Lecture 15, 11 October 2005

Conservation Biology
ECOL 406R/506R
University of Arizona
Fall 2005

Kevin Bonine
Kathy Gerst

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Conservation Biology 406R/506R

1. Conservation Genetics (Ch6)
2. Populations (Ch7)
3. Thank Rob Robichaux
4. Holldobler talk, Mannan Talk

LAB: In Field Friday, 1230-1600h

LAB+: Field Trip Friday –> Sunday, 21-23 October

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Reminder - Seminar Wednesday, 12 October 2005

This week's seminar will be presented by:

Dr. William Mannan
Professor of Wildlife Ecology
School of Natural Resources
University of Arizona

Topic:

"Identifying habitat sinks: a case study of Cooper's hawks in an urban environment"

Date, time and location:

12 October, 2005
1:00-2:00pm (NOTE NEW TIME)
Room 225 Biological Sciences East

All are encouraged to attend

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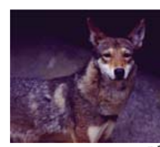
Introgression

RED WOLF (*Canis rufus*)
Coyotes, Gray wolves, Dogs



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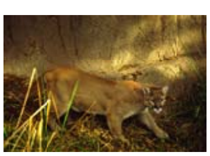
Applications of Genetics to Conservation Biology

-Molecular Taxonomy
-Populations, Gene Flow, Phylogeography
-Relatedness - Kinship, Paternity, Individual ID



Dr. Melanie Culver
SNR, UA

Molecular Taxonomy

Using molecules
(ie. DNA-based techniques)
for systematic study
or to define taxonomic units
(species, subspecies, ESUs and MUs)

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Molecular Taxonomy: Molecules versus Morphology

- Cryptic species (sibling species)
- Morphological variation without genetic variation

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Molecular Taxonomy: Conservation Relevance

- Unrecognized species may go extinct
- Incorrect species recognition
  - Non-optimal partitioning of management resources
  - Problems with hybridization
- Incorrect subspecies or population recognition
  - Non-optimal partitioning of management resources
  - Problems with introgression

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Populations, Gene Flow, Phylogeography

-Compare genetic traits among populations
-Resolve substructure among populations
-Infer movement patterns among individuals
-Infer historical events for species

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Population, Gene Flow, Phylogeography: Conservation Relevance

- Determine units for management
- Heterozygosity estimates
  - Population bottlenecks
  - Hardy-Weinberg assumptions (mutation, migration, selection, drift, inbreeding)
- PVA (Population Viability Analysis)
- MVP (Minimum Viable Population Size)
- Effective population size
  - Number of breeding individuals

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Relatedness (Kinship, Paternity and Individual ID)

Application of molecular genetic techniques, using hypervariable, repetitive DNA

(ie. microsatellites, minisatellites)

to questions of kinship, paternity or individual ID

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Kinship, Paternity, Individual ID:

- Infer relatedness among individuals
  - First order, second order, etc.
- Infer paternity (maternity)
- Reproductive success (male, female)
- Interpret reproductive strategies
  - Monogamy, harem, female choice, etc.
- Interpret behaviors
  - Dispersal (male, female), care giving, others
- Individual ID
  - Populations size estimates
  - Forensics

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Kinship, Paternity, Individual ID: Conservation Relevance

- Knowledge to aid management
  - Family structure
  - Reproductive strategy
  - Behavior
  - Dispersal
  - Inbreeding
  - Forensics/law enforcement

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Important Techniques: Phylogenetic Analysis

- Resolve evolutionary relationships (species, subspecies, populations, individuals)
- Tool used to determine Evolutionarily Significant Units (ESUs)
  - Also resolves Management Units (MUs)

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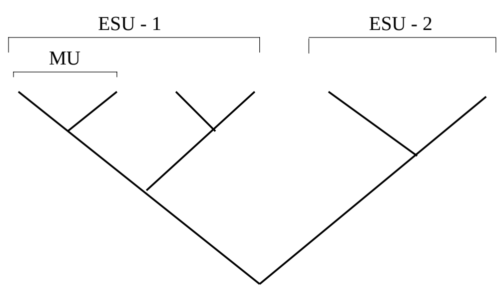
Phylogenetic tree with ESUs and MUs



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Phylogenetic Analysis: Phylogeography

- Combines phylogeny with geographical locations of populations
- Three likely outcomes for geographical populations
  - Equally different branches of tree
  - Shallow structure
  - Monophyletic group

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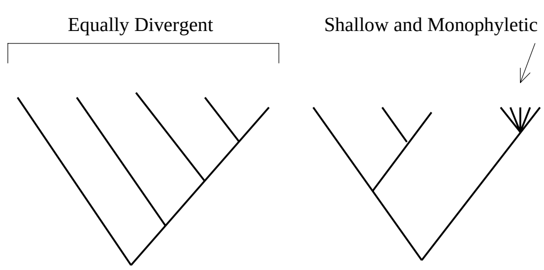
Phylogenetic Analysis: Phylogeography



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Non-Invasive Sampling

- Allows sampling without disturbance to individual
- Rare or hard to capture species
- Examples (hair, scat, feathers, saliva/cheek swab, regurgitated pellets, dried blood, biopsy dart, museum tissues

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Non-Invasive Sampling: Applications

- Species ID
- Individual ID
- Sex Determination (Sex Ratio)
- Gene Flow
- Previously described applications for genetics in conservation biology

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Non-Invasive Sampling: Pros and Cons

- Allow studies that are not possible by other methods
- Error/failure rates associated with having very minimal amount of DNA
- Use fresh tissues when possible to avoid potential errors

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Examples

- Taxonomy, Population Subdivision, Gene Flow, Phylogeography
  - Puma (cougar, mountain lion)
- Kinship and Paternity
  - Madagascar Fish-Eagle
- Species Inventory
  - Mammals at SNP using non-invasive methods

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Subspecies Taxonomy, Phylogeography, Gene Flow: Puma (cougar, mountain lion)

32 Puma subspecies, as of the early 1900s

Objectives

- Does current population differentiation reflect
  - Trinomial descriptions?
  - Physical or ecological barriers?
  - Isolation by distance?
- Are current levels of genetic variation the same within each population?
- Does population structure and genetic variation reflect
  - Historic migrations?
  - Historic dispersals?
  - Historic bottlenecks?

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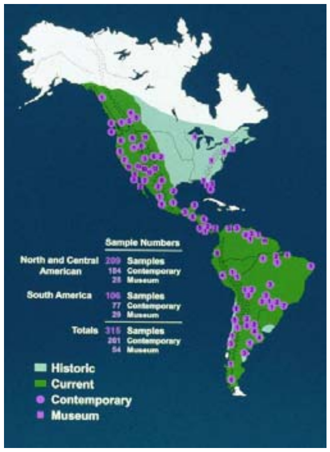
Modern and museum puma samples collected, total of 315



Molecular Methods Used

- Mitochondrial gene sequencing
  - 16SrRNA
  - NADH-5
  - ATPase8
- Nuclear microsatellite length determination
  - 10 domestic cat microsatellite loci

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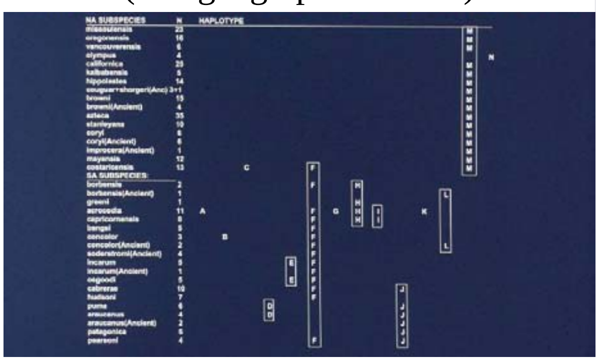
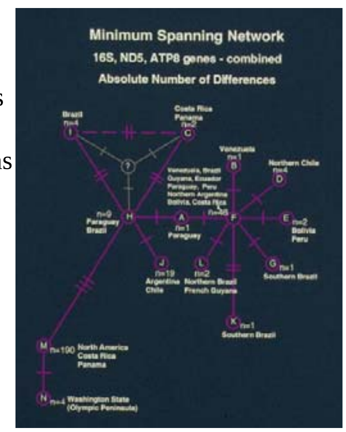
Mitochondrial DNA Haplotypes (in a geographical cline)



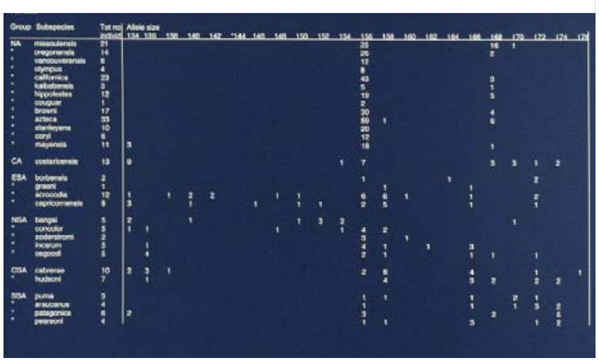
-Ancestral haplotypes

-2 historical radiations

-NA is most recently founded population



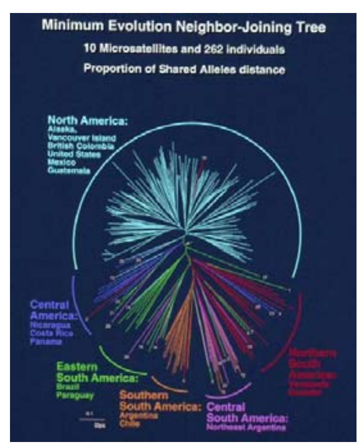
Microsatellite Alleles at FCA008



-Geographic clustering of individuals

~Six groups identified

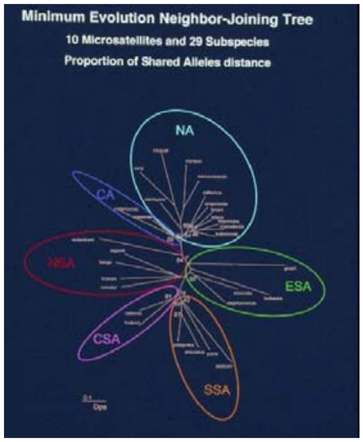
2 distance methods agree



-Subspecies associate into same 6 groups

-Statistical support from bootstrap values

-2 distance methods agree



Wright’s Fst Estimates and Slatkin’s Migration Estimates

mtDNA

	NA	CA	ESA	NSA	CSA	SSA
NA	–	0.1	0.1	0.02	0.03	0.1
CA	*0.784	–	8.3	0.5	1.6	1.6
ESA	*0.815	0.057	–	0.8	2.3	2.2
NSA	*0.958	*0.492	0.384	–	4.2	0.5
CSA	*0.935	0.233	*0.177	*0.107	–	1.3
SSA	*0.835	0.240	*0.186	*0.526	*0.281	–

(Fst near 0 = little divergence) (Migrants/generation)

microsatellites

	NA	CA	ESA	NSA	CSA	SSA
NA	–	4.0	4.4	8.0	2.2	0.9
CA	*0.110	–	2.3	3.5	3.5	1.2
ESA	*0.103	*0.179	–	15.7	4.8	1.0
NSA	*0.059	*0.126	*0.031	–	6.0	1.1
CSA	*0.186	*0.126	*0.094	*0.077	–	2.4
SSA	*0.367	*0.288	*0.330	*0.316	*0.172	–

Summary:
-6 groups identified using microsatellites
-mtDNA haplotypes overlayed onto map, supports 6 groups
-Location of 2 ancestral haplotypes

Major restrictions to gene flow:
-Amazon River
-Rio Parana
-Rio Negro
-Andes?

Fossil Record versus Molecular Divergence Estimates

- Oldest fossils in North and South America date to 0.2-0.3 Mya
- From mtDNA mutation rate of 1.15%/My, divergence for extant puma lineages is 390,000 years ago
- From mutation rate of 5×10^{-9}/yr for microsatellite flanking regions, pumas are less than 230,000 years old

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Historical Inferences

- Extant pumas originated in Brazillian Highlands (ancestral haplotypes)
- Fossil record suggests dispersal to NA soon after the common origin in Brazil
- 2 historical radiation events occurred

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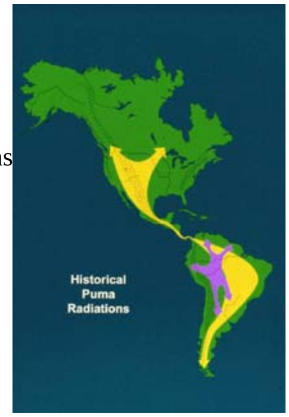
-Ancestor to puma crosses land-bridge ~2-3 Mya

-Puma origin in Brazilian Highlands ~300,000 ya

2 Major historical radiations

-One locally distributed

-One broad ranging



Puma Bottlenecks

- Subspecies-level
  - North America low overall genetic variation
- Population-level
  - Florida monomorphic at 8/10 microsatellite loci
  - Olympic Peninsula and Vancouver Island, monomorphic at 5/10 microsatellite loci

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Puma Conclusions

- Pumas originated in Brazil approximately 300,000 years ago
- Possible extirpation and recolonization in North America (Pleistocene age?)
- Molecular data does not support 32 subdivisions, instead 6 groups
- Pumas are fairly panmictic within 6 groups

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Conservation Implications

-Maintain habitat connectivity within 6 large groups

-Management should consider effects of bottlenecked populations

-Eastern cougar, Florida panther and Yuma puma management take into account revised subspecies

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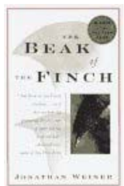

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http://www.rit.edu/~rhrsbi/GalapagosPages/DarwinFinch.html

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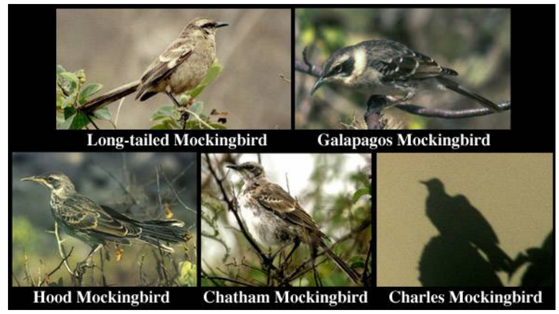

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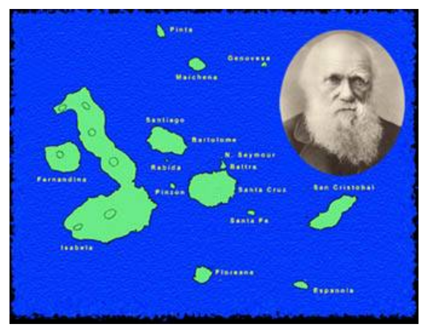

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Galapagos Marine Iguana (Iguanidae)

Only lizard to feed at sea
-algae, seaweed

Up to 10 or 12 m deep
Up to a hour-long dives for large males
(Darwin shipmate)

Highly social
8,000 indivs/ km of coast

16 islands
Cold upwelling water nourishes algae

Fernandina/Isabela
males to 10+ kg
females to almost 3 kg

Genovesa
males only to 1 kg
females to < 1kg

Why? → Water temperature and current strength

Amblyrhynchus cristatus

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Martin Wikelski, Princeton

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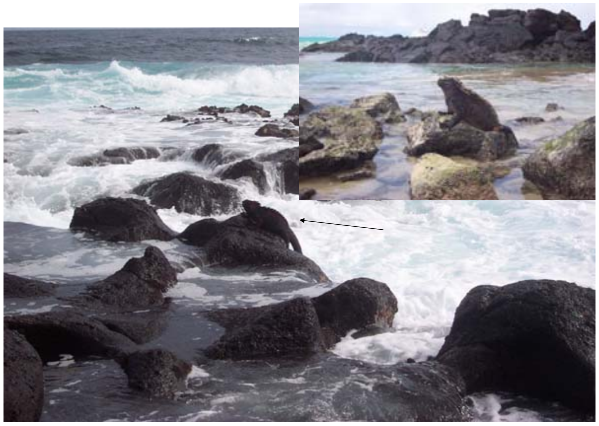
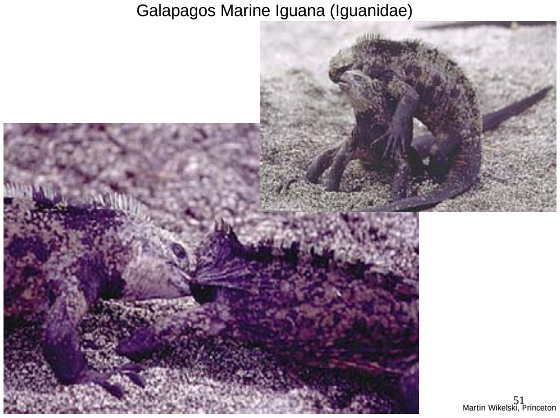


Katrina Mangin

Galapagos Marine Iguana (Iguanidae)



Martin Wikelski, Princeton

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Galapagos Marine Iguana (Iguanidae)

El Nino → lack of food (Why?)

Starvation b/c high cost of salt excretion

Animals may lose 15% body length
-bone absorption

Only adult vertebrate known to regularly shrink
(astronauts)

Largest animals die
-sexual selection
-natural selection

Amblyrhynchus cristatus

Martin Wikelski, Princeton

What is population viability analysis? (PVA)

Thanks to Margaret Evans, 2003

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Population viability analysis is
a quantitative analysis of population dynamics
with the goal of assessing extinction risk

Demographic Data →	Mathematical Analysis →	Prediction of extinction risk
•survival and fertility throughout an organism's life cycle •population size over time •birth and death rates	•matrix model •time series analysis •branching process •stochastic birth-death process •reaction-diffusion equation	•population growth rate (λ) •extinction probability •time to extinction •future population size or structure

Simulation vs. Summary Statistics (role of sampling, endangered species)

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Table 1.1 Potential uses of PVA "products"

Category of Use	*Specific Use*	*Examples*
Assessment of extinction risk	Assessing the extinction risk of a single population	Shaffer 1981, Shaffer and Samson 1985, Lande 1988a
	Comparing relative risks of two or more populations	Menges 1990, Forsman et al. 1996, Allendorf et al. 1997
	Analyzing and synthesizing monitoring data	Menges and Gordon 1996, Gerber et al. 1999,
Guiding management	Identifying key life stages or demographic processes as management targets	Crouse et al. 1987
	Determining how large a reserve needs to be to gain a desired level of protection from extinction	Shaffer 1981, Armbruster and Lande 1993
	Determining how many individuals to release to establish a new population	Bustamante 1996, Howells and Edwards Jones 1997, Marshall and Edwards Jones 1998, South et al. 2000
	Setting limits on the harvest (or take) from a population that are compatible with its continued existence	Nantel et al. 1996, Ratsirarson et al. 1996, Caswell et al. 1998, Tufto et al. 1999
	Deciding how many populations are needed to protect a species from regional or global extinction	Menges 1990, Lindenmayer and Possingham 1996

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Why do we do population "viability" analysis?

U. S. Endangered Species Act (1973)
codifies in law a national policy of avoiding the extinction of species

U. S. National Forest Management Act (1976)
"[f]ish and wildlife habitat shall be managed to maintain viable populations of existing native and desired nonnative vertebrate species in the planning area…In order to insure that viable populations will be maintained, habitat must be provided to support at least a minimum number of reproductive individuals and the habitat must be well distributed so that those individuals can interact with others in the planning area"

U. S. Marine Mammal Protection Act (1994 amendments)
stock assessment process

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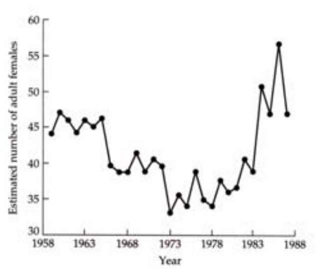
What do I mean by "population dynamics"?

populations are dynamic, not static

Grizzly bears,
Yellowstone National Park



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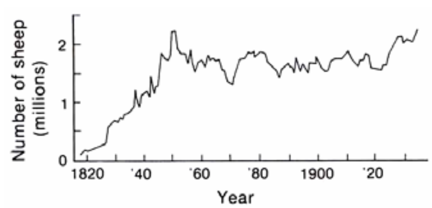
populations are dynamic, not static

Sheep on the island of Tasmania



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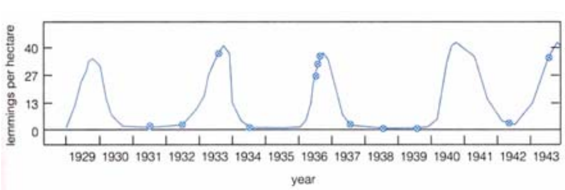
populations are dynamic, not static



Lemmings

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