UCLA Department of Statistics

Spatial Models for Bird Origin Assignment Using Genetic and Isotopic Data

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Project Background

Ongoing research at the Center for Tropical Research (CTR) at UCLA seeks to identify patterns of continental scale migratory connections

- Current methods are too coarse for most applications
- Large amounts of data are available (>150,000 feather samples from >500 species)
    - Genetic data - microsatellites, mitochondrial haplotypes, SNPs (soon)
    - Isotopic data - δ^2H

Species of interest

Hermit Thrush
Catharus guttatus

Photo by John Ingram

138 Individuals
14 Locations
6 Loci
9-27 Alleles

Wilson's Warbler
Wilsonia pusilla

© Glenn Bartley

163 Individuals
8 Locations
9 Loci
15-31 Alleles

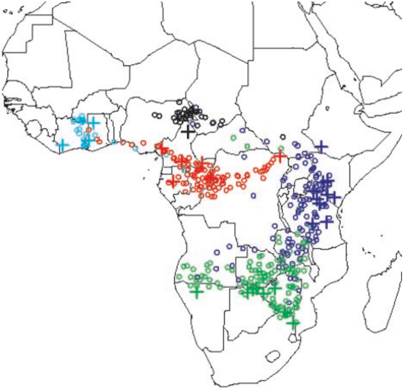
Model Framework

Assuming that the genetic(G) and isotopic(I) models are conditionally independent, then for a sample S and location k:

$$\begin{aligned}P(k|S,G,I) \propto\ & P(S|k,G,I)\ \pi(k)\\ &= P(S_G,S_I|k,G,I)\ \pi(k)\\ &= P(S_G|k,G,I)\ P(S_I|k,G,I)\ \pi(k)\\ &= P(S_G|k,G)\ P(S_I|k,I)\ \pi(k)\end{aligned}$$

Previous work

Wasser, et. al [2004] developed an approach for assigning genetic samples from illegal ivory shipments to geographic locations.



Model Basics

Using a multinomial error structure

$$p(y_{l\cdot k}|f_{l\cdot k}) = \frac{s_{lk}!}{\prod_i y_{lik}!} \prod_i (f_{lik})^{y_{lik}}$$

where:

- f_{lik} is the allele frequency of allele i from locus l at location k.
- y_{lik} is the count of allele i from locus l at location k.
- $s_{lk} = \sum_i y_{lik}$ is the total count of alleles from locus l at location k.

Modeling allele frequency

Allele frequencies are modeled using normalized values:

$$f_{lik} = \frac{\exp(\theta_{lik})}{\sum_j \exp(\theta_{ljk})}$$

where θ_{li} is a gaussian process:

$$\underset{[r\times 1]}{\boldsymbol{\theta}_{li}} \sim \text{MVN}(\underset{[r\times 1]}{\mathbf{M}_{li}}, \underset{[r\times r]}{\boldsymbol{\Sigma}})$$

Model Parameters

Mean

$$\underset{[r\times 1]}{\mathbf{M}_{li}} = \xi_l \ \eta_{li} \ \mathbf{1}_{[r,1]}$$

$$\xi_l \sim \text{Unif}(-\infty, \infty)$$

$$\eta_{li} \sim \text{N}(0, \beta_l)$$
$$\beta_l \sim \text{Unif}(0, 10^6)$$

Variance

$$\{\boldsymbol{\Sigma}\}_{k_1,k_2} = \sigma(d_{k_1,k_2}|\boldsymbol{\alpha})$$

Assumes process is stationary and isotropic

Covariance Functions

Powered Exponential Covariance:

$$\sigma(d|\boldsymbol{\alpha}) = \alpha_0 \exp\left[-\left(\frac{d}{\alpha_1}\right)^{\alpha_2}\right] + \alpha_3 \; I_{d=0}$$

Matérn Covariance:

$$\sigma(d|\boldsymbol{\alpha}) = \alpha_0 \frac{1}{\Gamma(\alpha_2)\; 2^{(\alpha_2-1)}} \left(\frac{d}{\alpha_1}\right)^{\alpha_2} K_{\alpha_2}\left(\frac{d}{\alpha_1}\right) + \alpha_3 \; I_{d=0}$$

with the following priors on $\boldsymbol{\alpha}$:

$$\alpha_0, \log(\alpha_1), \log(\alpha_2), \alpha_3 \sim \text{Unif}$$

Model Fitting via MCMC

All parameters are updated by random walk Metropolis Hasting with normal jump proposals.

However, we first reparameterize as follows:

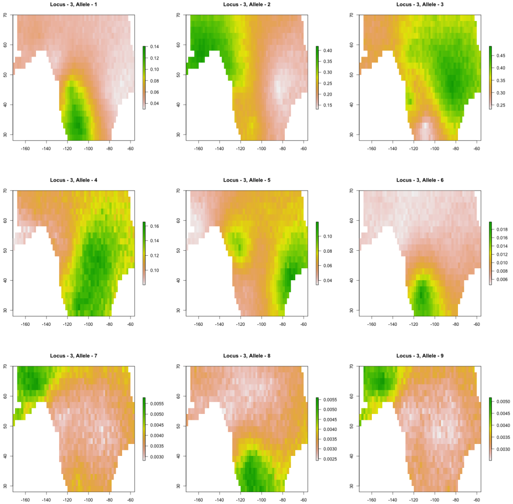
$$\underset{[r\times 1]}{\mathbf{V}_{li}} \sim \text{MVN}(0, \underset{[r\times r]}{\mathbf{\Sigma}})$$

$$\underset{[r\times 1]}{\mathbf{V}_{li}} = \underset{[r\times r]}{\text{Chol}(\mathbf{\Sigma})} \cdot \underset{[r\times 1]}{\mathbf{X}_{li}}$$

where

$$\{\mathbf{X}_{li}\}_k \sim \text{N}(0,1)$$

Allele Frequency - Hermit Thrush - Locus 3



Probability of a Sample

For a sample S with alleles i_l and j_l at locus l and location k

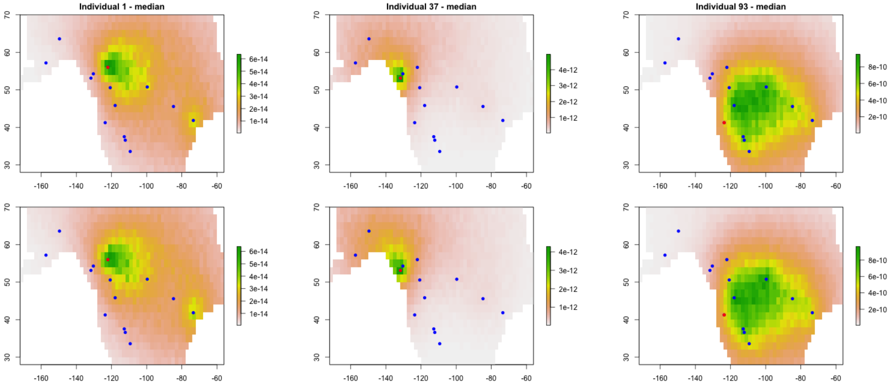
$$p(S|f,k) = \prod_l p_l(i_l, j_l|f,k)$$

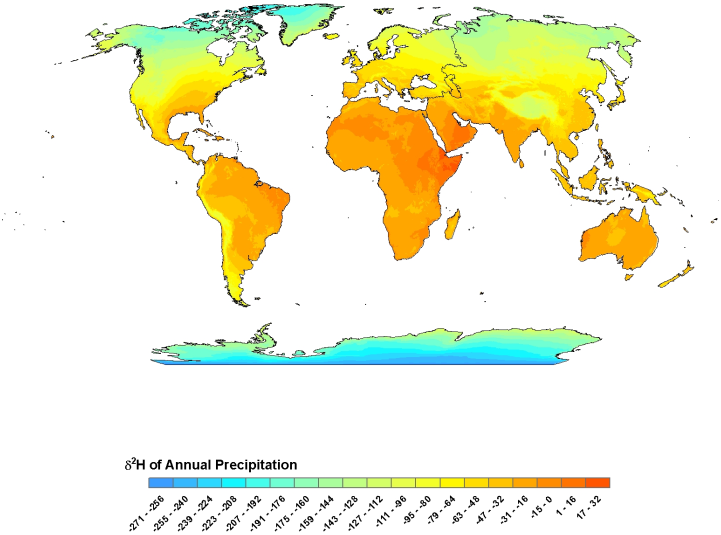
$$p_l(i_l, j_l|f,k) = \begin{cases} \gamma \; p_l(i_l|f,k) + (1-\gamma)\; p_l(i_l|f,k)^2 & \text{if } i_l = j_l \\ (1-\gamma)\; p(i_l|f,k)\; p(j_l|f,k) & \text{if } i_l \neq j_l \end{cases}$$

$$p_l(i_l|f,k) = (1-\delta) f_{lik} + \delta/m_l$$

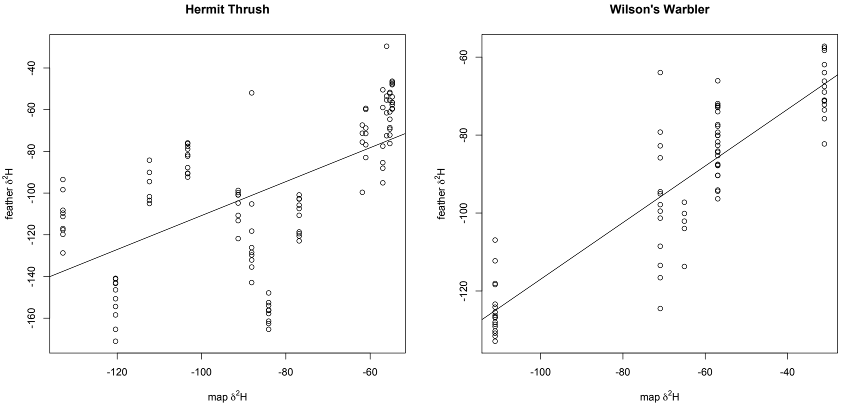
where δ is the probability only one of the alleles amplified and γ is the probability of a genotyping error.

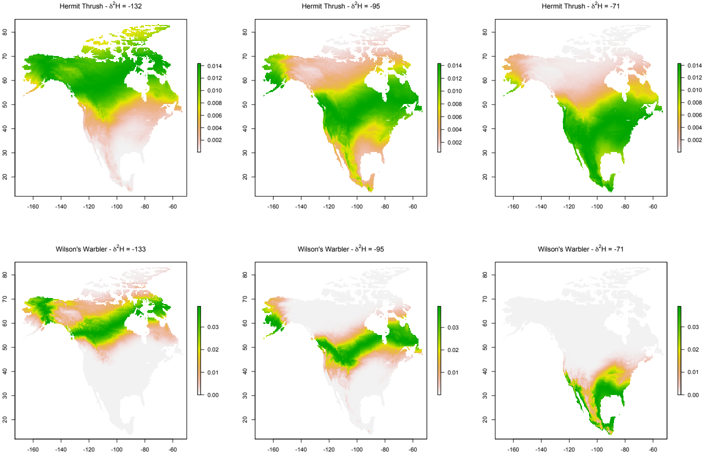
Spatial Posteriors - Hermit Thrush



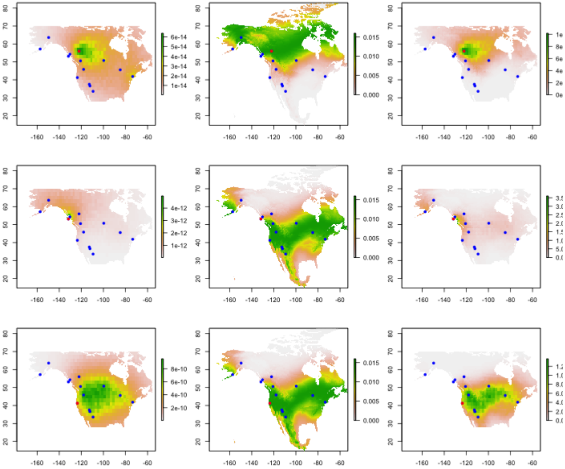

δ^2H of Annual Precipitation
-271 - -256
-255 - -240
-239 - -224
-223 - -208
-207 - -192
-191 - -176
-175 - -160
-159 - -144
-143 - -128
-127 - -112
-111 - -96
-95 - -80
-79 - -64
-63 - -48
-47 - -32
-31 - -16
-15 - 0
1 - 16
17 - 32

Mapping isotope values

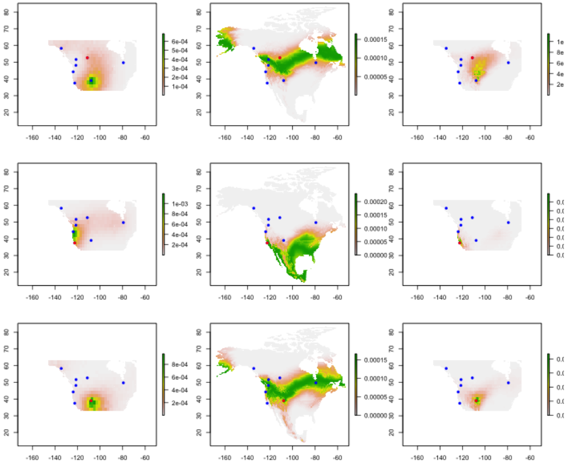



Hermit Thrush - δ^2H = -132
Hermit Thrush - δ^2H = -95
Hermit Thrush - δ^2H = -71
Wilson's Warbler - δ^2H = -133
Wilson's Warbler - δ^2H = -95
Wilson's Warbler - δ^2H = -71
80
70
60
50
40
30
20
-160
-140
-120
-100
-80
-60
0.014
0.012
0.010
0.008
0.006
0.004
0.002
0.03
0.02
0.01
0.00

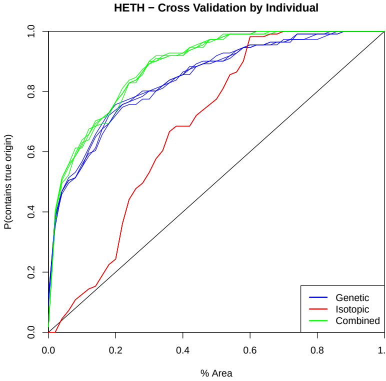
Combined - Hermit Thrush

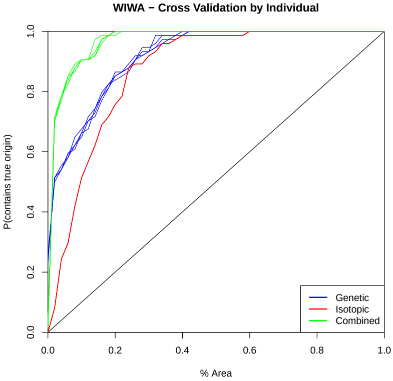


Combined - Wilson's Warbler

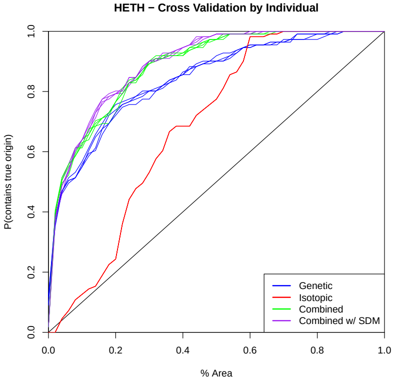


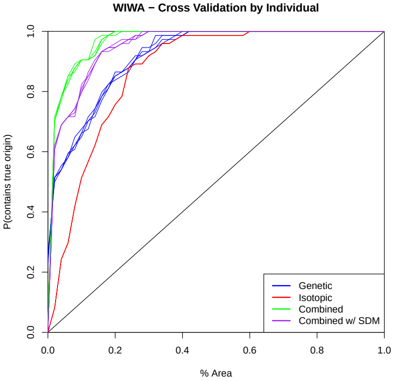
Classifier Results





Classifier Results + SDM





Conclusion

- Simple unified framework for combining Genetic and Isotopic models
- Combined results dramatically outperform either model alone
- Future Work
  - Fully bayesian isoscape model
  - Refine SDM priors
- R packages (available soon):
  - Genetic - Rscat
  - Isotopic - isoscape

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Genetic Methods:

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Isotopic Methods:

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- Andrew Schuh, Colorado State

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