Maximizing Evolutionary Potential Under Climate Change in Southern California Protected Areas

Principal Investigators: Dr. Thomas B Smith
Co-Investigators: Dr. Seth Riley, Dr. Katy Semple Delaney, Dr. Ryan Harrigan, and Dr. Henri Thomassen

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Project Description

Efforts to prioritize conservation areas have typically relied on indices that include levels of endemism, species richness, and degree of threat[1]. However, it has long been recognized that measures of species richness alone may fail to capture essential evolutionary processes that promote and sustain diversity[2-8]. To avoid extinction in the face of climate change, populations may either move to more favorable habitat, or adaptively respond to changing conditions. With increasing fragmentation of formerly continuous habitat, dispersal to new areas may be severely limited. It is important, therefore, to develop ways of prioritizing regions that include not only areas with high species richness and where species might move, but also regions that maximize a species' adaptive potential. A suitable approach to do this is to protect as much intraspecific morphological and genetic variation as possible, so as to increase the probability that one or more populations will be adapted to new climate conditions.

By identifying areas within the study region that harbor higher genetic variation, we have determined high priority areas that may influence conservation decisions. Understanding how these areas may change in response to impending climate change is of paramount importance. We have also ensured the toolbox of methods and data analysis pipeline for this project will be made available for use by LCC and other land managers. Finally, we have developed these methods to be of general utility to regions outside the Santa Monica Mountains National Recreation Area. While ecological and climate factors other than those found to be important in Southern California are likely playing a role in other regions, the framework established here can be easily transferred to other model systems.

Basic Approach and Scope of Work

We used existing genetic[9] data from 15-20 sites (depending on species) of the following bird and reptile species to identify areas important for conservation in the Santa Monica Mountains NRA: wrentit (*Chamaea fasciata*), western fence lizard (*Sceloporus occidentalis*), side-blotched lizard (*Uta stansburiana*), and western skink (*Plestiodon skiltonianus*). These species have contrasting vagilities and food niches, and occupy different strata of the vegetation. The species are common, with widespread distributions in California, although the wrentits are mostly limited to coastal chaparral habitat. All four species occur throughout much of the Santa Monica Mts. NRA. We used satellite remotely sensed and climate data, in conjunction with recently developed spatially explicit ecological modeling techniques[10] to project genetic diversity across the landscape. In local to regional scale studies (with environmental layers at spatial resolutions of ~ 20m - 1km), environmental parameters can be used in a correlative approach to indirectly discern patterns of biodiversity[11]. Spaceborne measurements can provide information on primary productivity, climate, and habitat structure, factors that are thought to be important in determining the distribution, composition, and local amounts of biodiversity[12-14]. Recent advances in GIS technologies and spatial statistics have increased the predictive power of spatial analyses by refining approaches that first identify and quantify associations between environmental variables and biodiversity[10,15,16]. These statistical associations can then be used to project patterns of diversity across a landscape, resulting in continuous predictions of alpha- or beta diversity, even in unsampled areas. Our approach consisted of three main steps:

1) Identify spatially explicit population structure across the SMMNRA

2) Predict the distribution of genetic variation across the study landscape

3) Project how this genetic variation is likely to change under climate change

Genetic Data

Genetic data used in this study consisted of genotype data taken from previous research in the Santa Monica Mountains National Recreation Area[9]. The data sets for each species included geo-referenced genotypes for each sampled individual, with multiple individuals per location (GPS location information in UTM, datum NAD27 zone11; Table 1). The definition of 'locations' in this data set was made through an *a priori* decision based on the spatial clustering of the pitfalls arrays in the sampling sites. Consequently some locations included multiple pitfall arrays.

Table 1: Details on genetic data; number of loci, total number of samples, number of locations, and range of number of samples per location.

Species name	# of loci	Total # samples	# of locations	Samples per location
Western skink (*Plestiodon skiltonianus*)	6	225	15	5-29
Western fence lizard (*Sceloporus occidentalis*)	8	239	17	8-18
Side-blotched lizard (*Uta stansburiana*)	8	215	15	2-18
Wrentit (*Chamaea fasciata*)	7	105	10	3-18

Environmental Data

Environmental variables used were of two types. First, low-resolution environmental data which allows for analyzing regional-scale processes, and consisted of a set of climate variables from the WorldClim database and satellite remotely sensed variables at 30 arcsec resolution (Table 2). Temperature was expected to influence genetic variation in these species, because three out of the four study species are cold-blooded, and therefore in their activity highly dependent on the temperature of the surrounding environment. Furthermore, precipitation was expected to be important, because the Santa Monica Mountains are a relatively arid area. Removing highly correlated variables with Pearson cross-correlations > 0.9, and keeping variables that are often used or ease interpretation, the following climate variables were selected for further analyses: Annual Mean Temperature (BIO01), Mean Diurnal Temperature Range (Mean of monthly maximum temp minus minimum temperature; (BIO02)), Temperature Seasonality (standard deviation * 100; (BIO04)), Maximum Temperature of warmest Month (BIO05), Minimum Temperature of Coldest Month (BIO06), Annual Precipitation (BIO12), Precipitation Seasonality (Coefficient of Variation; (BIO15), Precipitation of Warmest Quarter (BIO18), and Precipitation of Coldest Quarter (BIO19).

Second a set of remotely sensed data variables was used. These included Moderate Resolution Imaging Spectroradiometer (MODIS), we included the Normalized Difference Vegetation Index (NDVI) (calculated from the red and near infrared reflection of the earth's surface) and its standard deviation (NDVIstd) as a measure of greenness and seasonality, as well as percent tree cover, computed from the Vegetation Continuous Field (VCF) for the year 2001. We used radar data from the Quick Scatterometer (QuickSCAT), delivering information about near-surface moisture content, and a Digital Elevation Model (DEM) from the Shuttle Radar Topography Mission (SRTM) at 30 arc second resolution.

Table 2: List of low-resolution environmental variables used in the analysis.

Data Record	Instrument	Ecological Attributes	Variables Derived
NDVI	Satellite-MODIS	Vegetation Density	NDVI mean, NDVIstd
VCF	Satellite-MODIS	Forest cover & heterogeneity	Tree
Scatterometer-Backscatter	Satellite-QSCAT	Surface moisture	QSCATaug
WorldClim	Station-Network	Bioclimatic variables	BIO01, BIO02, BIO04, BIO05, BIO06, BIO12, BIO15, BIO18, BIO19

In addition to this lower-resolution data, we also included high-resolution (30 m) remotely sensed data, derived from the ASTER mission. The red (RED; band 2) and far infrared (FIR; band 3n) bands served as basis to compute NDVI as follows:

$$NDVI = (RED - NIR) / (RED + NIR)$$

Band 11 was also used, which contains temperature data that does not need further processing. In addition to these data sets from the ASTER layers, high-resolution elevation data and a tree cover data set in 30 m resolution were used as environmental predictors[17].

Table 3: List of high-resolution environmental variables used in the analysis.

Data Record	Instrument	Ecological Attributes	Variables Derived
Light & Temperature bands	Satellite-ASTER	Light reflection, Temperature	NDVI, Temp
DEM	SRTM	Elevation + Topography	Elevation
VCF	Satellite-MODIS	Tree cover + heterogeneity	Tree

Finally, previous work suggested that highway 101 may act as a dispersal barrier[22], reducing gene flow between populations. We therefore included this barrier hypothesis by generating a GIS rater layer where the area south of the 101 was coded as 0 and north of the 101 as 1. This in effect includes the 101 as a strong barrier between populations on opposite sides of the road.

Determining Spatially Explicit Population Structure

Microsatellite data was converted to pairwise distances using GenAlEx[18]. We analyzed population structure for each of the four target taxa using the program Geneland[19] in the R computer language[20] so that population structure could be determined in a spatially explicit manner. Genetic data was combined with location information to calculate a Bayesian inference of population structure. Models were run for 500,000 iterations with a thinning interval of 100 using all existing genetic data for each species separately. It should be noted here that Geneland and its inference methods do not include any environmental predictors. Rather, the genetic structure and geographic coordinates of each location's samples are compared and used to infer the number of populations present in the study region, as well as the most likely membership to each one of those populations for every pixel within the study region.

Predicting Genetic Variation Across the Study Region

Generalized Dissimilarity Modelling (GDM) is models beta-diversity across a landscape. Specifically, it is a matrix regression technique and predicts biotic turnover/ dissimilarity between sites based upon environmental dissimilarity and geographic distance. The advantages of GDM are that it makes few assumptions regarding the relationship between environment and genetic diversity and can explicitly take into account the potential influence of geographic distance (i.e. isolation-by-distance) on generating population divergence. It can also fit nonlinear relationships of environmental variables to biological variation by using an I-spline basis function and it provides an assessment of model performance is made through permutations. Additional useful information given by GDM is the relative importance of individual environmental variables in explaining the observed genetic diversity[21]. GDM is a two-step method: first, dissimilarities of a set of predictor variables are fitted to the genetic or phenotypic dissimilarities (the response variables). In an iterative process, predictor variables are added to and removed from the model, and only the variables that significantly improve the model are retained. Specifically, predictor variables are introduced to the model in random order and the variation in the response variable explained by the inclusion of that variable is compared to that without the variable (ΔD). Second, over many iterations the predictor variable is added again, but with the values randomized among sampling sites, resulting in a random distribution of ΔD_{rand}. ΔD is compared to ΔD_{rand}, based on which the predictor variable is either retained or dropped. Generalized dissimilarity models were run using an Avenue script in ArcView v 3.2 in conjunction with a SPlus v 4 script obtained from the authors of GDM [21].

To create spatially explicit projections of genetic variation across the landscape, all GDM runs consisted of 5000 randomly distributed classification training samples and 50 final GDM classes. As a means to contrast hypotheses regarding environmental differences, dispersal barriers, and geographic distance, we ran models with different sets of predictor variables. First, all predictor variables were entered (full model). Importance of any of those variables in a model would implicate its role in maintaining divergence between populations. To evaluate cross-correlations among predictor variables, in the remaining models the following subsets of the predictor variables were entered: only environmental variables, only geographic distance, or only the highway barrier. The percentages of the variation explained by each model were compared to assess which parameter set best explained the observed genetic variation.

To estimate the sensitivity of the models to the spatial resolution of the environmental variables, various combinations of high- and low-resolution data were used in our models. These consisted of using the full high-resolution variable set as a basis and adding single low-resolution variables (Tree, SRTM, NDVIstd, QSCATaug) that had performed well in previous analyses of low-resolution layers. Subsequently, all high- and low- resolution variables were used to set up a full model including both resolutions. In addition, high-resolution data was reaggregated to generate three medium- resolution data sets with 150 m (Factor 5), 300 m (Factor 10) and 600 m (Factor 20) resolutions. Further processing in ArcMap10 was performed on the full model results to visualize genetic variation for each species.

Projecting Genetic Change Under Climate Change

When projected onto estimated future environmental conditions, predictions of genetic diversity can be used to understand its spatio-temporal dynamics under various scenarios of changing environmental conditions. To assess the potential impact of future climate change on genetic diversity in our study species, we first created a model for only current climatic conditions (i.e. without vegetation and elevation variables), and subsequently projected these genotype-climate association onto predicted future climate layers from the IPCC 4th Assessment Report A1B climate change scenario for 2080-2090. Confidence intervals around climate change scenarios tend to become broader with predictions further into the future. Nevertheless, as the 2080-2090 predictions represent more extreme climate change scenarios, they were the focus of our modeling efforts (Models for 2050-260 were also produced, and will be made available online and by request). In fact, the 2080 predictions of atmospheric CO_2 concentrations may be reached much sooner, as current emissions already exceed the trajectories of the highest scenarios. Thus, projections of genetic variation on the 2080-2090 climate scenarios may be relevant for purposes of our study. From the predictions of genetic variation under current and future climate, we generated a change map for each of the target taxa, showing the level of predicted change in genetic variation between current conditions and those for the period 2080-2090.

Results

Determining Spatially Explicit Population Structure

For each of the four target taxa, population structure was determined using existing genetic data and geographic locations. For three of the taxa (Side-blotched lizard, western fence lizard, and wrentit) significant population structure was observed across the study region, divided largely into two populations, one northern and one southern within the SMMNRA (Figs 1-3). In each target taxon, this split between the two populations aligned almost perfectly to a region north of the CA-101 Highway and a region south of this major freeway. Consultation with scientists at the SMMNRA and previous research[9,22] has supported the hypothesis that this freeway and others can act as major barriers to dispersal and gene flow of relatively low vagility species, and our results from analyses of population structure confirm this.

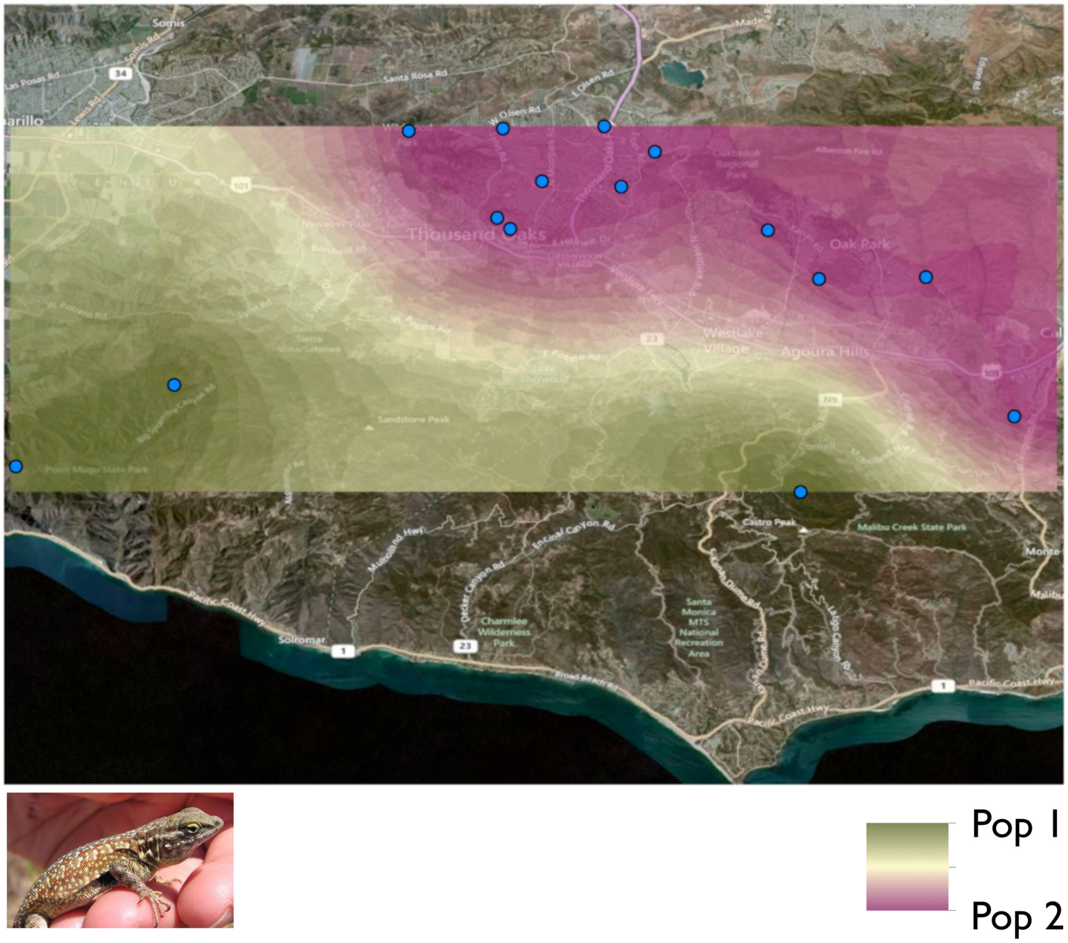

Fig. 1. Population structure of the Side-blotched lizard (*Uta stansburiana*) as determined by Geneland. Colors represent probability of belonging to one of two populations. Although sampling was sparse in the southern region, these locations are more genetically similar than geographically closer locations north of the CA-101.

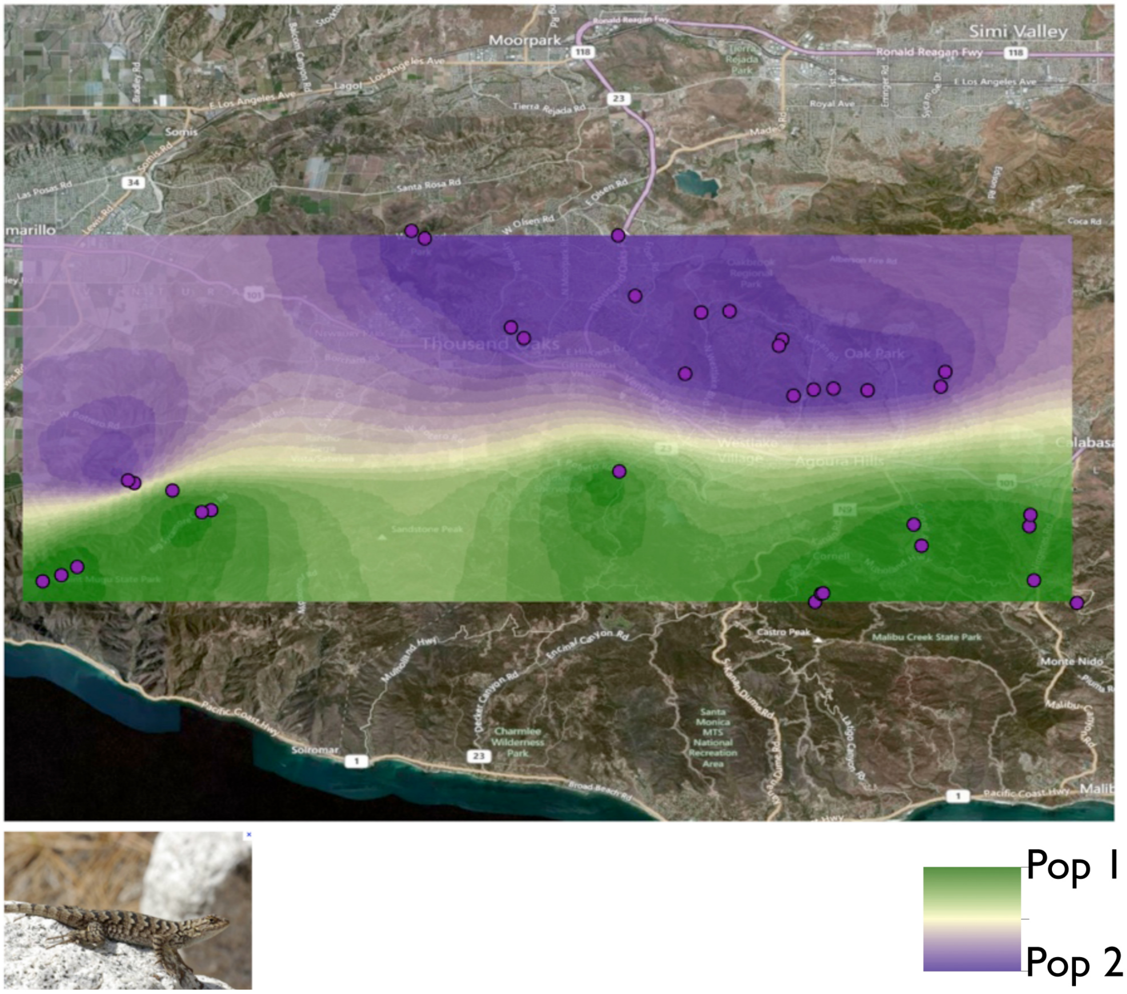

Fig. 2. Population structure of the western fence lizard (*Sceloporus occidentalis*) as determined by Geneland. Colors represent probability of belonging to one of two populations. Two southwest locations (in purple here) are more closely related to locations north of the CA-101, suggesting that despite acting as a clear barrier, some gene flow across the freeway may occur.

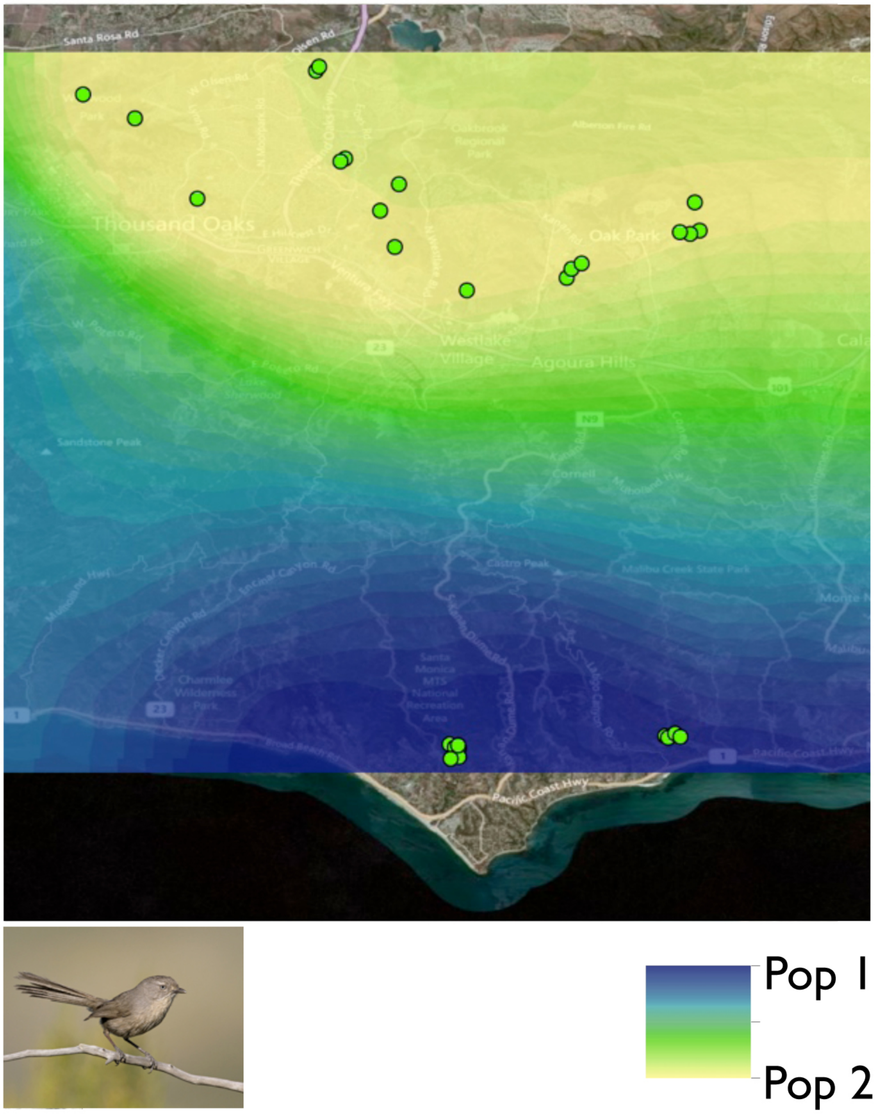

Fig. 3. Population structure of the wrentit (*Chamaea fasciata*) as determined by Geneland. Colors represent probability of belonging to one of two populations. Despite the ability to fly, wrentits are known as a low vagility species and may still be limited in dispersal by the same major barriers that terrestrial vertebrates encounter.

For the final taxon (western skink), no major barriers to dispersal were observed and the most likely number of populations observed was six (Fig. 4). Interestingly, locations that were more genetically related on either side of the CA-101 in this species corresponded to known underpasses or connecting corridors (several corridors in the east of the 23 highway and in the Agoura Hills region), and could represent locations where dispersal and gene flow are possible. It is possible that for this species, the freeway does not present the same type of barrier to gene flow as in the other three species studied.

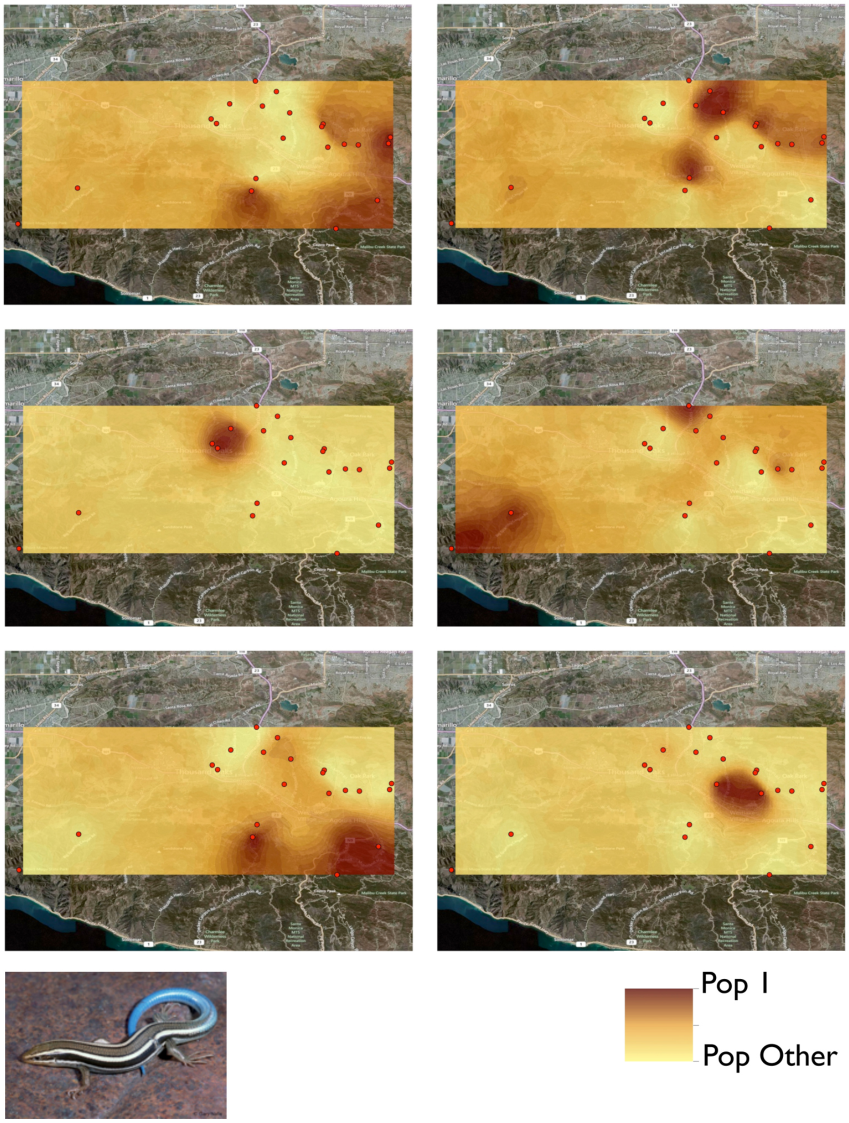

Fig. 4. Population structure of the western skink (*Plestiodon skiltonianus*) as determined by Geneland. Color represents probability of belonging to one of six populations. For this species, the CA-101 seems to act as less of a barrier to dispersal and gene flow, particularly along the eastern edge of the study region.

Predicting Genetic Variation Across the Landscape

Side-blotched lizard (*Uta stansburiana*)

The most important variables explaining genetic variation in the side-blotched lizard (*Uta stansburiana*) were tree cover, surface moisture (QSCAT), vegetation cover (as measured by NDVI), and a mixture of temperature (bio1, bio2) and precipitation variables (bio18). The maximum amount of genetic deviation explained by our full model was 50.2 %, suggesting that much of the variation seen in neutral genetic markers can be attributed to differences in environmental variables across locations. In this species, only 5.2 % of the genetic variation was explained by geographic distance between locations, suggesting patterns of genetic variation do not follow simple, linear gradients.

Table 4. Most important variables and variation explained for all GDM runs for the side-blotched lizard (*Uta stansburiana*).

Resolution		Predictive Variables	Predicted Deviation [%]
High	Full	Eucl	5.15
Reaggregated	Factor 5	Temp & Eucl	7.05
	Factor 10	Temp, Tree & Eucl	11.83
	Factor 20	Temp	15.15
Mixed	High + Tree	Tree (low) , Eucl & Tree	16.10
	High + SRTM	Eucl & Tree	9.80
	High NDVIstd	Eucl, Tree & NDVIstd (low)	10.71
	High + QSCATaug	QSCATaug & Tree	19.12
	High + Low	QSCATaug, NDVI (low), BIO01, Tree (low), 101	79.84
Low	Full	QSCATaug, NDVI, BIO01, Tree, 101	79.84
	NoEnv	Eucl	5.15
	NoEucl	QSCATaug, NDVI, BIO01, Tree, 101	79.84

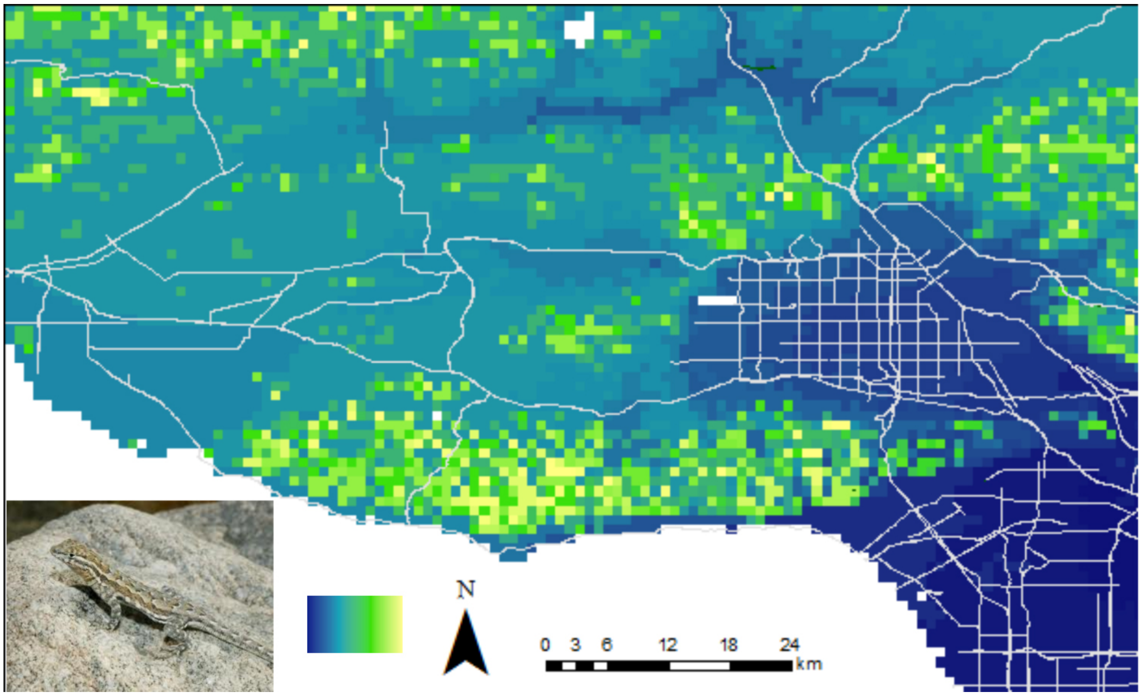

Fig. 5. Prediction of genetic turnover in the side-blotched lizard in Southern California based on GDM analyses. High genetic diversity in this species was seen along the Southern Coast, a center region east of highway CA-23, and a northeastern region in the Angeles National Forest.

Western fence lizard (*Sceloporus occidentalis*)

Modeling results for the western fence lizard suggests that the majority of genetic variation can be explained by environmental variation, particularly by surface moisture, tree cover, and temperature. Our best model under the GDM framework explained nearly 88% of the total genetic deviation across locations for this species. Importantly, geographic distance explained none of the genetic variation observed, again suggesting that population structure can likely be attributed to selection by local environmental conditions rather than by isolation-by-distance.

Table 5. Most important variables and variation explained for all GDM runs for the western fence lizard (*Sceloporus occidentalis*).

Resolution		Predictive Variables	Predicted Deviation [%]
High	Full	Elevation & Temp	34.28
Reaggregated	Factor 5	Temp & Elevation	39.67
	Factor 10	Tree, Temp & Elevation	70.05
	Factor 20	Temp, Elevation & Tree	37.19
Mixed	High + Tree	Tree	74.77
	High + SRTM	SRTM, Temp & Tree	19.37
	High + NDVIstd	Temp	20.56
	High + QSCATaug	QSCATaug, Tree & Temp	87.60
	High + Low	Tree, BIO01	80.67
Low	Full	Tree, BIO01, 101	79.70
	NoEnv	-	0
	NoEucl	Tree, BIO01, 101	79.70

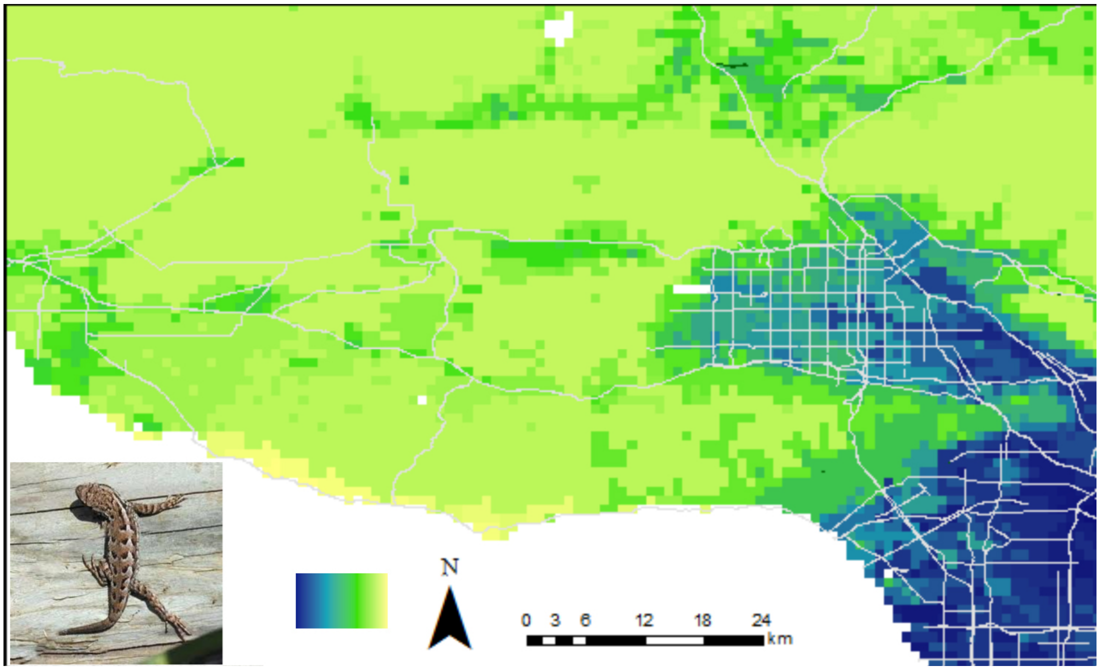

Fig. 6. Prediction of genetic turnover in the western fence lizard in Southern California based on GDM analyses. High genetic diversity in this species was seen in four distinct regions: along the Southern Coast, in a center region east of highway CA-23, in a northeastern region in the Angeles National Forest, and along a western portion of the SMMNRA centered in the Oxnard area.

Western skink (*Plestiodon skiltonianus*)

Results from GDM analyses for the western skink indicate that up to 45% of the genetic deviation in this species can be explained by environmental variables. While geographic distance played a role in explaining some of this variation (~8%), the most important variables in our model were vegetation (as determined by NDVI) and elevation.

Table 6. Most important variables and variation explained for all GDM runs for the western skink (*Plestiodon skiltonianus*).

Resolution		**Predictive Variables**	**Predicted Deviation [%]**
High	Full	Eucl & Elevation	9.12
Reaggregated	Factor 5	Eucl & Elevation	10.60
	Factor 10	Eucl & Elevation	11.80
	Factor 20	Elevation & Eucl	19.51
Mixed	High + Tree	Eucl & Elevation	9.12
	High + SRTM	SRTM (low) & Eucl	22.41
	High + NDVIstd	Elevation, Eucl & NDVIstd (low)	23.11
	High + QSCATaug	Elevation & Eucl	21.80
	High + Low	NDVI (low) , Eucl, SRTM (low)	44.63
Low	Full	NDVI (low) , Eucl, SRTM (low)	44.62
	NoEnv	Eucl	7.80
	NoEucl	NDVI, QSCATaug, SRTM	44.62
LCP	Full	Dist. Matrix, NDVI (low), Eucl, SRTM (low)	48.21

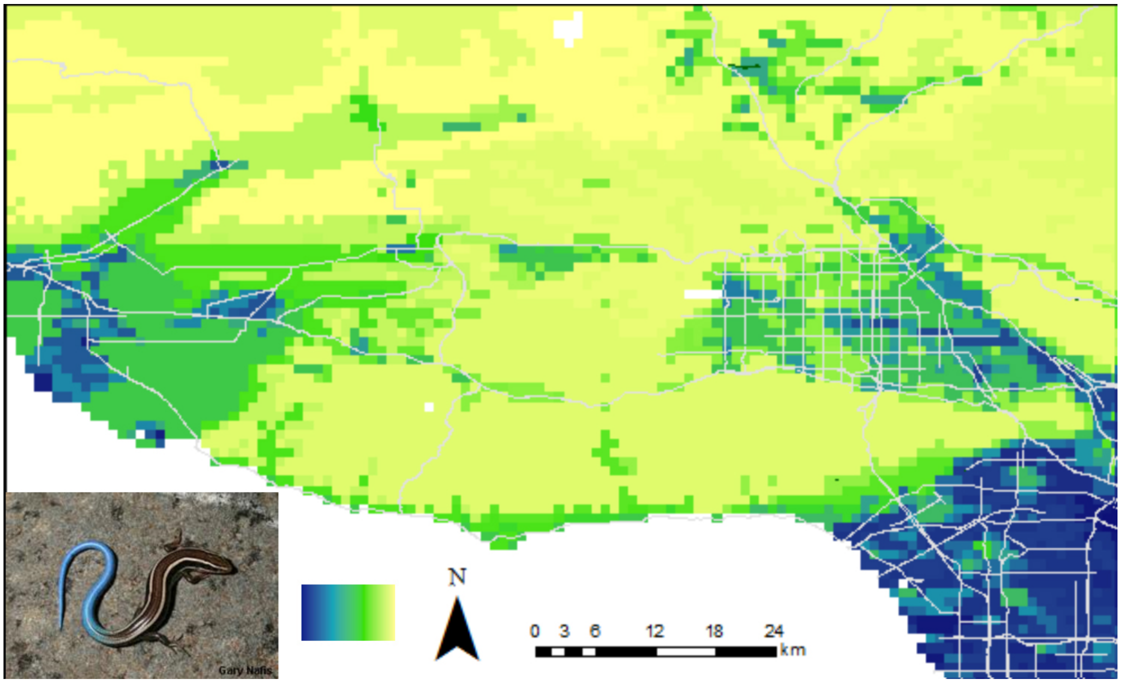

Fig. 7. Prediction of genetic turnover in the western skink in Southern California based on GDM analyses. High genetic diversity in this species was seen in four distinct regions: along the Southern Coast, in a center region east of highway CA-23, in a northeastern region in the Angeles National Forest, and along a western portion of the SMMNRA centered in the Oxnard area.

Wrentit (*Chamaea fasciata*)

Genetic deviation in the wrentit was found to be explained by three environmental variables, elevation, temperature, and vegetation (Table 7). A maximum of 97.5% of genetic deviation was explained by our best model for this species, and models explained equal genetic variation even when geographic distance was excluded from analyses, suggesting distance alone does little to explain genetic variation in this species.

Table 7. Most important variables and variation explained for all GDM runs for wrentit (*Chamaea fasciata*).

Resolution		Predictive Variables	Predicted Deviation [%]
High		Elevation & Temp	3.81
Reaggregated	Factor 5	Elevation	1.26
	Factor 10	Elevation	0.20
	Factor 20	Elevation	1.94
Mixed	High + Tree	Elevation & Temp	3.81
	High + SRTM	Temp	59.46
	High + NDVIstd	Temp	97.50
	High + QSCATaug	Temp	59.46
	High + Low	NDVIstd	71.93
Low	Full	NDVIstd	69.72
	NoEnv	-	0
	NoEucl	NDVIstd	69.72
LCP	Full	NDVIstd	71.93

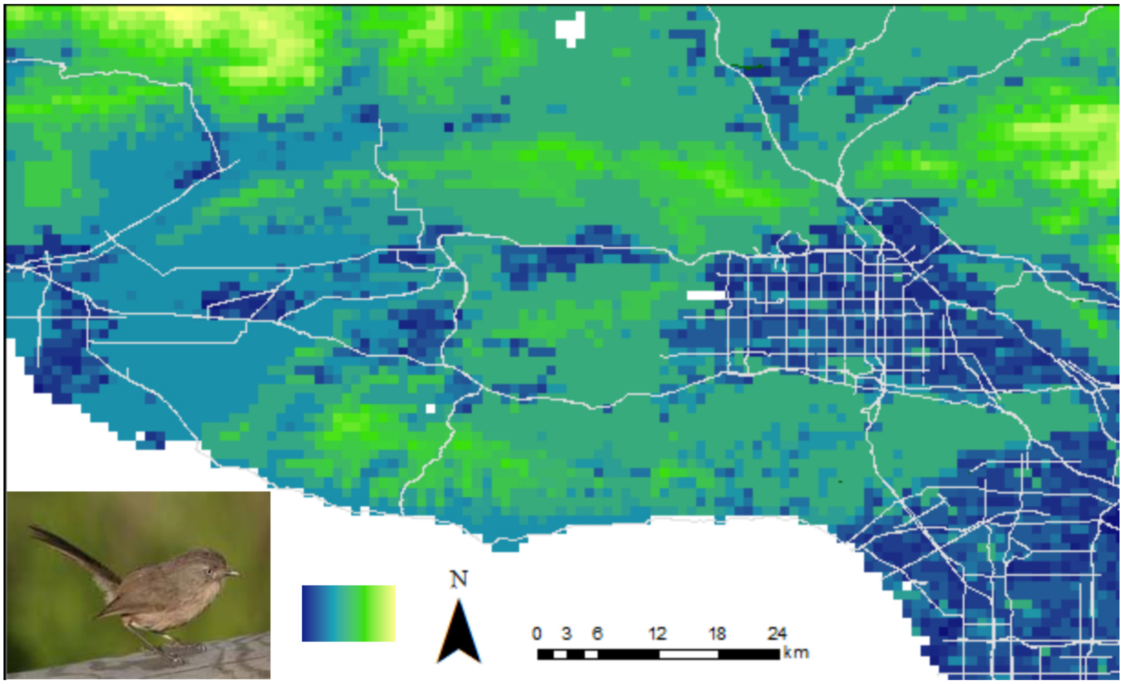

Fig. 8. Prediction of genetic turnover in the wrentit in Southern California based on GDM analyses. High genetic diversity in this species was seen in four distinct regions: along the Southern Coast, in a center region east of highway CA-23, in a northeastern region in the Angeles National Forest, and along a western portion of the SMMNRA centered in the Oxnard area.

Identifying Current Genetic Variation Hotspots

Examining each of the target taxa individually, we found a variety of environmental variables play a role in explaining genetic variation, and a range of explanatory power in our models (from 44.6% to 97.5%). However, geographically, several key locations were consistently found to harbour high genetic variation across all taxa. By examining predictive maps for each of our target taxa, we identified four key areas within the study region that represent hotspots in terms of genetic variation in these species (Fig. 9).

Southern Coast: The first of these hotspots was identified in the southernmost region of the SMMNRA, in an area south of the CA-101 and centered around the Malibu area. In fact, much of this coastline was found to exhibit high genetic variation in all four target taxa.

Central/Simi Valley: Another hotspot was identified in the center region of the SMMNRA, in an area divided by the CA-23 highway and including the Simi Valley at the eastern extent and Arroyo Vista and Moorpark on the west. Each of the four species demonstrated high genetic variation in this area, supporting previous findings that this area contains high genetic variation[9].

Northeastern/Angeles National Forest: A northern region on either side of the I-5 highway was found to contain high genetic variation on all four target taxa. This region extended into the Angeles National Forest on the eastern border, and the Santa Clarita Woodlands Park on the western side.

Western/Oxnard: The last of the genetic variation hotspots was identified in the western extent of the SMMNRA, centered in the Oxnard area. In three of the four target taxa analysed, this region contained a high amount of genetic variation across a relatively small geographic area.

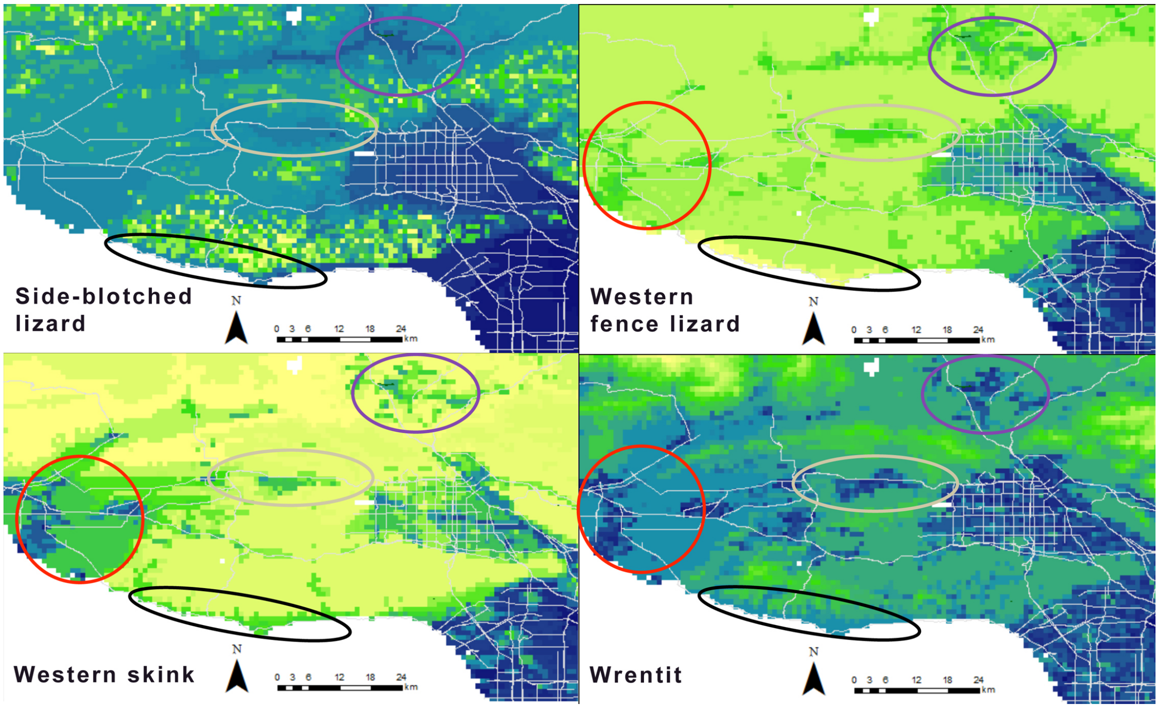

Fig. 9. Four identified hotspots of genetic variation in the Santa Monica Mountains National Recreation Area. High genetic diversity is seen four distinct regions: along the Southern Coast (black circle), in a center region east of highway CA-23 (gray circle), in a northeastern region in the Angeles National Forest (purple circle), and along a western portion of the SMMNRA centered in the Oxnard area (red circle). Although genetic variation was low for the side-blotched lizard in this last area, the remaining three taxa exhibited high variation across this relatively small region.

Projecting Variation Change Under Climate Change

By using the relationship between genetic variation and environmental variables under current climate conditions, we were then able to construct projections of how genetic variation may change under changing climate conditions. Results from the four target taxa are presented below, with general conclusions following.

Whereas spatial patterns of genetic variation under current climate conditions are similar, projected changes in these patterns vary considerable among species. Projections for the side-blotched lizard were not possible, because a model using only current climate, instead of both climate and vegetation variables, did not explain any genetic variation. Because spatial patterns of vegetation are highly unclear under future climate conditions, we could, therefore, not create a future prediction for this species.

Predicted changes for the western fence lizard are relatively uniform across the study area, except for particularly large changes in the northwest and east (Fig. 10). In contrast, changes in the western skink are predicted to be high in the Oxnard area and into the Angeles National Forest (Fig. 11). Genetic changes in the wrentit are generally predicted to be higher than in the two other species, and are highly spatially heterogeneous (Fig. 12).

Western fence lizard (*Sceloporus occidentalis*)

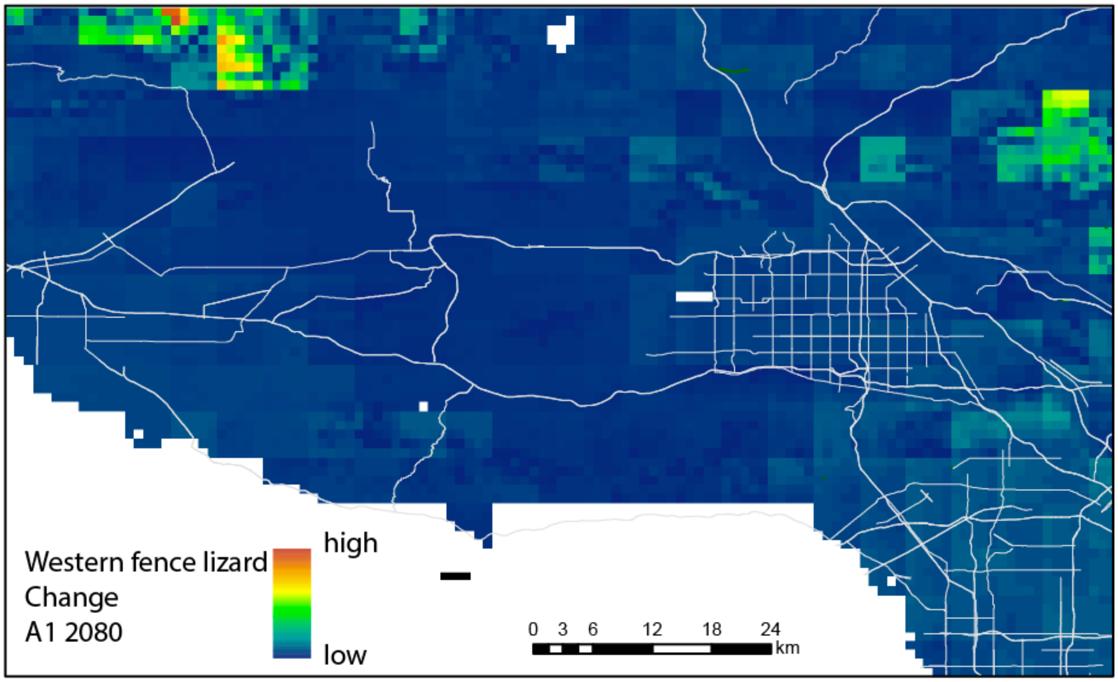

Fig. 10. Identified areas of change in genetic variation in the western fence lizard in Southern California by the year 2080, under an A1 climate scenario.

Western skink (*Plestiodon skiltonianus*)

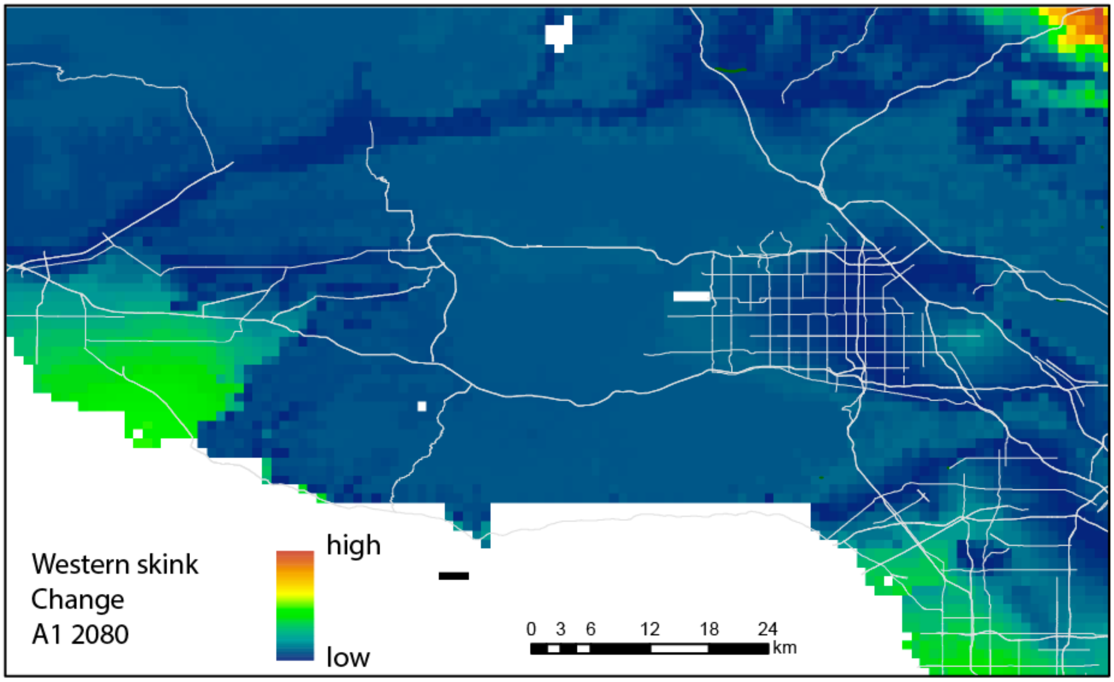

Fig. 11. Identified areas of change in genetic variation in the western skink in Southern California by the year 2080, under an A1 climate scenario.

Wrentit (*Chamaea fasciata*)

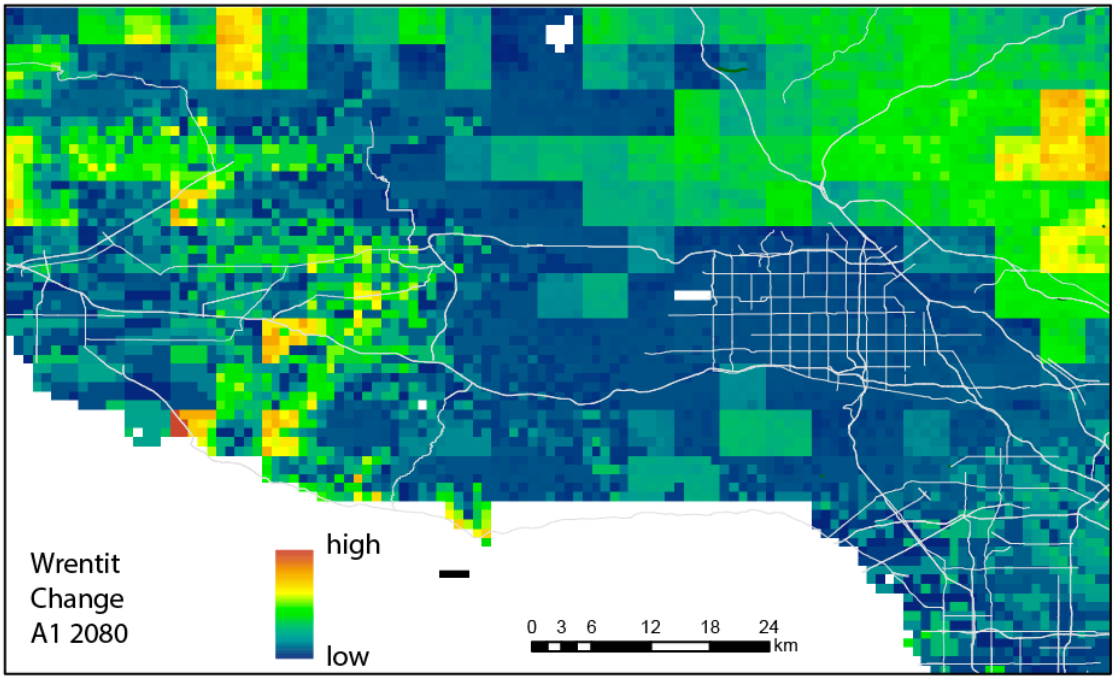

Fig. 12. Identified areas of change in genetic variation in the wrentit in Southern California by the year 2080, under an A1 climate scenario.

Discussion and Management Considerations

Climate change poses an urgent and significant threat to biodiversity[23,24]. Species may be unable to respond to climate change unless they have the capacity to shift their ranges. However, range shifts may not be possible for multiple reasons, including relatively low vagilities (or disparities in vagility within mutualistic species), isolation of populations due to habitat fragmentation, new biotic interactions resulting from a different species composition, or elevational constraints. Hence, many populations will have no choice but to adapt to changing climate conditions *in situ*. A prudent conservation strategy therefore is to design reserves that maximize intraspecific variation. Our results provide the first assessments of the utility of intraspecific genetic and morphological variation for conservation prioritization in the SMMNRA.

It has previously been suggested that the CA-101 highway is a considerable barrier to dispersal, and hence gene flow[22]. Analyses of population structure not taking into account local environmental conditions support this hypothesis. A clear north-south gradient exists in three of the four study species, with a sharp transition concurrent with the location of the highway. Yet, taking into account the potential effect of selection due to local environmental conditions revealed that habitat may be the most important driver of population divergence. Nevertheless, in two species, the CA-101 was selected by the model as a significant contributor to explaining genetic variation. These results suggest that this highway may indeed be a barrier to gene flow for small reptiles and birds, and warrant further research with respect to the strength of the barrier and potential ways to mitigate its impact. At least one of our target taxa, the western skink, demonstrated significant dispersal and connected populations across this barrier, suggesting either natural or anthropogenically-created (sewers, drainpipes) corridors may in fact serve as useful aids to gene flow and dispersal. An understanding of these major barriers and their varying impacts on genetic diversity in an urban environment is of paramount importance under a changing environment.

In the face of climate change, habitat fragmentation is a major concern, potentially worsening the direct impacts of changing climate conditions in at least two ways. First, barriers will prevent populations from tracking their optimal habitat conditions, leaving adaptation to new conditions as the only means to ensure long-term survival. Second, effective population sizes can be reduced to the extent that they suffer from inbreeding, resulting in the loss of the genetic diversity that is key to the ability to adapt to new conditions. Therefore, it is imperative that efforts be undertaken to maintain dispersal and gene flow between subpopulations.

Despite differences in vagilities and ecological requirements, spatial patterns of genetic variation are largely concordant between the four studied species. These results suggest that a limited number of species could serve as a surrogate for much of the ecological community. In our work in Ecuador, where we modeled genetic variation in seven different species, we found a similar concordance between important areas for conservation among our study species. Thus, conservation efforts that aim at incorporating intraspecific variation into the design of reserves may measure and model genetic diversity in a set of common species that are easy to sample. In addition, we have now applied our conservation prioritization framework to areas at medium (Ecuador) and small (SMMNRA) scales, with similar results with respect to the use of surrogates, suggesting that the framework is useful at multiple spatial scales and in different regions of the world.

The importance of maximizing a species' adaptive potential is emphasized by our predictions of future genetic variation. Even though the exact nature of the future response to changing climate conditions remains unclear, our modeling efforts suggest that the spatial patterns of necessary changes are highly diverse among different species. Indeed, long-term studies of different great tit (*Parus major*) populations in Europe suggest that responses may even vary within species[25]. Because of this uncertainty in potential responses, it will be risky to identify areas that will be climatically stable over time. However, protecting all possible environmentally-associated standing genetic variation will maximize a species' chances to adapt to new conditions. For our study species in the SMMNRA - and likely for a larger set of species for which these four can act as surrogates - this can be done, for example, by identifying areas covering the widest range of genetic variation (or colors in the maps presented in Fig. 9). An efficient strategy is to protect those areas with high levels of genetic variation, i.e. those where many colors are covered in a small area. As such, the four areas highlighted in Fig. 9 can efficiently protect most of the genetic variation in these species. With relatively few species, potentially important areas for protection can be identified visually. However, with more species, the design of areas to protect features of biodiversity is typically formulated as a constrained optimization problem in which the objective is to establish protected areas that meet the representation targets for the features while taking up as little land area as possible[26]. Socio-economic data can be included as part of the constraint on land use. Reserve selection software often used include Marxan[27], Zonation[28], and ResNet[26], which was used for the work in Ecuador[3]. The output of the models of intraspecific variation will be partitioned into classes that represent populations similar for that trait. Classes will be treated in the reserve selection software similarly to species occurrences. That is, a set of reserves is selected based on the requirement that at least a target percentage of the occurrences of each surrogate (i.e., genetic/morphological class or species) should be represented in those reserves. Thus, areas harboring high variation will be preferentially selected, but unique variation will also be protected.

Specific Management Recommendations

- Identify and research corridors allowing for increased connectivity across anthropogenic barriers (CA-101, CA-23, CA-5)
- Investigate additional species (particularly threatened and endangered) within the SMMNRA to determine if identified regions of high genetic variation in common species also contain high genetic diversity in rare species
- Explore land acquisition opportunities in the regions identified harboring high genetic variation in the four target taxa, particularly in those areas falling outside the SMMNRA
- Continue close monitoring of population structure in these and other taxa to best understand temporal change in populations under future climate change

Conclusions and Future Research

Despite the fact that much of the Santa Monica Mountains National Recreation Area (SMMNRA) is comprised of either federally- or privately-owned land that does not face the same increase in urbanization as developing countries do, identifying regions that harbor the highest genetic diversity provides managers and stakeholders the ability to target these areas for further study and research efforts. Endangered or less common species in these areas may be particularly vulnerable to small disturbances in habitat availability or large-scale climate changes that occur in existing habitats. Providing habitat to more 50 threatened or endangered species, the SMMNRA is considered a Mediterranean ecosystem conservation hotspot, and how these less common species will cope with current and future climate change is largely unknown. In addition, our analyses have identified currently unprotected regions north of the CA-101 that contain high amounts of genetic variation in the taxa studied. These locations (west of Simi Valley and west of the Angeles National Forest) could prove to be ideal targets for focused conservation and land acquisition efforts.

Despite identifying regions containing high genetic variation and their changes under climate change revealed in these analyses, additional research would greatly aid in confirming that these regions also harbor high genetic variation in other species. Of particular interest would be those species that are likely to be most impacted by changing climate, such as endangered native plant and insect species that are unable to rapidly move to new habitats. In addition, applying these models to other regions, specifically those that are not afforded the same level of current protection as the SMMNRA, could support the generalizability of our results. We have demonstrated our measures of genetic variation and their link to environmental variability can be a useful tool to capture adaptive potential here in a California LCC, and in tropical regions[3], but their application to other LCC regions in the United States remains unexplored. We are hopeful that the current study acts as impetus for applying the developed methods to additional species and regions in efforts to best inform future management and conservation decisions.

Project Outcomes

1) Two postdoctoral researchers were trained under this project, each under part-time contribution
2) One graduate student from the Department of Ecology and Evolutionary Biology gained experience in genetic analyses and geographic information systems
3) Two undergraduates (one ULCA, one University of Tubingen) assisted and gained knowledge about local biodiversity, use of the R statistical package, and genetic analyses in the R framework
4) Collaborations between UCLA and the Santa Monica Mountains National Recreation Area established; these include the addition of three additional datasets from 3 new target taxa (bobcats, gray foxes, and tree frogs) to be included in further analyses
5) Presentations, in-person scientific meetings, and collaborations were produced to disseminate results of this work

Products/Data Sharing

1) Genetic distances across the SMMNRA established and to be made publically available
2) Spatially interpolated maps of population structure and assignment publically available for each of the four target taxa
3) Current Maps of Generalized Dissimilarity Models for each of the four target taxa
4) Future Projected Maps of Genetic Variation Change publically available for two decades (2050, 2080) under the A1 Climate Scenario. Additional decades and scenarios made available upon request.
5) Data and results to be uploaded to the Climate Commons
6) Manuscript to be submitted to Evolutionary Applications in preparation (submission date - January 2014), focused on four target taxa
7) Additional manuscript examining morphological data in four target taxa as well as the inclusion of 3 additional taxa (2 mammals, 1 amphibian) to be completed in Spring 2014
8) Results to date presented to CA-LCC webinar (February 2013) and at various scientific meetings (IALE, Rhode Island, 2012, presented by R. Harrigan, and ESEB, Lisbon, Portugal, 2013, presented by Henri Thomassen)
9) Continued collaboration with SMMNRA researchers (Seth Riley, Katy Semple Delaney) on future publications and conservation and management of rare or endangered species within the SMMNRA

References

[**1**] Myers et al. 2000 Nature 403:853-858

[**2**] Thomassen et al. 2010 Evol Appl 3:1-16

[**3**] Thomassen et al. 2011 Evol Appl 4:397-413

[**4**] Smith et al. 1993 Biodivers Lett 1:164-167

[**5**] Crandall et al. 2000 Trends Ecol Evol 15:290-295

[**6**] Moritz 2002 Syst Biol 51:238-254

[**7**] Forest et al. 2007 Nature 445:757-760

[**8**] Smith & Grether 2008 In: Carroll & Fox (Eds) Oxford University Press, Oxford

[**9**] Delaney et al. 2010 PloS ONE:e12767

[**10**] Thomassen et al. 2010 Mol Ecol 19:3532-3548

[**11**] Turner et al. 2003 Trends Ecol Evol 18:306-314

[**12**] Gaston et al. 2000 J Appl Ecol 37:39-59

[**13**] Nagendra et al. 2001 Internatl J Remote Sens 22:2377-2400

[**14**] Justice et al. 1998 IEEE Trans Geosci Remote Sens 36:1228-1249

[**15**] Foll & Gaggiotti 2006 Genetics 174:875-891

[**16**] Joost et al. 2007 Mol Ecol 16:3955-3969

[**17**] http://asterweb.jpl.nasa.gov/gdm.asp

[**18**] Peakall and Smouse 2012 Bioinformatics 28:2537-2539

[**19**] Guillot et al. 2005 Mol Ecol Notes 5:712-715

[**20**] R Core Team 2013 R: A language for statistical computing http://www.R-project.org

[**21**] Ferrier et al. 2007 Diversity Distrib 13:252-264

[**22**] Riley et al. 2006 Mol Ecol 15:1733-1741

[**23**] Fischlin et al. 2007 Climate Change 2007: IPCC 4th Assessment Cambridge: 211-272

[**24**] Sinervo et al. 2010 Science 328:894-899

[**25**] Marcel et al. 2003 Proc Roy Soc B 270:367-372

[**26**] Sarkar et al. 2009 Spatial Conservation Prioritization: Quantitative Methods and Computational Tools Cambridge University Press: 235-248

[**27**] Ball and Possingham 2009 Spatial Conservation Prioritization: Quantitative Methods and Computational Tools Cambridge University Press: 185-195

[**28**] Moilanen and Kujala 2006 Zonation spatial conservation planning framework and software v. 1.0