Lecture 21

More Spatial Random Effects Models

Colin Rundel

04/10/2017

Spatial Assignment of Migratory Birds

Background

Using intrinsic markers (genetic and isotopic signals) for the purpose of inferring migratory connectivity.

- Existing methods are too coarse for most applications
- Large amounts of data are available (>150,000 feather samples from >500 species)
- Genetic assignment methods are based on Wasser, et al. (2004)
- Isotopic assignment methods are based on Wunder, et al. (2005)

Data - DNA microsatellites and $\delta^2\mathrm{H}$

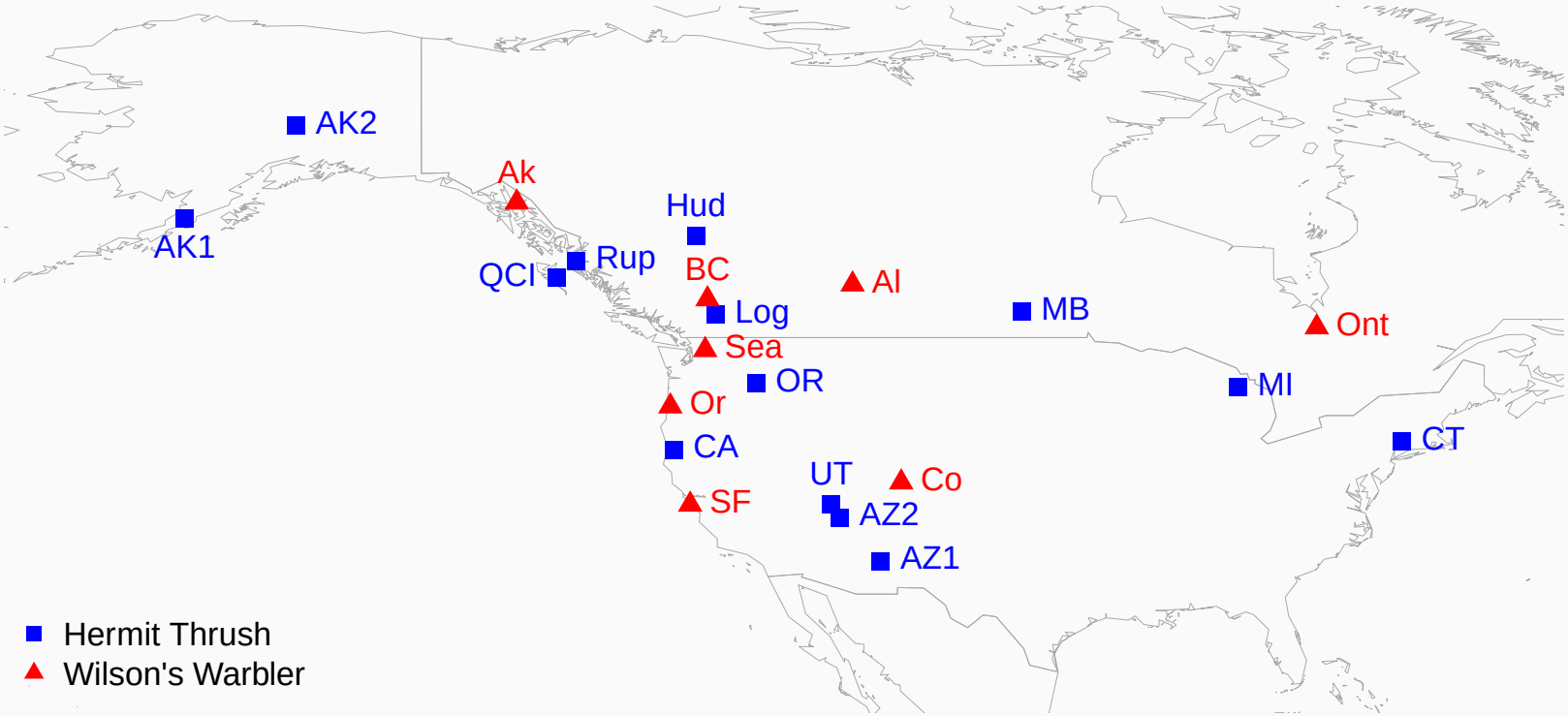
Hermit Thrush (*Catharus guttatus*)

- 138 individuals
- 14 locations
- 6 loci
- 9-27 alleles / locus

Wilson's Warbler (*Wilsonia pusilla*)

- 163 individuals
- 8 locations
- 9 loci
- 15-31 alleles / locus

Sampling Locations



Allele Frequency Model

For the allele i, from locus l, at location k

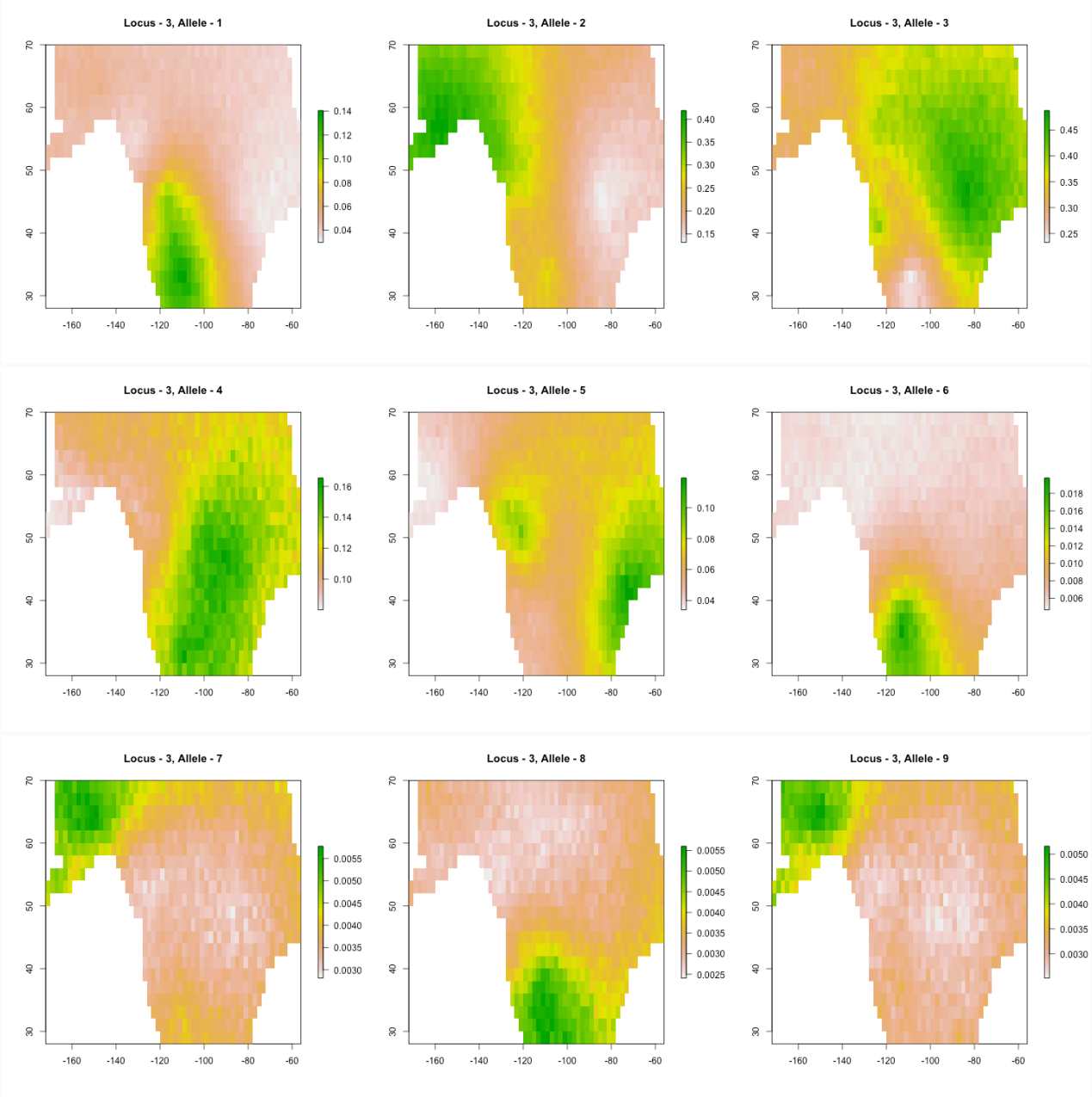
$$\boldsymbol{y}_{\cdot lk} | \boldsymbol{\Theta} \sim \mathcal{N}\left(\sum_i y_{ilk},\ \boldsymbol{f}_{\cdot lk}\right)$$

$$f_{ilk} = \frac{\exp(\Theta_{ilk})}{\sum_i \exp(\Theta_{ilk})}$$

$$\boldsymbol{\Theta}_{il} | \boldsymbol{\alpha}, \boldsymbol{\mu} \sim \mathcal{N}(\boldsymbol{\mu}_{il},\ \boldsymbol{\Sigma})$$

$$\{\Sigma\}_{ij} = \sigma^2\ \exp\left(-\left(\{d\}_{ij}\, r\right)^{\psi}\right) + \sigma_n^2\, 1_{i=j}$$

Predictions by Allele (Locus 3)



Genetic Assignment Model

Assignment model assuming Hardy-Weinberg equilibrium and allowing for genotyping (δ) and single amplification (γ) errors.

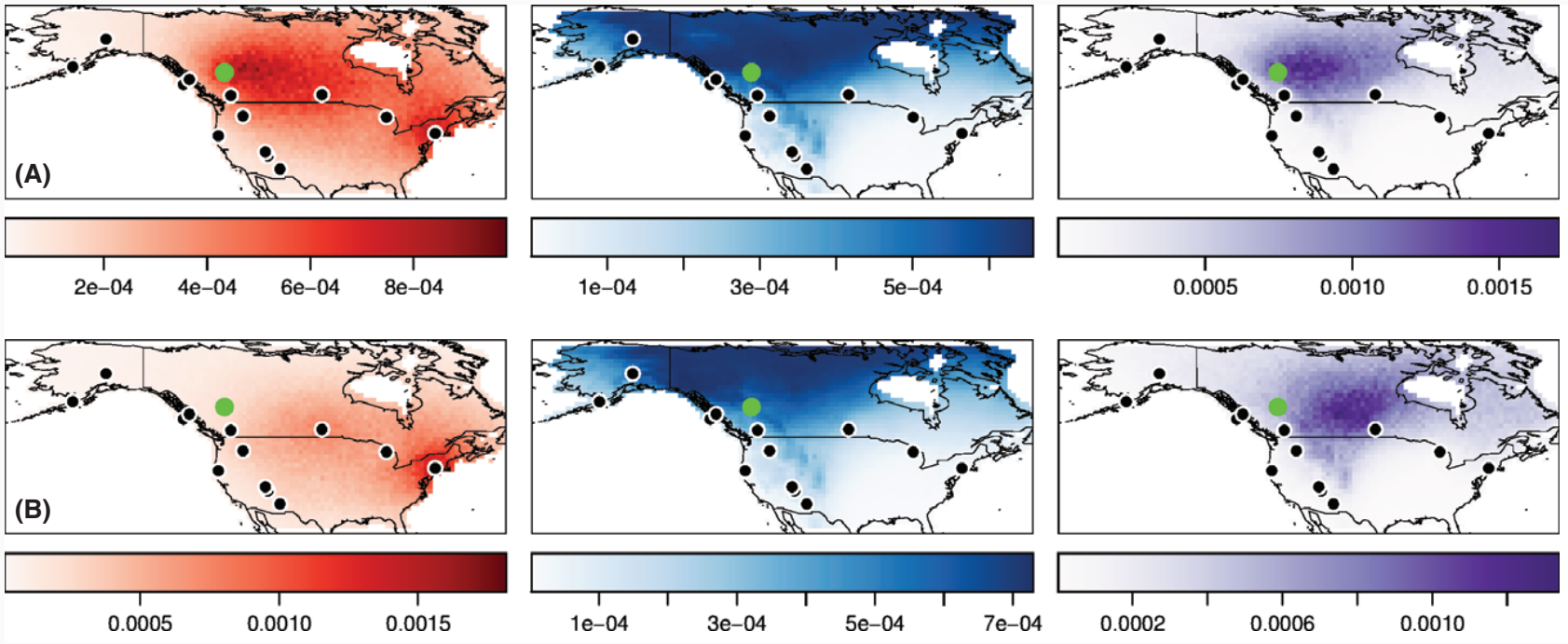
$$P(S_G|\boldsymbol{f}, k) = \prod_l P(i_l, j_l|\boldsymbol{f}, k)$$

$$P(i_l, j_l|\boldsymbol{f}, k) = \begin{cases} \gamma P(i_l|\boldsymbol{f}, k) + (1-\gamma)P(i_l|\tilde{\boldsymbol{f}}, k)^2 & \text{if } i = j \\ (1-\gamma)P(i_l|\boldsymbol{f}, k)P(j_l|\boldsymbol{f}, k) & \text{if } i \neq j \end{cases}$$

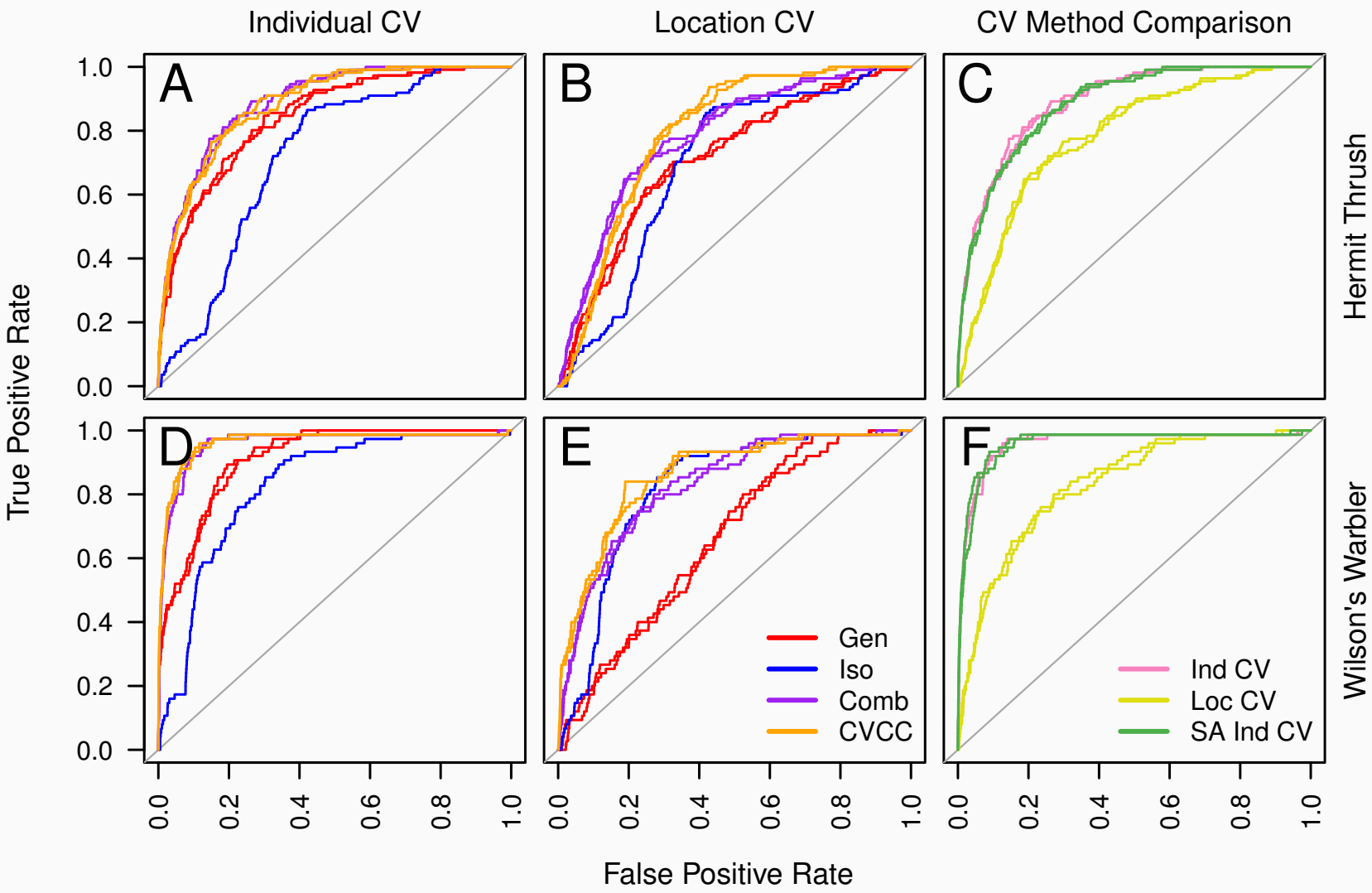
$$P(i_l|\boldsymbol{f}, k) = (1-\delta)f_{lik} + \delta/m_l$$

Combined Model

Genetic Isotopic Combined



Model Assessment



Migratory Connectivity