

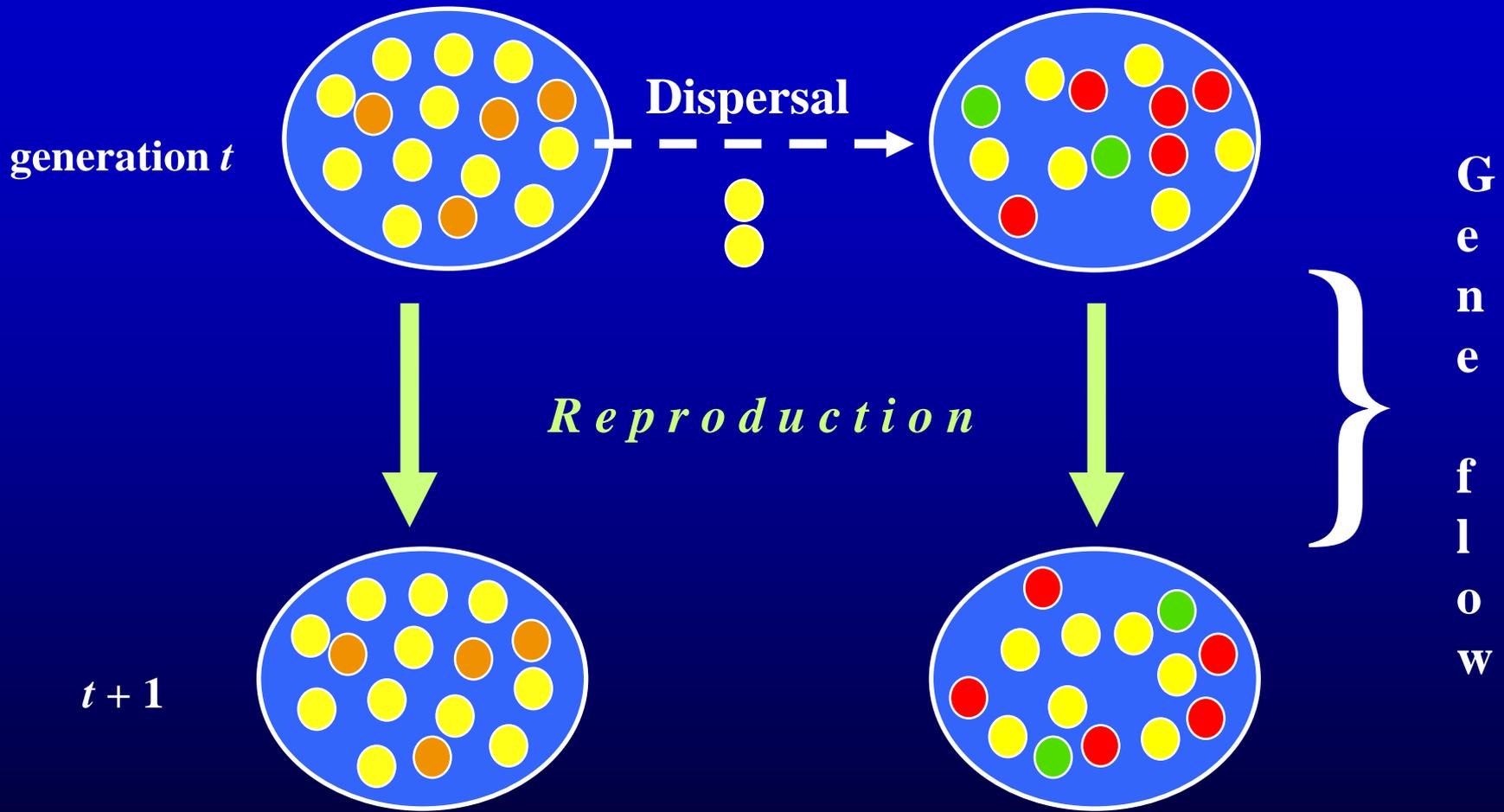
Estimating Gene Flow and Movement Among Populations

Amy Vandergast

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

avandergast@usgs.gov

Dispersal vs. Gene Flow



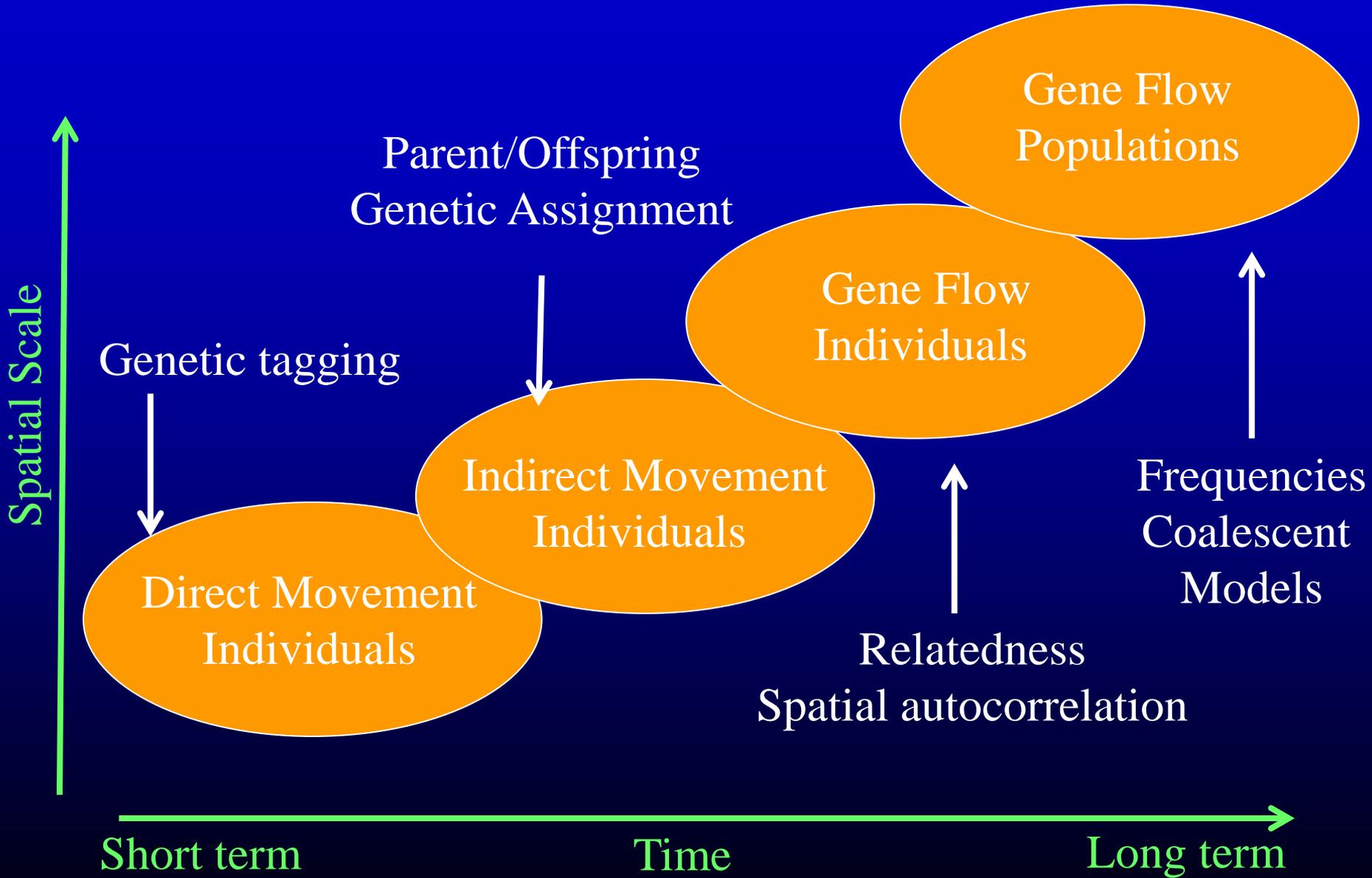


Management Questions and Uses

- How do we define a population?
- Are individuals dispersing and successfully breeding among populations?
- Within more continuously distributed species, what is the average dispersal/gene flow distance?
- Is there directionality to dispersal and gene flow?
- What landscape features, behaviors, ecological traits appear to promote or impede gene flow among populations?
- Is dispersal sex-biased?
- Has dispersal or gene flow changed in response to some perturbation or management action?
- Parameterizing spatially explicit population models.

Categories of migration estimates

- **Direct (observed)**
vs. **indirect (inferred from genetic similarity)**
- **Short-term (1 to \approx 10's of generations)**
vs. **long-term (1000's of generations or more)**
- **Population-based averages**
vs. **individual-based**



Data Considerations

- **Multiple loci**
 - **10-20 highly variable microsatellite loci**
 - **SNPs**
 - **More loci = better resolution**
- **Adequate sample sizes:**
 - **Enough individuals to analyze frequencies (20-30 per population)**
 - **Spatial coverage**
 - **For landscape-level inference, more sites=better resolution**

Movement of Individuals

Genetic “capture-recapture”

Journal of Zoology. Print ISSN 0952-8369

Mark–recapture by genetic tagging reveals restricted movements by bush rats (*Rattus fuscipes*) in a fragmented landscape

R. Peakall¹, D. Ebert¹, R. Cunningham² & D. Lindenmayer²

¹ School of Botany and Zoology, The Australian National University, Canberra, ACT, Australia

² Centre for Resource and Environmental Studies, The Australian National University, Canberra, ACT, Australia



Abstract

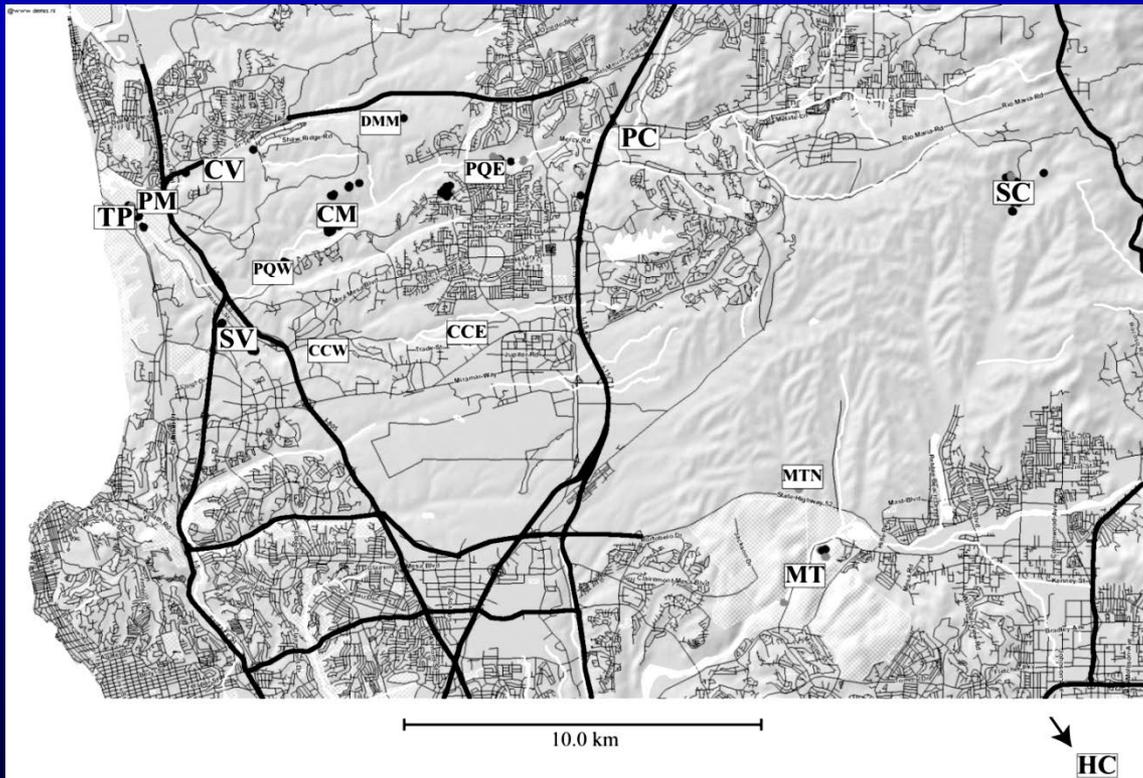
We applied genetic tagging (the identification of individuals by genetic markers) as part of a demographic and genetic analysis of a manipulative study of bush rats *Rattus fuscipes* in a fragmented landscape in south-eastern Australia. Our study comprised bush rat populations from 30 remnant patches embedded within an extensive exotic pine plantation. Genetic tagging was applied at 12 sites where eight or more animals were encountered in the initial census. Out of a total of 701 DNA samples, we determined (by genetic analysis at 11 microsatellite loci) that

←recapture;
s fuscipes.

and Zoology,
sity,
Tel: 612-
3

Very low recapture rates from "genetic tagging"

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



Minimal dispersal among fragments

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



Benefits and Caveats

- **Non-invasive DNA sources (scat, hair etc.)**
 - **Avoid handling/stressing animals**
 - **Sample degradation increases genotyping errors**
- **May require large sample sizes, particularly to estimate migration rates**
 - **Similar to other mark/recapture methods**
 - **263 scat piles → 184 capture events → 32 recaptures**
- **Results are interpretable within the bounds of the sampling scheme.**



Inferred Movement of Individuals, Intergenerational

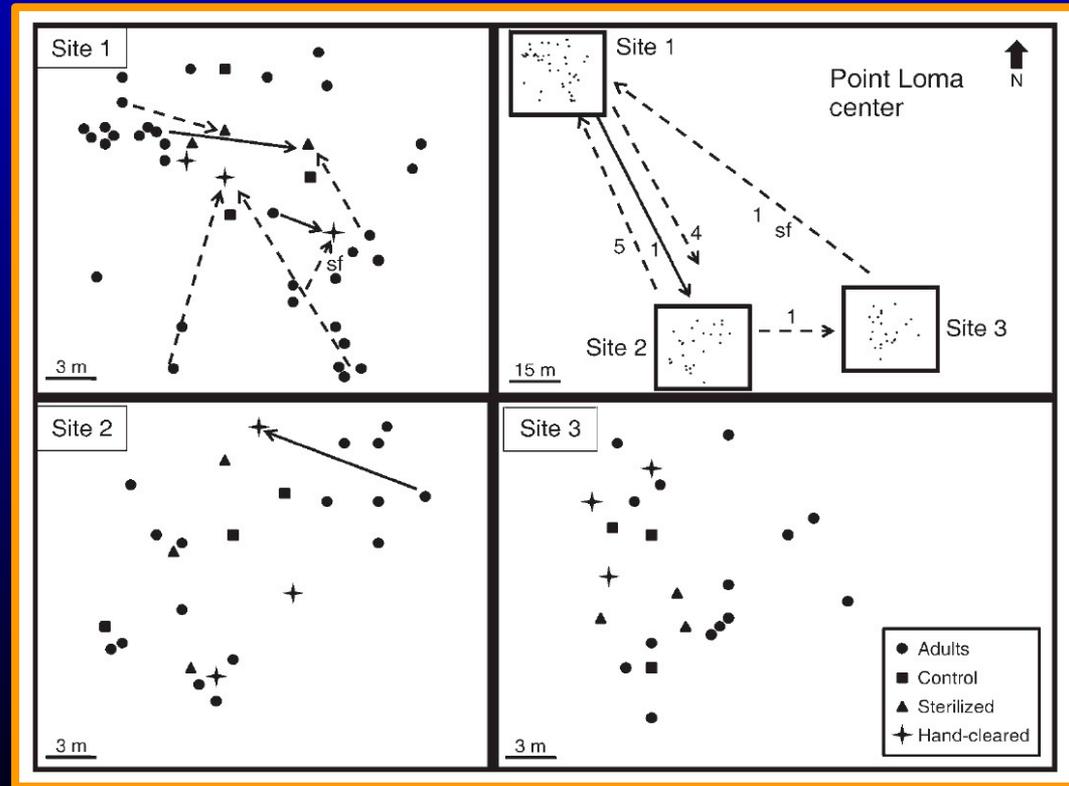
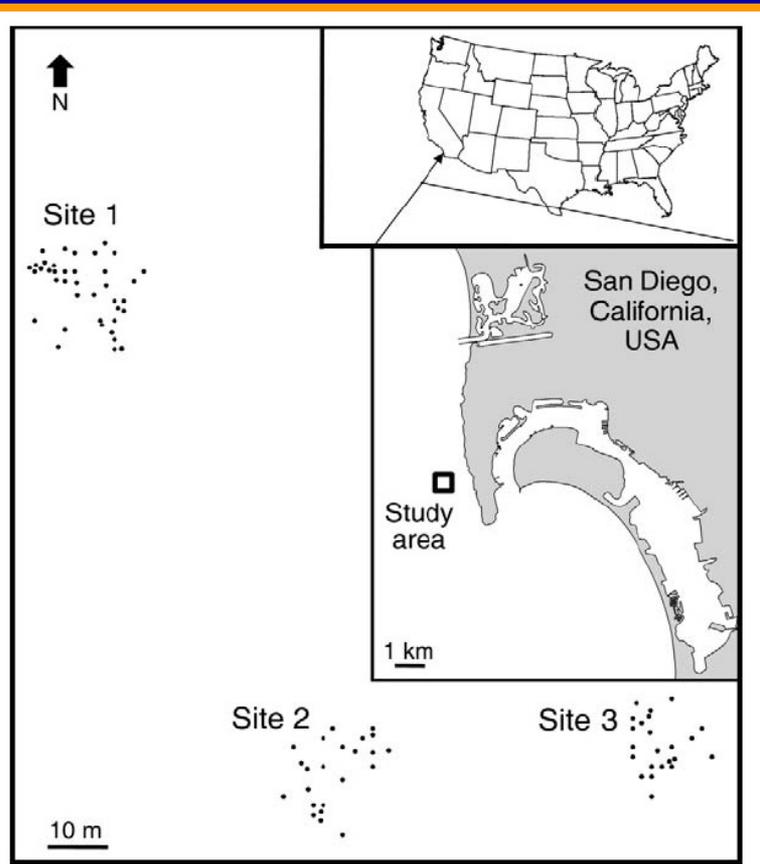
Parentage analysis

- **Likelihood-based analysis to identify parent/offspring based on multilocus genotypes.**
- **Sibship can also be inferred in the same way**
- **Examples with tree/shrub gene flow and seed and pollen movement.**

Parent/Offspring

Parentage analysis: Carney et al. (in press)

Kelp forests in southern California



Full Sibs

Coastal Cactus Wrens Parentage Analysis:

- Identified 6 pairs of full sibs with high confidence
- Maximum distance of 500 m



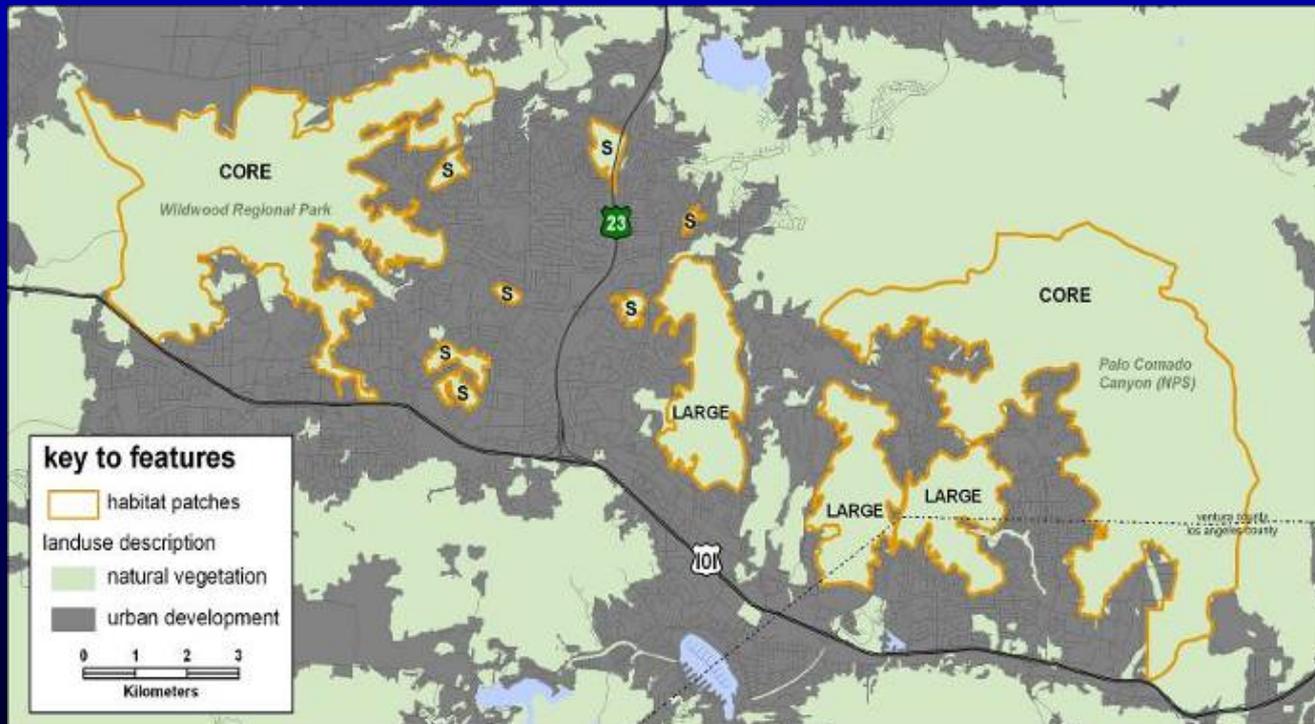
Photo by Alex Houston

Genetic Clustering to infer movement

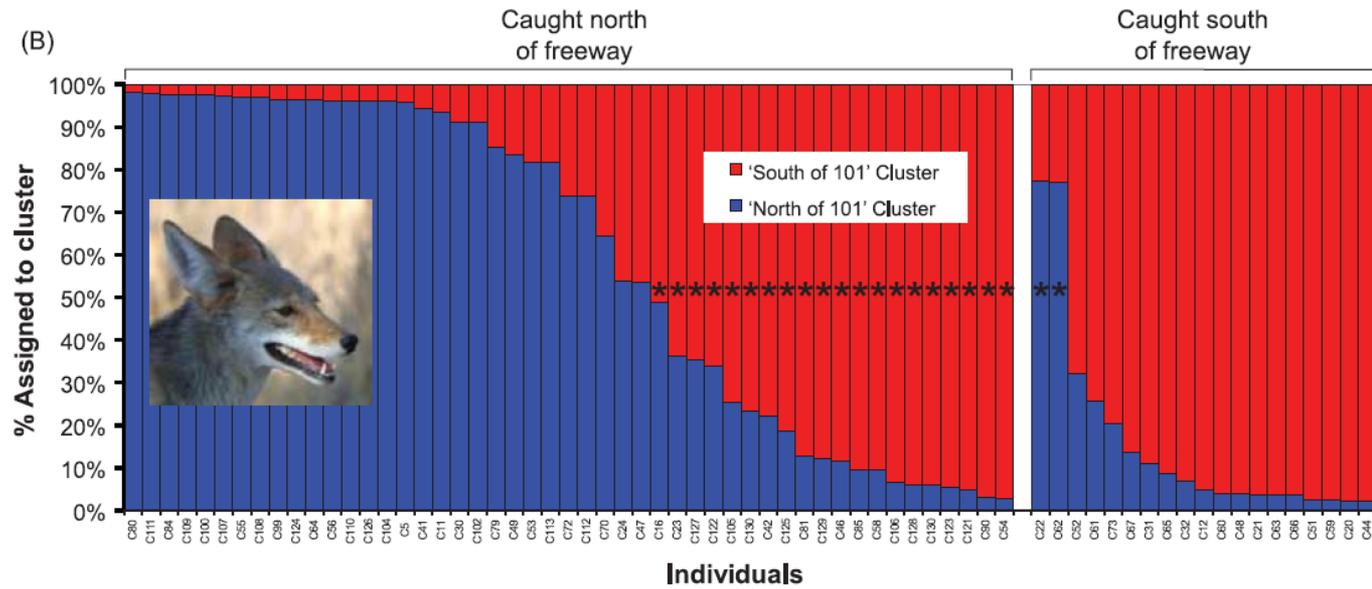
Santa Monica Mountains Coyote & Bobcat movement & genetics

Radio-tracked animals

Microsatellite markers



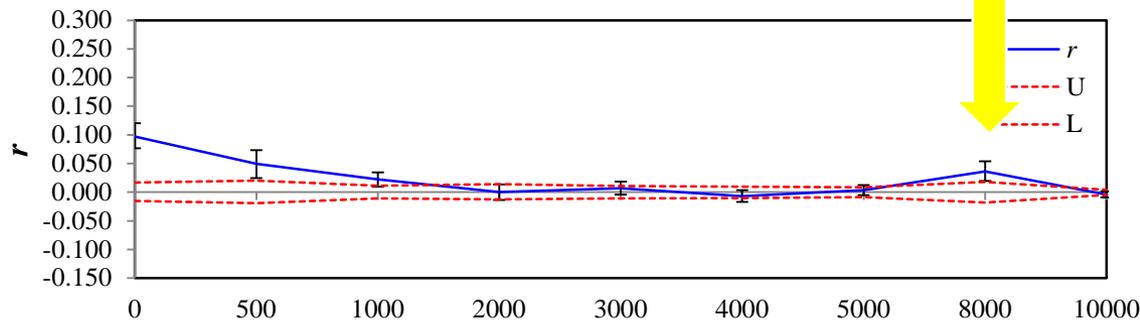
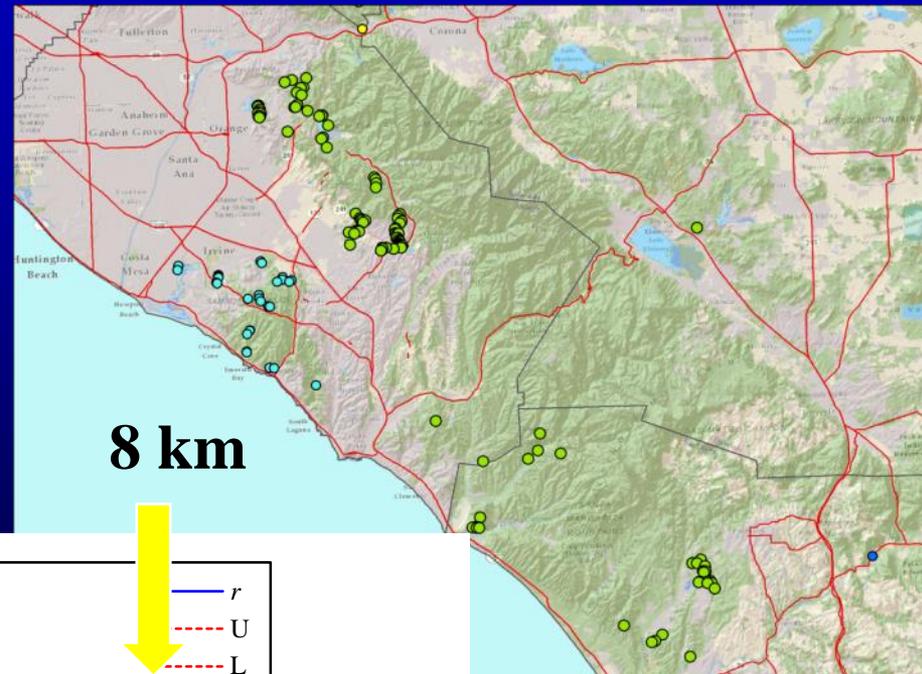
Freeway Barrier



Individual-based gene flow

Spatial Autocorrelation in individual genetic relatedness:

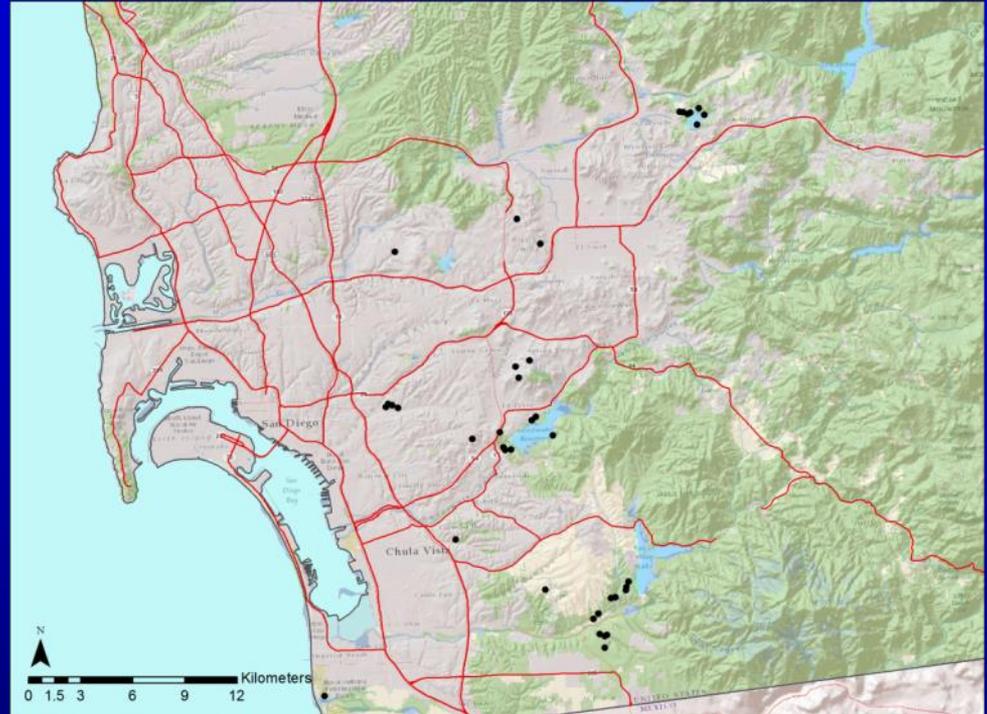
- Plot the genetic relatedness among individuals grouped at different distance classes
- Positive observed values (blue) indicate that individuals are more similar genetically than random (red dashed lines)



Cactus Wrens: San Diego

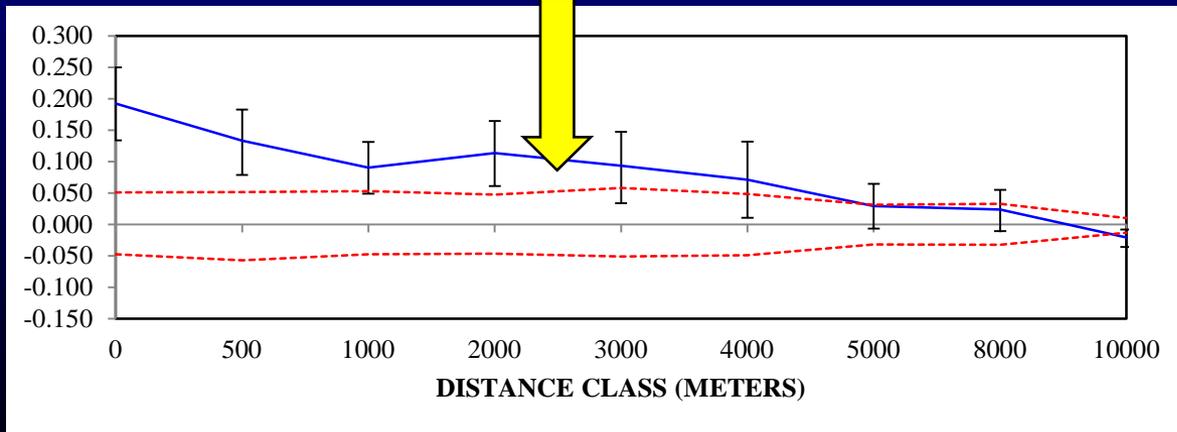


Photo by Steve Brad

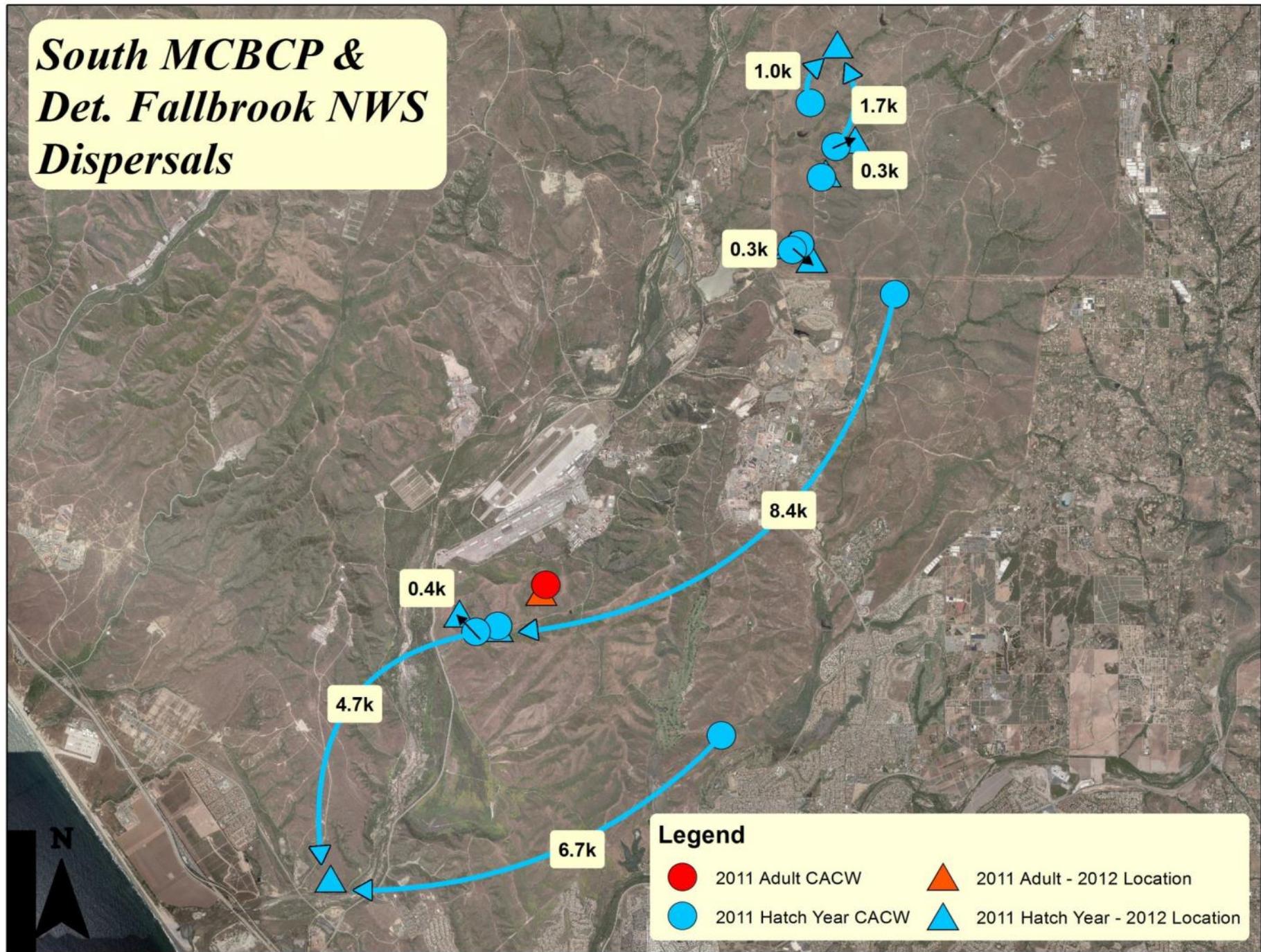


2-4 km

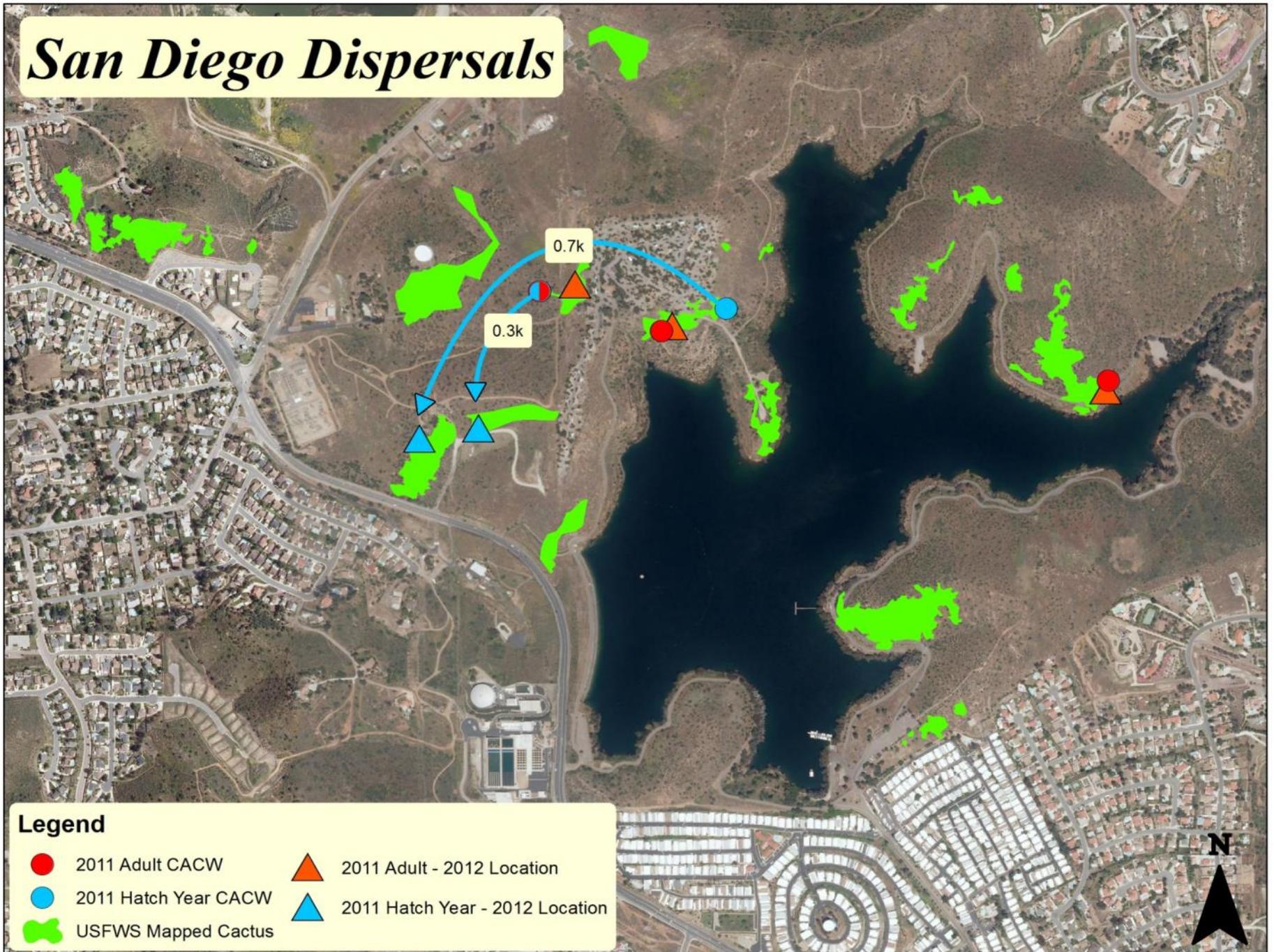
R



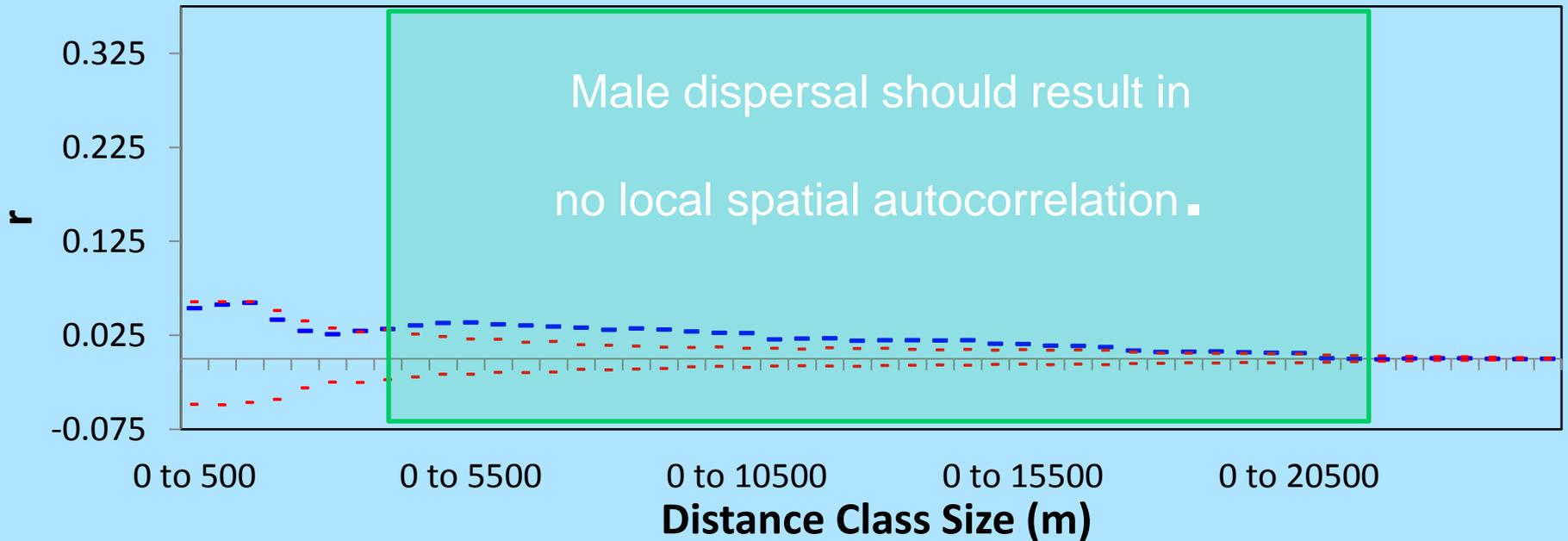
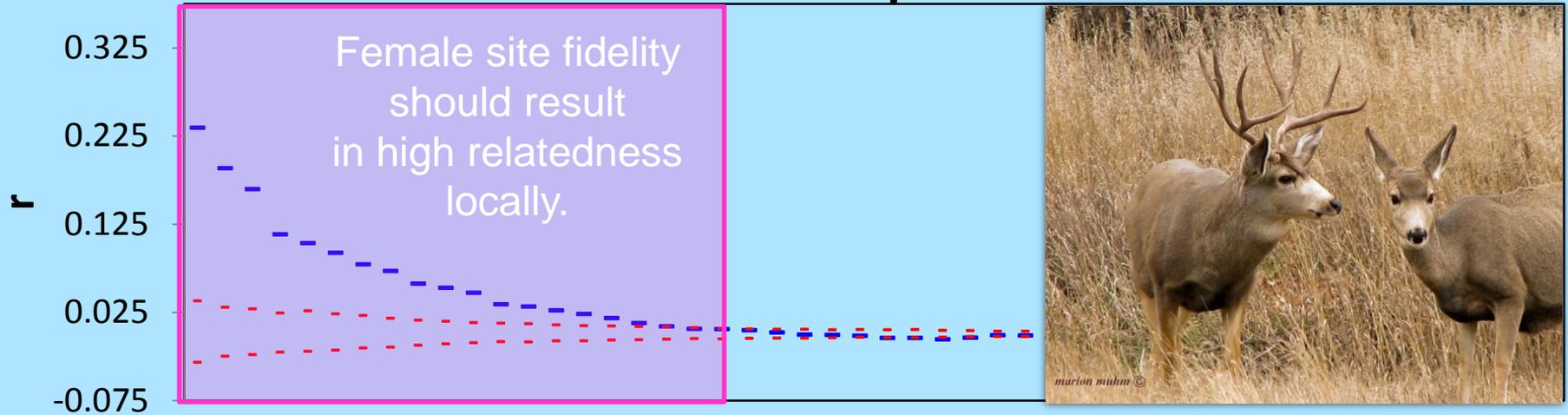
South MCBCP & Det. Fallbrook NWS Dispersals



San Diego Dispersals



Patterns of Female and Male Spatial Autocorrelation



Gene flow among populations

- **Estimate population genetic differentiation (FST)**
 - **The proportion of genetic diversity due to allele frequency differences among populations**
- **Coalescent models**
 - **Simultaneously estimate effective immigration and emigration rates, population size, time since divergence etc.**
- **Multi-generational averages**

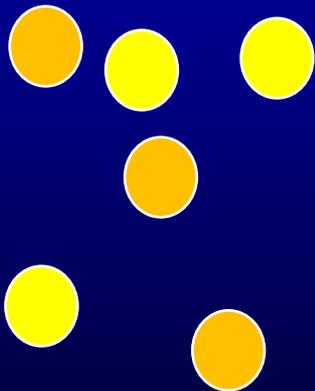
Drift + gene flow in a simple model

Gene flow (number of migrants per generation) could be estimated from F_{ST} in a very simple model ...

Assuming equilibrium between drift and gene flow.

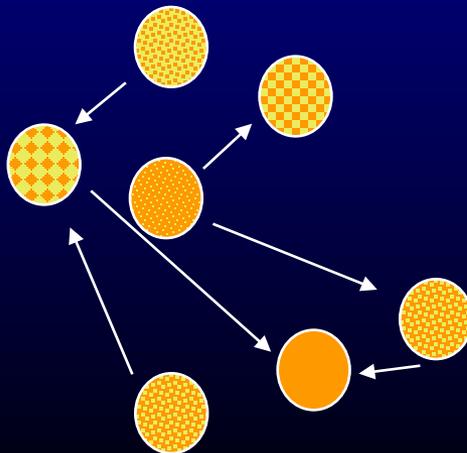
No gene flow;
only drift

$F_{ST} = 1$



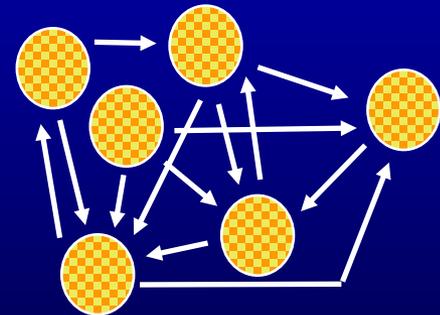
Both gene flow and
drift important

$F_{ST} < 1$

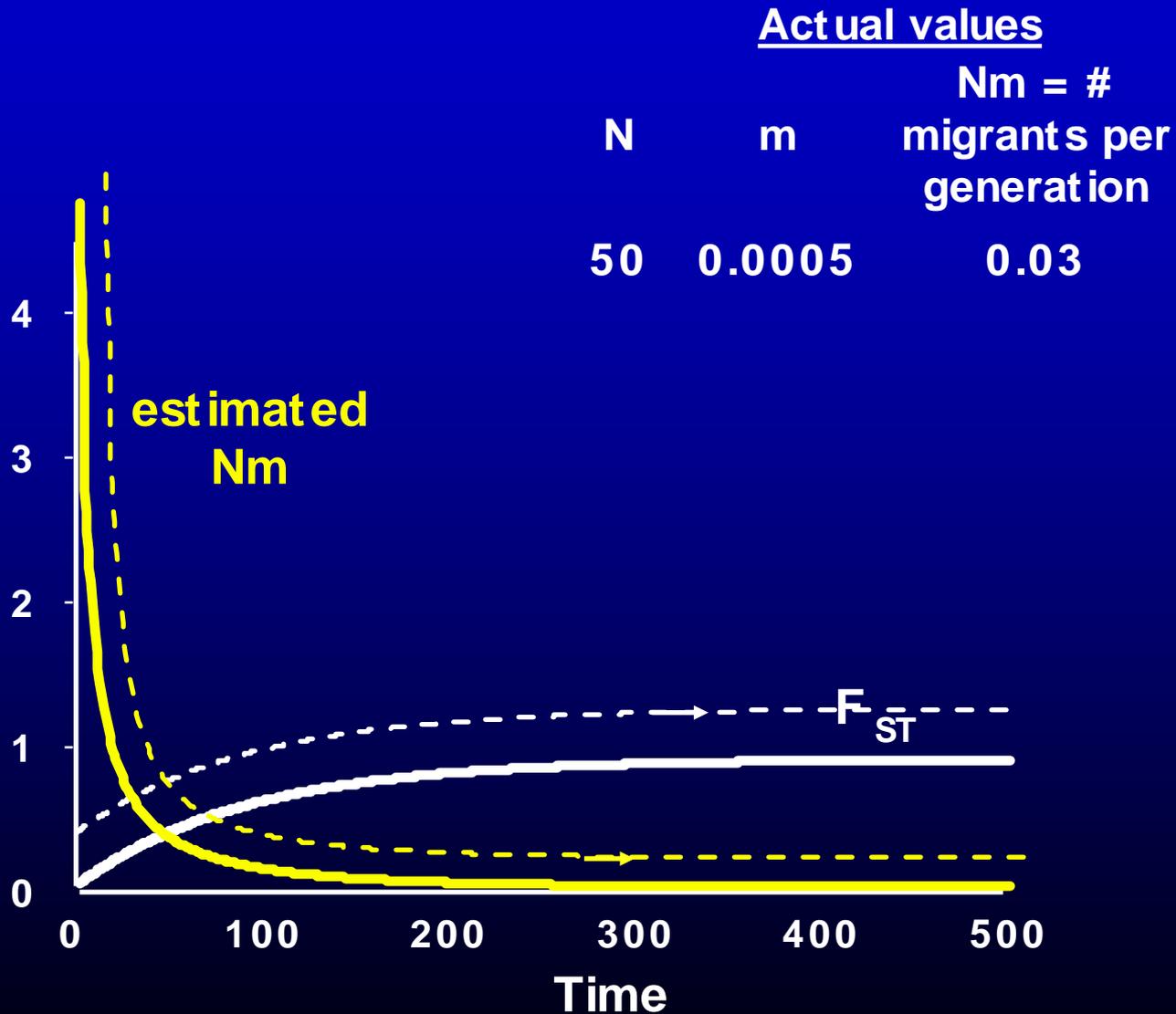


Gene flow high
relative to drift

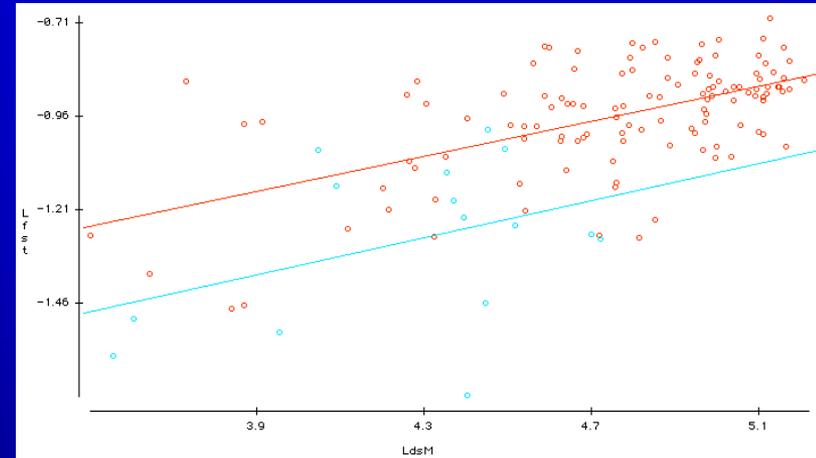
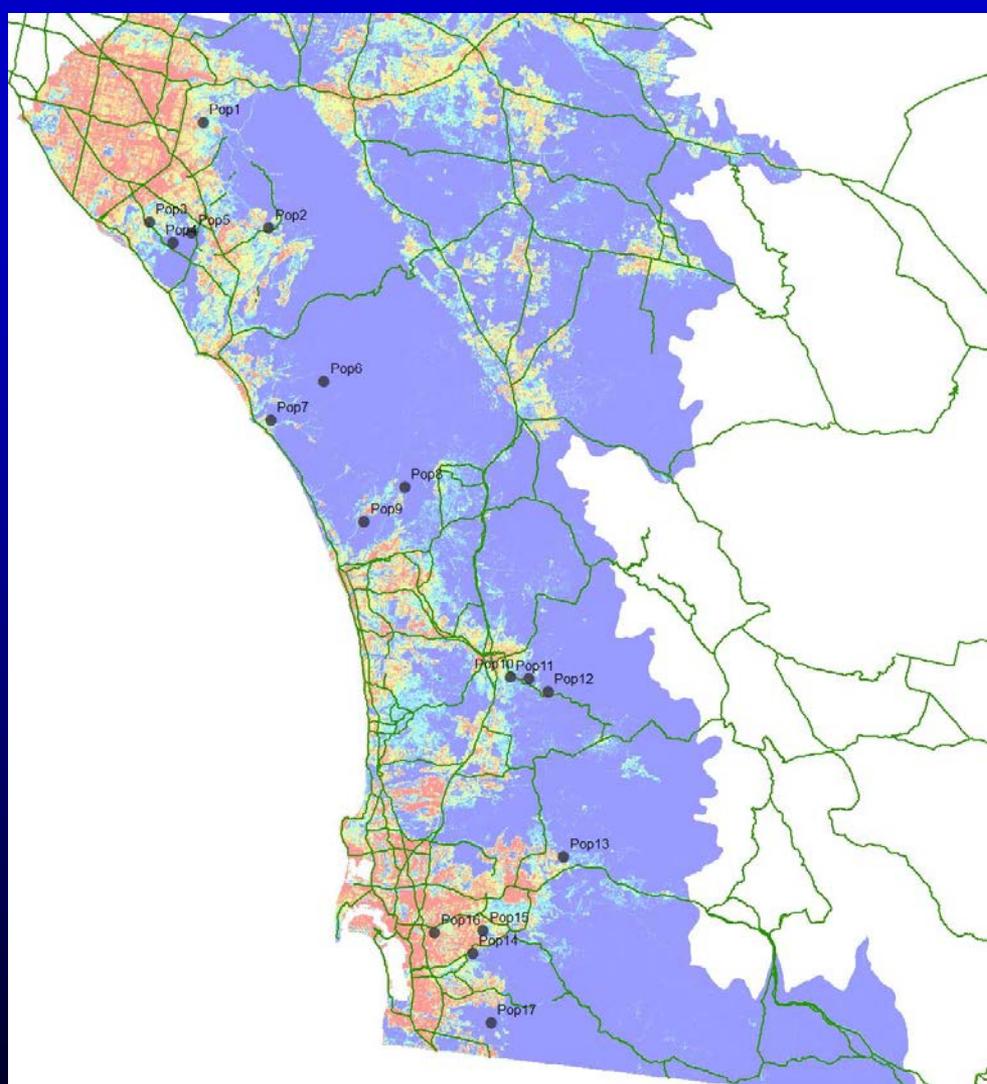
$F_{ST} = 0$



Recent Reduction in Gene Flow



Effect of urban fragmentation?



- **Correlation between pairwise F_{ST} and geographic distance- indicates stepping stone gene flow.**
- **Statistically higher F_{ST} s between populations separated by urban development**



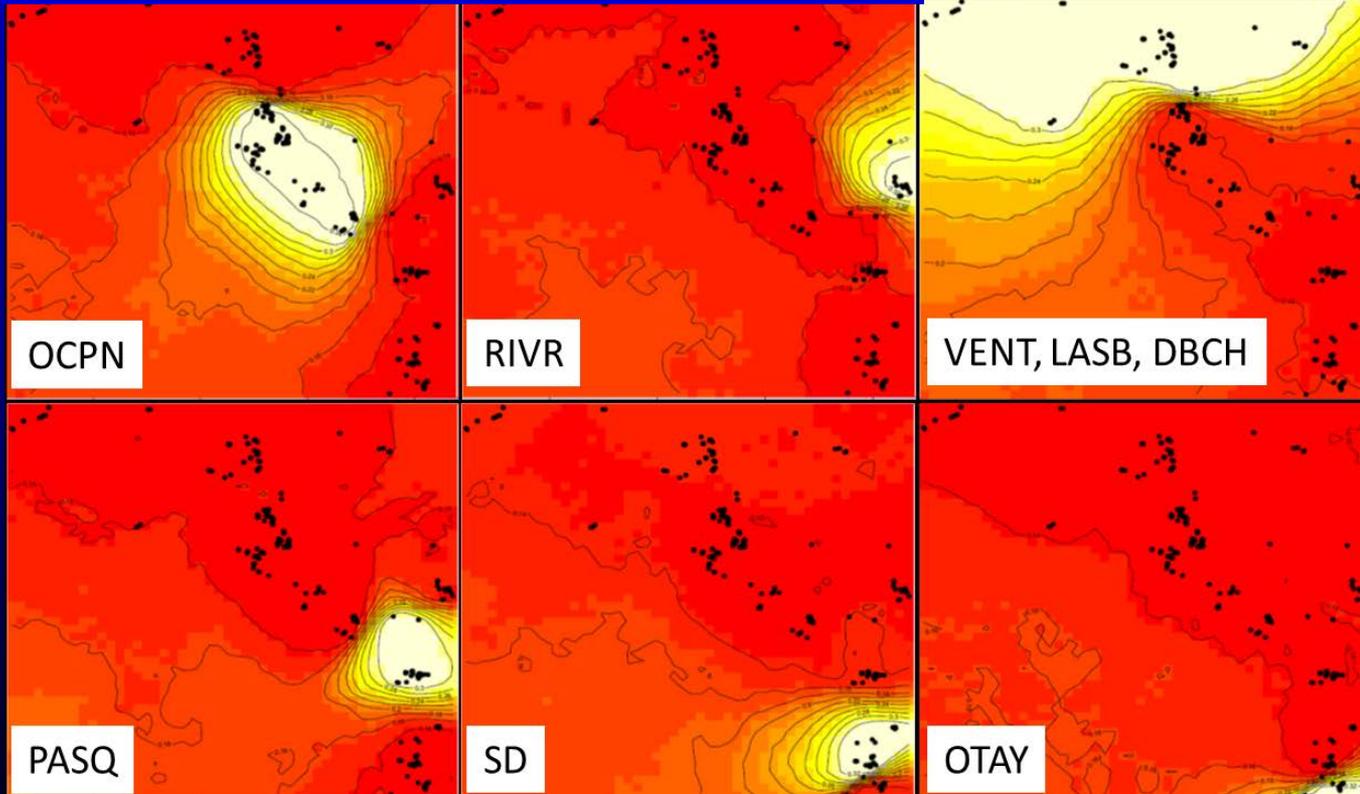
Defining Populations

- **Bayesian clustering algorithms try to recreate current population affiliations from observed genetic data.**
 - Estimate the number of clusters by minimizing linkage disequilibrium.
 - Useful when demarcation of geographic populations is difficult
- **Or test a null hypothesis of panmixia among pre-defined groups with contingency tables or randomization tests**
 - Useful when groups of individuals are more geographically defined.

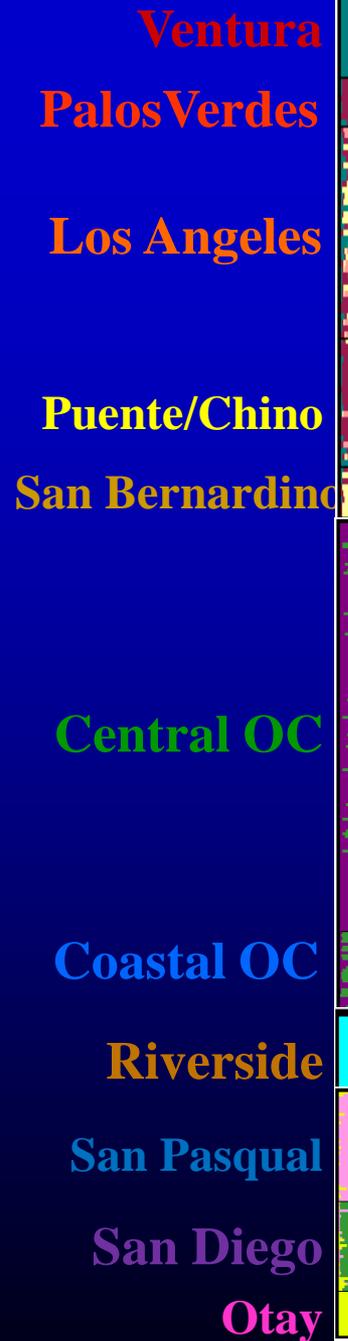
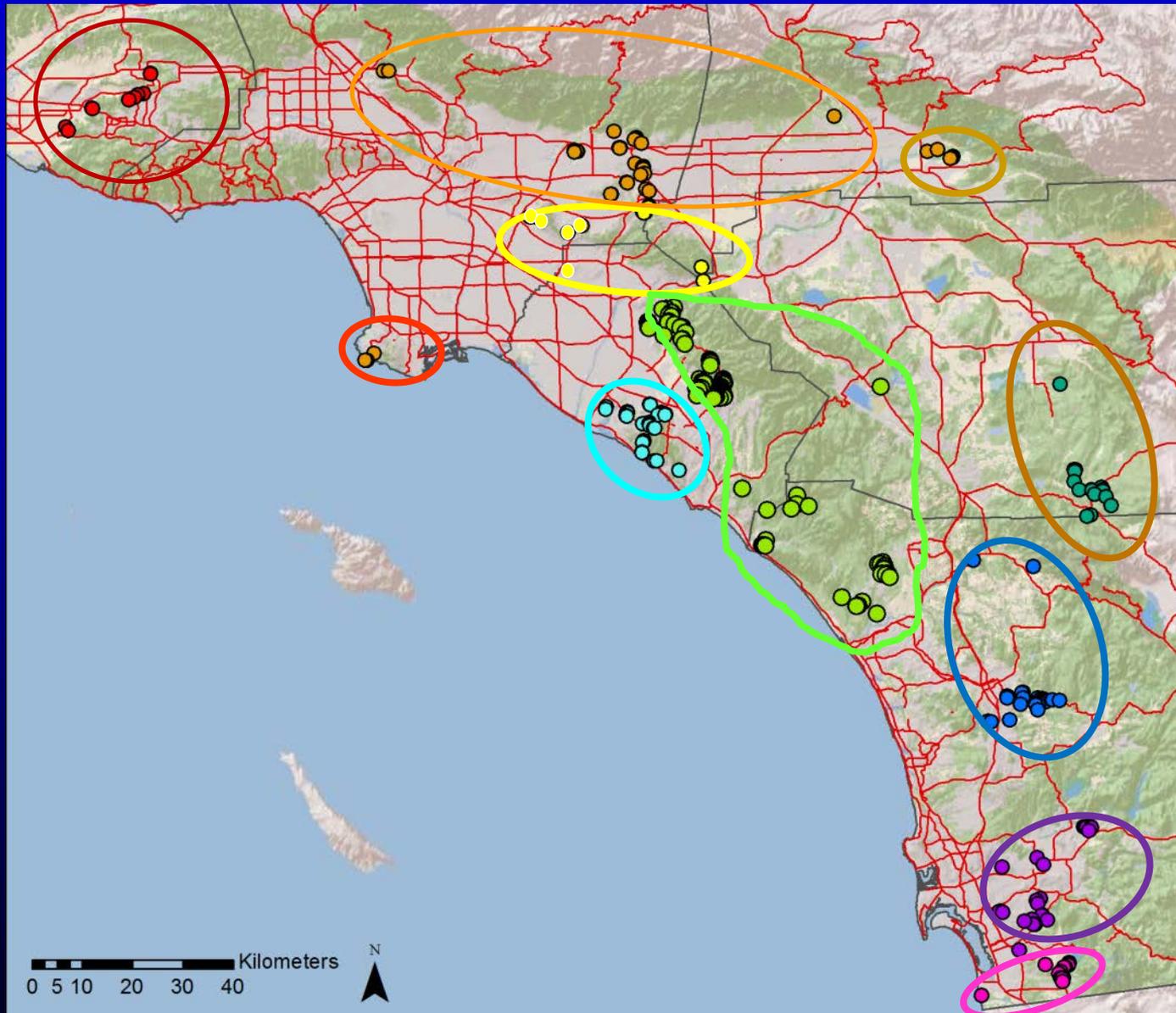
Genetic Clusters: Bayesian Assignment

Geneland Results

- 6 major clusters
- Further structuring within LA and OC



11 Genetic Clusters



Bayesian clustering algorithms

- **Clustering results can be influenced by the sampling regime.**
- **Genetically defined populations may not necessarily correspond to the appropriate unit of management.**



It all comes back to the questions...

- How do we define a population?
- Are individuals dispersing and successfully breeding among populations?
- Within more continuously distributed species, what is the average dispersal/gene flow distance?
- Is there directionality to dispersal and gene flow?
- What landscape features, behaviors, ecological traits appear to promote or impede gene flow among populations?
- Is dispersal sex-biased?
- Has dispersal or gene flow changed in response to some perturbation or management action?
- Parameterizing spatially explicit population models.