# 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

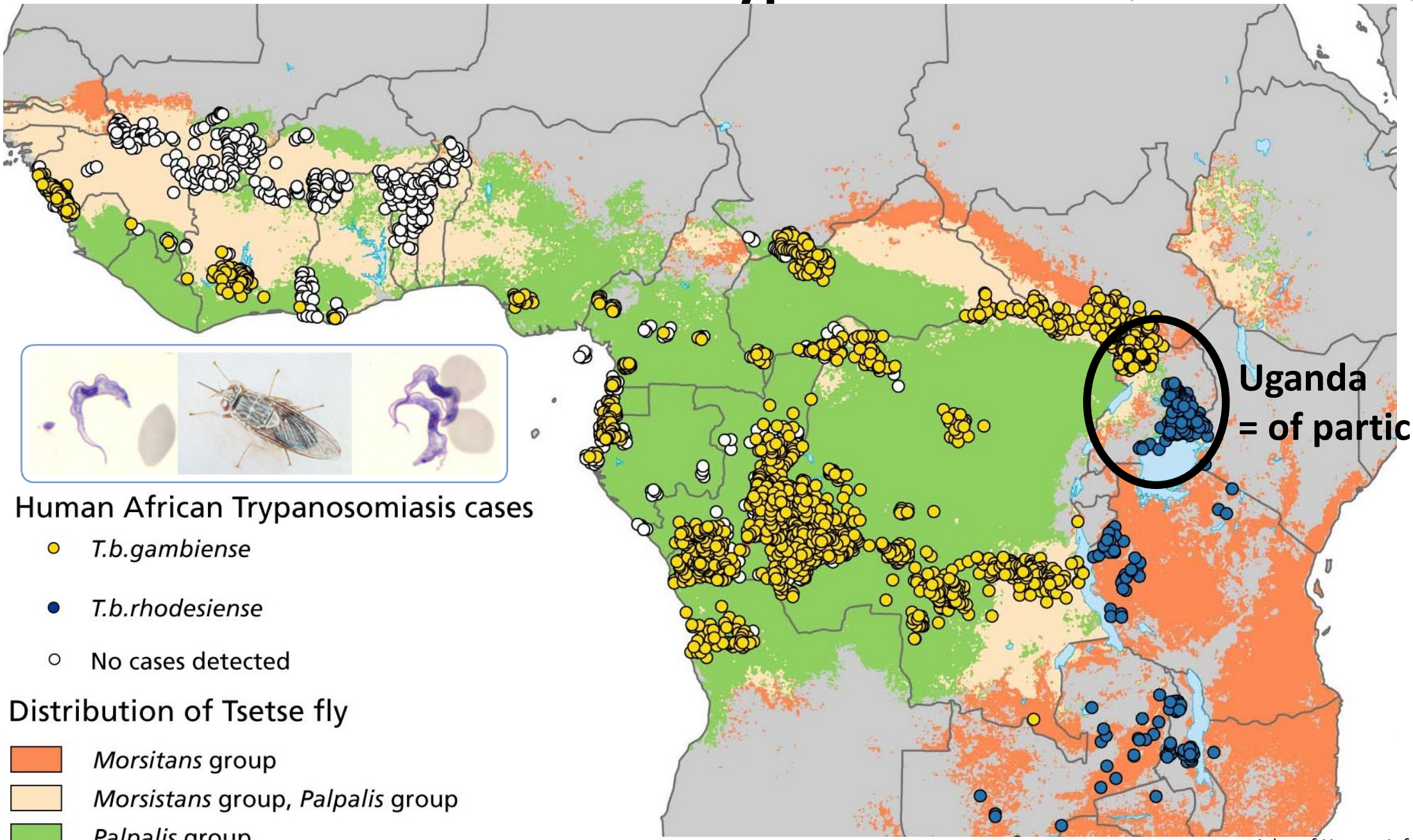
- **Method Development**
  - Inspiration: Tsetse

- **Method Validation**
  - Simulations
  - Empirical: Subterranean Termites

# Tsetse

Tsetse (*Glossina fuscipes*) in Uganda

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




Atlas of Human Infectious Diseases (2012)

# 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***

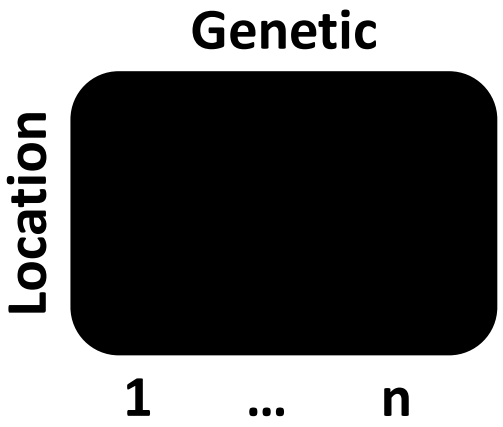
***Land Cover***

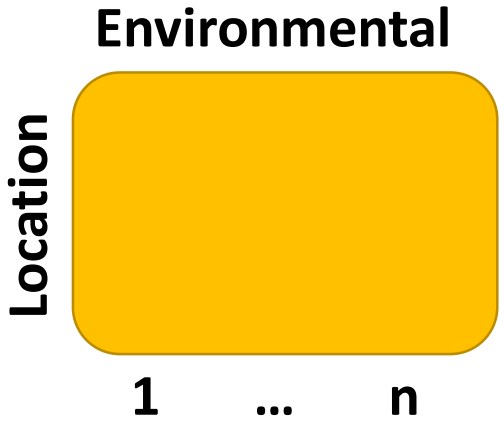
***Distance from Water Bodies***

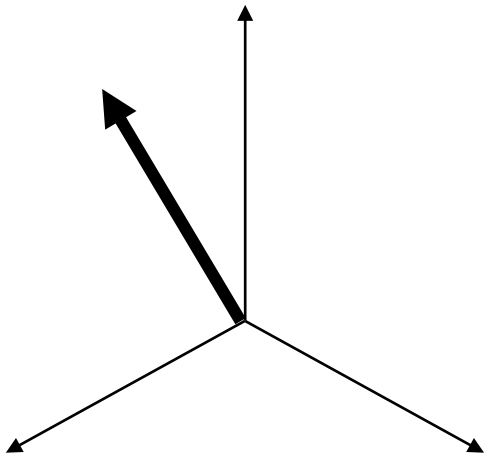
Random Effect:

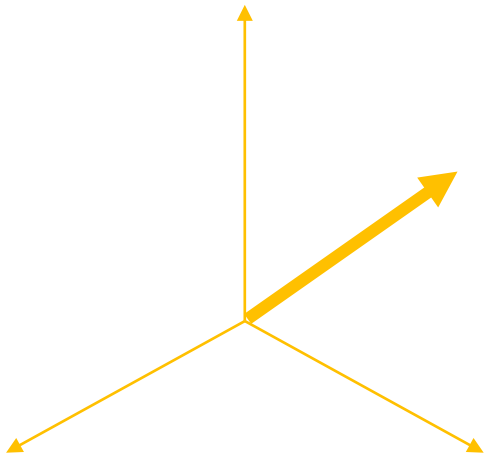
*Spatial Location*

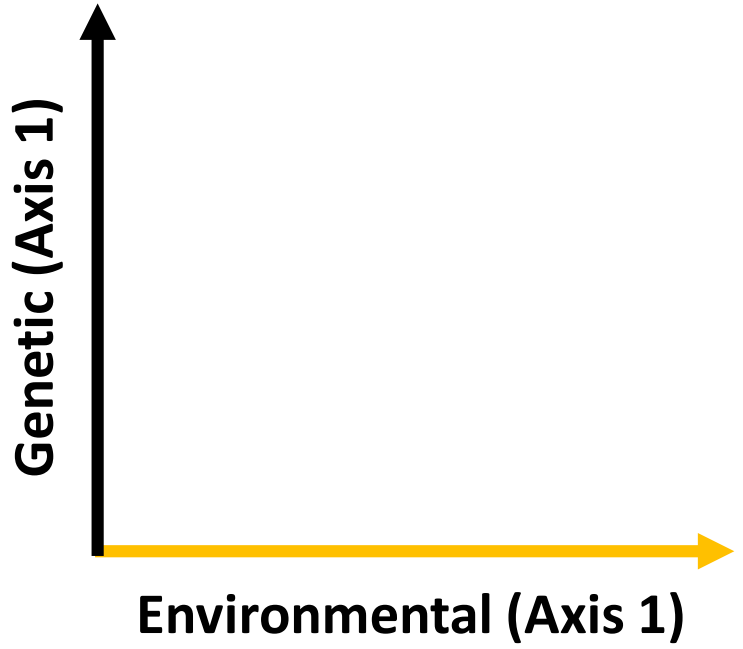
# The Method – Pt. 1: Multivariate Transformation







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

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

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

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

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

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

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

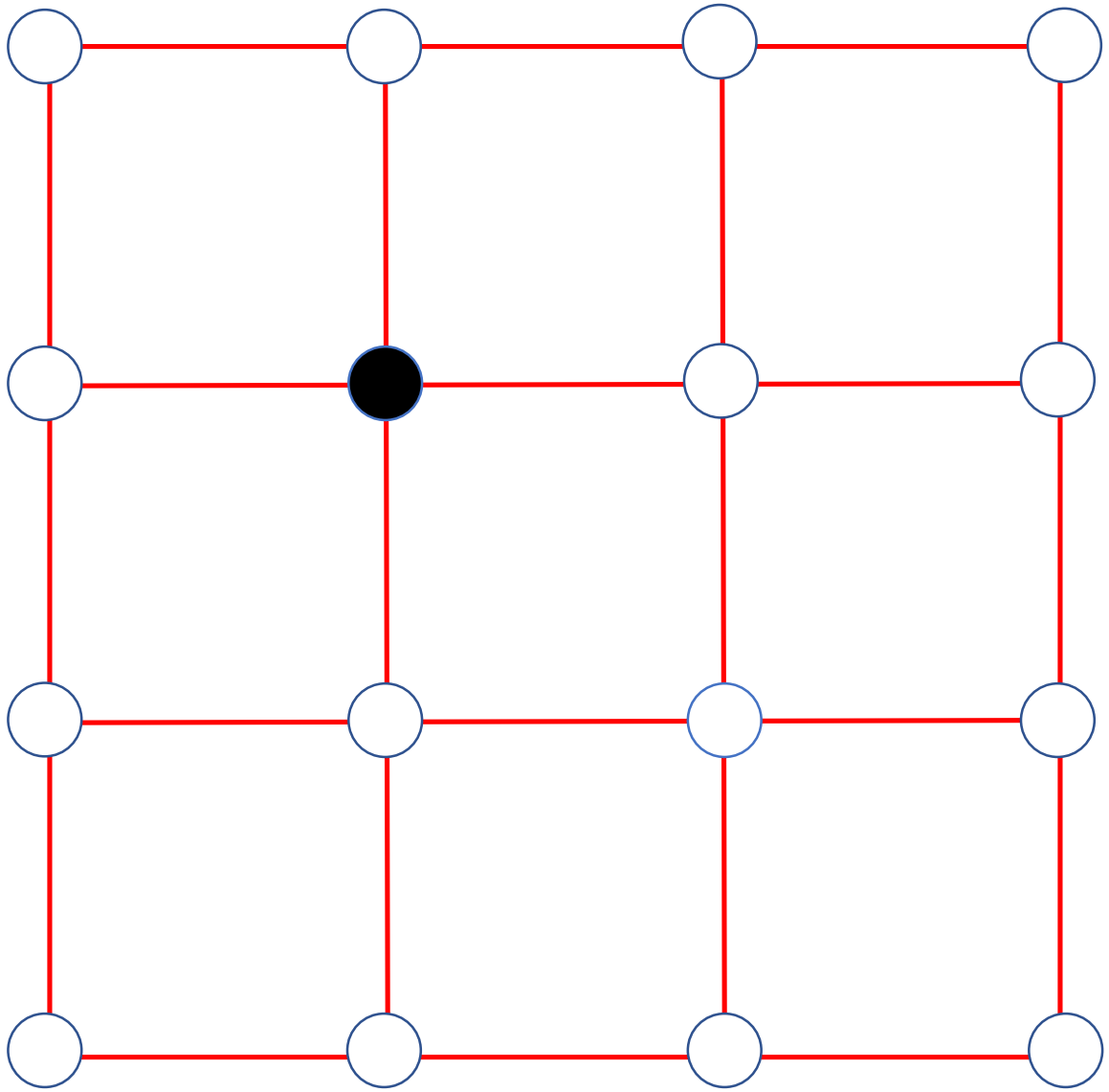
# (Bayesian) Interpolation

**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

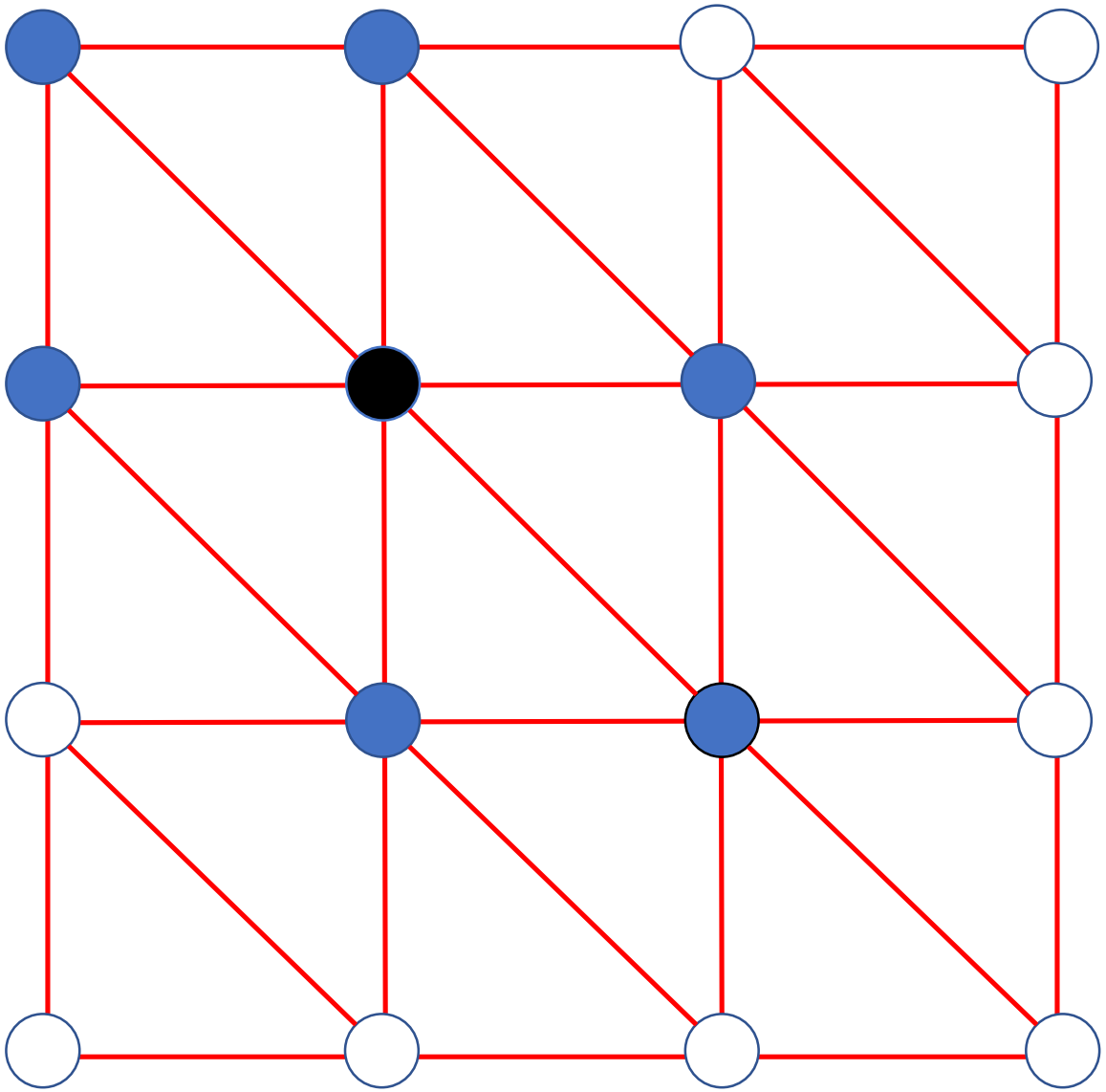


Sampled locations

Unsampled locations

# Interpolation

## Mesh (triangulation)

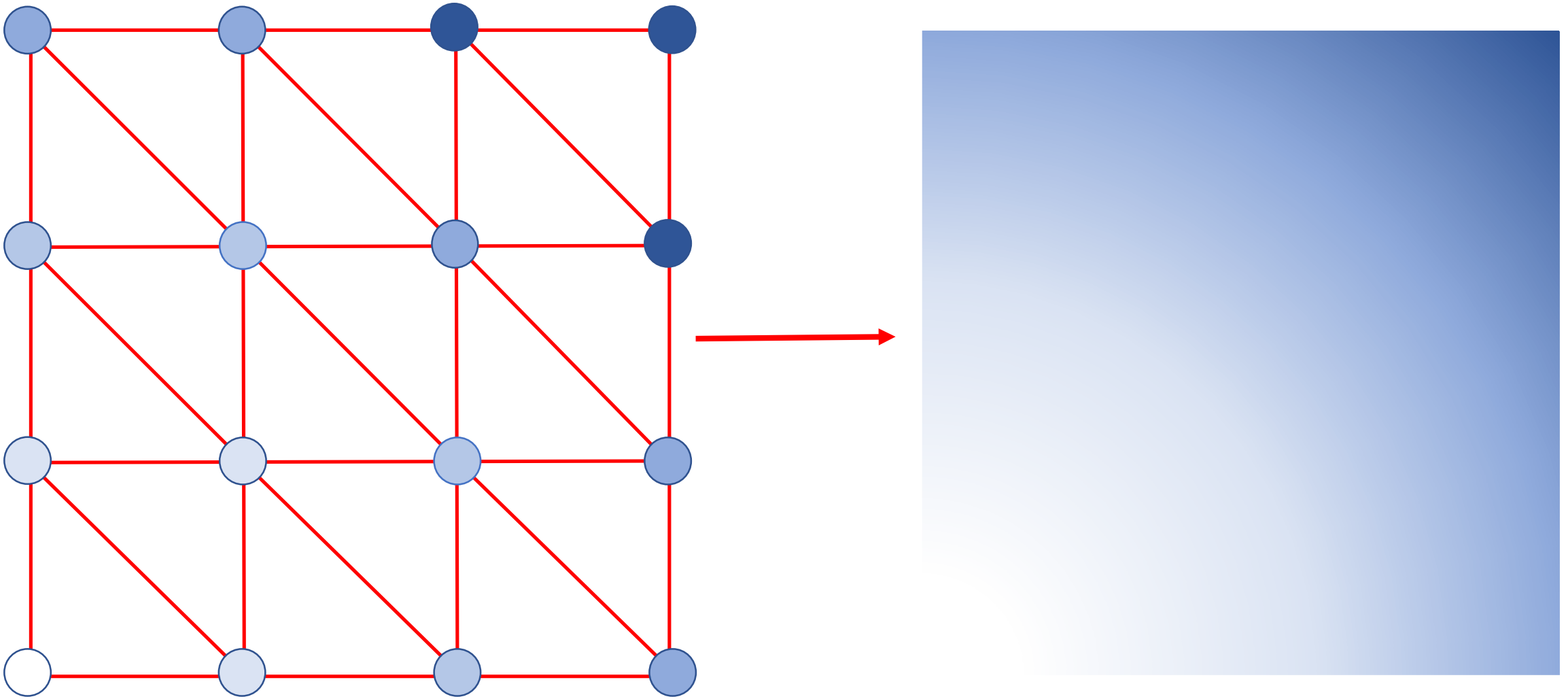


Sampled locations

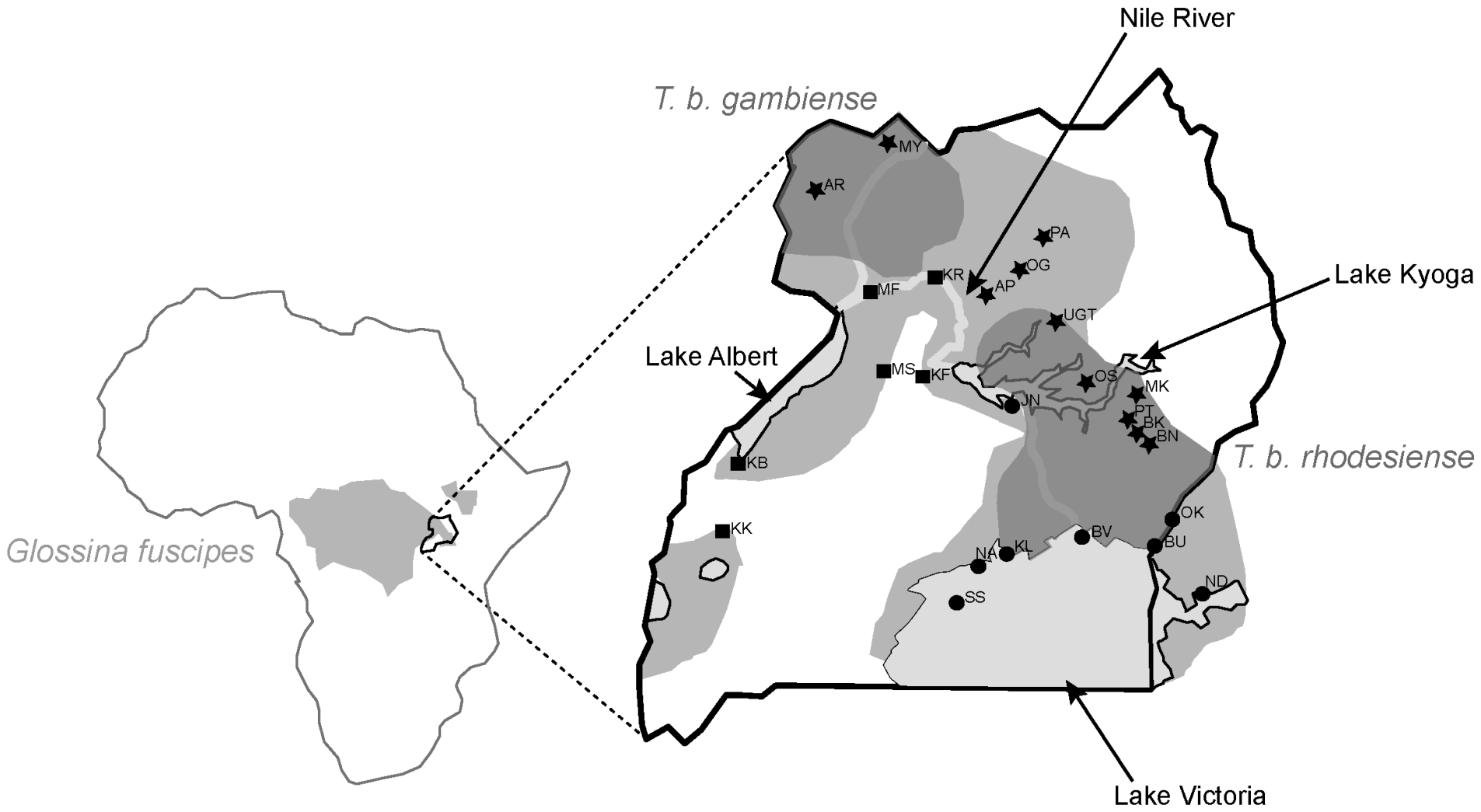
Neighboring locations

# Interpolation

## From Discrete to Continuous Gene Flow

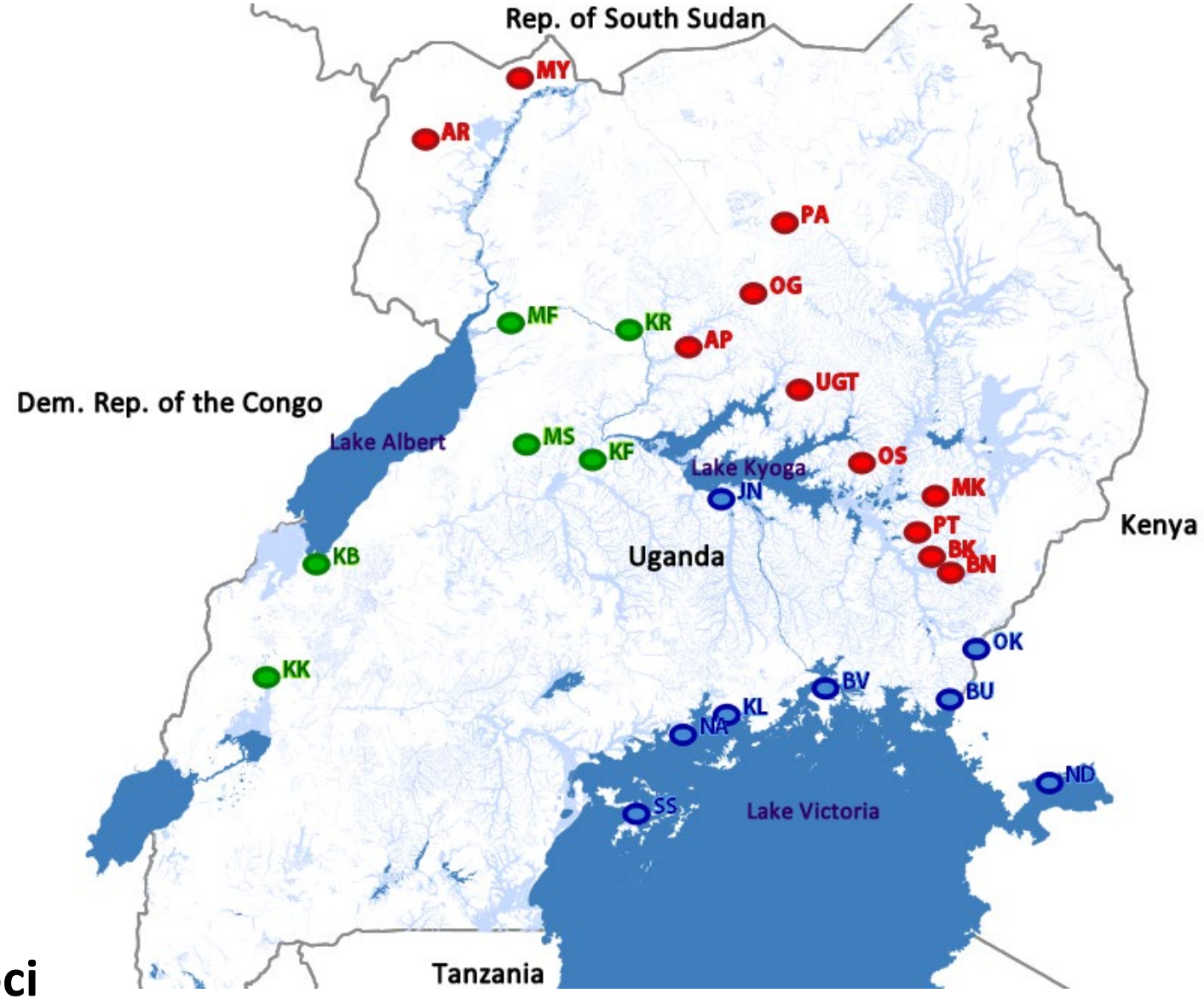


# Sampling Sites




**Tsetse in Uganda: 25 sites**

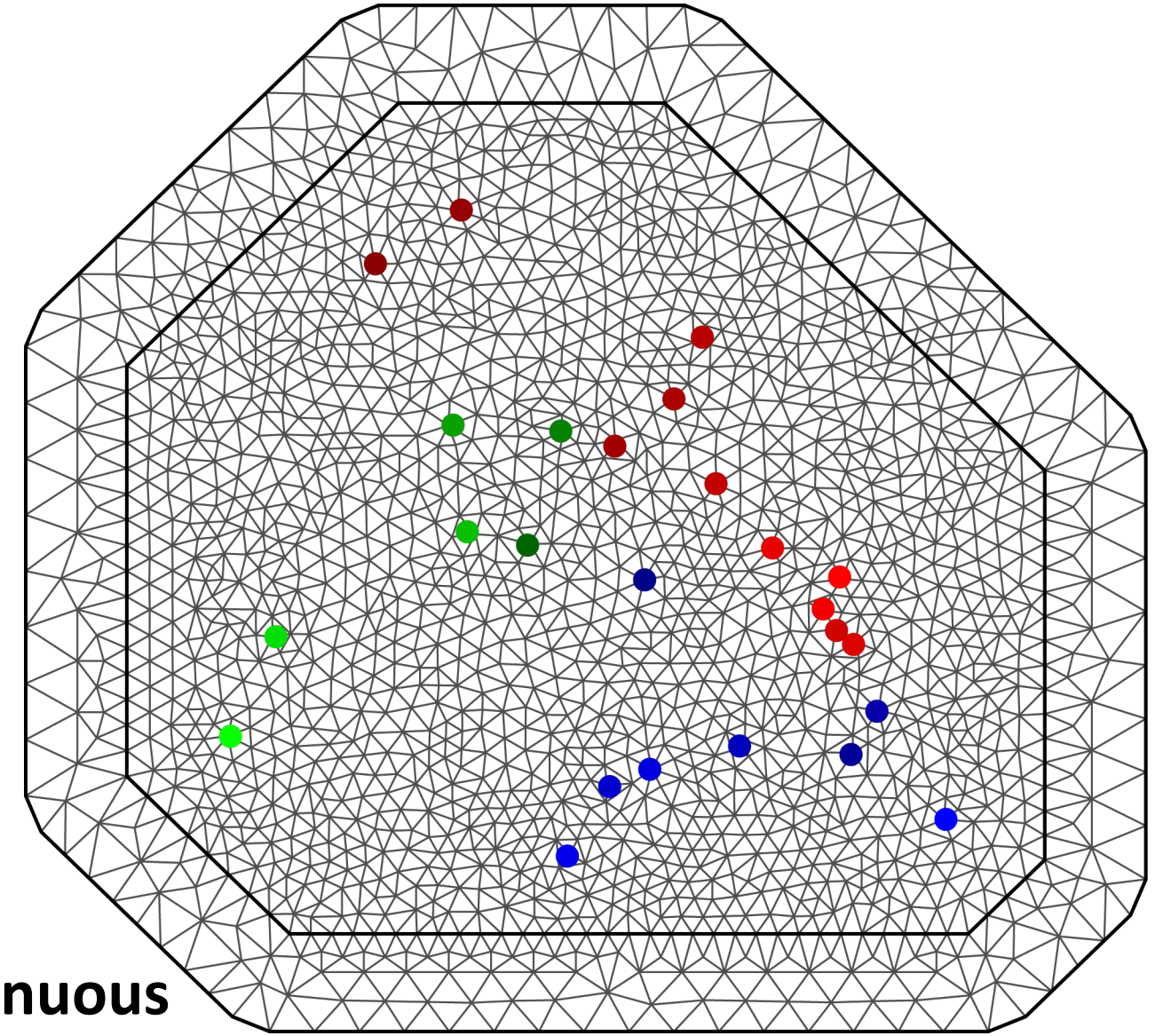
# Genetic Populations




**11 microsatellite loci**

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

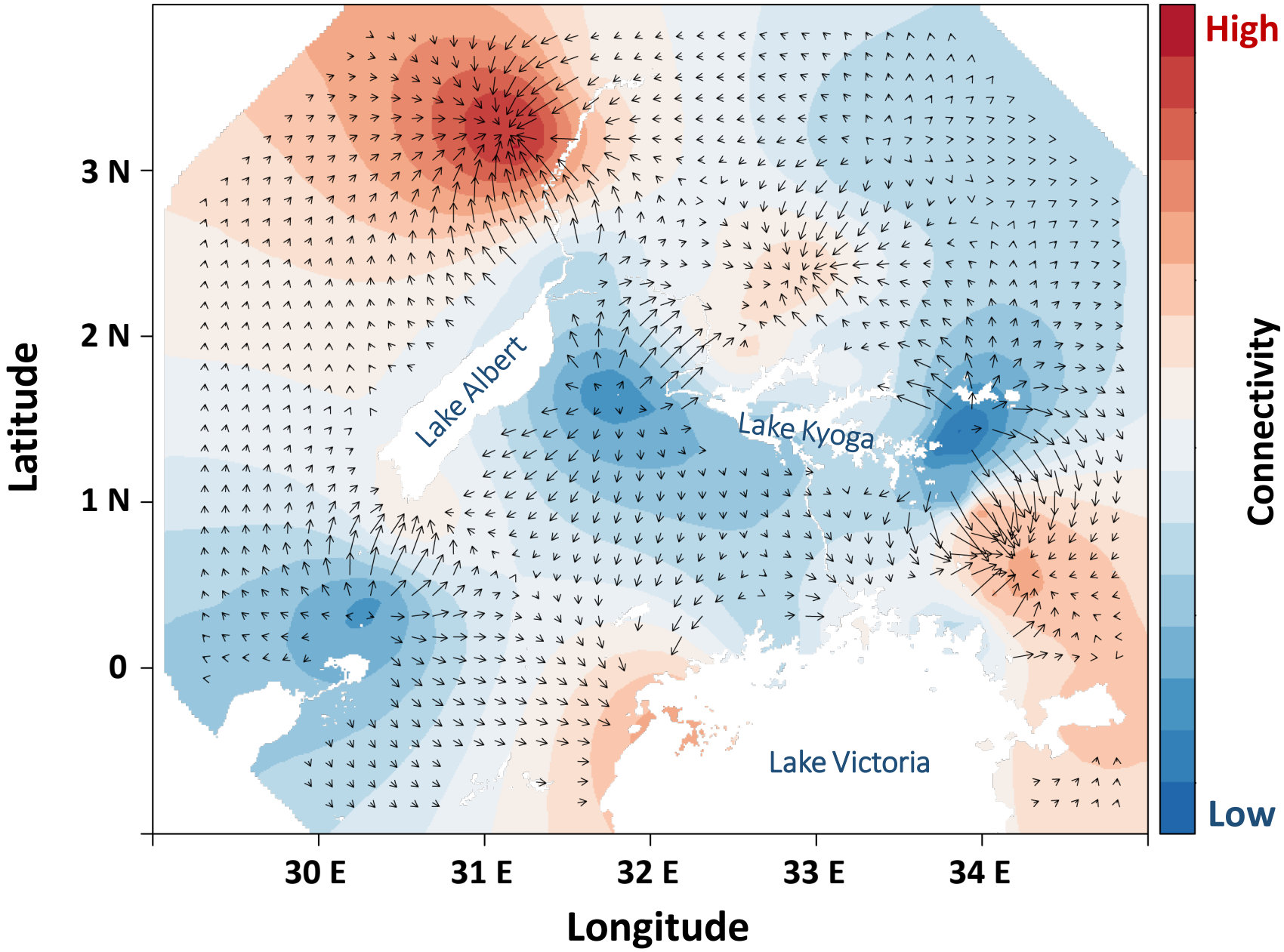
# Mesh



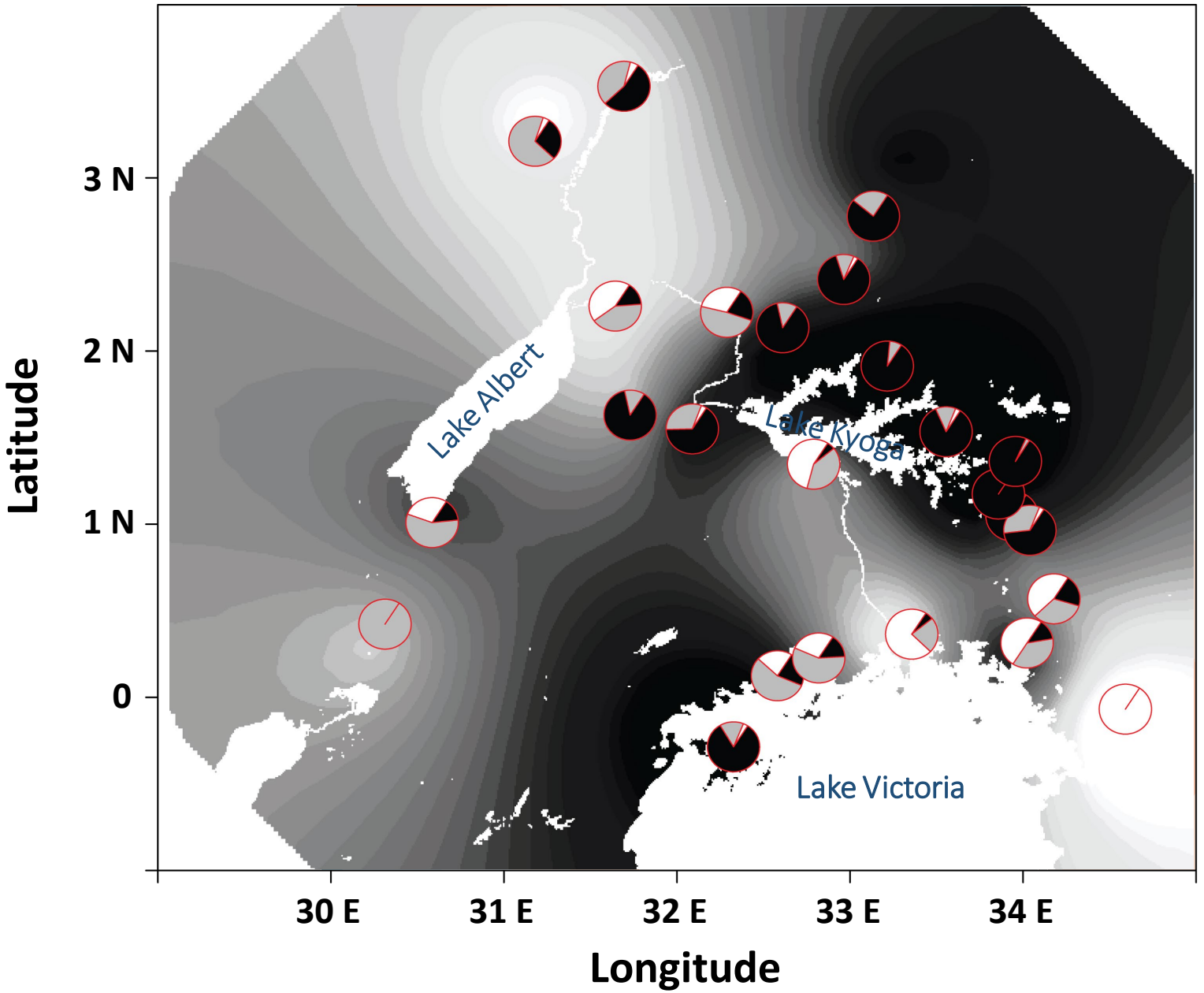
**Going from discrete to continuous**

# Neutral Gene Flow

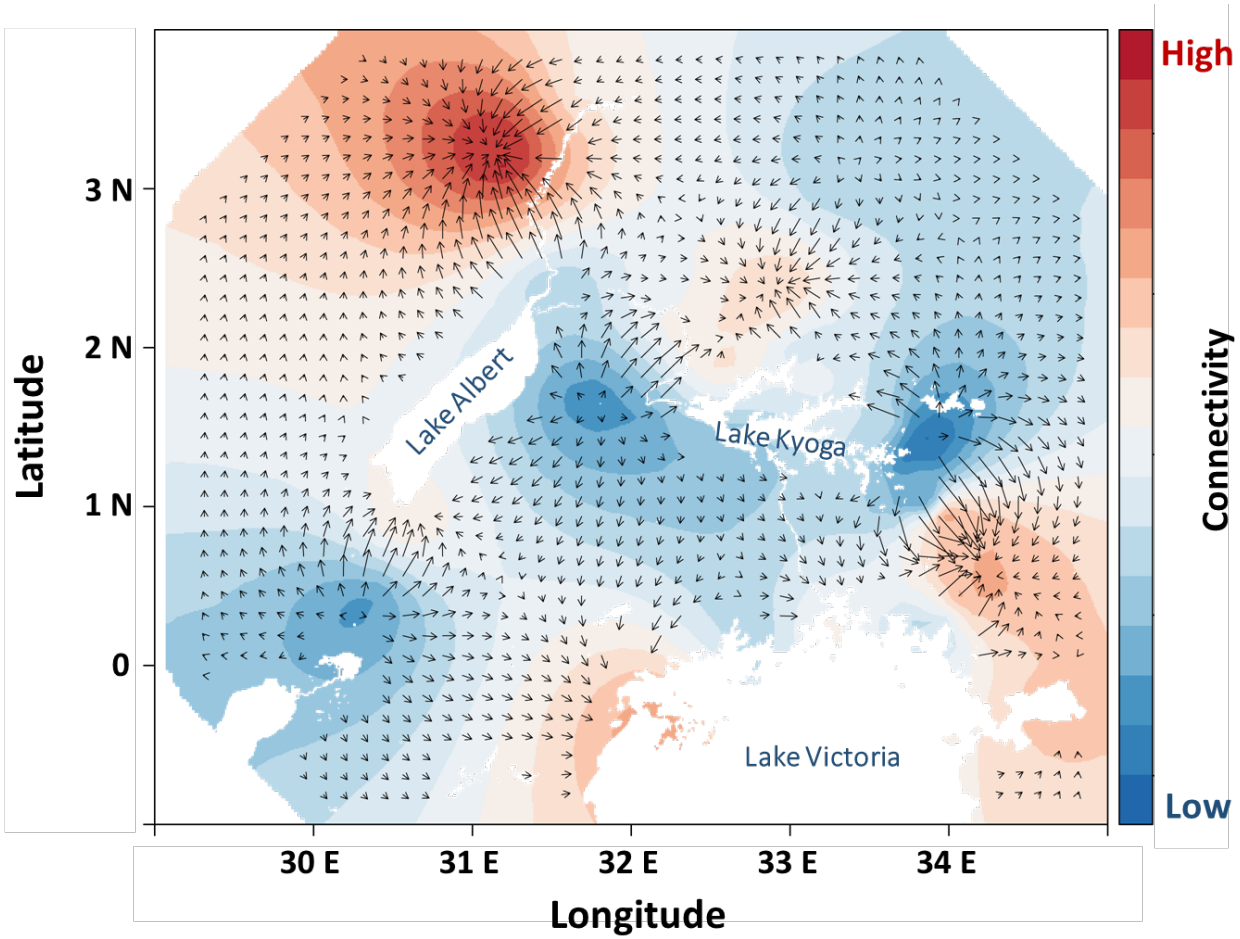
**Vector Field:**
**Magnitude and Direction of Gene Flow**

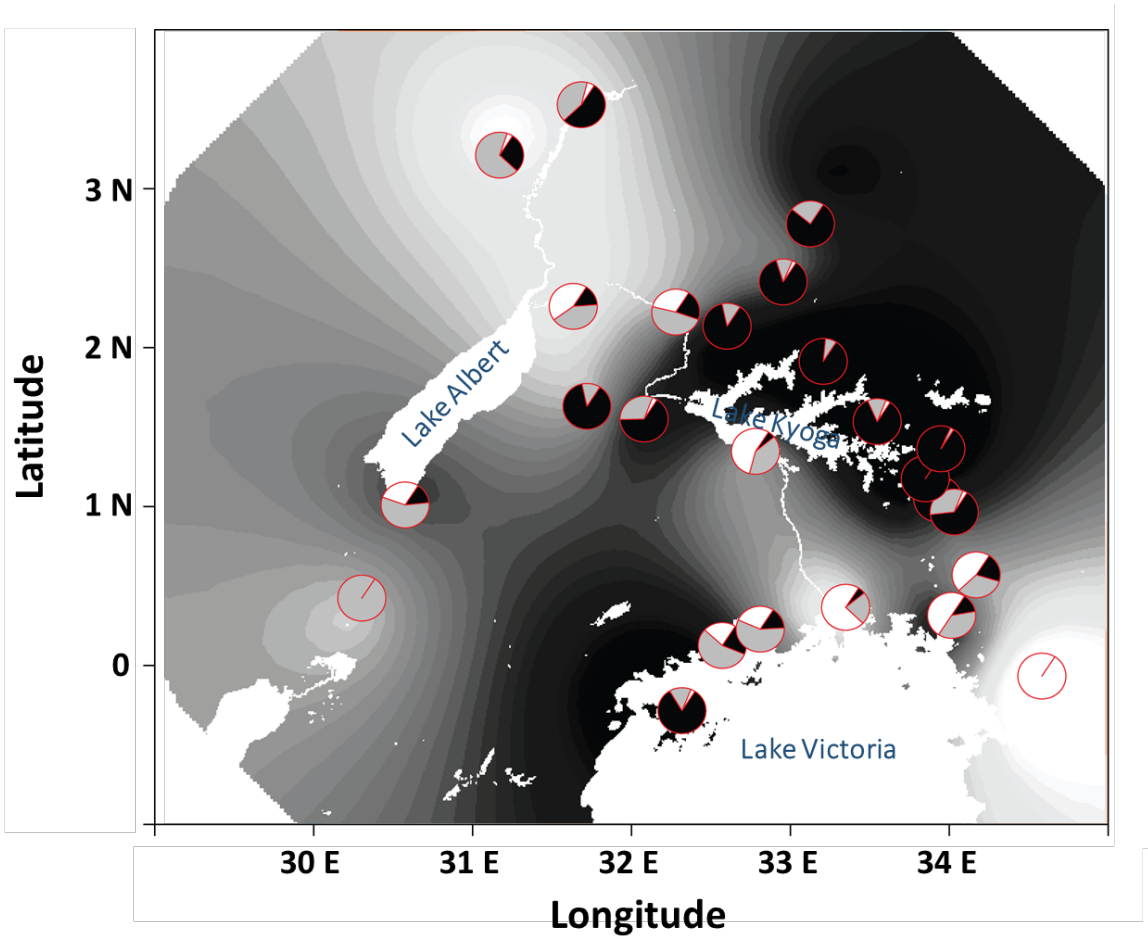


# (Positive) Selection

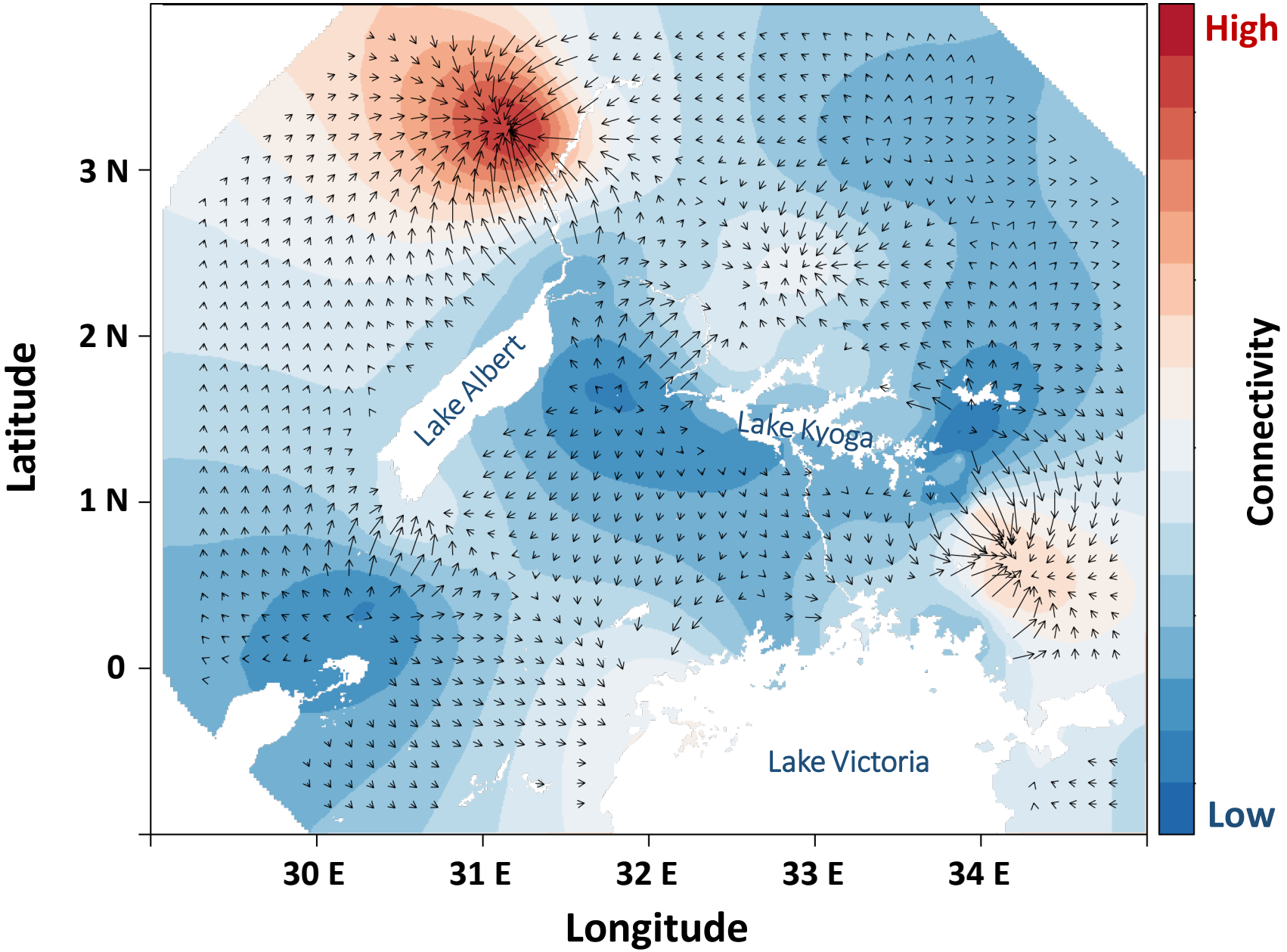


# Neutral Gene Flow + Selection



# = Adaptive Gene Flow



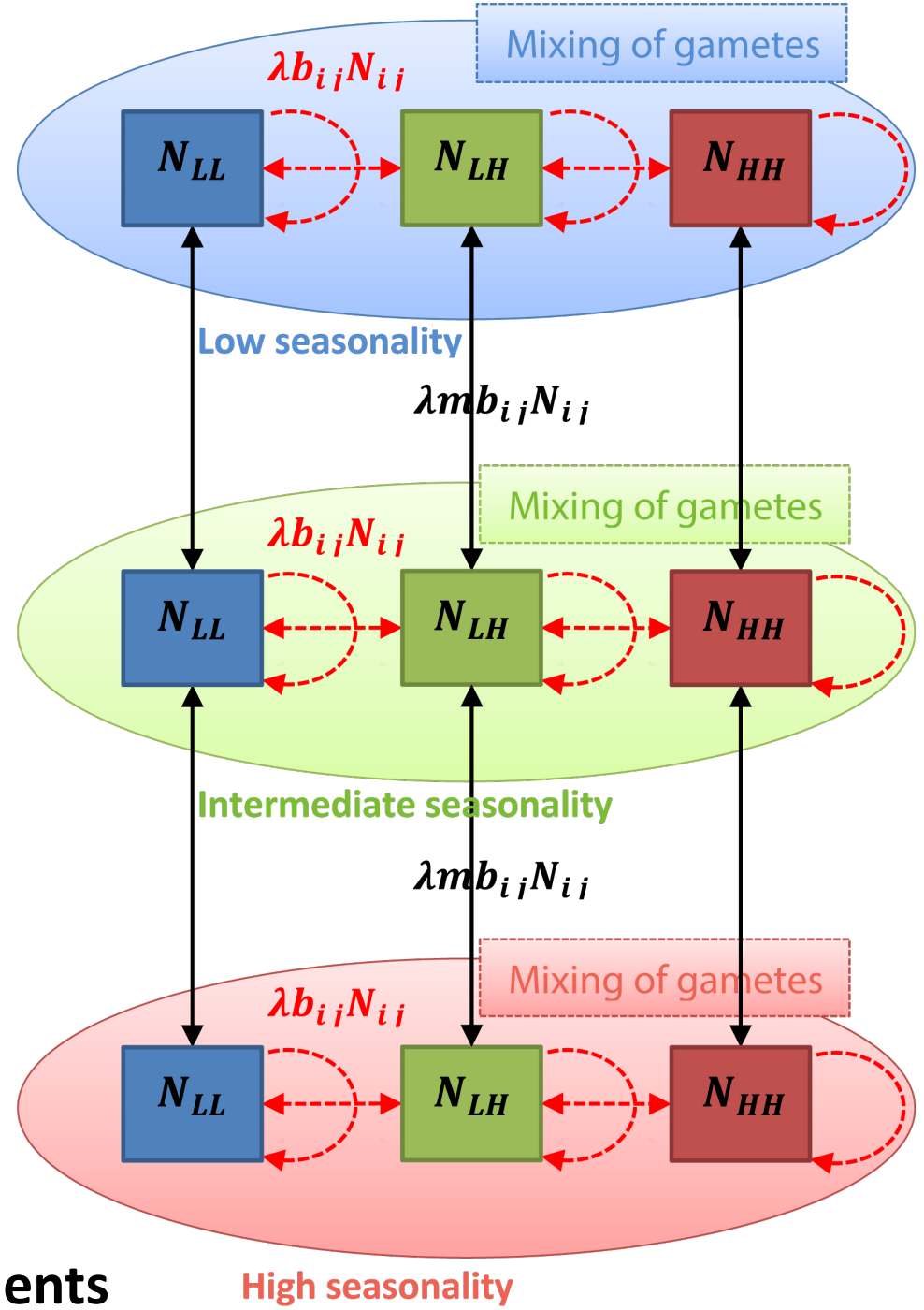
# Results: Neutral and Adaptive Models

| *Fixed Effects* | *Neutral Gene Flow* | *Adaptive Allele L* | *Adaptive Allele H* |
|---|---|---|---|
| | **mean** | **mean** | **mean** |
| Intercept | 4.464 | -0.066 | 0.653 |
| x | -0.087 | -0.047 | -0.047 |
| **y** | **0.380** | **0.617** | **0.255** |
| **Precip. 1** | 0.015 | **-0.988** | -0.009 |
| **Precip. 2** | 0.019 | **0.370** | 0.056 |
| **Temp. 1** | -0.014 | **0.255** | **0.141** |
| 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 | **-0.278** | **0.135** |
| Land Cover | -0.002 | 0.008 | -0.020 |

# Divergence:
# Forward Simulation

***b = survivorship:***

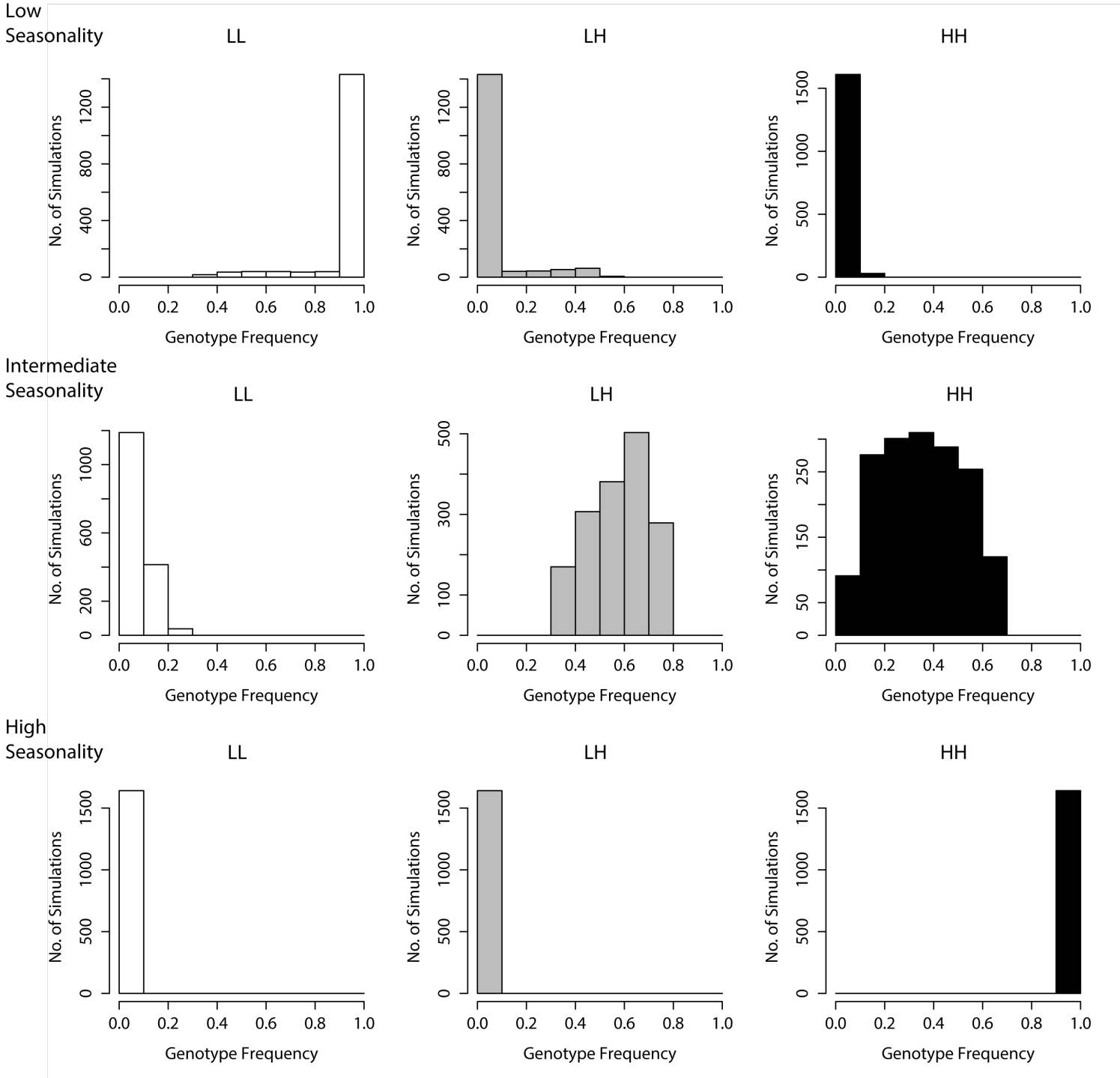
| | LL | LH | HH |
|---|---|---|---|
| Low Seasonality | 0.48 | 0.35 | 0.14 |
| Intermediate Seasonality | 0.16 | 0.44 | 0.18 |
| High Seasonality | 0.03 | 0.13 | 0.84 |




**Spatially-varying selection:**

**Different genotypes selected in different environments**

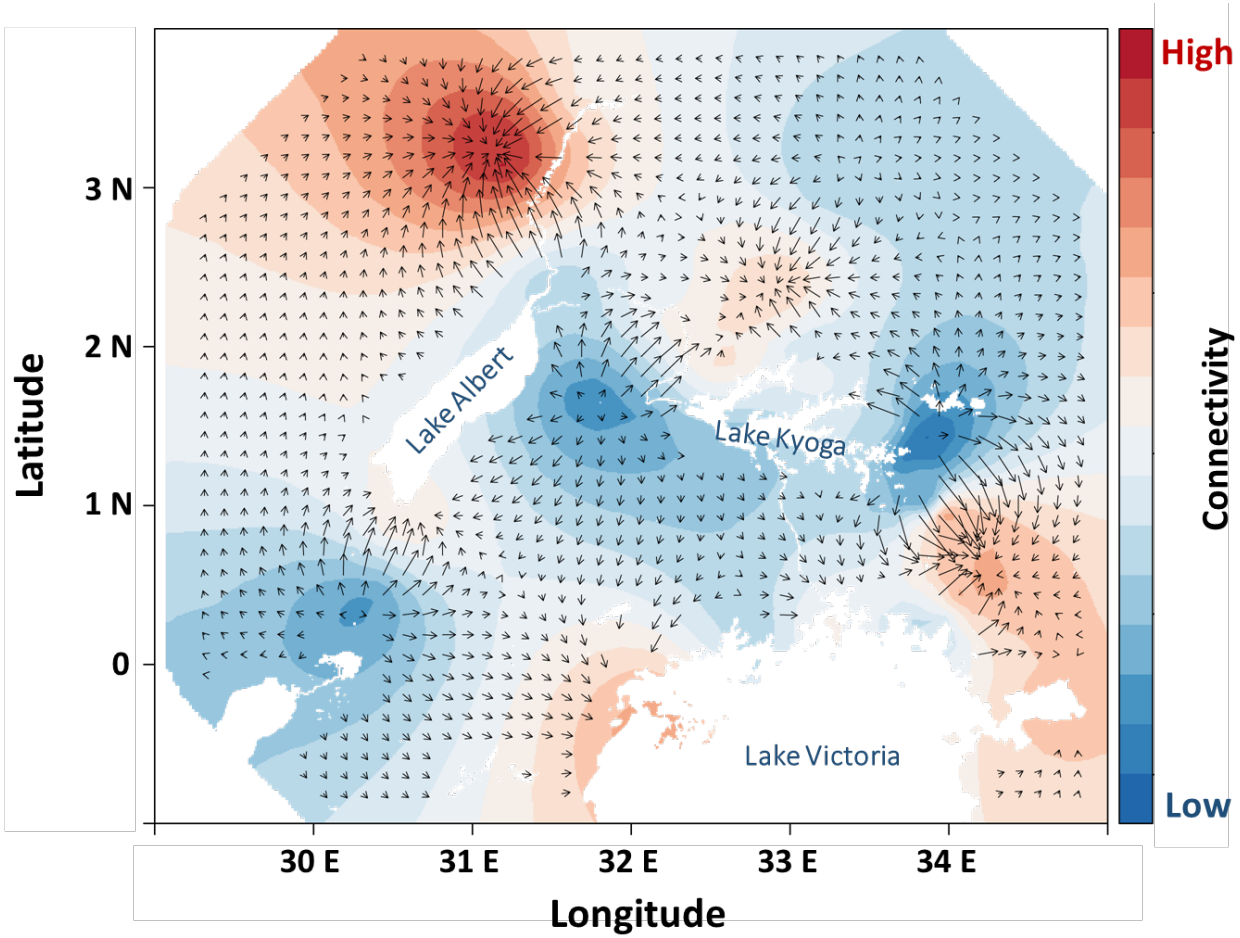
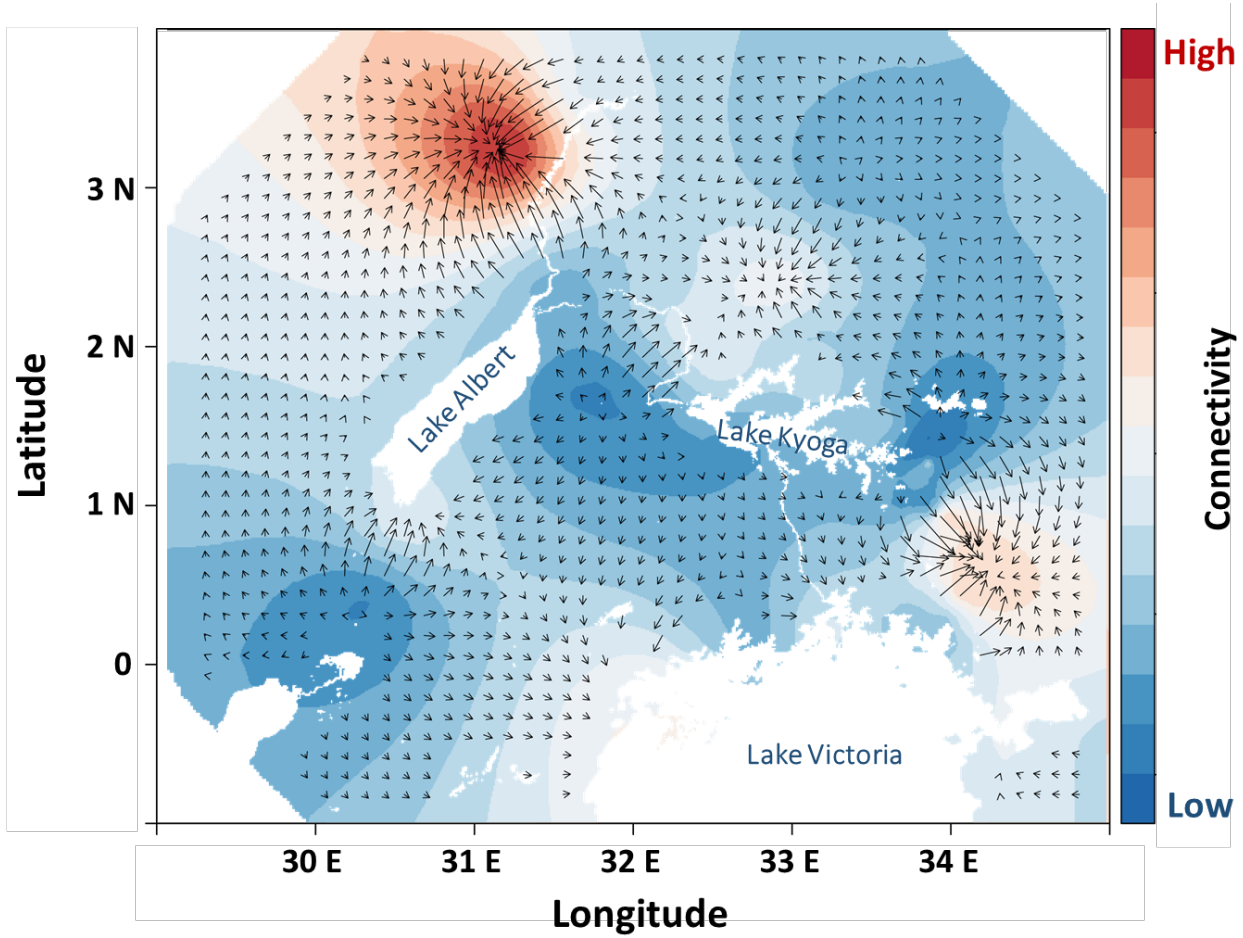
# Divergence:
# Forward Simulation




# Spatially-varying selection:

## Persistence of heterozygotes

# Landscape Connectivity

Which areas to target?

**Importance of accounting for selection**