

# Landscape Connectivity: Neutral And Adaptive Genetic Variation Across Space

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# Landscape Connectivity: Importance

- Which areas to target?
  - Conservation of endangered species
  - Control of invasive species
  - Pest/disease management

# The Story

- **Method Development**
  - Inspiration: Tsetse
- **Method Validation**
  - Simulations
  - Empirical: Subterranean Termites

# Tsetse

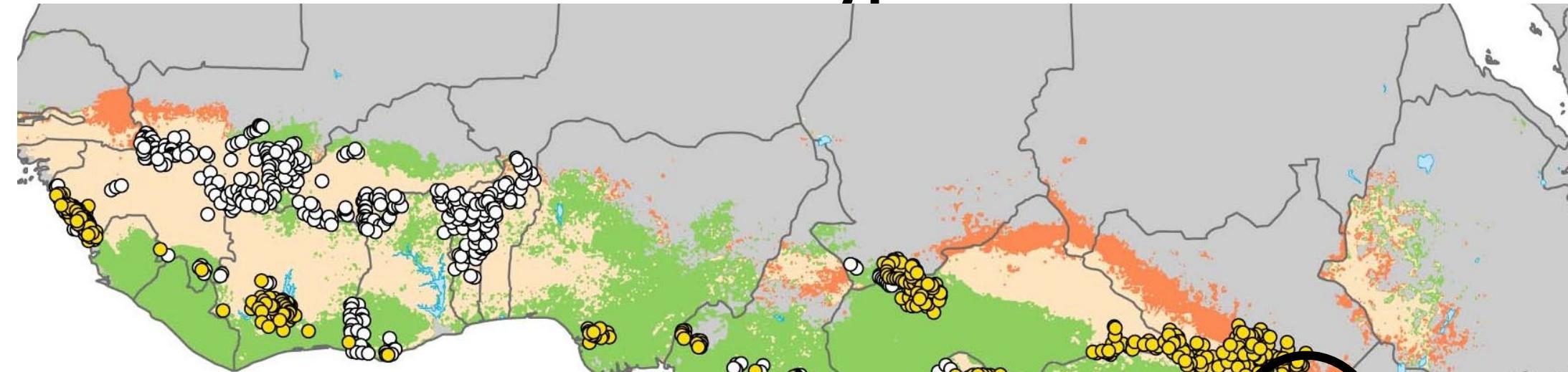


Tsetse (*Glossina fuscipes*) in Uganda



Subterranean termites  
(*Reticulitermes flavipes*)  
in the Eastern U.S.

# Tsetse = Vectors of African Trypanosomiasis (Fatal if Untreated)



Human African Trypanosomiasis cases

- *T.b.gambiense*
- *T.b.rhodesiense*
- No cases detected

Distribution of Tsetse fly

- *Morsitans* group
- *Morsitans* group, *Palpalis* group
- *Palpalis* group

# **Question**

**How are populations of tsetse connected and what are the practical (epidemiological/economical) implications?**

# **Motivation**

**Model connectivity WITHOUT parameterizing resistance (to movement) of landscape features**

# **Goal**

**Model continuous gene flow**

**Unconstrained (neutral)**

**Constrained (by selection; adaptive)**

# **Aims**

**Calculate metric in sampled locations**

**Interpolate metric in unsampled locations**

# **Modeling Gene Flow**

Response variable: **Gene flow**

Fixed effects: **Environmental variables**

Random effect: **Spatial locations**

# Modeling Gene Flow

## Mixed Model (Fixed and Random Effects)

Fixed Effects:

*Longitude*

*Latitude*

*Precipitation*

*Temperature*

*Vegetation*

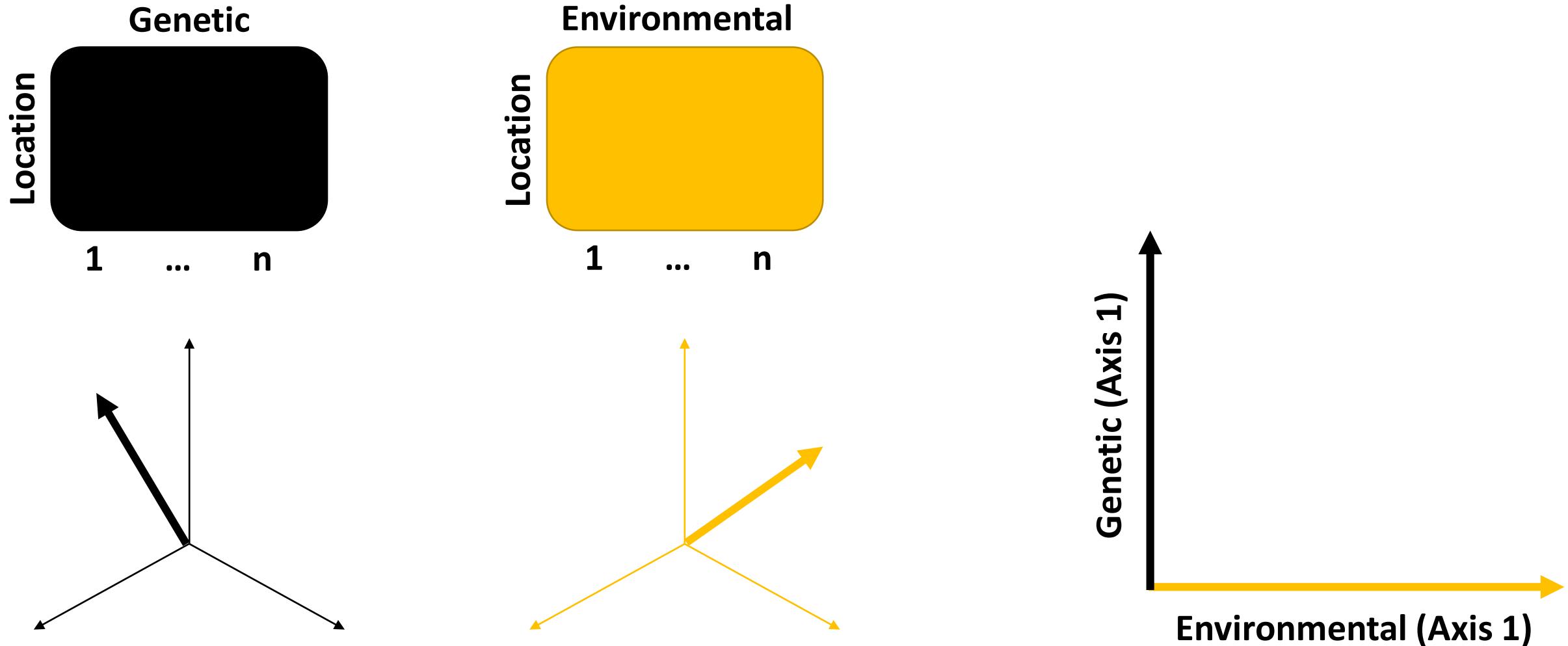
*Land Cover*

*Distance from Water Bodies*

Random Effect:

*Spatial Location*

# The Method – Pt. 1: Multivariate Transformation



# The Method – Pt. 2: Gene Flow at Discrete Points

**Neutral flow:**  $F_p = \frac{(\sum_{k=1}^n N_{pk})^2}{\sum_{k=1}^n N_{pk}^2}; F_{ip} = F_p$

**Interpolation:**  $F_i \sim \beta_{0_i} + \beta_{x_i} x_i + \beta_{y_i} y_i + \beta_{ij}^T C I_{ij} + f(s_i)$

**Presence/Absence Selected Alleles:**  $A_i | \pi_i \sim \text{Binom}(n_i, \pi_i)$

**Interpolated Log-Odds:**  $\text{logit}(\pi_i) \sim \beta_{0_i} + \beta_{x_i} x_i + \beta_{y_i} y_i + \beta_{ij}^T C I_{ij} + f(s_i)$

**Adaptive flow:**  $AF_i = \frac{(\sum_{j=1}^n A_{ij})^F}{\sum_{j=1}^n A_{ij}^F}$

# The Method – Pt. 3: Continuous Gene Flow

**Neutral flow:**  $F_p = \frac{(\sum_{k=1}^n N_{pk})^2}{\sum_{k=1}^n N_{pk}^2}; F_{ip} = F_p$

**Interpolation:**  $F_i \sim \beta_{0_i} + \beta_{x_i} x_i + \beta_{y_i} y_i + \beta_{ij}^T C I_{ij} + f(s_i)$

**Presence/Absence Selected Alleles:**  $A_i | \pi_i \sim \text{Binom}(n_i, \pi_i)$

**Interpolated Log-Odds:**  $\text{logit}(\pi_i) \sim \beta_{0_i} + \beta_{x_i} x_i + \beta_{y_i} y_i + \beta_{ij}^T C I_{ij} + f(s_i)$

**Adaptive flow:**  $AF_i = \frac{(\sum_{j=1}^n A_{ij})^F}{\sum_{j=1}^n A_{ij}^F}$

# (Bayesian) Interpolation

**Skipping complex mathematical details, including:**

**Covariance function to model spatial dependence (discrete space)**

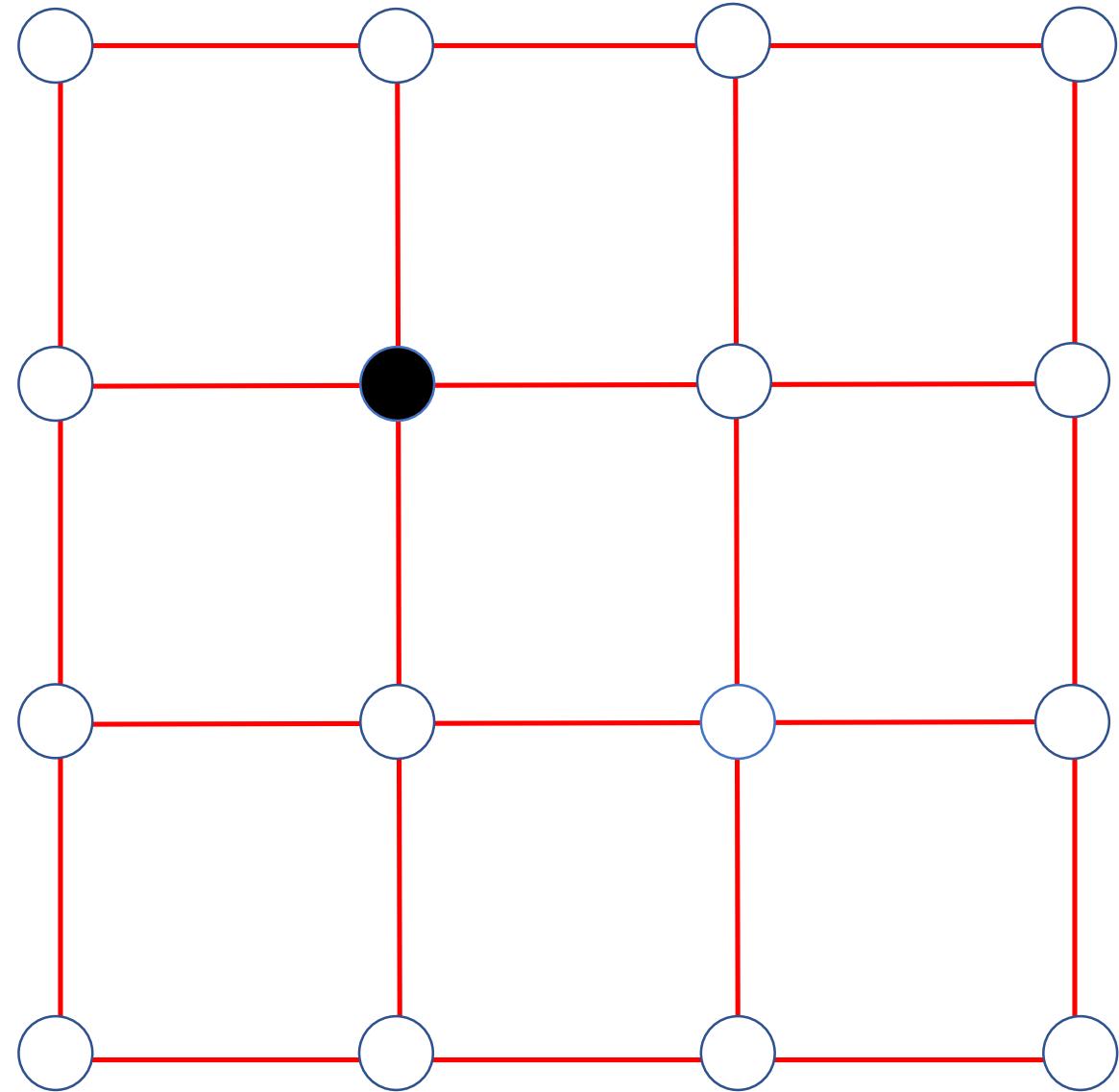
**Continuous-space approximation (using stochastic partial differential equations)**

# Interpolation

Finding neighboring locations

● Sampled locations

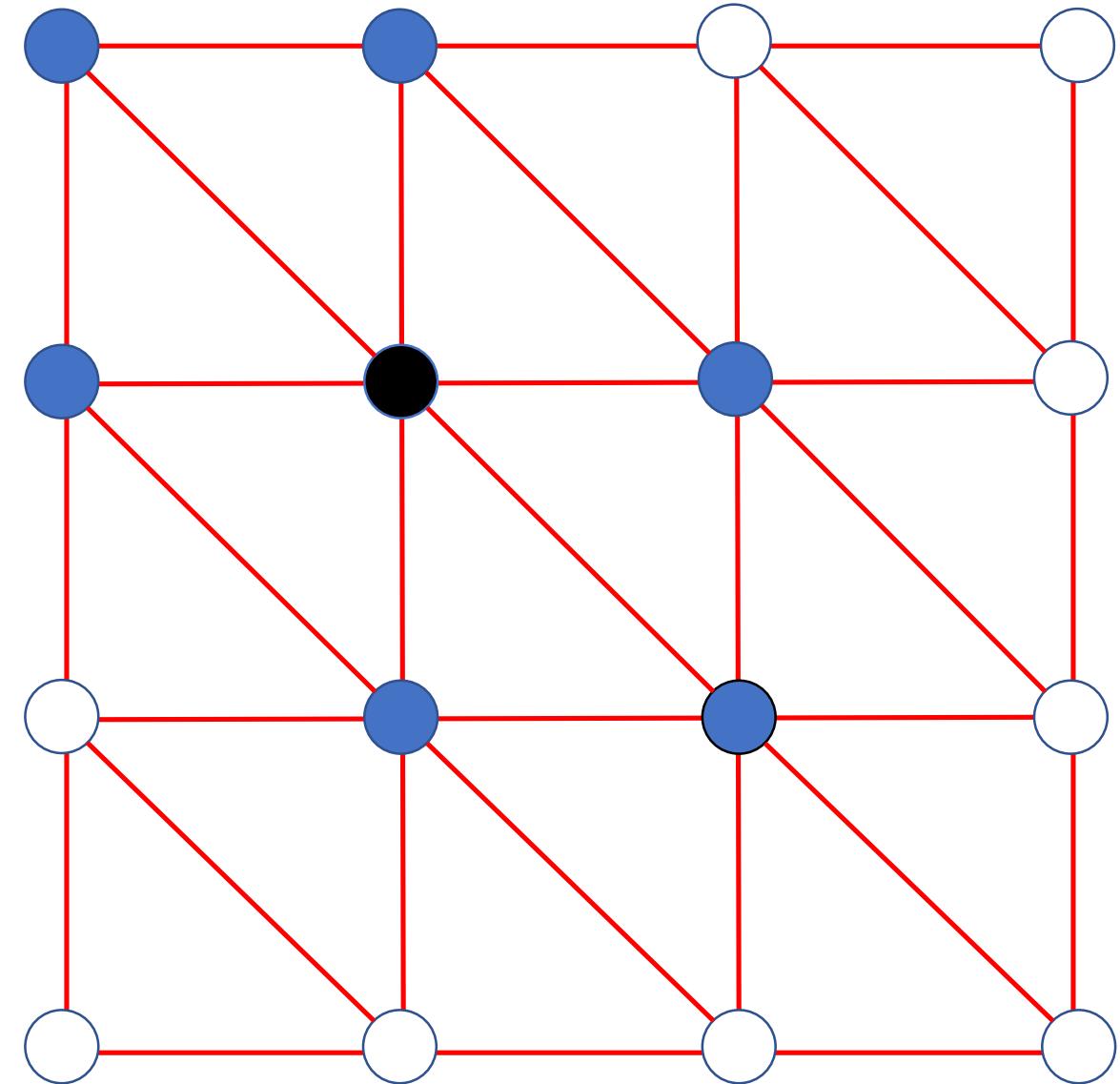
○ Unsampled locations



# Interpolation

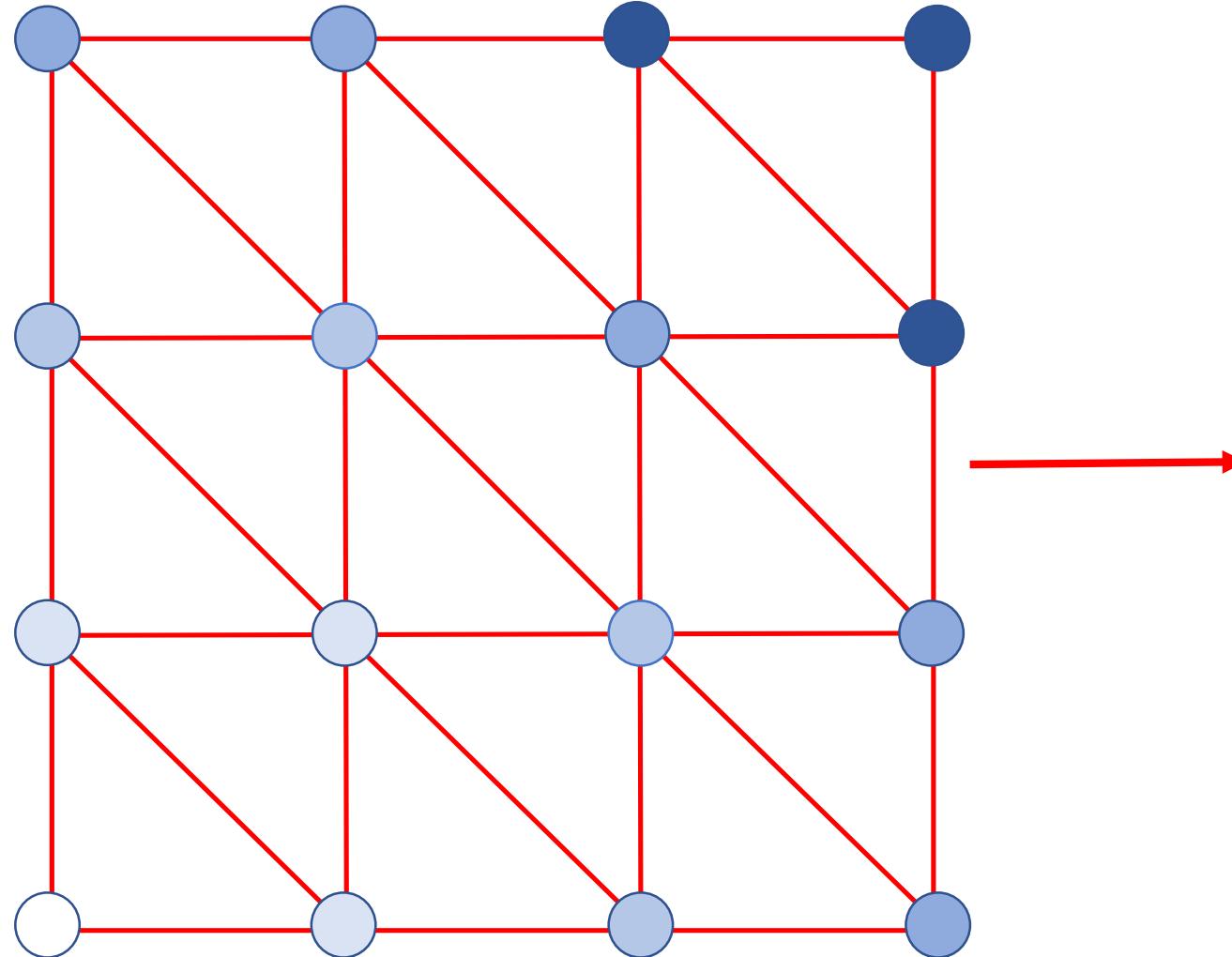
## Mesh (triangulation)

- Sampled locations
- Neighboring locations

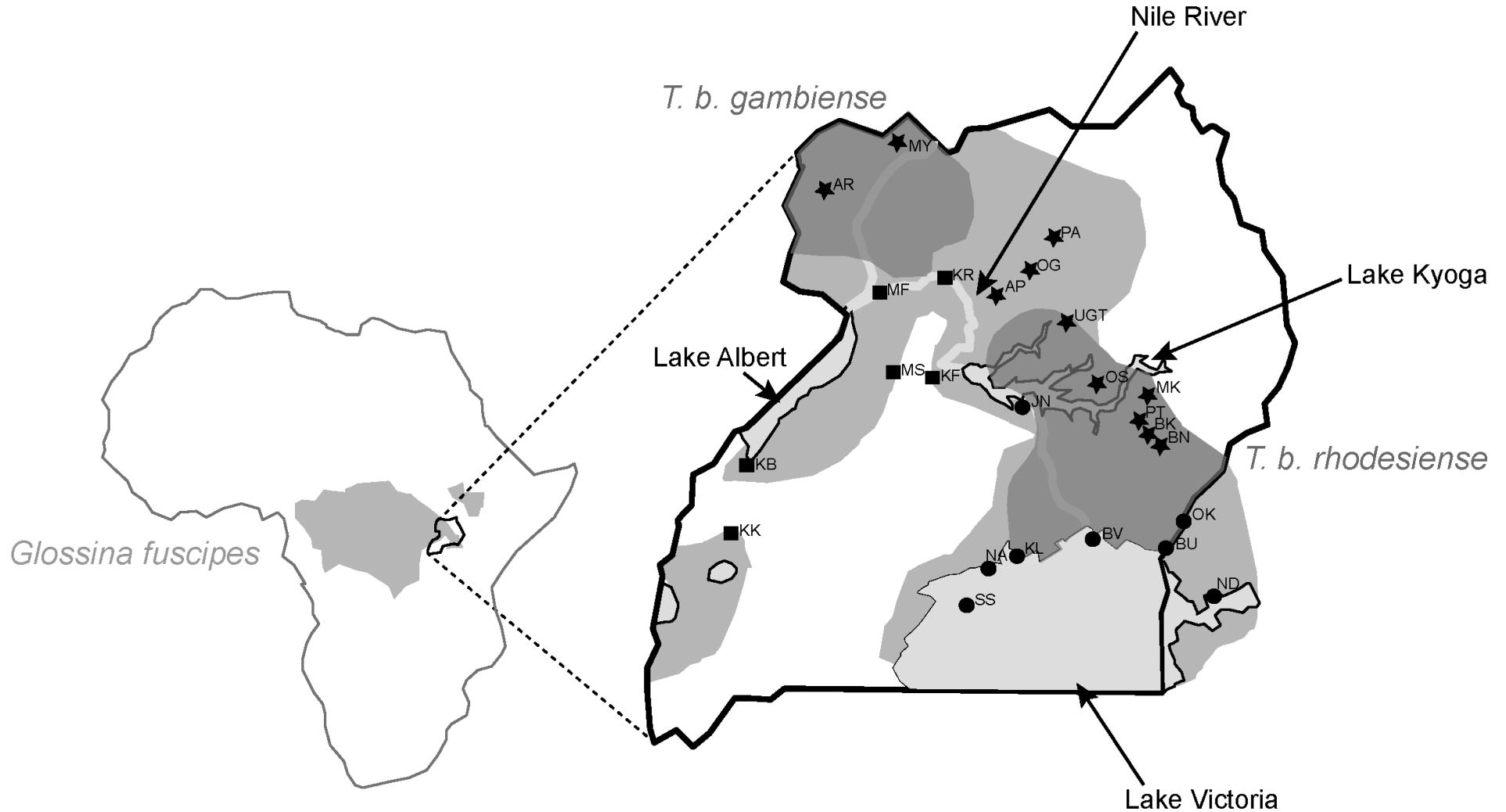


# Interpolation

## From Discrete to Continuous Gene Flow

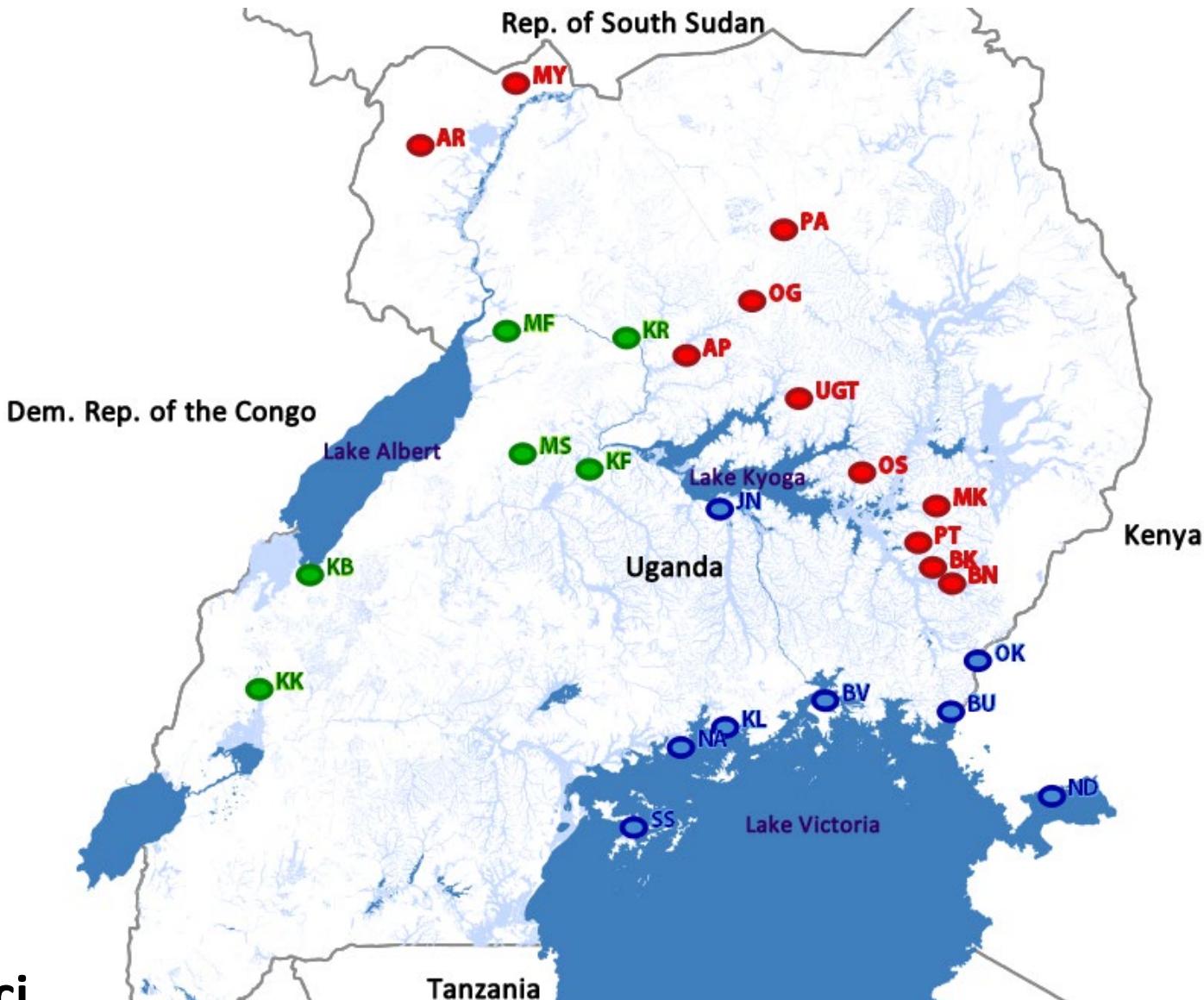


# Sampling Sites



Tsetse in Uganda: 25 sites

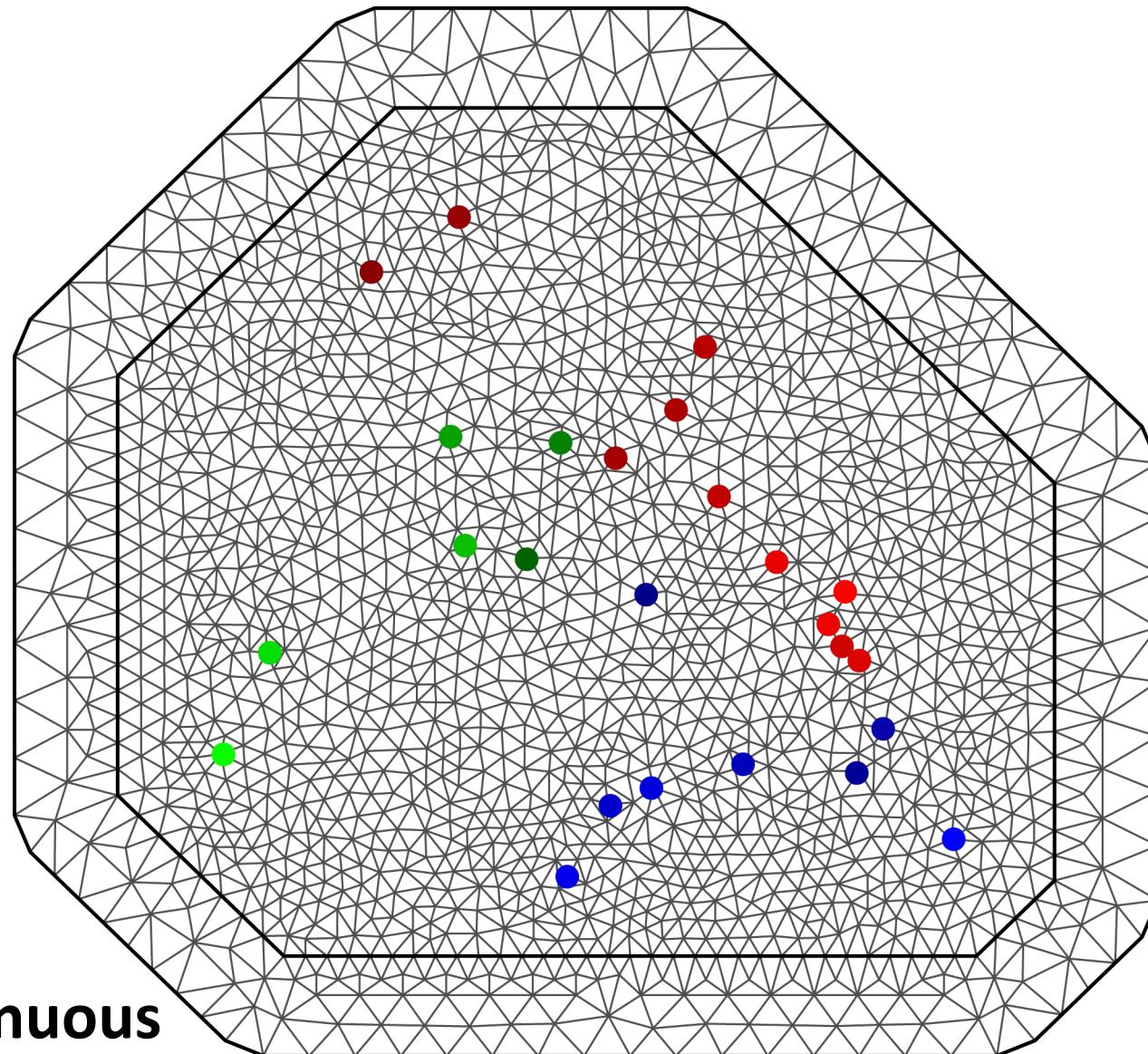
# Genetic Populations



11 microsatellite loci

965 individuals, 25 sites, 3 populations (9 sub-populations)

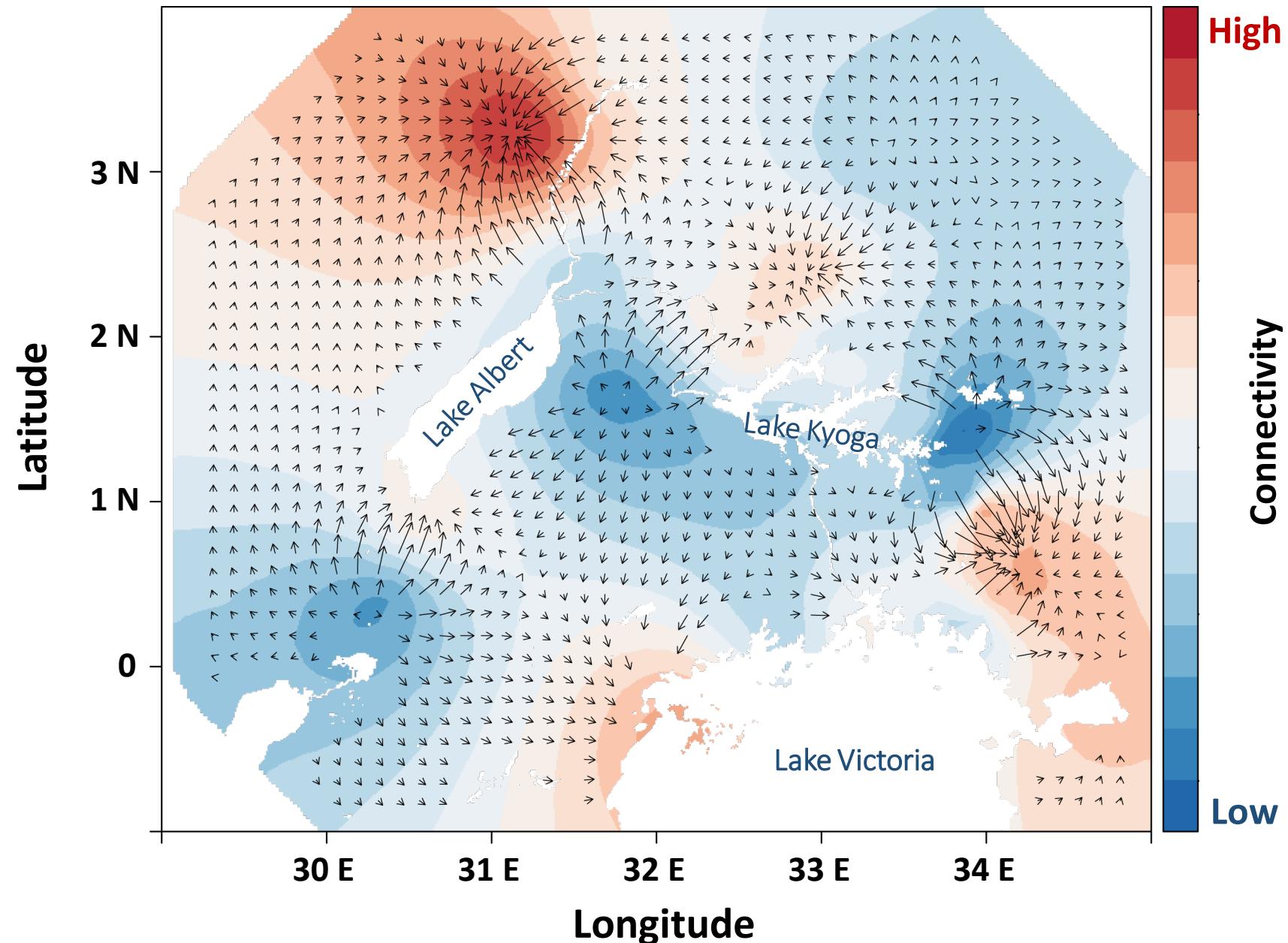
# Mesh



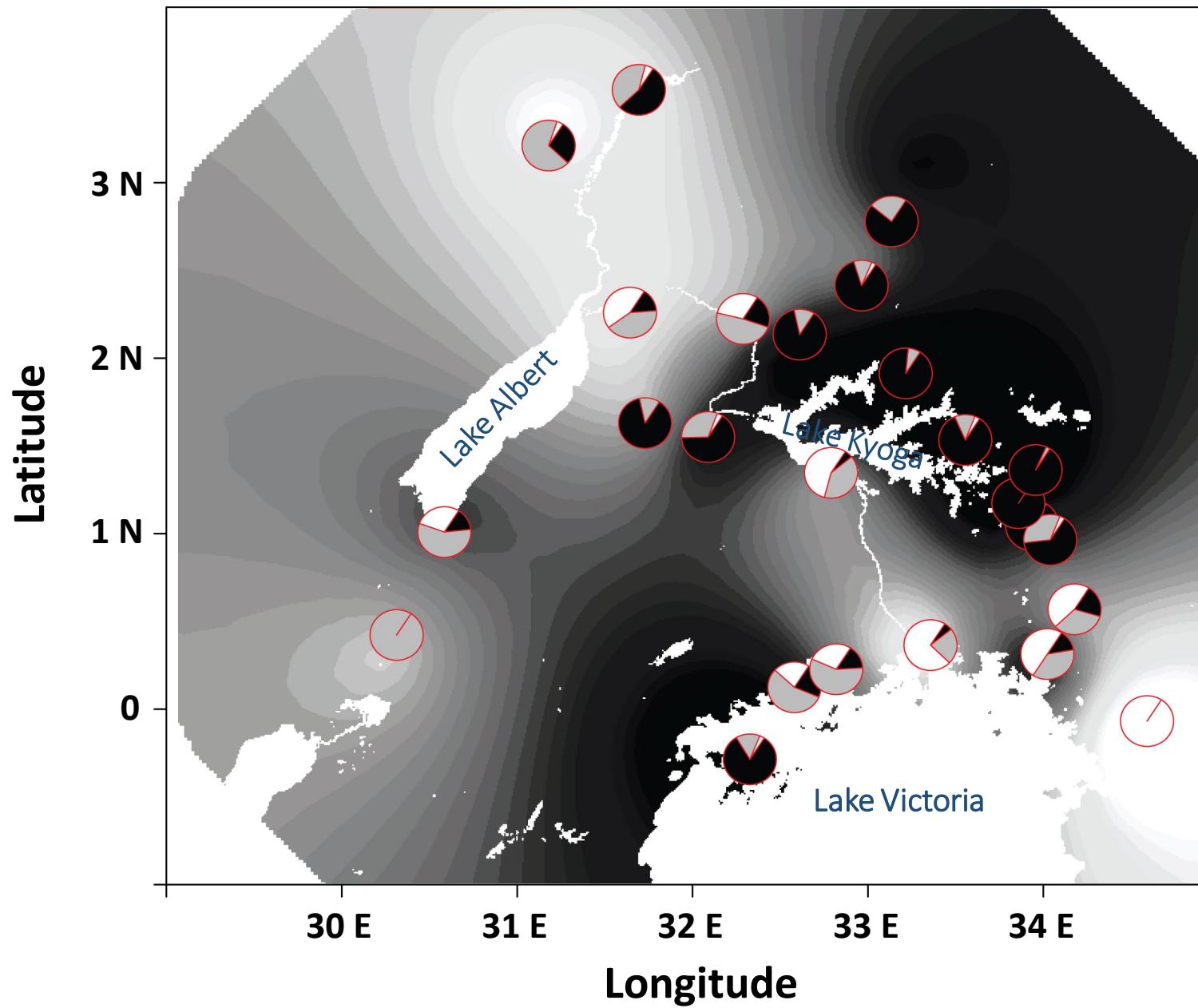
**Going from discrete to continuous**

# Neutral Gene Flow

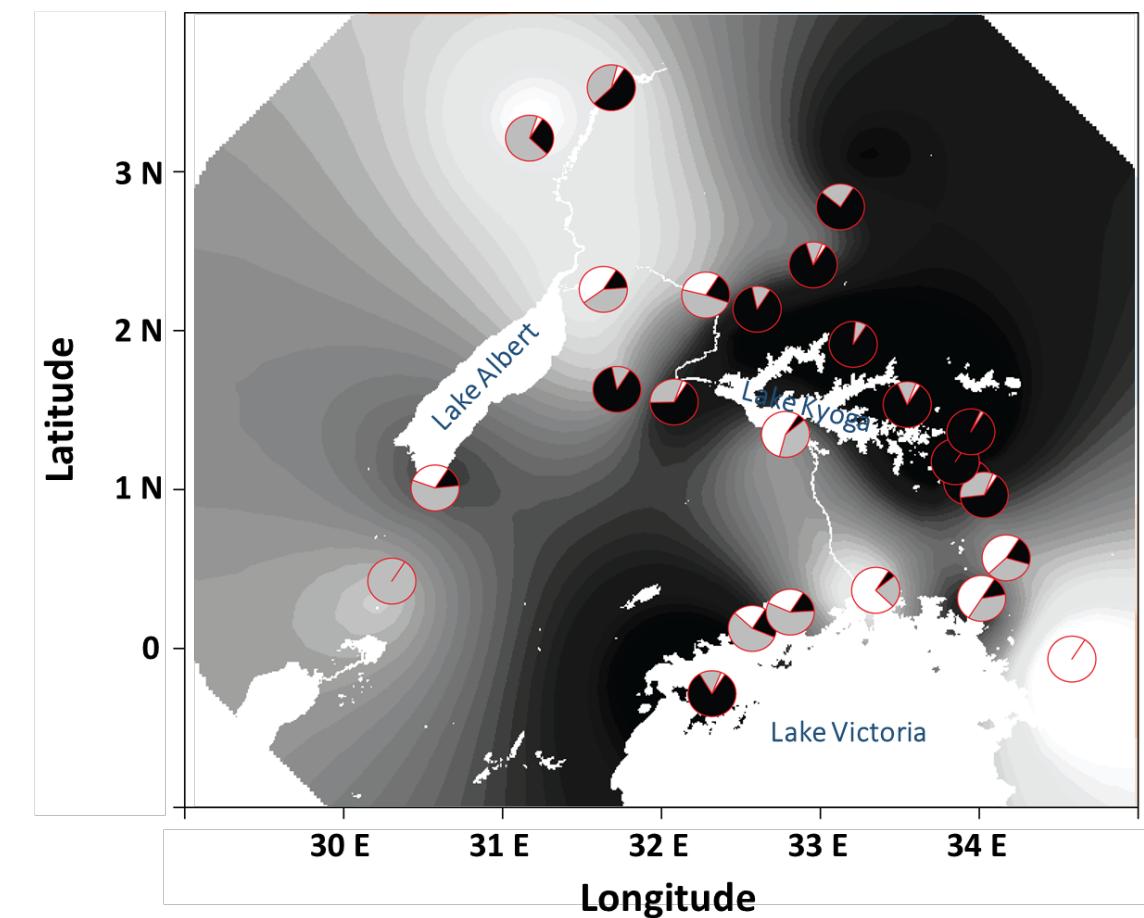
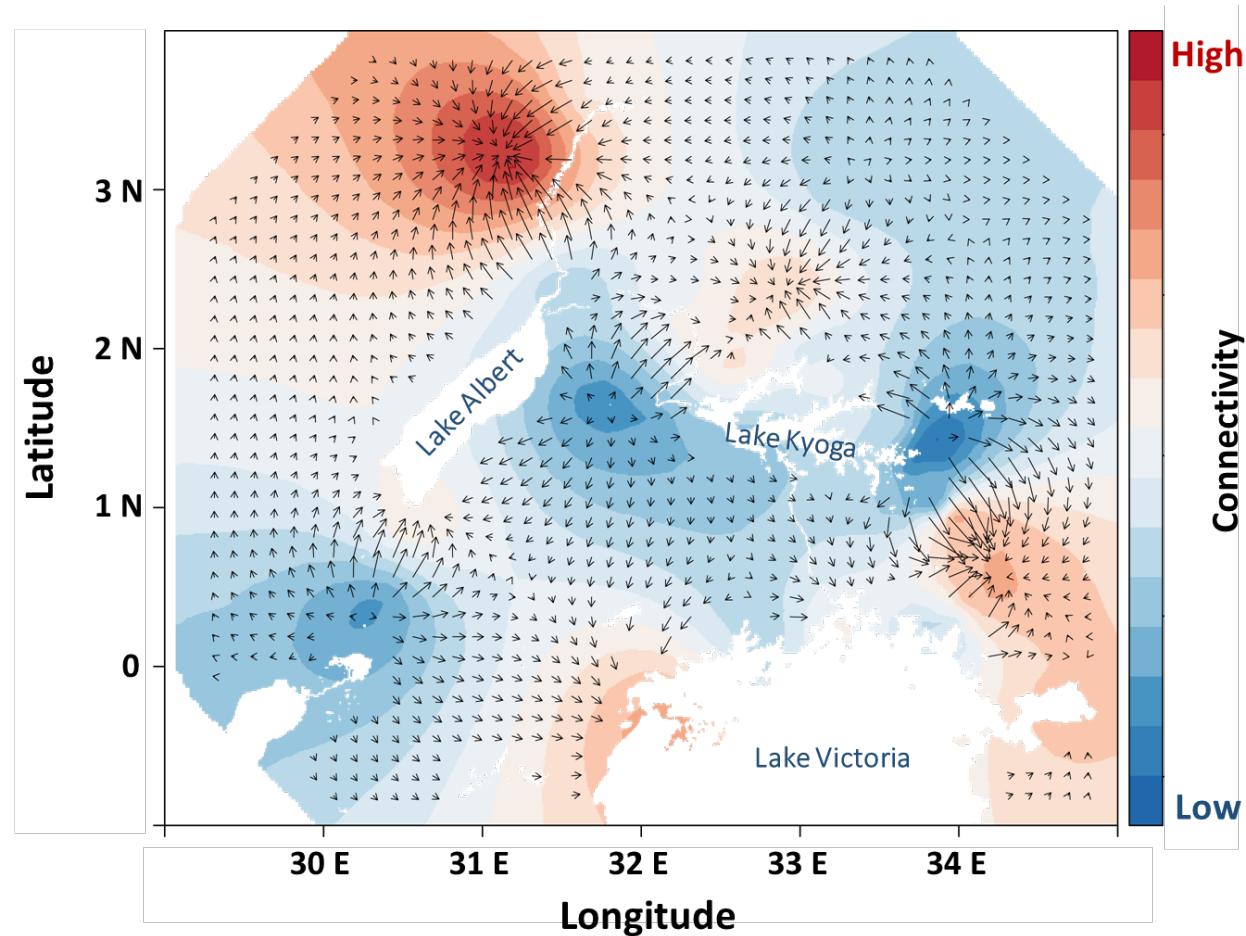
**Vector Field:**  
**Magnitude and Direction**  
**of Gene Flow**



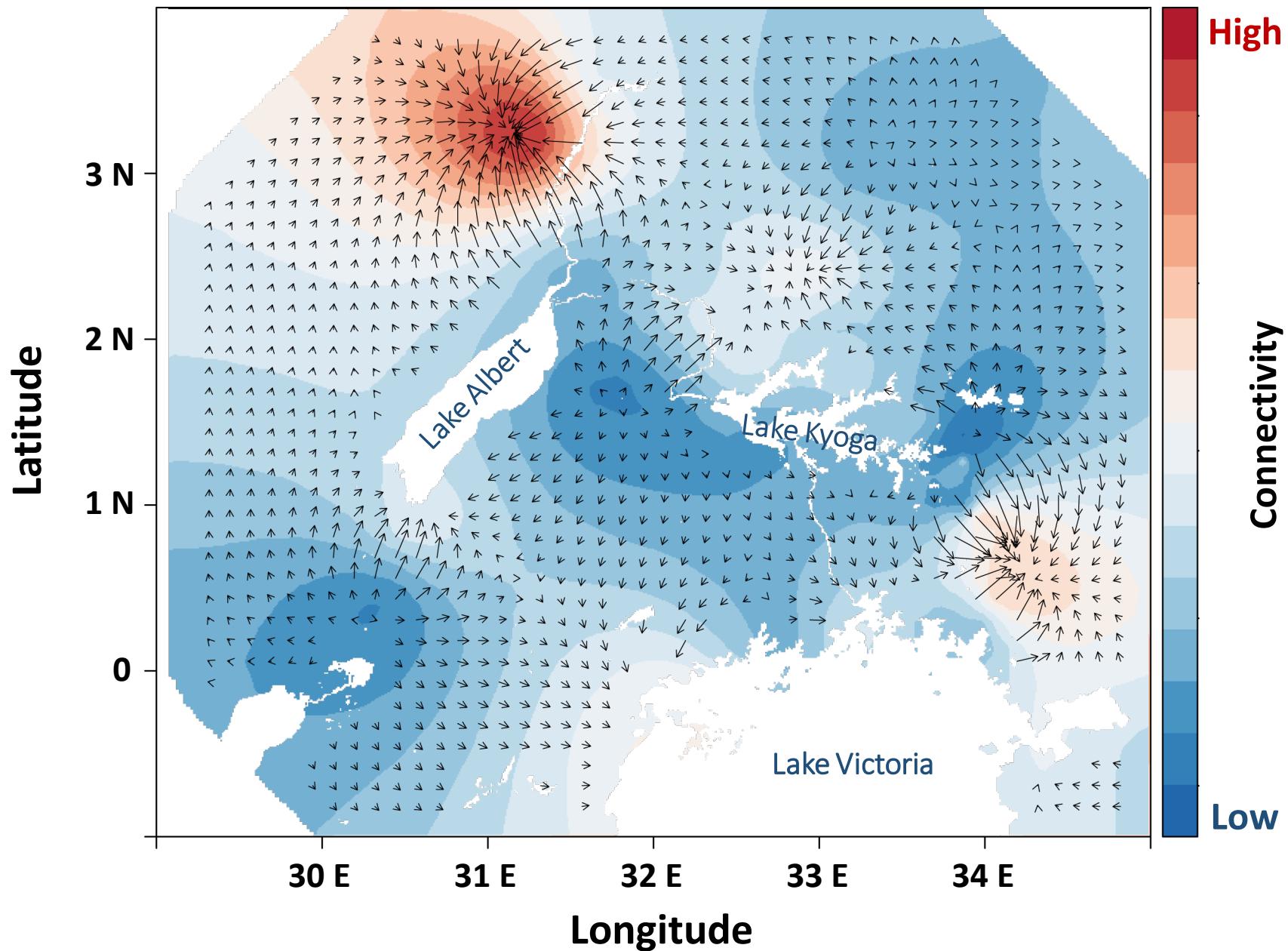
# (Positive) Selection



# Neutral Gene Flow + Selection



# = Adaptive Gene Flow



# Results: Neutral and Adaptive Models

<i>Fixed Effects</i>	<i>Neutral Gene Flow</i>	<i>Adaptive Allele L</i>	<i>Adaptive Allele H</i>
	mean	mean	mean
Intercept	4.464	-0.066	0.653
x	-0.087	-0.047	-0.047
y	<b>0.380</b>	<b>0.617</b>	<b>0.255</b>
Precip. 1	0.015	<b>-0.988</b>	-0.009
Precip. 2	0.019	<b>0.370</b>	0.056
Temp. 1	-0.014	<b>0.255</b>	<b>0.141</b>
Temp. 2	0.008	0.052	-0.063
Veg. 1	0.001	0.051	0.032
Veg. 2	0.003	-0.040	-0.023
Dist. Wat.	-0.008	<b>-0.278</b>	<b>0.135</b>
Land Cover	-0.002	0.008	-0.020

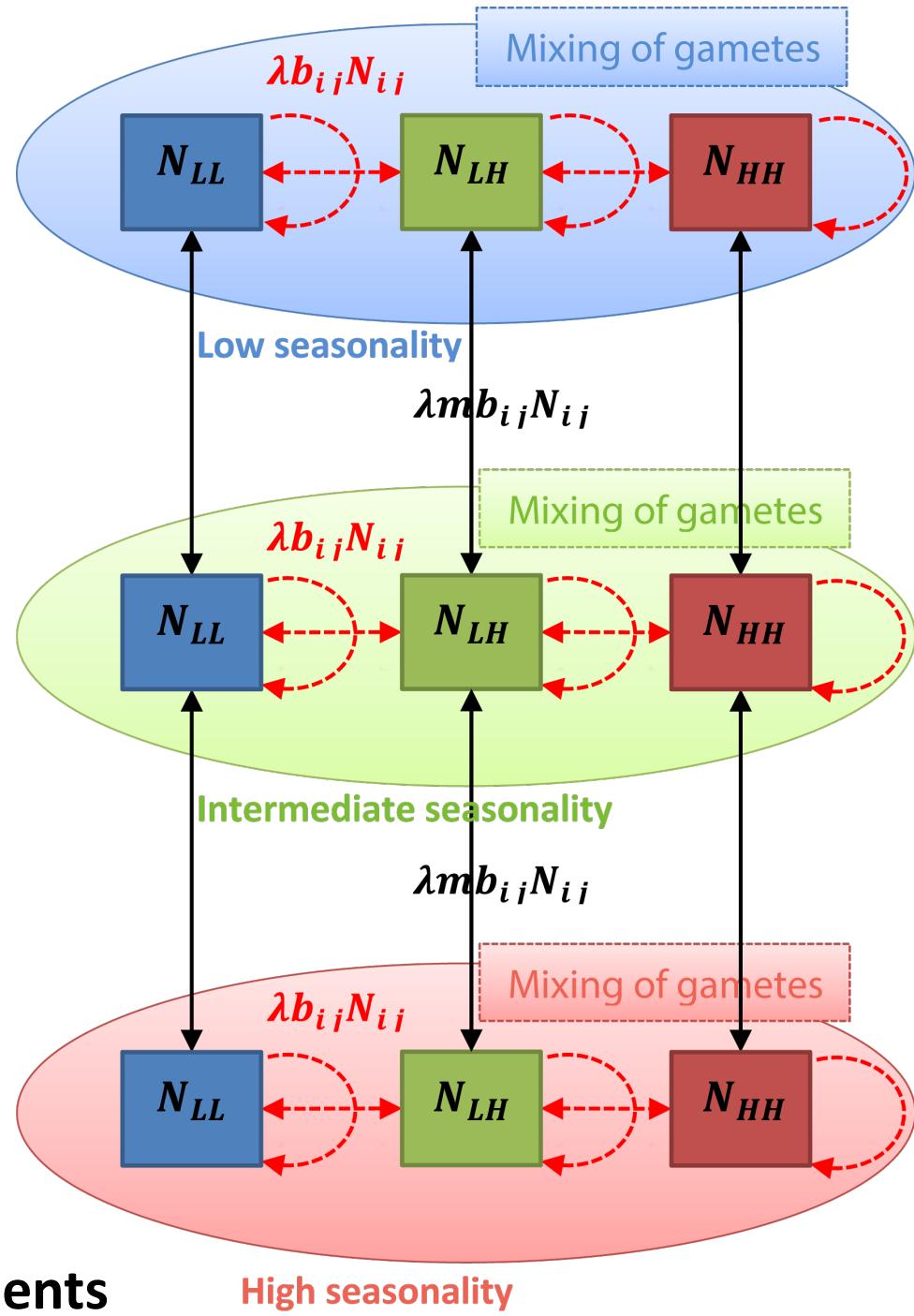
# Divergence: Forward Simulation

*b = survivorship:*

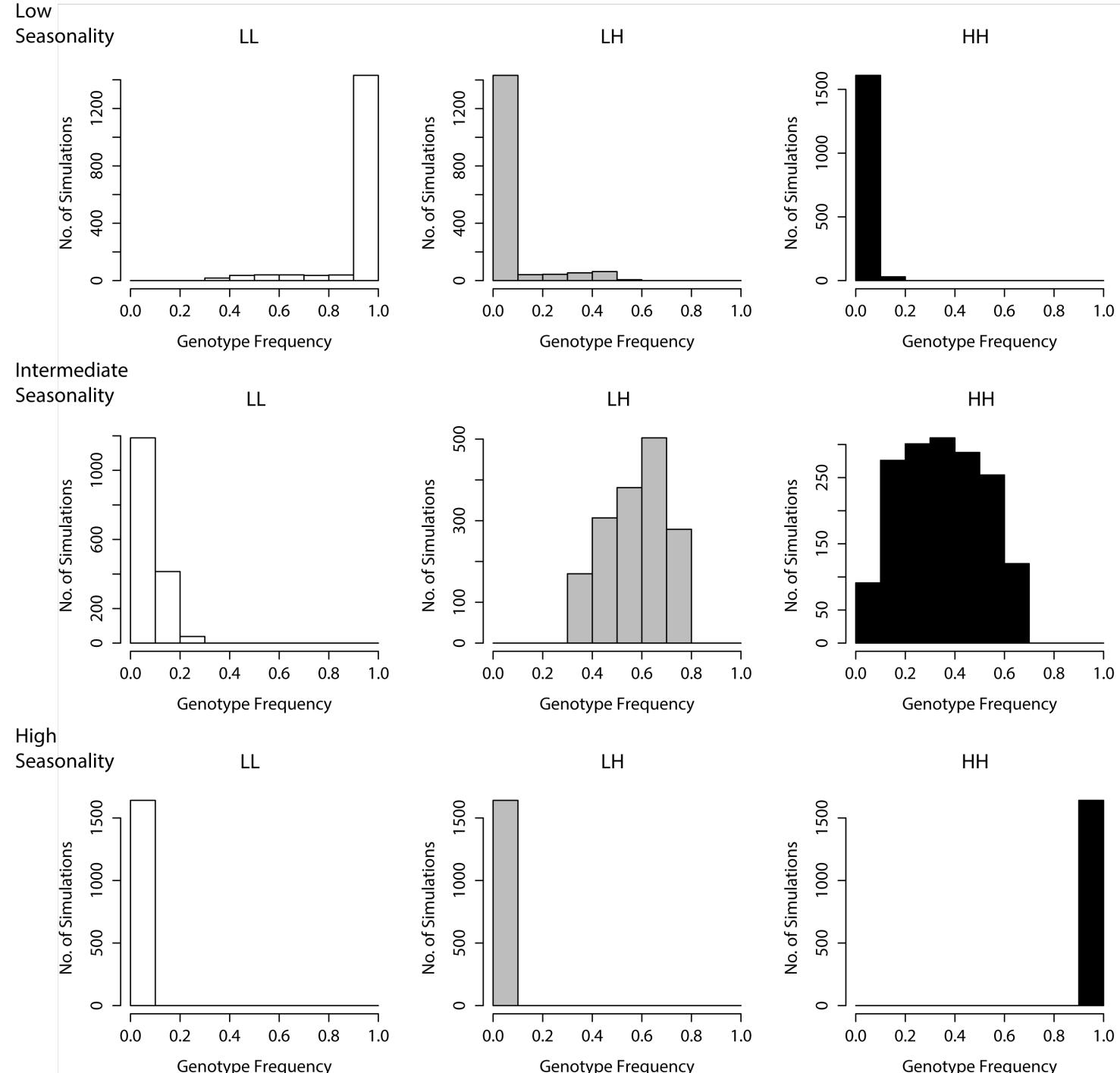
	LL	LH	HH
Low Seasonality	0.48	0.35	0.14
Intermediate Seasonality	0.16	0.44	0.18
High Seasonality	0.03	0.13	0.84

Spatially-varying selection:

Different genotypes selected in different environments



# Divergence: Forward Simulation

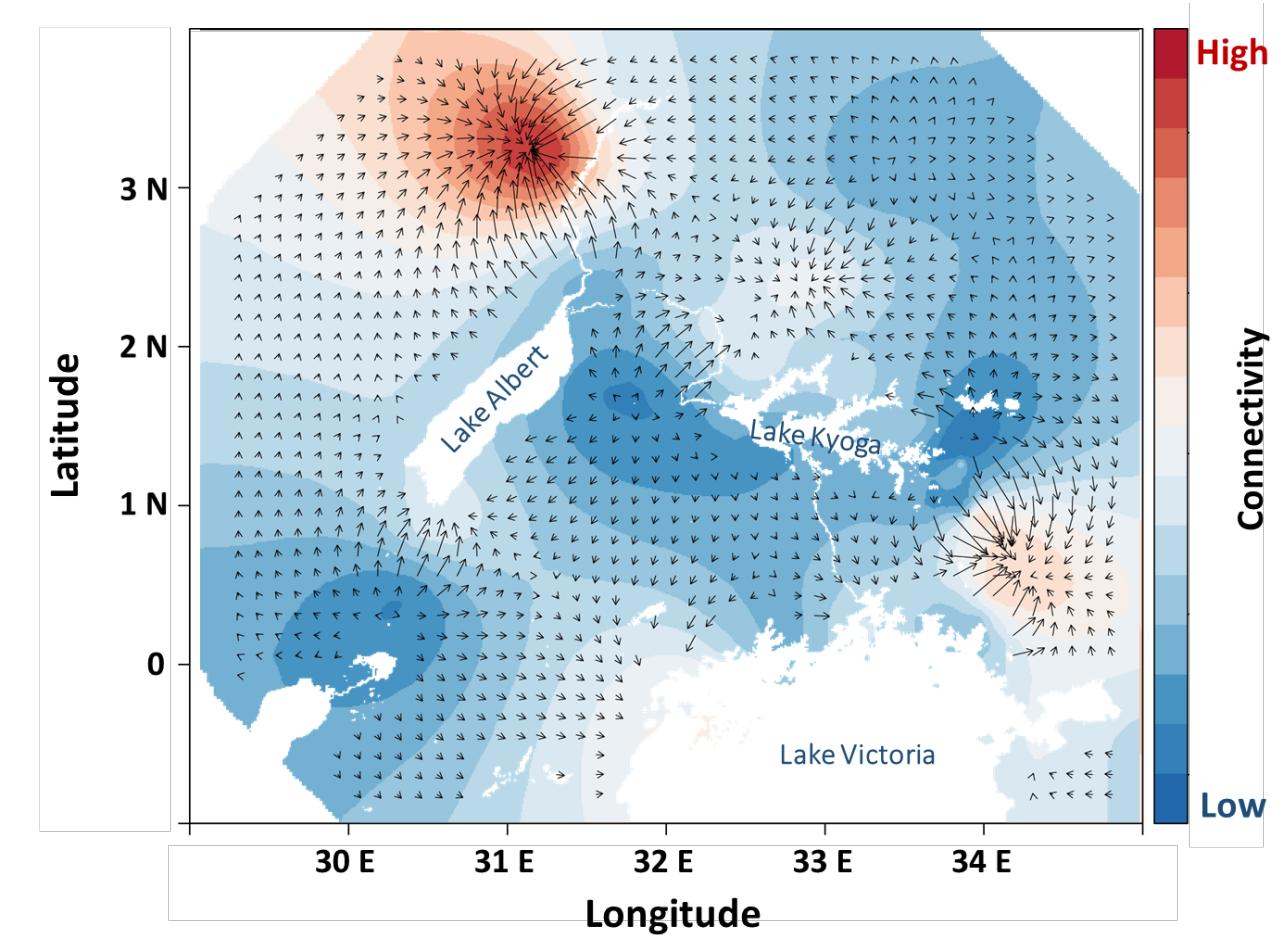
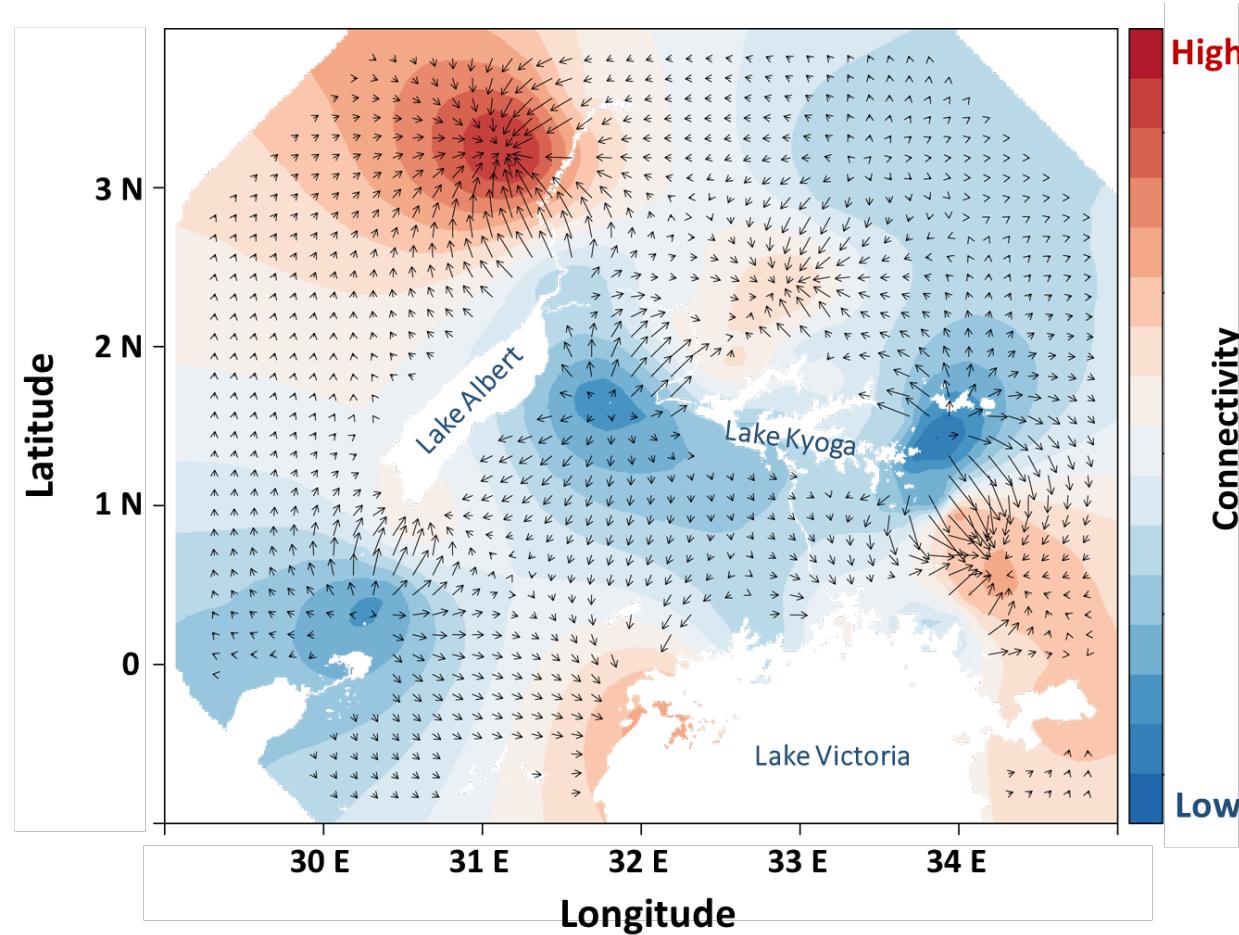


Spatially-varying selection:  
Persistence of heterozygotes

# Landscape Connectivity

Which areas to target?

Importance of accounting for selection



# Continuous Gene Flow: Other Methods

**Spatial (environment not included); do not account for selection**



## 2016: Estimated Effective Migration Surface

Visualizing spatial population structure with estimated effective migration surfaces

Desislava Petkova<sup>1,2</sup>, John Novembre<sup>3</sup>, and Matthew Stephens<sup>1,3</sup>

## 2017: Landscape Relatedness

Landscape relatedness: detecting contemporary fine-scale spatial structure in wild populations

Anita J. Norman  · Astrid V. Stronen · Geir-Arne Fuglstad · Aritz Ruiz-Gonzalez · Jonas Kindberg · Nathaniel R. Street · Göran Spong

## 2018: conStruct

Inferring Continuous and Discrete Population Genetic Structure Across Space

Gideon S. Bradburd,<sup>\*,1</sup> Graham M. Coop,<sup>,2</sup> and Peter L. Ralph<sup>,2</sup>

# **Testing the Method: Simulations**

# Simulations: Neutral and Selected Loci

## Sampling

### 1. Uniform

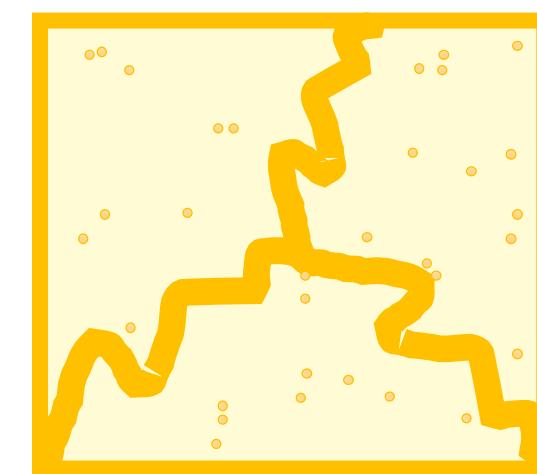
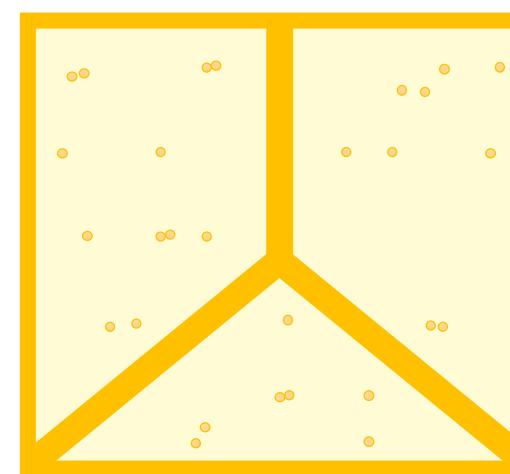
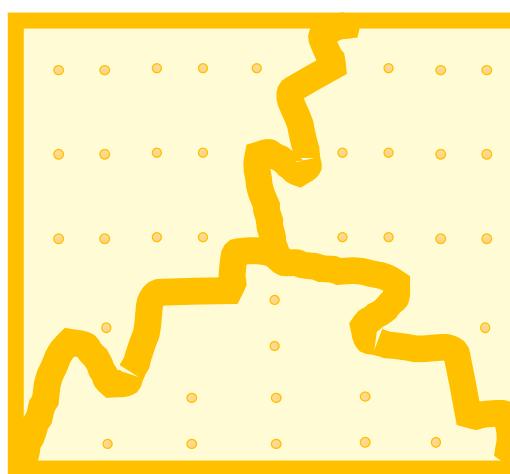
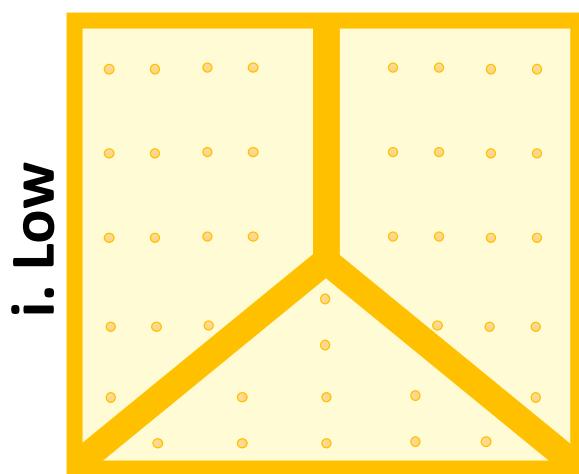
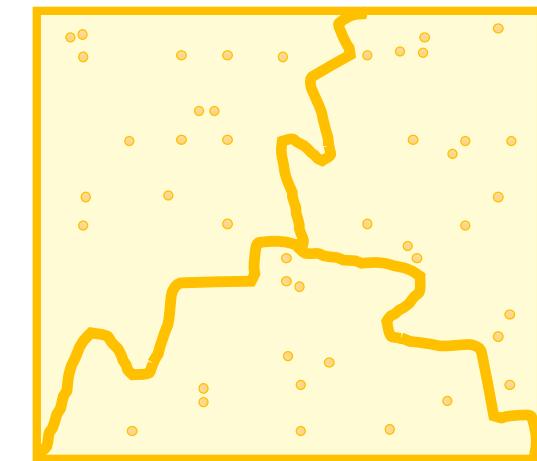
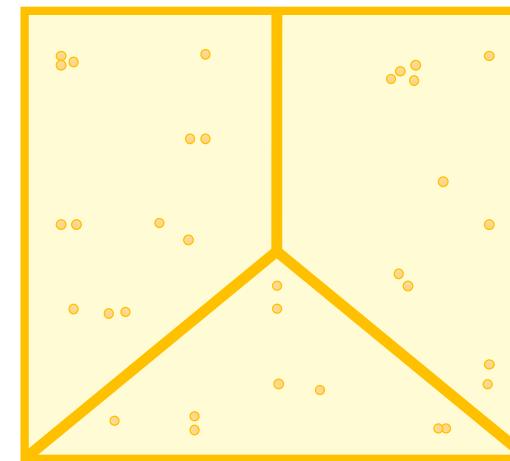
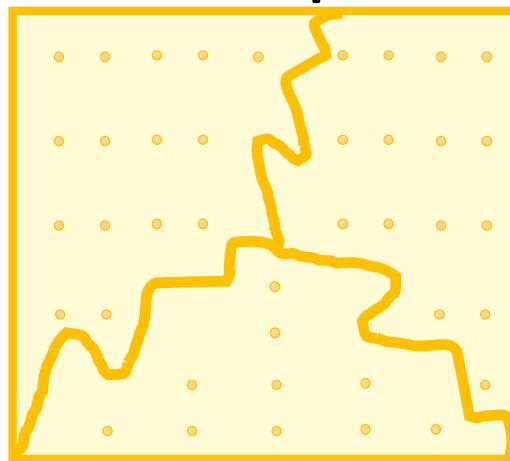
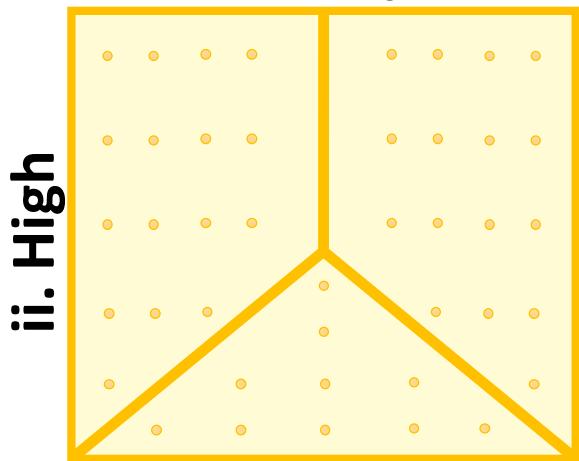
### 2. Non-uniform

#### Boundary Shape

##### A. Simple

##### B. Complex

Boundary Permeability



# Acknowledgements

- Dr. Gisella Caccone (Yale University)
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  - Dr. Brice Noonan
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  - Dr. Rodney Dyer (VCU)

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