more area identified for protection protects more obligate species, comes up against the feasibility of how much land can actually be protected. Given that we cannot protect as much land as we would prefer, the approach that identifies the least amount of land that protects the most species' essential habitats is most likely achievable.

Species requisite habitats could be added to a sage-grouse umbrella to ameliorate inadequate protection for sympatric species, which would produce a multi-species umbrella that encompasses all obligate species, *sensu* Lambeck (1997), but this can only be done if there is available information about the habitat requirements of the sympatric species. If there is

information about the habitat requirements of all the species under consideration, then single- or multi- species umbrella approaches are superfluous. Umbrella species approaches are used as a shortcut in planning when there is inadequate information for planning for sympatric species. Now that this information is available and procedures for utilizing it have been developed, the umbrella species approach provides no advantages other than requiring less time and resources.

Using models of fundamental habitat (Chapter 1) and a SCP approach to combine these models into multi-species habitat configurations that include specified amounts of the highest value fundamental habitats (Chapter 2), produces a biome-wide configuration of habitat that is predicted to support the persistence of all sympatric species. Different conservation scenarios can be explored with emphasis on particular species or land parcels, and the effects on the overall multi-species plan can be compared. This approach has the additional advantage of being able to use the models of fundamental habitats for conservation planning for individual species, in addition to planning for obligate taxa *en bloc* across the biome.

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CONCLUSION

I successfully developed methods to overcome the barriers to modeling fundamental habitats for the obligate taxa of a biome, at high resolutions, whole population extents, and incorporating habitat connectivity to produce habitat locations and configurations that are most likely to support species persistence. These fundamental habitat maps for each species were then combined using a systematic conservation optimization approach to produce a multi-species habitat configuration map that is most likely to support the persistence of the obligate taxa of this biome (Figure C1). This is an advancement for systematic conservation planning and can be used for more detailed and effective conservation planning for the taxa of any U.S. or Canadian biome, and other biomes as more covariate data layers become available.

These models only represent a snapshot in time; conditions are always changing and therefore habitat suitability is changing. In fact, climate and land use changes are accelerating (Pressey et al. 2007, Steffen et al. 2018, Ellis 2021, Saunders et al. 2023), and we do not know how different taxa and ecosystems will react to these changes, including to changes in the climate, like different amounts of moisture, different temperatures, and different timing of biological phenomena (phenology). Different organisms react differently based upon their abilities to tolerate, adapt, compete, or move (Parmesan 2006, Bennett et al. 2021, Hof 2021, Muñoz et al. 2021). Predicting the effects of climate change on species and ecosystems has very high uncertainty (Wiens and Hobbs 2015, Beaumont et al. 2016, Urban et al. 2016, Taheri et al. 2021). As conditions change, the fundamental habitat models can be rerun with updated environmental data layers and new species occurrence data, to estimate changes in species distributions and habitat associations, and these models can be input into the optimization algorithm to see whether the multi-species optimal habitat configuration solutions change.

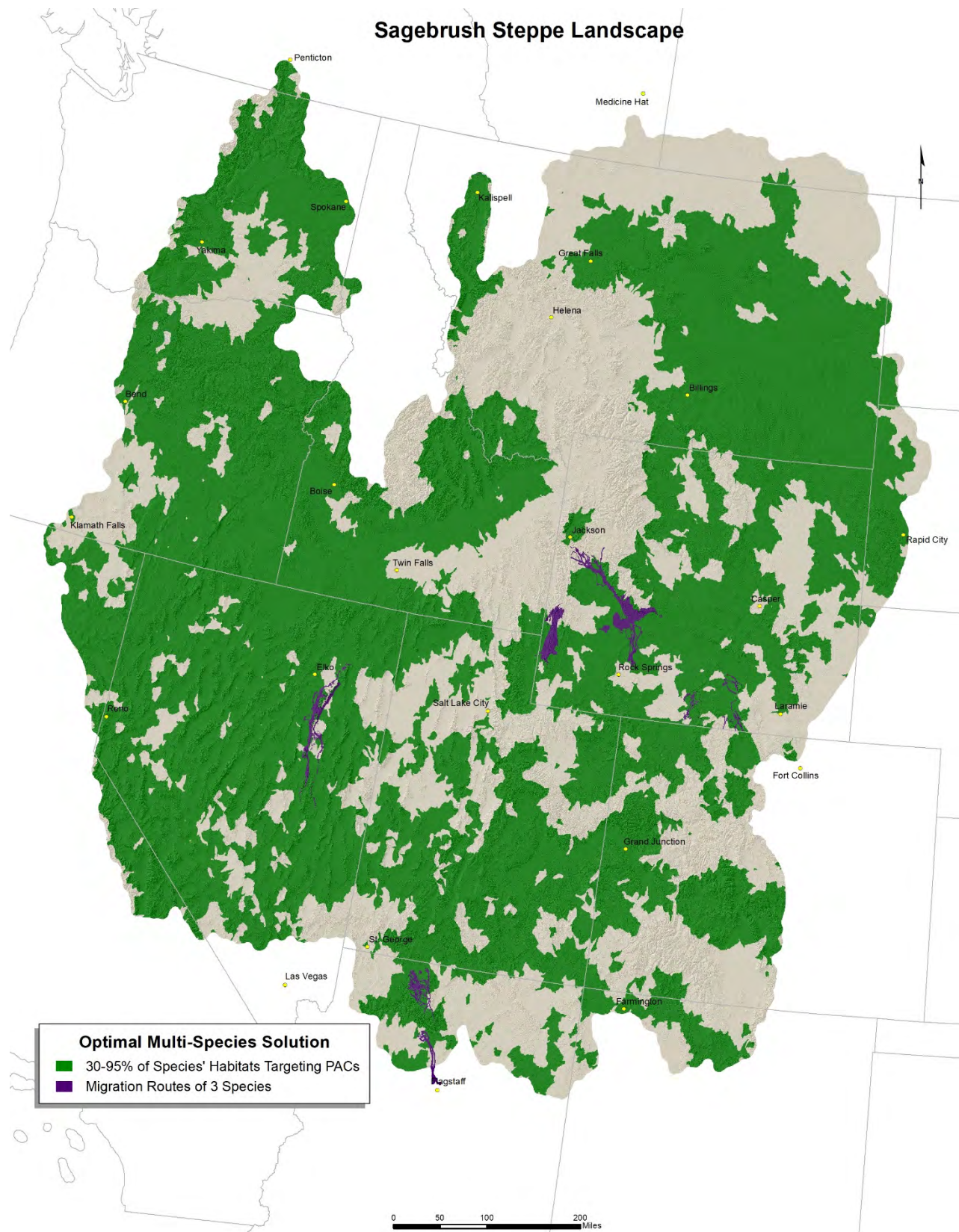


Figure C.1. Habitat optimization targeting Sage-grouse Priority Areas for Conservation (USFWS Wyoming Ecological Services 2014) includes 30% to 95% highest value fundamental habitats, plus the critical migration routes of 3 ungulate species. This land, if appropriately managed, is predicted to sustain the persistence of 165 obligate taxa of this biome.

There are several potential sources of uncertainty in these models (Langford et al. 2009), e.g., whether locations of observations are accurate (although this is less of concern since most observers these days have phones with built in GPS); non-systematic sampling; differences in observer's abilities to identify species; whether environmental/habitat data layers accurately spatially represent actual conditions; whether environmental/habitat variables (covariate data layers) were the factors that species used to determine their habitat preferences; whether species observations were in marginal habitats (i.e., that species were just traversing through) or sink habitats that would not support species populations; scales inappropriate for habitat selection; and ultimately, whether the identified habitats can actually support these species' populations.

I attempted to mitigate as many of these sources of uncertainty as possible. For instance, I ameliorated the sampling bias in the models; created the models incorporating multiple scales from 10m x 10m pixel size to biome extents; made sure the covariate data and species location data were collected during the same time period; and used the same procedures for each model, allowing the modeling routine to select covariates from the same set of high-resolution data layers (I did not weight or subjectively select covariate layers, to inconsistently try to better fit some models to the data) - to ensure model outputs would be consistent, comparable, and combinable for multi-species applications. The multi-species habitat optimization routine finds the same exact solution every time, given the same input data, so the optimal solutions identified contain no uncertainty other than that inherent in the underlying input data layers. However, even with consistency and following best practices, it is nearly impossible to assess the real-world validity of models such as these (Langford et al. 2009, McIntosh et al. 2018, Sinclair et al. 2018).

Model outputs should therefore be treated as hypotheses and applied via 'learn as you go' experimental design (Jarnevich et al. 2015, Hone and Krebs 2023), while monitoring population responses (Barrows et al. 2005). To assess whether the identified habitat types, amounts, and

multi-species configurations can actually sustain species populations, the identified habitats would need to be managed to protect species and the responses of populations monitored, along with any other stressors that may affect the populations, to ascertain cause and effects (Cabeza and Moilanen 2001, Hone and Krebs 2023). A feasible way to accomplish this would be design an adaptive management approach (Atkinson et al. 2004, Barrows et al. 2005, Fleishman et al. 2021), and use focal species to monitor population responses (Lambeck 1997, Bradford et al. 1998, O'Connell et al. 2000). Focal species *sensu* Lambeck (1997) can also be used to monitor ecological processes and ecological integrity (Noss et al. 1997), e.g., monitoring pygmy rabbit populations can serve as an indicator of overgrazing or other deleterious disturbances.

There are many factors that affect the persistence of species (e.g., land use and climate change, invasive species, tree encroachment, resource extraction, development, disturbance, livestock grazing, pollution). To effectively address the threats to species persistence, the first step is to identify the types, amounts, and configurations of habitats that each species requires, to assure that management prescriptions are done in places most likely to succeed. There are many proposed prescriptions for the type of management that needs to be implemented to protect the native taxa of this biome. Determining where to apply those management prescriptions, to be most effective, was the goal of this study.

In attempting to implement conservation plans, there is always tension between wanting to manage landscapes to best benefit native taxa versus considering the interests of stakeholders and the people that rely upon these landscapes for their livelihoods (DeFries and Nagendra 2017). Since much of these areas are in private landholdings or leases, the only way to succeed in conserving native taxa is to gain support and cooperation from stakeholders and private land managers (Coad et al. 2019). There is a body of research on the most effective ways to get stakeholder support for conservation efforts (Forbes et al. 2003, Dietz and Stern 2008). The

approach that seems most promising, is to present the (often legally decreed, e.g., for listed species) conservation objectives to stakeholders and allow them to devise the plan to reach the specified goals; have conservation professionals review the plan to determine whether it meets required conservation thresholds, and if it doesn't; send it back to the stakeholders to revise, until it does meet the conservation thresholds in a way the stakeholders can live with. This bottom-up stakeholder involved planning, as opposed to top-down planning coming from outsiders, seems to reinforce stakeholders' understanding of the issues and promotes acceptance of the solution, while adhering to the best conservation science (Gleason et al. 2010, Sayce et al. 2013, Duvall et al. 2017).

A comprehensive conservation plan (Figure C1) covers a large portion (63.3%) of the biome to target for conservation of native species, however, this land does not need to be set aside for biodiversity protection. Setting aside areas as off-limits to human activity for the protection of native taxa is infeasible because of human uses of the land and ineffective because conditions are rapidly changing (Mora and Sale 2011, Mace 2014, Maheshwari and Bhatnagar 2021, Wauchope et al. 2022). Human activity already affects most of the lands and waters of Earth and will continue to do so (Steffen et al. 2018, Maheshwari 2020, Ellis 2021, Folke et al. 2021). These lands can be managed as "working landscapes" as currently done by the NRCS Working Lands for Wildlife (NRCS 2021) to involve private land owners in the conservation of sage-grouse. This initiative would just need to be expanded to manage other obligate taxa habitats as identified in these models, which is starting to be done by the Working Lands for Wildlife - Sage Grouse Initiative (<https://www.wfw.org/wildlife/sage-grouse/about-the-initiative>), the U.S. Fish & Wildlife Service Partners Program (<https://www.fws.gov/program/partners-fish-and-wildlife>), the USGS Sagebrush Landscape Collaborative (<https://www.usgs.gov/special-topics/bipartisan-infrastructure-law-investments/science/sagebrush-keystone-initiative>), and others.

This conservation planning approach is intended to be a “living” plan and can and should be changed with new information. Moilanen et al. (2009) assert that the goals of conservation prioritization approaches are to “inform the conservation decision-making process” and “identify efficient actions in space and time that will deliver the best possible conservation outcomes”. The methodologies developed here allow this to be done by providing procedures that can be applied to identify areas of a biome to focus management efforts, to protect the viability of the obligate taxa of the biome, and to identify areas where more intensive development may be sited to have the least impact on native species. Using publicly available species location data and national biotic and abiotic datasets for model covariates, these methods can be replicated for any biome in the U.S. and Canada, and can be used in other biomes globally with adequate data for modeling.

These models are the best we can do with the data we have, but are incomplete and have inherent uncertainty. As more accurate data for more species and environmental conditions become available, the models can and should be updated. This study provides methods to use increased publicly collected data to create high-resolution, biome-scale models and incorporate habitat connectivity at multiple scales relevant to species. This approach can also incorporate other conservation objectives, which are easily modified, to provide a decision support process to plan for the conservation of all native species in a landscape. Because of the uncertainty inherent in any modeling procedure, the results of these models should be treated as hypotheses and implemented via an adaptive management process, monitoring, assessing, and adapting management applications as they are implemented.

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APPENDIX A

LIST OF SAGEBRUSH STEPPE-ASSOCIATED SPECIES

The crossed-out species in the list were not included, either because there were no observation records available within the study area (name crossed out); or for plants, they were not imperiled at NatureServe Levels G1, G2, T1 or T2 (rankings crossed out); or because raptor habitats were not modeled using observations. The “Group” designation was used to determine the group of species (observations) used to estimate the area sampled for each species group. A check in the “Obs” column indicates that there were not enough observations of the species in the study area to model their suitable habitat, so the actual (buffered) observation locations were used for multi-species conservation planning.

<u>Obs</u>	<u>Common Name</u>	<u>Scientific Name</u>	<u>Group</u>	<u>Ranking</u>
	Plants (51 included)			
	Dermatocarpon lorenzianum	<i>Dermatocarpon lorenzianum</i>	Lichen	G2
	Vagrant aspicilia	<i>Aspicilia fruticulosa</i>	Lichen	G3
	Woven spored lichen	<i>Texosporium sancti-jacobi</i>	Lichen	G3
	Bartram's tortula moss	<i>Tortula bartramii</i>	Moss	G3
	Gold Butte moss	<i>Didymodon nevadensis</i>	Moss	G4
	Nye County fishhook cactus	<i>Sclerocactus nyensis</i>	Cactus	G1
✓	Blaine's pincushion	<i>Sclerocactus blainei</i>	Cactus	G2
	Mesa Verde fishhook cactus	<i>Sclerocactus mesae-verdae</i>	Cactus	G2
	Simpson hedgehog cactus	<i>Pediocactus simpsonii</i>	Cactus	G5
	Contracted ricegrass	<i>Achnatherum contractum</i>	Graminoids	G3
	Henderson's needlegrass	<i>Achnatherum hendersonii</i>	Graminoids	G3
	Swallen's needlegrass	<i>Achnatherum swallenii</i>	Graminoids	G3
	Nodding melicgrass	<i>Melica stricta</i>	Graminoids	G4
	Thurber's needlegrass	<i>Achnatherum thurberianum</i>	Graminoids	G5
	Blue gramma	<i>Bouteloua gracilis</i>	Graminoids	G5
	Bottlebrush squirrel-tail	<i>Elymus elymoides</i>	Graminoids	G5
	Great Basin wildrye	<i>Leymus cinereus</i>	Graminoids	G5
	Least muhly	<i>Muhlenbergia minutissima</i>	Graminoids	G5
	Green needlegrass	<i>Nassella viridula</i>	Graminoids	G5
	Desert needlegrass	<i>Pappostipa speciosa</i>	Graminoids	G5
	Little-seed mountain ricegrass	<i>Piptatheropsis micrantha</i>	Graminoids	G5
	Desert dodder	<i>Cuscuta denticulata</i>	Vines	G4
✓	Grouse Creek rockcress	<i>Arabis falcatoria</i>	Forbs/herbs	G1
✓	Elko rockcress	<i>Arabis falcifruca</i>	Forbs/herbs	G1
✓	Ophir rockcress	<i>Arabis ophira</i>	Forbs/herbs	G1
	Fremont County rockcress	<i>Arabis pusilla</i>	Forbs/herbs	G1
✓	Troubled milkvetch	<i>Astragalus anxius</i>	Forbs/herbs	G1
	Skiff milkvetch	<i>Astragalus microcymbus</i>	Forbs/herbs	G1
	Whited's milkvetch	<i>Astragalus sinuatus</i>	Forbs/herbs	G1
✓	Barren Valley collomia	<i>Collomia renacta</i>	Forbs/herbs	G1
	Brandegge's buckwheat	<i>Eriogonum brandegeei</i>	Forbs/herbs	G1
	Frisco buckwheat	<i>Eriogonum soledium</i>	Forbs/herbs	G1
	Canyonlands lomatium	<i>Lomatium latilobum</i>	Forbs/herbs	G1
✓	Cusick's lupine	<i>Lupinus cusickii</i>	Forbs/herbs	G1
✓	Cordillia's beardtongue	<i>Penstemon floribundus</i>	Forbs/herbs	G1
	Gibben's beardtongue	<i>Penstemon gibbensii</i>	Forbs/herbs	G1
	Malheur wire-lettuce	<i>Stephanomeria malheurensis</i>	Forbs/herbs	G1
	Howell's thelypody	<i>Thelypodium howellii</i>	Forbs/herbs	G1
✓	Desert yellowhead	<i>Yermo xanthocephalus</i>	Forbs/herbs	G1
	Mystery wormwood	<i>Artemisia biennis var. diffusa</i>	Forbs/herbs	T1
	Steamboat buckwheat	<i>Eriogonum ovalifolium var. williamsiae</i>	Forbs/herbs	T1
	Aztec gilia	<i>Aliciella formosa</i>	Forbs/herbs	G2
	Sapphire rockcress	<i>Arabis fecunda</i>	Forbs/herbs	G2

<u>Obs</u>	<u>Common Name</u>	<u>Scientific Name</u>	<u>Group</u>	<u>Ranking</u>
	Clokey's milkvetch	<i>Astragalus aequalis</i>	Forbs/herbs	G2
	Gunnison milkvetch	<i>Astragalus anisus</i>	Forbs/herbs	G2
	Goose Creek milkvetch	<i>Astragalus anserinus</i>	Forbs/herbs	G2
	Beatley milkvetch	<i>Astragalus beatleyae</i>	Forbs/herbs	G2
✓	Cronquist's milkvetch	<i>Astragalus cronquistii</i>	Forbs/herbs	G2
	Debeque milkvetch	<i>Astragalus debequaeus</i>	Forbs/herbs	G2
	Gilman milkvetch	<i>Astragalus gilmanii</i>	Forbs/herbs	G2
✓	Mulford's milkvetch	<i>Astragalus mulfordiae</i>	Forbs/herbs	G2
✓	Fisher milkvetch	<i>Astragalus piscator</i>	Forbs/herbs	G2
✓	San Rafael milkvetch	<i>Astragalus rafaensis</i>	Forbs/herbs	G2
	Spring Mountain milkvetch	<i>Astragalus remotus</i>	Forbs/herbs	G2
	Toquima milkvetch	<i>Astragalus toquimanus</i>	Forbs/herbs	G2
✓	Currant milkvetch	<i>Astragalus uncialis</i>	Forbs/herbs	G2
✓	Aquarius Plateau Indian paintbrush	<i>Castilleja aquariensis</i>	Forbs/herbs	G2
	Gray cryptantha	<i>Cryptantha leucophaea</i>	Forbs/herbs	G2
	Bodie Hills cusickiella	<i>Cusickiella quadricostata</i>	Forbs/herbs	G2
	Windloving buckwheat	<i>Eriogonum anemophilum</i>	Forbs/herbs	G2
✓	Cusick's buckwheat	<i>Eriogonum cusickii</i>	Forbs/herbs	G2
✓	Sunnyside green gentian	<i>Frasera gypsicola</i>	Forbs/herbs	G2
	Sierra Valley ivesia	<i>Ivesia aperta</i>	Forbs/herbs	G2
	Ash Creek ivesia	<i>Ivesia paniculata</i>	Forbs/herbs	G2
	Grimy ivesia	<i>Ivesia rhypara</i>	Forbs/herbs	G2
	Plumas ivesia	<i>Ivesia sericoleuca</i>	Forbs/herbs	G2
	Webber ivesia	<i>Ivesia webberi</i>	Forbs/herbs	G2
	Grimes' vetchling	<i>Lathyrus grimesii</i>	Forbs/herbs	G2
	Slick spot peppergrass	<i>Lepidium papilliferum</i>	Forbs/herbs	G2
✓	Talapoosa Peak pearpod	<i>Lepidium tiehmii</i>	Forbs/herbs	G2
✓	Colorado desert-parsley	<i>Lomatium concinnum</i>	Forbs/herbs	G2
	Ochoco desert-parsley	<i>Lomatium ochocense</i>	Forbs/herbs	G2
✓	Packard's desert-parsley	<i>Lomatium packardiae</i>	Forbs/herbs	G2
	Rose-flower desert-parsley	<i>Lomatium roseanum</i>	Forbs/herbs	G2
	Smooth stickleaf	<i>Mentzelia mollis</i>	Forbs/herbs	G2
	Absaroka beardtongue	<i>Penstemon absarokensis</i>	Forbs/herbs	G2
	Idaho beardtongue	<i>Penstemon idahoensis</i>	Forbs/herbs	G2
✓	Inconspicuous scorpionweed	<i>Phacelia inconspicua</i>	Forbs/herbs	G2
	Fremont bladderpod	<i>Physaria fremontii</i>	Forbs/herbs	G2
✓	Prostrate bladderpod	<i>Physaria prostrata</i>	Forbs/herbs	G2
	Washington polemonium	<i>Polemonium pectinatum</i>	Forbs/herbs	G2
	Pygmy poreleaf	<i>Porophyllum pygmaeum</i>	Forbs/herbs	G2
	Alkali primrose	<i>Primula alcalina</i>	Forbs/herbs	G2
✓	Ertter's ragwort	<i>Senecio ertterae</i>	Forbs/herbs	G2
	Jan's catchfly	<i>Silene nachlingerae</i>	Forbs/herbs	G2
	Tufted globemallow	<i>Sphaeralcea caespitosa</i>	Forbs/herbs	G2
✓	Biennial prince's plume	<i>Stanleya confertiflora</i>	Forbs/herbs	G2
	Gypsum Townsend's aster	<i>Townsendia gypsophila</i>	Forbs/herbs	G2

<u>Obs</u>	<u>Common Name</u>	<u>Scientific Name</u>	<u>Group</u>	<u>Ranking</u>
✓	Owyhee clover	<i>Trifolium owyheense</i>	Forbs/herbs	G2
	Aase onion	<i>Allium aaseae</i>	Forbs/herbs	G3
	Meadow (Box) pussytoes	<i>Antennaria arcuata</i>	Forbs/herbs	G3
	Bodie Hills rockcress	<i>Arabis bodiensis</i>	Forbs/herbs	G3
	Wheel milkweed	<i>Asclepias uncialis</i>	Forbs/herbs	G3
	Challis milkvetch	<i>Astragalus amblytropis</i>	Forbs/herbs	G3
	Lemhi milkvetch	<i>Astragalus aquilonius</i>	Forbs/herbs	G3
	Palouse milkvetch	<i>Astragalus arrectus</i>	Forbs/herbs	G3
	Barr milkvetch	<i>Astragalus barrii</i>	Forbs/herbs	G3
	Brandege milkvetch	<i>Astragalus brandegei</i>	Forbs/herbs	G3
	Debris milkvetch	<i>Astragalus detritalis</i>	Forbs/herbs	G3
	Duchesne milkvetch	<i>Astragalus duchesnensis</i>	Forbs/herbs	G3
	Inyo milkvetch	<i>Astragalus inyoensis</i>	Forbs/herbs	G3
	Starveling milkvetch	<i>Astragalus jejunus var. jejunus</i>	Forbs/herbs	G3
	Grand Junction milkvetch	<i>Astragalus linifolius</i>	Forbs/herbs	G3
	Pauper milkvetch	<i>Astragalus misellus var. pauper</i>	Forbs/herbs	G3
	Ferron milkvetch	<i>Astragalus musiniensis</i>	Forbs/herbs	G3
	Nelson's milkvetch	<i>Astragalus nelsonianus</i>	Forbs/herbs	G3
	Picabo milkvetch	<i>Astragalus oniciformis</i>	Forbs/herbs	G3
	Peck's milkvetch	<i>Astragalus peckii</i>	Forbs/herbs	G3
	Ripley milkvetch	<i>Astragalus ripleyi</i>	Forbs/herbs	G3
	Trout Creek milkvetch	<i>Astragalus salmonis</i>	Forbs/herbs	G3
	Bitterroot milkvetch	<i>Astragalus scaphoides</i>	Forbs/herbs	G3
	Sandstone milkvetch	<i>Astragalus sesquiflorus</i>	Forbs/herbs	G3
	Little bun milkvetch	<i>Astragalus simplicifolius</i>	Forbs/herbs	G3
	Weak milkvetch	<i>Astragalus solitarius</i>	Forbs/herbs	G3
	Blue Mountain milkvetch	<i>Astragalus tegetarioides</i>	Forbs/herbs	G3
	Mud Flat milkvetch	<i>Astragalus yoder williamsii</i>	Forbs/herbs	G3
	Green-tinged Indian paintbrush	<i>Castilleja chlorotica</i>	Forbs/herbs	G3
	Pale Wallowa Indian paintbrush	<i>Castilleja oresbia</i>	Forbs/herbs	G3
	Intermountain evening-primrose	<i>Chylismia megalantha</i>	Forbs/herbs	G3
	Ownbey's thistle	<i>Cirsium ownbeyi</i>	Forbs/herbs	G3
	Bristle-flowered collomia	<i>Collomia macrocalyx</i>	Forbs/herbs	G3
	Erect cryptantha	<i>Cryptantha stricta</i>	Forbs/herbs	G3
	Welsh's cryptantha	<i>Cryptantha welshii</i>	Forbs/herbs	G3
	Evert's spring parsley	<i>Cymopterus evertii</i>	Forbs/herbs	G3
	Talus spring parsley	<i>Cymopterus lapidosus</i>	Forbs/herbs	G3
	Ripley's cymopterus	<i>Cymopterus ripleyi</i>	Forbs/herbs	G3
	Nevada willowherb	<i>Epilobium nevadense</i>	Forbs/herbs	G3
	Broad fleabane	<i>Erigeron latus</i>	Forbs/herbs	G3
	Needleleaf fleabane	<i>Erigeron nematophyllus</i>	Forbs/herbs	G3
	Piper's daisy	<i>Erigeron piperianus</i>	Forbs/herbs	G3
	Single-stem buckwheat	<i>Eriogonum acaule</i>	Forbs/herbs	G3
	Desert buckwheat	<i>Eriogonum desertorum</i>	Forbs/herbs	G3
	Ephedra buckwheat	<i>Eriogonum ephedroides</i>	Forbs/herbs	G3

<u>Obs</u>	<u>Common Name</u>	<u>Scientific Name</u>	<u>Group</u>	<u>Ranking</u>
	Dropleaf buckwheat	<i>Eriogonum exilifolium</i>	Forbs/herbs	G3
	Prostrate buckwheat	<i>Eriogonum proceiduum</i>	Forbs/herbs	G3
	Playa buckwheat	<i>Eriogonum salicornioides</i>	Forbs/herbs	G3
	Woodside buckwheat	<i>Eriogonum tumulosum</i>	Forbs/herbs	G3
	Cronquist's stickseed	<i>Hackelia cronquistii</i>	Forbs/herbs	G3
	Long-sepal globemallow	<i>Hiamna longisepala</i>	Forbs/herbs	G3
	Davis' peppergrass	<i>Lepidium davisii</i>	Forbs/herbs	G3
	Nuttall's desert parsley	<i>Lomatium nuttallii</i>	Forbs/herbs	G3
	Wyoming locoweed	<i>Oxytropis nana</i>	Forbs/herbs	G3
	Sand penstemon	<i>Penstemon arenicola</i>	Forbs/herbs	G3
	Pinto beardtongue	<i>Penstemon bicolor var. bicolor</i>	Forbs/herbs	G3
	Cary's beardtongue	<i>Penstemon caryi</i>	Forbs/herbs	G3
	Fremont's beardtongue	<i>Penstemon fremontii</i>	Forbs/herbs	G3
	Blueleaf beardtongue	<i>Penstemon glaucinus</i>	Forbs/herbs	G3
	Harrington's beardtongue	<i>Penstemon harringtonii</i>	Forbs/herbs	G3
	Lemhi beardtongue	<i>Penstemon lemhiensis</i>	Forbs/herbs	G3
	Pahute Mesa beardtongue	<i>Penstemon pahutensis</i>	Forbs/herbs	G3
	Beatley's phacelia	<i>Phacelia beatleyae</i>	Forbs/herbs	G3
	Playa phacelia	<i>Phacelia inundata</i>	Forbs/herbs	G3
	Mono County phacelia	<i>Phacelia monoensis</i>	Forbs/herbs	G3
	Opal phlox	<i>Phlox opalensis</i>	Forbs/herbs	G3
	Wholeleaf goldenweed	<i>Pyrrcoma insecticuriis</i>	Forbs/herbs	G3
	Snake River goldenweed	<i>Pyrrcoma radiata</i>	Forbs/herbs	G3
	Columbia yellowcress	<i>Rorippa columbiae</i>	Forbs/herbs	G3
	Silver chicken-sage	<i>Sphaeromeria argentea</i>	Forbs/herbs	G3
	Palmer's evening-primrose	<i>Tetrapteron palmeri</i>	Forbs/herbs	G3
	Sword Townsend-daisy	<i>Townsendia spathulata</i>	Forbs/herbs	G3
	Intermountain clover	<i>Trifolium andinum</i>	Forbs/herbs	G3
	Payson's tansy-mustard	<i>Descurainia incisa paysonii</i>	Forbs/herbs	F3
	Kellogg's onion	<i>Allium anceps</i>	Forbs/herbs	G4
	Douglas' onion	<i>Allium douglasii</i>	Forbs/herbs	G4
	Tolmie's onion	<i>Allium tolmiei</i>	Forbs/herbs	G4
	Munite prickly-poppy	<i>Argemone munita</i>	Forbs/herbs	G4
	Alvord milkvetch	<i>Astragalus alvordensis</i>	Forbs/herbs	G4
	Mourning milkvetch	<i>Astragalus atratus inseptus</i>	Forbs/herbs	G4
	Owyhee milkvetch	<i>Astragalus atratus owyheensis</i>	Forbs/herbs	G4
	John Day milkvetch	<i>Astragalus diaphanus</i>	Forbs/herbs	G4
	Geyer's milkvetch	<i>Astragalus geyeri var. geyeri</i>	Forbs/herbs	G4
	Gray's milkvetch	<i>Astragalus grayi</i>	Forbs/herbs	G4
	Spindle milkvetch	<i>Astragalus oophorus</i>	Forbs/herbs	G4
	Lavin's egg milkvetch	<i>Astragalus oophorus var. lavinii</i>	Forbs/herbs	G4
	Pink egg milkvetch	<i>Astragalus oophorus var. lonchocalyx</i>	Forbs/herbs	G4
	Oregon milkvetch	<i>Astragalus oregonus</i>	Forbs/herbs	G4
	Green River milkvetch	<i>Astragalus pubentissimus var.</i>	Forbs/herbs	G4

<u>Obs</u>	<u>Common Name</u>	<u>Scientific Name</u>	<u>Group</u>	<u>Ranking</u>
		<i>pubentissimus</i>		
	Ames milkvetch	<i>Astragalus pulsiferae</i> var. <i>suksdorfii</i>	Forbs/herbs	G4
	Four-wing milkvetch	<i>Astragalus tetraapterus</i>	Forbs/herbs	G4
	Cusick's Indian paintbrush	<i>Castilleja cusickii</i>	Forbs/herbs	G4
	Mt. Hamilton Indian paintbrush	<i>Castilleja dissitiflora</i>	Forbs/herbs	G4
	Yellow Indian paintbrush	<i>Castilleja flava</i>	Forbs/herbs	G4
	Country Indian paintbrush	<i>Castilleja flava</i> var. <i>rustica</i>	Forbs/herbs	G4
	Pale Indian paintbrush	<i>Castilleja pallescens</i>	Forbs/herbs	G4
	Parrothead Indian paintbrush	<i>Castilleja pilosa</i>	Forbs/herbs	G4
	Longspike Indian paintbrush	<i>Castilleja pilosa</i> var. <i>longispica</i>	Forbs/herbs	G4
	Steens Indian paintbrush	<i>Castilleja pilosa</i> var. <i>steenensis</i>	Forbs/herbs	G4
	Rough Indian paintbrush	<i>Castilleja scabrida</i>	Forbs/herbs	G4
	Thompson's Indian paintbrush	<i>Castilleja thompsonii</i>	Forbs/herbs	G4
	Yellowhair Indian paintbrush	<i>Castilleja xanthotricha</i>	Forbs/herbs	G4
	Western cabbage	<i>Caulanthus crassicaulis</i>	Forbs/herbs	G4
	Slender wild cabbage	<i>Caulanthus major</i>	Forbs/herbs	G4
	Hairy wild cabbage	<i>Caulanthus pilosus</i>	Forbs/herbs	G4
	Large-flowered chaenactis	<i>Chaenactis macrantha</i>	Forbs/herbs	G4
	Flesh-colored pincusion	<i>Chaenactis xantiana</i>	Forbs/herbs	G4
	Pygmy suncup	<i>Chylismiella pterosperma</i>	Forbs/herbs	G4
	Modoc hawksbeard	<i>Crepis modocensis</i>	Forbs/herbs	G4
	Tufted cryptantha	<i>Cryptantha caespitosa</i>	Forbs/herbs	G4
	Roundspike cryptantha	<i>Cryptantha humilis</i>	Forbs/herbs	G4
	Malheur cryptantha	<i>Cryptantha propria</i>	Forbs/herbs	G4
	Silky cryptantha	<i>Cryptantha sericea</i>	Forbs/herbs	G4
	Montana cryptantha	<i>Cryptantha sobolifera</i>	Forbs/herbs	G4
	Snake River cryptantha	<i>Cryptantha spiculifera</i>	Forbs/herbs	G4
	Wapah spring parsley	<i>Cymopterus ibapensis</i>	Forbs/herbs	G4
	Long-stalk spring parsley	<i>Cymopterus longipes</i>	Forbs/herbs	G4
	Fringed water-plantain	<i>Damasonium californicum</i>	Forbs/herbs	G4
	Pygmy monkeyflower	<i>Diplacus pygmaeus</i>	Forbs/herbs	G4
	White eatonella	<i>Eatonella nivea</i>	Forbs/herbs	G4
	Dwarf fleabane	<i>Erigeron nanus</i>	Forbs/herbs	G4
	Basin fleabane	<i>Erigeron pulcherrimus</i>	Forbs/herbs	G4
	Shortstem buckwheat	<i>Eriogonum brevicaule</i>	Forbs/herbs	G4
	Crosby's buckwheat	<i>Eriogonum crosbyae</i>	Forbs/herbs	G4
	Suksdorf's monkeyflower	<i>Erythranthe suksdorfii</i>	Forbs/herbs	G4
	White-margined wax plant	<i>Glyptopleura marginata</i>	Forbs/herbs	G4
	Cooper's rubberweed	<i>Hymenoxys cooperi</i>	Forbs/herbs	G4
	Lavender dwarf standing-cypress	<i>Ipomopsis polycladon</i>	Forbs/herbs	G4
	Wasatch desert-parsley	<i>Lomatium bicolor</i>	Forbs/herbs	G4
	Juniper desert-parsley	<i>Lomatium juniperinum</i>	Forbs/herbs	G4
	Oregon lupine	<i>Lupinus oregonus</i>	Forbs/herbs	G4
	Inch-high lupine	<i>Lupinus uncialis</i>	Forbs/herbs	G4

<u>Obs</u>	<u>Common Name</u>	<u>Scientific Name</u>	<u>Group</u>	<u>Ranking</u>
	Large-flower skeleton-plant	<i>Lygodesmia grandiflora</i>	Forbs/herbs	G4
	Torrey's desert-dandelion	<i>Malacothrix torreyi</i>	Forbs/herbs	G4
	Golden stickleaf	<i>Mentzelia pumila</i>	Forbs/herbs	G4
	Hill-monkeyflower	<i>Mimulus clivicola</i>	Forbs/herbs	G4
	Stoutstem threadplant	<i>Nemacladus rigidus</i>	Forbs/herbs	G4
	Coyote tobacco	<i>Nicotiana attenuata</i>	Forbs/herbs	G4
	Dwarf lousewort	<i>Pedicularis centranthera</i>	Forbs/herbs	G4
	Fuzzytongue penstemon	<i>Penstemon eriantherus</i>	Forbs/herbs	G4
	Larchleaf beardtongue	<i>Penstemon laricifolius</i>	Forbs/herbs	G4
	Glandular scorpionweed	<i>Phacelia glandulosa</i>	Forbs/herbs	G4
	Naked-stemmed phacelia	<i>Phacelia gymnoclada</i>	Forbs/herbs	G4
	Dense bladderpod	<i>Physaria nelsonii</i>	Forbs/herbs	G4
	Western bladderpod	<i>Physaria occidentalis</i>	Forbs/herbs	G4
	Desert combleaf	<i>Polyctenium fremontii</i>	Forbs/herbs	G4
	Milkwort knotweed	<i>Polygonum polygaloides</i>	Forbs/herbs	G4
	Slender woollyheads	<i>Psilocarphus tenellus</i>	Forbs/herbs	G4
	Dwarf skullcap	<i>Scutellaria nana</i>	Forbs/herbs	G4
	Rock tansy	<i>Sphaeromeria capitata</i>	Forbs/herbs	G4
	Baretwig neststraw	<i>Stylocline psilocarphoides</i>	Forbs/herbs	G4
	Torrey's bitterweed	<i>Tetraneuris torreyana</i>	Forbs/herbs	G4
	Westwater tumbled mustard	<i>Thelypodopsis elegans</i>	Forbs/herbs	G4
	Jones' Townsend-daisy	<i>Townsendia jonesii</i>	Forbs/herbs	G4
	Tufted Townsend-daisy	<i>Townsendia scapigera</i>	Forbs/herbs	G4
	Hairy Townsend-daisy	<i>Townsendia strigosa</i>	Forbs/herbs	G4
	Cushion milkvetch	<i>Astragalus aretioides</i> var. <i>sericoleucus</i>	Forbs/herbs	G4
	Hooked groundstar	<i>Ancistrocarphus filagineus</i>	Forbs/herbs	G5
	White sagebrush	<i>Artemisia ludoviciana</i>	Forbs/herbs	G5
	Don Meadow milkvetch	<i>Astragalus agrestis</i>	Forbs/herbs	G5
	Crescent milkvetch	<i>Astragalus amphioxys</i>	Forbs/herbs	G5
	<i>Astragalus cusickii</i> var. <i>sterilis</i>	<i>Astragalus cusickii</i> var. <i>sterilis</i>	Forbs/herbs	G5
	Horseshoe milkvetch	<i>Astragalus equisolensis</i>	Forbs/herbs	G5
	Newberry's milkvetch	<i>Astragalus newberryi</i>	Forbs/herbs	G5
	Snake River milkvetch	<i>Astragalus purshii</i> var. <i>ephiogenes</i>	Forbs/herbs	G5
	Northwestern Indian paintbrush	<i>Castilleja angustifolia</i>	Forbs/herbs	G5
	Applegate's Indian paintbrush	<i>Castilleja applegatei</i>	Forbs/herbs	G5
	Wyoming Indian paintbrush	<i>Castilleja linariifolia</i>	Forbs/herbs	G5
	Giant red Indian paintbrush	<i>Castilleja miniata</i>	Forbs/herbs	G5
	Broad-flowered pincushion	<i>Chaenactis stevioides</i>	Forbs/herbs	G5
	Plains spring-parsley	<i>Cymopterus acaulis</i>	Forbs/herbs	G5
	Yellowstone whitlow-grass	<i>Draba incerta</i>	Forbs/herbs	G5
	Few-seed whitlow-grass	<i>Draba oligosperma</i>	Forbs/herbs	G5
	Shockley's buckwheat	<i>Eriogonum shockleyi</i>	Forbs/herbs	G5
	Whitestem fraseria	<i>Frasera albicaulis</i>	Forbs/herbs	G5

<u>Obs</u>	<u>Common Name</u>	<u>Scientific Name</u>	<u>Group</u>	<u>Ranking</u>
	Western sweetvetch	<i>Hedysarum occidentale</i>	Forbs/herbs	G5
	Seaside heliotrope	<i>Heliotropium curassavicum</i>	Forbs/herbs	G5
	Fineleaf hymenopappus	<i>Hymenopappus filifolius</i>	Forbs/herbs	G5
	Stemless four-nerve daisy	<i>Hymenoxys acaulis</i>	Forbs/herbs	G5
	Ballhead standing-cypress	<i>Ipomopsis congesta</i>	Forbs/herbs	G5
	Spreading pygmyleaf	<i>Loeflingia squarrosa</i>	Forbs/herbs	G5
	Sagebrush bluebells	<i>Mertensia oblongifolia</i>	Forbs/herbs	G5
	Pale evening-primrose	<i>Oenothera pallida</i>	Forbs/herbs	G5
	Bessey's locoweed	<i>Oxytropis besseyi</i>	Forbs/herbs	G5
	Bristly combseed	<i>Pectocarya setosa</i>	Forbs/herbs	G5
	Narrow-leaf beardtongue	<i>Penstemon angustifolius</i>	Forbs/herbs	G5
	Thickleaf beardtongue	<i>Penstemon pachyphyllus</i>	Forbs/herbs	G5
	Sharpleaf twinpod	<i>Physaria acutifolia</i>	Forbs/herbs	G5
	Great Plains bladderpod	<i>Physaria arenosa</i>	Forbs/herbs	G5
	Chambers' twinpod	<i>Physaria chambersii</i>	Forbs/herbs	G5
	Hairy-foot plantain	<i>Plantago eriopoda</i>	Forbs/herbs	G5
	Basin-daisy	<i>Platyschukhria integrifolia</i>	Forbs/herbs	G5
	Douglas' knotweed	<i>Polygonum douglasii</i>	Forbs/herbs	G5
	California chicory	<i>Rafinesquia californica</i>	Forbs/herbs	G5
	Cutleaf thelypod	<i>Thelypodium laciniatum</i>	Forbs/herbs	G5
	Hooker's Townsend-daisy	<i>Townsendia hookeri</i>	Forbs/herbs	G5
	Pintwater rabbitbrush	<i>Chrysothamnus eremobius</i>	Sub/Dwarf shrubs	G1
✓	Kawich Range beardtongue	<i>Penstemon pudicus</i>	Sub/Dwarf shrubs	G1
	Granite buckwheat	<i>Eriogonum robustum</i>	Sub/Dwarf shrubs	G2
	Dwarf greasebush	<i>Glossopetalon pungens</i>	Sub/Dwarf shrubs	G2
	Smooth prickly phlox	<i>Linanthus glabrum</i>	Sub/Dwarf shrubs	G2
✓	Stemless beardtongue	<i>Penstemon acaulis</i>	Sub/Dwarf shrubs	G2
✓	Aquarius Plateau beardtongue	<i>Penstemon parvus</i>	Sub/Dwarf shrubs	G2
	Ward's beardtongue	<i>Penstemon wardii</i>	Sub/Dwarf shrubs	G2
	Cusick's giant hyssop	<i>Agastache cusickii</i>	Sub/Dwarf shrubs	G3
	Twisted buckwheat	<i>Eriogonum contortum</i>	Sub/Dwarf shrubs	G3
	Tunnel Springs beardtongue	<i>Penstemon concinnus</i>	Sub/Dwarf shrubs	G3
	Payson's beardtongue	<i>Penstemon paysoniorum</i>	Sub/Dwarf shrubs	G3
	Minidoka beardtongue	<i>Penstemon perpulcher</i>	Sub/Dwarf shrubs	G3
	Fuzzy sagebrush	<i>Artemisia papposa</i>	Sub/Dwarf shrubs	G4
	Pygmy sage	<i>Artemisia pygmaea</i>	Sub/Dwarf shrubs	G4
	Castle Lake bedstraw	<i>Galium glabrescens</i>	Sub/Dwarf shrubs	G4
	Desert wishbone-bush	<i>Mirabilis laevis</i>	Sub/Dwarf shrubs	G4
	Antelope Valley beardtongue	<i>Penstemon janishiae</i>	Sub/Dwarf shrubs	G4
	King's beardtongue	<i>Penstemon kingii</i>	Sub/Dwarf shrubs	G4
	Short-lobe penstemon	<i>Penstemon seorsus</i>	Sub/Dwarf shrubs	G4
	Woolly princesplume	<i>Stanleya tomentosa</i>	Sub/Dwarf shrubs	G4
	Black sagebrush	<i>Artemisia nova</i>	Sub/Dwarf shrubs	G5
	Scabland sagebrush	<i>Artemisia rigida</i>	Sub/Dwarf shrubs	G5
	Bud sagebrush	<i>Artemisia spinescens</i>	Sub/Dwarf shrubs	G5

<u>Obs</u>	<u>Common Name</u>	<u>Scientific Name</u>	<u>Group</u>	<u>Ranking</u>
	Rubber rabbitbrush	<i>Ericameria nauseosa</i>	Sub/Dwarf shrubs	G5
	Heermann's buckwheat	<i>Eriogonum heermannii</i>	Sub/Dwarf shrubs	G5
	Purple sage	<i>Salvia dorrii</i>	Sub/Dwarf shrubs	G5
	Woolly goldenweed	<i>Stenotus lanuginosus</i>	Sub/Dwarf shrubs	G5
	Packard's wormwood	<i>Artemisia packardiae</i>	Shrubs	G3
	Nuttall's horsebrush	<i>Tetradymia nuttallii</i>	Shrubs	G3
	Squaw-apple	<i>Peraphyllum ramosissimum</i>	Shrubs	G4
	Little sagebrush	<i>Artemisia arbuscula</i>	Shrubs	G5
	Bigelow sagebrush	<i>Artemisia bigelovii</i>	Shrubs	G5
	Plains silver sagebrush	<i>Artemisia cana cana</i>	Shrubs	G5
	Mountain silver sagebrush	<i>Artemisia cana viscidula</i>	Shrubs	G5
	Snowfield sagebrush	<i>Artemisia spiciformis</i>	Shrubs	G5
	Big sagebrush	<i>Artemisia tridentata</i>	Shrubs	G5
	Threetip sagebrush	<i>Artemisia tripartita</i>	Shrubs	G5
	Long-flowered snowberry	<i>Symphoricarpos longiflorus</i>	Shrubs	G5
	<u>Invertebrates (27 included)</u>			
	Salmon oregonian	<i>Cryptomastix harfordiana</i>	Molluscs	
	Hells Canyon land snail	<i>Cryptomastix populi</i>	Molluscs	
✓	Deschutes sideband	<i>Monadenia fidelis</i>	Molluscs	
	Mountainsnails	<i>Oreohelix spp.</i>	Molluscs	
	Northwest hesperian	<i>Vespericola columbianus</i>	Molluscs	
	Acastus checkerspot	<i>Chlosyne acastus</i>	Insects	
	Dotted blue butterflies	<i>Euphilotes spp.</i>	Insects	
	Skippers	<i>Hesperopsis spp.</i>	Insects	
	Spring Mountain comma skipper	<i>Hesperia comma mojavensis</i>	Insects	
	MacNeill's saltbush sootywing	<i>Hesperopsis gracielae</i>	Insects	
	Nevada viceroy	<i>Limenitis archippus</i>	Insects	
	Pahrnagat naucorid bug	<i>Pelocoris shoshone shoshone</i>	Insects	
	Northern crescent	<i>Phyciodes cocyta</i>	Insects	
	Sandhill skipper	<i>Polites sabuleti</i>	Insects	
	Atlantis fritillary	<i>Speyeria atlantis</i>	Insects	
	Northwestern fritillary	<i>Speyeria hesperis</i>	Insects	
	Wolf spider	<i>Alopecosa kochi</i>	Spiders	
	Sixspotted orbweaver	<i>Araniella displicata</i>	Spiders	
	Running crab spiders	<i>Ebo spp</i>	Spiders	
	Polymorphic long-jawed cobweaver	<i>Enoplognatha ovata</i>	Spiders	
	Hook-toothed money spider	<i>Erigone dentosa</i>	Spiders	
	Tangle-web spiders	<i>Euryopis spp</i>	Spiders	
	Western black widow	<i>Latrodectus hesperus</i>	Spiders	
✓	Fox's barrier orbweaver	<i>Metepeira foxi</i>	Spiders	
	Western lynx spider	<i>Oxyopes scalaris</i>	Spiders	
	Coppered white-cheeked jumping spider	<i>Pelegrina aeneola</i>	Spiders	
	Red-backed jumping spider	<i>Phidippus johnsoni</i>	Spiders	
	Leafbeetle jumping spider	<i>Sassacus papenhoei</i>	Spiders	

<u>Obs</u>	<u>Common Name</u>	<u>Scientific Name</u>	<u>Group</u>	<u>Ranking</u>
	Silver longjawed orbweaver	<i>Tetragnatha laboriosa</i>	Spiders	
	Protrudent long-legged cobweaver	<i>Theridion neomexicanum</i>	Spiders	
	Oblong running crab spider	<i>Tibellus oblongus</i>	Spiders	
	Grey ground crab spider	<i>Xysticus gulosus</i>	Spiders	
	Montane crab spider	<i>Xysticus montanensis</i>	Spiders	
<u>Amphibians (1 included)</u>				
	Great Basin spadefoot	<i>Spea intermontana</i>	Amphibians	
<u>Reptiles (19 included)</u>				
	Striped whipsnake	<i>Coluber taeniatus</i>	Reptiles	
	Grand Canyon rattlesnake	<i>Crotalus oreganus abyssus</i>	Reptiles	
	Midget faded rattlesnake	<i>Crotalus oreganus concolor</i>	Reptiles	
	Great Basin rattlesnake	<i>Crotalus oreganus lutosus</i>	Reptiles	
	Northern Pacific rattlesnake	<i>Crotalus oreganus oreganus</i>	Reptiles	
	Prairie rattlesnake	<i>Crotalus viridis</i>	Reptiles	
	Great Basin collared lizard	<i>Crotaphytus bicinctores</i>	Reptiles	
	Long-nosed leopard lizard	<i>Gambelia wislizenii</i>	Reptiles	
	Nightsnake	<i>Hypsiglena torquata</i>	Reptiles	
	Western milksnake	<i>Lampropeltis gentilis</i>	Reptiles	
	Pygmy horned lizard	<i>Phrynosoma douglasii</i>	Reptiles	
	Greater short-horned lizard	<i>Phrynosoma hernandesi</i>	Reptiles	
	Desert horned lizard	<i>Phrynosoma platyrhinos</i>	Reptiles	
	Great Basin gopher snake	<i>Pituophis catenifer</i>	Reptiles	
	Long-nosed snake	<i>Rhinocheilus lecontei</i>	Reptiles	
	Sagebrush lizard	<i>Sceloporus graciosus</i>	Reptiles	
	Desert spiny lizard	<i>Sceloporus magister</i>	Reptiles	
	Western ground snake	<i>Sonora semiannulata</i>	Reptiles	
	Side-blotched lizard	<i>Uta stansburiana</i>	Reptiles	
<u>Birds (23 included)</u>				
	Sharp-tailed grouse	<i>Tympanuchus phasianellus</i>	Galliformes	
	Short-eared owl	<i>Asio flammeus</i>	Owls	
	Western burrowing owl	<i>Athene cunicularia</i>	Owls	
	Golden eagle	<i>Aquila chrysaetos</i>	Raptors	
	Ferruginous hawk	<i>Buteo regalis</i>	Raptors	
	Swainson's hawk	<i>Buteo swainsoni</i>	Raptors	
	Prairie falcon	<i>Falco mexicanus</i>	Raptors	
	Grasshopper sparrow	<i>Ammodramus savannarum</i>	Song birds	
	Black-throated sparrow	<i>Amphispiza bilineata</i>	Song birds	
	Sagebrush sparrow	<i>Artemisiospiza nevadensis</i>	Song birds	
	Lark bunting	<i>Calamospiza melanocorys</i>	Song birds	
	Lark sparrow	<i>Chondestes grammacus</i>	Song birds	
	Gray flycatcher	<i>Empidonax wrightii</i>	Song birds	
	Brewer's blackbird	<i>Euphagus cyanocephalus</i>	Song birds	

<u>Obs</u>	<u>Common Name</u>	<u>Scientific Name</u>	<u>Group</u>	<u>Ranking</u>
	MacGillivray's warbler	<i>Geothlypis tolmiei</i>	Song birds	
	Loggerhead shrike	<i>Lanius ludovicianus</i>	Song birds	
	Virginia's warbler	<i>Leiothlypis virginiae</i>	Song birds	
	Sage thrasher	<i>Oreoscoptes montanus</i>	Song birds	
	Green-tailed towhee	<i>Pipilo chlorurus</i>	Song birds	
	Vesper sparrow	<i>Pooecetes gramineus</i>	Song birds	
	Rock wren	<i>Salpinctes obsoletus</i>	Song birds	
	Brewer's sparrow	<i>Spizella breweri</i>	Song birds	
	Clay-colored sparrow	<i>Spizella pallida</i>	Song birds	
	Western meadowlark	<i>Sturnella neglecta</i>	Song birds	
	Mountain plover	<i>Charadrius montanus</i>	Wading birds	
	Sandhill crane	<i>Antigone canadensis</i>	Wading birds	
	Long-billed curlew	<i>Numenius americanus</i>	Wading birds	
<u>Mammals (43 included)</u>				
	Pallid bat	<i>Antrozous pallidus</i>	Bats	
	Townsend's big-eared bat	<i>Corynorhinus townsendii</i>	Bats	
	Spotted bat	<i>Euderma maculatum</i>	Bats	
✓	Western mastiff bat	<i>Eumops perotis</i>	Bats	
✓	Western small-footed myotis	<i>Myotis ciliolabrum</i>	Bats	
	Long-eared myotis	<i>Myotis evotis</i>	Bats	
	Fringed myotis	<i>Myotis thysanodes</i>	Bats	
	Yuma myotis	<i>Myotis yumanensis</i>	Bats	
✓	Big free-tailed bat	<i>Nyctinomops macrotis</i>	Bats	
	White-tailed antelope squirrel	<i>Ammospermophilus leucurus</i>	Small mammals	
	Merriam's kangaroo rat	<i>Dipodomys merriami</i>	Small mammals	
	Chisel-toothed kangaroo rat	<i>Dipodomys microps</i>	Small mammals	
	Ord's kangaroo rat	<i>Dipodomys ordii</i>	Small mammals	
	Sagebrush vole	<i>Lemmyscus curtatus</i>	Small mammals	
	Dark kangaroo mouse	<i>Microdipodops megacephalus</i>	Small mammals	
	Cliff chipmunk	<i>Tamias dorsalis</i>	Small mammals	
	Least chipmunk	<i>Tamias minimus</i>	Small mammals	
	Northern grasshopper mouse	<i>Onychomys leucogaster</i>	Small mammals	
	Rock squirrel	<i>Otospermophilus variegatus</i>	Small mammals	
	Little pocket mouse	<i>Perognathus longimembris</i>	Small mammals	
	Great Basin pocket mouse	<i>Perognathus parvus</i>	Small mammals	
	Canyon mouse	<i>Peromyscus crinitus</i>	Small mammals	
	Piñon mouse	<i>Peromyscus truei</i>	Small mammals	
	Merriam's shrew	<i>Sorex merriami</i>	Small mammals	
	Preble's shrew	<i>Sorex preblei</i>	Small mammals	
	Botta's pocket gopher	<i>Thomomys bottae</i>	Small mammals	
	Wyoming pocket gopher	<i>Thomomys clusius</i>	Small mammals	
	Idaho pocket gopher	<i>Thomomys idahoensis</i>	Small mammals	
	Wyoming ground squirrel	<i>Urocitellus elegans</i>	Small mammals	
✓	Southern Idaho ground squirrel	<i>Urocitellus endemicus</i>	Small mammals	

<u>Obs</u>	<u>Common Name</u>	<u>Scientific Name</u>	<u>Group</u>	<u>Ranking</u>
	Piute ground squirrel	<i>Uroditellus mollis</i>	Small mammals	
✓	Townsend's ground squirrel	<i>Uroditellus townsendii</i>	Small mammals	
✓	Washington ground squirrel	<i>Uroditellus washingtoni</i>	Small mammals	
	Pygmy rabbit	<i>Brachylagus idahoensis</i>	Mesomammals	
	White-tailed prairie dog	<i>Cynomys leucurus</i>	Mesomammals	
	Black-tailed prairie dog	<i>Cynomys ludovicianus</i>	Mesomammals	
	Black-tailed jackrabbit	<i>Lepus californicus</i>	Mesomammals	
	White-tailed jackrabbit	<i>Lepus townsendii</i>	Mesomammals	
✓	Black-footed ferret	<i>Mustela nigripes</i>	Mesomammals	
	Kit fox	<i>Vulpes macrotis</i>	Mesomammals	
	Pronghorn	<i>Antilocapra americana</i>	Ungulates	
	Mule deer	<i>Odocoileus hemionus</i>	Ungulates	
	Bighorn sheep	<i>Ovis canadensis</i>	Ungulates	

APPENDIX B

164 OBLIGATE SAGEBRUSH STEPPE SPECIES INCLUDING IN STUDY

<u>Common Name</u>	<u>Species</u>	<u>Rank</u>	<u>Group</u>
<u>Plants (51)</u>			
Nye County fishhook cactus	<i>Sclerocactus nyensis</i>	G1	Cactus
Blaine's pincushion	<i>Sclerocactus blainei</i>	G2	Cactus
Grouse Creek rockcress	<i>Arabis falcatoria</i>	G1	Forb/herb
Elko rockcress	<i>Arabis falcifruta</i>	G1	Forb/herb
Ophir rockcress	<i>Arabis ophira</i>	G1	Forb/herb
<i>Astragalus anxius</i>	<i>Astragalus anxius</i>	G1	Forb/herb
Barren Valley collomia	<i>Collomia renacta</i>	G1	Forb/herb
Brandegee's buckwheat	<i>Eriogonum brandegeei</i>	G1	Forb/herb
Frisco buckwheat	<i>Eriogonum soredium</i>	G1	Forb/herb
Canyonlands lomatium	<i>Lomatium latilobum</i>	G1	Forb/herb
Cusick's lupine	<i>Lupinus cusickii</i>	G1	Forb/herb
Cordillia's beardtongue	<i>Penstemon floribundus</i>	G1	Forb/herb
Howell's thelypody	<i>Thelypodium howellii</i>	G1	Forb/herb
Desert yellowhead	<i>Yermo xanthocephalus</i>	G1	Forb/herb
Steamboat buckwheat	<i>Eriogonum ovalifolium</i> var. <i>williamsiae</i>	T1	Forb/herb
Gunnison milkvetch	<i>Astragalus anisus</i>	G2	Forb/herb
Goose Creek milkvetch	<i>Astragalus anserinus</i>	G2	Forb/herb
Cronquist's milkvetch	<i>Astragalus cronquistii</i>	G2	Forb/herb
Mulford's milkvetch	<i>Astragalus mulfordiae</i>	G2	Forb/herb
Fisher milkvetch	<i>Astragalus piscator</i>	G2	Forb/herb
San Rafael milkvetch	<i>Astragalus rafaensis</i>	G2	Forb/herb
Toquima milkvetch	<i>Astragalus toquimanus</i>	G2	Forb/herb
Currant milkvetch	<i>Astragalus uncialis</i>	G2	Forb/herb
Aquarius Plateau Indian paintbrush	<i>Castilleja aquariensis</i>	G2	Forb/herb
Bodie Hills cusickiella	<i>Cusickiella quadricostata</i>	G2	Forb/herb
Wind-loving buckwheat	<i>Eriogonum anemophilum</i>	G2	Forb/herb
Cusick's buckwheat	<i>Eriogonum cusickii</i>	G2	Forb/herb
Sunnyside green gentian	<i>Frasera gypsicola</i>	G2	Forb/herb
Sierra Valley ivesia	<i>Ivesia aperta</i>	G2	Forb/herb
Ash Creek ivesia	<i>Ivesia paniculata</i>	G2	Forb/herb
Grimy ivesia	<i>Ivesia rhypara</i>	G2	Forb/herb
Plumas ivesia	<i>Ivesia sericoleuca</i>	G2	Forb/herb
Webber ivesia	<i>Ivesia webberi</i>	G2	Forb/herb
Slick spot peppergrass	<i>Lepidium papilliferum</i>	G2	Forb/herb
Talapoosa Peak pearpod	<i>Lepidium tiehmii</i>	G2	Forb/herb
Colorado desert-parsley	<i>Lomatium concinnum</i>	G2	Forb/herb

<u>Common Name</u>	<u>Species</u>	<u>Rank</u>	<u>Group</u>
Packard's desert-parsley	Lomatium packardiae	G2	Forb/herb
Rose-flower desert-parsley	Lomatium roseanum	G2	Forb/herb
Smooth stickleaf	Mentzelia mollis	G2	Forb/herb
Idaho beardtongue	Penstemon idahoensis	G2	Forb/herb
Inconspicuous scorpionweed	Phacelia inconspicua	G2	Forb/herb
Prostrate bladderpod	Physaria prostrata	G2	Forb/herb
Ertter's ragwort	Senecio ertterae	G2	Forb/herb
Tufted globemallow	Sphaeralcea caespitosa	G2	Forb/herb
Biennial prince's plume	Stanleya confertiflora	G2	Forb/herb
Owyhee clover	Trifolium owyheense	G2	Forb/herb
Kawich Range beardtongue	Penstemon pudicus	G1	Subshrub/Dwarf shrub
Granite buckwheat	Eriogonum robustum	G2	Subshrub/Dwarf shrub
Stemless beardtongue	Penstemon acaulis	G2	Subshrub/Dwarf shrub
Aquarius Plateau beardtongue	Penstemon parvus	G2	Subshrub/Dwarf shrub
Ward's beardtongue	Penstemon wardii	G2	Subshrub/Dwarf shrub

Invertebrates (27)

Deschutes sideband	Monadenia fidelis		Molluscs
Mountainsnails	Oreohelix spp.		Molluscs
Acastus checkerspot	Chlosyne acastus		Insects
Dotted blue butterflies	Euphilotes spp.		Insects
Skippers	Hesperopsis spp.		Insects
Nevada viceroys	Limenitis archippus		Insects
Northern crescent	Phyciodes cocyta		Insects
Sandhill skipper	Polites sabuleti		Insects
Atlantis fritillary	Speyeria atlantis		Insects
Northwestern fritillary	Speyeria hesperis		Insects
Wolf spider	Alopecosa kochi		Spiders
Sixspotted orbweaver	Araniella displicata		Spiders
Running crab spiders	Ebo spp		Spiders
Polymorphic long-jawed cobweaver	Enoplognatha ovata		Spiders
Hook-toothed money spider	Erigone dentosa		Spiders
Tangle-web spiders	Euryopis spp		Spiders
Western black widow	Latrodectus hesperus		Spiders
Fox's barrier orbweaver	Metepeira foxi		Spiders
Western lynx spider	Oxyopes scalaris		Spiders
Coppered white-cheeked jumping spider	Pelegrina aeneola		Spiders
Red-backed jumping spider	Phidippus johnsoni		Spiders
Leafbeetle jumping spider	Sassacus papenhoei		Spiders
Silver longjawed orbweaver	Tetragnatha laboriosa		Spiders
Protrudent long-legged cobweaver	Theridion neomexicanum		Spiders
Oblong running crab spider	Tibellus oblongus		Spiders
Grey ground crab spider	Xysticus gulosus		Spiders

<u>Common Name</u>	<u>Species</u>	<u>Rank</u>	<u>Group</u>
Montane crab spider	Xysticus montanensis		Spiders
<u>Amphibians (1)</u>			
Great Basin spadefoot	Spea intermontana		Amphibians
<u>Reptiles (19)</u>			
Striped whipsnake	Coluber taeniatus		Reptiles
Grand Canyon rattlesnake	Crotalus oreganus abyssus		Reptiles
Midget faded rattlesnake	Crotalus oreganus concolor		Reptiles
Great Basin rattlesnake	Crotalus oreganus lutosus		Reptiles
Northern Pacific rattlesnake	Crotalus oreganus oreganus		Reptiles
Prairie rattlesnake	Crotalus viridis		Reptiles
Great Basin collared lizard	Crotaphytus bicinctores		Reptiles
Long-nosed leopard lizard	Gambelia wislizenii		Reptiles
Nightsnake	Hypsiglena torquata		Reptiles
Western milksnake	Lampropeltis gentilis		Reptiles
Pygmy horned lizard	Phrynosoma douglasii		Reptiles
Greater short-horned lizard	Phrynosoma hernandesi		Reptiles
Desert horned lizard	Phrynosoma platyrhinos		Reptiles
Great Basin gopher snake	Pituophis catenifer		Reptiles
Long-nosed snake	Rhinocheilus lecontei		Reptiles
Sagebrush lizard	Sceloporus graciosus		Reptiles
Desert spiny lizard	Sceloporus magister		Reptiles
Western ground snake	Sonora semiannulata		Reptiles
Side-blotched lizard	Uta stansburiana		Reptiles
<u>Birds (23)</u>			
Sharp-tailed grouse	Tympanuchus phasianellus		Galliformes
Short-eared owl	Asio flammeus		Owls
Western burrowing owl	Speotyto cunicularia		Owls
Grasshopper sparrow	Ammodramus savannarum		Song birds
Black-throated sparrow	Amphispiza bilineata		Song birds
Sagebrush sparrow	Artemisiospiza nevadensis		Song birds
Lark bunting	Calamospiza melanocorys		Song birds
Lark sparrow	Chondestes grammacus		Song birds
Gray flycatcher	Empidonax wrightii		Song birds
Brewer's blackbird	Euphagus cyanocephalus		Song birds
MacGillivray's warbler	Geothlypis tolmiei		Song birds
Loggerhead shrike	Lanius ludovicianus		Song birds
Virginia's warbler	Leiothlypis virginiae		Song birds
Sage thrasher	Oreoscoptes montanus		Song birds
Green-tailed towhee	Pipilo chlorurus		Song birds
Vesper sparrow	Poocetes gramineus		Song birds

<u>Common Name</u>	<u>Species</u>	<u>Rank</u>	<u>Group</u>
Rock wren	Salpinctes obsoletus		Song birds
Brewer's sparrow	Spizella breweri		Song birds
Clay-colored sparrow	Spizella pallida		Song birds
Western meadowlark	Sturnella neglecta		Song birds
Mountain plover	Charadrius montanus		Wading birds
Sandhill crane	Antigone canadensis		Wading birds
Long-billed curlew	Numenius americanus		Wading birds

Mammals (43)

Pallid bat	Antrozous pallidus		Bats
Townsend's big-eared bat	Corynorhinus townsendii		Bats
Spotted bat	Euderma maculatum		Bats
Western mastiff bat	Eumops perotis		Bats
Western small-footed myotis	Myotis ciliolabrum		Bats
Long-eared myotis	Myotis evotis		Bats
Fringed myotis	Myotis thysanodes		Bats
Yuma myotis	Myotis yumanensis		Bats
Big free-tailed bat	Nyctinomops macrotis		Bats
White-tailed antelope squirrel	Ammospermophilus leucurus		Small mammals
Merriam's kangaroo rat	Dipodomys merriami		Small mammals
Chisel-toothed kangaroo rat	Dipodomys microps		Small mammals
Ord's kangaroo rat	Dipodomys ordii		Small mammals
Sagebrush vole	Lemmyscus curtatus		Small mammals
Dark kangaroo mouse	Microdipodops megacephalus		Small mammals
Cliff chipmunk	Tamias dorsalis		Small mammals
Least chipmunk	Tamias minimus		Small mammals
Northern grasshopper mouse	Onychomys leucogaster		Small mammals
Rock squirrel	Otospermophilus variegatus		Small mammals
Little pocket mouse	Perognathus longimembris		Small mammals
Great Basin pocket mouse	Perognathus parvus		Small mammals
Canyon mouse	Peromyscus crinitus		Small mammals
Piñon mouse	Peromyscus truei		Small mammals
Merriam's shrew	Sorex merriami		Small mammals
Preble's shrew	Sorex preblei		Small mammals
Botta's pocket gopher	Thomomys bottae		Small mammals
Wyoming pocket gopher	Thomomys clusius		Small mammals
Idaho pocket gopher	Thomomys idahoensis		Small mammals
Wyoming ground squirrel	Urocitellus elegans		Small mammals
Southern Idaho ground squirrel	Urocitellus endemicus		Small mammals
Piute ground squirrel	Urocitellus mollis		Small mammals
Townsend's ground squirrel	Urocitellus townsendii		Small mammals
Washington ground squirrel	Urocitellus washingtoni		Small mammals

<u>Common Name</u>	<u>Species</u>	<u>Rank</u>	<u>Group</u>
Pygmy rabbit	<i>Brachylagus idahoensis</i>		Mesomammals
White-tailed prairie dog	<i>Cynomys leucurus</i>		Mesomammals
Black-tailed prairie dog	<i>Cynomys ludovicianus</i>		Mesomammals
Black-tailed jackrabbit	<i>Lepus californicus</i>		Mesomammals
White-tailed jackrabbit	<i>Lepus townsendii</i>		Mesomammals
Black-footed ferret	<i>Mustela nigripes</i>		Mesomammals
Kit fox	<i>Vulpes macrotis</i>		Mesomammals
Pronghorn	<i>Antilocapra americana</i>		Ungulates
Mule deer	<i>Odocoileus hemionus</i>		Ungulates
Bighorn sheep	<i>Ovis canadensis</i>		Ungulates

APPENDIX C

AMOUNT OF HABITAT OF EACH SPECIES AND PERCENTAGES INCLUDED IN OPTIMIZATION SCENARIOS

Species are listed in order of overall habitat they have available from lowest to highest amounts.

<u>Species</u>	<u>Cell Count</u>	<u>Ranges of habitat percentages included</u>			
		<u>90-20</u>	<u>90-30</u>	<u>95-20</u>	<u>95-30</u>
		<u>%</u>	<u>%</u>	<u>%</u>	<u>%</u>
Elko rockcress (<i>Arabis falcifracta</i>)	254,770	0.9	0.9	0.95	0.95
Barren Valley collomia (<i>Collomia renacta</i>)	375,304	0.9	0.9	0.95	0.95
Owyhee clover (<i>Trifolium owyheense</i>)	482,721	0.9	0.9	0.95	0.95
Southern Idaho ground squirrel (<i>Urocitellus endemicus</i>)	490,706	0.9	0.9	0.95	0.95
Grouse Creek rockcress (<i>Arabis falcatoria</i>)	505,638	0.9	0.9	0.95	0.95
Prostrate bladderpod (<i>Physaria prostrata</i>)	513,613	0.9	0.9	0.95	0.95
Washington ground squirrel (<i>Urocitellus washingtoni</i>)	634,480	0.9	0.9	0.95	0.95
Sunnyside green gentian (<i>Frasera gypsicola</i>)	643,165	0.9	0.9	0.95	0.95
Currant milkvetch (<i>Astragalus uncialis</i>)	687,092	0.9	0.9	0.95	0.95
Blaine's pincushion (<i>Sclerocactus blainei</i>)	795,639	0.9	0.9	0.95	0.95
Cordillia's beardtongue (<i>Penstemon floribundus</i>)	1,004,916	0.9	0.9	0.9	0.9
Cusick's lupine (<i>Lupinus cusickii</i>)	1,018,080	0.9	0.9	0.9	0.9
Fisher milkvetch (<i>Astragalus piscator</i>)	1,033,855	0.9	0.9	0.9	0.9
Ophir rockcress (<i>Arabis ophira</i>)	1,107,707	0.9	0.9	0.9	0.9
Cronquist's milkvetch (<i>Astragalus cronquistii</i>)	1,134,224	0.9	0.9	0.9	0.9
Aquarius Plateau Indian paintbrush (<i>Castilleja aquariensis</i>)	1,154,550	0.9	0.9	0.9	0.9
Western mastiff bat (<i>Eumops perotis</i>)	1,154,550	0.9	0.9	0.9	0.9
Inconspicuous scorpionweed (<i>Phacelia inconspicua</i>)	1,154,550	0.9	0.9	0.9	0.9
Ertter's ragwort (<i>Senecio ertterae</i>)	1,154,550	0.9	0.9	0.9	0.9
<i>Astragalus anxius</i> (<i>Astragalus anxius</i>)	1,155,496	0.9	0.9	0.9	0.9
Cusick's buckwheat (<i>Eriogonum cusickii</i>)	1,155,625	0.9	0.9	0.9	0.9
Desert yellowhead (<i>Yermo xanthocephalus</i>)	1,155,625	0.9	0.9	0.9	0.9
Mulford's milkvetch (<i>Astragalus mulfordiae</i>)	1,271,186	0.9	0.9	0.9	0.9
Talapoosa Peak pearpod (<i>Lepidium tiehmii</i>)	1,386,429	0.9	0.9	0.9	0.9
Deschutes sideband (<i>Monadenia fidelis</i>)	1,707,862	0.9	0.9	0.9	0.9
Black-footed ferret (<i>Mustela nigripes</i>)	2,304,516	0.8	0.8	0.8	0.8
Packard's desert-parsley (<i>Lomatium packardiae</i>)	2,309,100	0.8	0.8	0.8	0.8
Kawich Range beardtongue (<i>Penstemon pudicus</i>)	2,309,100	0.8	0.8	0.8	0.8
Stemless beardtongue (<i>Penstemon acaulis</i>)	2,310,174	0.8	0.8	0.8	0.8
San Rafael milkvetch (<i>Astragalus rafaelsensis</i>)	2,310,175	0.8	0.8	0.8	0.8
Colorado desert-parsley (<i>Lomatium concinnum</i>)	2,311,250	0.8	0.8	0.8	0.8
Aquarius Plateau beardtongue (<i>Penstemon parvus</i>)	2,311,250	0.8	0.8	0.8	0.8
Townsend's ground squirrel (<i>Urocitellus townsendii</i>)	2,311,250	0.8	0.8	0.8	0.8

Species	Cell Count	Ranges of habitat percentages included			
		90-20	90-30	95-20	95-30
		%	%	%	%
Western small-footed myotis (<i>Myotis ciliolabrum</i>)	3,195,152	0.8	0.8	0.8	0.8
Fox's barrier orbweaver (<i>Metepeira foxi</i>)	3,465,799	0.8	0.8	0.8	0.8
Big free-tailed bat (<i>Nyctinomops macrotis</i>)	3,465,800	0.8	0.8	0.8	0.8
Biennial prince's plume (<i>Stanleya confertiflora</i>)	3,465,800	0.8	0.8	0.8	0.8
Sierra Valley ivesia (<i>Ivesia aperta</i>)	20,977,004	0.75	0.75	0.75	0.75
Ash Creek ivesia (<i>Ivesia paniculata</i>)	23,003,554	0.75	0.75	0.75	0.75
Plumas ivesia (<i>Ivesia sericoleuca</i>)	24,755,853	0.75	0.75	0.75	0.75
Granite buckwheat (<i>Eriogonum robustum</i>)	26,543,281	0.75	0.75	0.75	0.75
Bodie Hills cusickiella (<i>Cusickiella quadricostata</i>)	30,200,536	0.75	0.75	0.75	0.75
Brandegee's buckwheat (<i>Eriogonum brandegeei</i>)	31,780,391	0.75	0.75	0.75	0.75
Slick spot peppergrass (<i>Lepidium papilliferum</i>)	32,092,318	0.75	0.75	0.75	0.75
Canyonlands lomatium (<i>Lomatium latilobum</i>)	33,165,168	0.75	0.75	0.75	0.75
Grand Canyon rattlesnake (<i>Crotalus oreganus abyssus</i>)	36,047,114	0.75	0.75	0.75	0.75
Webber ivesia (<i>Ivesia webberi</i>)	37,065,143	0.75	0.75	0.75	0.75
Idaho beardtongue (<i>Penstemon idahoensis</i>)	41,802,949	0.75	0.75	0.75	0.75
Toquima milkvetch (<i>Astragalus toquimanus</i>)	42,349,119	0.75	0.75	0.75	0.75
Nye County fishhook cactus (<i>Sclerocactus nyensis</i>)	43,546,957	0.75	0.75	0.75	0.75
Ward's beardtongue (<i>Penstemon wardii</i>)	45,953,690	0.75	0.75	0.75	0.75
Gunnison milkvetch (<i>Astragalus anisus</i>)	52,279,995	0.75	0.75	0.75	0.75
Steamboat buckwheat (<i>Eriogonum ovalifolium</i> var. <i>williamsiae</i>)	52,612,367	0.75	0.75	0.75	0.75
Frisco buckwheat (<i>Eriogonum soledium</i>)	58,401,582	0.75	0.75	0.75	0.75
Goose Creek milkvetch (<i>Astragalus anserinus</i>)	63,474,935	0.75	0.75	0.75	0.75
Howell's thelypody (<i>Thelypodium howellii</i>)	72,711,609	0.75	0.75	0.75	0.75
Tufted globemallow (<i>Sphaeralcea caespitosa</i>)	73,709,797	0.75	0.75	0.75	0.75
Rose-flower desert-parsley (<i>Lomatium roseanum</i>)	87,968,284	0.75	0.75	0.75	0.75
Wind-loving buckwheat (<i>Eriogonum anemophilum</i>)	95,156,421	0.75	0.75	0.75	0.75
Smooth stickleaf (<i>Mentzelia mollis</i>)	114,526,369	0.5	0.5	0.5	0.5
Grimy ivesia (<i>Ivesia rhypara</i>)	126,768,242	0.5	0.5	0.5	0.5
Northern Pacific rattlesnake (<i>Crotalus oreganus oreganus</i>)	137,709,241	0.5	0.5	0.5	0.5
Midget faded rattlesnake (<i>Crotalus oreganus concolor</i>)	195,842,006	0.5	0.5	0.5	0.5
Rock squirrel (<i>Otospermophilus variegatus</i>)	225,527,947	0.5	0.5	0.5	0.5
Wyoming pocket gopher (<i>Thomomys clusius</i>)	238,644,538	0.5	0.5	0.5	0.5
Pygmy horned lizard (<i>Phrynosoma douglasii</i>)	375,101,998	0.5	0.5	0.5	0.5
Merriam's kangaroo rat (<i>Dipodomys merriami</i>)	426,289,508	0.5	0.5	0.5	0.5
Chisel-toothed kangaroo rat (<i>Dipodomys microps</i>)	429,468,900	0.5	0.5	0.5	0.5
Little pocket mouse (<i>Perognathus longimembris</i>)	481,299,039	0.5	0.5	0.5	0.5
Piute ground squirrel (<i>Urocitellus mollis</i>)	482,215,554	0.5	0.5	0.5	0.5
Western ground snake (<i>Sonora semiannulata</i>)	486,906,094	0.5	0.5	0.5	0.5
Dark kangaroo mouse (<i>Microdipodops megacephalus</i>)	513,287,809	0.5	0.5	0.5	0.5
Silver longjawed orbweaver (<i>Tetragnatha laboriosa</i>)	535,578,028	0.5	0.5	0.5	0.5

Species	Cell Count	Ranges of habitat percentages included			
		90-20	90-30	95-20	95-30
		%	%	%	%
Idaho pocket gopher (<i>Thomomys idahoensis</i>)	560,717,644	0.5	0.5	0.5	0.5
Long-nosed snake (<i>Rhinocheilus lecontei</i>)	563,502,940	0.5	0.5	0.5	0.5
Long-nosed leopard lizard (<i>Gambelia wislizenii</i>)	582,270,353	0.5	0.5	0.5	0.5
Desert horned lizard (<i>Phrynosoma platyrhinos</i>)	614,046,137	0.4	0.4	0.4	0.4
Virginia's warbler (<i>Leiothlypis virginiae</i>)	637,012,888	0.4	0.4	0.4	0.4
Side-blotched lizard (<i>Uta stansburiana</i>)	662,109,816	0.4	0.4	0.4	0.4
Desert spiny lizard (<i>Sceloporus magister</i>)	676,668,340	0.4	0.4	0.4	0.4
White-tailed prairie dog (<i>Cynomys leucurus</i>)	708,659,255	0.4	0.4	0.4	0.4
Leafbeetle jumping spider (<i>Sassacus papenhoei</i>)	709,835,121	0.4	0.4	0.4	0.4
Western milksnake (<i>Lampropeltis gentilis</i>)	716,559,335	0.4	0.4	0.4	0.4
White-tailed antelope squirrel (<i>Ammospermophilus leucurus</i>)	735,599,229	0.4	0.4	0.4	0.4
Black-throated sparrow (<i>Amphispiza bilineata</i>)	746,041,966	0.4	0.4	0.4	0.4
Great Basin rattlesnake (<i>Crotalus oreganus lutosus</i>)	756,221,322	0.3	0.4	0.3	0.4
Lark bunting (<i>Calamospiza melanocorys</i>)	769,298,171	0.3	0.4	0.3	0.4
Sharp-tailed grouse (<i>Tympanuchus phasianellus</i>)	805,799,669	0.3	0.4	0.3	0.4
Grasshopper sparrow (<i>Ammodramus savannarum</i>)	807,695,970	0.3	0.4	0.3	0.4
Running crab spiders (<i>Ebo</i> spp)	818,655,296	0.3	0.4	0.3	0.4
Clay-colored sparrow (<i>Spizella pallida</i>)	828,795,694	0.3	0.4	0.3	0.4
Black-tailed prairie dog (<i>Cynomys ludovicianus</i>)	859,355,837	0.3	0.4	0.3	0.4
Pallid bat (<i>Antrozous pallidus</i>)	879,897,473	0.3	0.4	0.3	0.4
Acastus checkerspot (<i>Chlosyne acastus</i>)	885,871,796	0.3	0.4	0.3	0.4
Canyon mouse (<i>Peromyscus crinitus</i>)	888,387,211	0.3	0.4	0.3	0.4
Mountain plover (<i>Charadrius montanus</i>)	893,582,936	0.3	0.4	0.3	0.4
Cliff chipmunk (<i>Tamias dorsalis</i>)	898,198,829	0.3	0.4	0.3	0.4
Kit fox (<i>Vulpes macrotis</i>)	906,041,171	0.3	0.4	0.3	0.4
Botta's pocket gopher (<i>Thomomys bottae</i>)	923,445,255	0.3	0.4	0.3	0.4
Great Basin collared lizard (<i>Crotaphytus bicinctores</i>)	927,356,424	0.3	0.4	0.3	0.4
Great Basin pocket mouse (<i>Perognathus parvus</i>)	938,685,890	0.3	0.4	0.3	0.4
Prairie rattlesnake (<i>Crotalus viridis</i>)	990,519,322	0.3	0.4	0.3	0.4
Striped whipsnake (<i>Coluber taeniatus</i>)	1,000,439,998	0.2	0.3	0.2	0.3
Merriam's shrew (<i>Sorex merriami</i>)	1,002,675,482	0.2	0.3	0.2	0.3
Pygmy rabbit (<i>Brachylagus idahoensis</i>)	1,010,094,925	0.2	0.3	0.2	0.3
Nightsnake (<i>Hypsiglena torquata</i>)	1,042,866,759	0.2	0.3	0.2	0.3
Atlantis fritillary (<i>Speyeria atlantis</i>)	1,050,283,947	0.2	0.3	0.2	0.3
Spotted bat (<i>Euderma maculatum</i>)	1,072,451,968	0.2	0.3	0.2	0.3
Wyoming ground squirrel (<i>Uroditellus elegans</i>)	1,086,138,005	0.2	0.3	0.2	0.3
Piñon mouse (<i>Peromyscus truei</i>)	1,094,273,166	0.2	0.3	0.2	0.3
Preble's shrew (<i>Sorex preblei</i>)	1,094,736,291	0.2	0.3	0.2	0.3
Greater short-horned lizard (<i>Phrynosoma hernandesi</i>)	1,147,217,932	0.2	0.3	0.2	0.3
Black-tailed jackrabbit (<i>Lepus californicus</i>)	1,161,413,877	0.2	0.3	0.2	0.3

Species	Cell Count	Ranges of habitat percentages included			
		90-20	90-30	95-20	95-30
		%	%	%	%
Fringed myotis (<i>Myotis thysanodes</i>)	1,179,344,857	0.2	0.3	0.2	0.3
Northern grasshopper mouse (<i>Onychomys leucogaster</i>)	1,207,862,220	0.2	0.3	0.2	0.3
Ord's kangaroo rat (<i>Dipodomys ordii</i>)	1,210,189,110	0.2	0.3	0.2	0.3
Green-tailed towhee (<i>Pipilo chlorurus</i>)	1,210,333,841	0.2	0.3	0.2	0.3
Least chipmunk (<i>Tamias minimus</i>)	1,285,513,602	0.2	0.3	0.2	0.3
Long-billed curlew (<i>Numenius americanus</i>)	1,285,855,853	0.2	0.3	0.2	0.3
Grey ground crab spider (<i>Xysticus gulosus</i>)	1,291,673,708	0.2	0.3	0.2	0.3
Great Basin spadefoot (<i>Spea intermontana</i>)	1,296,110,335	0.2	0.3	0.2	0.3
Western black widow (<i>Latrodectus hesperus</i>)	1,301,930,201	0.2	0.3	0.2	0.3
Gray flycatcher (<i>Empidonax wrightii</i>)	1,317,913,969	0.2	0.3	0.2	0.3
MacGillivray's warbler (<i>Geothlypis tolmiei</i>)	1,355,659,807	0.2	0.3	0.2	0.3
Sagebrush lizard (<i>Sceloporus graciosus</i>)	1,372,281,223	0.2	0.3	0.2	0.3
Bighorn sheep (<i>Ovis canadensis</i>)	1,389,488,151	0.2	0.3	0.2	0.3
Sandhill crane (<i>Antigone canadensis</i>)	1,392,772,466	0.2	0.3	0.2	0.3
Western lynx spider (<i>Oxyopes scalaris</i>)	1,444,258,645	0.2	0.3	0.2	0.3
Sagebrush sparrow (<i>Artemisiospiza nevadensis</i>)	1,458,354,970	0.2	0.3	0.2	0.3
Sagebrush vole (<i>Lemmyscus curtatus</i>)	1,464,708,115	0.2	0.3	0.2	0.3
Great Basin gopher snake (<i>Pituophis catenifer</i>)	1,533,174,741	0.2	0.3	0.2	0.3
Mule deer (<i>Odocoileus hemionus</i>)	1,578,393,159	0.2	0.3	0.2	0.3
Wolf spider (<i>Alopecosa kochi</i>)	1,579,738,590	0.2	0.3	0.2	0.3
Yuma myotis (<i>Myotis yumanensis</i>)	1,627,876,944	0.2	0.3	0.2	0.3
Townsend's big-eared bat (<i>Corynorhinus townsendii</i>)	1,638,465,944	0.2	0.3	0.2	0.3
Pronghorn (<i>Antilocapra americana</i>)	1,678,466,144	0.2	0.3	0.2	0.3
Western burrowing owl (<i>Speotyto cunicularia</i>)	1,734,489,037	0.2	0.3	0.2	0.3
Long-eared myotis (<i>Myotis evotis</i>)	1,753,251,919	0.2	0.3	0.2	0.3
Coppered white-cheeked jumping spider (<i>Pelegrina aeneola</i>)	1,804,414,652	0.2	0.3	0.2	0.3
Red-backed jumping spider (<i>Phidippus johnsoni</i>)	1,811,336,150	0.2	0.3	0.2	0.3
Northwestern fritillary (<i>Speyeria hesperis</i>)	1,814,494,695	0.2	0.3	0.2	0.3
Western meadowlark (<i>Sturnella neglecta</i>)	1,830,632,998	0.2	0.3	0.2	0.3
Skippers (<i>Hesperopsis</i> spp.)	1,837,944,493	0.2	0.3	0.2	0.3
Brewer's blackbird (<i>Euphagus cyanocephalus</i>)	1,840,639,109	0.2	0.3	0.2	0.3
Loggerhead shrike (<i>Lanius ludovicianus</i>)	1,847,928,067	0.2	0.3	0.2	0.3
White-tailed jackrabbit (<i>Lepus townsendii</i>)	1,861,319,136	0.2	0.3	0.2	0.3
Vesper sparrow (<i>Pooecetes gramineus</i>)	1,861,542,960	0.2	0.3	0.2	0.3
Sage thrasher (<i>Oreoscoptes montanus</i>)	1,862,408,238	0.2	0.3	0.2	0.3
Hook-toothed money spider (<i>Erigone dentosa</i>)	1,878,778,471	0.2	0.3	0.2	0.3
Short-eared owl (<i>Asio flammeus</i>)	1,901,465,262	0.2	0.3	0.2	0.3
Northern crescent (<i>Phyciodes coccyta</i>)	1,912,358,430	0.2	0.3	0.2	0.3
Rock wren (<i>Salpinctes obsoletus</i>)	1,914,822,502	0.2	0.3	0.2	0.3
Lark sparrow (<i>Chondestes grammacus</i>)	1,919,323,159	0.2	0.3	0.2	0.3

<u>Species</u>	<u>Cell Count</u>	<u>Ranges of habitat percentages included</u>			
		<u>90-20</u>	<u>90-30</u>	<u>95-20</u>	<u>95-30</u>
		<u>%</u>	<u>%</u>	<u>%</u>	<u>%</u>
Tangle-web spiders (<i>Euryopis</i> spp)	1,925,761,134	0.2	0.3	0.2	0.3
Sixspotted orbweaver (<i>Araniella displicata</i>)	1,930,760,960	0.2	0.3	0.2	0.3
Polymorphic long-jawed cobweaver (<i>Enoplognatha ovata</i>)	1,943,482,350	0.2	0.3	0.2	0.3
Montane crab spider (<i>Xysticus montanensis</i>)	1,947,162,404	0.2	0.3	0.2	0.3
Nevada viceroy (<i>Limenitis archippus</i>)	1,948,368,055	0.2	0.3	0.2	0.3
Mountainsnails (<i>Oreohelix</i> spp.)	1,952,000,381	0.2	0.3	0.2	0.3
Sandhill skipper (<i>Polites sabuleti</i>)	1,955,155,666	0.2	0.3	0.2	0.3
Oblong running crab spider (<i>Tibellus oblongus</i>)	1,957,017,173	0.2	0.3	0.2	0.3
Brewer's sparrow (<i>Spizella breweri</i>)	1,957,300,810	0.2	0.3	0.2	0.3
Dotted blue butterflies (<i>Euphilotes</i> spp.)	1,962,652,527	0.2	0.3	0.2	0.3
Protrudent long-legged cobweaver (<i>Theridion neomexicanum</i>)	1,963,849,863	0.2	0.3	0.2	0.3

APPENDIX D

OPTIMIZED MULTI-SPECIES HABITATS COVERED BY SAGE-GROUSE UMBRELLAS

* Species highlighted in green are species that have more of their fundamental habitat protected by an umbrella than was considered essential to include in the optimization procedure to protect their persistence. Species highlighted in pink are species that have less of their fundamental habitat protected by an umbrella than was considered essential to include in the optimization procedure to protect their persistence.

Minimum area optimization covered by sage-grouse PAC umbrella

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Abundant Habitat Species				
Southern Idaho ground squirrel (<i>Urocitellus endemicus</i>)	0.95	8.8	23.5	100.0%
Cronquist's milkvetch (<i>Astragalus cronquistii</i>)	0.9	12.6	40.2	100.0%
Inconspicuous scorpionweed (<i>Phacelia inconspicua</i>)	0.9	9.9	26.5	100.0%
Mulford's milkvetch (<i>Astragalus mulfordiae</i>)	0.9	7.0	29.2	100.0%
Black-footed ferret (<i>Mustela nigripes</i>)	0.8	11.8	34.2	100.0%
San Rafael milkvetch (<i>Astragalus rafaensis</i>)	0.8	13.0	50.5	100.0%
Currant milkvetch (<i>Astragalus uncialis</i>)	0.95	10.1	28.8	97.0%
Cusick's lupine (<i>Lupinus cusickii</i>)	0.9	8.5	28.7	94.7%
Cusick's buckwheat (<i>Eriogonum cusickii</i>)	0.9	12.0	29.3	94.4%
Cordillia's beardtongue (<i>Penstemon floribundus</i>)	0.9	10.8	35.3	94.1%
Owyhee clover (<i>Trifolium owyheense</i>)	0.95	8.3	27.1	92.3%
Packard's desert-parsley (<i>Lomatium packardiae</i>)	0.8	9.9	24.5	90.9%
Fisher milkvetch (<i>Astragalus piscator</i>)	0.9	10.5	26.3	89.5%
Talapoosa Peak pearpod (<i>Lepidium tiehmii</i>)	0.9	5.6	22.9	89.2%
Ertter's ragwort (<i>Senecio ertterae</i>)	0.9	11.5	31.3	88.2%
Deschutes sideband (<i>Monadenia fidelis</i>)	0.9	14.7	38.8	87.1%
Canyonlands lomatium (<i>Lomatium latilobum</i>)	0.75	26.3	89.5	85.6%
Blaine's pincushion (<i>Sclerocactus blainei</i>)	0.95	8.8	27.6	84.6%
Sunnyside green gentian (<i>Frasera gypsicola</i>)	0.95	9.7	29.0	84.0%
Biennial prince's plume (<i>Stanleya confertiflora</i>)	0.8	11.3	29.6	83.7%
Aquarius Plateau beardtongue (<i>Penstemon parvus</i>)	0.8	8.7	31.0	82.8%
Big free-tailed bat (<i>Nyctinomops macrotis</i>)	0.8	11.3	36.5	80.0%
Western mastiff bat (<i>Eumops perotis</i>)	0.9	10.5	24.3	78.9%
Nye County fishhook cactus (<i>Sclerocactus nyensis</i>)	0.75	21.2	85.4	78.2%
Howell's thelypody (<i>Thelypodium howellii</i>)	0.75	14.2	87.6	77.9%
<i>Astragalus anxius</i> (<i>Astragalus anxius</i>)	0.9	11.0	34.9	77.8%
Granite buckwheat (<i>Eriogonum robustum</i>)	0.75	15.3	84.1	76.7%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Plumas ivesia (<i>Ivesia sericoleuca</i>)	0.75	11.2	79.5	75.4%
Aquarius Plateau Indian paintbrush (<i>Castilleja aquariensis</i>)	0.9	5.7	14.9	75.0%
Kawich Range beardtongue (<i>Penstemon pudicus</i>)	0.8	11.3	28.0	75.0%
Sierra Valley ivesia (<i>Ivesia aperta</i>)	0.75	16.4	78.3	74.7%
Webber ivesia (<i>Ivesia webberi</i>)	0.75	18.7	73.3	72.1%
Tufted globemallow (<i>Sphaeralcea caespitosa</i>)	0.75	18.6	73.9	71.7%
Ward's beardtongue (<i>Penstemon wardii</i>)	0.75	18.0	64.9	70.1%
Ash Creek ivesia (<i>Ivesia paniculata</i>)	0.75	20.4	75.5	68.8%
Rose-flower desert-parsley (<i>Lomatium roseanum</i>)	0.75	19.1	71.8	68.4%
Wind-loving buckwheat (<i>Eriogonum anemophilum</i>)	0.75	23.5	58.1	67.4%
Steamboat buckwheat (<i>Eriogonum ovalifolium</i> var. <i>williamsiae</i>)	0.75	19.6	76.3	67.3%
Stemless beardtongue (<i>Penstemon acaulis</i>)	0.8	11.3	31.2	66.7%
Western small-footed myotis (<i>Myotis ciliolabrum</i>)	0.8	12.7	29.6	66.0%
Fox's barrier orbweaver (<i>Metepeira foxi</i>)	0.8	13.0	31.9	63.5%
Slick spot peppergrass (<i>Lepidium papilliferum</i>)	0.75	17.5	83.5	62.8%
Gunnison milkvetch (<i>Astragalus anisus</i>)	0.75	17.8	82.6	62.6%
Washington ground squirrel (<i>Urocitellus washingtoni</i>)	0.95	11.6	35.0	60.7%
Ophir rockcress (<i>Arabis ophira</i>)	0.9	8.0	23.1	60.7%
Barren Valley collomia (<i>Collomia renacta</i>)	0.95	19.3	79.2	59.7%
Bodie Hills cusickiella (<i>Cusickiella quadricostata</i>)	0.75	30.4	94.9	59.4%
Toquima milkvetch (<i>Astragalus toquimanus</i>)	0.75	24.4	92.3	59.3%
Colorado desert-parsley (<i>Lomatium concinnum</i>)	0.8	15.0	29.2	57.6%
Brandegee's buckwheat (<i>Eriogonum brandegeei</i>)	0.75	20.5	79.7	53.8%
Frisco buckwheat (<i>Eriogonum soledium</i>)	0.75	20.3	76.1	52.9%
Townsend's ground squirrel (<i>Urocitellus townsendii</i>)	0.8	18.9	31.5	48.6%
Grand Canyon rattlesnake (<i>Crotalus oreganus abyssus</i>)	0.75	31.7	93.6	46.3%
Goose Creek milkvetch (<i>Astragalus anserinus</i>)	0.75	17.8	74.2	45.4%
Idaho beardtongue (<i>Penstemon idahoensis</i>)	0.75	20.1	57.7	43.0%
Prostrate bladderpod (<i>Physaria prostrata</i>)	0.95	11.2	21.6	40.0%
Grouse Creek rockcress (<i>Arabis falcatoria</i>)	0.95	3.2	6.2	21.7%
Elko rockcress (<i>Arabis falcifracta</i>)	0.95	4.1	4.1	3.3%
Desert yellowhead (<i>Yermo xanthocephalus</i>)	0.9	0	0	0.0%

Intermediate Habitat Species

Midget faded rattlesnake (<i>Crotalus oreganus concolor</i>)	0.5	8.8	21.3	86.7%
Smooth stickleaf (<i>Mentzelia mollis</i>)	0.5	18.4	66.9	76.6%
Grimy ivesia (<i>Ivesia rhypara</i>)	0.5	24.2	81.0	70.6%
Western ground snake (<i>Sonora semiannulata</i>)	0.5	15.6	83.4	62.2%
Dark kangaroo mouse (<i>Microdipodops megacephalus</i>)	0.5	18.1	90.4	61.4%
Chisel-toothed kangaroo rat (<i>Dipodomys microps</i>)	0.5	18.5	93.9	60.0%
Merriam's kangaroo rat (<i>Dipodomys merriami</i>)	0.5	20.0	73.5	59.6%
Long-nosed snake (<i>Rhinocheilus lecontei</i>)	0.5	23.0	86.1	59.5%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Little pocket mouse (<i>Perognathus longimembris</i>)	0.5	18.6	84.5	58.4%
Long-nosed leopard lizard (<i>Gambelia wislizenii</i>)	0.5	23.7	90.0	55.1%
Piute ground squirrel (<i>Urocyon mollis</i>)	0.5	22.0	91.6	54.5%
Pygmy horned lizard (<i>Phrynosoma douglasii</i>)	0.5	15.6	81.2	53.5%
Northern Pacific rattlesnake (<i>Crotalus oreganus oreganus</i>)	0.5	16.0	95.5	53.0%
Silver longjawed orbweaver (<i>Tetragnatha laboriosa</i>)	0.5	11.7	85.3	53.0%
Rock squirrel (<i>Otospermophilus variegatus</i>)	0.5	13.8	87.7	51.2%
Idaho pocket gopher (<i>Thomomys idahoensis</i>)	0.5	12.0	67.5	45.7%
Wyoming pocket gopher (<i>Thomomys clusius</i>)	0.5	23.4	75.6	36.0%

Limited Habitat Species

Black-tailed prairie dog (<i>Cynomys ludovicianus</i>)	0.4	39.3	87.7	70.1%
Desert spiny lizard (<i>Sceloporus magister</i>)	0.4	15.2	78.7	61.0%
Desert horned lizard (<i>Phrynosoma platyrhinos</i>)	0.4	21.6	84.6	58.1%
Side-blotched lizard (<i>Uta stansburiana</i>)	0.4	24.3	98.4	58.0%
Great Basin collared lizard (<i>Crotaphytus bicinctores</i>)	0.4	38.6	97.9	57.5%
White-tailed prairie dog (<i>Cynomys leucurus</i>)	0.4	30.9	94.7	57.2%
White-tailed antelope squirrel (<i>Ammospermophilus leucurus</i>)	0.4	27.9	91.9	56.2%
Black-throated sparrow (<i>Amphispiza bilineata</i>)	0.4	26.5	99.4	56.2%
Mountain plover (<i>Charadrius montanus</i>)	0.4	24.9	95.9	55.7%
Canyon mouse (<i>Peromyscus crinitus</i>)	0.4	27.4	88.6	55.0%
Botta's pocket gopher (<i>Thomomys bottae</i>)	0.4	26.7	86.7	54.4%
Great Basin pocket mouse (<i>Perognathus parvus</i>)	0.4	24.6	84.0	54.0%
Pallid bat (<i>Antrozous pallidus</i>)	0.4	17.7	89.9	53.6%
Acastus checkerspot (<i>Chlosyne acastus</i>)	0.4	40.3	94.1	53.5%
Leafbeetle jumping spider (<i>Sassacus papenhoei</i>)	0.4	14.2	91.6	53.0%
Lark bunting (<i>Calamospiza melanocorys</i>)	0.4	37.8	98.5	53.0%
Running crab spiders (<i>Ebo</i> spp)	0.4	15.8	96.3	53.0%
Kit fox (<i>Vulpes macrotis</i>)	0.4	22.0	90.0	52.4%
Cliff chipmunk (<i>Tamias dorsalis</i>)	0.4	13.2	76.9	51.6%
Virginia's warbler (<i>Leiothlypis virginiae</i>)	0.4	17.5	84.2	49.9%
Grasshopper sparrow (<i>Ammodramus savannarum</i>)	0.4	30.9	91.9	49.5%
Western milksnake (<i>Lampropeltis gentilis</i>)	0.4	18.2	89.5	46.5%
Sharp-tailed grouse (<i>Tympanuchus phasianellus</i>)	0.4	35.0	99.7	46.1%
Clay-colored sparrow (<i>Spizella pallida</i>)	0.4	21.9	97.0	45.9%
Great Basin rattlesnake (<i>Crotalus oreganus lutosus</i>)	0.4	36.7	96.9	44.2%
Prairie rattlesnake (<i>Crotalus viridis</i>)	0.4	16.3	67.5	42.4%
Striped whipsnake (<i>Coluber taeniatus</i>)	0.3	13.5	63.9	67.2%
Nightsnake (<i>Hypsiglena torquata</i>)	0.3	23.6	88.4	57.1%
Gray flycatcher (<i>Empidonax wrightii</i>)	0.3	34.8	97.7	54.6%
Fringed myotis (<i>Myotis thysanodes</i>)	0.3	20.2	91.8	54.5%
Yuma myotis (<i>Myotis yumanensis</i>)	0.3	29.3	81.2	54.3%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Sagebrush lizard (<i>Sceloporus graciosus</i>)	0.3	25.4	95.8	53.9%
Sagebrush sparrow (<i>Artemisospiza nevadensis</i>)	0.3	37.0	93.9	53.7%
Black-tailed jackrabbit (<i>Lepus californicus</i>)	0.3	24.1	98.9	53.7%
Pygmy rabbit (<i>Brachylagus idahoensis</i>)	0.3	23.8	95.3	53.4%
Sagebrush vole (<i>Lemmiscus curtatus</i>)	0.3	24.0	79.5	53.3%
Preble's shrew (<i>Sorex preblei</i>)	0.3	22.2	89.2	53.3%
Long-billed curlew (<i>Numenius americanus</i>)	0.3	23.6	96.0	53.2%
Spotted bat (<i>Euderma maculatum</i>)	0.3	23.8	97.9	53.1%
Merriam's shrew (<i>Sorex merriami</i>)	0.3	19.3	99.5	53.1%
Ord's kangaroo rat (<i>Dipodomys ordii</i>)	0.3	22.2	89.9	53.1%
Long-eared myotis (<i>Myotis evotis</i>)	0.3	21.9	85.9	53.0%
White-tailed jackrabbit (<i>Lepus townsendii</i>)	0.3	13.8	78.9	53.0%
Atlantis fritillary (<i>Speyeria atlantis</i>)	0.3	15.0	79.5	53.0%
Northern grasshopper mouse (<i>Onychomys leucogaster</i>)	0.3	22.0	92.9	53.0%
Least chipmunk (<i>Tamias minimus</i>)	0.3	18.1	87.7	53.0%
Grey ground crab spider (<i>Xysticus gulosus</i>)	0.3	20.3	83.4	53.0%
Western black widow (<i>Latrodectus hesperus</i>)	0.3	15.7	99.5	53.0%
MacGillivray's warbler (<i>Geothlypis tolmiei</i>)	0.3	20.6	94.4	53.0%
Sandhill crane (<i>Antigone canadensis</i>)	0.3	18.8	95.4	53.0%
Western lynx spider (<i>Oxyopes scalaris</i>)	0.3	20.4	89.0	53.0%
Great Basin gopher snake (<i>Pituophis catenifer</i>)	0.3	33.9	97.5	53.0%
Mule deer (<i>Odocoileus hemionus</i>)	0.3	22.9	96.0	53.0%
Wolf spider (<i>Alopecosa kochi</i>)	0.3	22.4	83.5	53.0%
Western burrowing owl (<i>Speotyto cunicularia</i>)	0.3	50.6	100.0	53.0%
Coppered white-cheeked jumping spider (<i>Pelegrina aeneola</i>)	0.3	22.3	84.3	53.0%
Red-backed jumping spider (<i>Phidippus johnsoni</i>)	0.3	26.1	88.7	53.0%
Northwestern fritillary (<i>Speyeria hesperis</i>)	0.3	37.7	98.0	53.0%
Western meadowlark (<i>Sturnella neglecta</i>)	0.3	33.3	97.9	53.0%
Skippers (<i>Hesperopsis</i> spp.)	0.3	39.6	98.3	53.0%
Brewer's blackbird (<i>Euphagus cyanocephalus</i>)	0.3	26.3	98.2	53.0%
Loggerhead shrike (<i>Lanius ludovicianus</i>)	0.3	37.6	97.9	53.0%
Vesper sparrow (<i>Pooecetes gramineus</i>)	0.3	35.0	98.3	53.0%
Hook-toothed money spider (<i>Erigone dentosa</i>)	0.3	14.1	81.0	53.0%
Short-eared owl (<i>Asio flammeus</i>)	0.3	50.6	100.0	53.0%
Northern crescent (<i>Phyciodes cocyta</i>)	0.3	43.2	98.1	53.0%
Rock wren (<i>Salpinctes obsoletus</i>)	0.3	34.1	99.8	53.0%
Tangle-web spiders (<i>Euryopis</i> spp)	0.3	19.3	68.9	53.0%
Sixspotted orbweaver (<i>Araniella displicata</i>)	0.3	20.3	82.9	53.0%
Polymorphic long-jawed cobweaver (<i>Enoplognatha ovata</i>)	0.3	13.5	62.5	53.0%
Montane crab spider (<i>Xysticus montanensis</i>)	0.3	20.6	75.7	53.0%
Nevada viceroy (<i>Limenitis archippus</i>)	0.3	43.2	97.5	53.0%
Mountainsnails (<i>Oreohelix</i> spp.)	0.3	17.0	67.5	53.0%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Sandhill skipper (<i>Polites sabuleti</i>)	0.3	48.6	93.0	53.0%
Oblong running crab spider (<i>Tibellus oblongus</i>)	0.3	20.6	64.9	53.0%
Brewer's sparrow (<i>Spizella breweri</i>)	0.3	37.2	97.9	53.0%
Dotted blue butterflies (<i>Euphilotes</i> spp.)	0.3	46.2	97.6	53.0%
Protrudent long-legged cobweaver (<i>Theridion neomexicanum</i>)	0.3	15.5	82.4	53.0%
Sage thrasher (<i>Oreoscoptes montanus</i>)	0.3	34.8	99.0	53.0%
Great Basin spadefoot (<i>Spea intermontana</i>)	0.3	27.6	87.6	53.0%
Pronghorn (<i>Antilocapra americana</i>)	0.3	24.2	95.8	52.9%
Bighorn sheep (<i>Ovis canadensis</i>)	0.3	24.3	96.0	52.9%
Green-tailed towhee (<i>Pipilo chlorurus</i>)	0.3	19.0	92.6	52.7%
Piñon mouse (<i>Peromyscus truei</i>)	0.3	26.6	95.6	52.6%
Greater short-horned lizard (<i>Phrynosoma hernandesi</i>)	0.3	25.5	99.1	48.3%
Wyoming ground squirrel (<i>Urocitellus elegans</i>)	0.3	12.2	73.9	48.3%
Townsend's big-eared bat (<i>Corynorhinus townsendii</i>)	0.3	14.6	82.1	46.9%
Lark sparrow (<i>Chondestes grammacus</i>)	0.3	33.3	83.5	42.4%

Minimum area optimization covered by priority sage-grouse habitat umbrella

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
<u>Abundant Habitat Species</u>				
Southern Idaho ground squirrel (<i>Urocitellus endemicus</i>)	0.95	8.8	23.5	100.0%
Cronquist's milkvetch (<i>Astragalus cronquistii</i>)	0.9	12.6	40.2	100.0%
Inconspicuous scorpionweed (<i>Phacelia inconspicua</i>)	0.9	9.9	26.5	100.0%
San Rafael milkvetch (<i>Astragalus rafaensis</i>)	0.8	13.0	50.5	100.0%
Mulford's milkvetch (<i>Astragalus mulfordiae</i>)	0.9	7.1	29.2	97.2%
Currant milkvetch (<i>Astragalus uncialis</i>)	0.95	10.1	28.8	97.0%
Black-footed ferret (<i>Mustela nigripes</i>)	0.8	12.0	34.2	97.0%
Cusick's lupine (<i>Lupinus cusickii</i>)	0.9	8.5	28.7	94.7%
Cusick's buckwheat (<i>Eriogonum cusickii</i>)	0.9	12.0	29.3	94.4%
Cordillia's beardtongue (<i>Penstemon floribundus</i>)	0.9	10.8	35.3	94.1%
Owyhee clover (<i>Trifolium owyheense</i>)	0.95	8.3	27.1	92.3%
Packard's desert-parsley (<i>Lomatium packardiae</i>)	0.8	9.9	24.5	90.9%
Fisher milkvetch (<i>Astragalus piscator</i>)	0.9	10.5	26.3	89.5%
Talapoosa Peak pearpod (<i>Lepidium tiehmii</i>)	0.9	5.6	22.9	89.2%
Ertter's ragwort (<i>Senecio ertterae</i>)	0.9	11.5	31.3	88.2%
Deschutes sideband (<i>Monadenia fidelis</i>)	0.9	14.7	38.8	87.1%
Canyonlands lomatium (<i>Lomatium latilobum</i>)	0.75	26.3	89.5	85.3%
Sunnyside green gentian (<i>Frasera gypsicola</i>)	0.95	9.7	29.0	84.0%
Aquarius Plateau beardtongue (<i>Penstemon parvus</i>)	0.8	8.7	31.0	82.8%
Blaine's pincushion (<i>Sclerocactus blainei</i>)	0.95	9.2	27.6	80.8%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Big free-tailed bat (<i>Nyctinomops macrotis</i>)	0.8	11.3	36.5	80.0%
Western mastiff bat (<i>Eumops perotis</i>)	0.9	10.5	24.3	78.9%
Astragalus anxius (<i>Astragalus anxius</i>)	0.9	11.0	34.9	77.8%
Granite buckwheat (<i>Eriogonum robustum</i>)	0.75	15.3	84.1	76.7%
Howell's thelypody (<i>Thelypodium howellii</i>)	0.75	14.2	87.6	76.3%
Nye County fishhook cactus (<i>Sclerocactus nyensis</i>)	0.75	21.5	85.4	76.2%
Plumas ivesia (<i>Ivesia sericoleuca</i>)	0.75	11.2	79.5	75.1%
Sierra Valley ivesia (<i>Ivesia aperta</i>)	0.75	16.5	78.3	74.4%
Biennial prince's plume (<i>Stanleya confertiflora</i>)	0.8	11.9	29.6	73.5%
Webber ivesia (<i>Ivesia webberi</i>)	0.75	18.7	73.3	72.1%
Ward's beardtongue (<i>Penstemon wardii</i>)	0.75	18.1	64.9	69.8%
Tufted globemallow (<i>Sphaeralcea caespitosa</i>)	0.75	18.9	73.9	68.9%
Ash Creek ivesia (<i>Ivesia paniculata</i>)	0.75	20.5	75.5	68.5%
Steamboat buckwheat (<i>Eriogonum ovalifolium</i> var. <i>williamsiae</i>)	0.75	19.6	76.3	67.3%
Western small-footed myotis (<i>Myotis ciliolabrum</i>)	0.8	12.7	29.6	66.0%
Kawich Range beardtongue (<i>Penstemon pudicus</i>)	0.8	11.6	28.0	65.6%
Wind-loving buckwheat (<i>Eriogonum anemophilum</i>)	0.75	23.8	58.1	65.5%
Fox's barrier orbweaver (<i>Metepeira foxi</i>)	0.8	13.0	31.9	63.5%
Gunnison milkvetch (<i>Astragalus anisus</i>)	0.75	17.8	82.6	62.3%
Rose-flower desert-parsley (<i>Lomatium roseanum</i>)	0.75	17.8	68.9	62.0%
Washington ground squirrel (<i>Urocitellus washingtoni</i>)	0.95	11.6	35.0	60.7%
Ophir rockcress (<i>Arabis ophira</i>)	0.9	8.0	23.1	60.7%
Bodie Hills cusickiella (<i>Cusickiella quadricostata</i>)	0.75	30.6	94.9	58.3%
Stemless beardtongue (<i>Penstemon acaulis</i>)	0.8	10.3	27.6	57.6%
Colorado desert-parsley (<i>Lomatium concinnum</i>)	0.8	15.0	29.2	57.6%
Barren Valley collomia (<i>Collomia renacta</i>)	0.95	19.6	79.2	57.3%
Slick spot peppergrass (<i>Lepidium papilliferum</i>)	0.75	17.9	83.5	57.0%
Toquima milkvetch (<i>Astragalus toquimanus</i>)	0.75	22.9	92.3	56.1%
Brandegee's buckwheat (<i>Eriogonum brandegeei</i>)	0.75	20.5	79.7	53.8%
Aquarius Plateau Indian paintbrush (<i>Castilleja aquariensis</i>)	0.9	5.0	14.9	53.6%
Frisco buckwheat (<i>Eriogonum soledium</i>)	0.75	20.4	76.1	51.5%
Townsend's ground squirrel (<i>Urocitellus townsendii</i>)	0.8	18.9	31.5	48.6%
Grand Canyon rattlesnake (<i>Crotalus oreganus abyssus</i>)	0.75	31.0	93.6	44.3%
Goose Creek milkvetch (<i>Astragalus anserinus</i>)	0.75	15.4	61.7	40.3%
Idaho beardtongue (<i>Penstemon idahoensis</i>)	0.75	20.0	48.6	40.1%
Prostrate bladderpod (<i>Physaria prostrata</i>)	0.95	7.0	16.9	22.9%
Grouse Creek rockcress (<i>Arabis falcatoria</i>)	0.95	3.2	6.2	21.7%
Elko rockcress (<i>Arabis falcifructa</i>)	0.95	0	0	0.0%
Desert yellowhead (<i>Yermo xanthocephalus</i>)	0.9	0	0	0.0%

Intermediate Habitat Species

Midget faded rattlesnake (<i>Crotalus oreganus concolor</i>)	0.5	8.8	21.3	86.7%
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	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Smooth stickleaf (<i>Mentzelia mollis</i>)	0.5	18.4	66.9	69.4%
Grimy ivesia (<i>Ivesia rhypara</i>)	0.5	23.1	80.0	62.7%
Western ground snake (<i>Sonora semiannulata</i>)	0.5	15.7	83.4	59.4%
Dark kangaroo mouse (<i>Microdipodops megacephalus</i>)	0.5	18.0	90.4	58.6%
Merriam's kangaroo rat (<i>Dipodomys merriami</i>)	0.5	20.2	73.5	58.4%
Chisel-toothed kangaroo rat (<i>Dipodomys microps</i>)	0.5	18.7	93.9	57.5%
Long-nosed snake (<i>Rhinocheilus lecontei</i>)	0.5	23.5	86.1	57.1%
Little pocket mouse (<i>Perognathus longimembris</i>)	0.5	19.0	84.5	56.0%
Long-nosed leopard lizard (<i>Gambelia wislizenii</i>)	0.5	24.2	90.0	52.9%
Piute ground squirrel (<i>Urocitellus mollis</i>)	0.5	22.5	91.6	52.0%
Northern Pacific rattlesnake (<i>Crotalus oreganus oreganus</i>)	0.5	16.2	95.5	50.8%
Silver longjawed orbweaver (<i>Tetragnatha laboriosa</i>)	0.5	11.7	85.3	50.8%
Pygmy horned lizard (<i>Phrynosoma douglasii</i>)	0.5	15.4	81.2	50.7%
Rock squirrel (<i>Otospermophilus variegatus</i>)	0.5	13.9	87.7	50.0%
Idaho pocket gopher (<i>Thomomys idahoensis</i>)	0.5	12.0	67.5	43.3%
Wyoming pocket gopher (<i>Thomomys clusius</i>)	0.5	23.0	75.6	33.6%

Limited Habitat Species

Black-tailed prairie dog (<i>Cynomys ludovicianus</i>)	0.4	39.2	87.7	69.7%
Desert spiny lizard (<i>Sceloporus magister</i>)	0.4	15.3	78.7	59.5%
Great Basin collared lizard (<i>Crotaphytus bicinctores</i>)	0.4	38.6	97.9	57.5%
Side-blotched lizard (<i>Uta stansburiana</i>)	0.4	24.7	98.4	56.0%
Desert horned lizard (<i>Phrynosoma platyrhinos</i>)	0.4	21.9	84.6	55.7%
White-tailed prairie dog (<i>Cynomys leucurus</i>)	0.4	31.0	94.7	54.5%
Black-throated sparrow (<i>Amphispiza bilineata</i>)	0.4	26.9	99.4	54.2%
White-tailed antelope squirrel (<i>Ammospermophilus leucurus</i>)	0.4	28.5	91.9	54.0%
Mountain plover (<i>Charadrius montanus</i>)	0.4	25.0	95.9	53.7%
Canyon mouse (<i>Peromyscus crinitus</i>)	0.4	27.7	88.6	52.9%
Botta's pocket gopher (<i>Thomomys bottae</i>)	0.4	27.1	86.7	52.8%
Great Basin pocket mouse (<i>Perognathus parvus</i>)	0.4	23.9	84.0	52.0%
Pallid bat (<i>Antrozous pallidus</i>)	0.4	17.8	89.9	51.6%
Acastus checkerspot (<i>Chlosyne acastus</i>)	0.4	40.4	94.1	51.3%
Leafbeetle jumping spider (<i>Sassacus papenhoei</i>)	0.4	14.4	91.6	50.8%
Lark bunting (<i>Calamospiza melanocorys</i>)	0.4	38.0	98.5	50.8%
Running crab spiders (<i>Ebo spp</i>)	0.4	15.9	96.3	50.8%
Kit fox (<i>Vulpes macrotis</i>)	0.4	22.4	90.0	50.2%
Cliff chipmunk (<i>Tamias dorsalis</i>)	0.4	13.2	76.9	49.8%
Virginia's warbler (<i>Leiothlypis virginiae</i>)	0.4	17.8	84.2	47.9%
Grasshopper sparrow (<i>Ammodramus savannarum</i>)	0.4	31.2	91.9	46.6%
Western milksnake (<i>Lampropeltis gentilis</i>)	0.4	18.0	83.6	44.5%
Sharp-tailed grouse (<i>Tympanuchus phasianellus</i>)	0.4	34.1	99.7	44.3%
Clay-colored sparrow (<i>Spizella pallida</i>)	0.4	21.9	97.0	44.0%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Great Basin rattlesnake (<i>Crotalus oreganus lutosus</i>)	0.4	35.6	94.5	42.3%
Prairie rattlesnake (<i>Crotalus viridis</i>)	0.4	16.3	67.5	40.1%
Striped whipsnake (<i>Coluber taeniatus</i>)	0.3	13.5	63.9	67.2%
Nightsnake (<i>Hypsiglena torquata</i>)	0.3	23.9	88.4	55.1%
Gray flycatcher (<i>Empidonax wrightii</i>)	0.3	34.8	97.7	52.6%
Fringed myotis (<i>Myotis thysanodes</i>)	0.3	20.4	91.8	52.4%
Yuma myotis (<i>Myotis yumanensis</i>)	0.3	29.2	81.2	52.3%
Black-tailed jackrabbit (<i>Lepus californicus</i>)	0.3	24.0	98.9	51.7%
Sagebrush sparrow (<i>Artemisiospiza nevadensis</i>)	0.3	36.8	93.9	51.6%
Sagebrush lizard (<i>Sceloporus graciosus</i>)	0.3	25.3	95.8	51.5%
Pygmy rabbit (<i>Brachylagus idahoensis</i>)	0.3	22.8	95.3	51.3%
Spotted bat (<i>Euderma maculatum</i>)	0.3	23.6	97.9	51.3%
Sagebrush vole (<i>Lemmiscus curtatus</i>)	0.3	23.1	79.5	51.0%
Great Basin spadefoot (<i>Spea intermontana</i>)	0.3	27.8	87.6	51.0%
Long-billed curlew (<i>Numenius americanus</i>)	0.3	23.6	96.0	50.9%
Merriam's shrew (<i>Sorex merriami</i>)	0.3	19.1	99.5	50.9%
Ord's kangaroo rat (<i>Dipodomys ordii</i>)	0.3	22.3	89.9	50.8%
Long-eared myotis (<i>Myotis evotis</i>)	0.3	21.6	85.9	50.8%
White-tailed jackrabbit (<i>Lepus townsendii</i>)	0.3	13.7	78.9	50.8%
Atlantis fritillary (<i>Speyeria atlantis</i>)	0.3	15.1	79.5	50.8%
Northern grasshopper mouse (<i>Onychomys leucogaster</i>)	0.3	21.5	92.9	50.8%
Least chipmunk (<i>Tamias minimus</i>)	0.3	18.2	87.7	50.8%
Grey ground crab spider (<i>Xysticus gulosus</i>)	0.3	20.4	83.4	50.8%
Western black widow (<i>Latrodectus hesperus</i>)	0.3	15.9	99.5	50.8%
MacGillivray's warbler (<i>Geothlypis tolmiei</i>)	0.3	20.9	94.4	50.8%
Sandhill crane (<i>Antigone canadensis</i>)	0.3	19.0	95.4	50.8%
Western lynx spider (<i>Oxyopes scalaris</i>)	0.3	20.6	89.0	50.8%
Great Basin gopher snake (<i>Pituophis catenifer</i>)	0.3	34.2	97.5	50.8%
Mule deer (<i>Odocoileus hemionus</i>)	0.3	23.3	96.0	50.8%
Wolf spider (<i>Alopecosa kochi</i>)	0.3	22.7	83.5	50.8%
Western burrowing owl (<i>Speotyto cunicularia</i>)	0.3	49.8	100.0	50.8%
Coppered white-cheeked jumping spider (<i>Pelegrina aeneola</i>)	0.3	22.6	84.3	50.8%
Red-backed jumping spider (<i>Phidippus johnsoni</i>)	0.3	26.3	88.7	50.8%
Northwestern fritillary (<i>Speyeria hesperis</i>)	0.3	37.7	98.0	50.8%
Western meadowlark (<i>Sturnella neglecta</i>)	0.3	33.4	97.9	50.8%
Skippers (<i>Hesperopsis</i> spp.)	0.3	39.6	98.3	50.8%
Brewer's blackbird (<i>Euphagus cyanocephalus</i>)	0.3	26.5	98.2	50.8%
Loggerhead shrike (<i>Lanius ludovicianus</i>)	0.3	37.6	97.9	50.8%
Vesper sparrow (<i>Pooecetes gramineus</i>)	0.3	34.9	98.3	50.8%
Hook-toothed money spider (<i>Erigone dentosa</i>)	0.3	14.2	81.0	50.8%
Short-eared owl (<i>Asio flammeus</i>)	0.3	49.4	100.0	50.8%
Northern crescent (<i>Phyciodes cocyta</i>)	0.3	43.4	98.1	50.8%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Rock wren (<i>Salpinctes obsoletus</i>)	0.3	34.5	99.8	50.8%
Tangle-web spiders (<i>Euryopis</i> spp)	0.3	19.4	68.9	50.8%
Sixspotted orbweaver (<i>Araniella displicata</i>)	0.3	20.4	82.9	50.8%
Polymorphic long-jawed cobweaver (<i>Enoplognatha ovata</i>)	0.3	13.5	62.5	50.8%
Montane crab spider (<i>Xysticus montanensis</i>)	0.3	20.6	75.7	50.8%
Nevada viceroy (<i>Limenitis archippus</i>)	0.3	43.2	97.5	50.8%
Mountainsnails (<i>Oreohelix</i> spp.)	0.3	17.1	67.5	50.8%
Sandhill skipper (<i>Polites sabuleti</i>)	0.3	48.9	93.0	50.8%
Oblong running crab spider (<i>Tibellus oblongus</i>)	0.3	20.8	64.9	50.8%
Brewer's sparrow (<i>Spizella breweri</i>)	0.3	37.1	97.9	50.8%
Dotted blue butterflies (<i>Euphilotes</i> spp.)	0.3	46.5	97.6	50.8%
Protrudent long-legged cobweaver (<i>Theridion neomexicanum</i>)	0.3	15.5	82.4	50.8%
Sage thrasher (<i>Oreoscoptes montanus</i>)	0.3	34.5	99.0	50.7%
Piñon mouse (<i>Peromyscus truei</i>)	0.3	26.6	95.6	50.7%
Bighorn sheep (<i>Ovis canadensis</i>)	0.3	24.7	96.0	50.7%
Pronghorn (<i>Antilocapra americana</i>)	0.3	23.9	95.8	50.6%
Green-tailed towhee (<i>Pipilo chlorurus</i>)	0.3	19.1	92.6	50.4%
Preble's shrew (<i>Sorex preblei</i>)	0.3	22.0	89.2	50.4%
Greater short-horned lizard (<i>Phrynosoma hernandesi</i>)	0.3	25.4	99.1	46.2%
Wyoming ground squirrel (<i>Uroditellus elegans</i>)	0.3	12.1	59.1	45.5%
Townsend's big-eared bat (<i>Corynorhinus townsendii</i>)	0.3	14.6	82.1	45.2%
Lark sparrow (<i>Chondestes grammacus</i>)	0.3	33.0	83.5	40.2%

Minimum area optimization covered by general sage-grouse habitat umbrella

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
<u>Abundant Habitat Species</u>				
Cronquist's milkvetch (<i>Astragalus cronquistii</i>)	0.9	12.6	40.2	100.0%
Inconspicuous scorpionweed (<i>Phacelia inconspicua</i>)	0.9	9.9	26.5	100.0%
San Rafael milkvetch (<i>Astragalus rafaensis</i>)	0.8	12.8	50.5	97.3%
Southern Idaho ground squirrel (<i>Uroditellus endemicus</i>)	0.95	9.0	23.5	95.8%
Cordillia's beardtongue (<i>Penstemon floribundus</i>)	0.9	10.8	35.3	94.1%
Mulford's milkvetch (<i>Astragalus mulfordiae</i>)	0.9	7.3	29.2	91.7%
Currant milkvetch (<i>Astragalus uncialis</i>)	0.95	10.8	28.8	90.9%
Fisher milkvetch (<i>Astragalus piscator</i>)	0.9	10.5	26.3	89.5%
Talapoosa Peak pearpod (<i>Lepidium tiehmii</i>)	0.9	5.6	22.9	89.2%
Deschutes sideband (<i>Monadenia fidelis</i>)	0.9	14.7	38.8	87.1%
Canyonlands lomatium (<i>Lomatium latilobum</i>)	0.75	26.9	89.5	83.0%
Aquarius Plateau beardtongue (<i>Penstemon parvus</i>)	0.8	8.7	31.0	82.8%
Big free-tailed bat (<i>Nyctinomops macrotis</i>)	0.8	11.3	36.5	80.0%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Western mastiff bat (<i>Eumops perotis</i>)	0.9	10.5	24.3	78.9%
Blaine's pincushion (<i>Sclerocactus blainei</i>)	0.95	9.7	27.6	76.9%
Granite buckwheat (<i>Eriogonum robustum</i>)	0.75	15.4	84.1	75.7%
Plumas ivesia (<i>Ivesia sericoleuca</i>)	0.75	11.1	79.5	73.6%
Sierra Valley ivesia (<i>Ivesia aperta</i>)	0.75	16.6	78.3	72.9%
<i>Astragalus anxius</i> (<i>Astragalus anxius</i>)	0.9	10.3	34.9	72.2%
Howell's thelypody (<i>Thelypodium howellii</i>)	0.75	14.4	87.6	71.3%
Webber ivesia (<i>Ivesia webberi</i>)	0.75	19.0	73.3	70.3%
Owyhee clover (<i>Trifolium owyheense</i>)	0.95	8.7	27.1	69.2%
Nye County fishhook cactus (<i>Sclerocactus nyensis</i>)	0.75	22.6	85.4	68.5%
Cusick's lupine (<i>Lupinus cusickii</i>)	0.9	8.8	28.7	68.4%
Ward's beardtongue (<i>Penstemon wardii</i>)	0.75	18.1	64.9	67.2%
Western small-footed myotis (<i>Myotis ciliolabrum</i>)	0.8	12.7	29.6	66.0%
Steamboat buckwheat (<i>Eriogonum ovalifolium</i> var. <i>williamsiae</i>)	0.75	19.6	76.3	65.9%
Ash Creek ivesia (<i>Ivesia paniculata</i>)	0.75	20.9	75.5	65.4%
Black-footed ferret (<i>Mustela nigripes</i>)	0.8	12.5	28.0	63.6%
Washington ground squirrel (<i>Urocitellus washingtoni</i>)	0.95	11.6	35.0	60.7%
Packard's desert-parsley (<i>Lomatium packardiae</i>)	0.8	8.9	24.5	60.6%
Sunnyside green gentian (<i>Frasera gypsicola</i>)	0.95	9.9	27.2	60.0%
Wind-loving buckwheat (<i>Eriogonum anemophilum</i>)	0.75	24.7	58.1	59.5%
Tufted globemallow (<i>Sphaeralcea caespitosa</i>)	0.75	19.8	73.9	59.4%
Gunnison milkvetch (<i>Astragalus anisus</i>)	0.75	17.7	82.6	59.0%
Ertter's ragwort (<i>Senecio ertterae</i>)	0.9	13.9	31.3	58.8%
Ophir rockcress (<i>Arabis ophira</i>)	0.9	7.6	23.1	57.1%
Cusick's buckwheat (<i>Eriogonum cusickii</i>)	0.9	9.2	29.3	55.6%
Brandegee's buckwheat (<i>Eriogonum brandegeei</i>)	0.75	20.6	79.7	52.8%
Rose-flower desert-parsley (<i>Lomatium roseanum</i>)	0.75	17.0	68.9	50.9%
Barren Valley collomia (<i>Collomia renacta</i>)	0.95	20.4	79.2	50.3%
Townsend's ground squirrel (<i>Urocitellus townsendii</i>)	0.8	18.9	31.5	48.6%
Toquima milkvetch (<i>Astragalus toquimanus</i>)	0.75	18.3	81.3	48.4%
Bodie Hills cusickiella (<i>Cusickiella quadricostata</i>)	0.75	34.0	94.9	47.7%
Fox's barrier orbweaver (<i>Metepeira foxi</i>)	0.8	12.6	31.9	46.2%
Colorado desert-parsley (<i>Lomatium concinnum</i>)	0.8	14.9	29.2	45.5%
Kawich Range beardtongue (<i>Penstemon pudicus</i>)	0.8	12.0	26.3	43.8%
Slick spot peppergrass (<i>Lepidium papilliferum</i>)	0.75	19.2	83.5	43.3%
Frisco buckwheat (<i>Eriogonum soredium</i>)	0.75	20.2	76.1	42.8%
Biennial prince's plume (<i>Stanleya confertiflora</i>)	0.8	10.5	25.3	34.7%
Grand Canyon rattlesnake (<i>Crotalus oreganus abyssus</i>)	0.75	27.1	92.0	32.1%
Idaho beardtongue (<i>Penstemon idahoensis</i>)	0.75	18.4	44.7	29.2%
Goose Creek milkvetch (<i>Astragalus anserinus</i>)	0.75	11.6	35.2	27.6%
Aquarius Plateau Indian paintbrush (<i>Castilleja aquariensis</i>)	0.9	3.0	9.8	25.0%
Stemless beardtongue (<i>Penstemon acaulis</i>)	0.8	12.9	27.6	18.2%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Elko rockcress (<i>Arabis falcifracta</i>)	0.95	0	0	0.0%
Grouse Creek rockcress (<i>Arabis falcatoria</i>)	0.95	0	0	0.0%
Prostrate bladderpod (<i>Physaria prostrata</i>)	0.95	0.0	0.0	0.0%
Desert yellowhead (<i>Yermo xanthocephalus</i>)	0.9	0	0	0.0%

Intermediate Habitat Species

Midget faded rattlesnake (<i>Crotalus oreganus concolor</i>)	0.5	8.8	21.3	86.7%
Merriam's kangaroo rat (<i>Dipodomys merriami</i>)	0.5	20.8	73.5	53.7%
Smooth stickleaf (<i>Mentzelia mollis</i>)	0.5	18.3	66.9	52.7%
Western ground snake (<i>Sonora semiannulata</i>)	0.5	16.2	83.4	51.9%
Dark kangaroo mouse (<i>Microdipodops megacephalus</i>)	0.5	17.9	90.4	51.5%
Chisel-toothed kangaroo rat (<i>Dipodomys microps</i>)	0.5	19.3	93.9	50.4%
Long-nosed snake (<i>Rhinocheilus lecontei</i>)	0.5	25.1	86.1	50.2%
Little pocket mouse (<i>Perognathus longimembris</i>)	0.5	20.0	84.5	48.8%
Long-nosed leopard lizard (<i>Gambelia wislizenii</i>)	0.5	25.6	90.0	46.2%
Grimy ivesia (<i>Ivesia rhypara</i>)	0.5	19.0	73.1	45.2%
Piute ground squirrel (<i>Urocyonax mollis</i>)	0.5	24.0	91.6	44.8%
Rock squirrel (<i>Otospermophilus variegatus</i>)	0.5	14.4	87.7	43.3%
Pygmy horned lizard (<i>Phrynosoma douglasii</i>)	0.5	15.2	81.2	43.0%
Northern Pacific rattlesnake (<i>Crotalus oreganus oreganus</i>)	0.5	17.3	95.5	40.8%
Silver longjawed orbweaver (<i>Tetragnatha laboriosa</i>)	0.5	11.5	85.3	40.8%
Idaho pocket gopher (<i>Thomomys idahoensis</i>)	0.5	11.0	39.2	29.6%
Wyoming pocket gopher (<i>Thomomys clusius</i>)	0.5	10.6	33.0	15.9%

Limited Habitat Species

Black-tailed prairie dog (<i>Cynomys ludovicianus</i>)	0.4	38.5	87.7	67.1%
Great Basin collared lizard (<i>Crotaphytus bicinctores</i>)	0.4	39.4	97.9	55.8%
Desert spiny lizard (<i>Sceloporus magister</i>)	0.4	15.7	78.7	54.4%
Side-blotched lizard (<i>Uta stansburiana</i>)	0.4	26.1	98.4	48.5%
Botta's pocket gopher (<i>Thomomys bottae</i>)	0.4	28.2	86.7	47.6%
White-tailed prairie dog (<i>Cynomys leucurus</i>)	0.4	31.0	94.7	47.3%
Desert horned lizard (<i>Phrynosoma platyrhinos</i>)	0.4	23.3	84.6	47.3%
Black-throated sparrow (<i>Amphispiza bilineata</i>)	0.4	28.5	99.4	46.8%
Mountain plover (<i>Charadrius montanus</i>)	0.4	25.8	95.9	46.2%
White-tailed antelope squirrel (<i>Ammospermophilus leucurus</i>)	0.4	30.8	91.9	45.8%
Canyon mouse (<i>Peromyscus crinitus</i>)	0.4	29.2	88.6	44.8%
Great Basin pocket mouse (<i>Perognathus parvus</i>)	0.4	22.5	82.9	44.3%
Pallid bat (<i>Antrozous pallidus</i>)	0.4	18.0	89.9	44.1%
Kit fox (<i>Vulpes macrotis</i>)	0.4	23.5	90.0	42.4%
Cliff chipmunk (<i>Tamias dorsalis</i>)	0.4	13.5	76.9	41.9%
Acastus checkerspot (<i>Chlosyne acastus</i>)	0.4	41.1	94.1	41.2%
Leafbeetle jumping spider (<i>Sassacus papenhoei</i>)	0.4	15.2	91.6	40.8%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Lark bunting (<i>Calamospiza melanocorys</i>)	0.4	38.5	98.5	40.8%
Running crab spiders (Ebo spp)	0.4	16.5	96.3	40.8%
Virginia's warbler (<i>Leiothlypis virginiae</i>)	0.4	19.1	84.2	38.5%
Grasshopper sparrow (<i>Ammodramus savannarum</i>)	0.4	32.3	89.5	33.7%
Sharp-tailed grouse (<i>Tympanuchus phasianellus</i>)	0.4	29.6	99.7	33.5%
Western milksnake (<i>Lampropeltis gentilis</i>)	0.4	17.8	83.6	33.4%
Clay-colored sparrow (<i>Spizella pallida</i>)	0.4	21.3	97.0	32.2%
Great Basin rattlesnake (<i>Crotalus oreganus lutosus</i>)	0.4	27.8	94.5	30.5%
Prairie rattlesnake (<i>Crotalus viridis</i>)	0.4	16.9	67.5	25.8%
Striped whipsnake (<i>Coluber taeniatus</i>)	0.3	12.9	43.1	65.2%
Nightsnake (<i>Hypsiglena torquata</i>)	0.3	24.9	88.4	48.0%
Fringed myotis (<i>Myotis thysanodes</i>)	0.3	21.6	91.8	44.1%
Gray flycatcher (<i>Empidonax wrightii</i>)	0.3	36.1	97.7	43.9%
Yuma myotis (<i>Myotis yumanensis</i>)	0.3	29.4	81.2	43.8%
Spotted bat (<i>Euderma maculatum</i>)	0.3	23.9	97.9	43.3%
Black-tailed jackrabbit (<i>Lepus californicus</i>)	0.3	24.7	98.9	43.1%
Pygmy rabbit (<i>Brachylagus idahoensis</i>)	0.3	20.9	83.0	42.8%
Piñon mouse (<i>Peromyscus truei</i>)	0.3	27.2	95.6	42.6%
Sagebrush sparrow (<i>Artemisiospiza nevadensis</i>)	0.3	36.2	93.9	42.5%
Great Basin spadefoot (<i>Spea intermontana</i>)	0.3	27.8	87.6	42.4%
Sagebrush lizard (<i>Sceloporus graciosus</i>)	0.3	25.2	95.8	41.3%
Merriam's shrew (<i>Sorex merriami</i>)	0.3	18.5	99.5	40.9%
Long-eared myotis (<i>Myotis evotis</i>)	0.3	21.1	85.9	40.8%
White-tailed jackrabbit (<i>Lepus townsendii</i>)	0.3	12.9	66.5	40.8%
Atlantis fritillary (<i>Speyeria atlantis</i>)	0.3	15.7	79.5	40.8%
Northern grasshopper mouse (<i>Onychomys leucogaster</i>)	0.3	18.3	86.1	40.8%
Least chipmunk (<i>Tamias minimus</i>)	0.3	18.4	87.7	40.8%
Grey ground crab spider (<i>Xysticus gulosus</i>)	0.3	21.4	83.4	40.8%
Western black widow (<i>Latrodectus hesperus</i>)	0.3	16.7	99.5	40.8%
MacGillivray's warbler (<i>Geothlypis tolmiei</i>)	0.3	22.6	94.4	40.8%
Sandhill crane (<i>Antigone canadensis</i>)	0.3	19.3	95.4	40.8%
Western lynx spider (<i>Oxyopes scalaris</i>)	0.3	21.8	89.0	40.8%
Great Basin gopher snake (<i>Pituophis catenifer</i>)	0.3	35.7	97.5	40.8%
Mule deer (<i>Odocoileus hemionus</i>)	0.3	24.8	96.0	40.8%
Wolf spider (<i>Alopecosa kochi</i>)	0.3	24.0	83.5	40.8%
Western burrowing owl (<i>Speotyto cunicularia</i>)	0.3	46.4	99.5	40.8%
Coppered white-cheeked jumping spider (<i>Pelegrina aeneola</i>)	0.3	23.8	84.3	40.8%
Red-backed jumping spider (<i>Phidippus johnsoni</i>)	0.3	27.1	85.3	40.8%
Northwestern fritillary (<i>Speyeria hesperis</i>)	0.3	37.5	98.0	40.8%
Western meadowlark (<i>Sturnella neglecta</i>)	0.3	33.8	97.9	40.8%
Skippers (<i>Hesperopsis</i> spp.)	0.3	39.5	98.3	40.8%
Brewer's blackbird (<i>Euphagus cyanocephalus</i>)	0.3	27.2	98.2	40.8%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Loggerhead shrike (<i>Lanius ludovicianus</i>)	0.3	37.6	97.9	40.8%
Vesper sparrow (<i>Pooecetes gramineus</i>)	0.3	34.4	98.3	40.8%
Hook-toothed money spider (<i>Erigone dentosa</i>)	0.3	14.5	81.0	40.8%
Short-eared owl (<i>Asio flammeus</i>)	0.3	44.7	100.0	40.8%
Northern crescent (<i>Phyciodes cocyta</i>)	0.3	42.8	98.1	40.8%
Rock wren (<i>Salpinctes obsoletus</i>)	0.3	36.0	99.8	40.8%
Tangle-web spiders (<i>Euryopis</i> spp)	0.3	20.1	68.9	40.8%
Sixspotted orbweaver (<i>Araniella displicata</i>)	0.3	21.3	82.9	40.8%
Polymorphic long-jawed cobweaver (<i>Enoplognatha ovata</i>)	0.3	13.8	62.5	40.8%
Montane crab spider (<i>Xysticus montanensis</i>)	0.3	20.4	75.7	40.8%
Nevada viceroy (<i>Limenitis archippus</i>)	0.3	43.0	97.5	40.8%
Mountainsnails (<i>Oreohelix</i> spp.)	0.3	17.6	67.5	40.8%
Sandhill skipper (<i>Polites sabuleti</i>)	0.3	50.4	93.0	40.8%
Oblong running crab spider (<i>Tibellus oblongus</i>)	0.3	21.4	64.9	40.8%
Brewer's sparrow (<i>Spizella breweri</i>)	0.3	36.8	97.9	40.8%
Dotted blue butterflies (<i>Euphilotes</i> spp.)	0.3	47.1	97.6	40.8%
Protrudent long-legged cobweaver (<i>Theridion neomexicanum</i>)	0.3	15.6	82.4	40.8%
Ord's kangaroo rat (<i>Dipodomys ordii</i>)	0.3	22.9	89.9	40.8%
Long-billed curlew (<i>Numenius americanus</i>)	0.3	23.7	96.0	40.8%
Sage thrasher (<i>Oreoscoptes montanus</i>)	0.3	33.0	99.0	40.7%
Sagebrush vole (<i>Lemmyscus curtatus</i>)	0.3	20.0	74.3	40.7%
Bighorn sheep (<i>Ovis canadensis</i>)	0.3	26.5	96.0	40.7%
Pronghorn (<i>Antilocapra americana</i>)	0.3	22.4	95.8	40.4%
Green-tailed towhee (<i>Pipilo chlorurus</i>)	0.3	19.9	92.6	40.4%
Preble's shrew (<i>Sorex preblei</i>)	0.3	22.2	89.2	38.0%
Greater short-horned lizard (<i>Phrynosoma hernandesi</i>)	0.3	25.1	99.1	35.2%
Townsend's big-eared bat (<i>Corynorhinus townsendii</i>)	0.3	13.5	58.7	34.0%
Wyoming ground squirrel (<i>Uroditellus elegans</i>)	0.3	11.4	52.4	32.9%
Lark sparrow (<i>Chondestes grammacus</i>)	0.3	32.6	83.5	27.2%

Sage-grouse PAC optimization covered by sage-grouse PAC umbrella

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
<u>Abundant Habitat Species</u>				
Inconspicuous scorpionweed (<i>Phacelia inconspicua</i>)	0.9	9.9	26.5	100.0%
Mulford's milkvetch (<i>Astragalus mulfordiae</i>)	0.9	7.0	29.2	100.0%
San Rafael milkvetch (<i>Astragalus rafaensis</i>)	0.8	13.0	50.5	100.0%
Black-footed ferret (<i>Mustela nigripes</i>)	0.8	11.9	34.2	97.0%
Sunnyside green gentian (<i>Frasera gypsicola</i>)	0.95	8.9	29.0	96.0%
Biennial prince's plume (<i>Stanleya confertiflora</i>)	0.8	10.5	29.6	95.9%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Southern Idaho ground squirrel (<i>Urocitellus endemicus</i>)	0.95	9.0	23.5	95.8%
Cronquist's milkvetch (<i>Astragalus cronquistii</i>)	0.9	13.0	40.2	95.8%
Cusick's lupine (<i>Lupinus cusickii</i>)	0.9	8.5	28.7	94.7%
Fisher milkvetch (<i>Astragalus piscator</i>)	0.9	10.0	26.3	94.7%
Talapoosa Peak pearpod (<i>Lepidium tiehmii</i>)	0.9	5.6	22.9	94.6%
Aquarius Plateau beardtongue (<i>Penstemon parvus</i>)	0.8	8.7	31.0	93.1%
Owyhee clover (<i>Trifolium owyheense</i>)	0.95	8.3	27.1	92.3%
Cusick's buckwheat (<i>Eriogonum cusickii</i>)	0.9	12.5	29.3	88.9%
Ertter's ragwort (<i>Senecio ertterae</i>)	0.9	11.5	31.3	88.2%
Currant milkvetch (<i>Astragalus uncialis</i>)	0.95	11.2	28.8	87.9%
Big free-tailed bat (<i>Nyctinomops macrotis</i>)	0.8	10.9	36.5	85.5%
Blaine's pincushion (<i>Sclerocactus blainei</i>)	0.95	8.8	27.6	84.6%
Canyonlands lomatium (<i>Lomatium latilobum</i>)	0.75	26.7	89.5	83.5%
<i>Astragalus anxius</i> (<i>Astragalus anxius</i>)	0.9	10.7	34.9	83.3%
Cordillia's beardtongue (<i>Penstemon floribundus</i>)	0.9	11.9	35.3	82.4%
Aquarius Plateau Indian paintbrush (<i>Castilleja aquariensis</i>)	0.9	5.4	14.9	82.1%
Packard's desert-parsley (<i>Lomatium packardiae</i>)	0.8	10.3	24.5	81.8%
Deschutes sideband (<i>Monadenia fidelis</i>)	0.9	15.4	38.8	80.6%
Western mastiff bat (<i>Eumops perotis</i>)	0.9	10.5	24.3	78.9%
Granite buckwheat (<i>Eriogonum robustum</i>)	0.75	15.4	84.1	78.1%
Nye County fishhook cactus (<i>Sclerocactus nyensis</i>)	0.75	21.4	86.4	77.0%
Webber ivesia (<i>Ivesia webberi</i>)	0.75	18.1	73.3	76.9%
Plumas ivesia (<i>Ivesia sericoleuca</i>)	0.75	11.1	79.5	74.8%
Sierra Valley ivesia (<i>Ivesia aperta</i>)	0.75	15.4	78.3	74.7%
Howell's thelypody (<i>Thelypodium howellii</i>)	0.75	13.9	87.6	74.0%
Wind-loving buckwheat (<i>Eriogonum anemophilum</i>)	0.75	22.5	58.1	72.9%
Ward's beardtongue (<i>Penstemon wardii</i>)	0.75	17.3	64.9	72.2%
Western small-footed myotis (<i>Myotis ciliolabrum</i>)	0.8	12.1	29.6	70.2%
Tufted globemallow (<i>Sphaeralcea caespitosa</i>)	0.75	18.0	73.9	66.9%
Colorado desert-parsley (<i>Lomatium concinnum</i>)	0.8	13.0	29.2	66.7%
Steamboat buckwheat (<i>Eriogonum ovalifolium</i> var. <i>williamsiae</i>)	0.75	19.9	76.3	66.3%
Toquima milkvetch (<i>Astragalus toquimanus</i>)	0.75	19.2	92.3	65.8%
Slick spot peppergrass (<i>Lepidium papilliferum</i>)	0.75	16.5	73.8	64.8%
Ash Creek ivesia (<i>Ivesia paniculata</i>)	0.75	20.1	75.5	64.6%
Ophir rockcress (<i>Arabis ophira</i>)	0.9	7.8	23.1	64.3%
Frisco buckwheat (<i>Eriogonum soredium</i>)	0.75	16.5	76.1	64.1%
Stemless beardtongue (<i>Penstemon acaulis</i>)	0.8	10.8	31.2	63.6%
Rose-flower desert-parsley (<i>Lomatium roseanum</i>)	0.75	19.9	73.2	63.1%
Bodie Hills cusickiella (<i>Cusickiella quadricostata</i>)	0.75	28.4	94.9	62.9%
Kawich Range beardtongue (<i>Penstemon pudicus</i>)	0.8	13.0	28.0	62.5%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Barren Valley collomia (<i>Collomia renacta</i>)	0.95	18.7	79.2	62.4%
Fox's barrier orbweaver (<i>Metepeira foxi</i>)	0.8	13.0	31.9	61.5%
Gunnison milkvetch (<i>Astragalus anisus</i>)	0.75	18.3	82.6	61.0%
Washington ground squirrel (<i>Uroditellus washingtoni</i>)	0.95	11.6	35.0	60.7%
Townsend's ground squirrel (<i>Uroditellus townsendii</i>)	0.8	15.7	31.5	60.0%
Prostrate bladderpod (<i>Physaria prostrata</i>)	0.95	7.9	21.6	57.1%
Brandegee's buckwheat (<i>Eriogonum brandegeei</i>)	0.75	20.8	79.7	52.8%
Goose Creek milkvetch (<i>Astragalus anserinus</i>)	0.75	18.4	74.2	50.7%
Grand Canyon rattlesnake (<i>Crotalus oreganus abyssus</i>)	0.75	30.5	92.5	49.7%
Idaho beardtongue (<i>Penstemon idahoensis</i>)	0.75	18.6	57.7	45.6%
Desert yellowhead (<i>Yermo xanthocephalus</i>)	0.9	2.3	8.9	26.3%
Grouse Creek rockcress (<i>Arabis falcatoria</i>)	0.95	3.2	6.2	21.7%
Elko rockcress (<i>Arabis falcifruca</i>)	0.95	2.5	4.1	6.7%

Intermediate Habitat Species

Midget faded rattlesnake (<i>Crotalus oreganus concolor</i>)	0.5	8.8	21.3	86.7%
Smooth stickleaf (<i>Mentzelia mollis</i>)	0.5	18.3	66.9	76.2%
Grimy ivesia (<i>Ivesia rhypara</i>)	0.5	24.9	81.0	72.7%
Western ground snake (<i>Sonora semiannulata</i>)	0.5	15.0	83.4	64.9%
Dark kangaroo mouse (<i>Microdipodops megacephalus</i>)	0.5	18.3	90.4	63.8%
Merriam's kangaroo rat (<i>Dipodomys merriami</i>)	0.5	19.3	73.5	63.4%
Long-nosed snake (<i>Rhinocheilus lecontei</i>)	0.5	21.3	86.1	62.6%
Chisel-toothed kangaroo rat (<i>Dipodomys microps</i>)	0.5	17.9	93.9	62.1%
Little pocket mouse (<i>Perognathus longimembris</i>)	0.5	17.7	84.5	60.6%
Piute ground squirrel (<i>Uroditellus mollis</i>)	0.5	20.3	91.6	59.0%
Long-nosed leopard lizard (<i>Gambelia wislizenii</i>)	0.5	22.1	90.0	58.6%
Pygmy horned lizard (<i>Phrynosoma douglasii</i>)	0.5	15.7	81.2	57.6%
Northern Pacific rattlesnake (<i>Crotalus oreganus oreganus</i>)	0.5	15.6	94.0	56.2%
Silver longjawed orbweaver (<i>Tetragnatha laboriosa</i>)	0.5	11.5	85.3	56.2%
Rock squirrel (<i>Otospermophilus variegatus</i>)	0.5	12.9	87.7	55.4%
Wyoming pocket gopher (<i>Thomomys clusius</i>)	0.5	20.1	75.6	51.1%
Idaho pocket gopher (<i>Thomomys idahoensis</i>)	0.5	11.9	67.5	51.0%

Limited Habitat Species

Black-tailed prairie dog (<i>Cynomys ludovicianus</i>)	0.4	39.5	87.7	69.7%
Desert spiny lizard (<i>Sceloporus magister</i>)	0.4	14.9	78.7	62.5%
White-tailed prairie dog (<i>Cynomys leucurus</i>)	0.4	28.8	94.7	61.9%
Desert horned lizard (<i>Phrynosoma platyrhinos</i>)	0.4	20.1	84.6	61.6%
Side-blotched lizard (<i>Uta stansburiana</i>)	0.4	22.7	98.4	60.7%
Black-throated sparrow (<i>Amphispiza bilineata</i>)	0.4	24.5	99.4	59.9%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
White-tailed antelope squirrel (<i>Ammospermophilus leucurus</i>)	0.4	25.7	91.9	59.9%
Mountain plover (<i>Charadrius montanus</i>)	0.4	23.2	95.9	59.6%
Canyon mouse (<i>Peromyscus crinitus</i>)	0.4	25.1	88.6	59.2%
Cliff chipmunk (<i>Tamias dorsalis</i>)	0.4	12.7	76.9	58.2%
Pallid bat (<i>Antrozous pallidus</i>)	0.4	16.7	89.9	57.8%
Virginia's warbler (<i>Leiothlypis virginiae</i>)	0.4	16.6	84.2	57.3%
Great Basin pocket mouse (<i>Perognathus parvus</i>)	0.4	25.2	83.5	57.3%
Botta's pocket gopher (<i>Thomomys bottae</i>)	0.4	24.8	86.7	57.0%
Kit fox (<i>Vulpes macrotis</i>)	0.4	20.3	90.0	56.9%
Acastus checkerspot (<i>Chlosyne acastus</i>)	0.4	37.3	94.1	56.7%
Leafbeetle jumping spider (<i>Sassacus papenhoei</i>)	0.4	13.7	83.6	56.2%
Lark bunting (<i>Calamospiza melanocorys</i>)	0.4	35.6	98.5	56.2%
Running crab spiders (<i>Ebo spp</i>)	0.4	15.2	96.3	56.2%
Grasshopper sparrow (<i>Ammodramus savannarum</i>)	0.4	27.8	91.9	54.7%
Great Basin collared lizard (<i>Crotaphytus bicinctores</i>)	0.4	39.5	97.9	52.8%
Western milksnake (<i>Lampropeltis gentilis</i>)	0.4	17.7	89.5	51.3%
Sharp-tailed grouse (<i>Tympanuchus phasianellus</i>)	0.4	33.8	99.9	50.8%
Clay-colored sparrow (<i>Spizella pallida</i>)	0.4	19.9	90.2	50.4%
Great Basin rattlesnake (<i>Crotalus oreganus lutosus</i>)	0.4	39.3	99.9	48.5%
Prairie rattlesnake (<i>Crotalus viridis</i>)	0.4	15.5	67.5	48.2%
Striped whipsnake (<i>Coluber taeniatus</i>)	0.3	18.4	74.6	83.9%
Nightsnake (<i>Hypsiglena torquata</i>)	0.3	22.6	88.4	60.3%
Gray flycatcher (<i>Empidonax wrightii</i>)	0.3	33.1	97.7	59.5%
Fringed myotis (<i>Myotis thysanodes</i>)	0.3	19.4	91.8	59.3%
Sagebrush sparrow (<i>Artemisospiza nevadensis</i>)	0.3	36.3	93.9	58.5%
Pygmy rabbit (<i>Brachylagus idahoensis</i>)	0.3	24.7	95.3	58.2%
Piñon mouse (<i>Peromyscus truei</i>)	0.3	24.8	95.6	57.9%
Great Basin spadefoot (<i>Spea intermontana</i>)	0.3	26.5	87.6	57.2%
Sagebrush lizard (<i>Sceloporus graciosus</i>)	0.3	25.1	95.8	57.2%
Preble's shrew (<i>Sorex preblei</i>)	0.3	22.3	89.2	57.1%
Sagebrush vole (<i>Lemmiscus curtatus</i>)	0.3	27.1	84.4	57.0%
Black-tailed jackrabbit (<i>Lepus californicus</i>)	0.3	23.2	98.9	56.9%
Long-billed curlew (<i>Numenius americanus</i>)	0.3	21.6	96.0	56.7%
Pronghorn (<i>Antilocapra americana</i>)	0.3	25.2	95.8	56.6%
Spotted bat (<i>Euderma maculatum</i>)	0.3	22.9	97.9	56.5%
Yuma myotis (<i>Myotis yumanensis</i>)	0.3	29.7	81.2	56.5%
Ord's kangaroo rat (<i>Dipodomys ordii</i>)	0.3	21.4	89.9	56.4%
Merriam's shrew (<i>Sorex merriami</i>)	0.3	19.1	99.5	56.3%
White-tailed jackrabbit (<i>Lepus townsendii</i>)	0.3	15.0	78.9	56.2%
Long-eared myotis (<i>Myotis evotis</i>)	0.3	23.1	85.9	56.2%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Atlantis fritillary (<i>Speyeria atlantis</i>)	0.3	15.3	78.1	56.2%
Northern grasshopper mouse (<i>Onychomys leucogaster</i>)	0.3	23.0	92.8	56.2%
Least chipmunk (<i>Tamias minimus</i>)	0.3	19.1	82.7	56.2%
Grey ground crab spider (<i>Xysticus gulosus</i>)	0.3	19.4	83.4	56.2%
Western black widow (<i>Latrodectus hesperus</i>)	0.3	15.1	99.5	56.2%
MacGillivray's warbler (<i>Geothlypis tolmiei</i>)	0.3	20.2	94.4	56.2%
Sandhill crane (<i>Antigone canadensis</i>)	0.3	18.0	95.4	56.2%
Western lynx spider (<i>Oxyopes scalaris</i>)	0.3	19.0	89.0	56.2%
Great Basin gopher snake (<i>Pituophis catenifer</i>)	0.3	31.8	97.5	56.2%
Mule deer (<i>Odocoileus hemionus</i>)	0.3	22.4	96.0	56.2%
Wolf spider (<i>Alopecosa kochi</i>)	0.3	21.3	78.5	56.2%
Western burrowing owl (<i>Speotyto cunicularia</i>)	0.3	51.1	100.0	56.2%
Coppered white-cheeked jumping spider (<i>Pelegrina aeneola</i>)	0.3	21.9	84.3	56.2%
Red-backed jumping spider (<i>Phidippus johnsoni</i>)	0.3	24.4	88.7	56.2%
Northwestern fritillary (<i>Speyeria hesperis</i>)	0.3	38.4	97.2	56.2%
Western meadowlark (<i>Sturnella neglecta</i>)	0.3	31.3	97.9	56.2%
Skippers (<i>Hesperopsis</i> spp.)	0.3	38.6	98.3	56.2%
Brewer's blackbird (<i>Euphagus cyanocephalus</i>)	0.3	25.0	98.2	56.2%
Loggerhead shrike (<i>Lanius ludovicianus</i>)	0.3	35.9	97.9	56.2%
Vesper sparrow (<i>Poocetes gramineus</i>)	0.3	34.7	95.4	56.2%
Hook-toothed money spider (<i>Erigone dentosa</i>)	0.3	13.9	81.0	56.2%
Short-eared owl (<i>Asio flammeus</i>)	0.3	52.2	100.0	56.2%
Northern crescent (<i>Phyciodes cocyta</i>)	0.3	43.4	96.0	56.2%
Rock wren (<i>Salpinctes obsoletus</i>)	0.3	32.9	99.8	56.2%
Tangle-web spiders (<i>Euryopis</i> spp)	0.3	18.9	68.9	56.2%
Sixspotted orbweaver (<i>Araniella displicata</i>)	0.3	19.5	82.9	56.2%
Polymorphic long-jawed cobweaver (<i>Enoplognatha ovata</i>)	0.3	13.4	61.5	56.2%
Montane crab spider (<i>Xysticus montanensis</i>)	0.3	20.9	75.7	56.2%
Nevada viceroy (<i>Limenitis archippus</i>)	0.3	41.2	97.5	56.2%
Mountainsnails (<i>Oreohelix</i> spp.)	0.3	16.7	64.8	56.2%
Sandhill skipper (<i>Polites sabuleti</i>)	0.3	47.2	93.0	56.2%
Oblong running crab spider (<i>Tibellus oblongus</i>)	0.3	20.6	64.9	56.2%
Brewer's sparrow (<i>Spizella breweri</i>)	0.3	38.0	97.9	56.2%
Dotted blue butterflies (<i>Euphilotes</i> spp.)	0.3	46.2	95.4	56.2%
Protrudent long-legged cobweaver (<i>Theridion neomexicanum</i>)	0.3	15.7	82.4	56.2%
Sage thrasher (<i>Oreoscoptes montanus</i>)	0.3	35.6	99.0	56.2%
Bighorn sheep (<i>Ovis canadensis</i>)	0.3	23.7	96.0	56.1%
Green-tailed towhee (<i>Pipilo chlorurus</i>)	0.3	20.2	93.6	56.0%
Wyoming ground squirrel (<i>Urocitellus elegans</i>)	0.3	13.1	82.1	54.3%
Townsend's big-eared bat (<i>Corynorhinus townsendii</i>)	0.3	15.1	82.4	52.7%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Greater short-horned lizard (<i>Phrynosoma hernandesi</i>)	0.3	25.0	99.1	52.5%
Lark sparrow (<i>Chondestes grammacus</i>)	0.3	32.1	83.5	48.0%

Sage-grouse PAC optimization covered by priority sage-grouse habitat umbrella

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
<u>Abundant Habitat Species</u>				
Inconspicuous scorpionweed (<i>Phacelia inconspicua</i>)	0.9	9.9	26.5	100.0%
San Rafael milkvetch (<i>Astragalus rafaensis</i>)	0.8	13.0	50.5	100.0%
Mulford's milkvetch (<i>Astragalus mulfordiae</i>)	0.9	7.1	29.2	97.2%
Southern Idaho ground squirrel (<i>Urocitellus endemicus</i>)	0.95	9.0	23.5	95.8%
Cronquist's milkvetch (<i>Astragalus cronquistii</i>)	0.9	13.0	40.2	95.8%
Cusick's lupine (<i>Lupinus cusickii</i>)	0.9	8.5	28.7	94.7%
Fisher milkvetch (<i>Astragalus piscator</i>)	0.9	10.0	26.3	94.7%
Talapoosa Peak pearpod (<i>Lepidium tiehmii</i>)	0.9	5.6	22.9	94.6%
Black-footed ferret (<i>Mustela nigripes</i>)	0.8	12.1	34.2	93.9%
Aquarius Plateau beardtongue (<i>Penstemon parvus</i>)	0.8	8.7	31.0	93.1%
Owyhee clover (<i>Trifolium owyheense</i>)	0.95	8.3	27.1	92.3%
Cusick's buckwheat (<i>Eriogonum cusickii</i>)	0.9	12.5	29.3	88.9%
Ertter's ragwort (<i>Senecio ertterae</i>)	0.9	11.5	31.3	88.2%
Currant milkvetch (<i>Astragalus uncialis</i>)	0.95	11.2	28.8	87.9%
Big free-tailed bat (<i>Nyctinomops macrotis</i>)	0.8	10.9	36.5	85.5%
Sunnyside green gentian (<i>Frasera gypsicola</i>)	0.95	9.9	29.0	84.0%
Biennial prince's plume (<i>Stanleya confertiflora</i>)	0.8	11.0	29.6	83.7%
<i>Astragalus anxius</i> (<i>Astragalus anxius</i>)	0.9	10.7	34.9	83.3%
Canyonlands lomatium (<i>Lomatium latilobum</i>)	0.75	26.8	89.5	83.2%
Cordillia's beardtongue (<i>Penstemon floribundus</i>)	0.9	11.9	35.3	82.4%
Packard's desert-parsley (<i>Lomatium packardiae</i>)	0.8	10.3	24.5	81.8%
Blaine's pincushion (<i>Sclerocactus blainei</i>)	0.95	9.2	27.6	80.8%
Deschutes sideband (<i>Monadenia fidelis</i>)	0.9	15.4	38.8	80.6%
Western mastiff bat (<i>Eumops perotis</i>)	0.9	10.5	24.3	78.9%
Granite buckwheat (<i>Eriogonum robustum</i>)	0.75	15.4	84.1	77.8%
Webber ivesia (<i>Ivesia webberi</i>)	0.75	18.1	73.3	76.7%
Plumas ivesia (<i>Ivesia sericoleuca</i>)	0.75	11.2	79.5	74.2%
Sierra Valley ivesia (<i>Ivesia aperta</i>)	0.75	15.5	78.3	74.1%
Nye County fishhook cactus (<i>Sclerocactus nyensis</i>)	0.75	22.0	86.4	74.1%
Ward's beardtongue (<i>Penstemon wardii</i>)	0.75	17.4	64.9	71.0%
Howell's thelypody (<i>Thelypodium howellii</i>)	0.75	14.2	87.6	70.6%
Western small-footed myotis (<i>Myotis ciliolabrum</i>)	0.8	12.1	29.6	70.2%
Wind-loving buckwheat (<i>Eriogonum anemophilum</i>)	0.75	23.1	58.1	68.3%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Colorado desert-parsley (<i>Lomatium concinnum</i>)	0.8	13.0	29.2	66.7%
Steamboat buckwheat (<i>Eriogonum ovalifolium</i> var. <i>williamsiae</i>)	0.75	19.9	76.3	66.1%
Ophir rockcress (<i>Arabis ophira</i>)	0.9	7.8	23.1	64.3%
Ash Creek ivesia (<i>Ivesia paniculata</i>)	0.75	20.3	75.5	63.5%
Tufted globemallow (<i>Sphaeralcea caespitosa</i>)	0.75	18.5	73.9	62.6%
Fox's barrier orbweaver (<i>Metepeira foxi</i>)	0.8	13.0	31.9	61.5%
Frisco buckwheat (<i>Eriogonum soredium</i>)	0.75	16.8	76.1	61.0%
Bodie Hills cusickiella (<i>Cusickiella quadricostata</i>)	0.75	28.9	94.9	61.0%
Washington ground squirrel (<i>Uroditellus washingtoni</i>)	0.95	11.6	35.0	60.7%
Aquarius Plateau Indian paintbrush (<i>Castilleja aquariensis</i>)	0.9	4.7	14.9	60.7%
Gunnison milkvetch (<i>Astragalus anisus</i>)	0.75	18.3	82.6	60.7%
Townsend's ground squirrel (<i>Uroditellus townsendii</i>)	0.8	15.7	31.5	60.0%
Toquima milkvetch (<i>Astragalus toquimanus</i>)	0.75	17.9	92.3	59.7%
Barren Valley collomia (<i>Collomia renacta</i>)	0.95	19.1	79.2	58.5%
Slick spot peppergrass (<i>Lepidium papilliferum</i>)	0.75	17.0	73.8	57.5%
Rose-flower desert-parsley (<i>Lomatium roseanum</i>)	0.75	18.1	73.2	55.1%
Kawich Range beardtongue (<i>Penstemon pudicus</i>)	0.8	13.7	28.0	53.1%
Brandege's buckwheat (<i>Eriogonum brandegeei</i>)	0.75	20.8	79.7	52.8%
Stemless beardtongue (<i>Penstemon acaulis</i>)	0.8	9.8	27.6	51.5%
Grand Canyon rattlesnake (<i>Crotalus oreganus abyssus</i>)	0.75	29.6	91.2	46.3%
Goose Creek milkvetch (<i>Astragalus anserinus</i>)	0.75	15.8	61.7	43.2%
Idaho beardtongue (<i>Penstemon idahoensis</i>)	0.75	18.5	48.6	41.1%
Prostrate bladderpod (<i>Physaria prostrata</i>)	0.95	4.5	16.9	34.3%
Grouse Creek rockcress (<i>Arabis falcatoria</i>)	0.95	3.2	6.2	21.7%
Desert yellowhead (<i>Yermo xanthocephalus</i>)	0.9	0.6	2.0	21.1%
Elko rockcress (<i>Arabis falcifruca</i>)	0.95	0	0	0.0%

Intermediate Habitat Species

Midget faded rattlesnake (<i>Crotalus oreganus concolor</i>)	0.5	8.8	21.3	86.7%
Smooth stickleaf (<i>Mentzelia mollis</i>)	0.5	18.3	66.9	67.7%
Grimy ivesia (<i>Ivesia rhypara</i>)	0.5	23.8	80.0	62.4%
Western ground snake (<i>Sonora semiannulata</i>)	0.5	15.3	83.4	60.7%
Merriam's kangaroo rat (<i>Dipodomys merriami</i>)	0.5	19.6	73.5	60.6%
Dark kangaroo mouse (<i>Microdipodops megacephalus</i>)	0.5	18.2	90.4	59.5%
Long-nosed snake (<i>Rhinocheilus lecontei</i>)	0.5	22.0	86.1	58.7%
Chisel-toothed kangaroo rat (<i>Dipodomys microps</i>)	0.5	18.2	93.9	58.2%
Little pocket mouse (<i>Perognathus longimembris</i>)	0.5	18.2	84.5	56.7%
Long-nosed leopard lizard (<i>Gambelia wislizenii</i>)	0.5	22.7	90.0	55.2%
Piute ground squirrel (<i>Uroditellus mollis</i>)	0.5	20.9	91.6	55.0%
Pygmy horned lizard (<i>Phrynosoma douglasii</i>)	0.5	15.6	81.2	53.6%
Rock squirrel (<i>Otospermophilus variegatus</i>)	0.5	13.1	87.7	52.5%
Northern Pacific rattlesnake (<i>Crotalus oreganus oreganus</i>)	0.5	15.9	94.0	52.5%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Silver longjawed orbweaver (<i>Tetragnatha laboriosa</i>)	0.5	11.6	85.3	52.5%
Idaho pocket gopher (<i>Thomomys idahoensis</i>)	0.5	11.8	67.5	46.9%
Wyoming pocket gopher (<i>Thomomys clusius</i>)	0.5	19.4	75.6	45.5%
<u>Limited Habitat Species</u>				
Black-tailed prairie dog (<i>Cynomys ludovicianus</i>)	0.4	39.5	87.7	69.4%
Desert spiny lizard (<i>Sceloporus magister</i>)	0.4	15.1	78.7	59.8%
Desert horned lizard (<i>Phrynosoma platyrhinos</i>)	0.4	20.6	84.6	57.7%
White-tailed prairie dog (<i>Cynomys leucurus</i>)	0.4	29.0	94.7	57.5%
Side-blotched lizard (<i>Uta stansburiana</i>)	0.4	23.3	98.4	57.4%
Black-throated sparrow (<i>Amphispiza bilineata</i>)	0.4	25.2	99.4	56.6%
Mountain plover (<i>Charadrius montanus</i>)	0.4	23.5	95.9	56.3%
White-tailed antelope squirrel (<i>Ammospermophilus leucurus</i>)	0.4	26.5	91.9	56.2%
Canyon mouse (<i>Peromyscus crinitus</i>)	0.4	25.7	88.6	55.5%
Cliff chipmunk (<i>Tamias dorsalis</i>)	0.4	12.8	76.9	54.8%
Pallid bat (<i>Antrozous pallidus</i>)	0.4	16.9	89.9	54.5%
Botta's pocket gopher (<i>Thomomys bottae</i>)	0.4	25.4	86.7	54.1%
Great Basin pocket mouse (<i>Perognathus parvus</i>)	0.4	24.2	83.5	54.1%
Virginia's warbler (<i>Leiothlypis virginiae</i>)	0.4	16.9	84.2	53.3%
Kit fox (<i>Vulpes macrotis</i>)	0.4	20.7	90.0	53.3%
Acastus checkerspot (<i>Chlosyne acastus</i>)	0.4	37.8	94.1	53.0%
Great Basin collared lizard (<i>Crotaphytus bicinctores</i>)	0.4	39.5	97.9	52.8%
Leafbeetle jumping spider (<i>Sassacus papenhoei</i>)	0.4	13.9	83.6	52.5%
Lark bunting (<i>Calamospiza melanocorys</i>)	0.4	36.0	98.5	52.5%
Running crab spiders (<i>Ebo</i> spp)	0.4	15.5	96.3	52.5%
Grasshopper sparrow (<i>Ammodramus savannarum</i>)	0.4	28.3	91.9	50.1%
Western milksnake (<i>Lampropeltis gentilis</i>)	0.4	17.5	83.6	47.5%
Sharp-tailed grouse (<i>Tympanuchus phasianellus</i>)	0.4	32.9	99.9	47.4%
Clay-colored sparrow (<i>Spizella pallida</i>)	0.4	19.9	90.2	47.0%
Great Basin rattlesnake (<i>Crotalus oreganus lutosus</i>)	0.4	37.6	99.5	45.0%
Prairie rattlesnake (<i>Crotalus viridis</i>)	0.4	15.6	67.5	44.2%
Striped whipsnake (<i>Coluber taeniatus</i>)	0.3	18.2	74.6	83.6%
Nightsnake (<i>Hypsiglena torquata</i>)	0.3	22.9	88.4	57.1%
Gray flycatcher (<i>Empidonax wrightii</i>)	0.3	33.2	97.7	56.0%
Fringed myotis (<i>Myotis thysanodes</i>)	0.3	19.8	91.8	55.6%
Sagebrush sparrow (<i>Artemisiospiza nevadensis</i>)	0.3	36.1	93.9	54.8%
Pygmy rabbit (<i>Brachylagus idahoensis</i>)	0.3	23.5	95.3	54.5%
Piñon mouse (<i>Peromyscus truei</i>)	0.3	25.0	95.6	54.3%
Great Basin spadefoot (<i>Spea intermontana</i>)	0.3	26.7	87.6	53.7%
Black-tailed jackrabbit (<i>Lepus californicus</i>)	0.3	23.2	98.9	53.5%
Sagebrush lizard (<i>Sceloporus graciosus</i>)	0.3	25.0	95.8	53.4%
Spotted bat (<i>Euderma maculatum</i>)	0.3	22.8	97.9	53.2%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Yuma myotis (<i>Myotis yumanensis</i>)	0.3	29.6	81.2	53.2%
Sagebrush vole (<i>Lemmyscus curtatus</i>)	0.3	25.8	82.1	53.1%
Long-billed curlew (<i>Numenius americanus</i>)	0.3	21.8	96.0	53.0%
Pronghorn (<i>Antilocapra americana</i>)	0.3	24.8	95.8	52.8%
Ord's kangaroo rat (<i>Dipodomys ordii</i>)	0.3	21.5	89.9	52.7%
Merriam's shrew (<i>Sorex merriami</i>)	0.3	18.9	99.5	52.6%
Preble's shrew (<i>Sorex preblei</i>)	0.3	22.1	89.2	52.5%
White-tailed jackrabbit (<i>Lepus townsendii</i>)	0.3	14.8	78.9	52.5%
Long-eared myotis (<i>Myotis evotis</i>)	0.3	22.6	85.9	52.5%
Atlantis fritillary (<i>Speyeria atlantis</i>)	0.3	15.6	78.1	52.5%
Northern grasshopper mouse (<i>Onychomys leucogaster</i>)	0.3	22.3	92.8	52.5%
Least chipmunk (<i>Tamias minimus</i>)	0.3	19.3	82.7	52.5%
Grey ground crab spider (<i>Xysticus gulosus</i>)	0.3	19.7	83.4	52.5%
Western black widow (<i>Latrodectus hesperus</i>)	0.3	15.3	99.5	52.5%
MacGillivray's warbler (<i>Geothlypis tolmiei</i>)	0.3	20.7	94.4	52.5%
Sandhill crane (<i>Antigone canadensis</i>)	0.3	18.2	95.4	52.5%
Western lynx spider (<i>Oxyopes scalaris</i>)	0.3	19.4	89.0	52.5%
Great Basin gopher snake (<i>Pituophis catenifer</i>)	0.3	32.3	97.5	52.5%
Mule deer (<i>Odocoileus hemionus</i>)	0.3	23.0	96.0	52.5%
Wolf spider (<i>Alopecosa kochi</i>)	0.3	21.7	78.5	52.5%
Western burrowing owl (<i>Speotyto cunicularia</i>)	0.3	49.9	100.0	52.5%
Coppered white-cheeked jumping spider (<i>Pelegrina aeneola</i>)	0.3	22.4	84.3	52.5%
Red-backed jumping spider (<i>Phidippus johnsoni</i>)	0.3	24.8	88.7	52.5%
Northwestern fritillary (<i>Speyeria hesperis</i>)	0.3	38.4	97.2	52.5%
Western meadowlark (<i>Sturnella neglecta</i>)	0.3	31.7	97.9	52.5%
Skippers (<i>Hesperopsis</i> spp.)	0.3	38.6	98.3	52.5%
Brewer's blackbird (<i>Euphagus cyanocephalus</i>)	0.3	25.4	98.2	52.5%
Loggerhead shrike (<i>Lanius ludovicianus</i>)	0.3	36.0	97.9	52.5%
Vesper sparrow (<i>Pooecetes gramineus</i>)	0.3	34.7	95.4	52.5%
Hook-toothed money spider (<i>Erigone dentosa</i>)	0.3	14.0	81.0	52.5%
Short-eared owl (<i>Asio flammeus</i>)	0.3	50.6	100.0	52.5%
Northern crescent (<i>Phyciodes cocyta</i>)	0.3	43.6	96.0	52.5%
Rock wren (<i>Salpinctes obsoletus</i>)	0.3	33.4	99.8	52.5%
Tangle-web spiders (<i>Euryopsis</i> spp)	0.3	19.1	68.9	52.5%
Sixspotted orbweaver (<i>Araniella displicata</i>)	0.3	19.6	82.9	52.5%
Polymorphic long-jawed cobweaver (<i>Enoplognatha ovata</i>)	0.3	13.4	61.5	52.5%
Montane crab spider (<i>Xysticus montanensis</i>)	0.3	20.8	75.7	52.5%
Nevada viceroy (<i>Limenitis archippus</i>)	0.3	41.5	97.5	52.5%
Mountainsnails (<i>Oreohelix</i> spp.)	0.3	16.9	64.8	52.5%
Sandhill skipper (<i>Polites sabuleti</i>)	0.3	47.8	93.0	52.5%
Oblong running crab spider (<i>Tibellus oblongus</i>)	0.3	20.8	64.9	52.5%
Brewer's sparrow (<i>Spizella breweri</i>)	0.3	37.9	97.9	52.5%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Dotted blue butterflies (Euphilotes spp.)	0.3	46.6	95.4	52.5%
Protrudent long-legged cobweaver (Theridion neomexicanum)	0.3	15.7	82.4	52.5%
Sage thrasher (Oreoscoptes montanus)	0.3	35.1	99.0	52.5%
Bighorn sheep (Ovis canadensis)	0.3	24.3	96.0	52.4%
Green-tailed towhee (Pipilo chlorurus)	0.3	20.4	93.6	52.3%
Wyoming ground squirrel (Uroditellus elegans)	0.3	13.1	82.1	49.6%
Townsend's big-eared bat (Corynorhinus townsendii)	0.3	15.0	82.4	49.3%
Greater short-horned lizard (Phrynosoma hernandesi)	0.3	24.9	99.1	48.7%
Lark sparrow (Chondestes grammacus)	0.3	31.8	83.5	44.1%

Sage-grouse PAC optimization covered by general sage-grouse habitat umbrella

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
<u>Abundant Habitat Species</u>				
Inconspicuous scorpionweed (Phacelia inconspicua)	0.9	9.9	26.5	100.0%
San Rafael milkvetch (Astragalus rafaensis)	0.8	12.8	50.5	97.3%
Southern Idaho ground squirrel (Uroditellus endemicus)	0.95	9.0	23.5	95.8%
Cronquist's milkvetch (Astragalus cronquistii)	0.9	13.0	40.2	95.8%
Fisher milkvetch (Astragalus piscator)	0.9	10.0	26.3	94.7%
Aquarius Plateau beardtongue (Penstemon parvus)	0.8	8.7	31.0	93.1%
Talapoosa Peak pearpod (Lepidium tiehmii)	0.9	5.7	22.9	91.9%
Mulford's milkvetch (Astragalus mulfordiae)	0.9	7.3	29.2	91.7%
Big free-tailed bat (Nyctinomops macrotis)	0.8	10.9	36.5	85.5%
Currant milkvetch (Astragalus uncialis)	0.95	11.6	28.8	84.8%
Cordillia's beardtongue (Penstemon floribundus)	0.9	11.9	35.3	82.4%
Canyonlands lomatium (Lomatium latilobum)	0.75	27.3	89.5	81.2%
Deschutes sideband (Monadenia fidelis)	0.9	15.4	38.8	80.6%
Western mastiff bat (Eumops perotis)	0.9	10.5	24.3	78.9%
Blaine's pincushion (Sclerocactus blainei)	0.95	9.7	27.6	76.9%
Granite buckwheat (Eriogonum robustum)	0.75	15.6	84.1	75.3%
Webber ivesia (Ivesia webberi)	0.75	18.5	73.3	72.6%
Astragalus anxius (Astragalus anxius)	0.9	10.7	34.9	72.2%
Plumas ivesia (Ivesia sericoleuca)	0.75	11.1	79.5	71.8%
Sierra Valley ivesia (Ivesia aperta)	0.75	15.8	78.3	71.5%
Western small-footed myotis (Myotis ciliolabrum)	0.8	12.1	29.6	70.2%
Owyhee clover (Trifolium owyheense)	0.95	8.7	27.1	69.2%
Cusick's lupine (Lupinus cusickii)	0.9	8.8	28.7	68.4%
Nye County fishhook cactus (Sclerocactus nyensis)	0.75	23.2	86.4	67.7%
Ward's beardtongue (Penstemon wardii)	0.75	17.4	64.9	66.5%
Howell's thelypody (Thelypodium howellii)	0.75	14.4	87.6	64.4%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Steamboat buckwheat (<i>Eriogonum ovalifolium</i> var. <i>williamsiae</i>)	0.75	19.9	76.3	64.2%
Sunnyside green gentian (<i>Frasera gypsicola</i>)	0.95	9.6	27.2	64.0%
Black-footed ferret (<i>Mustela nigripes</i>)	0.8	12.5	28.0	63.6%
Washington ground squirrel (<i>Uroditellus washingtoni</i>)	0.95	11.6	35.0	60.7%
Townsend's ground squirrel (<i>Uroditellus townsendii</i>)	0.8	15.7	31.5	60.0%
Ash Creek ivesia (<i>Ivesia paniculata</i>)	0.75	20.8	75.5	60.0%
Ertter's ragwort (<i>Senecio ertterae</i>)	0.9	13.9	31.3	58.8%
Wind-loving buckwheat (<i>Eriogonum anemophilum</i>)	0.75	24.3	58.1	58.6%
Gunnison milkvetch (<i>Astragalus anisus</i>)	0.75	18.2	82.6	57.4%
Colorado desert-parsley (<i>Lomatium concinnum</i>)	0.8	12.5	29.2	54.5%
Ophir rockcress (<i>Arabis ophira</i>)	0.9	8.2	23.1	53.6%
Brandege's buckwheat (<i>Eriogonum brandegeei</i>)	0.75	21.0	79.7	51.8%
Packard's desert-parsley (<i>Lomatium packardiae</i>)	0.8	9.4	24.5	51.5%
Tufted globemallow (<i>Sphaeralcea caespitosa</i>)	0.75	20.0	73.9	51.0%
Cusick's buckwheat (<i>Eriogonum cusickii</i>)	0.9	9.7	29.3	50.0%
Bodie Hills cusickiella (<i>Cusickiella quadricostata</i>)	0.75	32.3	94.9	49.7%
Toquima milkvetch (<i>Astragalus toquimanus</i>)	0.75	15.2	62.6	48.8%
Barren Valley collomia (<i>Collomia renacta</i>)	0.95	20.3	79.2	48.5%
Rose-flower desert-parsley (<i>Lomatium roseanum</i>)	0.75	16.8	54.2	43.5%
Frisco buckwheat (<i>Eriogonum soledium</i>)	0.75	17.4	76.1	43.3%
Slick spot peppergrass (<i>Lepidium papilliferum</i>)	0.75	18.6	73.8	41.8%
Biennial prince's plume (<i>Stanleya confertiflora</i>)	0.8	9.4	25.3	40.8%
Kawich Range beardtongue (<i>Penstemon pudicus</i>)	0.8	13.9	26.3	37.5%
Grand Canyon rattlesnake (<i>Crotalus oreganus abyssus</i>)	0.75	24.8	88.7	31.0%
Fox's barrier orbweaver (<i>Metepeira foxi</i>)	0.8	16.1	31.9	28.8%
Aquarius Plateau Indian paintbrush (<i>Castilleja aquariensis</i>)	0.9	2.7	9.8	28.6%
Idaho beardtongue (<i>Penstemon idahoensis</i>)	0.75	17.4	44.7	26.0%
Goose Creek milkvetch (<i>Astragalus anserinus</i>)	0.75	12.1	43.6	25.9%
Stemless beardtongue (<i>Penstemon acaulis</i>)	0.8	10.0	27.6	18.2%
Prostrate bladderpod (<i>Physaria prostrata</i>)	0.95	1.1	1.1	2.9%
Elko rockcress (<i>Arabis falcifruca</i>)	0.95	0	0	0.0%
Grouse Creek rockcress (<i>Arabis falcatoria</i>)	0.95	0	0	0.0%
Desert yellowhead (<i>Yermo xanthocephalus</i>)	0.9	0	0	0.0%

Intermediate Habitat Species

Midget faded rattlesnake (<i>Crotalus oreganus concolor</i>)	0.5	8.8	21.3	86.7%
Merriam's kangaroo rat (<i>Dipodomys merriami</i>)	0.5	20.7	73.5	52.9%
Western ground snake (<i>Sonora semiannulata</i>)	0.5	16.0	83.4	50.2%
Dark kangaroo mouse (<i>Microdipodops megacephalus</i>)	0.5	18.0	90.4	49.6%
Smooth stickleaf (<i>Mentzelia mollis</i>)	0.5	18.1	66.9	49.5%
Long-nosed snake (<i>Rhinocheilus lecontei</i>)	0.5	24.2	86.1	48.5%
Chisel-toothed kangaroo rat (<i>Dipodomys microps</i>)	0.5	19.0	93.9	48.4%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Little pocket mouse (<i>Perognathus longimembris</i>)	0.5	19.6	84.5	46.9%
Long-nosed leopard lizard (<i>Gambelia wislizenii</i>)	0.5	24.7	90.0	45.6%
Piute ground squirrel (<i>Urocitellus mollis</i>)	0.5	22.9	91.6	44.5%
Rock squirrel (<i>Otospermophilus variegatus</i>)	0.5	13.7	87.7	43.2%
Pygmy horned lizard (<i>Phrynosoma douglasii</i>)	0.5	15.4	81.2	42.7%
Grimy ivesia (<i>Ivesia rhypara</i>)	0.5	19.4	73.1	42.7%
Northern Pacific rattlesnake (<i>Crotalus oreganus oreganus</i>)	0.5	17.4	94.0	39.4%
Silver longjawed orbweaver (<i>Tetragnatha laboriosa</i>)	0.5	11.4	85.3	39.4%
Idaho pocket gopher (<i>Thomomys idahoensis</i>)	0.5	11.1	36.0	28.6%
Wyoming pocket gopher (<i>Thomomys clusius</i>)	0.5	11.4	30.8	21.3%

Limited Habitat Species

Black-tailed prairie dog (<i>Cynomys ludovicianus</i>)	0.4	38.5	87.7	65.9%
Desert spiny lizard (<i>Sceloporus magister</i>)	0.4	15.7	78.7	52.5%
Great Basin collared lizard (<i>Crotaphytus bicinctores</i>)	0.4	40.2	97.9	51.4%
Side-blotched lizard (<i>Uta stansburiana</i>)	0.4	25.2	98.4	47.6%
White-tailed prairie dog (<i>Cynomys leucurus</i>)	0.4	29.4	94.7	46.7%
Desert horned lizard (<i>Phrynosoma platyrhinos</i>)	0.4	22.4	84.6	46.6%
Black-throated sparrow (<i>Amphispiza bilineata</i>)	0.4	27.2	99.4	46.6%
Mountain plover (<i>Charadrius montanus</i>)	0.4	24.5	95.9	46.2%
Botta's pocket gopher (<i>Thomomys bottae</i>)	0.4	27.0	86.7	46.2%
White-tailed antelope squirrel (<i>Ammospermophilus leucurus</i>)	0.4	29.4	91.9	45.2%
Canyon mouse (<i>Peromyscus crinitus</i>)	0.4	27.6	88.6	44.5%
Pallid bat (<i>Antrozous pallidus</i>)	0.4	17.4	89.9	44.0%
Great Basin pocket mouse (<i>Perognathus parvus</i>)	0.4	22.6	82.9	43.6%
Cliff chipmunk (<i>Tamias dorsalis</i>)	0.4	13.1	76.9	43.2%
Kit fox (<i>Vulpes macrotis</i>)	0.4	22.0	90.0	42.4%
Acastus checkerspot (<i>Chlosyne acastus</i>)	0.4	39.9	94.1	39.8%
Leafbeetle jumping spider (<i>Sassacus papenhoei</i>)	0.4	14.9	83.6	39.4%
Lark bunting (<i>Calamospiza melanocorys</i>)	0.4	37.0	98.5	39.4%
Running crab spiders (<i>Ebo</i> spp)	0.4	16.3	96.3	39.4%
Virginia's warbler (<i>Leiothlypis virginiae</i>)	0.4	18.6	84.2	39.2%
Grasshopper sparrow (<i>Ammodramus savannarum</i>)	0.4	29.8	89.5	33.2%
Sharp-tailed grouse (<i>Tympanuchus phasianellus</i>)	0.4	27.9	99.9	32.8%
Western milksnake (<i>Lampropeltis gentilis</i>)	0.4	17.1	83.6	32.6%
Clay-colored sparrow (<i>Spizella pallida</i>)	0.4	19.5	90.2	31.4%
Great Basin rattlesnake (<i>Crotalus oreganus lutosus</i>)	0.4	28.2	96.9	29.3%
Prairie rattlesnake (<i>Crotalus viridis</i>)	0.4	16.3	67.5	25.7%
Striped whipsnake (<i>Coluber taeniatus</i>)	0.3	15.6	74.6	77.4%
Nightsnake (<i>Hypsiglena torquata</i>)	0.3	24.2	88.4	47.5%
Fringed myotis (<i>Myotis thysanodes</i>)	0.3	21.4	91.8	43.5%
Gray flycatcher (<i>Empidonax wrightii</i>)	0.3	34.8	97.7	43.5%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Pygmy rabbit (<i>Brachylagus idahoensis</i>)	0.3	21.4	83.0	42.5%
Yuma myotis (<i>Myotis yumanensis</i>)	0.3	29.6	81.2	42.5%
Piñon mouse (<i>Peromyscus truei</i>)	0.3	26.0	95.6	42.4%
Sagebrush sparrow (<i>Artemisiospiza nevadensis</i>)	0.3	35.7	93.9	42.1%
Spotted bat (<i>Euderma maculatum</i>)	0.3	23.5	97.9	42.1%
Great Basin spadefoot (<i>Spea intermontana</i>)	0.3	27.1	87.6	41.7%
Black-tailed jackrabbit (<i>Lepus californicus</i>)	0.3	23.9	98.9	41.6%
Sagebrush lizard (<i>Sceloporus graciosus</i>)	0.3	24.6	95.8	39.9%
Long-billed curlew (<i>Numenius americanus</i>)	0.3	22.1	96.0	39.7%
Sagebrush vole (<i>Lemmys curtatus</i>)	0.3	21.3	80.8	39.6%
Merriam's shrew (<i>Sorex merriami</i>)	0.3	18.4	99.5	39.5%
Ord's kangaroo rat (<i>Dipodomys ordii</i>)	0.3	22.3	89.9	39.5%
White-tailed jackrabbit (<i>Lepus townsendii</i>)	0.3	13.6	66.8	39.4%
Long-eared myotis (<i>Myotis evotis</i>)	0.3	21.7	85.9	39.4%
Atlantis fritillary (<i>Speyeria atlantis</i>)	0.3	16.4	78.1	39.4%
Northern grasshopper mouse (<i>Onychomys leucogaster</i>)	0.3	18.4	86.1	39.4%
Least chipmunk (<i>Tamias minimus</i>)	0.3	19.9	82.7	39.4%
Grey ground crab spider (<i>Xysticus gulosus</i>)	0.3	21.1	83.4	39.4%
Western black widow (<i>Latrodectus hesperus</i>)	0.3	16.3	99.5	39.4%
MacGillivray's warbler (<i>Geothlypis tolmiei</i>)	0.3	22.8	94.4	39.4%
Sandhill crane (<i>Antigone canadensis</i>)	0.3	18.6	95.4	39.4%
Western lynx spider (<i>Oxyopes scalaris</i>)	0.3	21.0	89.0	39.4%
Great Basin gopher snake (<i>Pituophis catenifer</i>)	0.3	34.4	97.5	39.4%
Mule deer (<i>Odocoileus hemionus</i>)	0.3	25.1	96.0	39.4%
Wolf spider (<i>Alopecosa kochi</i>)	0.3	23.5	78.5	39.4%
Western burrowing owl (<i>Speotyto cunicularia</i>)	0.3	45.7	99.5	39.4%
Coppered white-cheeked jumping spider (<i>Pelegrina aeneola</i>)	0.3	24.0	84.3	39.4%
Red-backed jumping spider (<i>Phidippus johnsoni</i>)	0.3	26.1	85.3	39.4%
Northwestern fritillary (<i>Speyeria hesperis</i>)	0.3	38.0	94.5	39.4%
Western meadowlark (<i>Sturnella neglecta</i>)	0.3	32.4	97.9	39.4%
Skippers (<i>Hesperopsis</i> spp.)	0.3	38.7	98.3	39.4%
Brewer's blackbird (<i>Euphagus cyanocephalus</i>)	0.3	26.6	98.2	39.4%
Loggerhead shrike (<i>Lanius ludovicianus</i>)	0.3	36.2	97.9	39.4%
Vesper sparrow (<i>Pooecetes gramineus</i>)	0.3	34.2	95.4	39.4%
Hook-toothed money spider (<i>Erigone dentosa</i>)	0.3	14.3	81.0	39.4%
Short-eared owl (<i>Asio flammeus</i>)	0.3	44.2	100.0	39.4%
Northern crescent (<i>Phyciodes coccyta</i>)	0.3	43.0	88.5	39.4%
Rock wren (<i>Salpinctes obsoletus</i>)	0.3	35.5	99.8	39.4%
Tangle-web spiders (<i>Euryopsis</i> spp)	0.3	19.9	68.9	39.4%
Sixspotted orbweaver (<i>Araniella displicata</i>)	0.3	20.8	82.9	39.4%
Polymorphic long-jawed cobweaver (<i>Enoplognatha ovata</i>)	0.3	13.8	61.5	39.4%
Montane crab spider (<i>Xysticus montanensis</i>)	0.3	20.6	75.7	39.4%

	Habitat %	Habitat Value		%
	<u>Included</u>	<u>Avg</u>	<u>Max</u>	<u>Uncovered</u>
Nevada viceroy (<i>Limenitis archippus</i>)	0.3	41.6	97.5	39.4%
Mountainsnails (<i>Oreohelix</i> spp.)	0.3	17.6	64.8	39.4%
Sandhill skipper (<i>Polites sabuleti</i>)	0.3	49.9	93.0	39.4%
Oblong running crab spider (<i>Tibellus oblongus</i>)	0.3	21.6	64.9	39.4%
Brewer's sparrow (<i>Spizella breweri</i>)	0.3	37.5	97.9	39.4%
Dotted blue butterflies (<i>Euphilotes</i> spp.)	0.3	47.6	92.8	39.4%
Protrudent long-legged cobweaver (<i>Theridion neomexicanum</i>)	0.3	15.8	82.4	39.4%
Pronghorn (<i>Antilocapra americana</i>)	0.3	23.0	95.8	39.4%
Sage thrasher (<i>Oreoscoptes montanus</i>)	0.3	33.4	99.0	39.4%
Bighorn sheep (<i>Ovis canadensis</i>)	0.3	26.8	96.0	39.3%
Green-tailed towhee (<i>Pipilo chlorurus</i>)	0.3	21.2	93.6	39.1%
Preble's shrew (<i>Sorex preblei</i>)	0.3	22.4	89.2	36.7%
Townsend's big-eared bat (<i>Corynorhinus townsendii</i>)	0.3	13.9	69.3	34.1%
Greater short-horned lizard (<i>Phrynosoma hernandesi</i>)	0.3	24.7	99.1	34.0%
Wyoming ground squirrel (<i>Urocitellus elegans</i>)	0.3	12.6	75.3	32.5%
Lark sparrow (<i>Chondestes grammacus</i>)	0.3	31.0	83.5	26.9%

APPENDIX E

ARCPY AND R CODE USED IN THE STUDY

R CODE

For Maxent models:

Converts .dbf files to .csv files for use as SWD files in Maxent

```
#setwd("../R_Code")
setwd("../Species")
## load packages
require(foreign)
require(xfun)
## get list of dbf files in target folder
file_list = list.files(pattern="*.csv", recursive = TRUE)
## iterate thru dbf files formatting them as SWD files and exporting as csv files
for (i in seq_along(file_list)) {
  filename = file_list[[i]]
  SWD <- read.csv(filename, as.is = TRUE)
  colnames(SWD)[colnames(SWD)=="ndvi_dif"] <- "ndvi_diff"
  out = sans_ext(filename)
  outname = paste(out, "csv", sep=".")
  write.csv(SWD, filename, row.names = FALSE)
}
head(SWD)
```

Combines individual .csv files together into a single .csv file

```
## load packages
library(foreign)
setwd("../Species/birds/passerines")
file_list = list.files(pattern="*_SWD2.csv")
# create empty list
datalist = list()
## open individual csv files adding their records to one list to be bound into a new dataframe
for (i in seq_along(file_list)) {
  #i=6
  filename = file_list[[i]]
  SWD <- read.csv(filename, as.is = TRUE)
  #head(SWD)
  dat <- data.frame(SWD)
  datalist[[i]] <- dat # add it to your list
}
## turn list into dataframe
bigDF = do.call(rbind, datalist)
head(bigDF)
tail(bigDF)
```

```

## Save dataframe as csv file
write.csv(bigDF, file = '../Species/birds/passerines_SWD.csv', row.names = FALSE)
#test
bigSWD <- read.csv('../Species/birds/passerines_SWD.csv', as.is = TRUE)
head(bigSWD)
tail(bigSWD)
setwd("../R_Code")

```

Fixes field names in Maxent species SWD (.csv) files

```

## load packages
require(foreign)
require(xfun)
## get list of dbf files in target folder
setwd("../Species/plants/forbs")
file_list = list.files(pattern="*_SWD.csv")
## iterates thru .csv files in folder, reformats field names and exports
for (i in seq_along(file_list)) {
  filename = file_list[[i]]
  #setwd("H:/Maxent/Species/reptiles")
  SWD <- read.csv(filename, as.is = TRUE)
  head(SWD)
  #SWD <- SWD[ -c(1) ]
  #colnames(SWD)[colnames(SWD)=="Longitude"] <- "longitude"
  #colnames(SWD)[colnames(SWD)=="Latitude"] <- "latitude"
  colnames(SWD)[colnames(SWD)=="tmin_stepp"] <- "tmin_steppe"
  colnames(SWD)[colnames(SWD)=="tmax_stepp"] <- "tmax_steppe"
  colnames(SWD)[colnames(SWD)=="prcp_stepp"] <- "prcp_steppe"
  colnames(SWD)[colnames(SWD)=="patches_gr"] <- "patches_grass"
  colnames(SWD)[colnames(SWD)=="patches_sa"] <- "patches_sage"
  colnames(SWD)[colnames(SWD)=="patches_sh"] <- "patches_shrub"
  colnames(SWD)[colnames(SWD)=="steppe_slo"] <- "steppe_slope"
  colnames(SWD)[colnames(SWD)=="steppe_ele"] <- "steppe_elev"
  colnames(SWD)[colnames(SWD)=="steppe_asp"] <- "steppe_aspcat"
  colnames(SWD)[colnames(SWD)=="steppe_lc_"] <- "steppe_lc_nr"
  #newfield <- "Crotalus_spp"
  #newfield <- sub("_SWD.csv", "", filename)
  #SWD[, "species"] <- newfield
  #newSWD <- SWD[c(22,1:21)]
  #head(newSWD)
  #out = sans_ext(filename)
  #outname = paste(out, "csv", sep=".")
  #outname = paste0("../Species/reptiles/", filename)
  #setwd("../Species/reptiles/")
  write.csv(SWD, filename, row.names = FALSE)
}
## test
SWD <- read.csv(filename, as.is = TRUE)
head(SWD)

```

```

setwd("../R_Code")
## individual fixes
#SWD1 <- read.csv(file =
'H:/Maxent/Species/inverts/BAMONA/csv/Limenitis_archippus_pts_SWD.csv', as.is = TRUE)
#SWD2 <- read.csv(file = '../Species/inverts/insects/Limenitis_archippus_pts_SWD.csv', as.is =
TRUE)
#head(SWD1)
#head(SWD2)
#SWDfinal <- rbind(SWD1,SWD2)
#write.csv(SWDfinal, file = '../Species/inverts/insects/Limenitis_archippus_pts_SWD.csv',
row.names = FALSE)

```

Randomly selects a specified number of records for use as background points in Maxent

```

setwd("../R_Code")
setwd("../Background")
## load packages
library(dplyr)
library(foreign)
library(xfun)
## get list of SWD files in target folder
file_list = list.files(pattern="*pt100ha_SWD.csv")
## iterate thru SWD files selecting a random set of 50,000 records and saving as a new file
for (i in seq_along(file_list)) {
  filename = file_list[[i]]
  SWD <- read.csv(filename, as.is = TRUE)
  newSWD <- sample_n(SWD, 100000)
  strip = sans_ext(filename)
  out = sub("_SWD", "_Samp100k_SWD", strip)
  outname = paste(out, "csv", sep=".")
  write.csv(newSWD, outname, row.names = FALSE)
}
## test
sampleSWD <- read.csv('../Background/rept_pt100ha_Samp100k_SWD.csv', as.is = TRUE)
head(sampleSWD)
tail(sampleSWD)
## Individual files
SWD <- read.csv('../Background/wading_birds_SWD.csv', as.is = TRUE)
head(SWD)
newSWD <- sample_n(SWD, 100000)
strip = sans_ext('../Background/wading_birds_SWD.csv')
out = sub("_SWD", "_Samp100k_SWD", strip)
outname = paste(out, "csv", sep=".")
write.csv(newSWD, outname, row.names = FALSE)
## Doesn't work, use Excel
#SWD <- read.csv(file = '../Background/rept_pt100ha_Samp100k_SWD.csv', as.is = TRUE)
#NoDat <- -9999
#newSWD[SWD=="NA"]<-NoDat

```

Fixes field names in Maxent background SWD (.csv) files and adds 'background' column to front of file

```
setwd("../Background")
## load packages
require(foreign)
require(xfun)
require(dplyr)
## get list of dbf files in target folder
file_list = list.files(pattern="*_SWD.csv")
## iterates thru .csv files in folder, reformats field names, adds 'background' column, and exports
for (i in seq_along(file_list)) {
  filename = file_list[[9]]
  SWD <- read.csv(filename, as.is = TRUE)
  head(SWD)
# SWD <- SWD[ -c(1) ]
# colnames(SWD)[colnames(SWD)=="X"] <- "longitude"
# colnames(SWD)[colnames(SWD)=="Y"] <- "latitude"
  colnames(SWD)[colnames(SWD)=="tmin_stepp"] <- "tmin_steppe"
  colnames(SWD)[colnames(SWD)=="tmax_stepp"] <- "tmax_steppe"
  colnames(SWD)[colnames(SWD)=="prcp_stepp"] <- "prcp_steppe"
  colnames(SWD)[colnames(SWD)=="patches_gr"] <- "patches_grass"
  colnames(SWD)[colnames(SWD)=="patches_sa"] <- "patches_sage"
  colnames(SWD)[colnames(SWD)=="patches_sh"] <- "patches_shrub"
  colnames(SWD)[colnames(SWD)=="steppe_slo"] <- "steppe_slope"
  colnames(SWD)[colnames(SWD)=="steppe_ele"] <- "steppe_elev"
  colnames(SWD)[colnames(SWD)=="steppe_asp"] <- "steppe_aspcat"
  colnames(SWD)[colnames(SWD)=="steppe_lc_"] <- "steppe_lc_nr"
  SWD[,"background"] <- "background"
  newSWD <- SWD[c(22,1:21)]
  head(newSWD)
  #out = sans_ext(filename)
  #outname = paste(out, "csv", sep=".")
  #outname = paste0("../Background/", filename)
  write.csv(newSWD, filename, row.names = FALSE)
  #rowNum = nrow(newSWD)
  #if(rowNum > 100000) {
  # sampSWD <- sample_n(newSWD, 100000)
  #
  # strip = sans_ext(filename)
  # out = sub("_SWD", "_Samp100k_SWD", strip)
  # extName = paste(out, "csv", sep=".")
  # newName = paste0("../Background/", extName)
  # write.csv(sampSWD, newName, row.names = FALSE)
  }
## test
SWD <- read.csv(filename, as.is = TRUE)
head(SWD)
SampSWD <- read.csv(file = '../Background/galliforms_Samp100k_SWD.csv', as.is = TRUE)
```

```

head(SampSWD)
setwd("../R_Code")
## fix individ
SWD <- read.csv(file = '../Species/reptiles/Crotalus_spp_SWD.csv', as.is = TRUE)
head(SWD)
write.csv(SWD, file = '../Species/reptiles/Lampropeltis_gentilis_SWD.csv', row.names =
FALSE)
SWD <- read.csv(file = '../Background/rept_pt100ha_SWD.csv', as.is = TRUE)
SWD[SWD=="NA"]<- -9999

```

For multi-species optimization:

Uses prioritizr package to run Gurobi optimization program for 164 species

```

setwd("E:/Study")
library(slam)
library(gurobi)
library(prioritizr)
library(sf)
library(readr)
# Percentage-of-habitat targets based on amount of habitat each species has available
targetdf <- read_csv("Hbtt30-95Percent.csv", col_names = FALSE)
targets <- c(targetdf, recursive = TRUE, use.names = FALSE)
print(targets)
# convert shapefile of HU polygons with avg-spp-hbtt data as columns into simple features format
sim_pu_sf <- st_read("HabitatAvg_HU12.shp")
fixed_sim_pu_sf <- st_zm(sim_pu_sf, drop=T, what='ZM')
featureNames <- setdiff(names(fixed_sim_pu_sf),
c("Cost", "PAC_Cost", "PAD_Cost", "Sage_Cost", "Avg_Cost", "geometry", "SqKm", "HU_ID"))
print(featureNames)
# create problem
p1 <- problem(fixed_sim_pu_sf, features = featureNames, "Cost") %>%
  add_min_set_objective() %>%
# add_relative_targets(0.3) %>%
  add_relative_targets(targets) %>%
  add_binary_decisions() %>%
  add_gurobi_solver(gap = 0)
## Other options
# add_boundary_penalties(penalty = 500, edge_factor = 0.5)
# add_feature_contiguity_constraints()
# add_gap_portfolio(number_solutions = 5, pool_gap = 0.2)
# solve the problem
s1 <- solve(p1)
# export the solution as a shapefile
#st_write(s1, "E:/Study/HU12_Optimization30.shp")
st_write(s1, "E:/Study/HU12_Optimization30-95_PAC3.shp")

```

ArcPy Code

Adds new fields to raster layers, copies data, and deletes old fields

```
import arcpy
import os
#import sys
from arcpy import env
from arcpy.sa import *
#stdoutOrigin=sys.stdout
#sys.stdout = open("log.txt", "w")
# Set environment settings
env.workspace = "/lustre/projects..."
# Get lists of codes and fieldnames
#codesTxt = open("Spp_Codes.txt", "r").read()
#codesTxt = codesTxt.replace('\n', '')
#codesList = codesTxt.split(",")
inFeature = "...Inputs/HabitatAvg_HU8.shp"
nameList = [f.name for f in arcpy.ListFields(inFeature)]
nameList.remove("FID")
nameList.remove("Shape")
fieldNames = [str(i) for i in nameList]
oldNames = fieldNames[:164]
newNames = fieldNames[164:]
# Add new fields, copy data, and delete old fields
#for code in codesList:
#  arcpy.AddField_management(inFeature, code, "DOUBLE")
for old, new in zip(oldNames, newNames):
    arcpy.CalculateField_management(inFeature, new, "!" + old + "!", "PYTHON")
    arcpy.DeleteField_management(inFeature, old)
#sys.stdout.close
#sys.stdout=stdoutOrigin
```

Extracts zonal statistics from raster layers and output to tables

```
import arcpy
import os
from arcpy import env
from arcpy.sa import *
arcpy.CheckOutExtension("Spatial")
# Set environment settings
env.workspace = ".../Inputs/SpeciesR_Mean"
# Set local variables
inZoneData = ".../Inputs/HydroUnits/Steppe_HU8.shp"
zoneField = "FID"
fieldList = ['MEAN']
inField = "Alo_kochi"
# Process: Zonal Stats to Table
for inRaster in arcpy.ListFiles("*.tif"):
    inRastName = os.path.splitext(inRaster)[0]
    outTable = "...Inputs/SpeciesHbttAvg81/" + inRastName + ".dbf"
```

```

    outzStats = ZonalStatisticsAsTable(inZoneData, zoneField, inRaster, outTable, "DATA",
"MEAN")
    arcpy.JoinField_management(inZoneData, zoneField, outzStats, "OID", inField)

```

Creates raster from .csv table of species counts

```

import csv
import arcpy
import os
from arcpy import env
from arcpy.sa import *
arcpy.CheckOutExtension("Spatial")
# Set environment settings
env.workspace = ".../Inputs/SpeciesR_Mean"
# Set local variables
csvFile = open("SppRm.csv")
reader = csv.reader(csvFile)
sppList = list(reader)
for elem in sppList:
    elem.append(1)
sppWSumTable = WSTable(sppList)
# Process: Weighted Sum
outWtdSum = WeightedSum(sppWSumTable)
outWtdSum.save("../Output/SpeciesR_sum.tif")

```

Creates regions of raster cells with equal values

```

import arcpy
import os
from arcpy import env
from arcpy.sa import *
arcpy.CheckOutExtension("Spatial")
# Set environment settings
env.workspace = ".../Output"
# Set local variables
inRast = "SpeciesR_sum.tif"
inTotalArea = 177216120
inAreaUnits = "HECTARES"
inNumberRegions = 10
# Execute Locate Regions
outRegions = LocateRegions(inRast, inTotalArea, inAreaUnits, inNumberRegions,
evaluation_method="HIGHEST_VALUE",
                        number_of_neighbors="EIGHT", no_islands="ISLANDS_ALLOWED",
region_seeds="LARGE",
                        region_resolution="HIGH", selection_method="COMBINATORIAL")
outRegions.save("../Output/SpeciesR_regions.tif")

```

Changes cell size of rasters using bilinear resampling

```

import arcpy
import os

```

```

from arcpy import env
from arcpy.sa import *
arcpy.CheckOutExtension("Spatial")
# Set environment settings
env.workspace = ".../Inputs/SpeciesR_Mean"
# Set local variables and run
for inRaster in arcpy.ListFiles("*.tif"):
    inRastName = os.path.splitext(inRaster)[0]
    outRastName = inRastName + "200.tif"
    outRaster = ".../Inputs/SpeciesR_Mean200/" + outRastName
    arcpy.Resample_management(inRaster, outRaster, "200", "BILINEAR")

```

Converts floating point value rasters to integer rasters

```

import arcpy
import os
from arcpy import env
from arcpy.sa import *
arcpy.CheckOutExtension("Spatial")
# Set environment settings
env.workspace = ".../Inputs/SpeciesR_Mean200"
# Set local variables and run
for inRaster in arcpy.ListFiles("*.tif"):
    inRastName = os.path.splitext(inRaster)[0]
    outRastName = inRastName + "i.tif"
    inRast = Raster(inRaster)
    outRaster = Int(inRast + 0.5)
    outRaster.save(".../Inputs/SpeciesR_Mean200_Int/" + outRastName)

```

Creates new raster layers of average values per zone (watersheds) for habitat rasters

```

import arcpy
import os
from arcpy import env
from arcpy.sa import *
arcpy.CheckOutExtension("Spatial")
# Set environment settings
env.workspace = ".../Inputs/Species_Restricted3"
# Set local variables
inZoneData = ".../Inputs/Steppe_HU12.shp"
zoneField = "FID"
outTable = "means.dbf"
# Process: Zonal Stats to Table
for inRaster in arcpy.ListFiles("*.tif"):
    inRastName = os.path.splitext(inRaster)[0]
    outTableName = inRastName + ".dbf"
    outzStats = ZonalStatisticsAsTable(inZoneData, zoneField, inRaster, outTable, "DATA",
"MEAN")
    outReclassify.save(".../Inputs/SpeciesR_Int3/" + outRastName)

```

Creates rasters with average cell values across multiple rasters

```
import arcpy
import os
from arcpy import env
from arcpy.sa import *
arcpy.CheckOutExtension("Spatial")
# Set environment settings
env.workspace = ".../Inputs/SpeciesR_Int4"
# Process: Average rasters and add normalized value field
for inRaster in arcpy.ListFiles("*.tif"):
    inRastName = os.path.splitext(inRaster)[0]
    outRastName = inRastName + ".m.tif"
    inRast2 = ".../Inputs/SpeciesR81_Frag4/" + inRastName + "_81f.tif"
    inRast3 = ".../Inputs/SpeciesR321_Frag4/" + inRastName + "_321f.tif"
    inRast4 = ".../Inputs/SpeciesR1001_Frag4/" + inRastName + "_1001f.tif"
    inRast5 = ".../Inputs/SpeciesR3163_Frag4/" + inRastName + "_3163f.tif"
    raster1 = arcpy.Raster(inRast2)
    raster2 = arcpy.Raster(inRast3)
    raster3 = arcpy.Raster(inRast4)
    raster4 = arcpy.Raster(inRast5)
    raster5 = arcpy.Raster(inRast5)
    outRast = Int(((raster1 + raster2 + raster3 + raster4 + raster5)/0.5) + 0.5)
    outRast.save(".../Inputs/SpeciesR_Mean4/" + outRastName)
```

Counts cells of raster layers equal to specified values and output as .csv files

```
import arcpy
import os
import csv
from arcpy import env
from arcpy.sa import *
arcpy.CheckOutExtension("Spatial")
# Set environment settings
env.workspace = "...Inputs/SpeciesR_Count"
# Set local variables
ctList = []
qry = "VALUE = 1"
csvFile = ".../CellCt30.csv"
# Process: Build list with count
for inRaster in arcpy.ListFiles("*.tif"):
    inRastName = os.path.splitext(inRaster)[0]
    with arcpy.da.SearchCursor(inRaster, ['VALUE','COUNT'], qry) as rows:
        for row in rows:
            ctList.append((inRastName, row[1]))
with open(csvFile, 'wb') as output:
    writer = csv.writer(output)
    writer.writerows(ctList)
```

Runs specified size floating window summing cell values into target cell

```
import arcpy
import os
from arcpy import env
from arcpy.sa import *
arcpy.CheckOutExtension("Spatial")
# Set environment settings
env.workspace = ".../Inputs/SpeciesR_Int4"
# Set local variables
nbr = NbrRectangle(1001, 1001, "CELL")
# Process: BlockStatistics and LookUp
for inRaster in arcpy.ListFiles("*.tif"):
    inRastName = os.path.splitext(inRaster)[0]
    outRastName = inRastName + "_1001.tif"
    outFocalStat = FocalStatistics(inRaster, nbr, "SUM")
    outFocalStat.save(".../Inputs/SpeciesR1001_4/" + outRastName)
```

Standardizes values of different scaled contiguity rasters

```
import arcpy
import os
from arcpy import env
from arcpy.sa import *
arcpy.CheckOutExtension("Spatial")
# Set environment settings
env.workspace = ".../Inputs/SpeciesR1001_4"
# Process: Map Algebra
for inRaster in arcpy.ListFiles("*.tif"):
    inRastName = os.path.splitext(inRaster)[0]
    outRastName = inRastName + "f.tif"
    raster1 = arcpy.Raster(inRaster)
    rasterMax = raster1.maximum
    outRaster = Int(((raster1 / rasterMax) * 10) + 0.5)
    outRaster.save(".../Inputs/SpeciesR1001_Frag4/" + outRastName)
```

Adds fields to rasters of species groups and populate with standardized counts

```
import arcpy
from arcpy import env
from arcpy.sa import *
# Set environment settings
env.workspace = ".../Inputs/Species_Group"
# Set local variables
fieldName1 = "Product"
expression1 = "!COUNT!*!LINK!"
fieldName2 = "Combo"
# Process: Add field and calculate values
for inRaster in arcpy.ListFiles("*.tif"):
    arcpy.AddField_management(inRaster, fieldName1, "LONG")
    arcpy.CalculateField_management(inRaster, fieldName1, expression1, "PYTHON")
```

```

max_value = float('-inf')
with arcpy.da.SearchCursor(inRaster, fieldName1) as cursor:
    for row in cursor:
        value = row[0]
        if value > max_value:
            max_value = value
expression2 = "(!Product!/\" + max_value + \")*10"
arcpy.AddField_management(inRaster, fieldName2, "FLOAT")
arcpy.CalculateField_management(inRaster, fieldName2, expression2, "PYTHON")

```

Reclassifies floating point cell values of 0-10 to integer categories 0, 1, 2... 10

```

import arcpy
import os
from arcpy import env
from arcpy.sa import *
arcpy.CheckOutExtension("Spatial")
# Set environment settings
env.workspace = ".../Inputs/Species_Restricted4"
# Set local variables
reclassField = "VALUE"
remap =
RemapRange([[0,0,0],[0,0.1,1],[0.1,0.2,2],[0.2,0.3,3],[0.3,0.4,4],[0.4,0.5,5],[0.5,0.6,6],[0.6,0.7,7],
[0.7,0.8,8],[0.8,0.9,9],[0.9,1,10]])
# Process: Reclassify
for inRaster in arcpy.ListFiles("*.tif"):
    inRastName = os.path.splitext(inRaster)[0]
    outRastName = inRastName + "11.tif"
    outReclassify = Reclassify(inRaster, reclassField, remap, "NODATA")
    outReclassify.save(".../Inputs/SpeciesR_Int4/" + outRastName)

```

Reclassifies habitat values 0-10 to 0 and 10-100 to 1 (nonhabitat and habitat)

```

import arcpy
import os
from arcpy import env
from arcpy.sa import *
arcpy.CheckOutExtension("Spatial")
# Set environment settings
env.workspace = ".../Inputs/SpeciesR_Mean30r"
# Set local variables
reclassField = "VALUE"
remap = RemapRange([[0,10,0],[10.1,100,1]])
# Process: Reclassify
for inRaster in arcpy.ListFiles("*.tif"):
    inRastName = os.path.splitext(inRaster)[0]
    outRastName = inRastName + "ct.tif"
    outReclassify = Reclassify(inRaster, reclassField, remap, "NODATA")
    outReclassify.save(".../Inputs/SpeciesR_Count/" + outRastName)

```