A landscape genetics approach to linkage planning in the Mojave Desert

Amy Vandergast
U.S. Geological Survey
Western Ecological Research Center
San Diego Field Station

avandergast@usgs.gov

- Robert Fisher (Research Biologist)
- Dustin Wood (Geneticist)
- Jonathan Richmond (Geneticist)
- Todd Esque & Ken Nussear (Henderson, NV)

SDFS Genetics Lab

- Est. 2005
- Landscape and conservation genetics of wild populations of animals in the western U.S.

SDFS Genetics: Research Directions

1. Describing and comparing patterns of genetic variation across landscapes and applications to conservation planning
2. Effects of recent habitat fragmentation on population connectivity, sequential landscape modeling
3. Rare species population genetics (defining ESUs, examining subspecies delineations, management units)
4. Molecular tools for monitoring
5. Molecular systematics

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What is landscape genetics?

- Combines methodologies from landscape ecology, population genetics and spatial statistics.
- High-resolution genetic data used to determine the influences of landscape features on gene flow and dispersal.
- Effective for understanding movement and gene flow in species where direct estimates of movement (through mark recapture, radio telemetry, etc.) are difficult to obtain.

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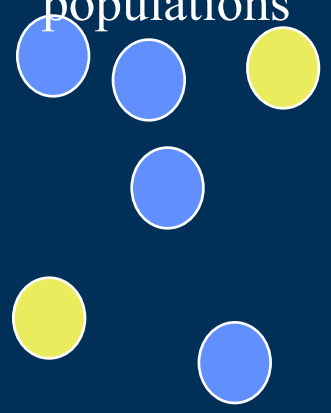
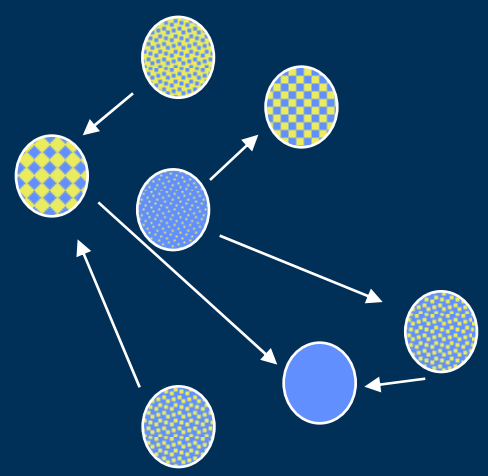
- Selectively neutral genetic markers provide estimates of gene flow (dispersal + successful reproduction)

- Measured as differences in allele frequencies between populations or individuals.

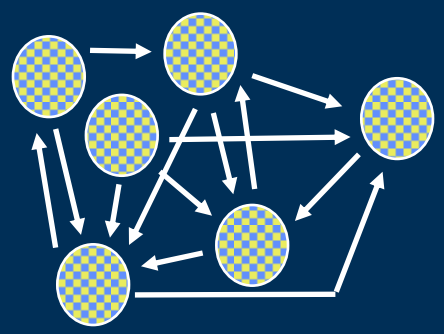
No gene flow between populations populations



Some gene flow between populations



High gene flow between populations



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Typical geographic analysis of genetic data

"Isolation by distance" plots.

A decrease in genetic similarity with increasing distance

* implies limited spatial movement

Slatkin 1993

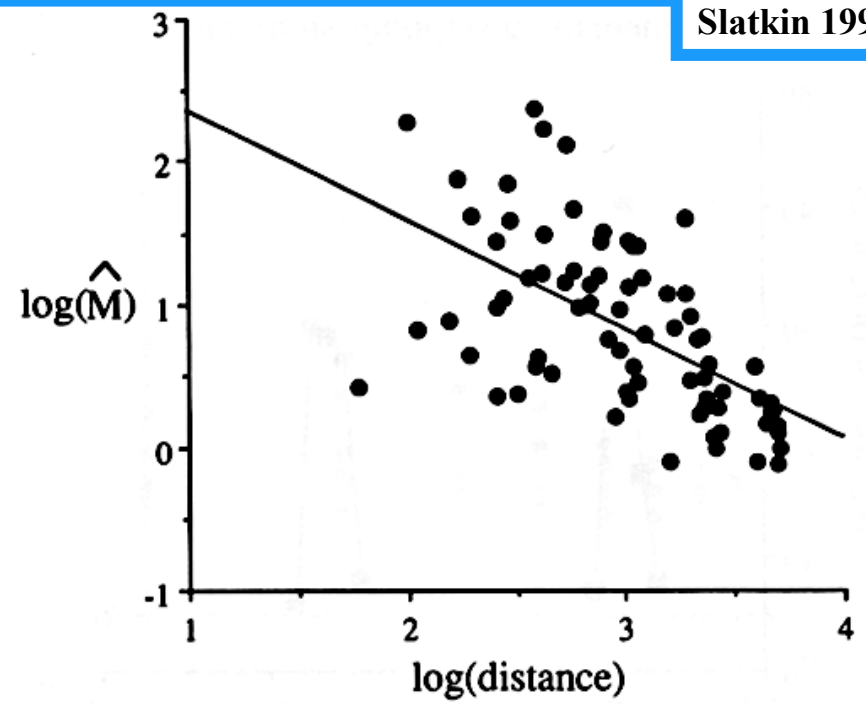

FIG. 10. $\text{Log}_{10}(\hat{M})$ plotted against $\log_{10}$(distance in km) for the glaucous wing gull, *Larus glaucescens*. Data are in Bell (1992) and were kindly provided by the author. Samples were taken from 14 locations on the west coast of North America. Sample sizes ranged from 8 to 20 individuals. Twenty-six polymorphic loci were surveyed. The line was generated using a conventional linear regression: $\log(\hat{M}) = 3.12 - 0.77 \log(d)$ with an R^2 value of 0.343.

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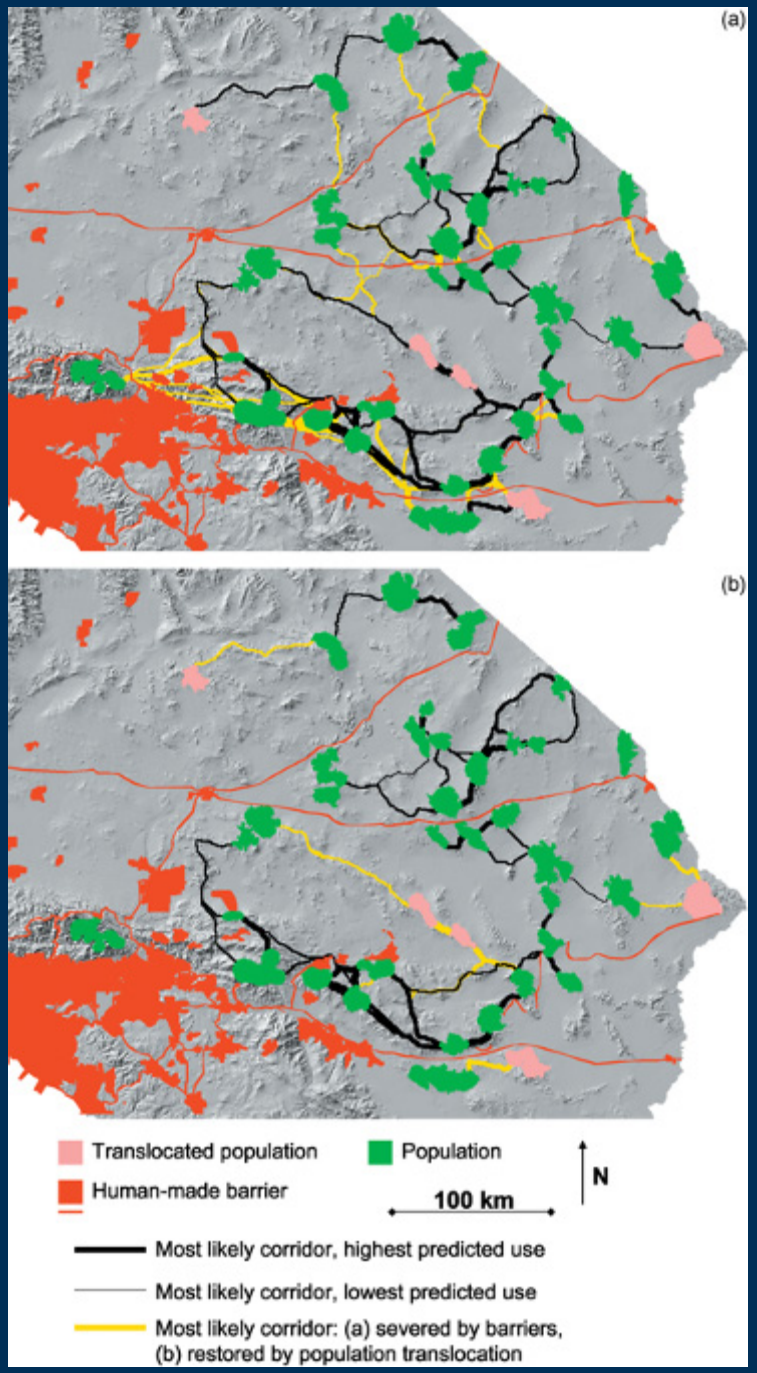
Newer Analyses: Desert Bighorn Sheep

- Does gene flow vary as a function of distance alone or distance + slope + road barriers?
- Created different "cost" models and tested fit to gene flow.
- From optimized model, identified dispersal corridors, using "least cost path"

Epps et al 2007 Journal of Applied Ecology **44:** 714–724



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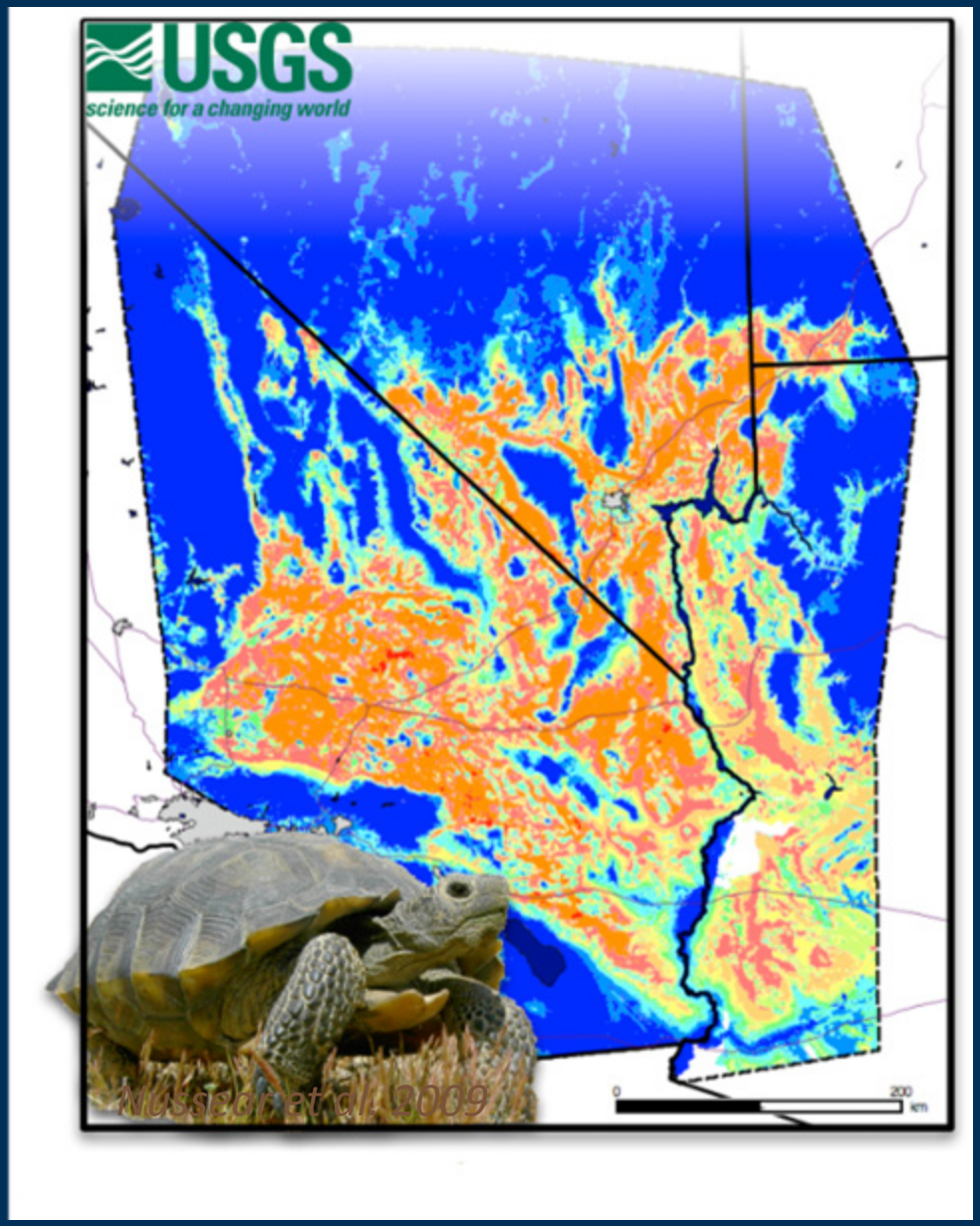
Newer Analyses: Desert Tortoise

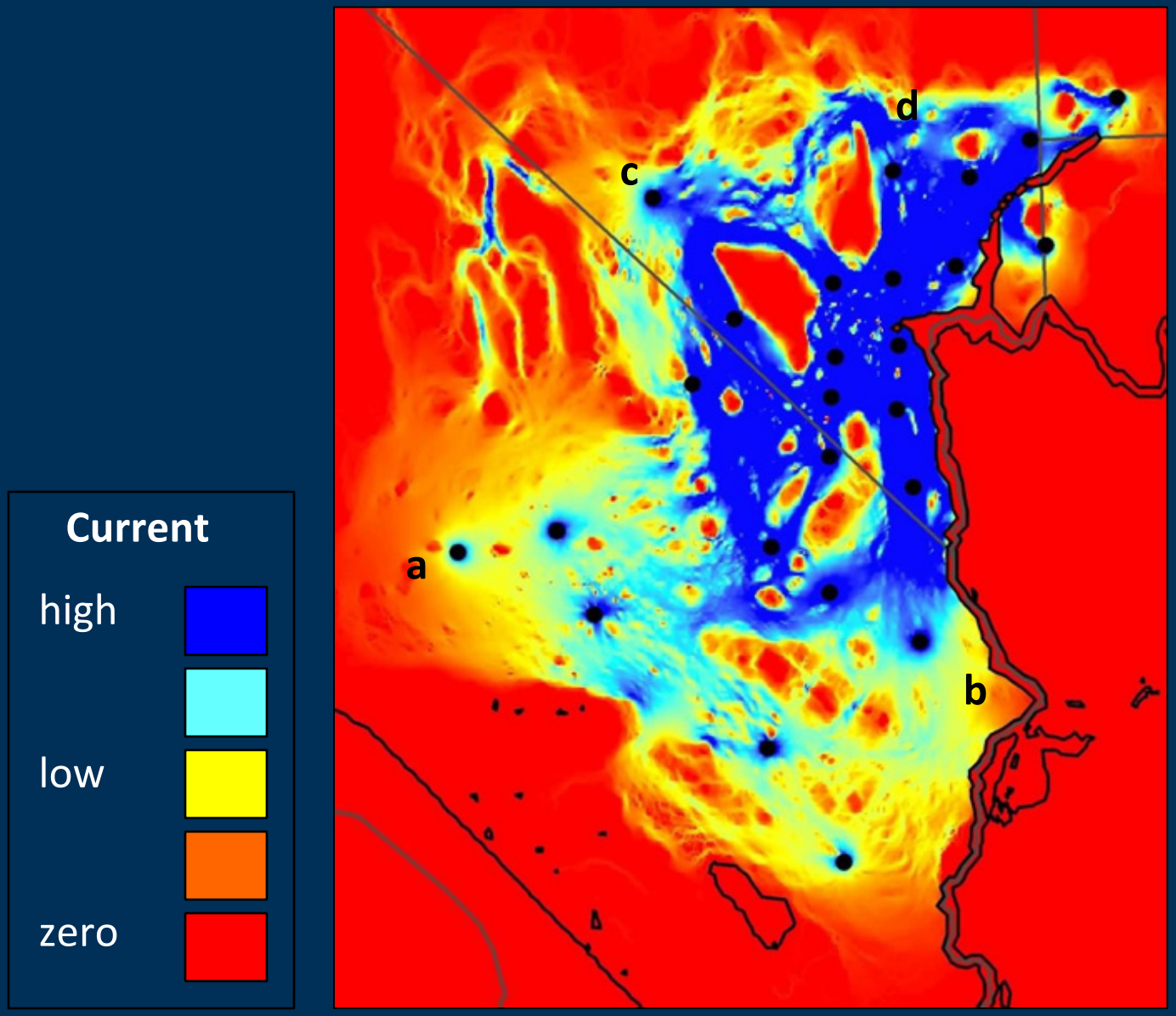


Potential Habitat Map

- Currently used by BLM, and consulting firms for decision-making on project proposals
- Available online to agencies and public

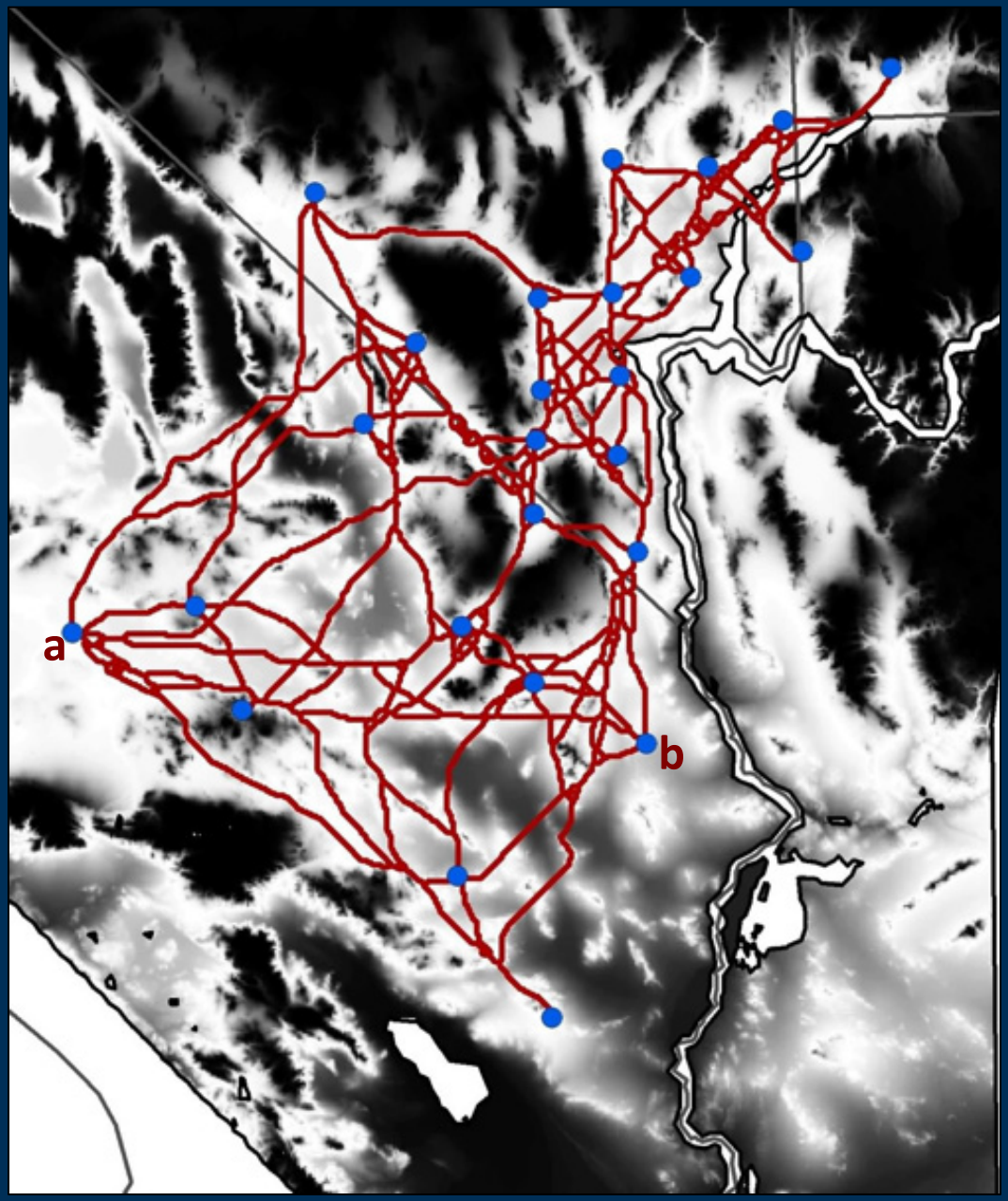
http://pubs.usgs.gov/of/2009/1102/

Desert Tortoise Genetic Connectivity



B. Hagerty 2009

Desert Tortoise Genetic Connectivity



Least cost path

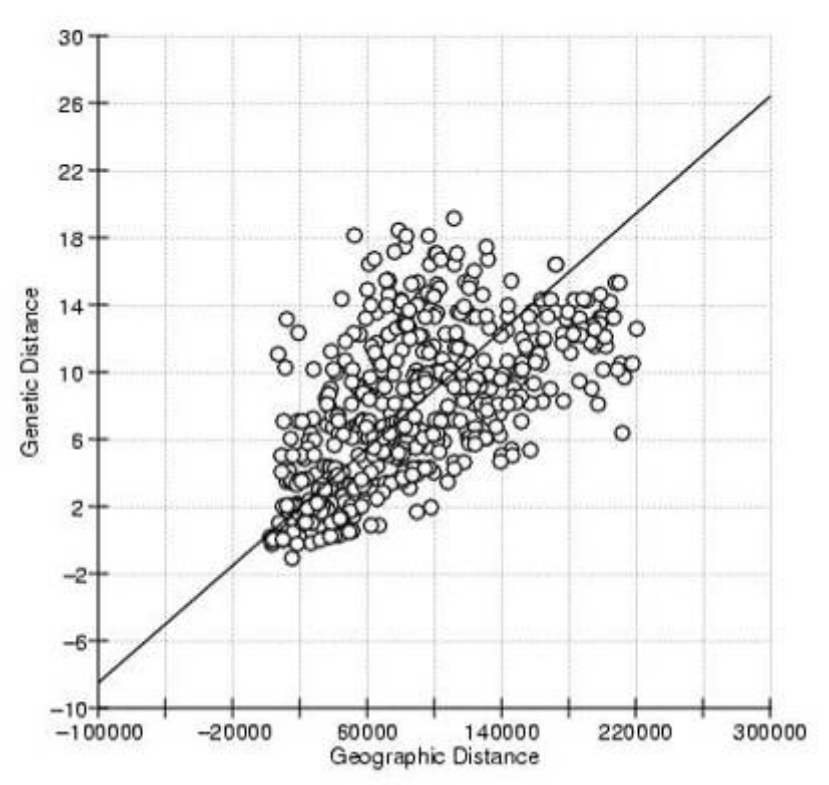
Movement between two locations through most suitable habitat

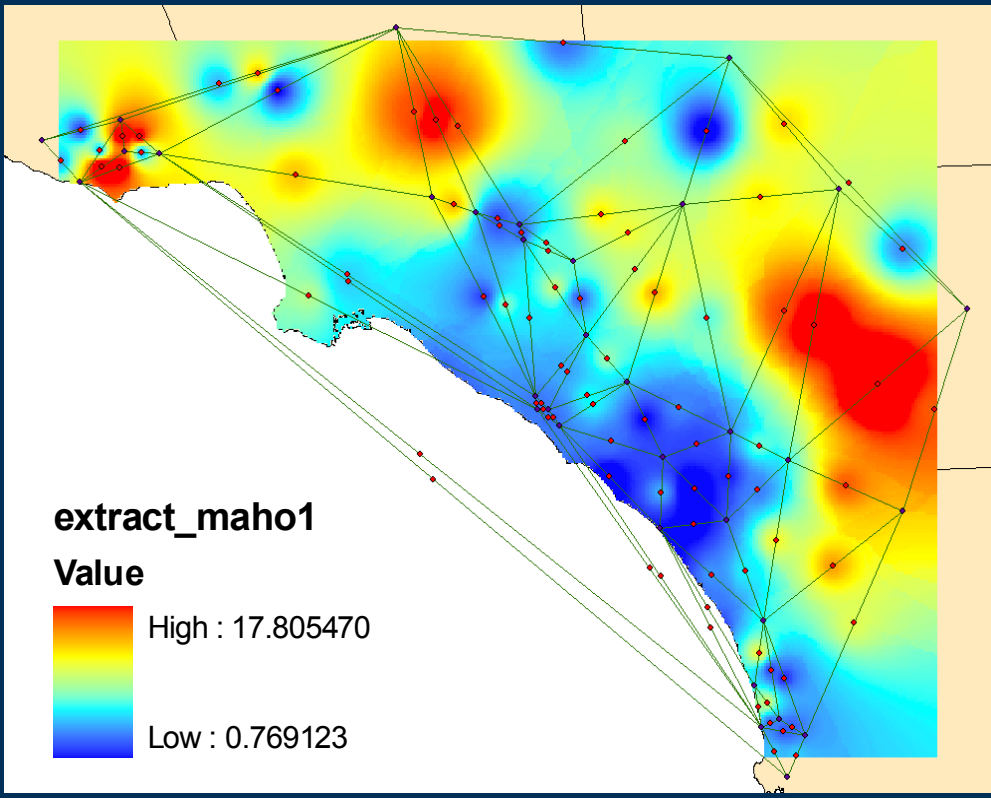
Cumulative least cost paths between all 25 locations ( )

B. Hagerty in review

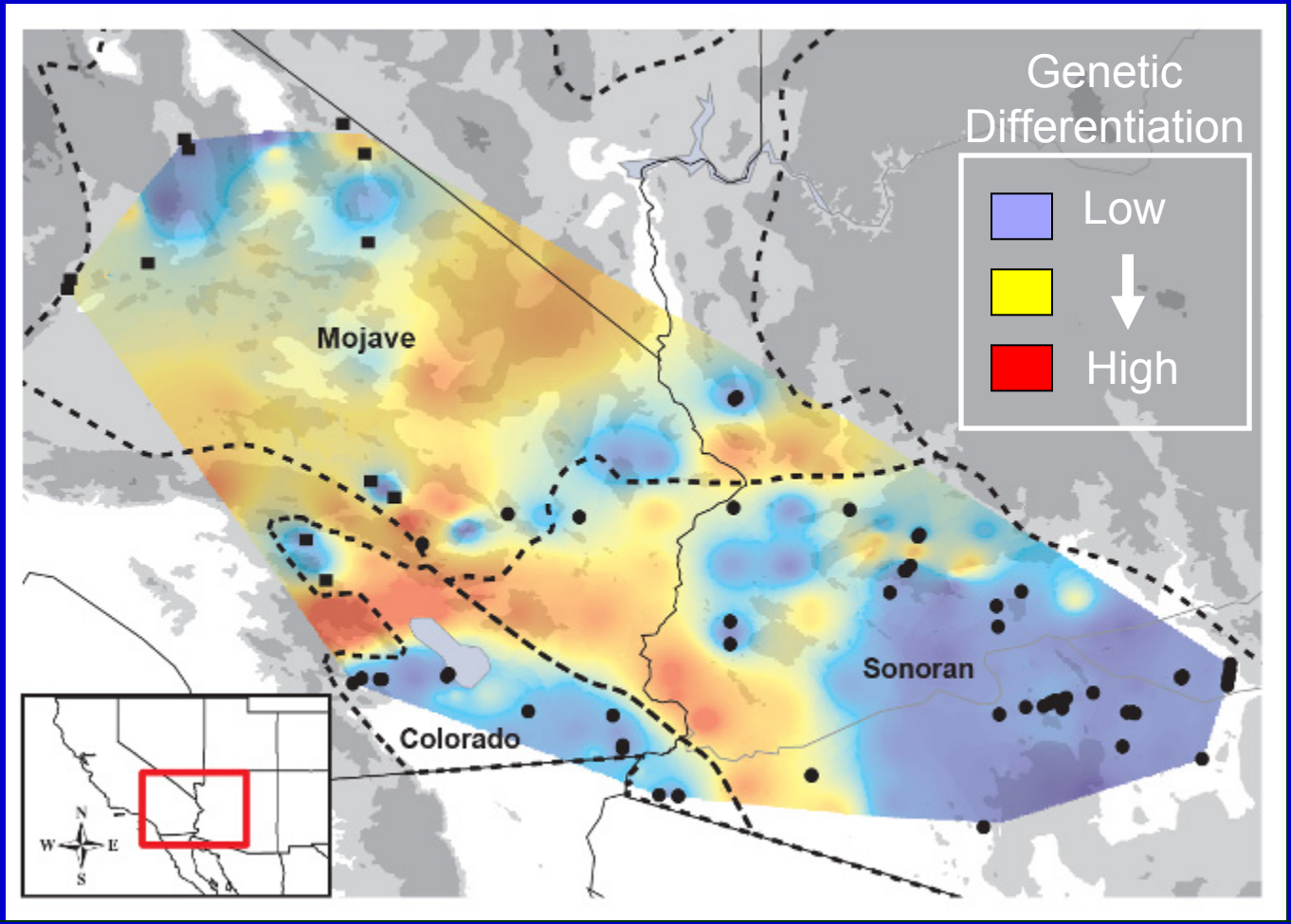
Newer analyses

Visualization of "genetic landscapes".





Western-shovel nosed snake, *Chionactus occipitalus*



Wood et al 2007 Conservation Genetics 9:1489-1507

Scaling landscape genetics from single species to entire communities

BIOLOGICAL CONSERVATION 141 (2008) 1648–1664

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Are hotspots of evolutionary potential adequately protected in southern California?

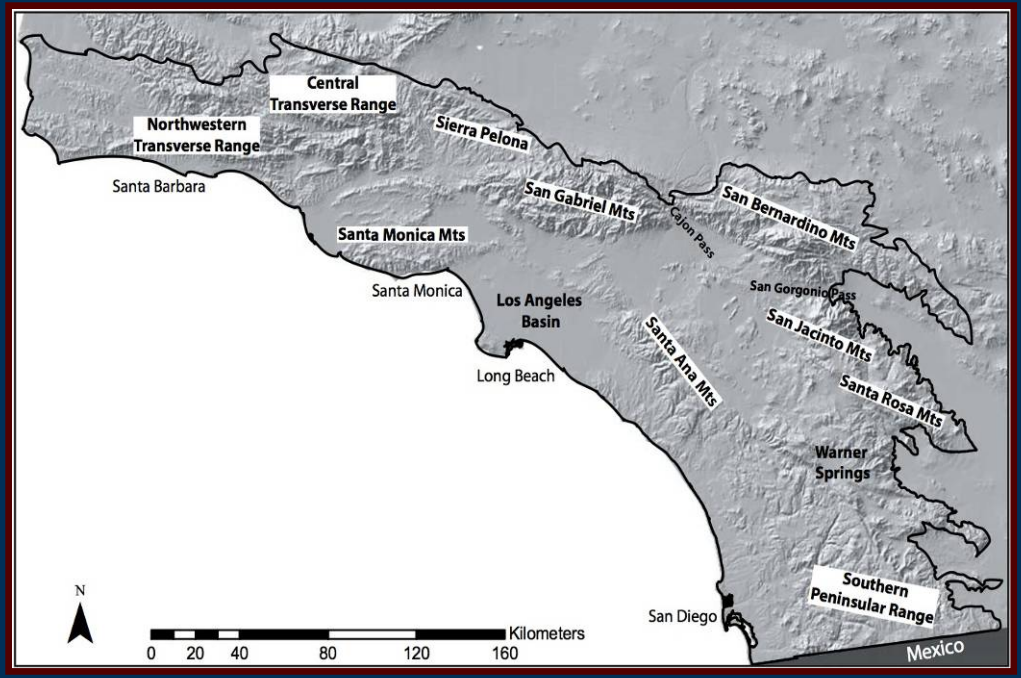
Amy G. Vandergast[a,*], *Andrew J. Bohonak*[b], *Stacie A. Hathaway*[a], *Joshua Boys*[b], *Robert N. Fisher*[a]

[a]*US Geological Survey, Western Ecological Research Center, San Diego Field Station. 4165 Spruance Road, Suite 200, San Diego, CA 92101, United States*

[b]*San Diego State University, Department of Biology, 5500 Campanile Drive, San Diego, CA 92182-4614, United States*

Scaling landscape genetics from single species to entire communities

- GIS-based approach for mapping "multi-species genetic landscapes" (MGLs).
- mtDNA datasets from 21 vertebrate and invertebrate species
- Focus on the SCCE
- Raw data obtained from study authors, standardized, and reanalyzed.



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Species

Invertebrates

Apomastus schlingeri/kristenae

Branchinecta sandiegonensis

Hemileuca electra

Stenopelmatus mahogani

Amphibians

Batrachoseps nigriventris

Batrachoseps major

Birds

Chamaea fasciata

Picoides albolarvatus

Toxostaoma redivivum

Mammals

Neotoma fuscipes

Neotoma lepida

Perognathus longimembris

Sorex ornatus

Reptiles

Emys marmorata

Plestiodon gilberti

Lampropeltis zonata

Lichanura trivirgata

Masticophis flagellum

Phrynosoma coronatum

Sceloporus occidentalis

Xantusia henshawi

Methods

- **Within each species:**

1. Calculate genetic divergence between each pair of collection locations
2. Visualize in a GIS using inverse distance weighted interpolation.
3. Calculate genetic variation within each collection site and visualize.

- **Across species:**

1. Average all species layers into a divergence MGL and a variation MGL at a 1 km^2 grid scale

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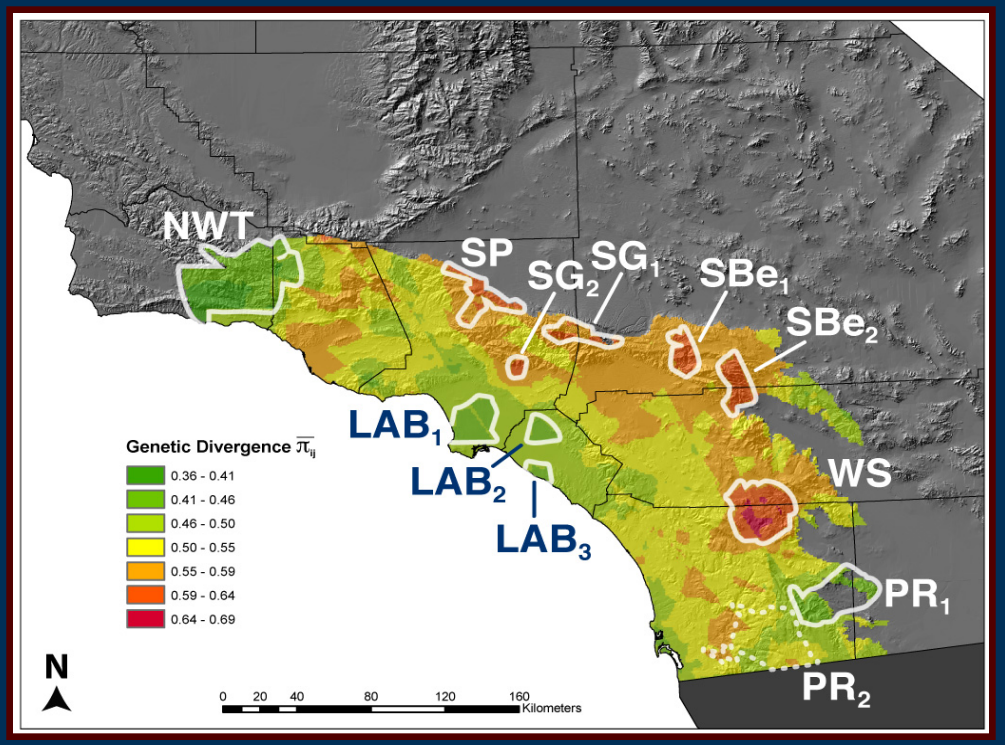
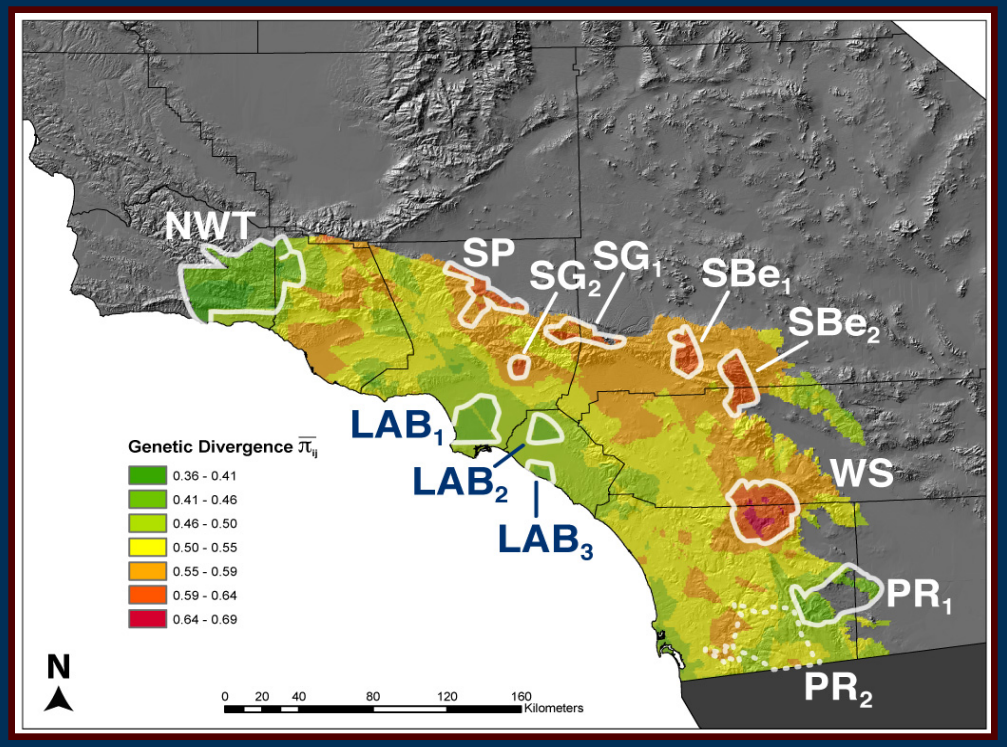
Genetic Divergence MGL



Divergence Hotspots

- Steep environmental gradients
- Represent secondary contact zones between previously isolated lineages
- Great potential for genetic change
- Except WS, all in So. Transverse Range
  - Vascular plant endemism (Munz 1935, Raven and Axelrod 1978)
  - Recontact and hybrid zones localized at mtn passes between ranges (Remington 1968)

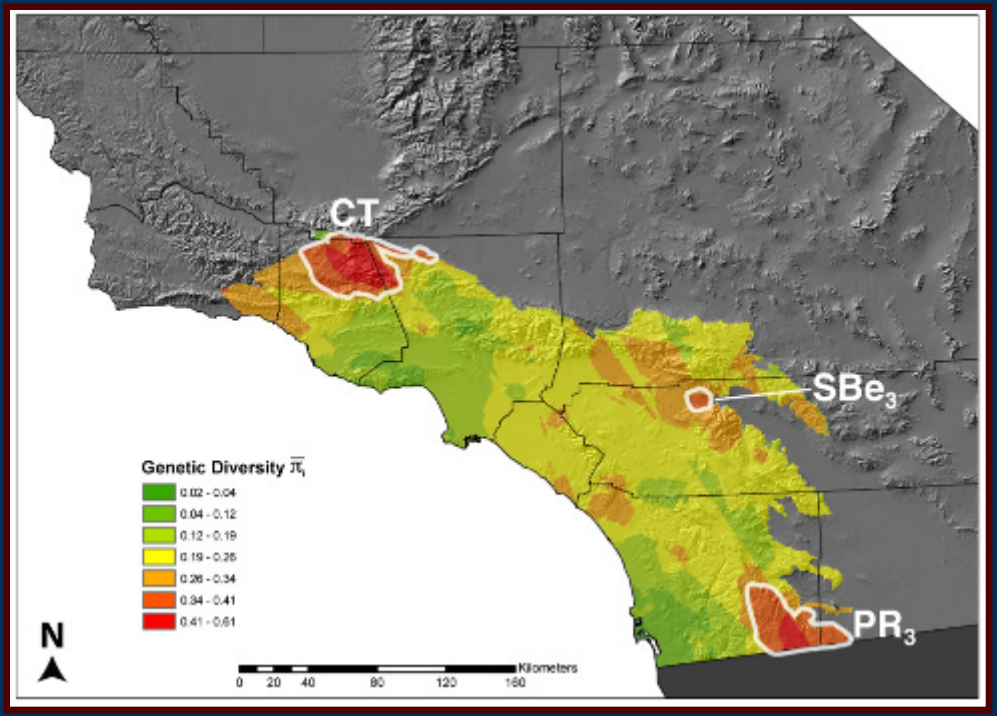
Genetic Divergence MGL



Connectivity Hotspots

- Represent recent and rapid range expansions
- High ongoing rates of gene flow
- When separated by areas of divergence, may represent regional gene pools
  - Deserve separate protection
- Within each area of high connectivity, corridors should be protected.

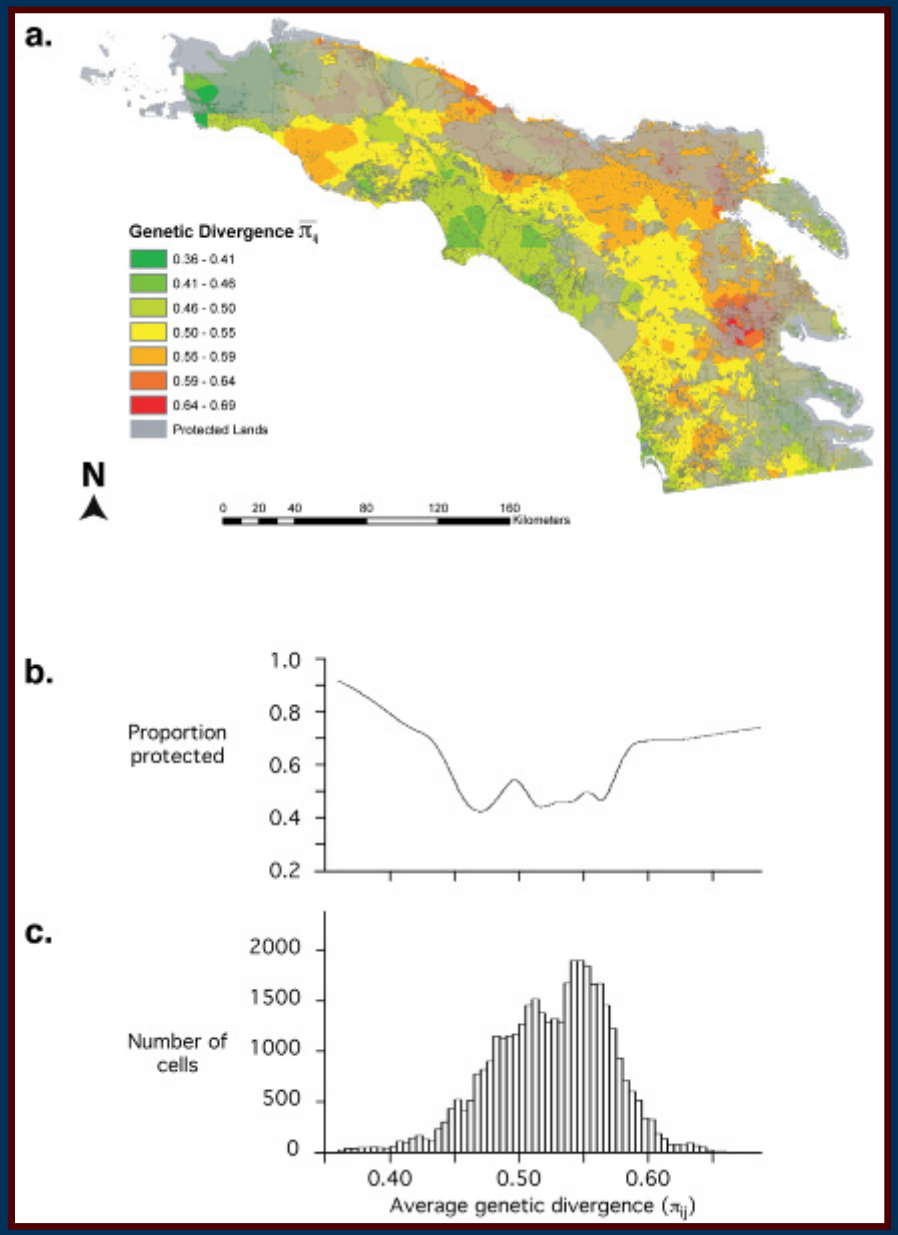
Genetic Diversity MGL

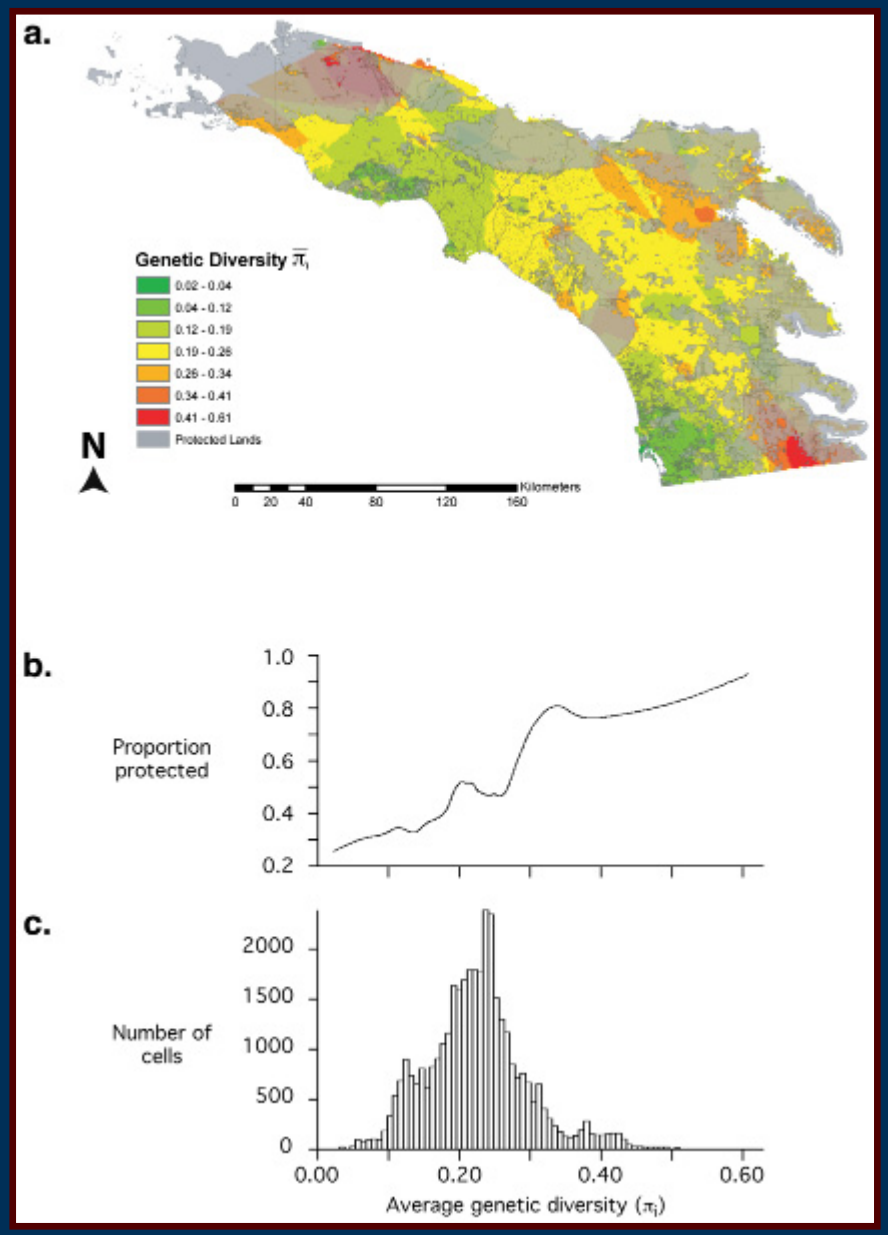


Diversity Hotspots

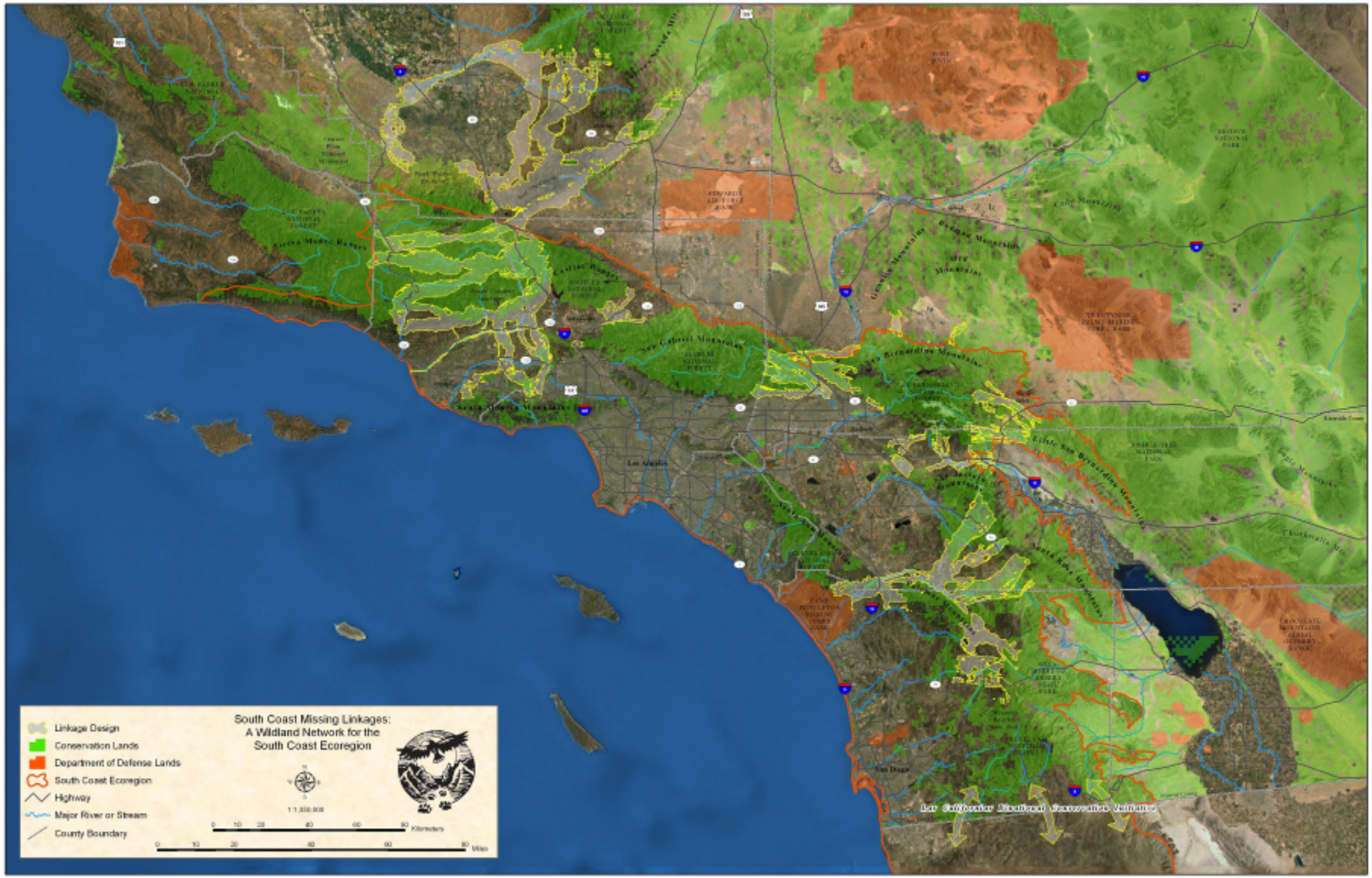
- Expected in areas containing older and larger populations
- Areas where gene pools from formerly separated lineages now meet
- Diversity = raw material for selection and evolution

Are Hotspots of Evolutionary Potential Protected?





Applications



Applications

- **Mapping approach provides an avenue to incorporate measures of evolutionary process into GIS-based assessments and land planning.**

- **Many different types of information should go into systematic conservation planning**
  - (richness, diversity, complementarity, land availability, restoration potential, etc.)

- **Southern California– ongoing efforts by TNC, South Coast Missing Linkages Project, MSCP etc.**

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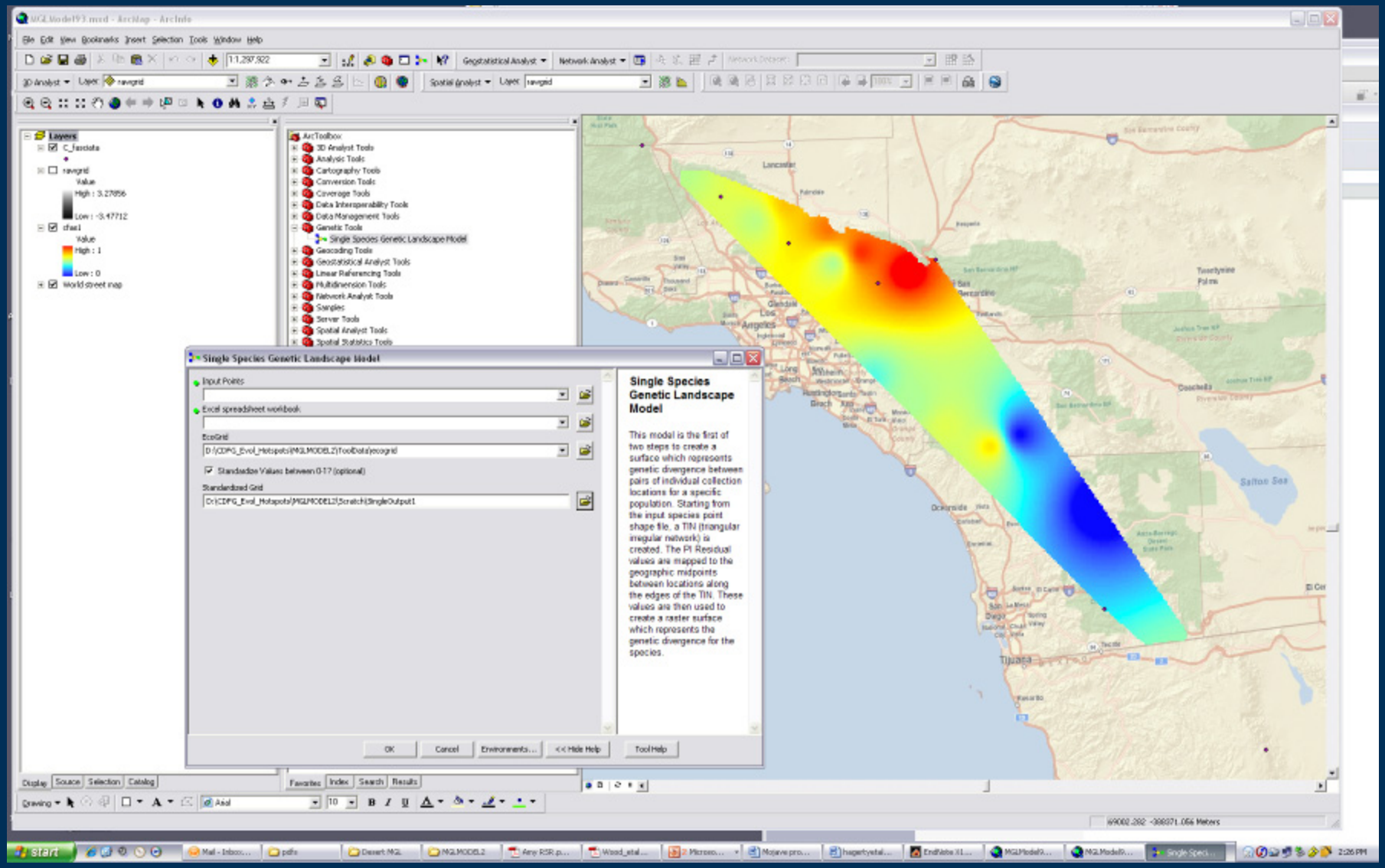
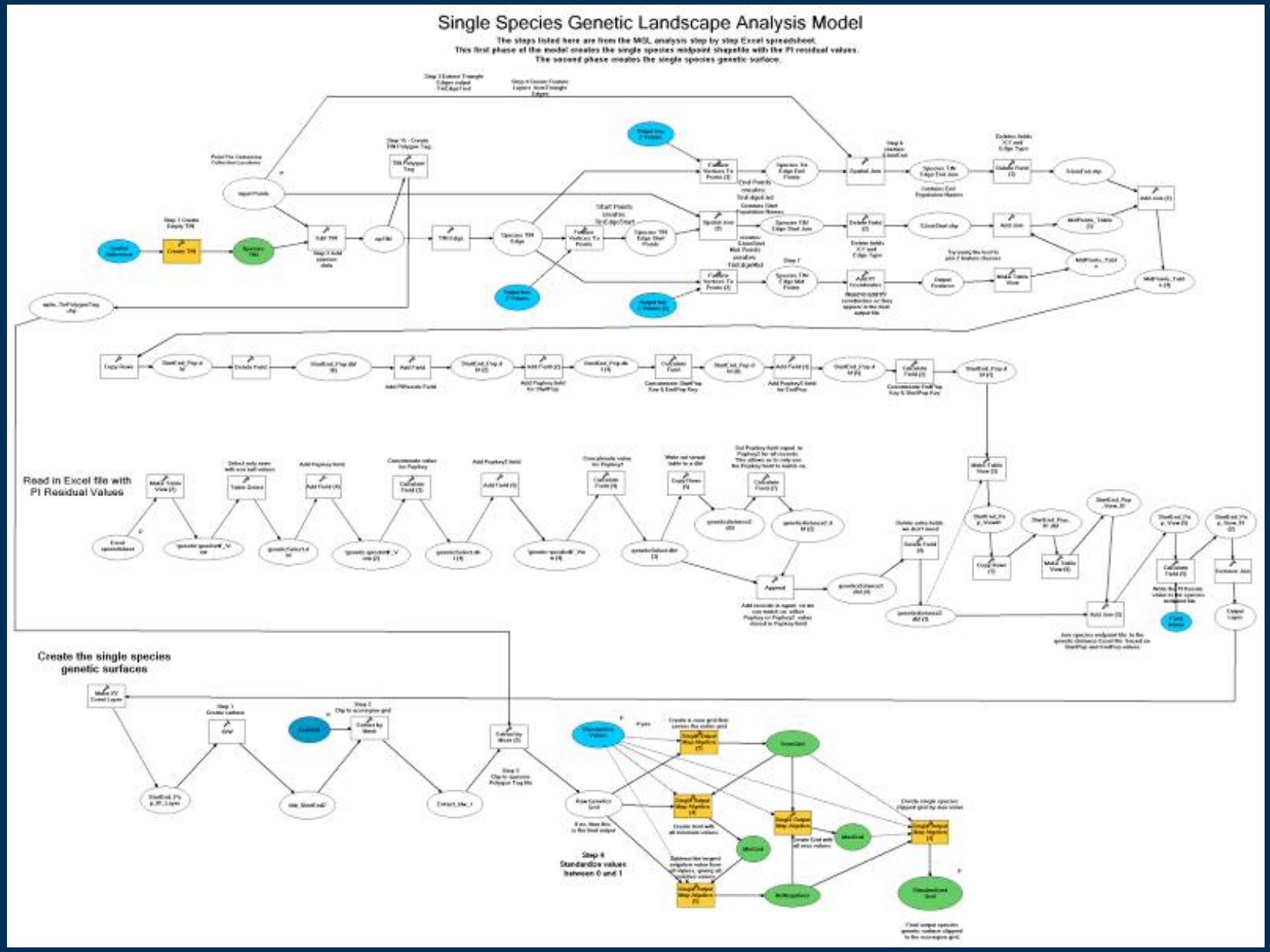
GIS tool to automate analysis

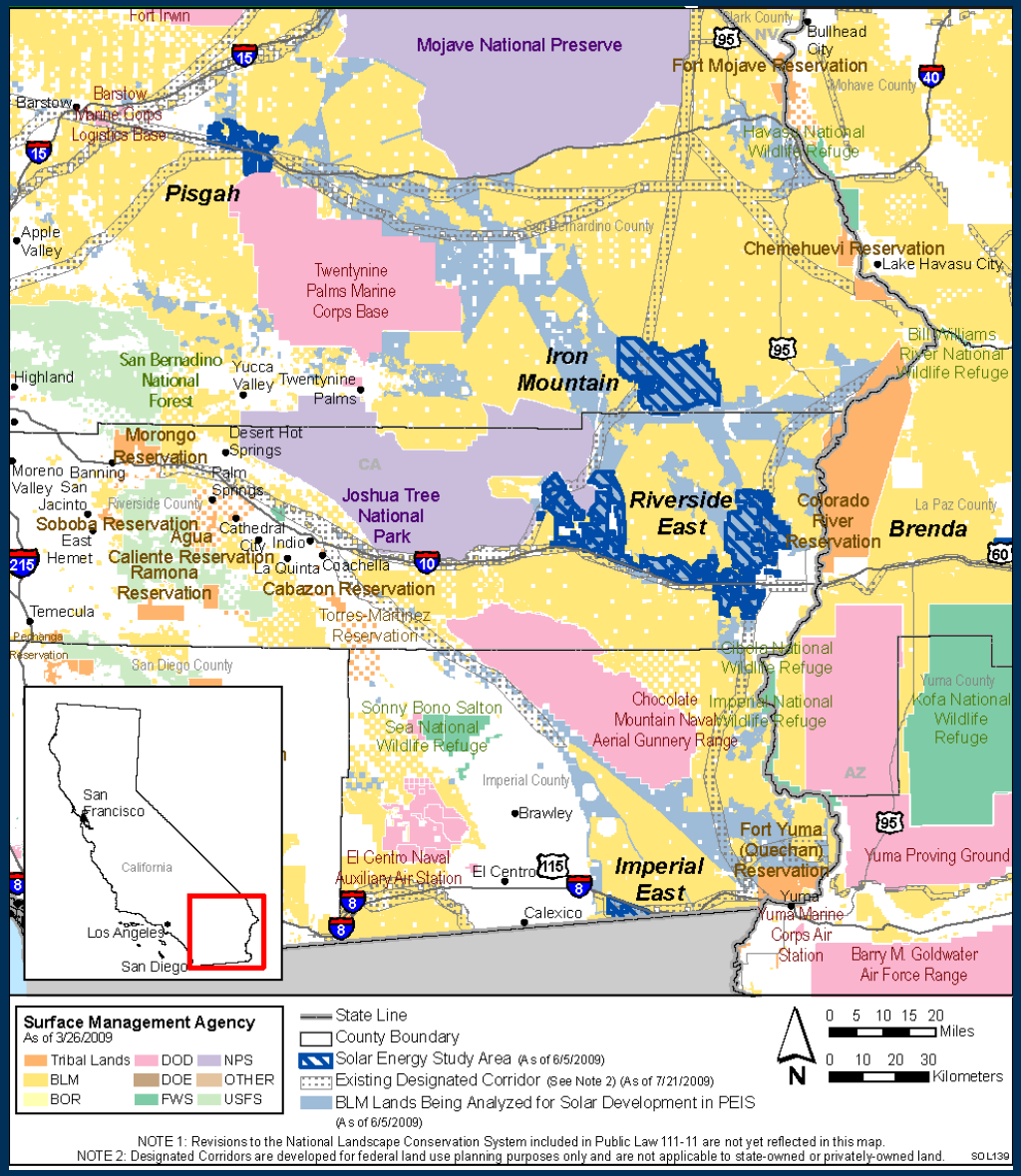


GIS tool to automate analysis



Rapid Assessment of Genetic Connectivity in the Mojave Desert

- Need scientifically defensible information on wildlife connectivity as soon as possible
- Solar energy development study areas



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Rapid Assessment of Genetic Connectivity in the Mojave Desert

Using published and available genetic datasets:

1. Broad Scale:
   - Genetic Landscapes across multiple species
   - Locate regions with high genetic diversity & connectivity (important adaptive reservoirs)
   - Locate gaps in available data where further genetic data should be collected

2. Fine Scale:
   - Habitat suitability modeling & genetic data
   - Maps of population connectivity (least cost paths)
   - Locate common movement corridors

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Available population genetic data

Mammals
Ovis canadensis
Spermophilus mohavensis
Canis latrans
Perognathus longimembris
Chaetodipus penicillatus

Invertebrates
Assiminea Spring snails
Homolonicus spiders
Tegeticula synthetica
Hyalella amphipods

Plants
Yucca brevifolia

Herpetofauna
Gopherus agassizii
Sceloporus magister
Xantusia vigilis
Lichanura trivirgata
Crotaphytus
Crotalus mitchelli
Plestiodon gilberti
Uma scoparia
Crotalus cerastes
Masticophis
Chionactus occipitalis
Bufo punctatus

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Habitat Strata

Low elevation creosote scrublands

Gopherus agassizii
Homolonicus spiders
Chaetodipus penicillatus
Spermophilus mohavensis
Chionactus occipitalis

High elevation forest and rock

Sceloporus magister
Xantusia vigilis
Lichanura trivirgata
Crotaphytus
Tegeticula synthetica
Yucca brevifolia
Crotalus mitchelli

Desert riparian (seeps and springs)

Bufo punctatus
Plestiodon gilberti
Assiminea Spring snails
Ovis canadensis
Hyalella amphipods

Dunes

Uma scoparia
Perognathus longimembris
Crotalus cerastes

Generalists

Masticophis
Canis latrans

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Proposed Timeline

- October 2009
  - Gather data sets
  - Create individual and multispecies genetic landscapes
  - Begin habitat modeling for select species
  - Portal for data sharing (SC Wildlands, TNC, others)
- Early Spring 2010
  - Preliminary report for PEIS
- Late Fall 2010
  - Final USGS publication (peer-reviewed)

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