Wildlife Connectivity Across The Central California Coast Region

A fine-scale multi-species modeling approach to inform management and restoration of wildlife corridors in a biodiversity hotspot

Mountain lion passing through Sedgwick Reserve (Photo: Kristen Zumdahl)

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1. INTRODUCTION

The southern central coast of California, situated within the California Floristic Province, is globally renowned for its rich biodiversity, including various endemic plant and animal species (Calsbeek et al., 2003). The region is considered to be one of the 36 global biodiversity hotspots, which are areas recognized for both exceptional biodiversity and high levels of threat (Habel et al., 2019). The central coast is a dynamic region, characterized by a mix of large urban populations, extensive agricultural lands, and relatively intact natural areas (Thorne et al., 2006). It also contains the largest stretch of undeveloped coastline remaining in Southern California, providing critical intact habitat for the region's biodiversity. However, increasing urbanization, infrastructure development, and agricultural expansion have resulted in significant habitat fragmentation. This fragmentation disrupts wildlife movement, limits access to resources, and disrupts ecological systems. Additionally, fragmented habitats can isolate wildlife populations, increasing the risk of inbreeding and genetic bottlenecks (Haddad et al., 2015). Habitat fragmentation can hinder a species' ability to adapt to climate change and obstruct their migration to new areas in response to shifting environmental conditions.

To address this challenge of fragmentation, conservation strategies such as wildlife crossings—overpasses and underpasses designed for wildlife—have been successfully implemented to reduce barriers to movement (Goldfarb, 2023). Other initiatives, including revegetation of wildlife corridors, wildlife-friendly fencing, and the creation of buffer zones around developed areas, have also shown potential to enhance habitat connectivity. Habitat connectivity is essential for species survival and long-term ecosystem health (van Strien & Grêt-Regamey, 2016). By maintaining or restoring connected landscapes, wildlife can move freely between areas to find food, mates, and suitable breeding grounds. Species can also shift their ranges in response to changing environmental conditions, enabling them to move to more suitable habitats if and when their current habitats become less suitable. There remains a need for more strategic, data-driven approaches to conservation and connectivity planning. Identifying, prioritizing, and protecting essential habitat cores and connectivity areas where interventions like wildlife crossings or corridor restoration are needed is crucial.

2. CASE STUDY BACKGROUND

The project goal is to identify and provide recommendations for improving habitat connectivity within the California central coast region, with a focus on addressing key animal movement barriers. To achieve this goal, the project will pursue the following objectives:

1. Identify and map least-cost corridors and movement barriers for three focal species.
2. Aggregate corridors and identify important overlapping linkage pathways across all species.
3. Recommend restoration and management strategies for improving habitat connectivity in identified barrier areas and around important core areas.

The project conservation target is to ensure that 30% of land within identified corridors is protected. In this analysis, protected lands are classified using the USGS Gap Analysis Project (GAP) Land Definitions. This conservation target aligns with the historic Kunming-Montreal Global Biodiversity Framework, which aims to conserve 30% of the Earth's land and oceans by 2030 (referred to as 30×30). The 30×30 initiative has been widely adopted globally, with nearly every country committing to this conservation goal (Convention on Biological Diversity, 2022; Gallo et al., 2023). Scientists agree that protecting at least 30% of land, freshwater, and oceans by 2030 is essential to addressing the dual crises of biodiversity loss and climate change facing the planet (The Nature Conservancy, n.d.). This widely accepted conservation target will serve as a goal for modeling multi-species wildlife connectivity across the California central coast region.

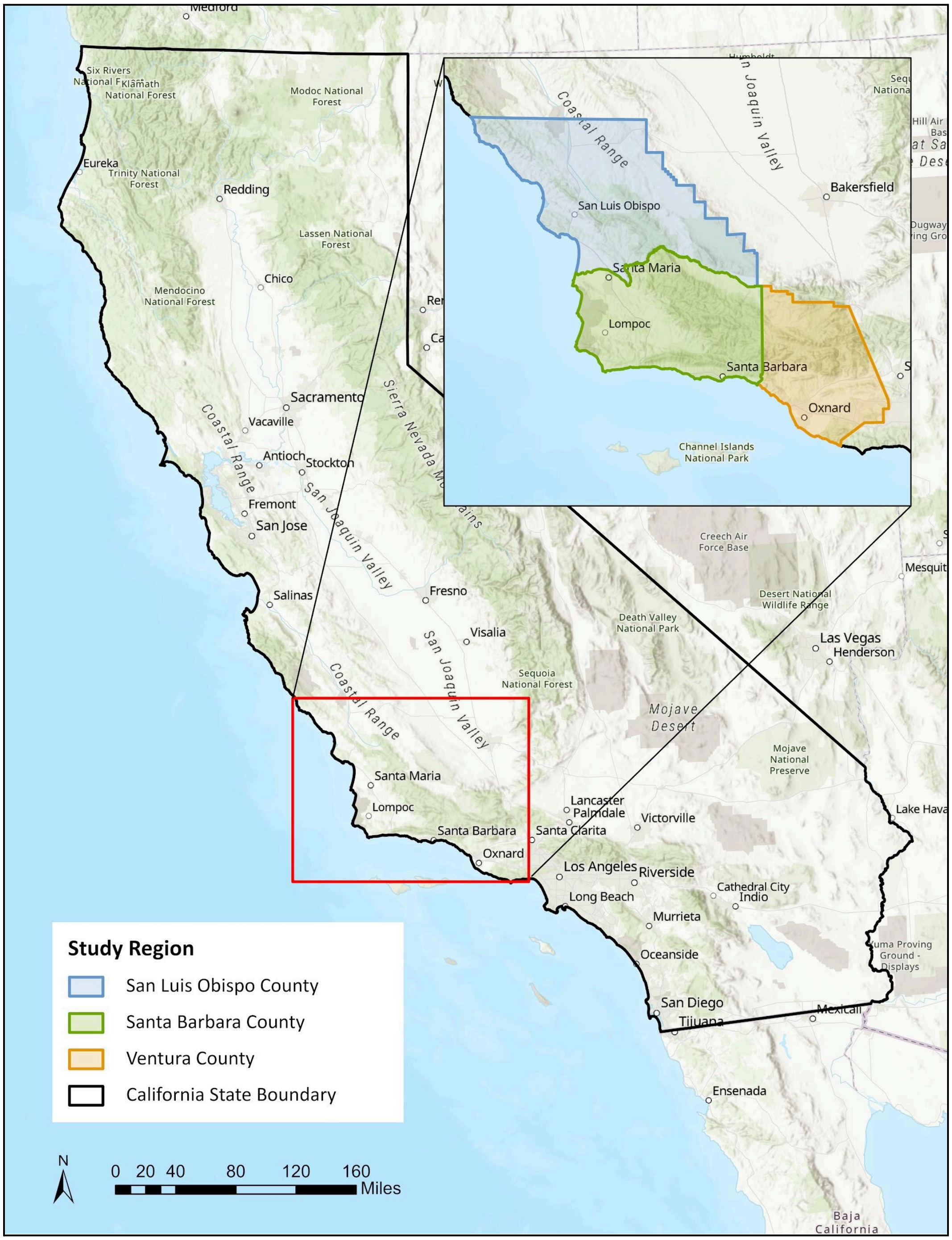

Figure 1. Connectivity Study Region. The extent of the final analyses encompasses San Luis Obispo, Santa Barbara, and Ventura counties within the California Central Coast region.

The project's geographic extent covers three counties within the central coast region—San Luis Obispo, Santa Barbara, and Ventura (Figure 1)—spanning a total area of 7,948 square miles (2,062 square kilometers). This region is home to significant ecological sites including Ellwood Mesa's Monarch Butterfly roosting area, the Jack and Laura Dangermond Preserve, the Guadalupe-Nipomo Dunes, Burton Mesa Reserve, and Sedgwick Preserve, all of which contribute to its ecological richness. The area supports various habitat types, including oak woodlands, mixed-conifer forests, grassland, chaparral, coastal scrub, and riparian habitats, each sustaining a diverse array of unique biodiversity (The Nature Conservancy, 2020).

3. METHODS

3.1 Focal Species

This connectivity analysis includes three focal species: mountain lion (*Puma concolor*), mule deer (*Odocoileus hemionus californicus*), and striped skunk (*Mephitis mephitis*) (Table 1). These species were selected to represent a range of habitat preferences, movement abilities, and ecological roles, ensuring the analysis addresses the connectivity needs of diverse wildlife species in the study region (Meurant, 2018; Breckheimer, 2014).

Mountain lions, an apex predator and flagship species of California's central coast, require large, contiguous habitats. They typically avoid human-dominated landscapes, making them an essential umbrella species for this analysis (Thorne, 2006; Fletcher, 2022). They are highly mobile, preferring open habitats with good visibility, and are particularly sensitive to landscape fragmentation at broader spatial scales (Minor et al., 2010; ICF, 2023).

Mule deer, a mid-sized species with moderate mobility, play a crucial role in maintaining ecological connectivity by moving through various habitats, including edge environments and open landscapes (Kie et al., 2002). Their movement patterns and habitat use make them a key representative of species that rely on medium-scale connectivity corridors.

The striped skunk, a smaller-bodied mammal with moderate mobility, complements the analysis by representing species that move across finer spatial scales and are less sensitive to fragmentation than larger mammals (ICF, 2023). Including this species ensures that the connectivity analysis accounts for wildlife with diverse movement abilities and habitat requirements.

Table 1. List of Focal Species. Focal species chosen for analysis are categorized by taxonomic group, movement type, and selection criteria.

Common Name	Scientific Name	Taxonomic Group	Movement Type	Selection Criteria	Home Range	Citation
Mountain lion	*Puma concolor*	Mammal (carnivore)	Passage	Area sensitive, Barrier sensitive, Umbrella, Flagship, Protected	40 sq. km	(Ahlborn & White, n.d.)

Striped skunk	*Mephitis mephitis*	Mammal (omnivore)	Passage	Barrier sensitive, Dispersal-limited	1 sq. km	(Ahlborn & White, n.d.-b; Rosatte et al., 2011)
Mule deer	*Odocoileus hemionus californicus*	Ungulate (herbivore)	Passage	Barrier sensitive, migratory	7 sq. km.	(Kie et al., 2002)

3.2 Core Areas

Core areas are key locations requiring linkages to support ecological connectivity (Sawyer et al., 2011). Core areas for the connectivity analysis were primarily selected based on the GAP designated protected areas, which represent lands with varying degrees of established conservation measures. These areas were chosen for their size and capacity to support the largest focal species, with the exception of Sedgwick Reserve, which was selected based on known wildlife usage of the reserve. Three patches of California red-legged frog habitat and two units of non-protected natural areas (Gaviota State Park and El Capitan State Beach) that were located in between adjacent protected areas were merged to form contiguous cores. Likewise, smaller protected areas that overlapped with larger ones were merged to form unified core areas.

Table 2. USGS Gap Analysis Project (GAP) Land Definitions.

GAP status code	Definition of land status
1	Areas managed for biodiversity to prevent conversion of natural land cover and maintain a natural state. Natural disturbance events can proceed or are mimicked in the management. (Ex. Wilderness Areas)
2	Areas managed for biodiversity to prevent conversion of natural land cover and maintain a natural state but management practices can degrade natural states and natural disturbance events can be suppressed (Ex. National Wildlife Refuges)
3	Areas having permanent protection from conversion of natural land cover for the majority of the area, but subject to extractive uses. It also confers protection to federally listed endangered and threatened species throughout the area. (Ex. National Forests)
4	Areas with no known mandate for biodiversity protection or conversion of natural habitat. The area generally allows conversion to unnatural land cover throughout or management intent is unknown. (Ex. Agricultural lands)

Stakeholder input was also central to the selection process, ensuring that locally significant areas and management priorities were incorporated. In particular, stakeholders noted the importance of critical habitats within Vandenberg Space Force Base (VSFB). A northern and southern section of VSFB was added to the core areas based on a regional core area analysis by the Conservation Biology Institute (Gatewood et al., 2017). This collaborative approach ensured the core area boundaries aligned with both ecological goals and place-based conservation priorities.

Table 3. List of Core Areas. Merged protected areas are grouped by numeric core area codes 1-10 and are categorized by designation type, managing unit, and GAP status code.

Core Area ID	Unit Name	Designation Type	Managing Unit	GAP Status
1	Santa Lucia Wilderness	Wilderness Area	U.S. Forest Service	1
	Garcia Wilderness	Wilderness Area	U.S. Forest Service	1
	Machesna Mountain Wilderness	Wilderness Area	U.S. Forest Service	1
	Las Piletas Ranch	Private Conservation	The Nature Conservancy	2
2	Carrizo Plain National Monument	National Monument	Bureau of Land Management	2
	Carrizo Plains Ecological Reserve	State Conservation Area	California Department of Fish and Wildlife	2
	Bitter Creek National Wildlife Refuge	National Wildlife Refuge	U.S. Fish and Wildlife Service	2
3	Chumash Wilderness	Wilderness Area	U.S. Forest Service	1
4	Sespe Wilderness	Wilderness Area	U.S. Forest Service	1
	Hopper Mountain National Wildlife Refuge	National Wildlife Refuge	U.S. Fish and Wildlife Service	2
5	Matilija Wilderness	Wilderness Area	U.S. Forest Service	1
6	Dick Smith Wilderness	Wilderness Area	U.S. Forest Service	1
	San Rafael Wilderness	Wilderness Area	U.S. Forest Service	1
7	Sedgwick Reserve	State Conservation Area	University of California	2
8	Vandenberg Space Force Base (Northern)	Military Land	Department of Defense	4
9	Jack and Laura Dangermond Preserve	Private Conservation	The Nature Conservancy	2
	Vandenberg Space Force Base (Southern)	Military Land	Department of Defense	4
10	Gaviota State Park	State Park Recreation	California Department of Parks and Recreation	4
	El Capitan State Beach	State Park Recreation	California Department of Parks and Recreation	4
	Arroyo Hondo Preserve	Private Conservation	Land Trust for Santa Barbara County	2
	Los Padres National Forest	National Forest	U.S. Forest Service	3

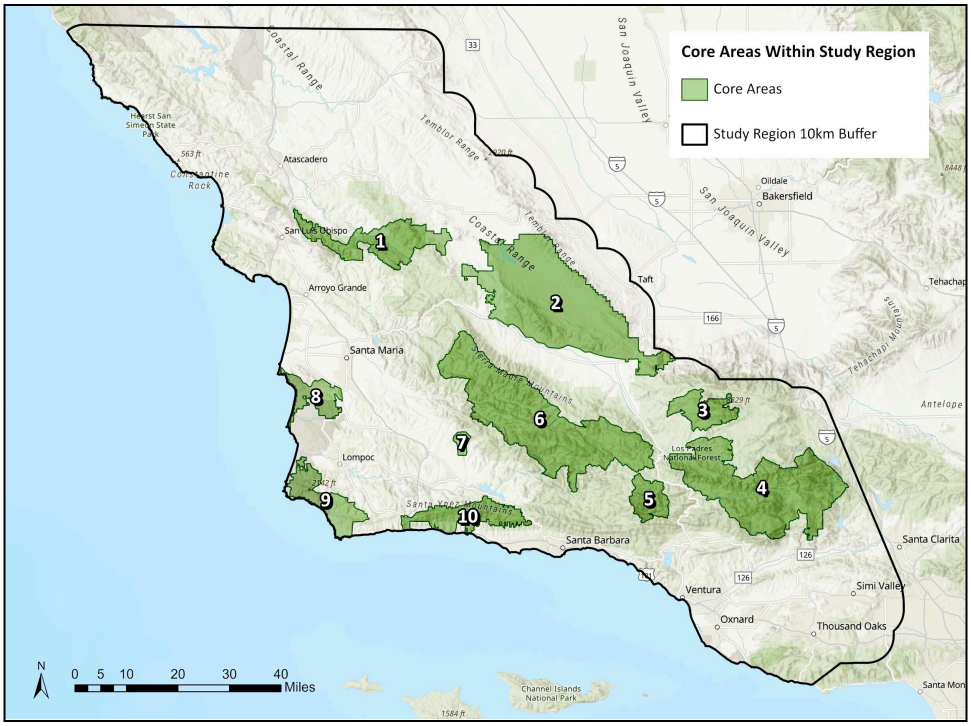

Figure 2. Core Areas Within the Study Region. Core areas shown in green are labeled by the corresponding numeric codes outlined in Table 3.

3.3 Species Occurrence Data and Environmental Variables

Species occurrence data was obtained from the Global Biodiversity Information Facility (GBIF) and filtered using the following criteria: presence records; observation types (machine observation, human observation); date range (1990–2020); geographic location (USA, California); dataset type (iNaturalist research grade); and media type (image).

Environmental predictor variables, including bioclimatic variables (Appendix A), vegetation type, elevation, distance to water, and distance to roads, were prepared in ArcGIS Pro at two resolutions—1 km and 270 m. The 1 km resolution was applied across the entire state of California to capture broad-scale patterns, ensure full geographic coverage, and incorporate more species occurrence points for model robustness. The 270 m resolution was applied only to Southern California, allowing for computationally compatible finer-scale analysis. This approach allows for the comparison of tradeoffs between extent and resolution, with the coarser resolution model incorporating large-scale patterns statewide and the finer resolution model offering more granularity over a smaller geographic area.

Distance to roads inaccurately showed roads as highly suitable habitat for species, most likely due to the nature of citizen-collected data recording species occurrences near roads. This contradicts established ecological knowledge; therefore, distance to roads was excluded from the analysis (van Strien & Grêt-Regamey, 2016).

- ***Bioclimatic variables*** (bioclims) were selected based on previous model calibrations for the same focal species that minimized overfitting (Krause et al., 2015). The four out of nineteen selected variables are BIO 1 (Annual Mean Temperature), which represents the yearly average of monthly temperatures; BIO 4 (Temperature Seasonality), capturing the variation in temperature throughout the year; BIO 12 (Annual Precipitation), which quantifies total precipitation over the year; and BIO 15 (Precipitation Seasonality), reflecting monthly variability in precipitation. 1 km resolution bioclim variables were sourced from WorldClim, while 270 m resolution bioclim variables were generated from the Basin Characterization Model (BCM) statistically downscaled monthly climate rasters (Flint et al., 2021). Monthly maximum temperature, monthly minimum temperature, and monthly precipitation rasters were processed to derive 30-year summaries of the selected bioclim variables from 1990-2020 (Appendix B).

- *Elevation* accounts for topographical influences on species distribution. A 30 arc second (1 km) resolution Digital Elevation Model (DEM) was sourced from WorldClim, and a 7.5 arc-second (250 m) Multi-resolution Terrain Elevation Data Model (GMTED) was sourced from USGS Earth Explorer and resampled to 270 m using bilinear interpolation.

- *Distance to Water* measures proximity to natural and artificial water sources using streamlines from the National Hydrography Dataset. A stream data set (natural perennial and artificial streams) was created from NHD Flowlines and merged with the California Department of Fish and Wildlife (CDFW) California Streams layer to form contiguous segments of selected stream types. The stream dataset was rasterized at 1 km and 270 m resolutions and made binary. Open Water, Woody Wetlands, and Emergent Herbaceous Wetlands were isolated from the 2021 National Land Cover Database, made binary, and merged with the rasterized stream layer. The final water layer was used to create a distance to water raster that calculates the distance of each cell to the nearest perennial water source (Krause et al., 2015).

- *Vegetation Type* categorizes habitat types based on the California Wildlife Habitat Relationships system. The data was obtained from the California Department of Forestry and Fire Protection (CAL FIRE) Fire and Resource Assessment Program (FRAP) which used California's "best available" land cover data, compiled from CDFW's VegCAMP program and USDA Forest Service Management and Analysis for Remote Sensing Laboratory to classify 63 vegetation types covering 1990-2022. The field "WHRNUM" was isolated as the raster value to keep the highest classification level for input into the model.

3.4 Resistance Surface

The resistance layer is critical in connectivity and corridor modeling, estimating the difficulty or "cost" of species movement through the landscape (Keeley et al., 2016). It is derived from habitat suitability models by inverting the suitability values, with areas of high habitat suitability corresponding to low resistance and vice versa. The resistance surfaces represent limitations to movement based on environmental conditions and species-specific ecological needs. These surfaces are inputted into connectivity models that identify the least-cost paths or corridors for species dispersal (Poor et al., 2024).

Species Distribution Modeling

Species distribution models (SDMs) were developed using the maximum entropy (Maxent) algorithm through Wallace, an R Shiny application designed for modeling suitable habitats. Maxent estimates the relative probability of species occurrence across a landscape by contrasting known species presence locations with background environmental conditions (Merow et al., 2013). For each focal species, two spatial resolution scenarios were run: a 1 km resolution model covering the entire state of California and a 270 m resolution model applied to the southern half of the state for computational compatibility. Multiple environmental variable combinations ("scenarios") were tested with both 1 km and 270 m data to examine how the inclusion and exclusion of bioclimatic variables, vegetation, elevation, roads, and distance to water affect model performance. A schematic of the overall workflow from SDM to connectivity analysis can be found in Appendix C.

- Scenario 1: Four bioclimatic variables (annual temperature, annual precipitation, precipitation seasonality, and temperature seasonality), vegetation, elevation, and distance to water.
- Scenario 2: Vegetation, elevation, and distance to water
- Scenario 3: Vegetation and elevation

Species occurrence points were spatially thinned for each species' home range size: striped skunk points were thinned to 1 km, mule deer to 7 km, and mountain lion to 12 km (reflecting the median home range size for female mountain lions). 10,000 background points were randomly generated for both scenarios. Models were evaluated using Checkerboard 2 (K=4) validation, a spatial cross-validation method that partitions occurrence data into bins based on fine- and coarse-grain spatial aggregation (aggregation factor = 2). This approach excludes a subset of training data during calibration and tests the model on the excluded data, providing a robust measure of accuracy while accounting for spatial autocorrelation (Muscarella et al., 2014). Checkerboard 2 was chosen for its ability to achieve spatial independence between training and testing subsets while maintaining a balanced representation of geographic and environmental variation (Mushagalusa et al., 2024). The MaxEnt model was optimized by systematically determining the optimal combination of feature types and regularization multiplier values. Regularization multipliers were tested at intervals of 0.5, ranging from 0.5 to 4, across feature type combinations including L, H, LQ, LQH, and LQHP (L: linear, Q: quadratic, H: hinge, P: product) (Appendix B).

Model performance was assessed using Area Under the Curve (AUC) and response curve analysis. AUC quantifies the model's ability to correctly classify species presence or absence, with values of 0.7 to 0.8 considered acceptable, 0.8 to 0.9 considered excellent, and more than 0.9 considered outstanding (Mandrekar, 2010). Response curve analysis showed the effect of key predictors on species occurrence. While we had a higher AUC for the LQHP feature combination with a regularized multiplier of 0.5, the response curves showed no clear relationship between the modeled suitability and each predictor variable, indicating that this model was overfit. The model with the second-highest AUC, a 270m resolution model with a feature combination of LQ and a regularized multiplier of 0.5, was selected based on its clear response curve relationships.

Resistance Raster Calculation

Habitat suitability surfaces are often inverted to calculate resistance using a linear inverse transformation, assuming that suitability and resistance to movement have a direct inverse relationship. However, this approach oversimplifies species movement behavior. In actuality, species may traverse lower-quality habitats during periods of movement (Keeley et al., 2016). An approach by Keeley et al. (2016) accounts for this by using a negative exponential transformation to convert the habitat suitability values from species distribution models to resistance:

$$Resistance = 100 - 99 \times \frac{((1 - exp(-c * h))}{(1 - exp(-c))},$$

where h is the habitat suitability value (0 to 1), and c is the scaling parameter. C values closer to 1 indicate a near-linear relationship between suitability and resistance, while increasing c values generate an increasingly nonlinear negative exponential function of suitability (Keeley et al., 2016; Poor et al., 2020). A non-linear c-value of 4 was applied for all species, based on the approach outlined in Jennings et al., 2020 and in comparison to previous studies using this method of approximating resistance (Ianella et al., 2024; Wang et al., 2024).

3.5 Connectivity Analysis

Connectivity modeling often relies on least-cost path analysis, which assumes animals have perfect knowledge of the landscape and travel along a single optimal route that minimizes movement costs (Williamson et al., 2020). This study applies the least-cost corridor methodology outlined by Beier et al. (2007) to identify potential wildlife movement pathways. This approach identifies least-cost corridors—routes offering the lowest resistance to movement—for each focal species between core habitat areas. Resistance rasters, representing the relative difficulty of movement across the landscape, and core habitat patches, critical for maintaining connectivity, served as key inputs. The analysis encompassed San Luis Obispo, Santa Barbara, and Ventura counties.

Circuitscape

Circuitscape, run through the Linkage Mapper Toolbox in ArcGIS Pro, was used to model least-cost corridors to identify connectivity pathways between core habitat areas. A network of potential linkages was constructed using adjacency data, calculated cost-weighted distances, and least-cost paths between core pairs. Least-cost corridors were then calculated and normalized to compare the relative movement cost across pathways. These corridors were mosaicked to produce a composite linkage map. Corridors that exceeded a species-specific cost-weighted distance threshold were truncated to maintain biological accuracy based on their home range size.

After mapping the corridors, a Barrier Mapper analysis was conducted to identify significant barriers affecting the quality and placement of the corridors. The inputs included the resistance rasters and the cost-weighted distance raster generated from the completed Linkage Pathways analysis. Additionally, a barrier detection radius of 1000m was specified, detecting barriers up to 2km across (McRae, 2012). Centrality Mapper was used to analyze the resulting linkage networks and calculate current flow centrality across the network. This analysis helped determine the importance of each core area in maintaining overall network connectivity (McRae, 2012).

Multi-species Aggregation

The three species corridors and least-cost paths were combined to form a least-cost corridor and least-cost path union, which allows for the identification of important habitat for all focal species to move between core areas (Krause et al., 2015). Redundant corridors were removed based on species overlap, resulting in cleaner linkage areas. The aggregated corridors were then evaluated to determine the number of species per linkage, elevational range, and vegetation cover. The attributes of the vegetation layer clipped to the corridors were exported for statistical analysis in RStudio (Appendix B).

4. RESULTS

4.1 Habitat Suitability

The 270 m resolution model scenario including all predictor variables (Scenario 1), a feature combination of LQ, and a regularized multiplier of 0.5 generated the AUC values in Table 4, which indicates excellent performance by the model. Habitat suitability from the SDMs generally align with CDFW predicted habitat for each species (CDFW Interagency Wildlife Task Group, n.d.). Highly suitable habitat is defined by the suitability threshold 0.67-1 and moderately suitable habitat is defined by a 0.34-0.66 threshold. Of the total modeled habitat area, 26% of habitat (5,229,912 ha) is considered highly or moderately suitable for the mountain lion, 19% (3,345,301 ha) for the striped skunk, and 36% (6,027,037 ha) for mule deer. Of the modeled habitat area within the buffered study region (2,093,484 ha), 62% of habitat (1,302,176 ha) is considered highly or moderately suitable for the mountain lion, 47% (987,970 ha) for the striped skunk, and 69% (1,448,093 ha) for mule deer. Species distribution models with habitat suitability thresholds are displayed in Appendix D.

Table 4. Area Under the Curve (AUC) Values Per Species Distribution Model.

Species	Mule Deer	Striped Skunk	Mountain Lion
AUC Value	0.84	0.89	0.87

4.2 Least-Cost Corridor Analysis

Results of the least-cost corridor analysis show both similar and varying patterns across the focal species. The least cost corridors consisted of 20 mountain lion corridors, 27 striped skunk corridors, and 17 mule deer corridors, with many species corridors overlapping.

Mountain Lion

Several least-cost paths from coastal cores travel through intermediate cores to reach central cores (Figure 3). For example, the least-cost path from Core 8 travels through Core 6 to reach Core 7 rather than traveling directly. Although these direct corridors have higher cost-weighted distance values and do not contain a least-cost path, they are still important for considering all possible species movement pathways. The widest mountain lion corridors are located around the Santa Ynez Foothills (Core 10) to areas of Los Padres National Forest (Cores 4, 5, 6) and the Jack and Laura Dangermond Preserve (Core 9), providing more opportunities for movement between these core areas (Figure 3). Corridors are narrowest at linkages to Core 2 (Carrizo Plains), which coincides with barrier centers with the highest improvement score (Figure 3).

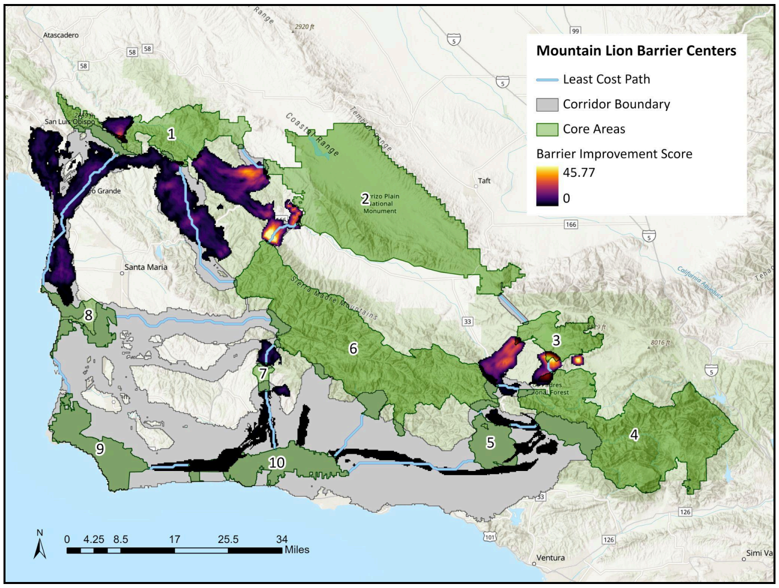

Figure 3. Mountain Lion Barrier Centers Between Core Areas. Areas with high barrier improvement scores are located in yellow at the western edge of Carrizo Plains (Core 2) and south of Chumash Wilderness (Core 3).

Striped Skunk

Least-cost paths for the striped skunk align closely with the truncated corridors (Figure 4). Striped skunks travel more directly between core areas, reflecting their wider range of suitable habitat. The widest corridors are located between the Santa Ynez Foothills (Core 10) to sections of Los Padres National Forest (Cores 4, 5, 6), indicating more movement opportunities between these core areas. The narrowest corridors are linkages to Core 2 (Carrizo Plains), which coincides with barrier centers with the highest improvement score (Figure 4).

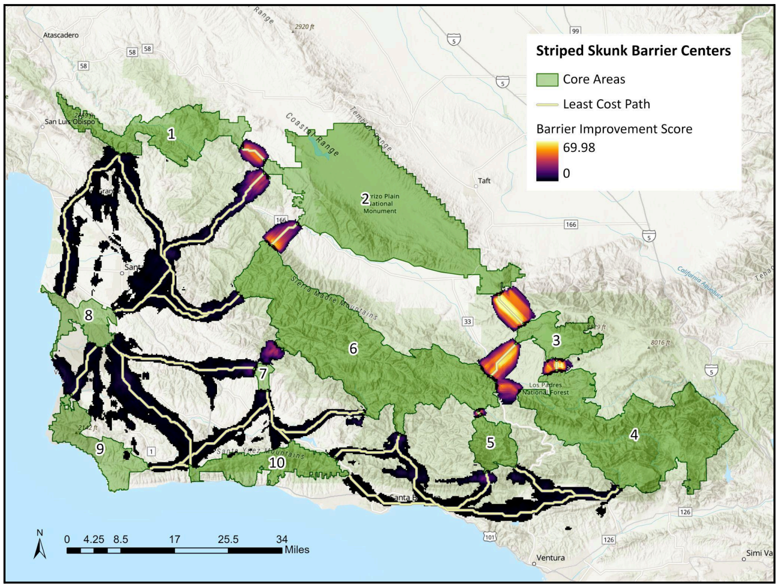

Figure 4. Striped Skunk Barrier Centers Between Core Areas. Areas with high barrier improvement scores are located in yellow in linkages from Core 3 to adjacent cores. Corridor boundaries aligned closely with the least cost path and are not shown for clearer visualization.

Mule Deer

Mule deer had the fewest number of least-cost paths and corridors (14). Compared to the other focal species, the mule deer's modeled connectivity travels through more intermediate cores to reach the central Los Padres National Forest Core (Core 6). The widest and narrowest corridors are located in the same areas as the mountain lion and striped skunk, between the Santa Ynez Foothills and Los Padres National Forest, and linkages to Carrizo Plains, respectively (Figure 5). Minimal barrier centers are located within the widest corridor. In contrast, the narrow corridors coincide with barrier centers with high improvement scores (Figure 5).

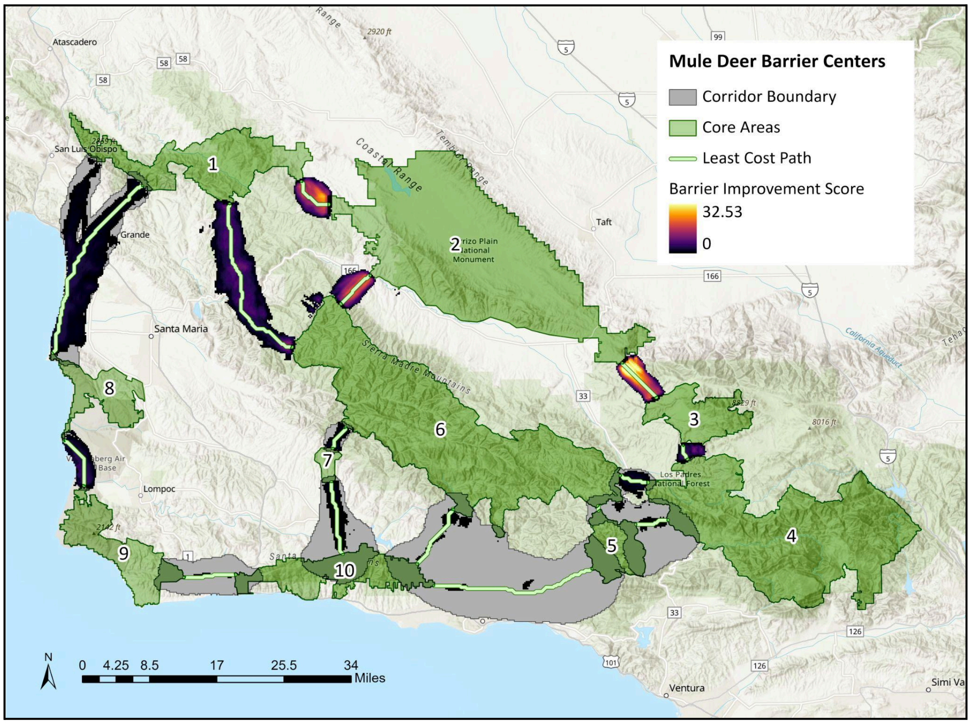

Figure 5. Mule Deer Barrier Centers Between Core Areas. The area with the highest barrier improvement score is highlighted in yellow between Cores 2 and 3.

Aggregate Connectivity

The area of the least-cost corridor union totals 450,881.64 hectares. Protected areas make up 11.24% of the aggregated corridors (50,688.92 ha). The linkages range in elevation from 119 m to 32,767 m. Linkages also cover a variety of vegetation types; for the total area of linkages, 52.5% were in shrub, 17.1% in herbaceous, and 16.4% in hardwood woodland (Figure 6). Aggregated corridors and least-cost paths show clusters of distinct least-cost paths in the widest corridor area between the Santa Ynez Foothills (Core 10) to sections of Los Padres National Forest (Cores 4, 5, 6), indicating this corridor as significant to overall species movement (Figure 7).

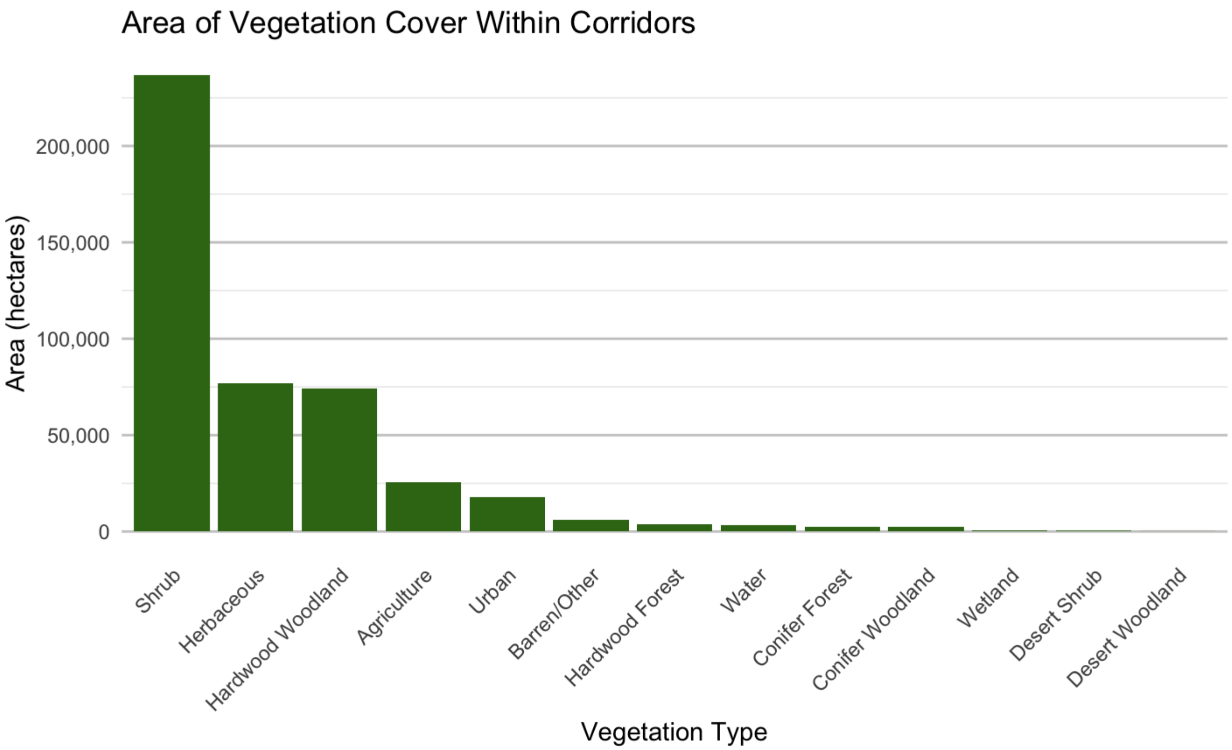

Figure 6. Area of Vegetation Cover within Corridors. Shrub vegetation was the dominant vegetation type within the aggregated corridors while desert vegetation covered the least amount of area.

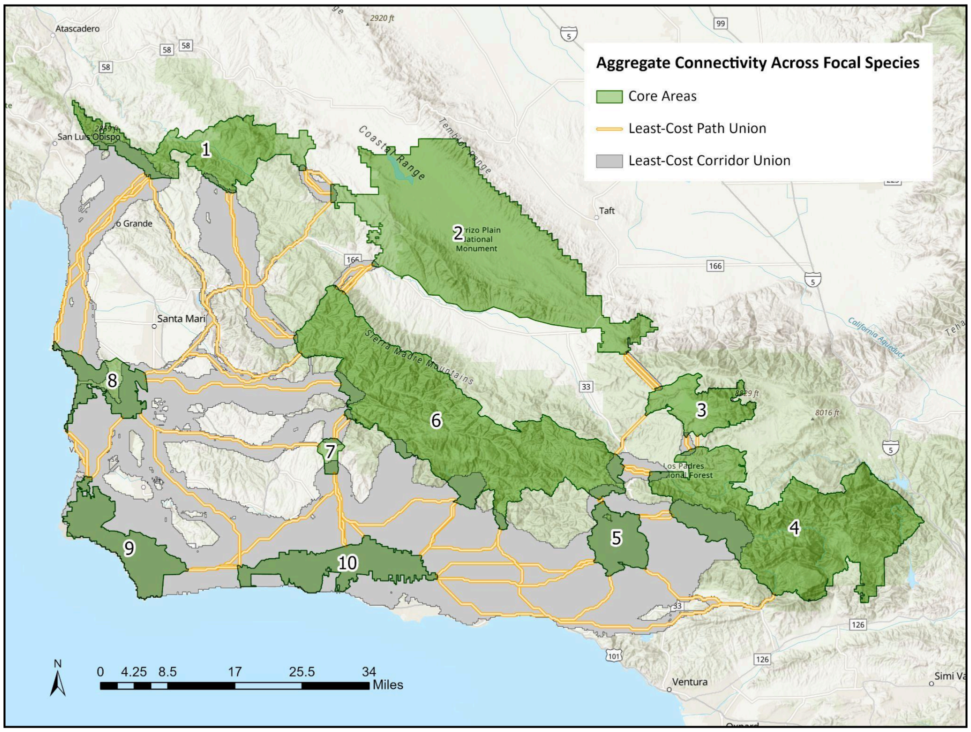

Figure 7. Least-Cost Corridor and Least-Cost Path Union Across Focal Species. A union of least-cost paths (orange) and corridors (grey) show significant overlap between species movement paths.

For many linkages, there was an overlap in the corridors of two species (Figure 8). There are significant linkages between Cores 1 and 2, 2 and 3, and 5/6/7 and 10 in which all three focal species utilize a portion of the corridor. Mule deer and mountain lions share several linkages between core areas, signifying the potential of these umbrella species to include other non-focal species within their corridors.

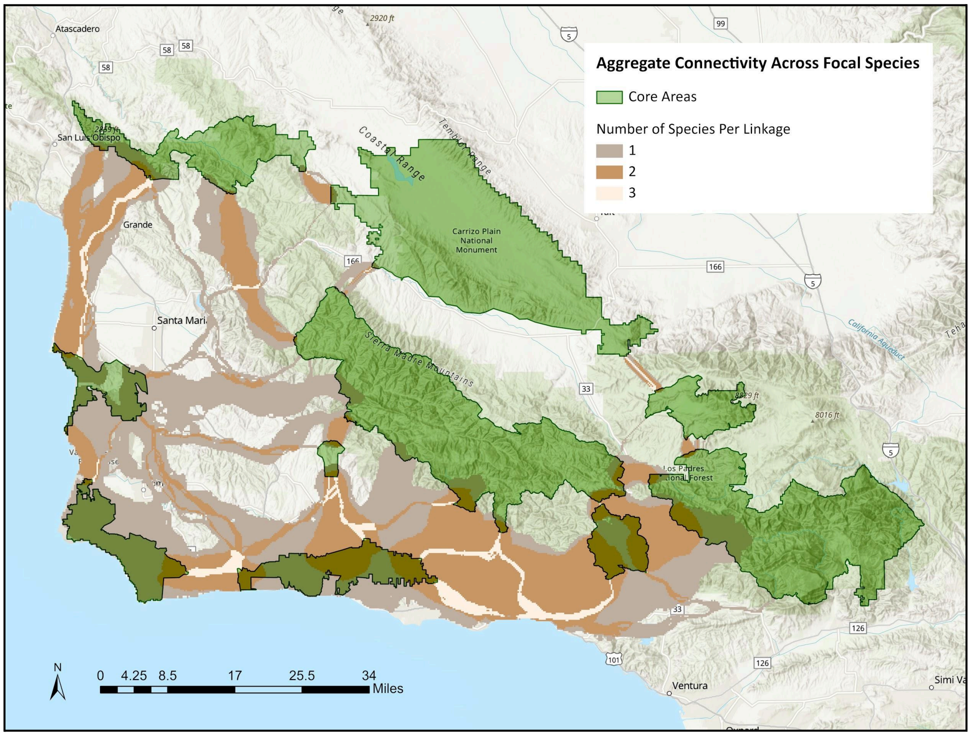

Figure 8. Aggregate Connectivity Across Focal Species. Aggregated corridors show the number of species using each linkage, with significant overlap between two out of three focal species in several corridors.

4.3 Centrality Analysis

Centrality analysis gave further insight into the importance of each core area in keeping the overall network connected. The resulting top current flow centrality scores highlight Core 7 (Sedgwick Reserve) and Core 8 (North Vandenberg) as the most important core areas for mountain lion connectivity. Core 6 (Dick Smith Wilderness and San Rafael Wilderness of Los Padres National Forest) was the most important core area for striped skunk and mule deer connectivity and had the highest average centrality score among all three focal species. These cores act as a “hub” for keeping the network connected and their loss would disconnect more than one core area from the rest of the network. Core areas with the lowest current flow centrality score were Core 3 (Chumash Wilderness) for striped skunk and mule deer connectivity and Core 2 (Carrizo Plains) for mountain lion connectivity. Core 2 had the lowest average centrality score across the focal species. These cores have the fewest linkages to other core areas and are least important for maintaining overall network connectivity. This reflects the notion that centrally located patches generally have higher centrality scores than those located at the boundary since connecting edge patches usually require a current to flow through the central patch (Carroll et al., 2011).

Table 6. Core Area Centrality Scores By Species Connectivity Analysis. Lowest scores per species analysis are highlighted in red and highest scores are highlighted in green.

Core Area	Centrality Score (mountain lion)	Centrality Score (striped skunk)	Centrality Score (mule deer)	Average Centrality Score
1	17.359475	13.145373	13.546235	14.68369433
2	9.567645	12.779852	12.751228	11.699575
3	15.347022	11.872093	11.945536	13.05488367
4	12.153129	15.077434	18.700971	15.31051133
5	15.347022	17.008113	20.367052	17.57406233
6	13.363856	26.271274	29.748672	23.127934
7	20.739633	13.347689	12.316616	15.46797933
8	20.644018	18.818768	13.377692	17.61349267
9	12.462958	14.543695	18.294121	15.100258
10	18.050184	21.245419	24.407664	21.23442233

5. DISCUSSION

5.1 Recommendations

Identifying key habitats and corridors is only the first step in conserving biodiversity and maintaining wildlife connectivity at a landscape scale. Equally important are stewardship and adaptive management, which are essential for creating resilient and functional landscapes. Currently, protected areas account for only 11.24% of the aggregate corridors, falling short of the project's conservation target of protecting 30% of land within these corridors. Protected status ensures proper land management to support species' well-being. Corridor linkages that are utilized by all 3 focal species should be prioritized for future conservation and protection status. These areas include linkages between Cores 1 and 2, 2 and 3, and 5/6/7 and 10 (Figure 8). The most critical core areas for mountain lion connectivity are Core 7 (Sedgwick Reserve) and Core 8 (North Vandenberg), while Core 6 (Dick Smith Wilderness and San Rafael Wilderness in Los Padres National Forest) is vital for striped skunk and mule deer. The continued conservation and proper management of these core areas is crucial for maintaining overall species connectivity, as the loss of these areas would disrupt the entire network.

Restoration efforts should be focused on areas with high barrier improvement scores. For all 3 focal species, the linkages between Core 2 (Carrizo Plains) and Core 6 (Dick Smith Wilderness and San Rafael Wilderness of Los Padres National Forest) as well as linkages between wilderness areas within Los Padres Forest (Cores 3, 4, and 6) had the highest barrier improvement scores. Common restoration strategies to improve and maintain wildlife corridors include reestablishing native vegetation and managing invasive species to improve overall quality of species habitat. Additionally, physical barriers can be mitigated by installing wildlife-friendly infrastructure such as culverts, underpasses, and overpasses that allow safe movement across roads and other anthropogenic structures. These combined efforts help facilitate connectivity, reduce fragmentation, and support the long-term viability of wildlife populations.

5.2 Limitations

Due to data limitations, this analysis was not conducted under future climate scenarios, which is useful for predicting shifts in habitat suitability and species movement corridors under climate change. Climate change is expected to cause significant ecological changes, including altered species distributions, migration patterns, and ecosystem dynamics. Species are projected to shift their ranges even under modest warming scenarios, and barriers to movement or limited dispersal may exacerbate population declines and increase extinction risks (Littlefield et al., 2017). Without incorporating long-term climate trends, conservation efforts risk prioritizing areas that may no longer support species in the future. Integrating projections of range shifts into conservation planning is essential for species protection and resilience (Littlefield et al., 2017).

Additionally, this analysis relied on static habitat and corridor models, which assume species presence data reflects true distributions, that these distributions remain consistent with environmental factors, and that the appropriate predictors are included (Franklin, 2010). However, these models do not account for dynamic environmental changes over time, limiting their ability to capture temporal variability induced by climate change. A dynamic modeling approach could enhance predictions by accounting for the combined impacts of climate change, land use alterations, and shifting disturbance regimes (Franklin, 2010; Littlefield et al., 2017). This would provide a more accurate reflection of species distributions and ecological dynamics in a changing climate.

Other data quality and availability limitations include a lack of higher-resolution climate data that would allow for more precise modeling of species distribution at finer regional scales. Data that was developed at 30 m resolution had to be resampled to match coarser 270 m resolution climate data for this analysis. Additionally, species occurrence points, collected from research-grade citizen science observations, are often spatially clustered around areas with high human activity, such as recreational areas and roads, rather than being naturally distributed across the landscape. This can introduce sampling bias into the SDMs and connectivity analysis by potentially underestimating or misrepresenting the importance of less-sampled but ecologically significant areas.

Due to this observed sampling bias and the exclusion of distance to roads as an environmental predictor variable, roads were not included in this analysis but are an important factor in accurately assessing connectivity. Roads can act as barriers to movement for many species and can influence connectivity by fragmenting habitats, altering animal movement patterns, and increasing mortality risk through vehicle collisions (Riley et al. 2014). This exclusion could lead to corridors appearing more continuous than they actually are, causing an overestimation of connectivity in areas intersected by roads.

5.3 Future Research

The findings and limitations of this study present several opportunities for future research. Empirical studies are necessary to assess whether the modeled corridors are actively used by the focal species. This ground-truthing is often done by deploying GPS collars or tags on target species to track their actual movement patterns across the landscape. Camera traps and genetic sampling can complement collaring studies by confirming the presence of species utilizing the corridors and assessing whether gene flow between populations is indicative of successful connectivity (Calderón et al., 2024). Field surveys can also help to identify physical barriers, anthropogenic activity, and habitat quality not accounted for in the model. These surveys can also inform movement feasibility in urban areas and which intervention strategies are most appropriate to improve connectivity in identified barrier areas (i.e. culverts, wildlife crossings).

Additional modeling can also enhance the findings of this study. Mapping pinch points in the corridors can inform where there are potential constrictions to movement, or “bottlenecks.” Similar fine-scale connectivity assessments have also conducted a land facet analysis to model and identify corridors of topographic similarity that may provide resilience to climate change (Krause et al., 2015). Furthermore, incorporating additional species in this analysis will enhance model robustness by capturing a wider range of ecological requirements, movement behaviors, and habitat needs, leading to corridors that better reflect diverse species interactions and ecosystem dynamics. This should include corridor species as well as passage species, which move through corridors across generations.

Methods for integrating roads into the analysis should also be investigated and tested. One possible approach is to create a separate resistance layer that assigns resistance values for distance to roads. Assignment of resistance values is often informed by a combination of expert opinion and empirical data (Wade et al. 2015). This layer can be combined with the resistance surface generated from the SDMs through weighted averaging to give more weight to the SDM-derived resistance layer while still ensuring a meaningful contribution of road resistance. Similarly, high human density areas may be unsuitable for wildlife habitat and movement. To account for this and aid in the selection of continuous corridors, urban areas can be delineated with census block housing density maps or impervious surface maps and masked from the corridors (Krause et al. 2015).

Lastly, a comparison of the modeled linkages to other conservation project data can inform how well the connectivity analysis captured regional conservation priorities. This can help integrate place-based significance into the model and ensure that stakeholder conservation goals are complemented by wildlife corridor restoration and management.

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Appendix

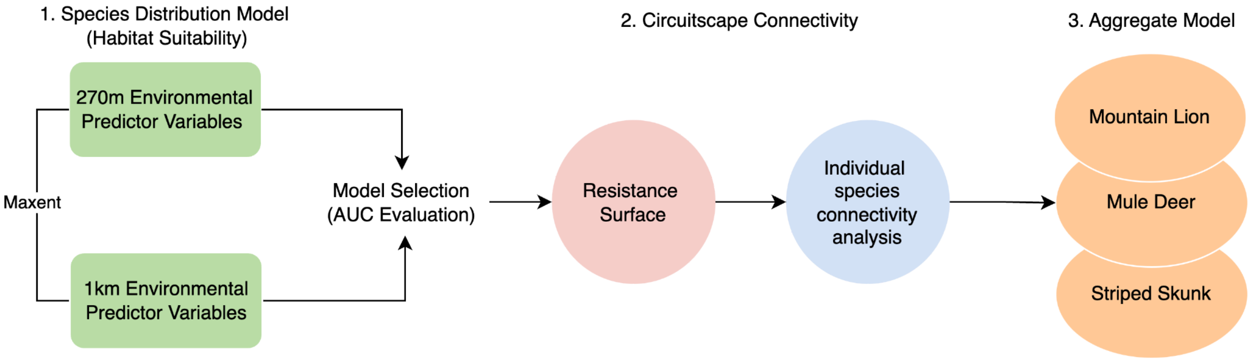
Appendix A. WorldClim Bioclimatic Variable Codes.

Code	Bioclimatic Variable
BIO1	Annual Mean Temperature
BIO2	Mean Diurnal Range
BIO3	Isothermality
BIO4	Temperature Seasonality
BIO5	Max Temperature of Warmest Month
BIO6	Min Temperature of Warmest Month
BIO7	Temperature Annual Range
BIO8	Mean Temperature of Wettest Quarter
BIO9	Mean Temperature of Coldest Quarter
BIO10	Mean Temperature of Warmest Quarter
BIO11	Mean Temperature of Coldest Quarter
BIO12	Annual Precipitation
BIO13	Precipitation of Wettest Month
BIO14	Precipitation of Driest Month
BIO15	Precipitation Seasonality
BIO16	Precipitation of Wettest Quarter
BIO17	Precipitation of Driest Quarter
BIO18	Precipitation of Warmest Quarter
BIO19	Precipitation of Coldest Quarter

Appendix B. GitHub Repository.

All code used in this report is hosted in a GitHub repository publicly accessible here: https://github.com/thuy-tienbui/connect-conserve.git

Appendix C. Modeling Workflow Diagram.



Appendix D. Species Distribution Models.

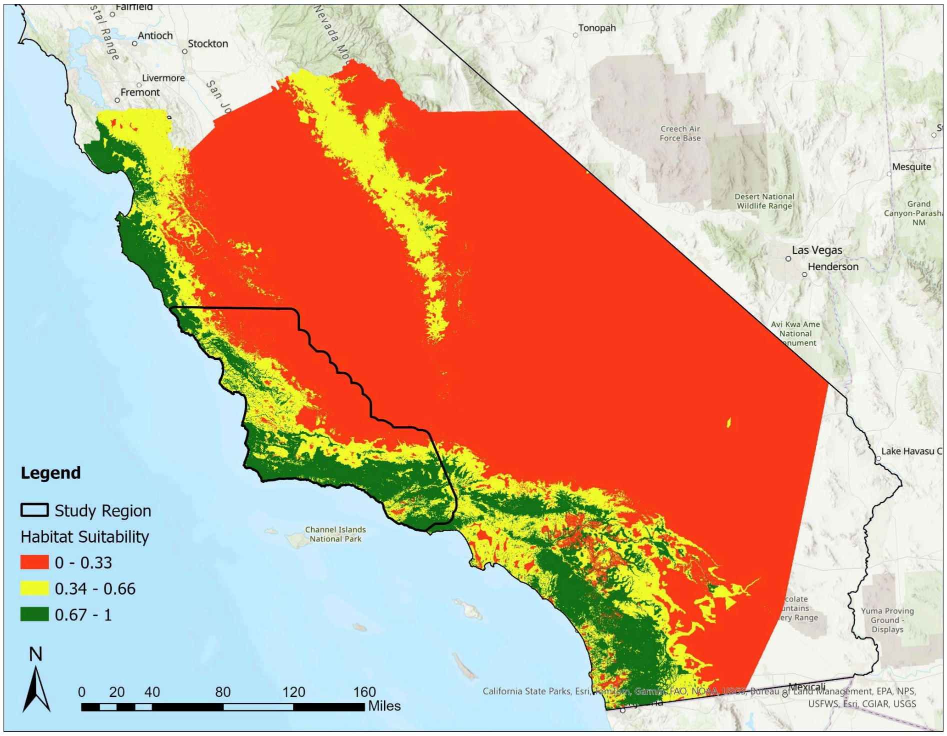


Figure D1. Mountain Lion (*Puma concolor*) Species Distribution Model. Green represents highly suitable habitat (0.67-1), yellow is moderately suitable (0.34-0.66), and red is low suitability (0-0.33). The study region contains 694,780.74 ha of highly suitable habitat.

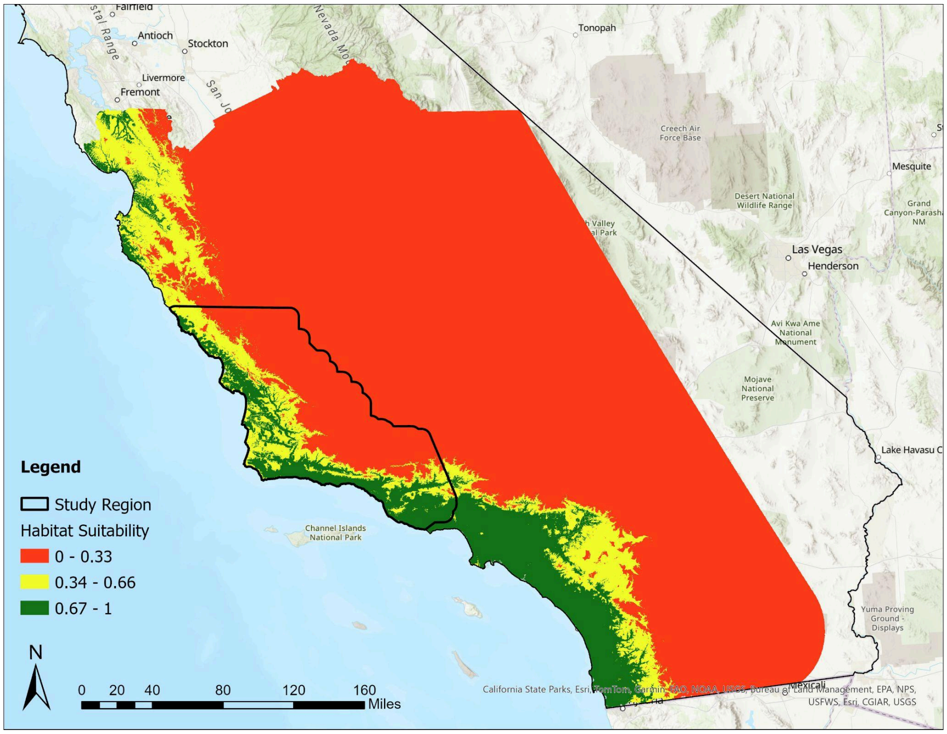


Figure D2. Striped skunk (*Mephitis mephitis*) Species Distribution Model. Green represents highly suitable habitat (0.67-1), yellow is moderately suitable (0.34-0.66), and red is low suitability (0-0.33). The study region contains 495,625.23 ha of highly suitable habitat.

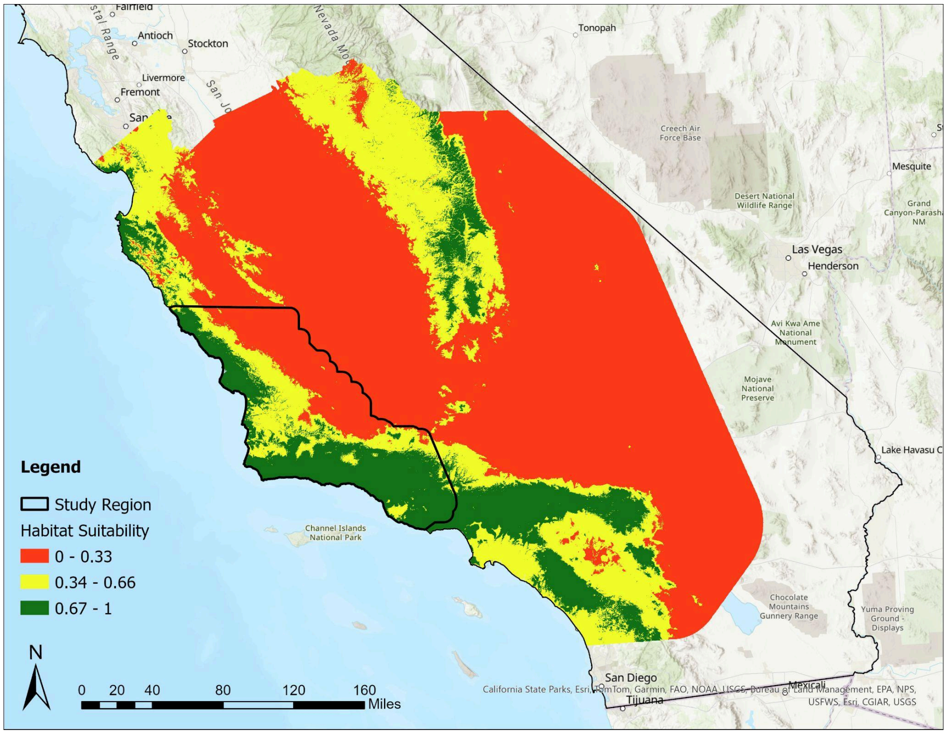


Figure D3. Mule Deer (*Odocoileus hemionus californicus*) Species Distribution Model.Green represents highly suitable habitat (0.67-1), yellow is moderately suitable (0.34-0.66), and red is low suitability (0-0.33). The study region contains 910,316.88 ha of highly suitable habitat.

Appendix E. Species Cost-Weighted Corridor Maps

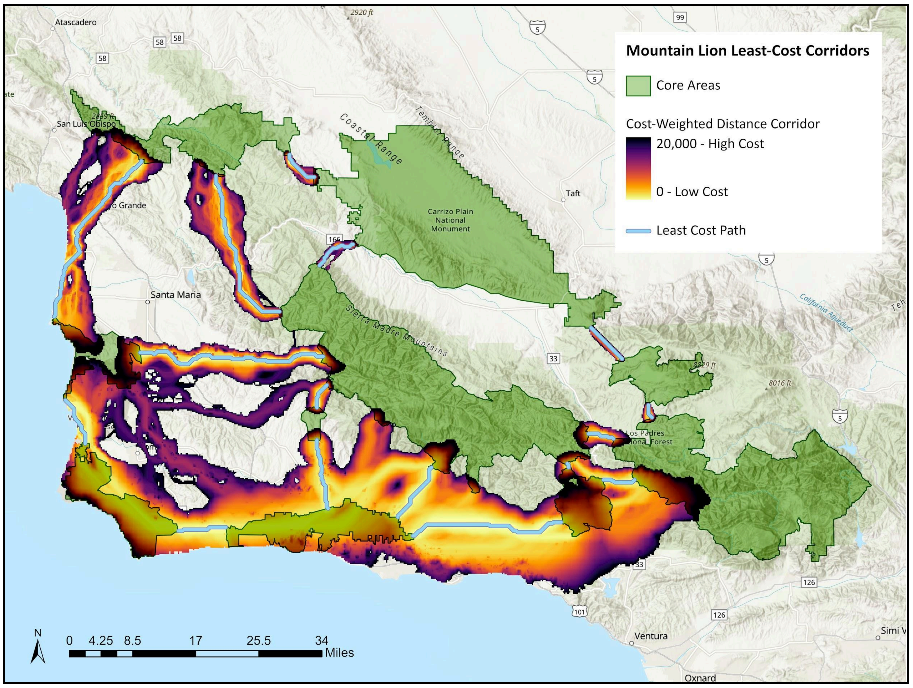


Figure E1. Mountain Lion Corridors and Least-Cost Paths Between Core Areas. Least-cost paths travel through areas of the corridor with the lowest movement difficulty along the total path from core to core (yellow regions).

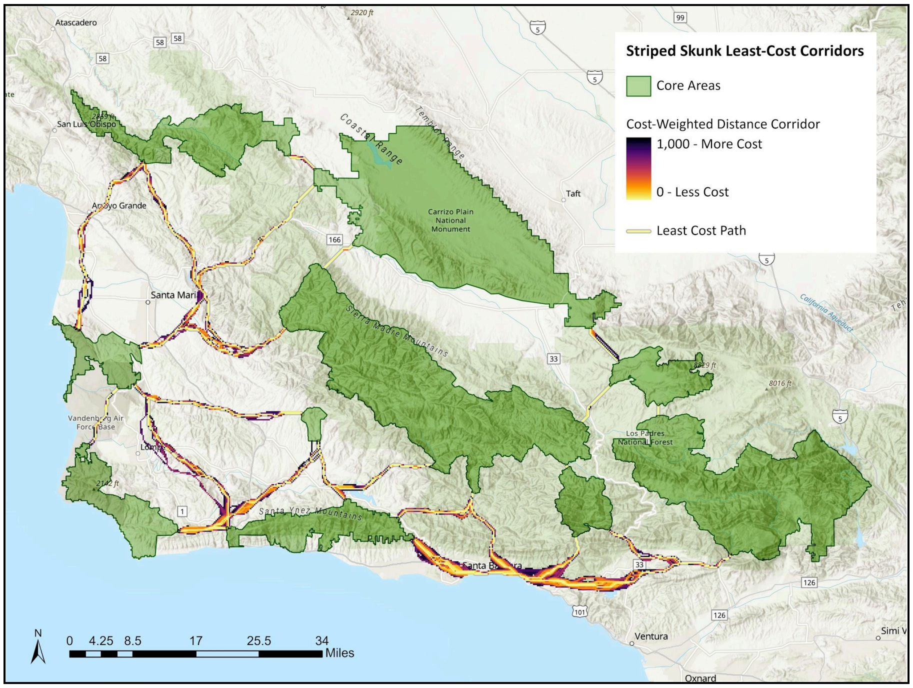


Figure E2. Striped Skunk Corridors and Least-Cost Path Between Core Areas. Least-cost paths travel through areas of the corridor with the lowest movement difficulty along the total path from core to core (yellow regions).

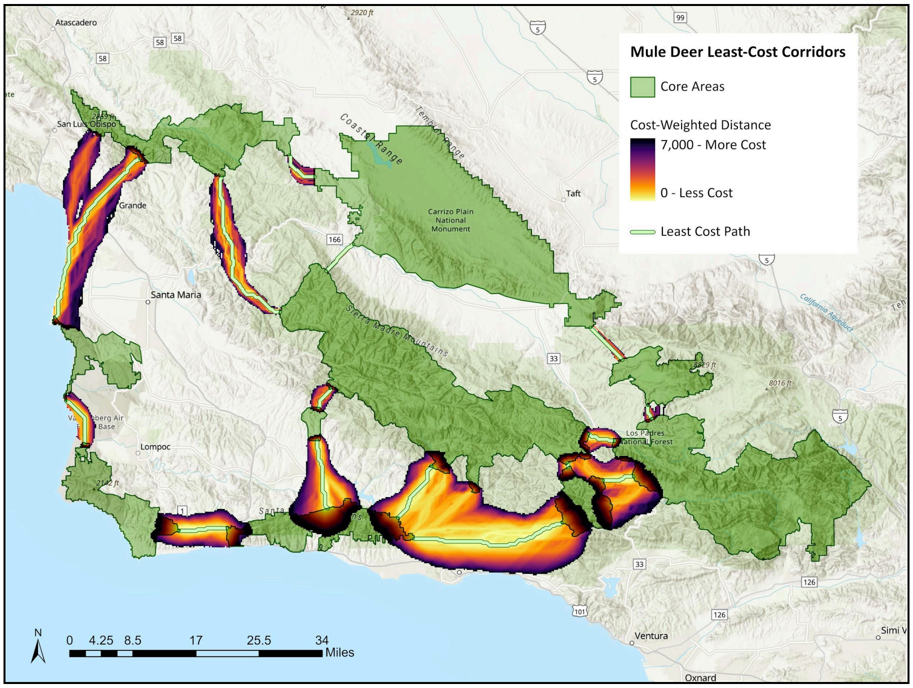


Figure E3. Mule Deer Corridors and Least-Cost Paths Between Core Areas. Least-cost paths travel through areas of the corridor with the lowest movement difficulty along the total path from core to core (yellow regions).

Appendix F. Data Sources Table.

The datum for all data is NAD83 with the exception of data at the global extent, which is in WGS84. All data is publicly available.

Name	Source	Format	Date Published	Spatial Extent	Resolution
7.5 Arc Second Global Multi-resolution Terrain Elevation Data Model (GMTED)	USGS Earth Explorer	Raster GeoTIFF	2010	Western United States	250m
30 Arc Second Digital Elevation Model (DEM)	WorldClim	Raster GeoTIFF	2017	Global	1km
California Vegetation by Wildlife Habitat Relationship Type	CAL FIRE FRAP	Raster GeoTIFF	2022	California	30m
California County Boundaries	CAL FIRE FRAP	Vector/Line Shapefile	2023	California	NA
TIGER Primary and Secondary Roads	USDA Geospatial Data Gateway	Vector/Line Shapefile	2020	California	NA
TIGER Streets	USDA Geospatial Data Gateway	Vector/Line Shapefile	2020	California	NA

National Land Cover Dataset (NLCD)	Multi-Resolution Land Characteristics (MRLC) Consortium	Raster GeoTIFF	2021	Western United States	30m
Protected Areas Database of the United States (PAD-US)	USGS Gap Analysis Project	Geodatabase	2021	California	NA
California Streams	CDFW Open Data	Vector/Line Shapefile	05-10-16	California	NA
National Hydrography Dataset	USGS National Map	Vector/Line Shapefile	2023	California	NA
WorldClim Bioclimatic Variables	WorldClim	Raster GeoTIFF	01-2020	Global	1km
Basin Characterization Model Climate Inputs 1896-2020	USGS ScienceBase	Raster GeoTIFF	05-29-2024	California	270m
Species Occurrence Points	Global Biodiversity Information Facility	Vector/Line Shapefile	Ongoing	Global	NA
CDFW Species Predicted Habitat	Biogeographic Information and Observation System (BIOS)	Raster GeoTIFF	03-02-2017	California	30m
Land Trust for Santa Barbara County Core Areas	Conservation Biology Institute	Vector/Line Shapefile	04-20-2018	Santa Barbara County	NA