GIS Applications to Museum Specimens

Joseph Grinnell (1877–1939)

At this point I wish to emphasize what I believe will ultimately prove to be the greatest value of our museum. This value will not, however, be realized until the lapse of many years, possibly a century, assuming that our material is safely preserved. And this is that the student of the future will have access to the original record of faunal conditions in California and the west wherever we now work."

- Founder and First Director of MVZ
- Ecological Niche Concept

Biogeography, niche evolution and changing climates

Arthur M. Sackler Colloquium of the National Academy of Sciences, held in Irvine, CA, December 11–13, 2008, in celebration of the Centennial of the Museum of Vertebrate Zoology at the University of California at Berkeley.

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Species distribution models

- based on current ecological niche constraints
- used to project future and past species distributions
- assumptions add uncertainty in model projections
 - structure of the models,
 - algorithms used to translate niche associations into distributional probabilities,
 - quality and quantity of data,
 - mismatches between the scales of modeling and data.

Niche Modeling and statistical phylogeography of the Western Jumping Mouse (*Zapus princeps*) : Testing alternative hypotheses

Jason L. Malaney

The Question

Assessing past geographical distributions and processes

Do communities remain intact through time OR do taxa respond to environmental change idiosyncratically?

comparative phylogeography across multiple species

Signals of introgression in taxa thru glacial cycles?

OR did taxa remain in sustained isolation?

Importance of Museums...

Documentation

- Provide verifiable evidence of who, what, when, where, how, why
- Data can then be used to ask interesting questions over evolutionary time
 - Where did organisms potentially occur in the past?
 - Where will organisms go with changes in climate?

Where did organisms potentially occur in the past? Calculate current distribution model Project to past - Paleoclimate distribution Propose alternative hypotheses of demography of organisms Test hypotheses empirically with multi-locus DNA data Effective population sizes – Ne relatedness of lineages – clades & trees Divergence dates - when splits between lineages occurred Relate these back to paleo-distributions and contemporary distributions Very strong story of <u>history</u> of organisms Natural history museums are fundamental...

Where will organisms go with changes in climate?

Calculate current distribution model Project to future - future distribution Helps with making decisions about conservation of lineages \rightarrow areas Helps to project if current activities may have future repercussions Very strong story of <u>future</u> of organisms Natural history museums are fundamental...

Strengths of phylogeography & coalescent modeling Statistical inference –

- Parametric Bootstrap
- GIS technologies ecological niche models
- Multiple independent markers
 Multiple species



Richards et al. 2007

Empirical Example

Are distributions of western North American mammals ephemeral or persistent historically?

Single Ancestor
Populations have recently fragmented from a common ancestor

Independent Refuge

Populations were disjunct, persisting in isolated pockets throughout glacial cycles

Admixture

No isolation during glaciations - populations repeatedly introgress
 Habitats coalesced and became less isolated

Hypothetical montane species distributions during interglacial periods

Single ancestor during glacial periods?

BUSH

Admixture during glacial periods?



Independent refuge during glacial periods?



Zapus princeps One of 3 species of Zapus Family Dipodidae Range: Western North America New Mexico to southern Yukon Habitat: Generally willow and aspen thickets along riparian zones Dense vegetation, highly fragmented in SW Biology: active 3-4 months, low natality, long generations, low densities



Methods

Tissues obtained from natural history collections
 DMNS, FMNH, MSB, MVZ, UAM, UMNH, and UWBM
 MtDNA

1140 base pairs of Cytochrome b gene

 295 Total specimens: 292 sequenced (28 from Patton and Conroy), 3 from GenBank

221 Zapus princeps, 65 Z. hudsonius, 8 Z. trinotatus, 1 Napaeozapus insignius

Nuclear DNA – 5 genes

 APOB – 367bp, BCRA – 919bp, EFG – 573, GBA – 528bp, MYH2 – 266bp

63 specimens representing major mtDNA clades
 Total: 3793bp

Specimens of Zapus princeps Edmonton

Calgary

san Francisco

Grea

DAHC

Ise

city

CALIFORNIA

BRITISH COLUMBIA

Vancouver

Seattle WASHINGTON

Portland

RESON

victoria

1000 Marth

wome

C40

135 Vegas SOUTH DAROTA SOUTH

chevenne nesusa

UNITED

Albuquerque

UEN NEICO

Denver

CHIORINO

ARIZONA

• Phoenix

Niche Models & Parameters

Set the stage for specific hypotheses

 Identify and calculate specific parameters which influence hypotheses – Empirical
 Phylogeny & Model of Evolution
 Effective Population Size – Ne

 Total and lineage

 Divergence Time - coalescent

Hypotheses



Admixture

Independent Refuge

Single Ancestor

LGM 18,000 ybp



Hypothesized refugia

Methods

Statistical phylogeography of Z. princeps Test alternative hypotheses of historical demography Model based coalescent techniques parametric bootstrap - MESQUITE Simulate genealogies & sequences – probability distribution **GTR** + I + Γ Metric - s of Slatkin and Maddison Compare empirical value to those generated randomly





0.7



Summary

Highly divergent Zapus princeps lineages
4 distinct, monophyletic, and novel lineages
Multiple markers

 structured lineages that exhibit high levels of deep historical differentiation

- May warrant taxonomic revisions
- Morphology

Jumping mice in western NA appear to have undergone sustained fragmentation

- Can not reject the independent refuge hypotheses
- Challenge is to disentangle alternative models

more specific parameterization within fragmentation model

Other montane species?
Comparative Phylogeography
Do communities remain intact through time OR do taxa respond to environmental change idiosyncratically?



Fossil Record





Zapus hudsonius