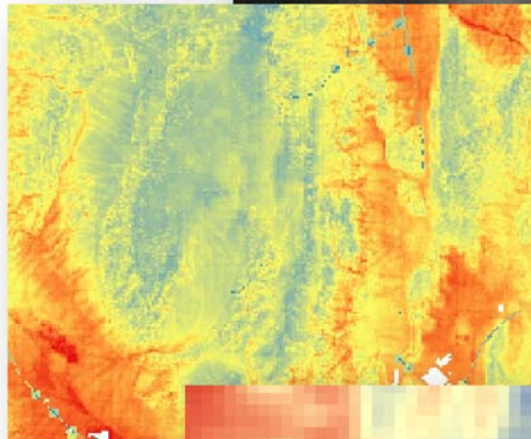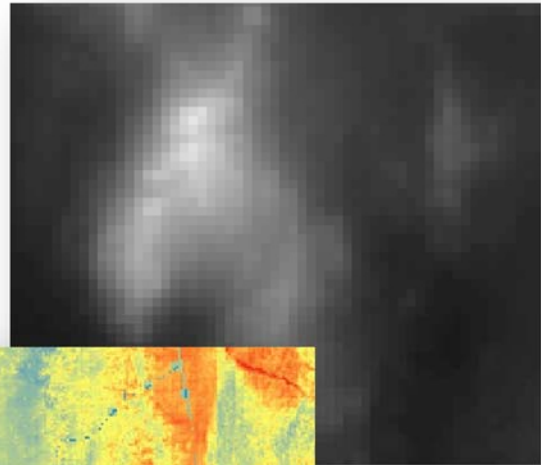# BIODIVERSITY HOTSPOT ANALYSIS

Biodiversity Layer and Report

Prepared for the:

desert conservation
P R O G R A M

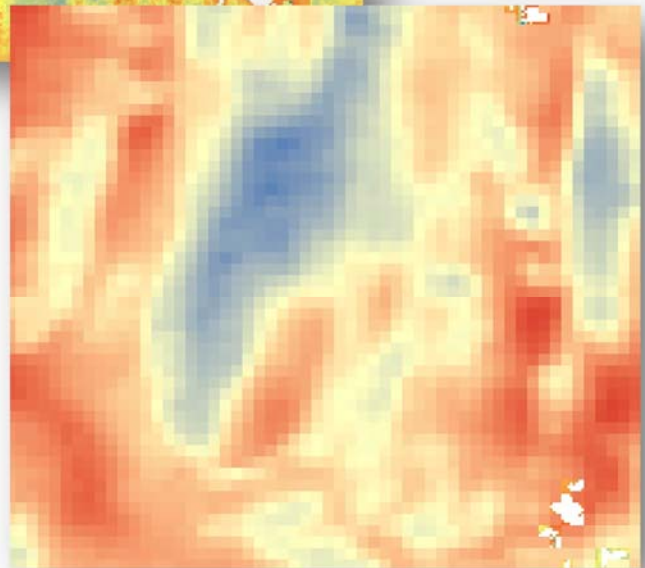4701 W. Russell Rd.
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INTRODUCTION

Quantifying biodiversity is an important yet challenging task for applied conservation and land management (Cardinale et al. 2012). Being able to implement regional biodiversity sampling projects requires both an acute need for quantifying biodiversity and extensive funding, often leaving such projects outside of the realm of local conservation and land management agencies, even when such information would be useful for land management. One promising solution is the repurposing of other data to derive estimates of biodiversity. For example, species distribution models (SDMs) are commonly-developed spatial tools used in conservation and management (Calabrese et al. 2013). SDMs for a single species provide little information on biodiversity, but when a sufficient number of SDMs are created for different species within a common spatial extent, spatially-explicit estimates of species richness (i.e., biodiversity) can be calculated. Following calculation of the stacked SDMs (SSDMs), a macroecological model can then be created to remove accumulated bias inherent in the process of building the component SDMs (Calabrese et al. 2013, Fithian et al. 2014). Finally, the macroecological model can be used in a geographic information system as a tool to examine spatial variation in biodiversity across the extent of the calculation area.

METHODS

Conceptual treatment of SDMs

Here in Clark County, Nevada, the Clark County Desert Conservation Program (DCP) has either commissioned or has access to SDMs for 55 plant, reptile, mammal, avian, and invertebrate species. Most of these species are covered under the current Multiple Species Habitat Conservation Plan, while a few are under consideration for inclusion under a potential future Plan amendment. The list of species chosen for deriving SDMs is not comprehensive of all species present within Clark County, and therefore any resultant estimates of biodiversity must be interpreted as 'biodiversity among this list of species', or alternatively, 'species richness'. Importantly, we can use the SSDM and landscape data to generate a macroecological model generalized to all species (Calabrese et al. 2013).

Data processing

The first step I conducted in data processing was to classify all SDMs provided by the DCP into one of three categories: suitable for use as provided (i.e., a continuous estimate of the relative probability of occurrence, scaled between zero and one), suitable for use after processing (e.g., species density estimates that can be scaled between zero and one), and unsuitable for this task (e.g., vector layers with qualitative classification of species' occurrence or a probability raster that was only generated for a small portion of Clark County). Some SDMs were habitat-based average observed avian densities rather than probability of occurrence estimates. For SDMs with density estimates that were all less than 1, the direct density estimate was retained as approximately equivalent to the probability of occurrence in that habitat cover type (i.e., low average observed densities = low probability of occurrence in a given plot). For density estimates that exceeded 1, densities were rescaled to a zero-to-one scale by dividing the observed value by the maximum value rounded up to the nearest tenth place to ensure all values were less

than 1. For 'suitable after processing' SDMs I assumed that within-species variation in density was a proxy variably for variation in probability of occurrence. While this is likely an assumption that is untenable among species, it is reasonable to assume that any bias or deviation from this assumption is constant within a species. Therefore any deviation is consistent across the SDM and therefore does not influence the use of the SDM as an index of spatial variation in biodiversity.

Simple spatial re-projection, raster snapping, or raster resampling were applied where necessary to standardize all of the SDMs to the same resolution (i.e., 250m x 250m), raster origin coordinates, and coordinate system (i.e., NAD83 UTM Z11N). All NoData cells were assigned a value of 0 prior to stacking. Some SDMs were resampled to a higher resolution (250m) than that of the original SDM (1km). In practice this meant that a grid cell that was previously 1km x 1km with a single raster value now was comprised of four grid cells, each 250m x 250m, and each with the same original raster value. In terms of spatial accuracy this falsely implies a higher resolution at the level of the individual SDM, but it is acceptable to do at the level of the SSDM because it allowed them to accommodate the resolution of the 250m SDMs. This approach maximized inclusion of all information from the highest resolution SDMs. Nonetheless, we note that some of the input SDMs were originally generated at a resolution of 1km and were later resampled to a resolution of 250m for compatibility. Some of the Great Basin Bird Observatory avian SDMs were generated at a higher resolution than the other SDMs. These were resampled to a 250m x 250m resolution taking the maximum value within the window to reflect the highest probability that a species was observed within the larger window.

Create p-SSDM

After all SDMs were assessed for suitability and were re-projected, snapped, and/or resampled I constructed the raw biodiversity hotspot map. Calabrese et al. (2013) found that applying thresholds to classifying binary species presence (e.g., converting continuous probabilities of presence to a yes/no present or absent state) was a highly biased method of stacking SDMs and consistently resulted in overpredicting species richness. Therefore I used two other methods that Calabrese et al. (2013) tested. First, I created a continuous index of local biodiversity by stacking all raw probability SDMs (i.e., stacking p-SDMs to create a single p-SSDM). This method side-steps defining arbitrary thresholds in defining whether or not a grid cell contains a species and instead serves as an index whereby the higher the biodiversity index value the higher the true number of species. The strength of creating a p-SSDM is that it has been proven to be considerably less biased than stacking SDMs with arbitrary presence/absence thresholds. The drawback to creating the p-SSDM model is that it represents an index of biodiversity of the list of species and therefore may contain latent bias with regards to true biodiversity depending on the level of (unknown) bias in which species were chosen to create SDMs. To resolve this I conducted a second analysis, whereby I modeled the p-SSDM biodiversity index as a function of environmental predictors to elucidate underlying macroecological patterns in biodiversity. The goal of this analysis was to test for, and if present to correct for, any biases in the p-SSDM (Calabrese et al. 2013). It assumes that the p-SSDM contained some bulk of information about underlying macroecological patterns in species

richness. It tested whether there was some bias in the p-SSDM, whether as a function of the p-SSDM being a non-random subset of all species in Clark County, biases induced by the varying modeling methods used to produce the individual p-SDMs, or biases inherent in the process of stacking p-SDMs (Calabrese et al. 2013).

Create macroecological model

To build the macroecological model I used the p-SSDM biodiversity raster layer as the response variable in a linear regression with five environmental predictor variables. The environmental predictor variables were chosen from the six most important variables identified by Inman et al. (2014) in a study on SDMs for 15 species across the Mojave Ecoregion. The five predictor variables used in this macroecological model were elevation, seasonal thermal change, surface texture, topographic position, and seasonal greenness timing (Table 1). Winter precipitation was the sixth environmental predictor variable initially included. However, winter precipitation was highly correlated ($r = 0.863$) with elevation and was excluded from further analysis because previous work has shown elevation to be a primary driver of regional variation in biodiversity (Mateo et al. 2012).

Table 1. Environmental predictor variables used in creation of the macroecological biodiversity model. Variables were selected as the six most influential variables for species distributions in the Mojave Ecoregion (Inman et al. 2014). All spatial data for variables were created or processed by Southwest Ecology (2018). This table adapted from Southwest Ecology (2018).

Variable	Unit	Description	Original source
Elevation	m	Elevation calculated using remote-sensed data	USGS National Elevation Dataset
Seasonal thermal change	Index	Higher values indicate higher disparity between summer and winter temperatures	Inman et al. 2014
Surface texture	°C x 100	Difference between mean daytime and nighttime surface temperatures	Inman et al. 2014
Topographic position	Index	Steady state wetness index as a function of both slope and the upstream contributing area per unit width orthogonal to the flow direction	USGS National Elevation Dataset
Seasonal greenness timing	Time	Date of the maximum value of the Normalized Difference Vegetation Index	Inman et al. 2014

I generated a systematic grid of sample points 2.25 km apart from each other to sample the biodiversity raster and environmental predictor variable rasters while ensuring even coverage across the county and minimizing spatial autocorrelation. After removing points from the sample grid that fell within DCP-defined 'disturbed' areas (i.e., a vector layer provided by DCP) there were 3,827 sample points. I sampled the raster layers and then used linear regression in Program R v.3.5 (R Core Team 2018) to derive the macroecological statistical model. I then used the coefficients from the statistical model in Raster Calculator to create the continuous macroecological predictive surface. All environmental raster layers were provided at a resolution of 1 km, so the output macroecological layer is at this resolution as well.

After creation of the p-SSDM and macroecological raster layers I ensured they were clipped to the boundaries of Clark County. I also converted all raster cells overlapping 'disturbed' areas to NoData using the disturbed vector layer provided by DCP. Finally, I resampled the p-SSDM using bilinear interpolation and subtracted this layer from the macroecological layer to assess broad geographic patterns in where and how the macroecological model rectified the biodiversity estimates of the p-SSDM.

Case study – reserve system design

I conducted two case studies to show how the p-SSDM and macroecological biodiversity models can be used in designing a new reserve system and in quantifying the biodiversity value of the reserve system. For the first case study I created two hypothetical identically-sized reserve units where the question is placement within a portion of northeast Clark County. For the second question I created four different-sized reserve units where the question is on a single large or several small reserve units whose placement within southwestern Clark County is fixed. Finally, I calculated zonal statistics for the Boulder City Conservation Easement (BCCE) to show how the current BCCE is related to both biodiversity models.

RESULTS

Initial processing for quality control resulted in 29 SDMs being classified as suitable, 11 SDMs classified as suitable after processing, and 15 SDMs classified as unsuitable (Appendix A). Most of the SDMS classified as suitable were generate by Southwest Ecology (2018). Most of the SDMs classified as suitable after processing were generated by Great Basin Bird Observatory as habitat cover-based avian density estimates. Most SDMs classified as unsuitable were plant SDMs generated by Hamilton and Kokos (2011) that only contained vectorized qualitative estimates of survey results (e.g., 'found', 'surveyed but not found', and 'not surveyed'). These SDMs provided qualitative information to which probabilities could not be assigned (e.g., 'not surveyed' does not equal 'not present'). A couple of unsuitable SDMs were originally generated only for a small subset of Clark County (e.g., portions of the Virgin River), and because they did not include occurrence probability estimates elsewhere, were unsuitable due to their minimal spatial extent.

Stacking the 40 p-SDMs to produce the p-SSDM layer proceeded smoothly once they were all in the same coordinate system, resolution, and no longer retained NoData cells. The output p-SSDM shows spatial variation in the index of biodiversity of the 40 species modeled in the list in Appendix A (Figure 1). This raster layer is a useful tool for examining spatial variation in biodiversity of the 40 assessed species across Clark County. General patterns in biodiversity of the 40 species showed higher diversity at lower elevations in Clark County, particularly along the Virgin and Muddy Rivers and surrounding Las Vegas

Figure 1. Biodiversity hotspots for the 40 species used to build the stacked species distribution model (p-SSDM). Raster cells are at a resolution of 250m.
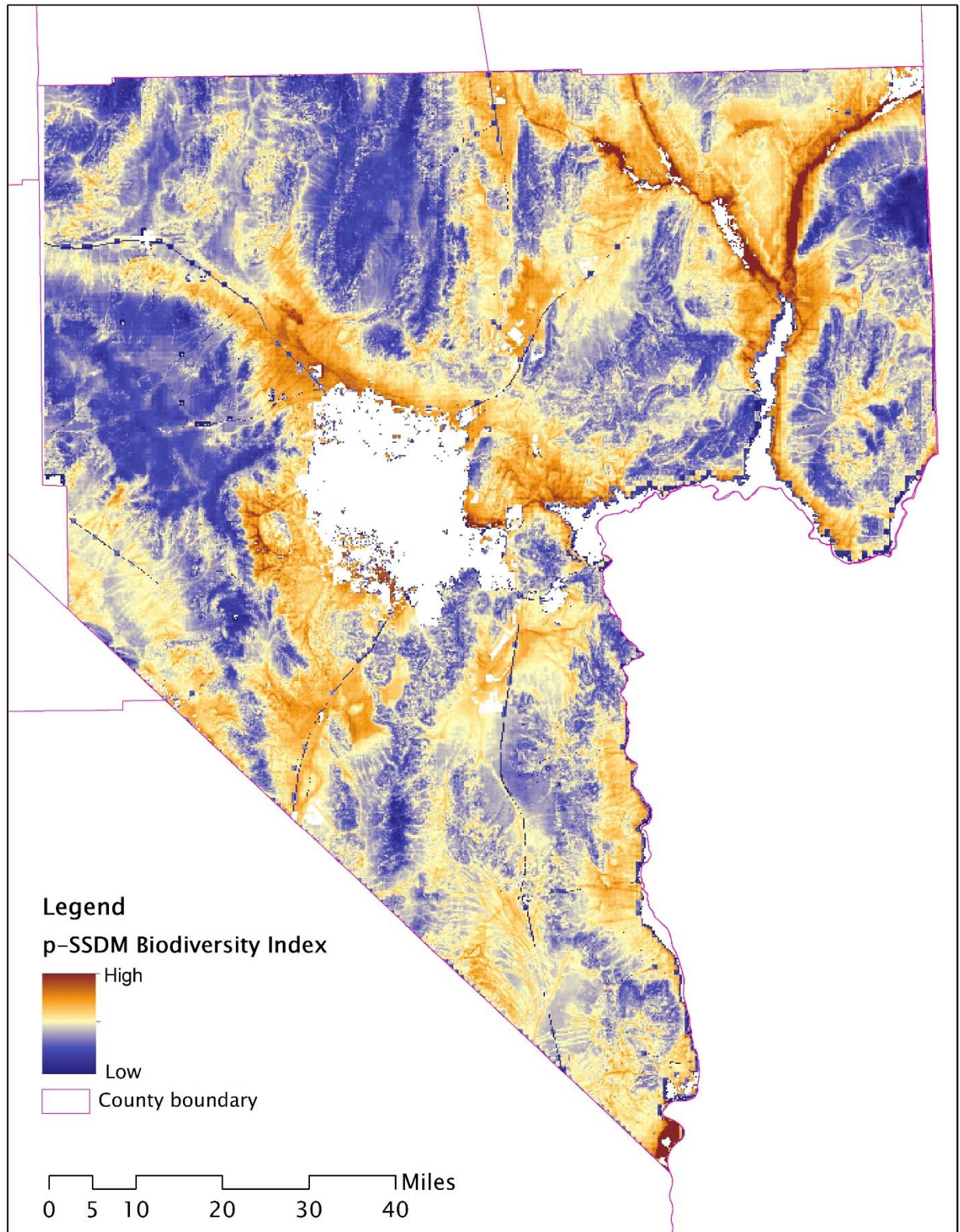
While the p-SSDM raster layer is useful for assessing biodiversity patterns of the 40 species included in the model, it would also be useful to assess biodiversity of all species. The macroecological model used the p-SSDM layer to extract general information on landscape features driving biodiversity and then re-applied those relationships across Clark County. It found that general species biodiversity decreased as elevation increased, was lower in areas with higher seasonal thermal change (i.e., decreased as the difference between summer and winter temperatures increased), was higher in areas with higher surface texture (i.e., a higher difference between daytime and nighttime temperatures), was higher in areas with a higher topographic position index (i.e., higher steady state wetness), and was higher in areas with later seasonal greenness timing (i.e., later maximum vegetation greenness). All relationships were statistically significant (Table 2). The five variables explained 27.7% of the variation in species biodiversity (Adjusted R^2 = 0.2768).

Table 2. Statistical results from the macroecological model describing spatial patterns in species biodiversity as a function of landscape variables in Clark County, Nevada, USA.

Variable	Coefficient	Std. Error	t-value	p-value
Intercept	10.144	0.507	22.56	< 0.001
Elevation	-0.0023	0.00009	-26.05	< 0.001
Seasonal thermal change	-0.0031	0.00052	-5.84	< 0.001
Surface texture	0.00236	0.00032	7.47	< 0.001
Topographic position	0.0652	0.0187	3.49	< 0.001
Seasonal greenness timing	0.3279	0.0317	10.34	< 0.001

General spatial patterns of biodiversity as predicted by the macroecological model were similar to the p-SSDM model in that biodiversity was predicted to be higher in low-elevation portions of the county (Figure 2). The Muddy and Virgin River corridors, while still predicted to have high general biodiversity, did not stand out as much as "epicenters" of biodiversity as they did in the p-SSDM model.

I generated the macroecological model to potentially adjust for sample selection bias in the species used to build the p-SSDM model. I tested for spatial bias in the p-SSDM model by overlaying both rasters and then subtracting the p-SSDM raster (Figure 1) from the macroecological raster (Figure 2) to generate a raster of differences between the two (Figure 3). In the difference raster, positive values (in green) indicate areas where the macroecological model predicted higher biodiversity than did the p-SSDM model, whereas negative values (in purple) represent areas where the macroecological model predicted lower biodiversity than did the p-SSDM model. Areas in white indicate substantial agreement between the two models. Thus this map shows where bias in the p-SSDM was rectified by the macroecological biodiversity, with respect to all-species biodiversity. The difference raster indicates that the p-SSDM model over-scored biodiversity in the Muddy and Virgin River corridors and west of Las Vegas, whereas the p-SSDM model underscored biodiversity east of Las Vegas and in the

northwest portion of the County. In spite of the differences, there was substantive overlap between the two biodiversity models with a Pearson's correlation coefficient of 0.475.

Figure 2. Map of general biodiversity hotspots derived from the macroecological biodiversity model. Raster cells are at a resolution of 1.0 km.
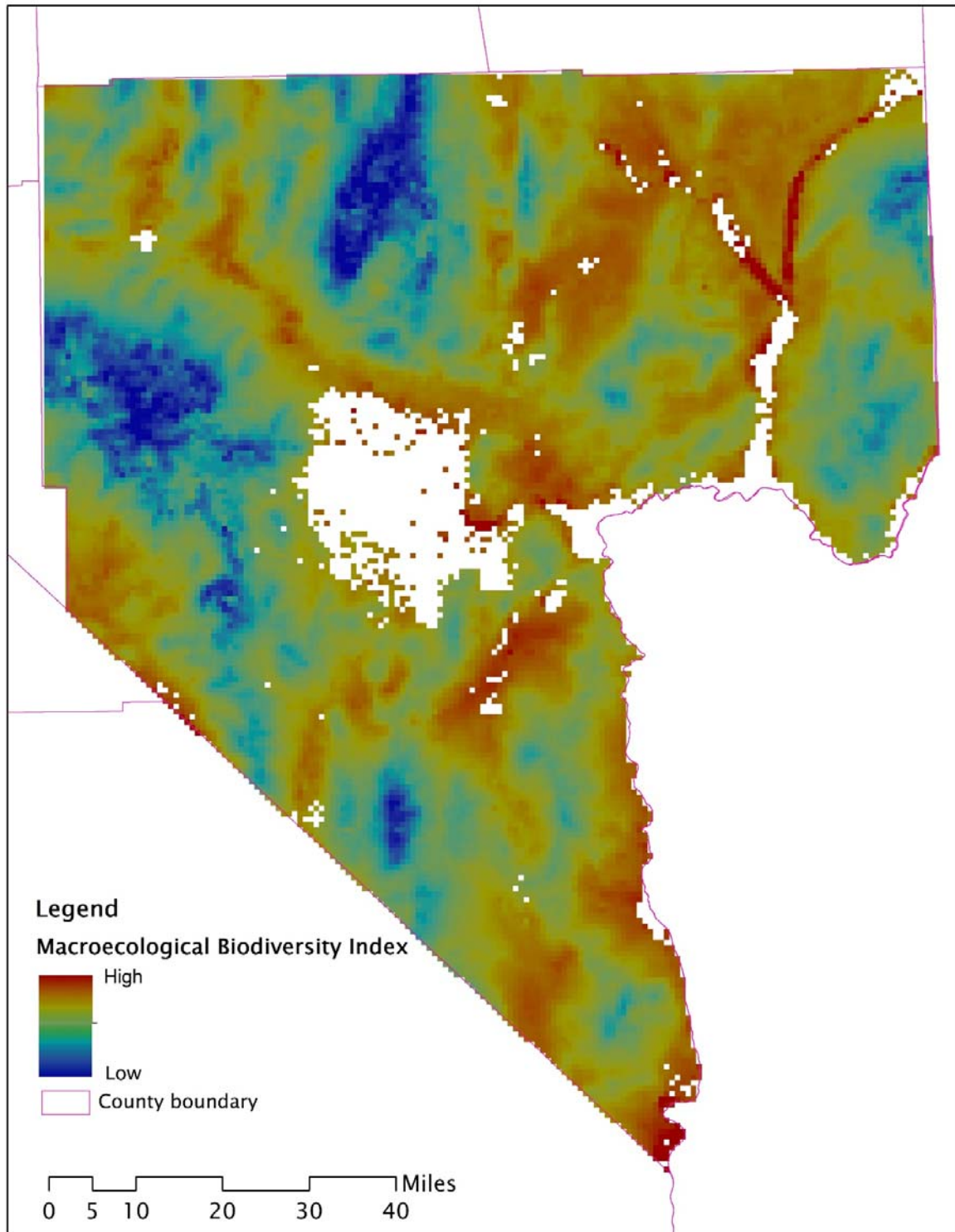
Figure 3. Map of the difference in biodiversity estimates from the stacked species distribution (p-SSDM) and macroecological models. Calculated by subtracting p-SSDM raster from the macroecological raster. Cell size resolution is 1.0 km.
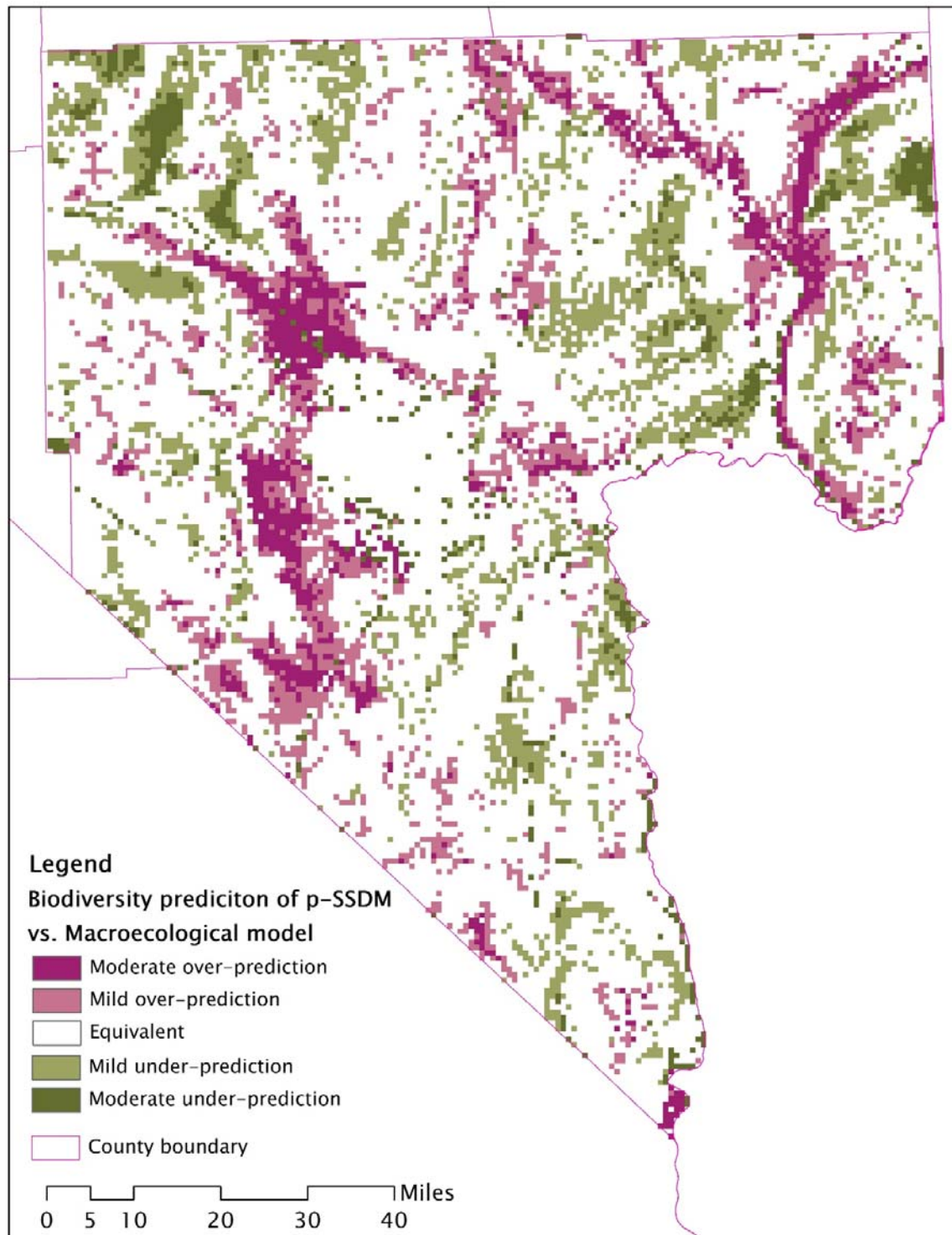
The first case study was a choice between two hypothetical locations (1a and 1b) for a single reserve unit in northeastern Clark County (Figure 4). Location 1a had a 15.7% higher average biodiversity index score for the p-SSDM model and a 12.0% higher average biodiversity score for the macroecological model (Table 3). Summed biodiversity scores within each of the reserve units followed a similar pattern, with 1a having 12.7 % higher p-SSDM scores than 1b and 12.6% higher macroecological scores.

Table 3. Biodiversity index values for choosing between two hypothetical reserve unit locations in northeastern Clark County, Nevada. Average and sum values calculated using the zonal statistics tool in Spatial Analyst.

Reserve Unit	Average		Sum	
	p-SSDM	Macroecological	p-SSDM	Macroecological
1a	9.6	10.3	6897.0	455.3
1b	8.3	9.2	6120.5	404.3

The second case study was more complex, in that it was evaluating a single large or several small hypothetical reserve units, none of whose boundaries could be changed (e.g., due to land ownership or other constraints). In other words, the choice was between making Unit 2a a reserve unit or Units 2b, 2c, and 2d into reserve units. Two contrasting findings emerged. For average biodiversity index scores, the three smaller units had 5.9% higher p-SSDM scores and 13.6% higher macroecological scores. However, for total summed scores, the single large unit had 19.7% higher p-SSDM scores and 5.4% higher macroecological scores. The opposing patterns are due to the different total areas of the units, with the single large unit being 71.35 km^2 versus a combined area of 55.14 km^2 for all three smaller units. Thus, if potential unit boundaries are fixed, any given point within the three smaller units would tend to have higher biodiversity, but at the level of the entire reserve, the single large unit would have higher total diversity.

Table 4. Biodiversity index values for choosing between one large or several small hypothetical reserve unit locations in southwestern Clark County, Nevada.

Reserve Unit	Average		Sum	
	p-SSDM	Macroecological	p-SSDM	Macroecological
2a	10.1	8.8	11306.3	601.4
2b, 2c, & 2d	10.7	10.0	9447.7	570.4

Figure 4. Location map of hypothetical case study reserve units and the Boulder City Conservation Easement. Background layer is the macroecological biodiversity layer, ranging from low biodiversity (blue) to high biodiversity (red).
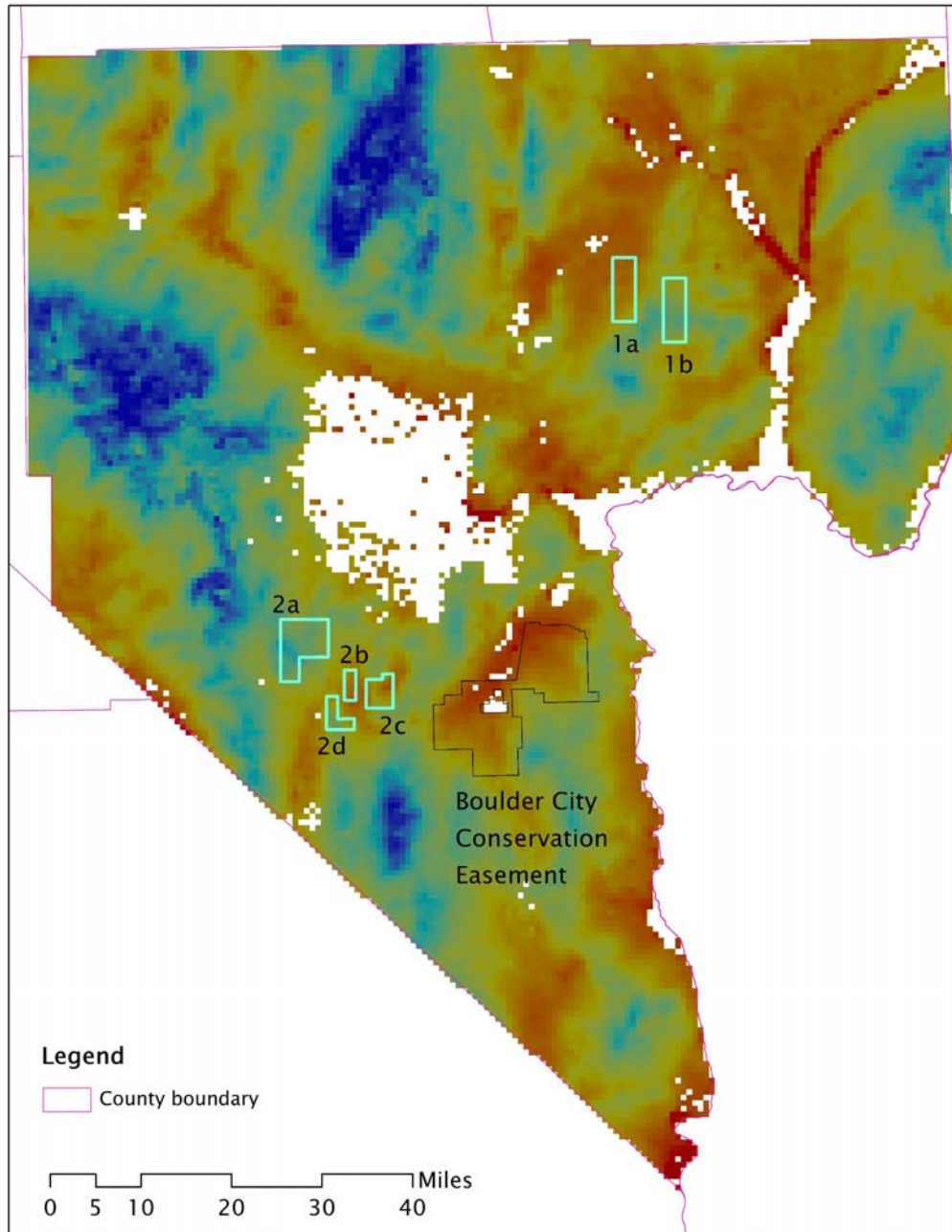
For reference, Table 5 also displays the biodiversity metrics for the BCCE and Clark County in its entirety. The BCCE has an average p-SSDM value 6.4% higher than the county-wide average and a macroecological score 10.6% higher than the county-wide average.

Table 5. Biodiversity index metrics for the Boulder City Conservation Easement and the entirety of Clark County, Nevada.

Reserve Unit	Average		Sum	
	p-SSDM	Macroecological	p-SSDM	Macroecological
BCCE	10.0	10.4	55622.1	3611.1
Clark County	9.4	9.4	2.9×10^6	1.8×10^5

All spatial products associated with this analysis have also been submitted to the DCP. Table 6 lists the relevant spatial layers to link them with their reference in this report.

Table 6. Spatial data inputs and outputs from creation of a 40-species biodiversity model and a macroecological biodiversity model in Clark County, Nevada, USA. Italics represent interchangeable labels for multiple rasters of the same spatial data type.

Spatial data	Filename	Figure in this report	Notes
Input species distribution models	'*speciescode_X*_final'	NA	Where 'X' is '250m' only if raster was resampled to 250m
Environmental predictor variables	'*envirovariable*_nad83z11'	NA	NA
p-SSDM biodiversity	'biodiversity_hotspots_pSSDM'	Figure 2	Stacked probability-of-occurrence species distribution model
Macroecological biodiversity	'biodiversity_hotspots_ macroecological'	Figure 3	Regression model of p-SSDM and environmental predictors
Difference biodiversity	'biodiversity_hotspots_Diff_ Macroecol_minus_pSSDM'	Figure 4	Overlay of biodiversity models, calculated as macroecological minus p-SSDM

DISCUSSION

The goal of this analysis was to leverage existing SDMs to generate a spatial model of variation in biodiversity across Clark County, Nevada. Forty of the 55 potential SDMs were suitable for this analysis, either a priori or after spatial processing, including reprojecting, resampling, snapping, and rescaling. Combining these probability-of-occurrence rasters yielded a stacked species distribution model (p-SSDM) that predicted spatial variation in biodiversity of the 40 species across Clark County. To adjust for potential bias induced by the selection of a handful of species out of all species in Clark County, I then created a macroecological model of total species biodiversity in Clark County as explained by five environmental predictor variables.

The p-SSDM raster layer is useful for conservation planning with respect to the 40 species used to build the p-SSDM. In contrast, the macroecological raster layer is useful for conservation planning for general biodiversity of all species including the 40 species used to build the p-SSDM. Both maps were generated using robust data, and the choice of which to use for conservation planning depends on the desired scope of biodiversity to capture. By and large the two models agreed, with a moderately strong correlation between the two and large portions of Clark County with equivalent biodiversity predictions among both models (Figure 4). The map of differences between models can be useful to highlight areas where, if the p-SSDM model is chosen, it should be recognized whether the p-SSDM is accurately representing general biodiversity (i.e., white areas), or is narrowly representing the 40 SDM species' diversity (i.e., purple or green areas).

The two case studies demonstrated different ways that either biodiversity layer can be used. The first case study was a simple "where should we put a 45.93 km^2 reserve area?" question. The second case study was a more nuanced, "which of these two fixed options should we choose as a reserve area?" question. In practice, designing reserve areas is likely even more nuanced depending on competing land uses, land ownership patterns, and landscape-level factors (e.g., risk of catastrophe, connectivity, etc.). Of particular note is the different ways that average biodiversity values versus summed biodiversity values can be used in a trade-off analysis. The larger a reserve unit, the higher the likely total biodiversity is within the unit, albeit perhaps as an aggregrevative function of low-diversity patches. In contrast, a small unit can also protect biodiversity by maximizing the biodiversity of any particular patch within the unit (i.e., protecting hotspots). These metrics apply to both the p-SSDM and macroecological models, and the choice between the two depends on the focal level for quantifying biodiversity (i.e., richness of the 40 SDM species or richness of general biodiversity). Hopefully these tools prove useful for analysis and land use planning to quantify biodiversity in Clark County, Nevada.

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Appendix A. List of species distribution models (SDMs) provided by Clark County Desert Conservation Program for potential inclusion in the biodiversity hotspot analysis. SDMs were classified with a suitability for inclusion status based upon the spatial characteristics of the SDM.

Common Name	Scientific Name	Taxon	Category	Reason
Bell's sparrow	*Artemisiospiza belli*	Birds	Suitable	NA
Botta's pocket gopher	*Thomomys bottae*	Mammals	Suitable	NA
Burrowing owl	*Athene cunicularia hypugea*	Birds	Suitable	NA
California leaf-nose bat	*Macrotus californicus*	Mammals	Suitable	NA
Desert iguana	*Dipsosaurus dorsalis*	Reptiles	Suitable	NA
Gila monster	*Heloderma suspectum cinctum*	Reptiles	Suitable	NA
Hoary bat	*Lasiurus cinereus*	Mammals	Suitable	NA
MacNeill's saltbush sootywing	*Hesperopsis gracielae*	Invertebrate	Suitable	NA
Mexican free-tailed bat	*Tadarida brasiliensis*	Mammals	Suitable	NA
Mojave shovel-nosed Snake	*Chionactis occipitalis*	Reptiles	Suitable	NA
Pallid bat	*Antrozous pallidus*	Mammals	Suitable	NA
Sidewinder	*Crotalus cerastes*	Reptiles	Suitable	NA
Silver-haired bat	*Lasionycteris noctivagans*	Mammals	Suitable	NA
Spotted leaf-nose snake	*Phyllorhynchus decurtatus*	Reptiles	Suitable	NA
Townsend's big-eared bat	*Corynorhinus townsendii*	Mammals	Suitable	NA
Western red bat	*Lasiurus blossevillii*	Mammals	Suitable	NA
Alkali mariposa lily	*Calochortus striatus*	Plants	Suitable	NA
Blue Diamond cholla	*Cylindropuntia multigeniculata*	Plants	Suitable	NA
Catchfly gentian	*Eustoma exaltatum*	Plants	Suitable	NA
Clarke phacelia	*Phacelia filiae*	Plants	Suitable	NA
Halfring milkvetch	*Astragalus mohavensis var. hemigyrus*	Plants	Suitable	NA
Joshua tree	*Yucca brevifolia*	Plants	Suitable	NA
Mokiak milkvetch	*Astragalus mokiacensis*	Plants	Suitable	NA
Polished blazingstar	*Mentzelia polita*	Plants	Suitable	NA
Rosy two-toned beardtongue	*Penstemon bicolor ssp. roseus*	Plants	Suitable	NA
Silverleaf sunray	*Enceliopsis argophylla*	Plants	Suitable	NA
Straw milkvetch	*Astragalus lentiginosus var. stramineus*	Plants	Suitable	NA

Common Name	Scientific Name	Taxon	Category	Reason
Threecorner milkvetch	*Astragalus geyeri var. triquetrus*	Plants	Suitable	NA
Yellow Two-toned beardtongue	*Penstemon bicolor ssp. bicolor*	Plants	Suitable	NA
Arizona Bell's vireo	*Vireo bellii arizonae*	Birds	Suitable after processing	Resolution / density estimates
Bendire's thrasher	*Toxostoma bendirei*	Birds	Suitable after processing	Resolution / density estimates
Costa's hummingbird	*Calypte costae*	Birds	Suitable after processing	Resolution / density estimates
Desert pocket mouse	*Chaetodipus penicillatus*	Mammals	Suitable after processing	Resolution / density estimates
Desert tortoise	*Gopherus agassizii*	Reptiles	Suitable after processing	Resolution / density estimates
Gilded flicker	*Colaptes chrysoides*	Birds	Suitable after processing	Resolution / density estimates
Golden eagle	*Aquila chrysaetos*	Birds	Suitable after processing	Resolution / density estimates
LeConte's thrasher	*Toxostoma lecontei*	Birds	Suitable after processing	Resolution / density estimates
Loggerhead shrike	*Lanius ludovicianus*	Birds	Suitable after processing	Resolution / density estimates
Phainopepla	*Phainopepla nitens*	Birds	Suitable after processing	Resolution / density estimates
Southwestern willow flycatcher	*Empidonax traillii extimus*	Birds	Suitable after processing	Resolution / density estimates
Desert kangaroo rat	*Dipodomys deserti*	Mammals	Unsuitable	Insufficient coverage
Regal ringneck snake	*Diadophis punctatus*	Reptiles	Unsuitable	Qualitative
Ridgeway's rail	*Rallus obsoletus yumanensis*	Birds	Unsuitable	Qualitative / insufficient coverage
Spotted bat	*Euderma maculatum*	Mammals	Unsuitable	Qualitative
Yellow-billed cuckoo	*Coccyzus americanus*	Birds	Unsuitable	Qualitative / insufficient coverage
Beaver Dam breadroot	*Pediomelum castoreum*	Plants	Unsuitable	Qualitative
Gold Butte moss	*Didymodon nevadensis*	Plants	Unsuitable	Qualitative

Common Name	Scientific Name	Taxon	Category	Reason
Las Vegas bearpoppy	*Arctomecon californica*	Plants	Unsuitable	Qualitative
Las Vegas buckwheat	*Eriogonum corymbosum var. nilesii*	Plants	Unsuitable	Qualitative
Pahrump Valley buckwheat	*Eriogonum bifurcatum*	Plants	Unsuitable	Qualitative
St. George blue-eyed grass	*Sisyrinchium radicatum*	Plants	Unsuitable	Qualitative
Sticky buckwheat	*Eriogonum viscidulum*	Plants	Unsuitable	Qualitative
Sticky ringstem	*Anulocaulis leiosolenus*	Plants	Unsuitable	Qualitative
White-margined beardtongue	*Arctomecon merriamii*	Plants	Unsuitable	Qualitative
White bearpoppy	*Penstemon albomarginatus*	Plants	Unsuitable	Qualitative