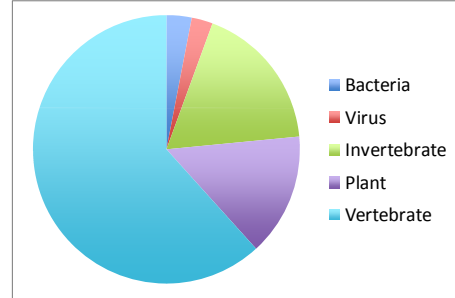


Landscape Genetics: Questions and Insights Part I

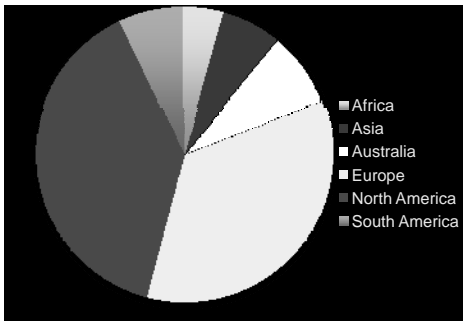
Andrew Storfer
 School of Biological Sciences
 Washington State University

Organismal groups



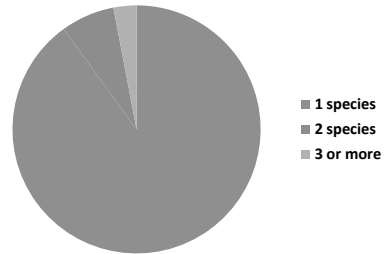
Current Gaps?

Geographic



Current Gaps?

of study species



Storfer et al submitted

Current Gaps?

Habitat Type

- 79% Terrestrial
- 15% Freshwater
- 6% Saltwater
- 40% Temperate Forests
- 10% Tropical Forests
- 11% Agricultural



Storfer et al submitted

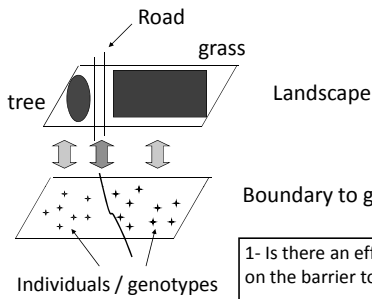
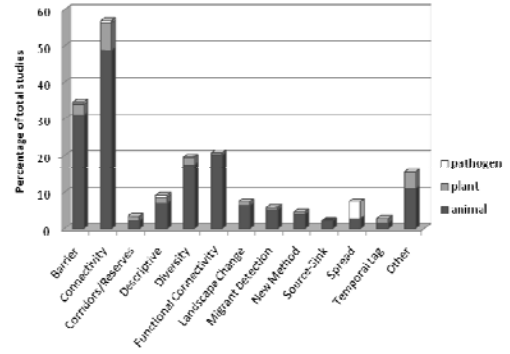
Interdisciplinarity?

	Study design	XY	Extent	Spatial Data	HW	LD
Ecology/conservation	.334	.309*	.362	.819	.642	.619
Genetics	.357	.150	.291	.701	.742	.670

Landscape genetics: Question Types

1. Effects of barriers
2. Habitat fragmentation
3. Landscape variables
4. Spatial and temporal scales
5. Species-specific hypothesis tests

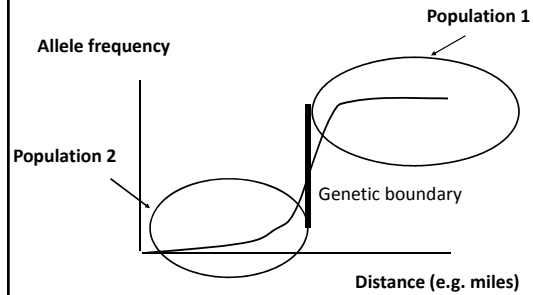
Question types:



- 1- Is there an effect of the road on the barrier to gene flow
- 2- Is there an effect of the habitat on the membership coefficient – related to connectivity

Barrier to gene flow:

Area of sharp variation in allele frequency

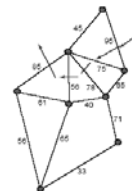


Barriers

- Methods
 - 1) Edge detection method
 - a) Monmonier's algorithm (Monmonier, 1973)
 - b) Wombling (Womble, 1951)
 - 2) Bayesian clustering methods
 - a) No spatial algorithms
STRUCTURE ; BAPS ; PARTITION
 - b) Spatial algorithms
Geneland; TESS ; BAPS 5 (Corander et al., 2008)
 - 3) Multivariate analysis (PCA): not widely used
 - 4) Graph theory

Edge detection methods

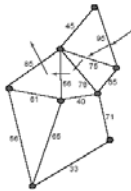
1- Monmonier maximum difference algorithm (Monmonier 1973)



Example of a hypothetical Delaunay triangulation (Manel et al. 2003)

Tops of triangles correspond to geographical position of the samples and are connected by the Delaunay triangulation approach

Genetic distance between two samples is given by the number indicated on each edge of the triangles. The first boundary is drawn with arrows



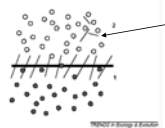
-The edge of the network with the largest associated distance is selected and used to extend a boundary perpendicular to the edge of the network

- The edge directly adjacent to the growing boundary with the largest genetic distance is selected to extend the boundary

-The two previous steps are repeated until the growing boundary meets another boundary or reach the edge of the area under study

Software : BARRIER (Manni et al. 2005) - AIS (Miller 2005) -R package adegenet (Jombart)

2-Wombling



Allele frequency calculated in each locality

-Allele frequencies transformed by interpolation
-partial derivative of allele frequencies is computed and the magnitude of the resulting slope is proportional to length of the rods

-Only magnitudes significant at 5% are represented The direction of the slopes = the direction of the rods.

-The 1 = rods that could be connected by a genetic discontinuity between green and white localities because their direction does not differ / The 2 corresponds to noise.

Algorithm: WOMBSOFT (Crida and Manel 2007)

Example of boundaries / populations detection methods: European Alpine Plants

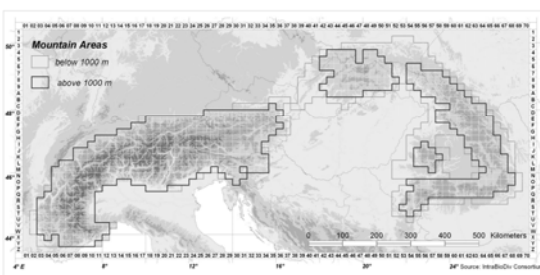
questions:

- 1) Are refugia correlated with areas of strong genetic diversity or is environment a better predictor of genetic diversity?
- 2) Is species diversity correlated with genetic diversity?

Before estimating the genetic diversity, we need to investigate the genetic structure

The Study Area

Alpes Carpathes

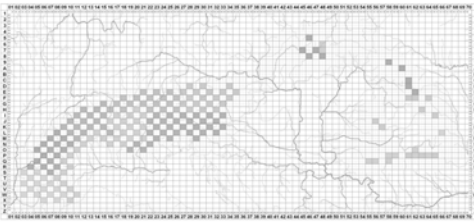


Mountain Areas
below 1000 m
above 1000 m

0 100 200 300 400 500 Kilometers

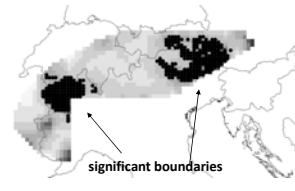
Data description

Sampling on a regular grid : pixels 23 x 25 km
Alps: 149 pixels
27 plant species sampled and genotyped for AFLP




Looking for boundaries using a wombling-based method

Sampling: 3 individus in 80 sites
Molecular markers: 250 AFLP



significant boundaries



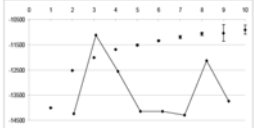
Luzula alpinopilosa

Legend:
• sampling points
values of the systematic function:
0 km 1 km 2 km

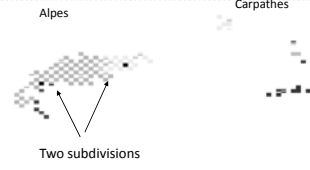
resolution of the grid :
80 pixels on x, 50 on y
each pixel is 8.4x7.4 km²
- bandwidth = 25 km

(Crida & Manel 2007)

Looking for populations using a Bayesian clustering method (STRUCTURE) - In the Alps and the Carpathes



1) Variation of the performance of the model in relation to K (number of assumed populations) → K=5



2) Probability of each individual to belong to its populations for K=5

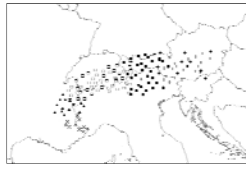
Conclusion: in this case population and boundary analysis lead to a similar pattern

Comparison of Bayesian clustering and edge detection methods for inferring boundaries in landscape genetics. (Safner et al. Submitted)

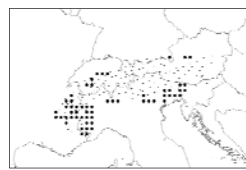
Algorithms	TESS	BAPS5	WOMBSOFT	AIS (Monmonier)
Model	Spatial Bayesian clustering	Spatial Bayesian clustering	No model. Non parametric. Weighted local regression	No model. Non parametric.
Spatial	Prior	Prior	x,y in the local weighted regression	Delaunay triangulation
Clustering criteria	LE between loci Allows for departure from HW	HWE and LE between loci	No	No
Data	Codominant	Co-dominant and Dominant	Co-dominant, Dominant and categorical	Co-dominant, Dominant, and Sequence

	TESS	BAPS5	WOMBSOFT	AIS (Monmonier)
Platforms	Windows, Unix/Linux	Windows, Unix/Linux Mac OS X	Windows, Unix/Linux Mac OS X	Windows
Reference	(Francois et al. 2006; Chen et al. 2007)	(Corander and Tang 2007)	(Crida and Manel 2007)	(Miller 2005)
URL	http://www-timc.imag.fr/Olivier.Francois/te ss.html	http://web.abo.fi/fak/mnf//mat e/jc/software/b aps.html	http://cran.r-project.org/web/packages/wom bsoft/index.htm l	http://www.marksgeneticssoftware.net/AISInfo.htm


Rhododendron dataset : 380 individuals, 120 AFLP



1-Six clusters identified by TESS



3-Boundary elements (black circles) detected by WOMBSOFT. Small crosses indicate sampling sites.






2-Four clusters identified by BAPS5.

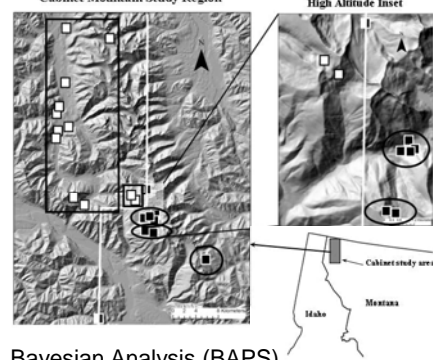
The algorithms do not converge toward the same conclusion!

Testing barrier influence: effect of altitude on genetic variation in long-toed salamanders (Andy Giordano; M.S., 2005)

- From sea level to >8000 ft.
- Distribution sparse at high altitudes and more contiguous at low altitudes
- Is altitude (i.e., mountains) a barrier to gene flow?
- Was late Pleistocene glaciation a barrier?

Cabinet Mountain Study Region



High Altitude Inset

Analysis: 7 microsatellite loci

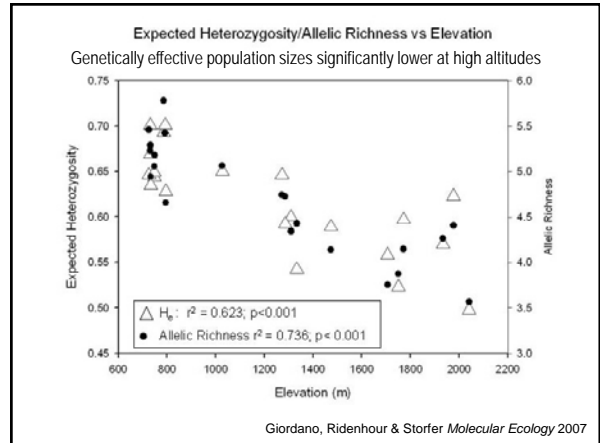
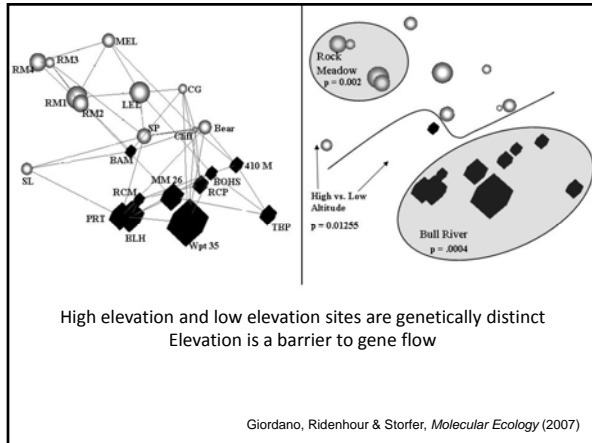
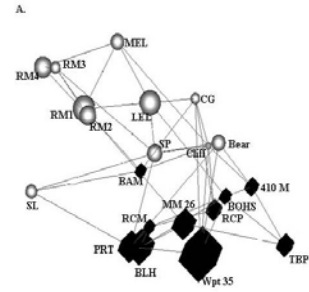
Bayesian Analysis (BAPS)
7 high altitude genetic clusters; 3 low altitude clusters

High versus low altitude sites

- 7 high altitude genetic clusters; 3 low altitude clusters
 - 93% pairwise F_{ST} values significant between high altitude site pairs
 - 49% of pairwise F_{ST} values were significant between low altitude site pairs
- High altitude sites (taken together) genetically distinct from low altitude sites
 - $F_{ST} = 0.24$ ($p = 0.001$)

Application of Graph Theory: Population Graphing (Dyer & Nason 2005)

- Helps visualize relationships between groups of sites.
- Partitions variance like F_{ST} measures utilized in an AMOVA.
 - Nodes represent sites with diameter proportional to within site variation
 - Edge lengths are proportional to among site variance
- Deficiency of edges was detected between high and low altitude populations



Long-toed salamander: classic Life History Trade-Offs

- | | |
|---|--|
| <ul style="list-style-type: none"> • Low Altitude (700-1200 m) <ul style="list-style-type: none"> – Eggs laid early – Larger egg clutches/ Smaller egg sizes – Larvae metamorphose within 2-3 mos. – Low topographic relief among sites | <ul style="list-style-type: none"> • High Altitude >1200 m <ul style="list-style-type: none"> – Eggs laid late (pond thawing) – smaller egg clutches/ larger egg sizes – Larvae over-winter prior to metamorphosis (>14mo) – High topographic relief among sites |
|---|--|

Question: Is life history variation phenotypically plastic or genetically controlled?

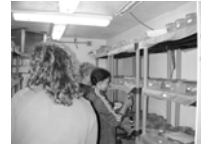
- Genetic isolation between low & high altitude sites suggests conditions for local adaptation (genetic)
 - Temperature gradients correlated w/ genetic differentiation in amphibians
- BUT, amphibians widely known to show plasticity in LH traits
 - Alternative hypothesis: Development characteristics are plastic

Conservation implications

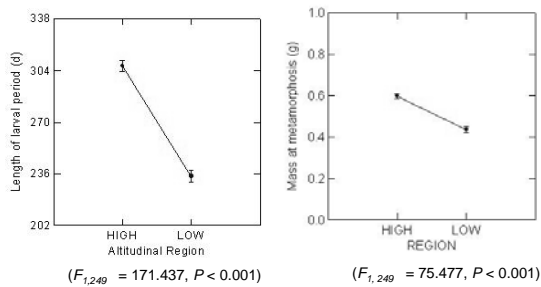
- Global temperatures predicted to increase, especially in temperate zones
 - If development time genetically controlled - may not metamorphose quickly enough if high elevation ponds become ephemeral
 - » Could lead to population declines
 - If plastic - may be able to respond, depending on range of plasticity

Experimental Design: Common Garden

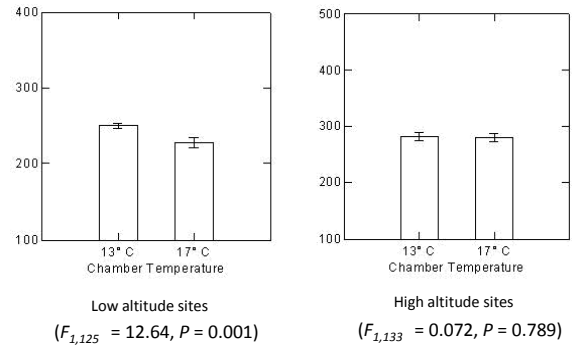
- Treatments (2 x 2 factorial design)
 - 2 environmental chambers - temperature:
 - 13°C current mean/ 17°C IPCC median prediction
 - altitudinal region
 - 7 low altitude sites (<1200 m)
 - 4 high altitude sites (>1200 m)
- Response variables
 - Larval period length
 - Mass at metamorphosis



Length of larval period/ Mass at metamorphosis



Effects of temperature on larval period



Barriers

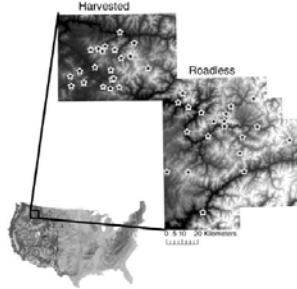
- General insights
- Initial studies – overlay
- More recently – Monmonier -> Wombling -> Assignment Methods
- Barrier examples:
 - Rivers – ↓ gene flow in mammals, reptiles, deer; ↑ gene flow in some amphibians, transgenic crops
 - Major ridgelines – ↓ gene flow in amphibians some mammals; ↑ gene flow in some small mammals
 - Anthropogenic barriers – unsuitable habitat, dams, development

Habitat fragmentation

- General insights
- Generally has negative consequences for gene flow and genetic diversity
 - Examples formica ants (Mäki-Petäys *et al.* 2005), common frogs (*Rana temporaria*; Johannson *et al.* 2005), alpine butterflies (*Parnassius smintheus*; Keyghobadi *et al.* 2005), and golden cheeked warblers (*Dendroica chrysoparia*), **but not** Amazon liverworts (*Radula flaccida*; Zartman *et al.* 2006), the tree species, *Sorbus aucuparia* (Bacles *et al.* 2004) or the yellow-footed antechinus (*Antechinus flavipes*; Lada *et al.* 2008)
- Can alter species movement patterns
 - E.g., roe deer more closely follow woodland corridors in fragmented landscape

Habitat fragmentation: Example tailed frogs in Idaho

- Habitat specialist, requires cold, fast flowing streams
- Do patterns of gene flow differ in harvested versus burned areas?



Do patterns of gene flow differ in harvested versus burned areas?

- Answer: YES
- Tailed frogs follow stream corridors more closely in harvested sites and primarily avoid unshaded areas in burned sites

Region	Path	Variables	Direction	r ²	AIC	AIC weight	
Harvested	LC stream	Topo distance	+	0.73	-775	0.8	
		PIP	-				
	LC canopy	Topo distance	+	0.74	-772	0.18	
		PIP	-				
	LC canopy/hl	Topo distance	+	0.71	-767	0.01	
		PIP	-				
LC canopy/hl	LC canopy/hl	Topo distance	+	0.74	-765	0.01	
		PIP	-				
		Canopy cover	-				
Roadless	LC hl	Fire distance	+	0.75	-854	0.92	
		hl	-				
	LC canopy	Topo distance	+	0.74	-848	0.05	
		IP	+				
	LC canopy/hl	LC canopy/hl	Fire distance	+	0.74	-847	0.03
			hl	-			