# Conserving adaptive variation: putting process on the map

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## Problem

- The conservation of evolutionary process has been acknowledged to be important, however…
- …little attention paid to adaptive variation, although this has to be maximized in the face of climate and land-use change.
- Few theoretical frameworks and computational methodologies to incorporate adaptive variation are available.

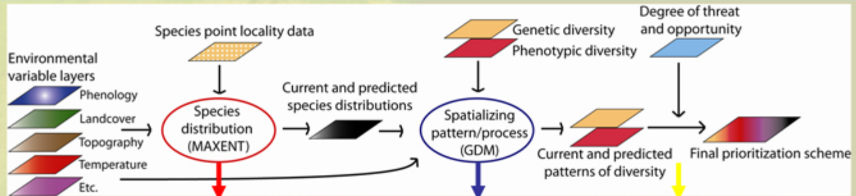
## Background

- For a long time conservation efforts have focused on areas of high species richness, endemism and level of threat.
- In addition to species, adaptive variation critical to conserve, to retain the potential for a response to changing environments
- This is especially important in the face of human induced climate and land-use change.
- Evolutionary processes have so far been included by: 1. a measure of phylogenetic diversity (e.g. branch lengths); 2. detailed knowledge of processes (but only available for limited number of geographic areas).
- *But* little attention for intra-specific adaptive variation and the mechanisms that generate and sustain it.

## Materials and Methods

- **MAXENT[1]**: ecological niche modeling approach using species presence data and climate as well as remotely sensed environmental information.
- **Generalized Dissimilarity Modeling (GDM[2])**: non-linear matrix regression, using splines to fit environmental differences to genetic or phenotypic differences. Uses iterative selection process to only include important environmental variables. In addition creates spatial predictions of genetic and phenotypic patterns into areas that were not sampled.
- Exemplifying the framework:
  - Target species: birds, frogs, bats
  - Target area: Ecuador


## Our proposed framework




1. Species distribution (niche) modeling to assess overall habitat suitability. Uses species presence data in conjunction with environmental layers.

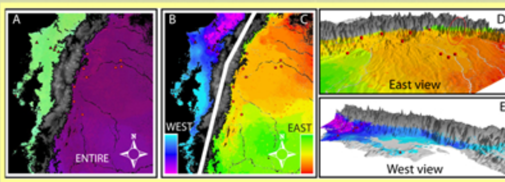
2. Spatializing genetic/phenotypic (response) pattern within species distribution. Two-step process: *a.* correlate environmental differences to response differences, based on set of sampling localities → function describing relation; *b.* predict pattern across the landscape using function from a. and environmental data.

3. Assessing degree of threat and opportunities for conservation. Takes into account threat to species and areas comprising the species' adaptive variation; input from local communities, government; etc.

## Wedgebilled Woodcreeper

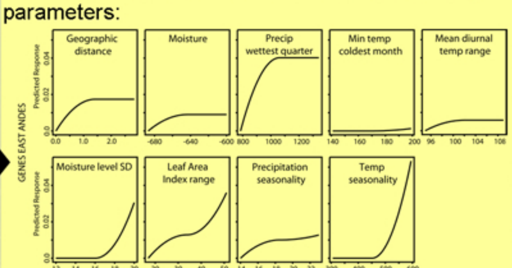
### *Genes* (136 AFLP loci)

| Region | % of total variance explained |
|---|---|
| Entire Ecuador | 95.2 |
| West of Andes | 98.5 |
| East of Andes | 72.2 |




Predictive maps of the genetic pattern based on 15 sampling localities (red dots). Differences in colors represent differences in the genes (see color bars). Analyses for: A) entire Ecuador; B) and E) west of the Andes; C) and D) east of the Andes.

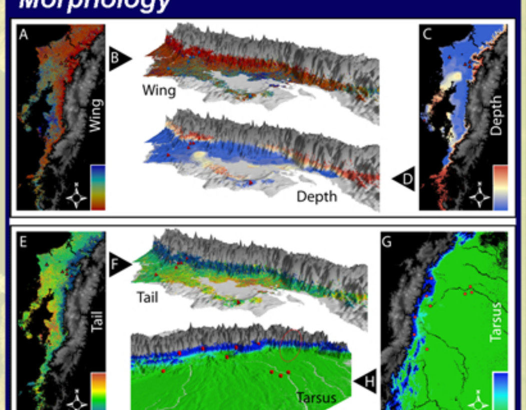
Genetic pattern in the east driven by the following parameters:




The maximum level of these response curves indicate the relative contribution of each variable to explaining the total variation. The slopes indicate rates of change.

In the west, different variables were important, indicating that different processes are shaping the genetic patterns on either side of the Andes.

### *Morphology*

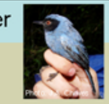


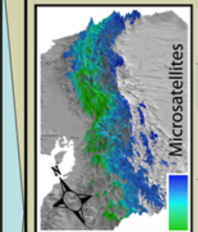

Several morphological features were well explained by environmental variables in either the east or the west of the Andes:

| Percentage of total variance explained | Ecuador | West of Andes | East of Andes |
|---|---|---|---|
| Tarsus length | 42.0 | 60.7 | *70.5* |
| Wing length | 47.9 | *91.7* | 22.0 |
| Tail length | 55.0 | *82.4* | 48.2 |
| Bill width | 8.5 | 59.2 | 23.7 |
| Bill depth | 48.5 | *92.5* | 27.2 |
| Exposed culmen | 13.4 | 63.9 | 18.9 |
| Combined | 31.8 | 73.4 | 42.0 |

Patterns are mainly driven by % treecover and various temperature measures.

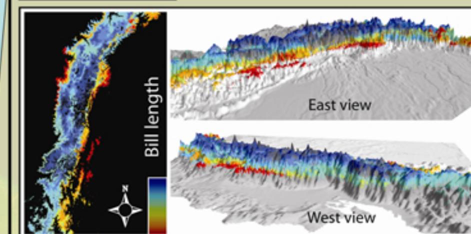
## Masked Flowerpiercer





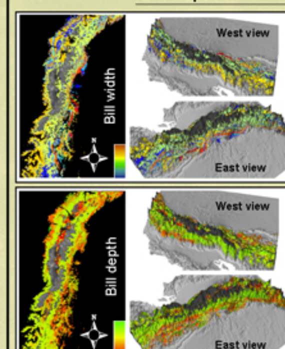

| | % of total variance explained |
|---|---|
| Microsatellites (8 loci) | 51.0* |
| Bill length | 70.8 |

* Relatively low % potentially due to homoplasy in microsatellite loci.




## Streak-necked Flycatcher

| | % of total variance explained |
|---|---|
| Bill width | 60.2 |
| Bill depth | 72.6 |

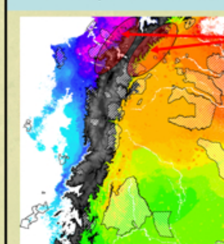



Genetic variation (microsatellites) was not well explained by environment.

This could indicate: 1) Homoplasy in microsatellites, or 2) gene flow across the Andes.

However, two morphological traits seem to be adaptive.

## Comparison to currently protected areas



Areas of particularly high turnover.

- Adaptive variation particularly along gradients from lowland to higher elevations.
- Especially high turnover for all studied species and traits along northwestern and northeastern slopes of Andes.
- Currently protected areas do not extend far enough into those regions or into the lowlands.

Hatched areas are currently protected (source: IUCN).

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### References

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2. Ferrier S, et al. (2007) Diversity Distrib 13:252-264.