Guidance Document for Fine-Scale Wildlife Connectivity Analysis

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I. Introduction

PURPOSE: This report is intended as a guidance document for California Department of Fish and Wildlife (Department) staff undertaking or reviewing a fine-scale wildlife connectivity analysis. The goal of such an analysis is to develop transparent, repeatable, data driven decision support tools to identify habitat connectivity areas to prioritize for conservation. Here we define a "fine-scale connectivity analysis" as a GIS-based corridor analysis using fine-scale landscape or vegetation base data (e.g., with a minimum mapping unit of 10 acres or smaller), using a raster cell size of <500 m, and connecting landscape blocks with a minimum block size of 100 ac.

BACKGROUND: Natural resource conservation and planning is a critical responsibility of the Department (https://www.wildlife.ca.gov/Explore.aspx) and identifying and mapping essential wildlife corridors and habitat linkages (Fish & Game Code 1930.5) is one component of this. Habitat loss and fragmentation are major threats to plant and animal communities across the globe (Buchmann *et al.* 2013). Identifying areas of high quality habitat and connectivity are essential to maintain viable populations in the future (Gilpin 1987). **Habitat connectivity** provides paths for movement across the landscape and is important for species to find food, cover and mates. Habitat connectivity can be achieved through the identification and conservation of **corridors**, specific movement paths. Corridors can be taken together to build a **linkage**, which provides ecological connectivity and movement paths for multiple species through an area. Habitat connectivity is particularly important for wide-ranging species or those that seasonally migrate (Thorne *et al.* 2006). Connectivity is also very important for adaptation to climate change to allow for species to move as habitat changes (Noss 1991). Barriers to connectivity include roads, development, and habitat conversion. Roads can result in high levels of mortality for some species (Riley *et al.* 2006; Meese *et al.* 2009). Development and habitat conversion can also impede movement across the landscape. A fine scale wildlife connectivity analysis incorporates information of species habitat and area needs with dispersal ability and landscape barriers to identify high quality habitat and linkage areas across the landscape.

This report includes examples from our case study analysis of wildlife connectivity across the northern Sierra Nevada foothills. Additional information on methods and analysis, as well as example code, can be found in the project report [`https://nrm.dfg.ca.gov/FileHandler.ashx?DocumentID=85358`] and on our website http://www.dfg.ca.gov/biogeodata/projects/connectivity.asp.

COMPONENTS OF THE ANALYSIS: We identified **wildlife linkages,** based on individual species habitat corridors for a set of focal species representative of the study area, as the main component of a wildlife connectivity analysis. **Riparian connections**, which provide important movement corridors to wildlife, particularly in developed areas (Hilty & Merenlender 2004); and **land facets**, corridors of topographically similar units (e.g., canyons, ridges) that address potential movement paths in the face of climate change (Beier & Brost 2010), can supplement wildlife linkages to capture other ecologically important connectivity areas. Taken together, provide a full spectrum of corridors to provide connectivity for wildlife in all habitat types and in areas with different levels of human impact. In some habitat types or areas of the state, additional consideration may need to be given to ecological processes that require movement across the landscape to maintain wildlife habitat such as transport of nitrogen from oceans inland (Helfield and Naiman 2001) or transport of sediment or sand (Griffiths *et al.* 2002).

We identified the following steps to complete a fine-scale connectivity analysis:

I. Define study area and scale of analysis
    a. Consider geographic context
    b. Define and identify landscape blocks
    c. Define minimum corridor width
II. Wildlife corridor component
    a. Select focal species
        i. Species selection criteria
        ii. Considerations for different taxonomic groups
    b. Develop data driven habitat models for focal species
    c. Apply urban mask
    d. Identify habitat patch size, configuration and dispersal distance variables for each species and develop habitat patch analysis
    e. Perform corridor analysis to identify areas of high quality habitat that can function as connections between landscape blocks for focal species
III. Building the Linkage
    a. Combine the results of the corridor and patch analysis to identify areas of wildlife connectivity for corridor users and dwellers.
IV. Riparian corridor component
    a. Identify riparian corridors that connect landscape blocks
V. Climate change component
    a. Perform land facet corridor analysis to identify connections of topographic similarity between landscape blocks

Appendix A outlines recommended mapping standards for fine-scale connectivity analysis.

For other guidance documents for wildlife connectivity modeling also see (Fischer & Fischenich 2000; Bennett 2003; Chetkiewicz *et al.* 2006; Beier *et al.* 2007; Beier *et al.* 2008; Aune *et al.* 2011; Shilling & Waetjen 2011; Rudnick *et al.* 2012; Cushman *et al.* 2013).

II. Study Area and Scale

The first steps of a wildlife connectivity analysis are to identify the study area and spatial scale of the analysis. There are many reasons to select a particular area for a wildlife connectivity project; the goals of the project and scale of available datasets should drive the selection of the study area and scale of analysis. Study area selection may be based on an area of conservation concern, or an area with known migration or other movement corridors. The study area may represent important areas of biodiversity or rare species. A study area may be selected because it is threatened by urban development, roads, logging, or habitat conversation (Aune *et al.* 2011).

The study area should be large enough to encompass natural processes such as movement between habitats, a disturbance regime (e.g., mosaic of habitats at different successional stages), or the maintenance of gene flow (e.g., supporting multiple populations). The California Essential Habitat Connectivity Project (Spencer *et al.* 2010) recommends that a fine-scale connectivity analysis should include a study area small enough that natural areas smaller than 10,000 acres (4047 ha) can be mapped and considered, but large enough to be meaningful for assessing connectivity; and the area should be of homogeneous environmental and planning context (e.g., Jepson Manual 10 ecoregions of California). The methods we outline here are for study areas at the USDA ecoregion “section” or finer resolution (sub-section)(Bailey *et al.* 1994). USDA ecoregion sections represent relatively environmentally homogenous regions of the state and range in size from approximately 750,000 to 8.5 million ha. We recommend analysis at the ecoregion section level for fine-scale wildlife connectivity models because computing power needs increase for larger areas and species habitat requirements may change across larger, environmentally heterogeneous areas.

The scale of a wildlife connectivity analysis varies depending on the species, area, and availability of data. Species selection will play a major role in the scale of the analysis (see section 3). Species have a range of different movement patterns at a range of scales (Bennett 2003). The different spatial scales can vary during different life stages, for example, aquatic to terrestrial, dispersal from natal range and seasonal migration (Table 1). The scale chosen should match the scale of habitats on the ground and the scale at which focal species perceive the landscape. This may range from tens of meters (e.g., small patches of specific habitat type, stream corridor) to hundreds of meters or more (e.g., larger patches of more common habitat types). Use of fine-scale vegetation maps allows for the identification of small, locally-important corridors that may not be accurately mapped in coarser-scale vegetation/habitat datasets. The raster cell size for analysis will largely be driven by the raster cell size of available base data sets. For fine-scale connectivity analyses, we recommend a raster cell size of <500 m to maintain the identification of small or narrow corridors.

EXAMPLE: Northern Sierra Nevada foothills

The northern Sierra Nevada foothills ecoregion section is approximately one million ha in size; and combined with a 30 km bufferit is 4.4 million ha. We chose this study area because of its importance in a planning context: it is under high development pressure, is bisected by several major highways, and a number of conservation plans are in progress. In addition, the availability of fine-scale vegetation data (2 acres minimum mapping unit) for this ecoregion section; the homogeneity of habitats and environments used by species across the study area for model evaluation; and the feasibility of the area for modeling (e.g., computing power needed) made the area an ideal candidate for our study. We used a raster cell size of 270 m for analysis. Although some datasets were available at 30 m for the ecoregion (e.g., vegetation, topography), we generalized these to 270 m to match the cell size of available climate data and to better match the accuracy of species occurrence locations.

a. Differing Needs by Geographic Region

Different geographic regions of the state are home to different suites of species, habitat types, and levels of urban development, land use, and agriculture. All of these factors may influence how a connectivity analysis is implemented. Defining the study area based on ecoregions helps to ensure that similar suites of habitat types and species are found throughout the study area, although urban development and agricultural use may vary within an ecoregion. For areas with high levels of urban development or agriculture, fine-scale vegetation or habitat maps delineating small patches of remaining habitat, as well as accurately mapped riparian corridors, are likely to be key components of a connectivity analysis. In all geographic regions of the state, availability of data and computing power will be limiting factors for conducting fine-scale connectivity analysis. Availability of appropriate datasets will determine the mapping scale and methodology that can be used.

b. Landscape Blocks

Landscape blocks are the areas of land to be connected by corridors. Landscape blocks can be defined many different ways depending on the goals of the study. Beier et al. (2011) suggest seven ways to define landscape blocks:

1) expert opinion mapped areas;
2) areas of high ecological integrity;
3) all or a subset of protected areas;
4) areas that meet quantitative conservation targets using optimization algorithms;
5) previously developed conservation maps;
6) maps of modeled or know habitat developed for a suite of species;
7) or preliminary natural landscape blocks modified with highways or other linear barriers.

Spencer et al. (2010) suggest defining landscape blocks by

1) land use;
2) ecological value or ownership, including protected areas;
3) highly fragmented “endangered” areas;
4) species important areas;
5) or areas with high biological integrity.

Any combination of these landscape block definitions may be suitable depending on the study area and project goals. We strongly recommend that landscape blocks have some type of protected status so the corridors have a long-term conservation planning context. USGS GAP conservation status designation can be used to determine conservation status (Table 1). A corridor connecting areas that may be highly modified or developed in the future may become a “bridge to nowhere”. We also suggest splitting landscape blocks by urban areas and areas within 50 m of major roads to identify barriers within blocks (Spencer *et al.* 2010). Local expert knowledge from Department staff, land trusts, and other local land management organizations is a key component of identifying a robust list of landscape blocks for any study area. Local experts can provide input on important habitat areas that may not be included in readily available GIS datasets, such as locally-important species habitat and movement areas, conservation agreements with private landowners, or newly acquired public lands.

Table 1. Definition of lands selected for landscape blocks.

GAP 1*	An area of permanent protection from conversion of natural land cover and a mandated management plan to maintain a natural state and disturbance events.
GAP 2*	An area of permanent protection from conversion of natural land cover and a mandated management plan to maintain a primarily natural state, but may receive uses that degrade the quality of existing natural communities, including suppression of natural disturbance.
GAP 3*	Multiple use public lands. An area of permanent protection from conversion of natural land cover for most of the area, but subject to extractive uses of either a broad, low intensity type, i.e. logging, or localized intense type, i.e. mining; protection to federally listed species throughout the area.
NCED	Privately owned conservation easement lands from the National Conservation Easement Database, which represents approximately 60% of the conservation easements in California. Data are from land trusts and public agencies. Conservation easements are legal agreements voluntarily entered into between landowners and conservation entities (agencies or land trusts) for the express purpose of protecting certain societal values such as open space or vital wildlife habitats.

*USGS GAP Analysis program protected areas conservation status code (http://gapanalysis.usgs.gov/padus/data/)

Landscape Block Configuration

minimum block size, distance between blocks and the number of blocks

The configuration of landscape blocks is also important. We recommend selecting enough landscape blocks across the study area to provide for realistic dispersal distance and connectivity throughout the study area. Blocks should be large enough to accommodate natural processes for the largest species such as a population patch (100,000 ha). To prevent modeling corridors shorter than the minimum corridor width (see below), we recommend adding a 1 km buffer to each block and aggregating any blocks with overlapping buffers. Adding a buffer to blocks also helps to generalize sensitive property boundary data (e.g., conservation easement data).

EXAMPLE: Northern Sierra Nevada foothills

We based our landscape blocks on protected lands managed primarily for biodiversity conservation (based on USGS GAP Analysis conservation status designations GAP 1 and 2); protected lands managed for multiple uses but representing large, contiguous natural areas with high ecological integrity (i.e., GAP 3 lands that intersect with Spencer et al. (2009) large intact blocks); and lands under conservation easement. This selection of landscape blocks represented lands with high habitat value that were expected to maintain this habitat value in the foreseeable future (Table 3). We included any blocks that were 100 acres or larger before the buffer was applied. After compiling a draft map of landscape blocks based on our criteria, we held a stakeholder meeting to acquire input from local experts including local, regional, and state government land management agencies, land trusts, non-profits, and ecologists and species experts.

c. Corridor Width

Individual corridor width may vary depending on the species, type of corridor, and scale of analysis. Riparian corridors and land facets (e.g., ridges, canyons) represent physical attributes of the landscape that are often quite narrow; generalizing them by making them wider, or selecting them based on a minimum width, may not be appropriate ecologically. Although individual corridors identified may be narrower, the final linkage should have an average minimum width of 1-2 km.

EXAMPLE: Northern Sierra Nevada foothills

Our linkages had an average minimum width of 1 km.

Table 2. Connectivity at multiple scales varying with species movement patterns (from Bennett 2003).

	Local scale (less than 1 km)	**Ecoregion Section (1-10’s km)**	**Ecoregion Province/Domain (10-100’s km)**
Habitat patch	small patches of vegetation; small forested areas; chain of wetlands	habitats large enough to support a population of breeding individuals; series of small reserves; landscape blocks	habitats along a mountain chain; system of rivers, lakes and wetlands along a flyway;
Habitat corridor	vegetated roadsides; forest corridors; fencerows; underpasses	riparian corridors; broad links of suitable habitat between protected areas	major river systems; mountain range; swaths of continuous rangeland, forest, desert
Habitat mosaics	mosaic of parks, gardens; vegetated pastures and farmland	mosaic of old growth forest and regenerating forest; natural vegetated rangeland; reclaimed pasture or farmland	state or national forest; national parks; wilderness areas; areas of related climate, vegetation zones
Species movement patterns	resident species, living within the same habitat year-round	resident species that move between several habitats to obtain different resources Seasonal migration between habitat types, altitudinal migrants	annual migration to nearby areas or different geographic regions

II. Building Wildlife Corridors

a. Focal Species Selection

Wildlife connectivity analysis should incorporate species-specific habitat and movement needs of wildlife in the study area, which requires the selection of focal species. Focal species provide the underpinning data of each linkage based on species habitat data. Focal species should be selected from a variety of taxonomic groups with diverse movement and habitat needs. The species chosen should be representative of the study area and the habitats it contains, and share traits with other species not selected (Beier *et al.* 2009). Beier et al. (2009) suggests selecting multiple and diverse focal species to design linkages that will buffer against uncertainty.

A good starting point to select focal species is a comprehensive species list of the study area. We recommend the California Wildlife Habitat Relationships (CWHR) system (http://www.dfg.ca.gov/biogeodata/cwhr/) for a list of all terrestrial vertebrate species, the threatened and endangered invertebrates list at http://www.dfg.ca.gov/wildlife/nongame/t_e_spp/invertebrates.html and a comprehensive list of California fish species at http://calfish.ucdavis.edu/species/ and http://www.dfg.ca.gov/marine/fishid.asp.

Once you have a complete list of species for your study area, we recommend defining selection criteria and ranking each species. Criteria for selecting focal species should be based on movement and habitat requirements, prioritizing species with movement as a key component of their life history (i.e., passage species) as well as species whose habitat and movement needs would encompass those of multiple species (Table 2). Priority for focal species selection is given to species with the following life history and conservation attributes:

- **Area-sensitive species**: species that occur in lower density but require large areas or species with greater need for corridor to survive.
- **Barrier-sensitive species**: species that are specifically sensitive to roads or other anthropogenic barriers in the landscape.
- **Umbrella species**: to collectively conserve other native species and key ecological processes.
- **Dispersal-limited species**: species that require movement as dictated by their life history characteristics, movement characteristics, and habitat preferences: movement by individual animals to access resources within their home range; movement between two smaller populations to maintain metapopulation persistence (immigration and emigration); or seasonal migration.
- **Habitat specialists**: species that are highly sensitive to loss or fragmentation of a specific habitat type.
- **Species of greater conservation need**: based on conservation status rankings/vulnerabilities.
- **Process-limited species:** species that move to maintain certain ecological processes such as disturbance, predator-prey interactions and dispersal to acquire new habitats.

Next, species that meet the selection criteria are evaluated to identify those that use the corridor to move through (**passage species**) and those that live in the corridor (**corridor dwellers**). Corridor dwellers may move within the corridor during their lifetime, but are likely to take multiple generations to move through the corridor. The list of passage species and corridor dwellers should then be further stratified across taxonomic groups (mammals, birds, reptiles, amphibians, fish, and plants) and by use of major habitat types in the study area, to represent the diversity of habitat requirements and movement needs across the ecoregion.

Collaboration with Department species experts and regional office biologists will help to narrow the list of focal species; identify those species for which data is available; and identify data sources for species location data, as well as life history and biogeographic information such as home range, patch size and dispersal distance. Species experts can also provide valuable review of habitat and connectivity models.

Considerations for Different Taxonomic Groups

Mammals: Large mammals with high mobility and large home-range size will likely make up the bulk of highly ranked species. Within these, species that occur at low density, species that are particularly barrier-sensitive (e.g., avoid crossing roads), and habitat specialists should be prioritized for inclusion as focal species. We recommend stratifying across groups within the mammals so that large predators and ungulates as well as small mammals and even bats are considered in the analysis.

Some migratory large mammals, such as mule deer, are known to use “traditional” migration routes, specific routes used by groups of animals year after year. The corridors identified in the type of analysis described here may coincide with these migration routes, but there may be additional factors influencing the traditional migration routes that are not considered in a least-cost corridors model. We recommend adding known migration corridors as an additional layer if available.

Birds: Birds are generally the least barrier-sensitive taxonomic group because of their ability to fly. Focal species selection should identify those species that tend to move along the ground (e.g., road runner) or migrate long distances on foot (e.g., mountain quail). In addition, habitat specialists that are limited by patches of specific habitat types for feeding or reproduction are good candidates for focal species.

Reptiles: Highly mobile or barrier sensitive (e.g., high road mortality) reptiles may be good candidates for inclusion as passage species. Habitat specialists, species of concern, and important prey species are good candidates for corridor dwellers.

Amphibians: Due to their small size and generally low mobility, amphibians are most likely to be included as corridor dwellers. Habitat specialists, species of concern, and important prey species are good candidates for focal species.

Fish: Inclusion of specific fish species would require an aquatic component not addressed in this report. The riparian connections described in this report are intended to capture riparian habitat as used by terrestrial species, although they also address fish habitat in a general way. However, they do not address other factors important to fish connectivity such as water flow and stream barriers (Schick & Lindley 2007).

Plants and vegetation: Due to their sessile nature, plants are corridor dwellers that may move through a corridor very slowly over multiple generations. Rare vegetation communities are unique assemblages of plants that may also have conservation status and protection. In general, plants or vegetation communities with conservation status would be the best candidates for focal species. However, inclusion of specific plant species may be more appropriate in a conservation plan that prioritizes habitat for species of concern, rather than a connectivity analysis meant to address movement across the landscape. Plant species are expected to move as climate conditions change. These potential movement paths may be captured by land facet corridors.

Species Literature Review

Understanding the biogeographic needs of focal species will help to build better models. The best resources for this information are species experts and the scientific literature. Information on focal species habitat use is needed for the distributions models. Species home range size is needed to estimate population and breeding patch size, and maximum dispersal distance is needed to evaluate distance between patches and continuity of habitat along corridors.

EXAMPLE: Northern Sierra Nevada foothills

We ranked 218 species occurring within our study area (Table 3). Based on this ranking, input from Department species experts and regional biologists, and an assessment of the species occurrence data and other species data available to build the models, we selected 30 focal species[1], stratified across taxonomic groups and major habitat types (i.e., oak woodland, chaparral, grassland), comprised of 9 passage species and 21 corridor dwellers.

Table 3. Focal species selection criteria for the northern Sierra Nevada foothills connectivity analysis. Rank 1 species were highest priority for inclusion.

Rank	Selection criteria
1	Area-sensitive: species that occur in low density but require large areas
2	Barrier-sensitive: species that are specifically sensitive to road development
3	Umbrella: species that are representative of a trophic group/guild, related species, rare species, mobility class, key ecological process or other collection of species
4	Dispersal-limited: species that require seasonal migration (fine scale movement)
5	Habitat specialist: species that are highly sensitive to habitat loss or fragmentation
6	Listed status: species of greater conservation need based on conservation status rankings

b. Habitat Models

To incorporate specific movement needs of focal species, a spatial habitat suitability model for each focal species is needed. The habitat model identifies potential suitable habitat for each species across the study area, allows for the delineation of core habitat areas and habitat patches for the patch

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[1] The full species list can be found online at https://nrm.dfg.ca.gov/FileHandler.ashx?DocumentID=61105&inline=1

analysis, and functions as the cost layer (i.e., inverse of habitat suitability) for the least-cost corridor analysis. There are two main approaches for habitat modeling: expert opinion based models and statistical models (i.e., species distribution models, SDMs) to estimate habitat suitability. We recommend statistical habitat models because they are data-driven and repeatable. When species specific data are not available to develop a SDM we recommend the techniques described in (Beier *et al.* 2007). Regardless of the modeling method chosen, a key component of model development is review and input from a wildlife expert with knowledge of the distribution and ecology of the species being modeled.

Species Distribution Models

Species distribution modeling (SDM), also known as ecological niche modeling (ENM), is one of the best available tools for producing species specific information necessary in conservation planning (Hannah 2003). Species distribution models integrate a wide range of spatial environmental data and known species point locations to estimate habitat suitability. The SDM output is a grid that ranks habitat suitability from 0-100 across the landscape based on the environmental conditions at known species locations. The output grid is assessed for accuracy by evaluating the habitat suitability predicted by the SDM at a set of species locations not used to build the model.

There are many SDM methods available; table 4 provides a list of the most popular. For our analysis we used Maxent. Maxent is a general-purpose machine learning method of maximum entropy (Phillips *et al.* 2006). Maxent estimates a species probability distribution by finding the probability distribution of maximum entropy, subject to a set of constraints that represent the information about the species distribution (Phillips *et al.* 2006). Maxent also allows for the use of presence-only data and categorical variables. Elith and others (2006) compared 12 SDM algorithms and found that Maxent performed better than other algorithms for modeling distributions with limited data points. For a tutorial on Maxent see (Phillips 2010).

Statistical models such as SDMs have the advantage of being transparent and repeatable, whereas expert opinion-based models, which require individuals to manually assign weights and resistance values to environmental factors (Beier et al. 2009), are subject to differences in estimates depending on the interpretation of the expert providing the ranking. Expert opinion models may also be limited by level of knowledge of the species, and may be most appropriate for those species for which habitat factors influencing habitat suitability and movement patterns are well studied.

Table 4. Species distribution models

Method(s)	**Model/software name**	**Species data type**	**Website**
Maximum Entropy	MAXENT	Presence and background	http://www.cs.princeton.edu/~schapire/maxent/
Ensemble of decision trees	RANDOM FOREST	Presence and absence	http://www.stat.berkeley.edu/~breiman/RandomForests/
Ecological Niche Factor Analysis	BIOMAPPER	Presence and absence	http://www2.unil.ch/biomapper/enfa.html
Genetic Algorithm (GARP)	GARP	Presence and pseudo-absence	http://www.nhm.ku.edu/desktopgarp/
Regression: GLM, GAM, BRT, MARS	Implemented in R	Presence and absence or pseudo-absence	**GLM** http://data.princeton.edu/R/glms.html **GAM** http://cran.r-project.org/web/packages/gam/index.html **BRT** http://statsr.wikispaces.com/Boosted+Regression+Trees **MARS** http://www.r-bloggers.com/statistical-learning-with-mars/

Expert Opinion Models

Expert opinion models can be used when data are unavailable for species distribution modeling. Beier *et al.* (2007) recommends techniques for expert-opinion models (corridor designer habitat model) for connectivity analysis. In California, CWHR provides habitat suitability ratings for terrestrial animal species in 65 habitat types at different structural stages (density and dbh). The CWHR Bioview module provides an output table of habitat suitability ratings from the CWHR database for a selected species that can be applied to a spatial habitat data file. The habitat data file is generally a list of polygons in a GIS data set representing vegetation class and structural stages (density and dbh). The Bioview output is produced as follows: First, for each species, a standard habitat suitability value is given for each vegetation type and structural stage. These data, based on expert opinion, show the suitability of the vegetation type and structural stage for the species, represented on a scale of 0 to 100 with 0 for no suitability, 33 for low suitability, 66 for medium suitability and 100 for high suitability. Values are provided for reproduction, cover and feeding (life stages). The arithmetic mean and geometric mean of the three life stage values are provided as the suitability values. These data can then be joined with the vegetation layer for representation in GIS to depict low to high suitability.

EXAMPLE: Northern Sierra Nevada foothills

Maxent Habitat Models: We used Maxent (Phillips *et al.* 2006) because it is one of the well-performing species distribution models available and it is also able to handle presence-only species data. We used species location data, a fine-scale vegetation map completed by the California Department of Fish and Wildlife (CDFW) Vegetation Classification and Mapping Program for the Sierra Nevada foothills region, bioclimatic variables derived from PRISM climate data, elevation, and distance to water as predictors. We implemented Maxent in R using the 'dismo' package (Hijmans *et al.*, 2011). The models were developed at 270 m spatial resolution with five replications using 10-fold cross-validation as a method of sample evaluation. We evaluated model performance in R using the model evaluation metric AUC (area under the curve) using the 'PresenceAbsence' package (Freeman and Moisen, 2008).

Our habitat models were developed statewide, so our models could be built using data from the diverse habitats across the state to improve model performance, but the results were only evaluated within our study area based on Department species experts' knowledge (Hernandez *et al.* 2006). A paucity of species occurrence data within our study area led us to primarily use species occurrence points outside our study area as a basis for the habitat suitability modeling. The lack of a wall-to-wall fine-scale vegetation map for the state required us to use a mosaic of the best available data from multiple sources. We were then limited to using the vegetation/habitat classification that was a common field among the various source datasets, the CWHR classification.

Expert Opinion Models: We used CHWR's Bioview module to create expert opinion habitat suitability maps. First, CWHR density and dbh codes were added to the NSNF vegetation map based on density and dbh data provided in the attribute table for the vegetation polygons. Next, the NSNF fine-scale vegetation map was merged with the FRAP 2006 multisource landcover dataset, which included CWHR codes for all other areas of the state, to create a statewide 30 m pixel vegetation dataset. The Bioview model was then run to obtain the mean habitat suitability rank[2] of each habitat stage for each of the 30 focal species, and the results were joined to the map. The 30 m pixel suitability maps were then generalized to 270 m pixels, using the average pixel value, for comparison with the 270 m SDM output maps.

c. Urban Mask

The urban mask should represent areas not suitable for wildlife habitat or wildlife movement. Habitat suitability rankings can be changed to zero within the urban mask when it is unsuitable for wildlife habitat, or corridors can be clipped by the urban mask when the habitat is unsuitable for wildlife movement. Urban areas can be delineated a number of ways such as with census block housing density maps, parcel zoning maps, or maps of impervious surfaces. In addition, bodies of water such as lakes should be included in areas unsuitable for terrestrial wildlife movement (i.e., corridor should not go through the middle of a lake).

EXAMPLE: Northern Sierra Nevada foothills

For our analysis we defined urban areas as 1) one or more housing unit per 5 acres[3] from the 2010 Census block housing and population density on habitat lands dataset

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[2] CHWR BioView arithmetic mean of habitat suitability ranks for reproduction, cover, and feeding

[3] Based on input from our Department wildlife experts, we used values of >1 housing unit per 5 acres, or 1 housing unit per 5 acres when 8 or more parcels are in one contiguous block, to define areas unsuitable for wildlife movement. We used values of ≥1 housing unit per 10 acres to define areas unsuitable as core habitat patches.

(http://www.census.gov/rdo/data/2010_census_redistricting_data_pl_94-171_summary_files.html), 2) commercial and industrial parcels based on zoning codes Industrial_Alb and COMM1_Alb from the California Digital Parcel Database, and 3) areas with >50% impervious surfaces (landcover classes 23 and 24) from the National Landcover Database (USGS 2006). Roads data are from the US Major Roads ESRI datasets and lakes are from the CDFW lakes dataset.

d. Habitat Patch Analysis

The patch analysis is used to identify all suitable habitat patches across the study area based on individual species habitat suitability, home range, patch size and dispersal distance data. Three types of habitat patches are defined: 1) **population patches** are able to support at least 50 individuals and are capable of supporting the species for several decades; 2) **breeding patches** are capable of supporting a breeding pair; and, 3) **other patches** are smaller than a breeding patch and can be used as move-through habitat to link to other patches.

The SDM output is the basis for the patch analysis. A threshold is applied to the original SDM output to identify all suitable habitat areas. Published information or species expert estimates of average home range size are used to determine minimum patch sizes. The corridor designer tool in ArcGIS is used to identify all suitable habitat patches across the study area and rank these as potential core areas (population patches), patches (breeding patches) or less than a patch (other patches). Contiguous suitable habitat larger than 25 times the recorded average home range size are recorded as potential core areas, and each area of contiguous suitable habitat as least 2 times the minimum recorded home range but less than the potential core area are recorded as a patch. A potential core area may sustain at least 50 individuals and are probably capable of supporting species for several decades. Patches can support at least one breeding pair and are probably useful to the species if the patch can be linked via dispersal to other patches or core areas.

Box A. Patch Analysis Steps

1. Use the Geomorphometry and Gradient Metrics toolbox, Statistics, Transformations Tool to **normalize** habitat models to 0-1. Output1
2. Raster Calculator, multiply output 1 with 100 to have habitat raster with values 0-100. Output2
3. Corridor designer toolbox, Habitat Modeling, Modify HSM 1 – Reclassify features in HSM. This tool reclassifies the habitat model pixels to 0 for Urban, Road and Lake areas.
4. Corridor designer toolbox, Habitat Modeling, Create habitat patch map tool. Inputs modified habitat model from previous step, threshold from threshold analysis and patch size for breeding patch and population match. Creates polygon layer attributed as 1=smaller than breeding patch, 2=breeding patch, 3=population patch.

Habitat patch analysis is conducted for both passage species and corridor dwellers. After the least-cost corridors for the passage species are complete, the habitat patches for corridor dwellers are overlaid on the corridors, and additional habitat for corridor dwellers is added to the final linkage as needed (see Corridor Analysis section below) to meet each species habitat patch needs.

e. Corridor Analysis

The goal of the corridor analysis is to define the land area that best connects two landscape blocks. There are a variety of spatial models to analyze landscape connectivity (Table 5) including least-cost path (Beier *et al.* 2007), friction analysis (Nikolakaki 2004) and electrical circuit theory (McRae & Beier 2007). Also see Cushman et al. (2013) for detailed description of the latest techniques. For a comparison of techniques see (Poor *et al.* 2012).

Table 5. Interactive tools for mapping and planning corridors data from (http://www.conservationcorridor.org/corridor-toolbox/)

Tools for mapping and planning corridors	**Website**
Connecting Landscapes	http://www.landscope.org/focus/connectivity/
Corridor Design	http://corridordesign.org/
Connectivity Analysis Toolkit	http://www.klamathconservation.org/science_blog/software/
Linkage Mapper	https://code.google.com/p/linkage-mapper/
Zonation	http://cbig.it.helsinki.fi/software/zonation/
The Yale Framework	http://yale.databasin.org/
The Circuitscape Project	https://sites.google.com/a/circuitscape.org/circuitscape/
Connect: Connectivity Modeling Toolbox	http://www.unc.edu/depts/geog/lbe/Connect/

The methods described here follow the least-cost corridor techniques described in Beier et al. (2007). This analysis identifies a least-cost corridor or the best potential route for each species between a set of landscape blocks based on habitat suitability. The data needed for a least-cost corridor analysis are a resistance raster and landscape blocks. The resistance raster is the inverse of the habitat suitability model, based on the assumption that the poorer the habitat for the species, the greater the “cost” to move through this habitat. The patch analysis identifies the habitat patches for each species within each landscape block. These habitat patches are ultimately what is connected in the corridor analysis. There may be multiple patches per landscape block. We recommend developing a least-cost corridor for each possible connection and using a rule-set to select the best individual species corridor.

The least-cost corridor output does not identify barriers, risk and dispersal ability. The model identifies the least-cost path between any two blocks, but in some cases the least cost path may still be too costly or otherwise unsuitable for wildlife movement. Therefore, it is important to evaluate each corridor. We suggest removing any urban areas or areas of unsuitable/non-restorable habitat from the corridors, and then inspecting if the corridor is still continuous. To evaluate if a corridor is useful for a species, it is important to examine the amount of suitable habitat in the corridor and how far apart habitat patches are. We suggest calculating the amount of habitat area to make sure it meets each species habitat need in each corridor and then measuring the distance between habitat patches in the corridor to ensure that patches of suitable habitat are not separated by distances greater than the maximum dispersal distance for that focal species. If the corridors do not meet these rules, then outside habitat patches adjacent to the corridor can be added to meet selection requirements. The size and distance among habitat patches must be adequate to support species movement; the shape of those habitats also plays a key role.

Box B. Rules to Select the Best Individual Species Corridor

We developed the following rule-set as selection criteria to determine if a corridor should be included:

1. Is the corridor continuous after urban mask is applied?
    a. If YES: proceed to #2
    b. If NO: delete corridor
2. Does the corridor provide sufficient habitat patches (breeding patch or larger)? What percentage of the corridor is in habitat patches?
    a. If YES: proceed to #3
    b. If NO: proceed to #4
3. Is the distance between patches inside the corridor within the species dispersal distance?
    a. If YES: include corridor, go to Box C.
    b. If NO: proceed to #4
4. Is there another corridor between the same two landscape blocks that does meet the selection criteria?
    a. If YES: delete corridor
    b. If NO: proceed to #5
5. Are there habitat patches nearby that could be included in the corridor to meet selection criteria?
    a. If YES: expand corridor to include additional patches, go back to #1
    b. If NO: delete corridor

Evaluation Steps

1. Remove urban mask areas from corridors. Visually inspect if corridor is continuous.
2. Calculate distance between patches.
    a. Clip patch layer with corridors
    b. Calculate distance between patches within corridor, use Conefor Inputs tool:
        i. Select Layers (corridor), Select ID Field (ID), Select Attribute Field (ID)
        ii. Calculate distance between all features
        iii. Calculate from Feature Edges
        iv. Select, ASCII Text File of Distance to Each Feature
        v. Specify output folder
        vi. If you want to see table of results check Open dBase and text file.
    c. Compare distance between patches with species dispersal distance
    d. If distance matches species dispersal distance move to step 2 if not look at next larger corridor slice (01 to 02)
3. What percentage of the corridor is suitable habitat patches?
    a. Clip habitat patch layer with corridors
    b. Calculate area of clipped patches
    c. Divide total area of corridor with patch area, multiply by 100 for percentage
4. Are there habitat patches bordering the corridor that can be included if needed?

Box C. Incorporating Corridor Dwellers and Selecting Final Corridors

1. Corridor dwellers: repeat corridor selection evaluation steps (see Box B) for all corridor dwellers, for every corridor that met the selection criteria for passage species. Create an attribute table field for each corridor dweller, and mark which corridors meet the selection criteria for that species.

After the incorporation of corridor dwellers, final corridors are selected from those that met the selection criteria detailed in Box B.

2. Corridor selection, select corridors that represent the most species
    a. First select corridors that connect multiple blocks
    b. Then select the corridors that cover the most species, i.e. if a corridor for BLBE connects three blocks but the corridor does not provide connections for other species, select the corridors that account for the most species

III. Building the Linkage

The linkage incorporates data and information for all the focal species including corridor dwellers. This analysis identifies multiple swaths of habitat that species have the potential to reside in or move through.

Least-Cost Union

The final least-cost corridors for all species are combined to generate a Least-Cost Union. The least-cost union represents all individual species corridors merged together, identifying the best swath of habitat available for focal species to move from one block to another.

Rules for Union Analysis

Pinch points, areas where habitat have been narrowed by surrounding development, can prevent species from moving through a corridor. To ensure that functional processes are protected, a corridor should have a minimum width. The minimum width of a corridor should be based on species needs (for corridor dwellers), or could be based on home range size (Beier *et al.* 2008). Two kilometers is suggested by many studies as a suitable distance. A wide linkage ensures the inclusion of a variety of habitats for other species not modeled, such as plants and pollinators, and allows for natural disturbance regimes to operate with minimal constraints from adjacent urban areas (Beier *et al.* 2006). A wide linkage also enhances the ability of the biota to respond to climate change and buffers against edge effects. In areas where the corridor is less than the minimum width, additional natural habitats should be added to either side of the union. If no natural habitats are available, agricultural land should be added because these lands have the potential to be restored.

Box D. Calculating Corridor Attributes

1. Calculate corridor length and width
    a. Dissolve corridor multipart to single part
    b. From Corridor Designer Evaluation tools, select the Batch Bottleneck analysis tool
        i. Select 1st landscape block
        ii. Select 2nd landscape block
        iii. Select corridor
        iv. Once Bottleneck Results are complete result will be shown in a table. Select 2000 as the Threshold Statistic.
        v. Record from left results box the Length
        vi. Record from middle results box Proportion
        vii. Add v and vi to attribute table

2. Count number of major road crossings
3. Calculate percentage of habitat in corridor

IV. Riparian Corridors

Riparian corridors are important areas that maintain connectivity throughout the state of California (Spencer *et al.* 2010) and provide areas for movement for many species including predators (Hilty & Merenlender 2004). Riparian corridors may serve multiple valuable ecological functions such as providing wildlife habitat, preserving water quality, and providing flood control. Riparian corridors are important for wildlife movement because they provide continuous swaths of cover, food, and water. They may also provide the only remaining natural swaths of habitat through highly modified landscapes.

> ***EXAMPLE: Northern Sierra Nevada foothills***
> We defined our riparian corridors as areas within 500 m of perennial streams with mapped riparian habitat. Even if riparian habitat was mapped on only one section of the stream, the entire length of the stream was included as the riparian corridor.

V. Climate Change Analysis

Animal and plant distributions are strongly influenced by climate, and species distributions are known to change over time as the climate changes. Plants and animals require corridors for movement to track climatic conditions as they change. However, there is a great deal of uncertainty in modeling these corridors, and the hypotheses produced by the models are difficult to test. One of the methods often used to plan for the impending effect of climate change on biodiversity is to design reserves and linkages using climate envelope models projected into future climate conditions based on predicted emission scenarios. However, there is uncertainty associated with the emission scenarios, the predicted future climatic conditions, as well as with how exactly the species will respond to a changing climate. This results in uncertainty that the climate envelope models will perform well in predicting reserves and linkages that wildlife can use in the future. For this reason, some authors suggest to focus rather on protecting corridors of physical landscape units defined by topography and/or soil parameters such as slopes, ridges, and canyons (Beier & Brost 2010).

Land Facets

Land facets are areas of the landscape with uniform topographic and geologic characteristics. Land facets are used to predict areas of habitat that are expected to be suitable in future climates without relying on models of future temperature and precipitation. We used a land facet analysis to identify corridors with uniform topographic and geologic features that will support species and species movement as climate conditions change over time. For a full description of land facets and analysis steps, see (Brost (2010)).

EXAMPLE: Northern Sierra Nevada foothills

We identified 3 categories of land facets across the study area and 11 individual facets:

Canyons: low elevation gentle canyons, high elevation steep canyons and high elevation gentle canyons;

Slopes: low elevation, flat, warm slopes, mid-elevation gentle, warm slopes, steep, cool slopes, steep, hot slopes, high elevation gentle hot slopes and high elevation steep slopes;

Ridges: low elevation gentle ridges, high elevation steep ridges and high elevation gentle ridges.

We modeled corridors between landscape blocks for each of the land facets identified.

Literature Cited

Aune, K., Beier, P., Hilty, J. & Shilling, F. (2011). Assessment and planning for ecological connectivity: A practical guide. The Wildlife Conservation Society Bozeman, MT, USA, p. 82.

Bailey, R.G., Avers, P.E., King, T. & McNab, W.H. (1994). Ecoregions and subregions of the United States. (eds. McNab, WH & Bailey, RG). USDA Forest Service Wahsington , DC.

Beier, P. & Brost, B. (2010). Use of Land Facets to Plan for Climate Change: Conserving the Arenas, Not the Actors. *Conservation Biology*, 24, 701-710.

Beier, P., Majka, D.R. & Jenness, J.S. (2007). Conceptual steps for designing wildlife corridors. p. 90.

Beier, P., Majka, D.R. & Newell, S.L. (2009). Uncertainty analysis of least-cost modeling for designing wildlife linkages. *Ecological Applications*, 19, 2067-2077.

Beier, P., Majka, D.R. & Spencer, W. (2008). Forks in the Road: Choices in Procedures for Designing Wildland Linkages. *Conservation Biology*, 22, 836-851.

Beier, P., Penrod, K., Luke, C., Spencer, W. & Cabanero, C. (2006). South Coast Missing Linkages: restoring connectivity to wildlands in the largest metropolian ara in the United States. In: *Connecitivty Conservation* (eds. Crooks, KR & Sanjayan, MA). Cambridge University Press Cambridge, UK.

Bennett, A.F. (2003). Linkages in the landscape: The role of corridors and connectivity in wildlife conservation. IUCN Gland, Switerland and Cambridge, UK, p. 254.

Brost, B. (2010). Use of land facets to design conservation corridors: Conserving the arenas, not the actors. In: *Forestry*. Northern Arizona University Flagstaff, AZ, p. 113.

Buchmann, C.M., Schurr, F.M., Nathan, R. & Jeltsch, F. (2013). Habitat loss and fragmentation affecting mammal and bird communities - The role of imterspecific competition and individual space use. *Ecological Informatics*, 14, 90-98.

Chetkiewicz, C.-L., St. Clair, C.C. & Boyce, M.S. (2006). Corridors for conservation: Integrating pattern and process. *Annual Review in Ecology, Evolution and Systematics*, 37, 317-342.

Cushman, S.A., McRae, B., Adriaensen, F., Beier, P., Shirley, M. & Zeller, K. (2013). Biological corridors and connectivity. In: *Key Topics in Conservation Biology 2*. John Wiley & Sons, pp. 384-404.

Elith*, J., H. Graham*, C., P. Anderson, R., Dudík, M., Ferrier, S., Guisan, A. *et al.* (2006). Novel methods improve prediction of species' distributions from occurrence data. *Ecography*, 29, 129-151.

Fischer, R.A. & Fischenich, J.C. (2000). Design recommendations for riparian corridors and vegetated buffer strips. In: *EMRRP Technical Notes Collection (ERDC TN-EMRRP-SR-24)*. US Army Engineer Research and Development Center Vicksburg, MS.

Gilpin, M.E. (1987). Spatial structure and population vulnerability. In: *Viable Populations for Conservation* (ed. Soule, ME). Cambridge University Press Cambridge, England, pp. 125-139.

Griffiths, P.G., Webb, R.H., Lancaster, N., Kaehler, C.A. & Lundstrom, S.C. (2002). Long-term Sand Supply to Coachella Valley Fringe-toed Lizard Habitat in the Northern Coachella Valley, California. U.S. Geological Survey Water-Resources Investigations Report.

Hannah, L. (2003). Regional Biodiversity Impact Assessments for Climate Change: A Guide for Protected Area Managers. In: *Buying Time: A User's Manual for Building Resistance and Resilience to Climate Change in Natural Systems* (eds. Hansen, LJ, Biringer, JL & Hoffman, JR). World Wildlife Fund Berlin, Germany, pp. 235-244.

Hernandez, P., Graham, C.H., Master, L.L. & Albert, D.L. (2006). The effect of sample size and species characteristics on performance of different species distribution modeling methods. *Ecography*, 29, 773-785.

Hilty, J. & Merenlender, A.M. (2004). Use of riparian corridors and vineyards by mammalian predators in Northern California. *Conservation Biology*, 18, 126-135.

McRae, B. & Beier, P. (2007). Circuit theory predicts gene flow in plant and animal populations. *Proceedings of the National Academy of Sciences of the United States of America*, 104, 19885-19890.

Meese, R.J., Shilling, F. & Quinn, J.F. (2009). CalTrans: Wildlife crossing guidance manual. Information Center for the Environment, Department of Environmental Science and Policy, University of California - Davis Davis, CA, USA.

Nikolakaki, P. (2004). A GIS site-selection process for habitat creation: estimating connectivity of habitat patches. *Landscape and Urban Planning*, 68, 77-94.

Noss, R.F. (1991). Landscape connectivity: Different functions at different scales. In: *Landscape linkages and biodiversity* (ed. Hudson, WE). Island Press Washington, D.C. USA.

Phillips, S.J. (2010). A brief tutorial on maxent. *Lessons in Conservation*, 107-135.

Phillips, S.J., Anderson, R.P. & Schapire, R.E. (2006). Maximum entropy modeling of species geographic distributions. *Ecological Modelling*, 190, 231-259.

Poor, E.E., Loucks, C., Jakes, A. & Urban, D.L. (2012). Comparing habitat suitability and connectivity modeling methods for conserving pronghorn migration. *PLos One*, 7, 1-12.

Riley, S.P.D., Pollinger, J.P., Sauvajot, R.M., York, E.C., Bromley, C., Fuller, T.K. *et al.* (2006). A southern California freeway is a physical and social barrier to gene flow in carnivores. *Molecular Ecology*, 15, 1733-1741.

Rudnick, D.A., Ryan, S.J., Beier, P., Cushman, S.A., Dieffenback, F., Epps, C.W. *et al.* (2012). The role of landscape connectivity in planning and implementing conservation and restoration priorities. *Issues in Ecology*, 16, 21.

Schick, R.S. & Lindley, S.T. (2007). Directed connectivity among fish populations in a riverine network. *Journal of Applied Ecology*, 44, 1116-1126.

Shilling, F. & Waetjen, D.P. (2011). Regional approach for connectivity analysis and design. University of California Davis for the California Department of Fish and Game Davis, CA, p. 82.

Spencer, W., Beier, P., Penrod, K., Winters, K., Paulman, C., Rustigian-Romsos, H. *et al.* (2010). California essential habitat connectivity project: A strategy for conserving a connected California. California Department of Transportation, California Department of Fish and Game and Federal Highways Administration Sacramento, CA, p. 313.

Thorne, J.H., Cameron, D. & Quinn, J.F. (2006). A conservation design for the central coast of California and the evaluation of mountain lions as an umbrella species. *Natural Areas Journal*, 26, 137-148.

USGS (2006). National Landcover Database. United States Geological Survey. Sioux Falls, SD.

Appendix A. Recommended Fine-scale Connectivity Mapping Standards

- Spatial scale of analysis
    - Raster cell size of <500 m
    - Corridors with a minimum width of 1 km
    - Corridors based on land cover or vegetation base data with a minimum mapping unit of 2 acres or smaller and a verified accuracy of >80%
    - Study area of USDA ecoregion section or smaller size
- Landscape blocks
    - Connect landscape blocks with a minimum block size of 100 ac
    - Protected status of landscape blocks should be considered. Blocks of unprotected lands should be included only when there is some certainty of their long-term conservation status.
    - Split landscape blocks by urban areas and areas within 50 m of major road
    - Employ local expert knowledge when identifying landscape blocks
    - Add a buffer to blocks equivalent to the minimum corridor width, and aggregate blocks based on the buffer
- Habitat suitability and corridor modeling for wildlife species
    - Select enough focal species to be representative of all taxonomic groups, movement types and habitat needs within the study area
    - Include both passage species and corridor dwellers
    - Use species-specific information on home range size, patch size requirements (population and breeding patches) and dispersal distance to assess each corridor
    - Model wildlife corridors between wildlife species core areas located within landscape blocks, and include connections for corridor dwellers based on patch analysis
    - Use transparent, repeatable (statistical) modeling methods when possible to develop habitat suitability models
    - Every habitat suitability model and set of corridors should be reviewed by a wildlife expert with detailed knowledge of that species, and refined based on their comments
    - Avoid modeling corridors into or through urban areas
- Prioritizing corridors
    - Corridors might be prioritized based on:
        - the number of landscape blocks they connect,
        - the number and/or types of species they provide movement of live-in habitat for,
        - if they also intersect riparian or climate change corridors,
        - the types of habitats they provide.

Corridor Attributes

- GIS shapefiles of the fine-scale corridors should include, at a minimum, the following attributes for each corridor:
    - A unique name or ID
    - A list of the blocks it connects
    - Corridor area and length
    - The number of major road crossings and names of roads
    - The composition of major vegetation types (percentage of corridor area in each type)
    - Percentage of corridor under conservation protection (e.g., GAP status 1, 2 and 3)

    For Wildlife Corridors:

    - A checklist of the species it provides movement or live-in habitat for
    - Percentage of area in the corridor providing habitat for the species
    - A count of the species it provides movement or live-in habitat for