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Using Population Genetics in Wildlife Monitoring Programs

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U.S. Geological Survey


Hurley
ZERMATT
STORE

Western Ecological Research Center
San Diego FS Conservation Genetics Lab

- Est. 2005
- Measuring genetic diversity within & among populations of T&E species
- Determining distinct population/subspecies boundaries
- Understanding the effects of habitat loss & fragmentation on genetic connectivity
- Invasion origins

Western Ecological Research Center
San Diego FS Conservation Genetics Lab

Alameda whipsnake*

Brown tree snake

California red-legged frog*

Coachella Valley fringe-toed lizard*

Jerusalem crickets

Mountain yellow-legged frog*

Narrow-headed gartersnake*

Riverside fairy shrimp*

San Diego fairy shrimp*

South Pacific skinks

Southwestern willow flycatcher*

Unarmored three-spine stickleback*

Western Pond Turtle

Western shovel-nosed snake

Western skink

When is genetic sampling useful?

Within Species

- **Measuring genetic diversity within a population, Ne: expansion, contraction**
- **Parentage**
- **Detection of recent migrants among patches**
- **Measuring gene flow (dispersal + successful breeding) among core areas**

When is genetic sampling useful?

Across Subspecies/ Species

- Determining relationships among species
- Defining ESUs
- Determining whether a difficult to detect/cryptic species is present

Multi-species Comparisons

- Evaluating how much genetic diversity is present and how it is distributed over space and time.
- Evaluating historical patterns of diversity and evolutionary processes

Types of Genetic Markers

- MtDNA/cpDNA sequences
- Nuclear sequences (introns, coding regions)
- Microsatellite markers
- AFLPs
- SNPs

Analyses and Temporal Scale of inference

1. Genealogy-based analyses
   - Mainly sequence data, single or multiple loci
   - Require new mutations to reach detectable levels or even fixation in local populations
   - Focus on the oldest evolutionary processes in the gene genealogy.
   - Contemporary changes in gene flow rates or patterns are not readily inferred from these methods.

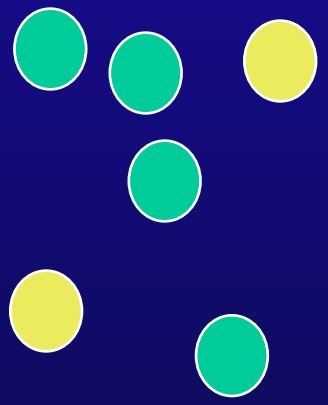
Analyses and Temporal Scale of inference

2. **Frequency-based similarity or distance measures (FST: AMOVA, IBD)**

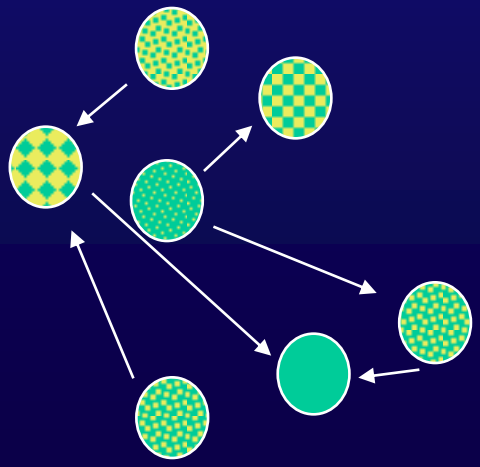
- All data types
- Drift-gene flow equilibrium on shorter time scales than genealogical analyses (10s to 1000s generations).
- The time required depends on whether gene flow (or effective population size) has increased or decreased, and the magnitude of the change.
- Can provide information even prior to a drift/gene flow equilibrium when comparative approaches are employed

Selectively neutral genetic markers provide estimates of gene flow (dispersal + successful reproduction) measured as differences in allele frequencies between populations or individuals.

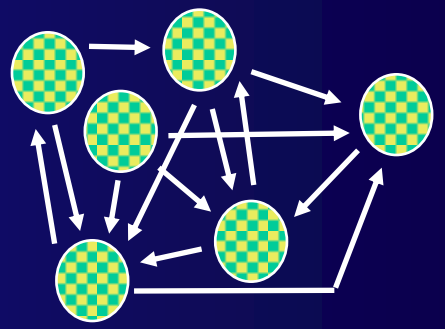
No gene flow between populations



Some gene flow between populations



High gene flow between populations



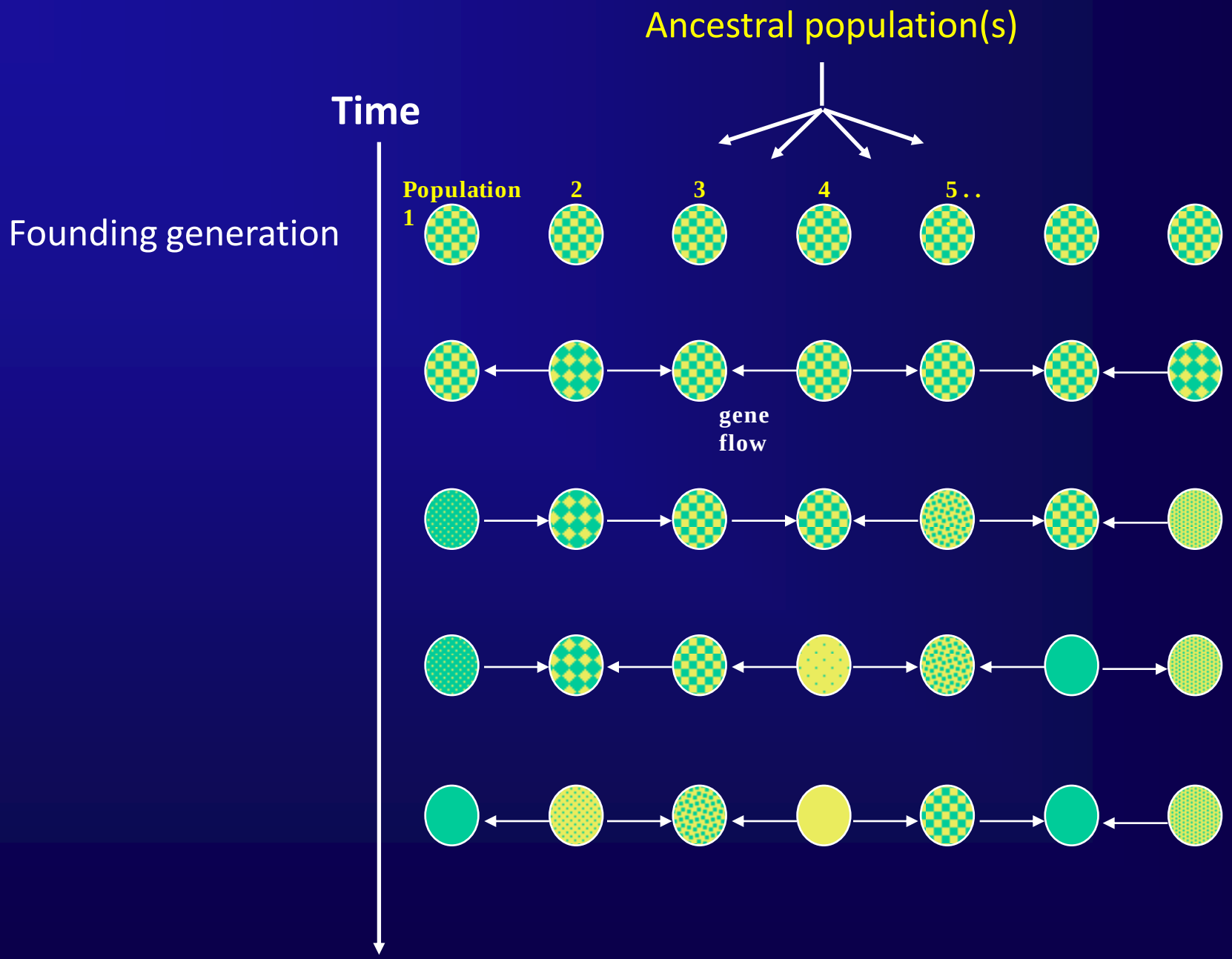
Non-equilibrium conditions

Measuring number of migrants from FST:

$$FST = 1/(1+4Nm)$$

- **Idealized population, equilibrium between drift and gene flow**

- **In most cases, human-induced landscape change is too recent to expect a drift/mutation equilibrium**
- **So FST/gene flow estimates reflect historical conditions**


Ancestral population(s)
Time
Founding generation
Population 1
2
3
4
5 . .
gene flow

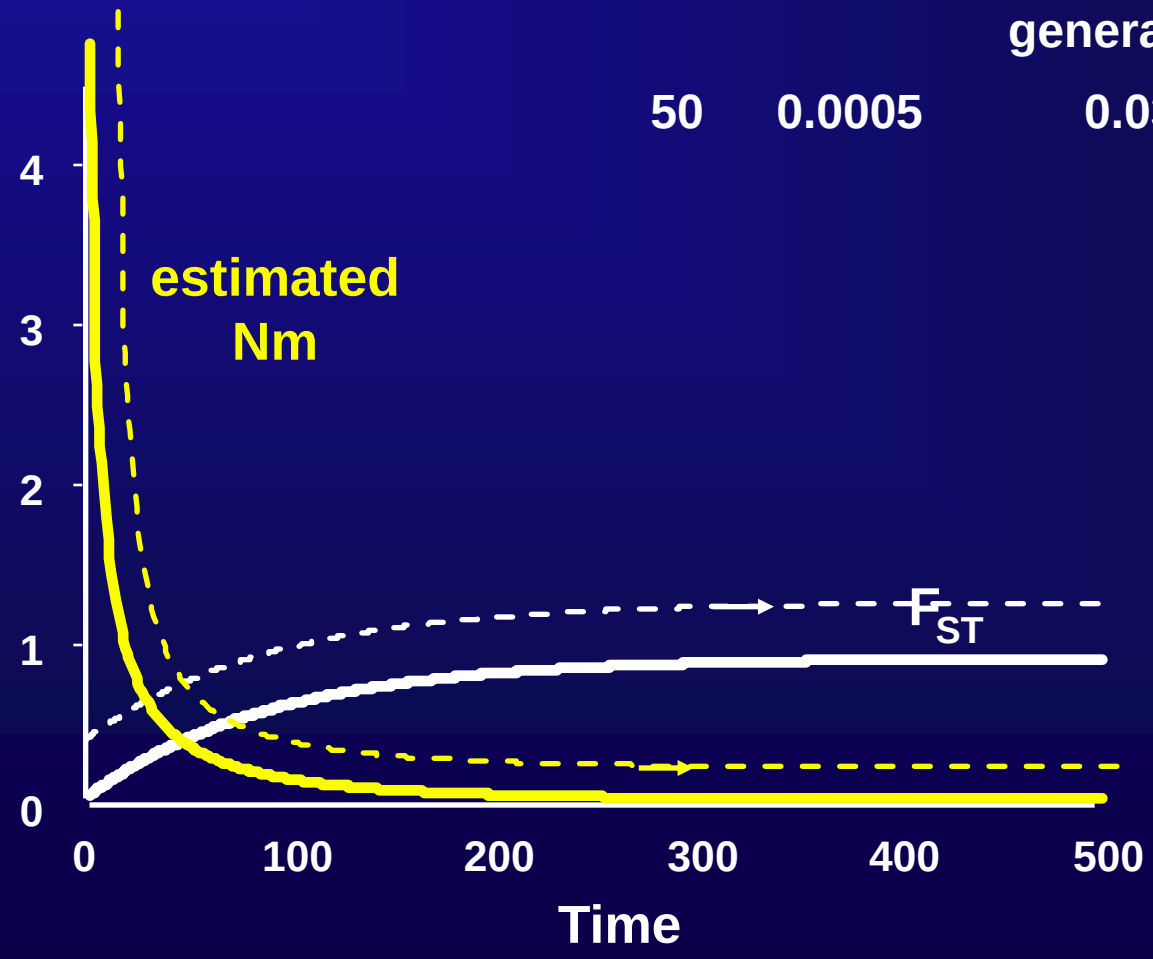
Solutions:

Comparative approach

Modeling approaches

Actual values

N	m	Nm = # migrants per generation
50	0.0005	0.03



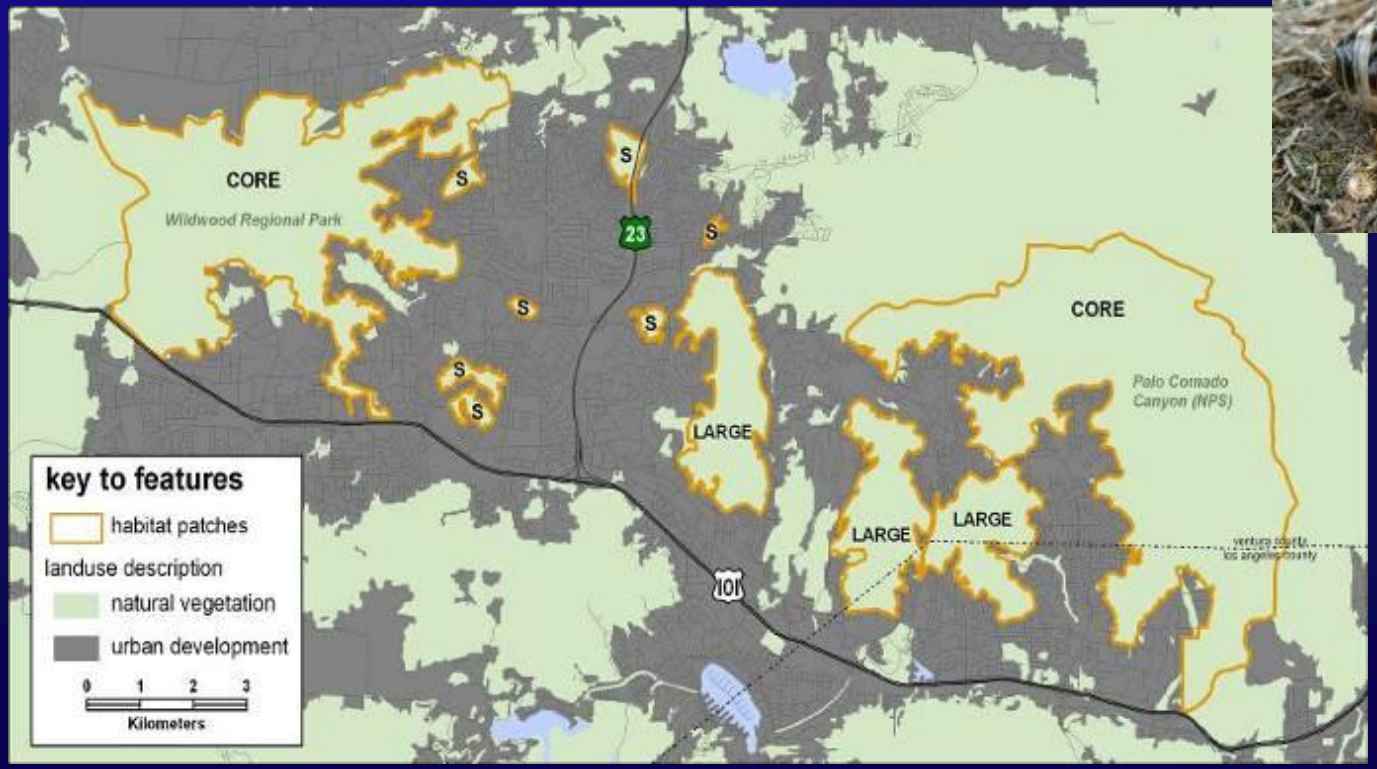
Analyses and Temporal Scale of inference

3. <u>Clustering algorithms (e.g., STRUCTURE)</u>

   - Commonly applied to microsatellite data
   - Define contemporary gene pool boundaries
   - Utilize linkage disequilibrium across loci-- statistically detectable for only a few generations after a unique genotype immigrates.

Example 1: Santa Monica Mountains

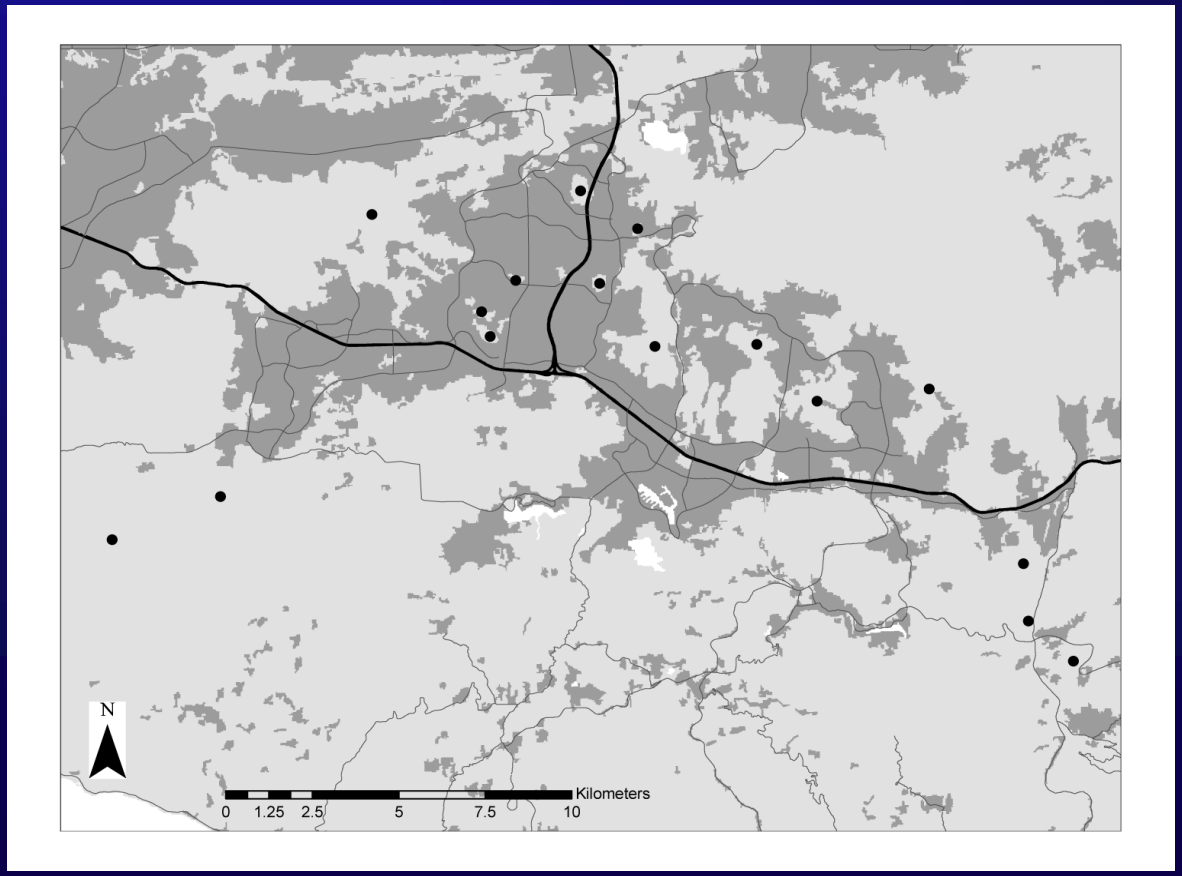
- Pitfall sampling of invertebrates in small and large fragments
- Genetic structure of a JC: mtDNA, ISSRs
- Assessed genetic connectivity among fragments
- Genetic diversity within fragments



Vandergast et al 2009 J. Insect Conservation

Genetic Results

- Compared genetic connectivity among fragments to that among sampling locations through contiguous habitat
- Found less connectivity among fragments and less genetic diversity within smaller and older fragments.



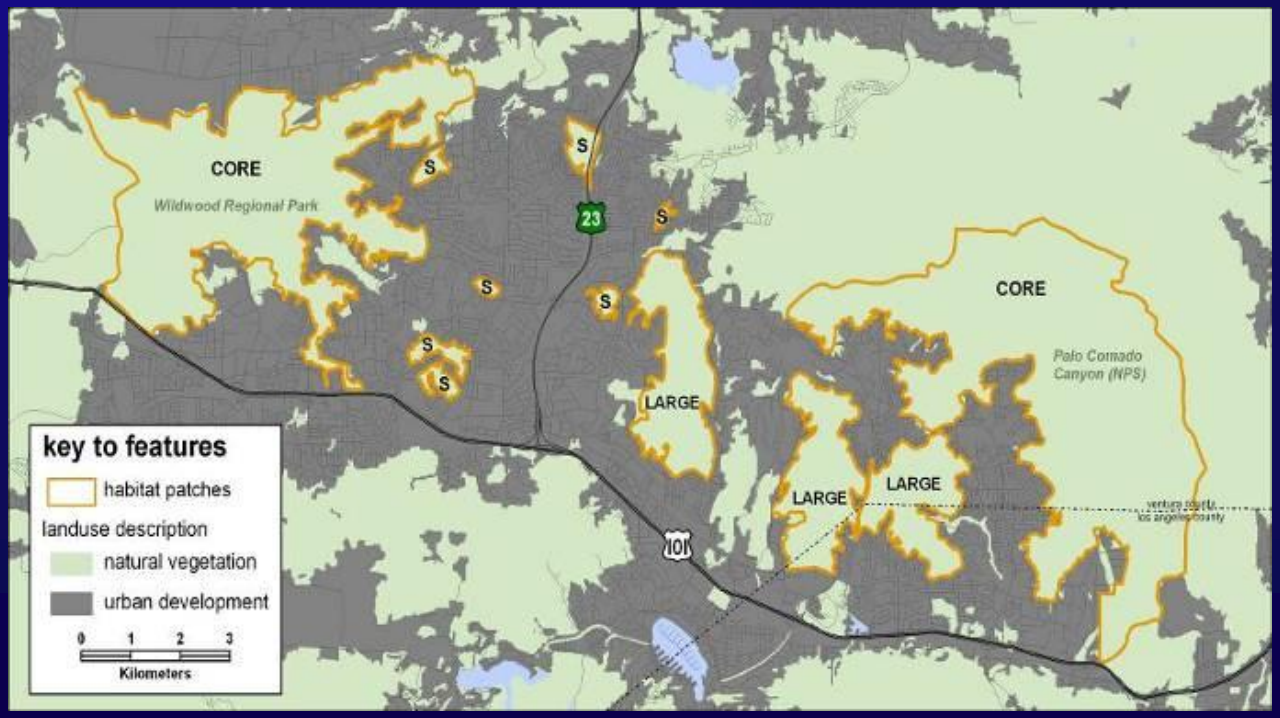
Added information with genetic sampling

- **Pitfall Capture Data Alone:**
  - # of individuals captured per unit effort was NOT correlated with patch size
  - Mean capture rate in small fragments was NOT lower than in larger patches and contiguous areas
  - Traditional monitoring approach does not detect a major decline.

- **Decline in genetic connectivity and diversity can increase the likelihood of population declines and eventual extinction.**
  - Reduced or no rescue effect for extirpated subpopulations
  - Loss of genetic variation reduces likelihood that a population can track environmental change.

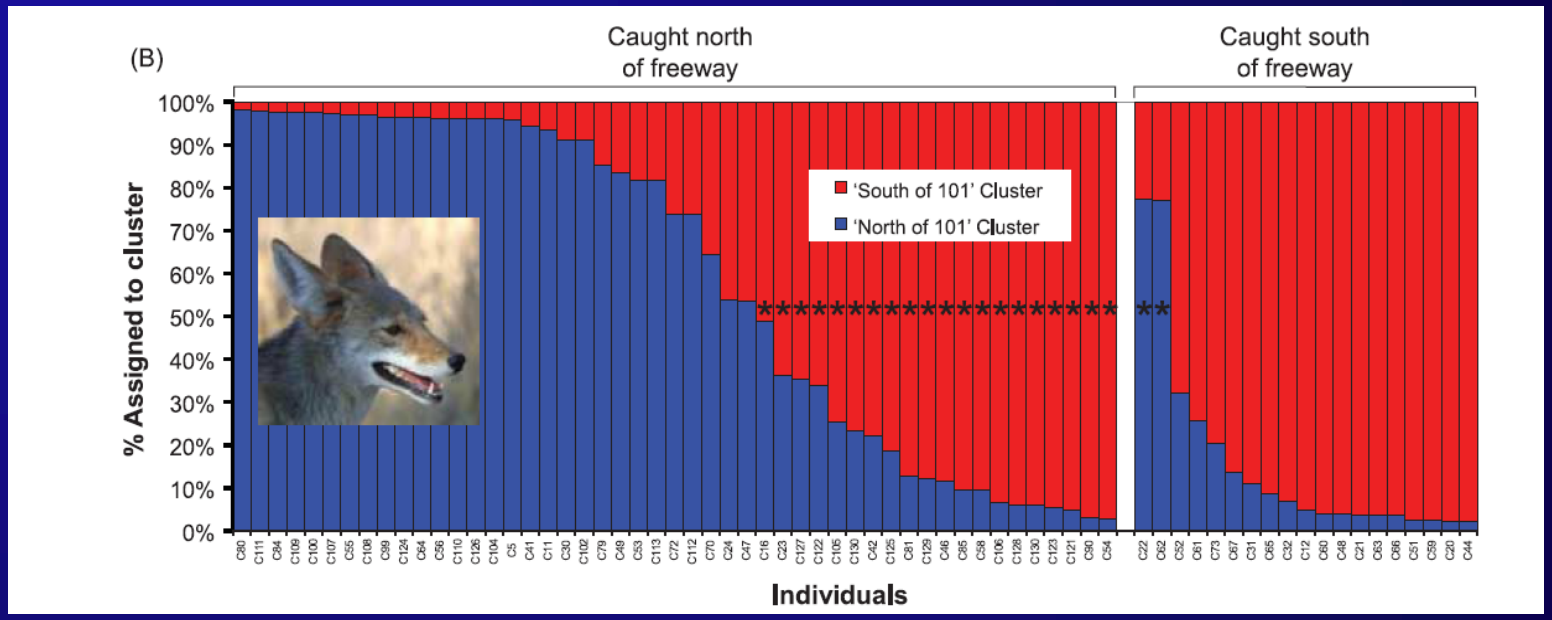
Example 2: Santa Monica Mountains Coyote & Bobcat movement & genetics

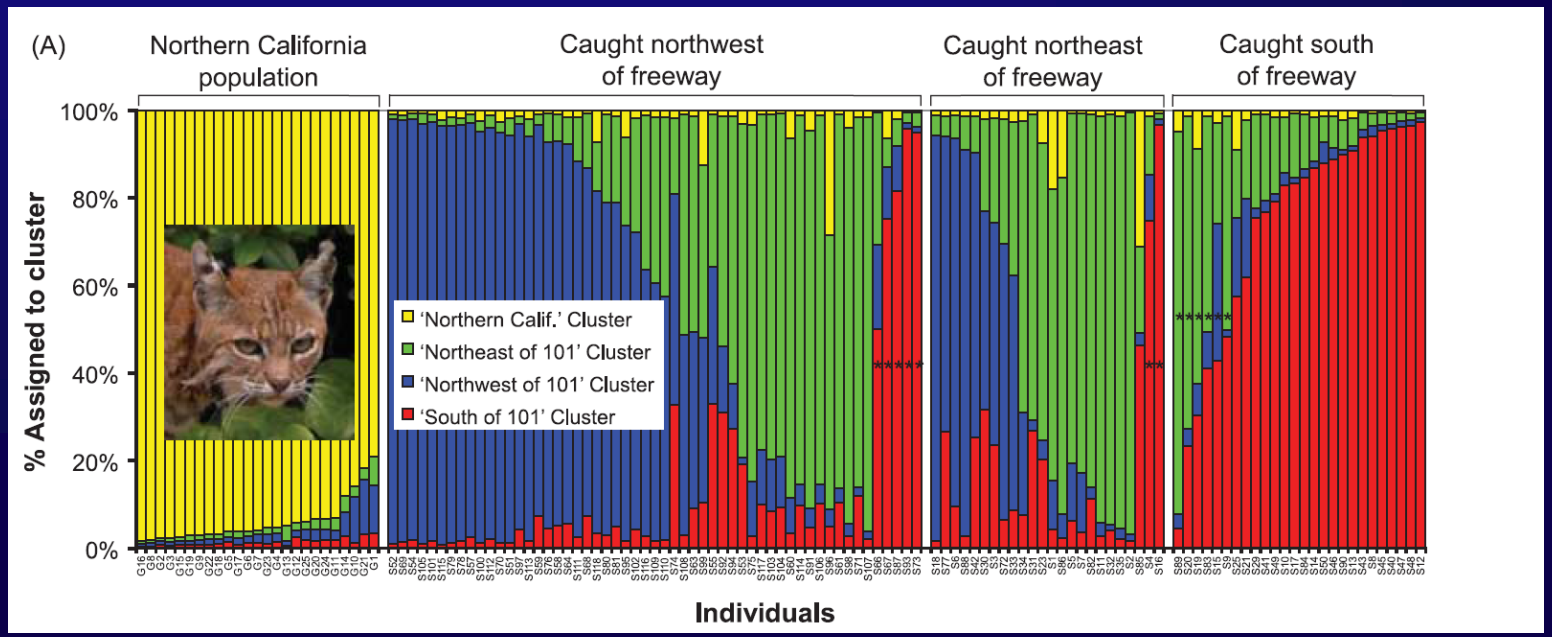
- Radio-tracked animals
- Microsatellite markers
- Genetic assignment tests to estimate current migration
- FST to estimate genetic differentiation/gene flow



Riley et al 2006 Molecular Ecology

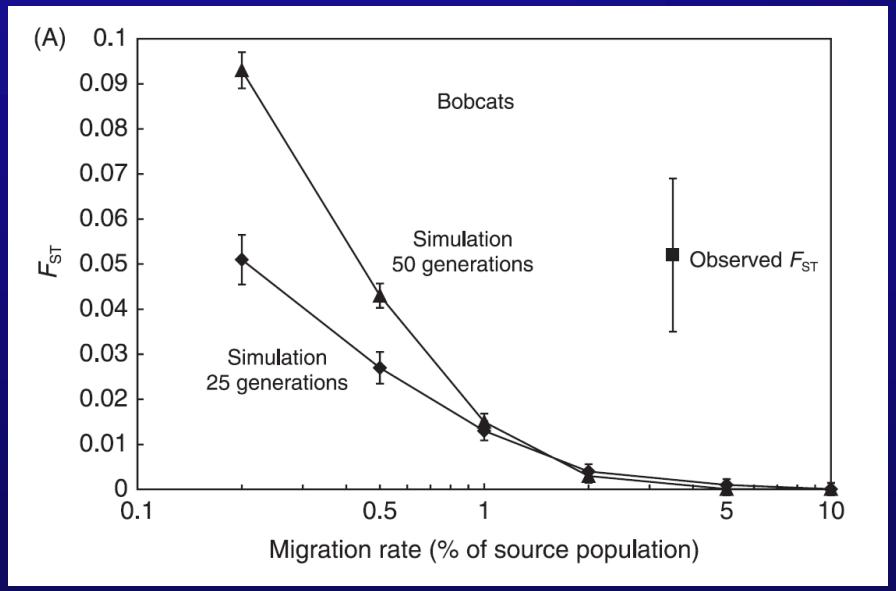
Results

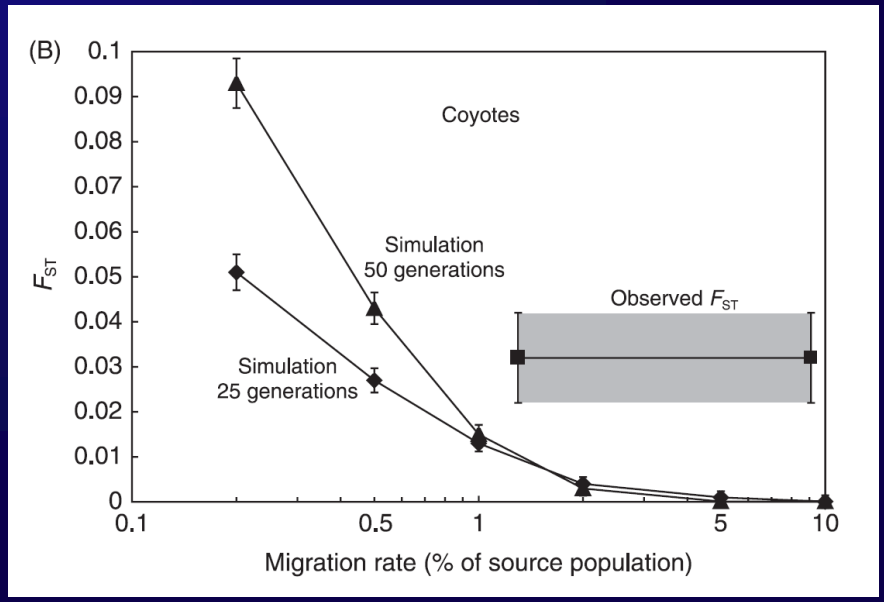

(B)
Caught north of freeway
Caught south of freeway
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
% Assigned to cluster
'South of 101' Cluster
'North of 101' Cluster
****
**
Individuals


(A)
Northern California population
Caught northwest of freeway
Caught northeast of freeway
Caught south of freeway
100%
80%
60%
40%
20%
0%
% Assigned to cluster
'Northern Calif.' Cluster
'Northeast of 101' Cluster
'Northwest of 101' Cluster
'South of 101' Cluster
*****
**
******
Individuals

Carnivore Results

- 5-35 % of surveyed individuals crossed freeways (Radio tracking and genetic assignment tests)
- Genetic differentiation/gene flow estimates: 0.5 ind/gen





Added information with genetic sampling

- High number of dispersing individuals that are not breeding and contributing to the gene pool

- Freeways artificially constrain home range boundaries, causing territory pile up– reduces reproductive opportunities for dispersing individuals.

Example 3: Mule Deer DNA Fingerprinting: Social Structure and Genetic Connectivity

www.dfg.ca.gov

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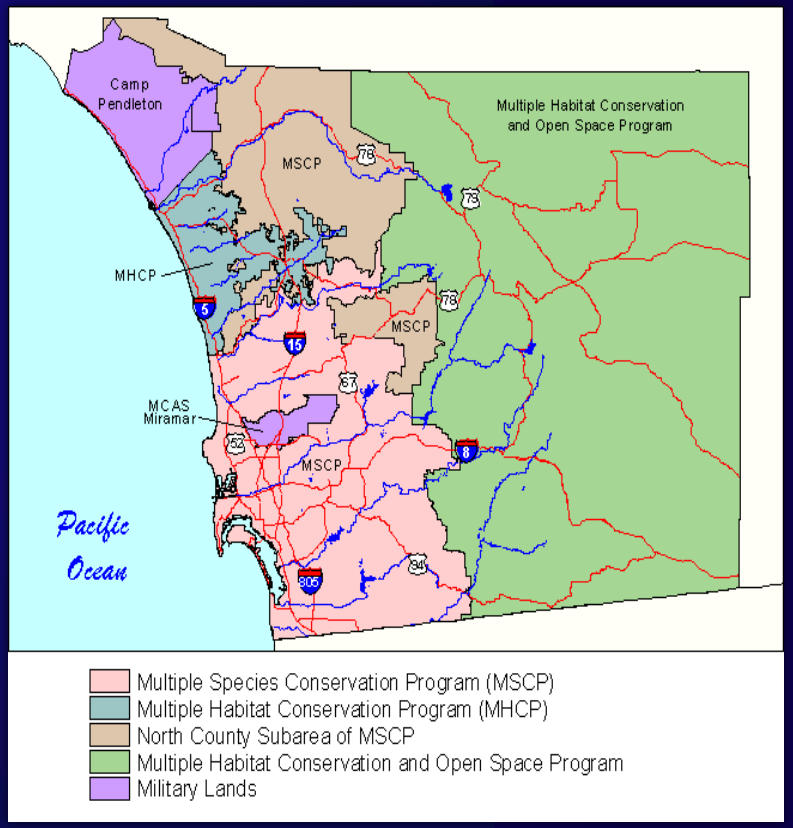
Why is the status of mule deer in urban San Diego of interest?

- MSCP monitoring
- Mule deer thought to be resilient to intense urbanization …
- … but no regional mark-recapture studies*
- … and tracking data that indicate habitat use may not translate to dispersal through an area.

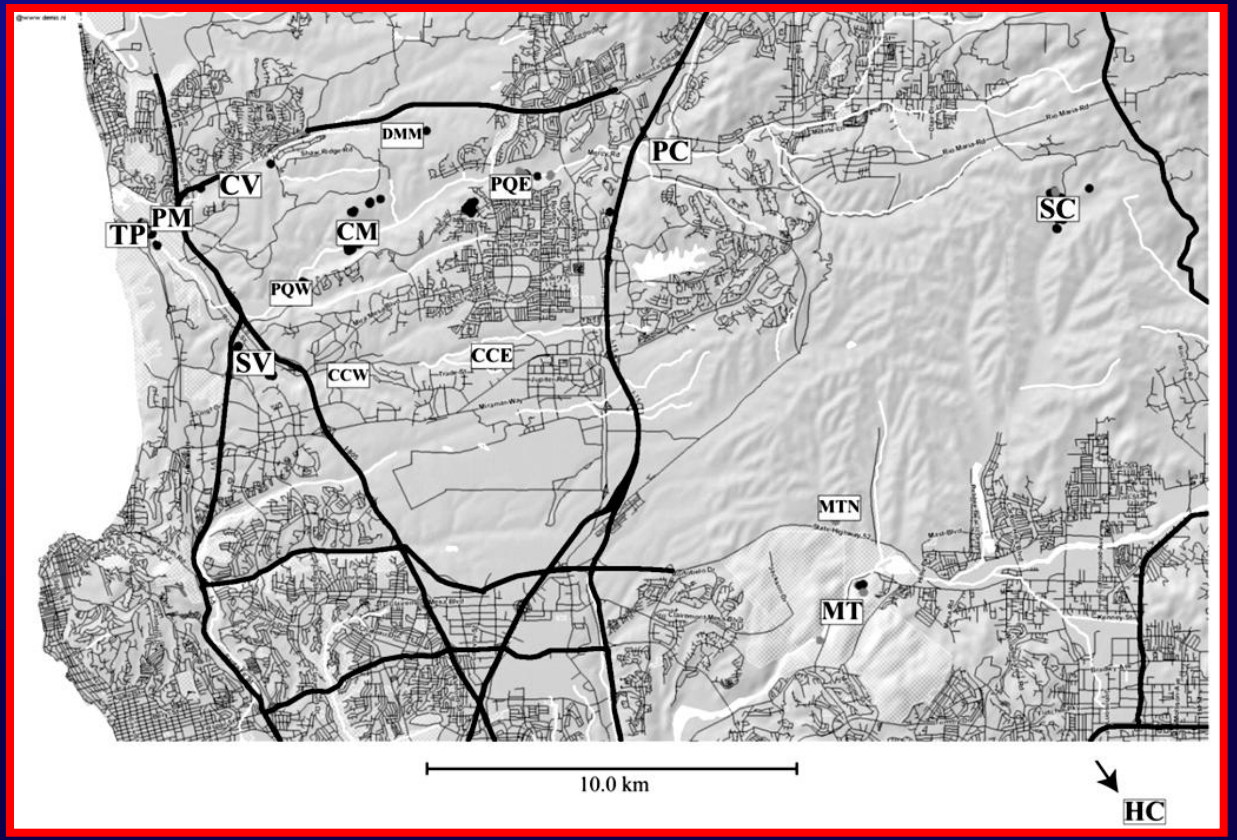


Mitelberg et al in review. Biological Conservation

Methods

- Fecal pellet collected 15 sites, 2 years (2005-2007)
- Microsatellites & Gender ID PCR test


Photo: Lani Noreke

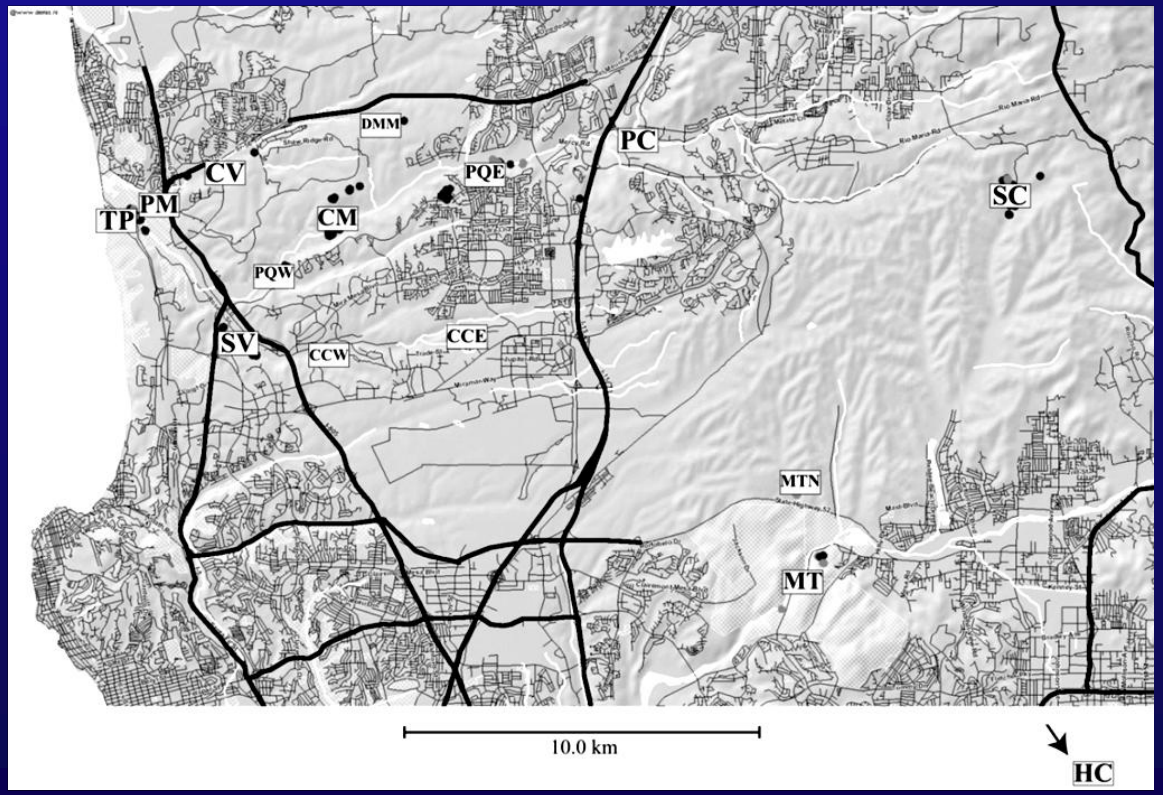


Data Analysis

1) Identify individuals and assess recapture rates
2) Assess genetic variation within the entire sampled region
3) Analyze breeding group & gene pool level structure

Very low recapture rates from "genetic tagging"

Almost 500 scat piles collected, 263 of sufficient quality for analysis
-> 152 unique individuals

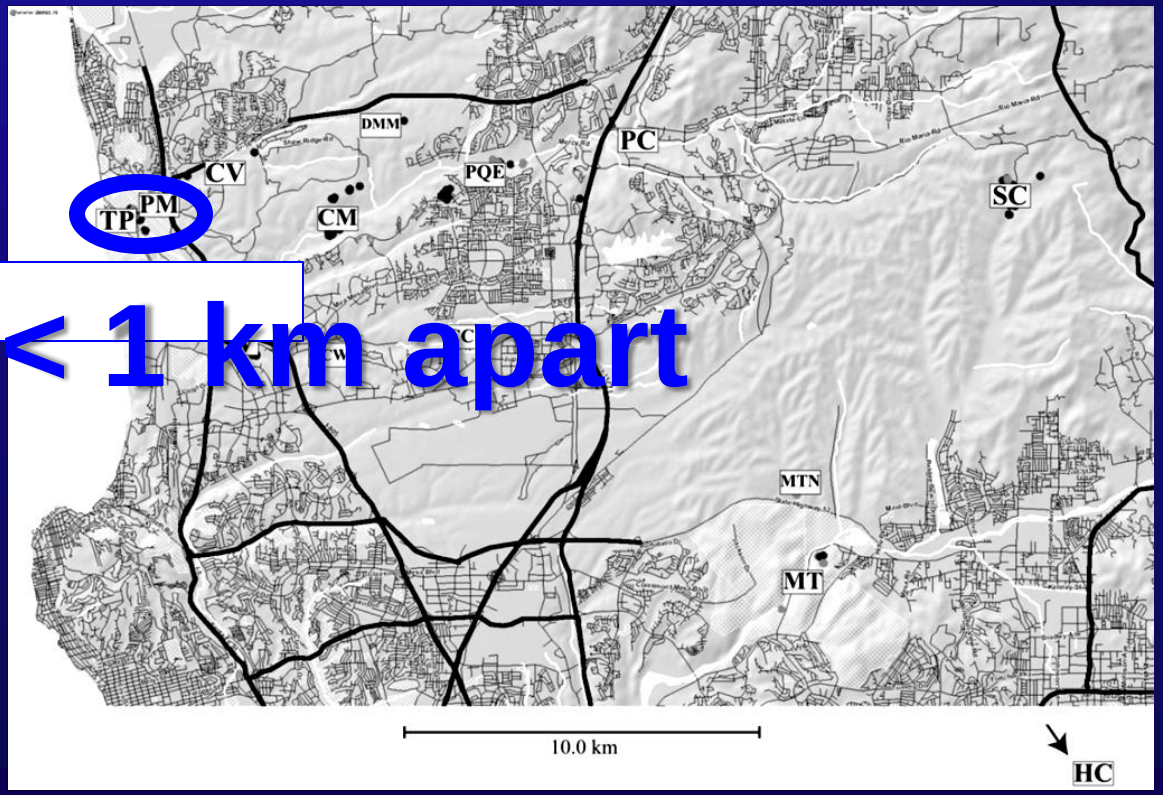


32 recaptures over 2 years
- 29 at same site
- only 3 recaptures at different sites

Minimal dispersal among fragments

Very low recapture rates from "genetic tagging"

Almost 500 scat piles collected, 263 of sufficient quality for analysis
-> 152 unique individuals



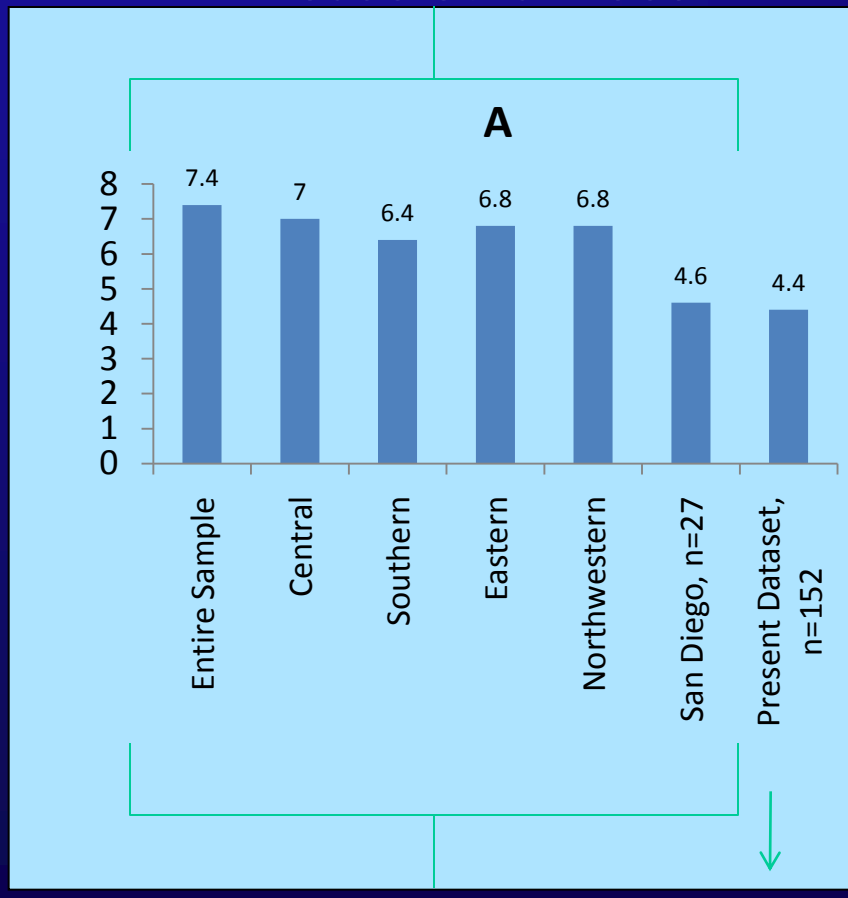
< 1 km apart

32 recaptures over 2 years
- 29 at same site
- only 3 recaptures at different sites

Minimal dispersal among fragments

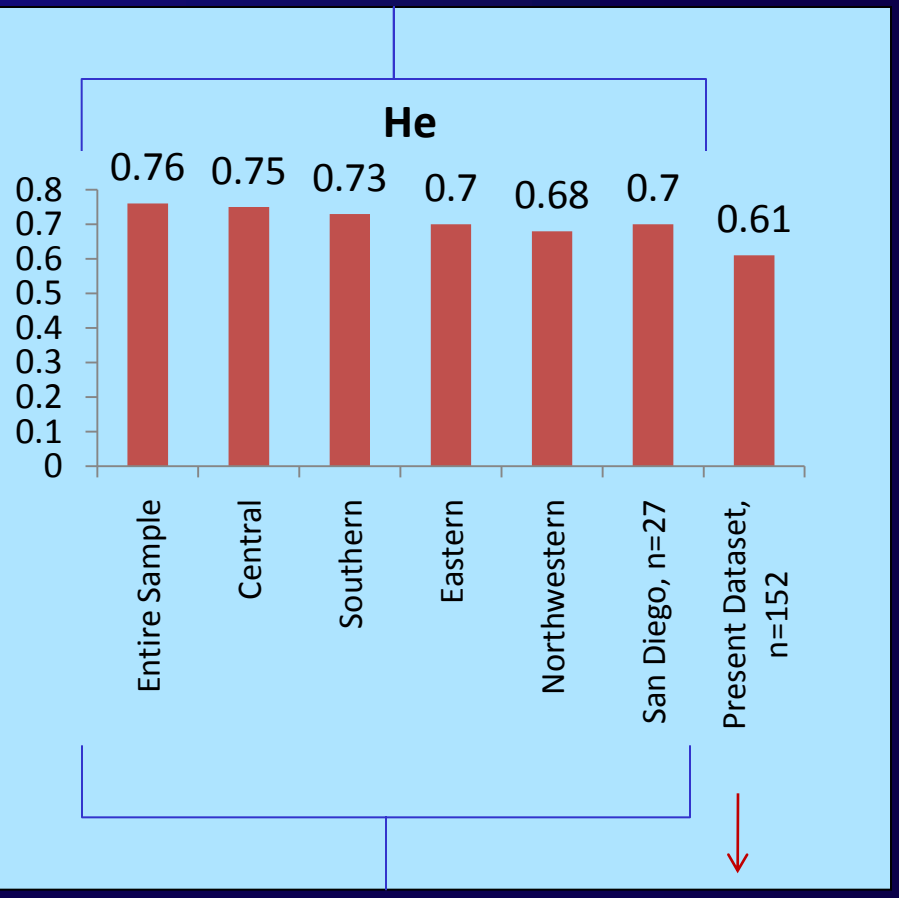
Low genetic diversity

Pease et. al 2009



1994-2004 2005-2007

Pease et. al 2009



1994-2004 2005-2007

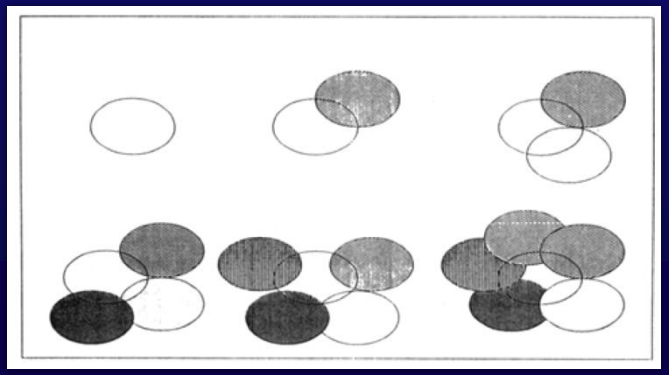
How does the breeding structure of mule deer affect fine-scale individual relatedness?

- Female offspring stay close to doe or move nearby

  → expect high relatedness locally for females, and a rapid decrease with distance

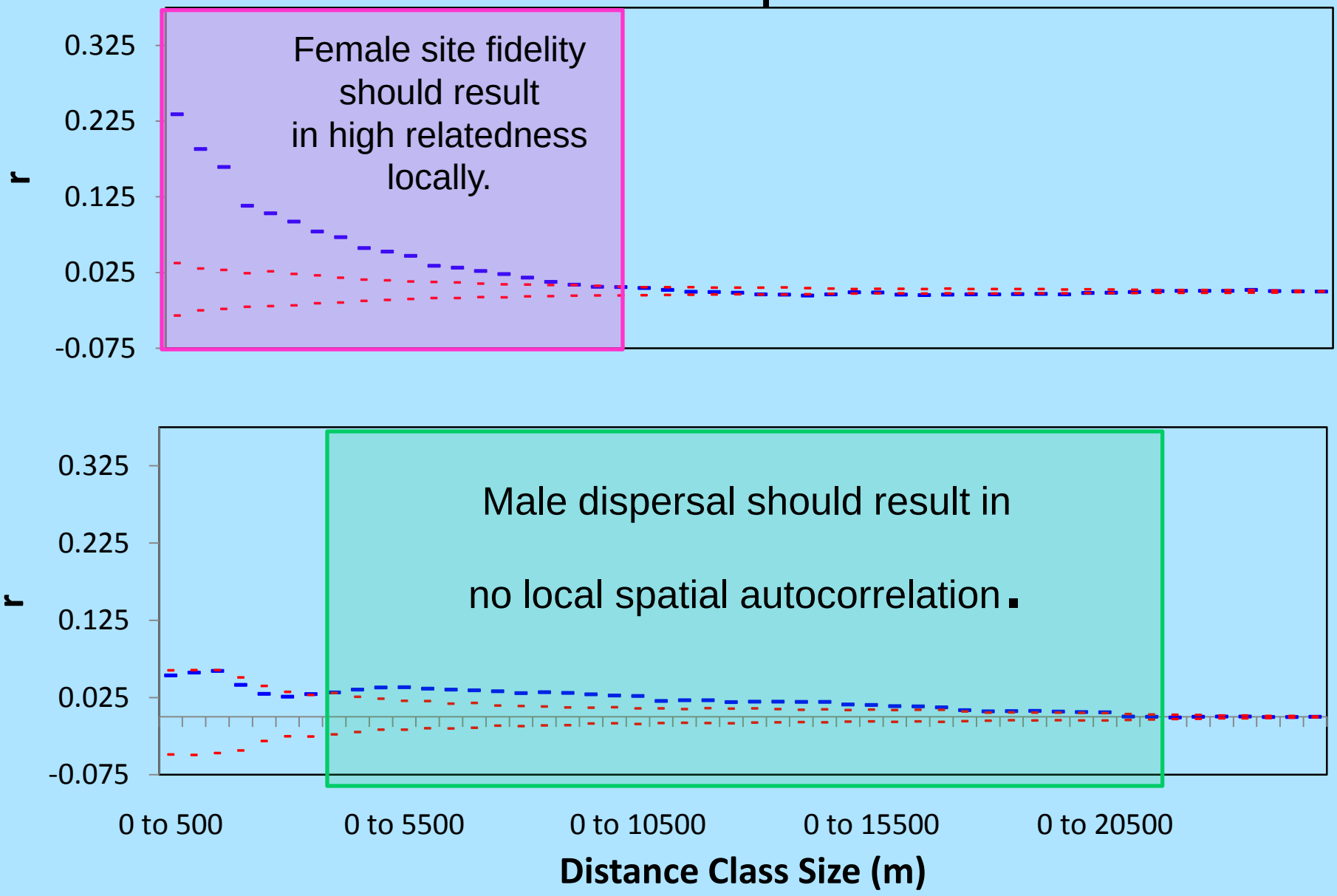
- Male offspring disperse to avoid inbreeding

  → expect no relatedness among closely spaced males



Rose-petal hypothesis: Porter et al. 1991

Patterns of Female and Male Spatial Autocorrelation



Summary: Genetic analysis of southern mule deer in San Diego

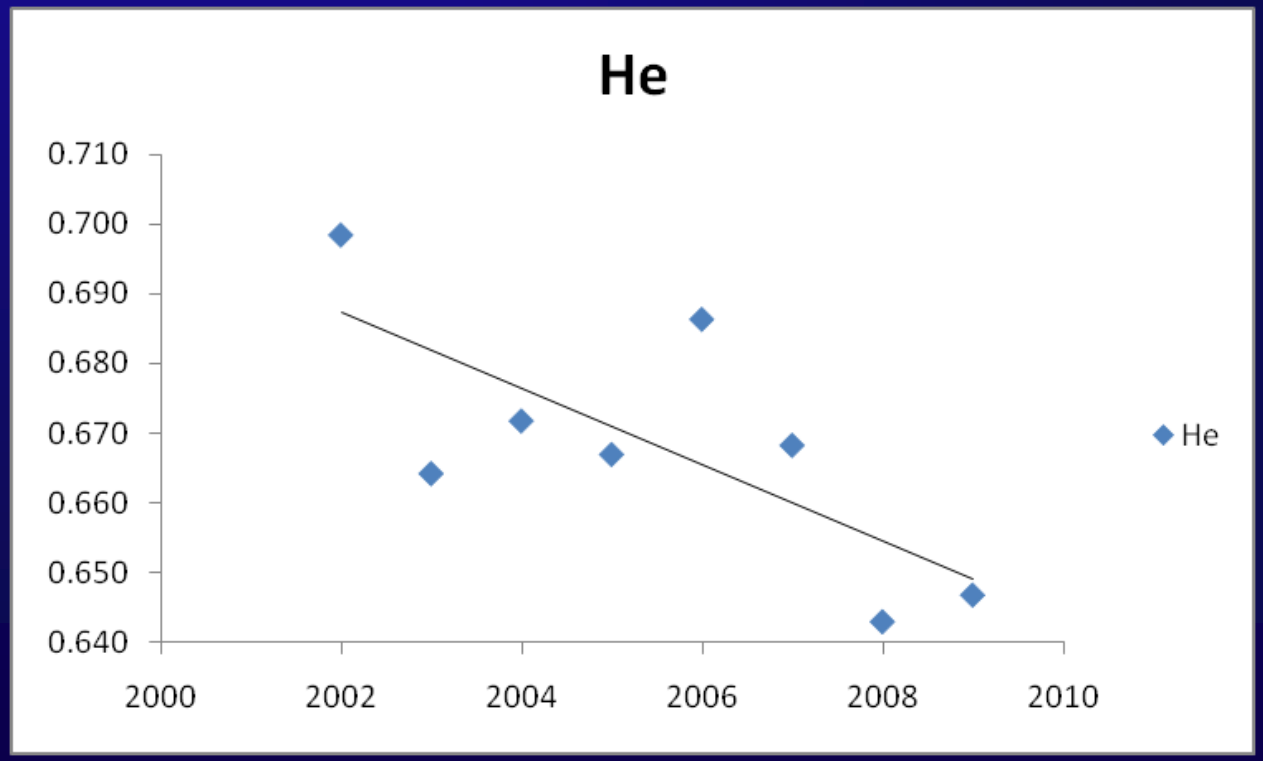
- Less genetic diversity than other CA mule deer.
- Restricted movement* among and even within urban fragments.
- N-S freeways potentially acting as barriers to gene flow.
- Genetic signature of recent reductions in population size for Torrey Pines
- High relatedness between neighboring females.
- Some relatedness among males at scale of approx. 10 km

Example 4: Southwestern Willow Flycatcher population monitoring

- Intensive population monitoring on Camp Pendleton over past 10 years (KUS)
- Genotyped birds present with 8 microsatellite markers
- FST to estimate genetic differentiation with only other known local population (Cleveland National Forest)
- Changes in genetic diversity over time, bottlenecks

Results

- Trend in decreasing genetic variation over time
- Low Ne: 108.1 (62.9 - 229.5), consistent with low N census
- Strong evidence for a recent or ongoing population bottleneck



Added information with genetic sampling

- Genetic drift strongly acting on this population that is undergoing a severe demographic decline.

<u>Future genotyping of nestlings and parentage analysis</u>

- What is the contribution of each individual to the next generation?
- Do extra pair copulations act to increase or decrease genetic variation beyond what would be expected under random mating?

- New birds detected in 2010

Conclusion

Population genetic techniques can compliment other field monitoring techniques

1. Mark/recapture with non-invasive sampling
2. Estimating recent migration
3. Estimating gene flow or genetic connectivity
4. Estimating effective population size
5. Examining demographic history
6. Sex Determination
7. Parentage
8. Detecting species presence (e-DNA, species specific gene amplification)
9. Choosing source populations for augmentation

Considerations

1. What are the population parameters of interest?
2. What are acceptable rates of error?
3. How often should monitoring occur?
4. Cost/benefits of different types of monitoring
5. Obtaining samples: how should these be distributed spatially and temporally?
6. Type of tissue, storage methods

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.