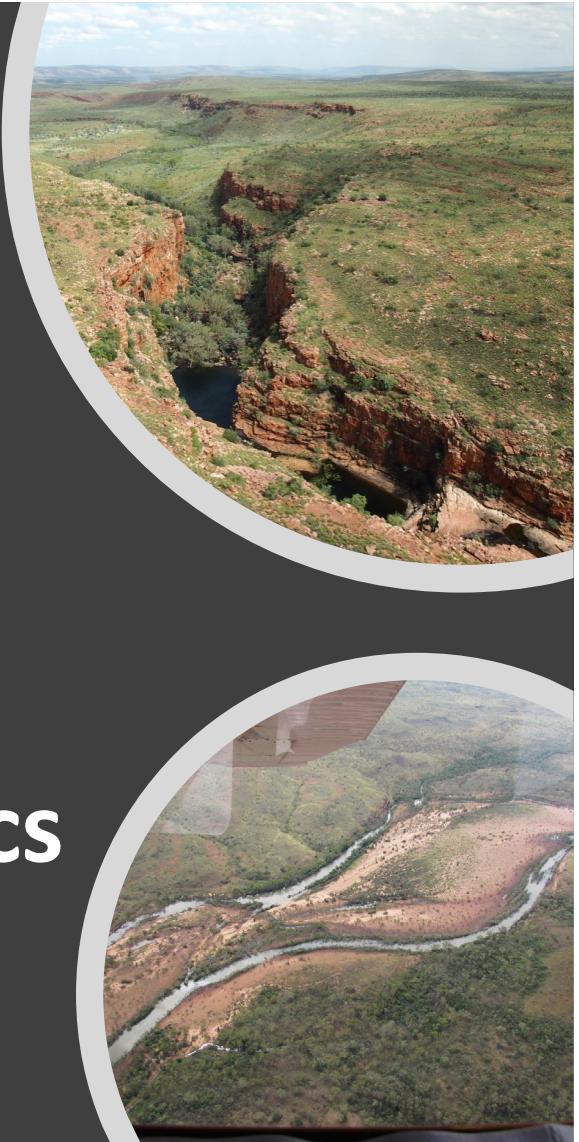
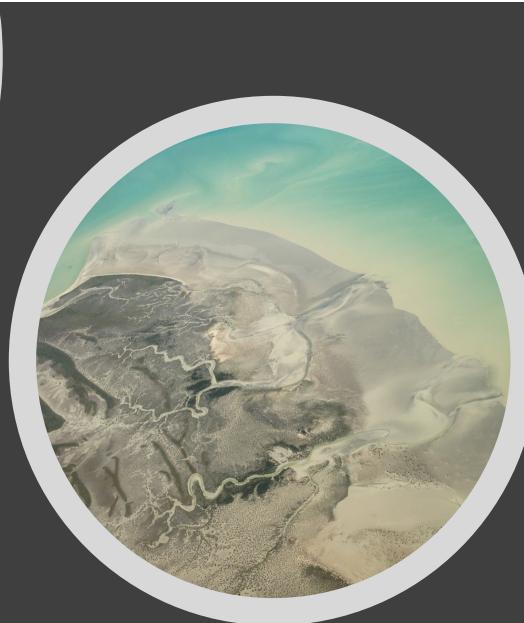
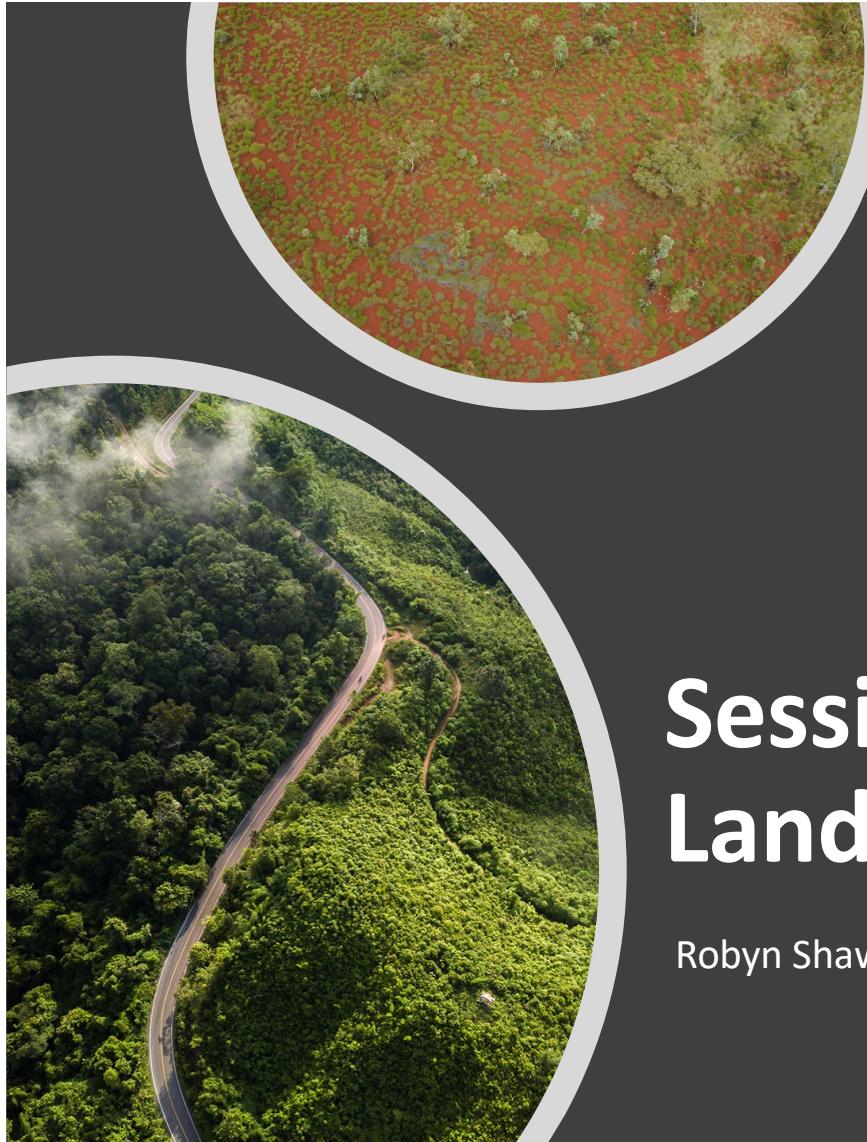
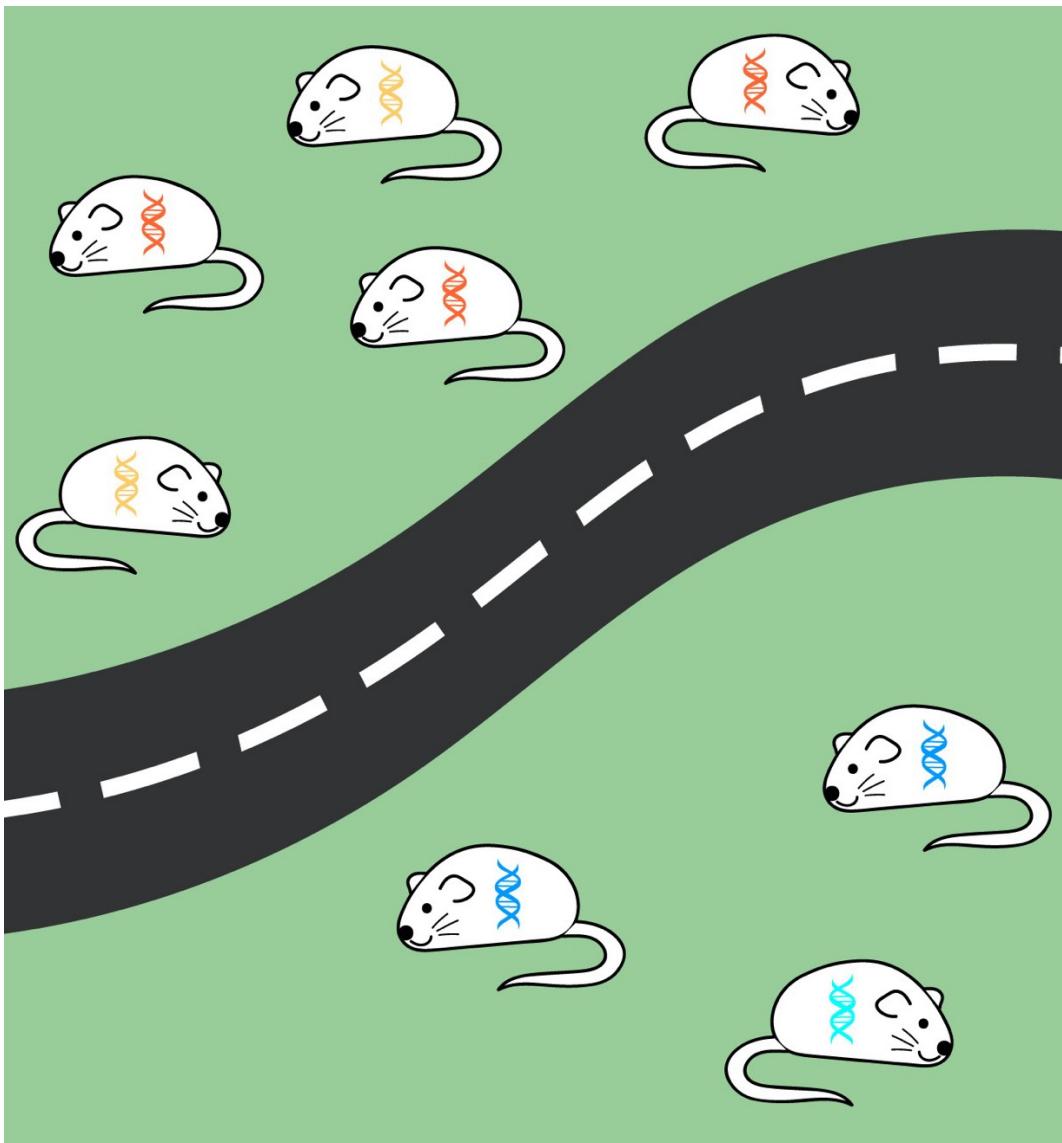


Session 8: Landscape Genetics

Robyn Shaw and Bernd Gruber



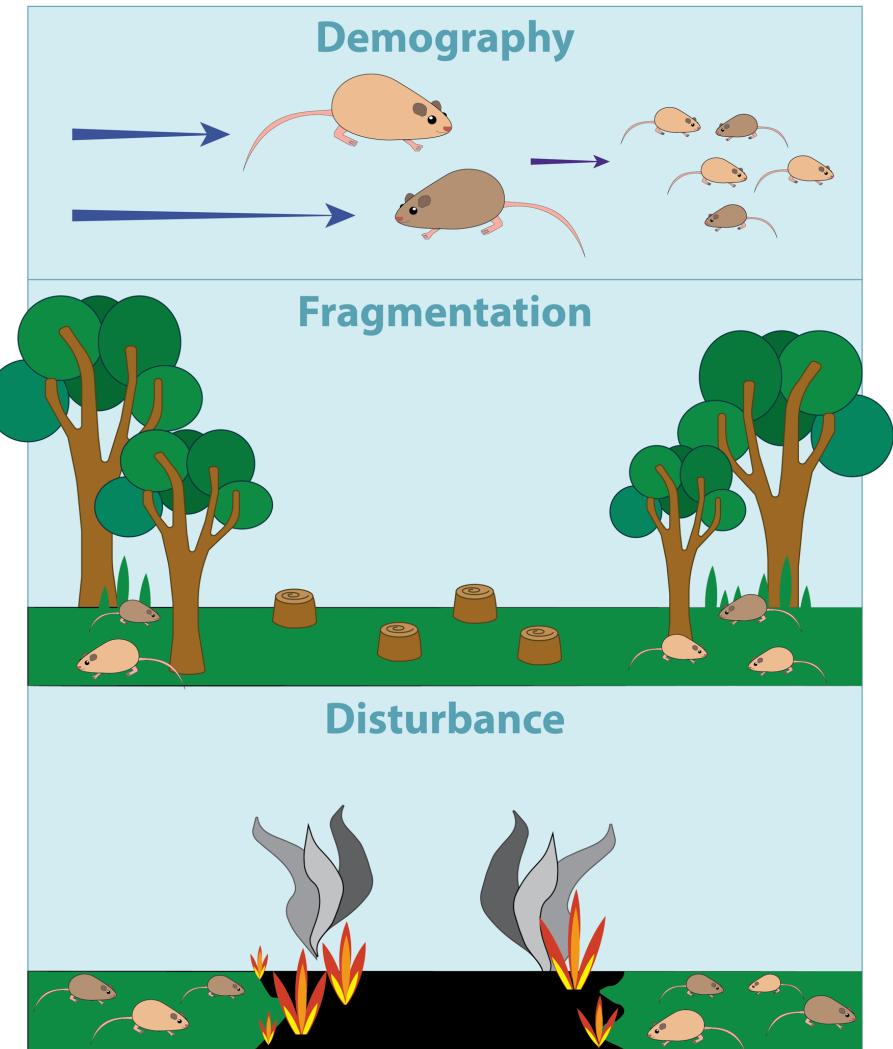


What is landscape genetics?

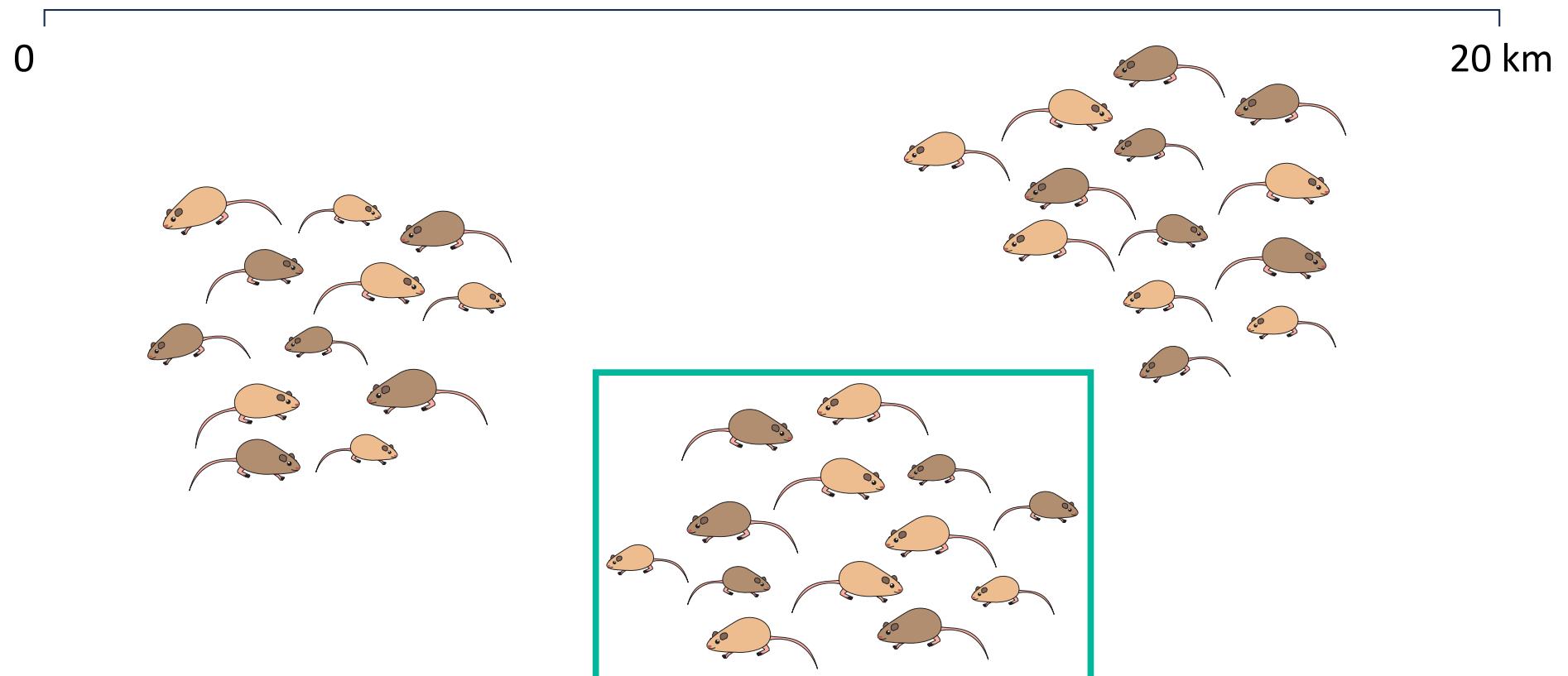
- Combines landscape ecology with population genetics
- Used to understand how landscape structure, composition and configuration influence gene flow, genetic drift, and selection
- We're going to focus on **dispersal** and **gene flow**

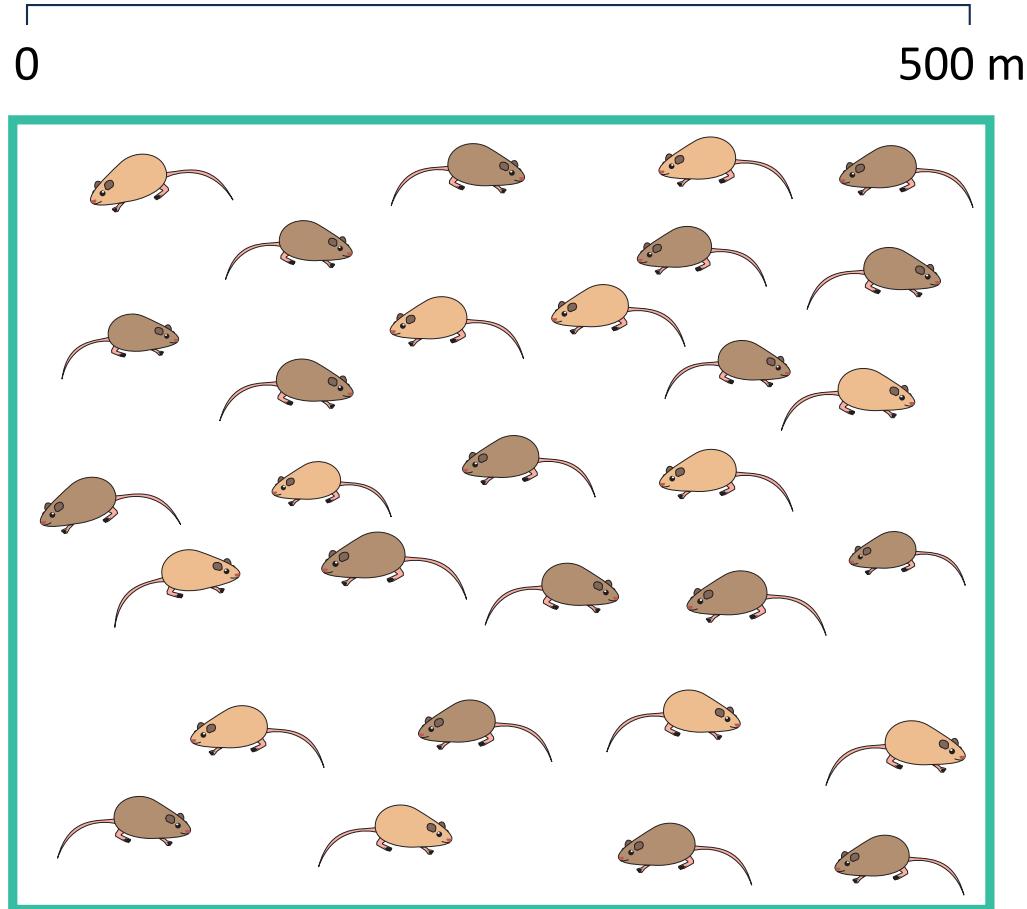
Why do we need to know about dispersal?

- Species-specific knowledge can act as a baseline to inform conservation strategies
- This can help us to determine:
 - How populations might be impacted by fragmentation or disturbance
 - Whether a population is at risk of becoming small and isolated, and losing genetic diversity through inbreeding and drift



Let's start with the basics: Individuals vs. populations



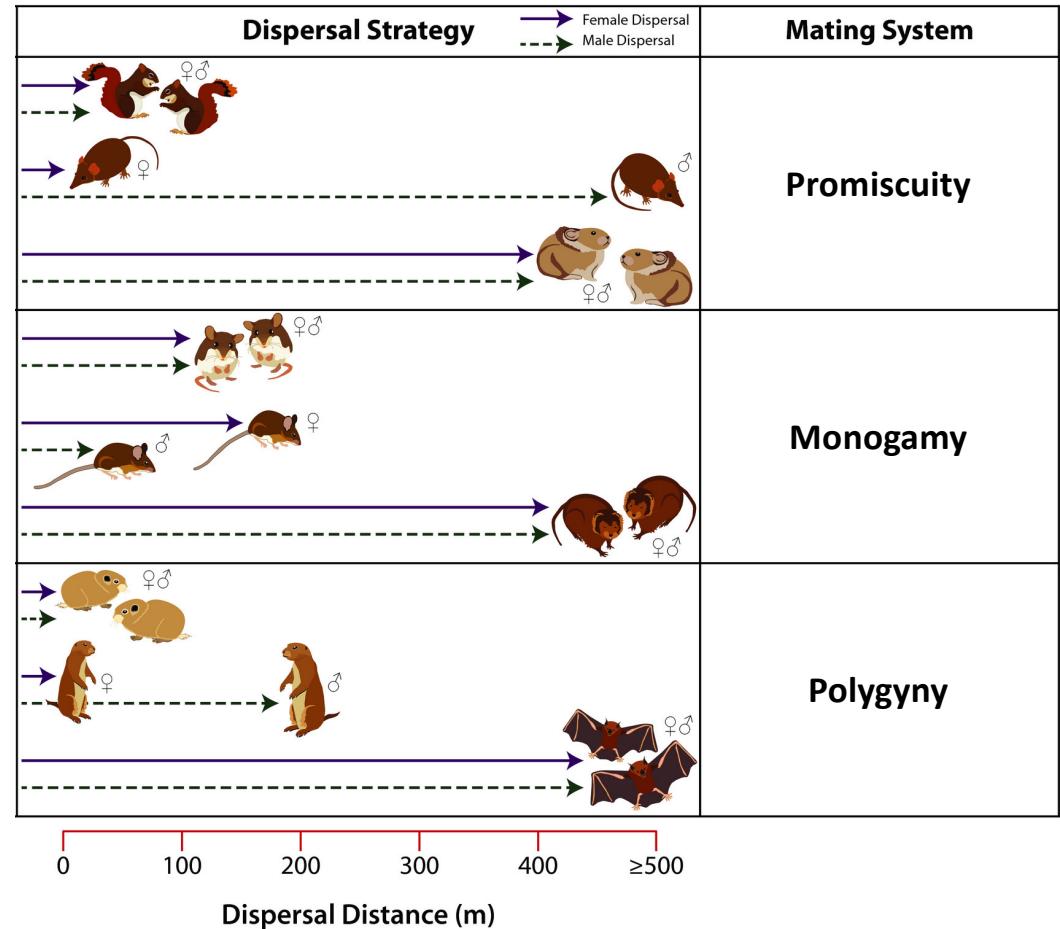


- **Demographic processes often occur within populations**
- **e.g., dispersal, mating, and social behaviours can play out over 10s-100s of metres**
- **These processes can shape patterns of fine-scale genetic structure**

Fine-scale genetic structure

- Dispersal strategies vary across species (and sometimes across populations)
- If one sex tends to disperse further than the other, we say dispersal is sex-biased
- This is reflected in patterns of fine-scale genetic structure:
 - Philopatry = genetic similarity among neighbouring individuals
 - Dispersal = neighbouring individuals are genetically dissimilar*

* Unless dispersal is unidirectional

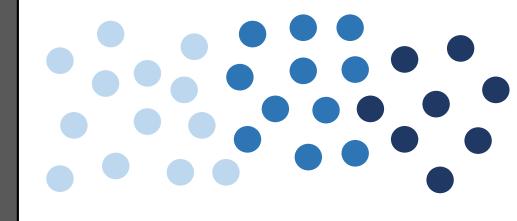


Modified figure from Shaw et al. (2018)

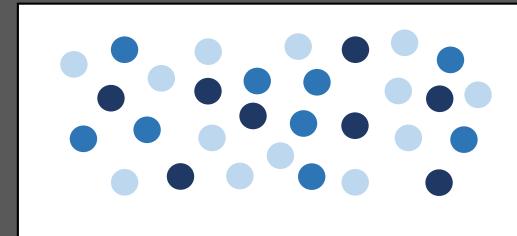
Genetic spatial autocorrelation

- Multivariate approach (combines all loci into a single analysis)
 - Calculates the autocorrelation coefficient "r" for pairs of individuals within a specified distance class
 - r is bounded by -1 (individuals are genetically dissimilar) and $+1$ (individuals are genetically similar)
 - Significant genetic spatial autocorrelation is detected when:
 - r falls outside of 95% null hypothesis confidence regions
- OR
- 95% bootstrap confidence intervals do not overlap zero

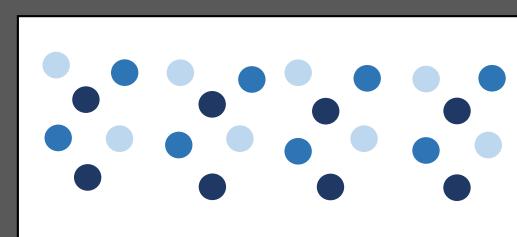
Positive spatial autocorrelation



Zero spatial autocorrelation



Negative spatial autocorrelation



REFS: Smouse & Peakall 1999; Peakall et al. 2003; Banks & Peakall 2012

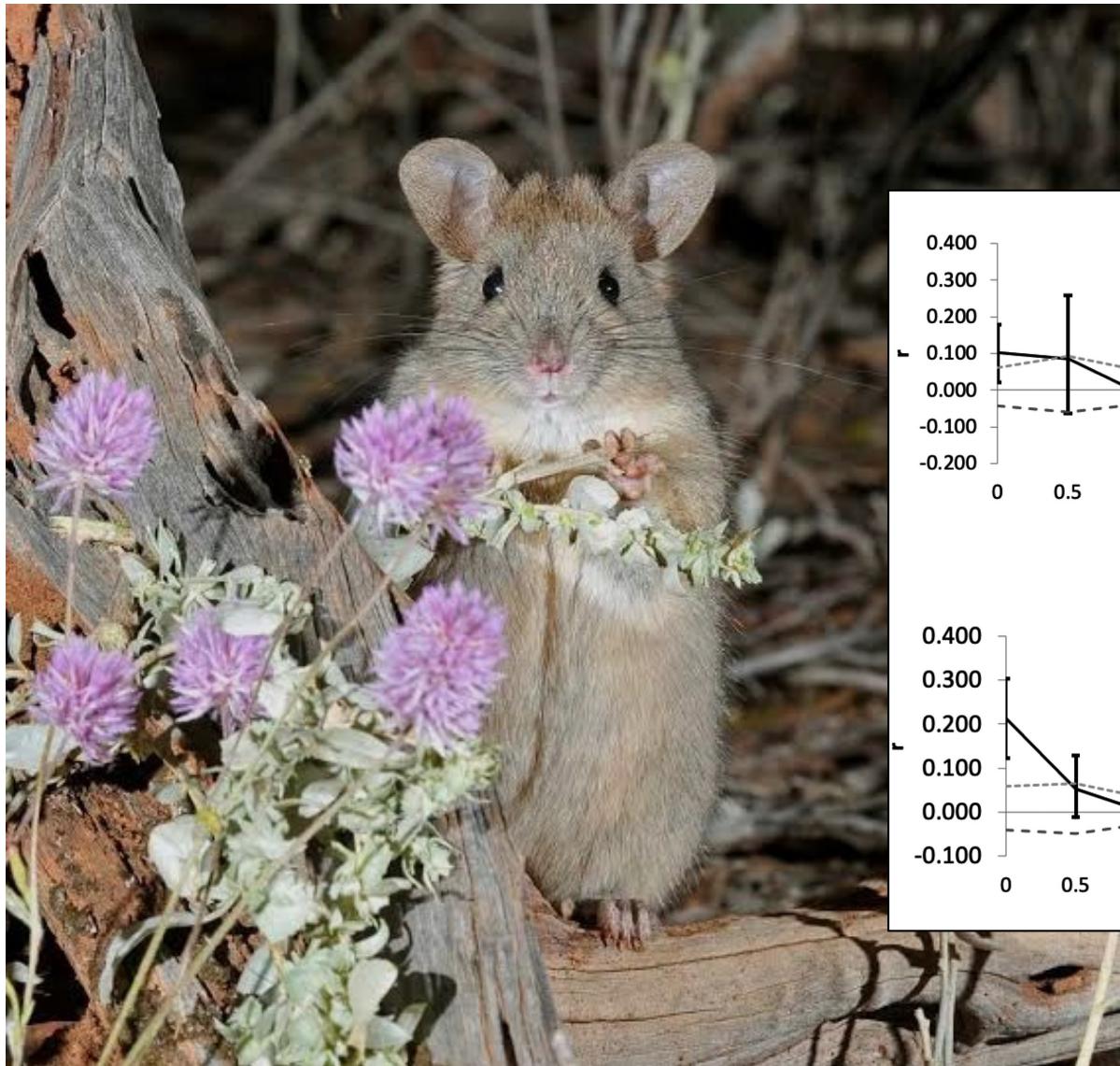


Example: Onley et al. (2022)

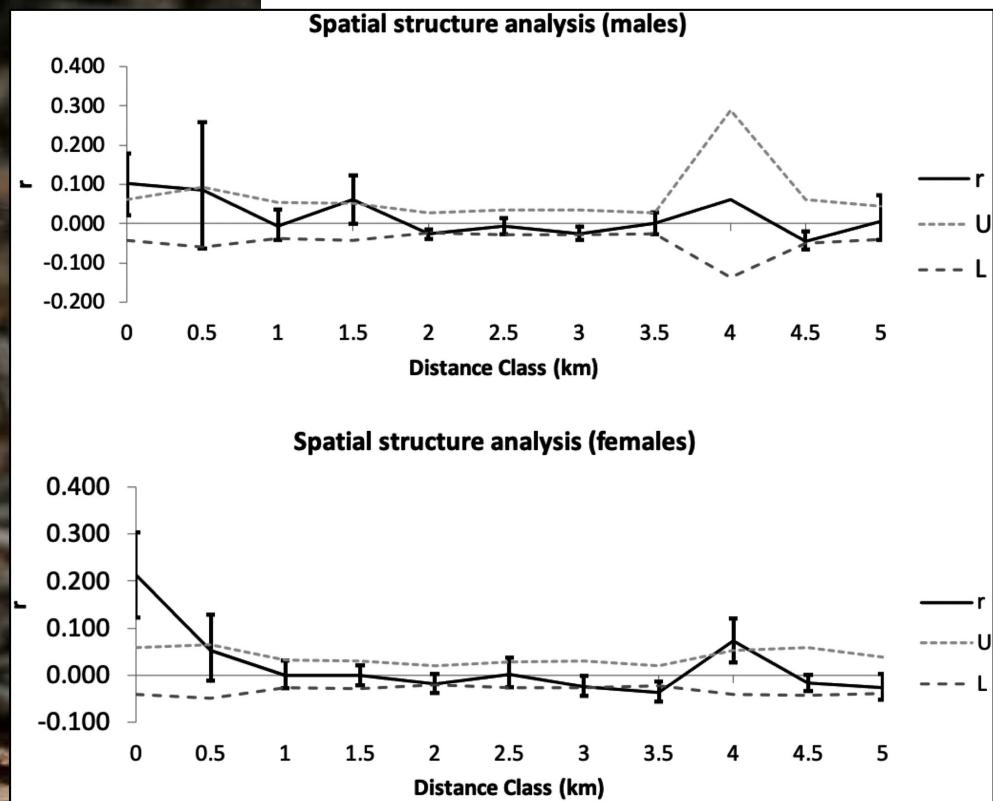
- Used spatial autocorrelation to maximise population viability in the greater stick-nest rat (*Leporillus conditor*)
- Knowledge of social structure and dispersal can inform translocation programmes
- Male-biased dispersal (1.5 km vs. 500 m in females)
- Suggest that founders should be harvested in over 1.5 km to maintain family structure, released over short distances of 300-500 m



Australian Wildlife
Conservancy



Example: Onley et al. (2022)



Australian Wildlife
Conservancy

Exercise: simulating dispersal

- There is a long history of simulations in population genetics, especially for evaluating tests for sex-biased dispersal
- Simulations are powerful – you can figure out the expected patterns under different conditions
- Gives you an indication as to whether the pattern is absent, or present but undetectable

Now you try!

Molecular Ecology (2002) 11, 1103–1114

Tests for sex-biased dispersal using bi-parentally inherited genetic markers

JÉRÔME GOUDET,^{*} NICOLAS PERRIN^{*} and PETER WASER[†]

^{*}Institute of Ecology, Biology Building, University of Lausanne, CH-1015 Lausanne, Switzerland, [†]Department of Biological Sciences, Purdue University, W. Lafayette IN 47907 USA

MOLECULAR ECOLOGY

Molecular Ecology (2012) 21, 2092–2105

doi: 10.1111/j.1365-294X.2012.05485.x

Genetic spatial autocorrelation can readily detect sex-biased dispersal

SAM C. BANKS¹ and ROD PEAKALL²

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Received: 7 November 2022 | Revised: 3 October 2023 | Accepted: 11 October 2023

DOI: 10.1111/mec.17174

ORIGINAL ARTICLE

MOLECULAR ECOLOGY WILEY

Episodic population fragmentation and gene flow reveal a trade-off between heterozygosity and allelic richness

Peta Hill¹ | Chris R. Dickman² | Russell Dinnage³ | Richard P. Duncan¹ |
Scott V. Edwards⁴ | Aaron Greenville² | Stephen D. Sarre¹ | Emily J. Stringer¹ |
Glenda M. Wardle² | Bernd Gruber¹

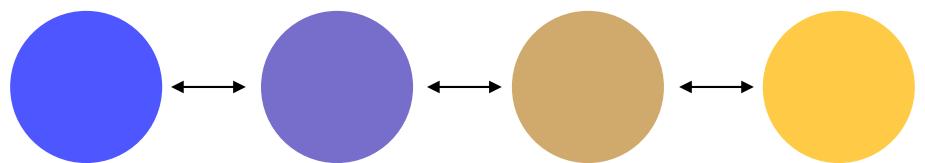


Limitations to dispersal

- Geographic distance
- Barriers
- Habitat quality/structure

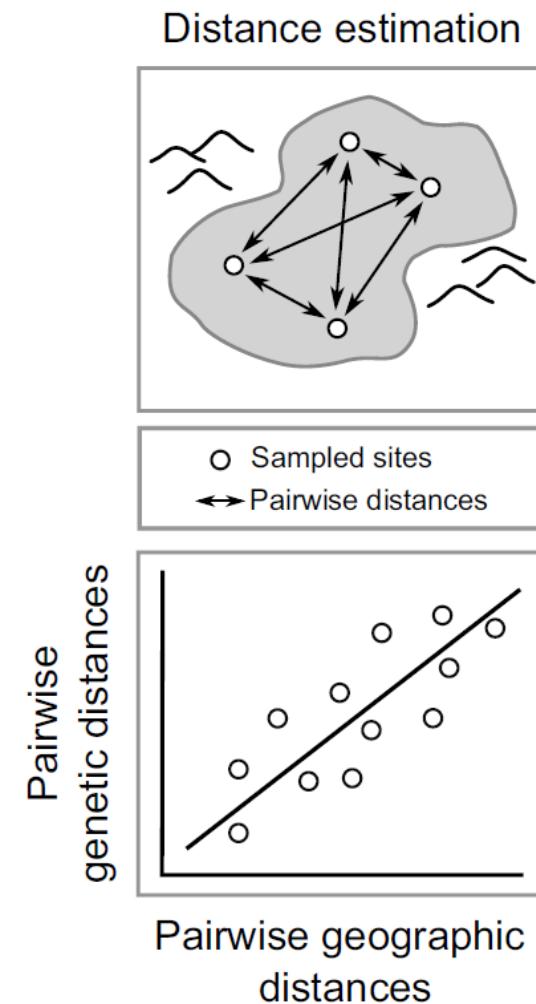
Geographic distance

- Isolation-by-distance (IBD)
- Individuals or populations that are geographically distant are less likely to share genetic material than those that are close
- Based on the "stepping-stone" model (Kimura & Weiss 1964)



Geographic distance

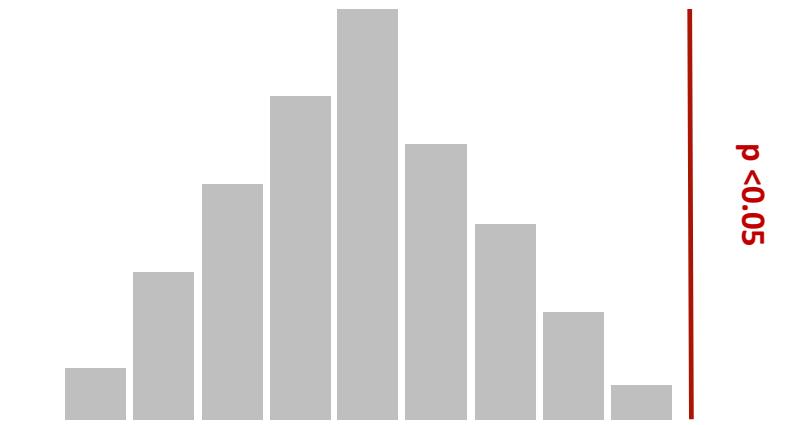
- We expect a linear relationship between geographic and genetic distance
- Distances can be calculated as:
 - Pairwise estimates of population differentiation; or
 - Individual-by-individual genetic distances



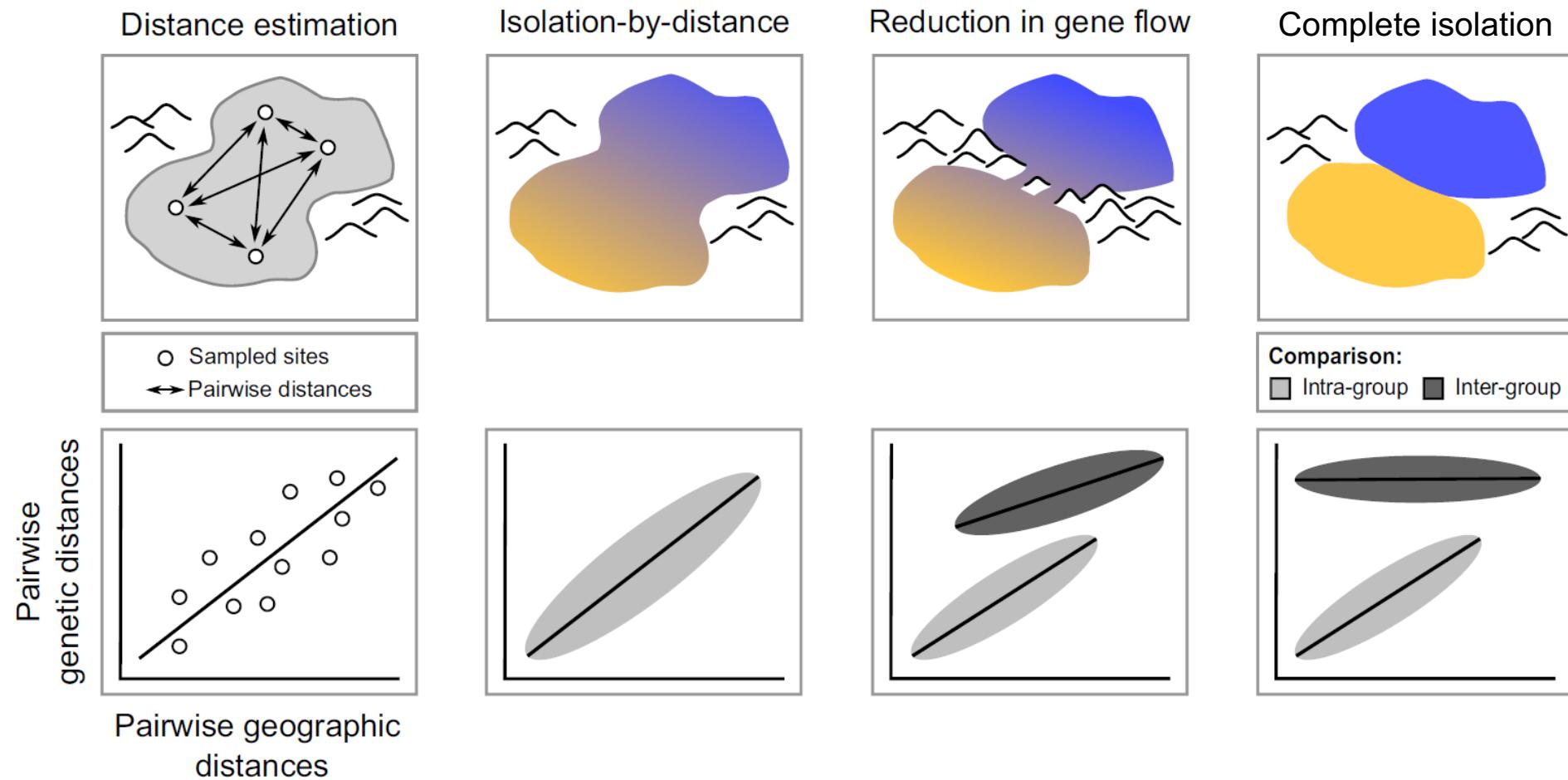
Modified figure from Prates et al. (2023)

Mantel test

- We can use Mantel tests for matrix correspondence to test for IBD (Mantel 1967)
- We can't perform a regression because pairwise data are non-independent
- Instead, we report the correlation between matrices and use permutations to test for significance



Example: Prates et al. (2023)



The Pilbara region of Western Australia



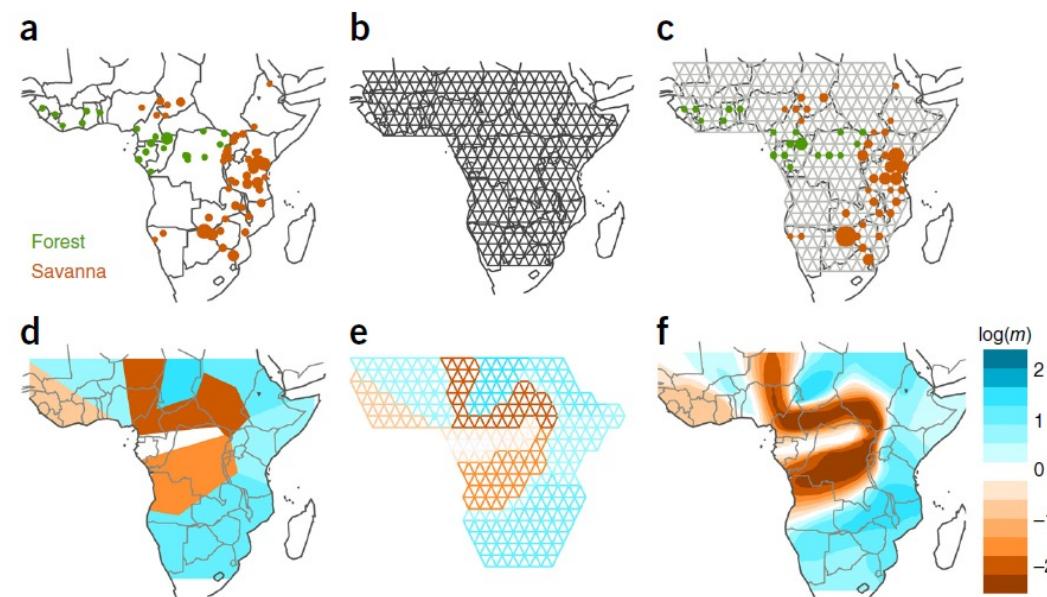
© Christian Fletcher 2017

Lesser hairy-footed dunnart (*Sminthopsis youngsonii*)



Estimated Effective Migration Surfaces (EEMS)

- Developed by Petkova et al. (2016)
- “visualize variation in effective migration across a habitat”

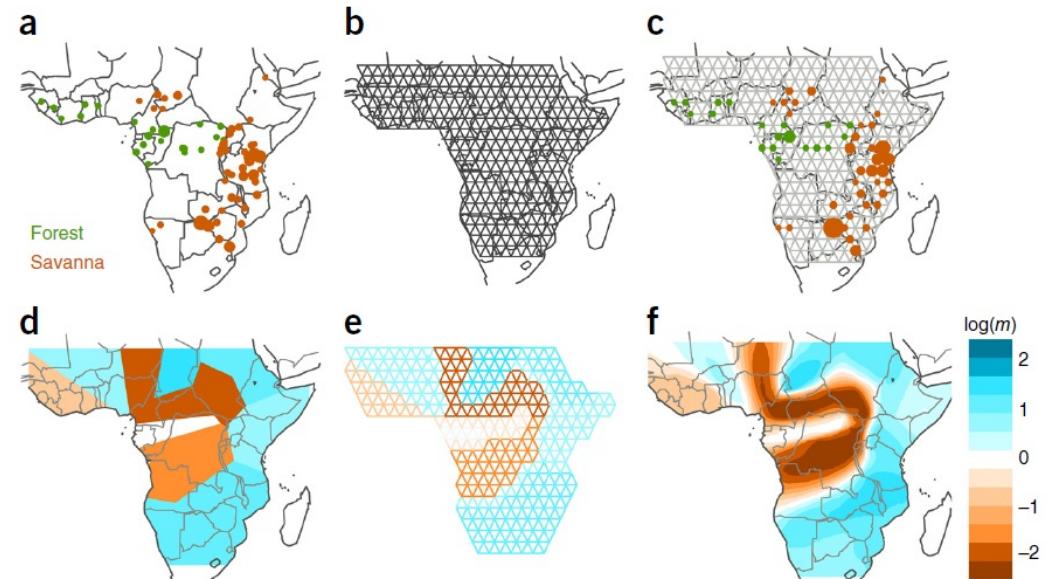


Visualizing spatial population structure with estimated effective migration surfaces

Desislava Petkova^{1,2}, John Novembre³ & Matthew Stephens^{1,3}

Estimated Effective Migration Surfaces (EEMS)

- a) genetic samples
- b) a dense triangular grid
- c) samples are assigned to demes on the grid
- d) migration rates according to a Voronoi tessellation
- e) Bayesian approach so expected dissimilarities match observed
- f) interpolation
($\log(m)=1$ is 10 higher than average m)



Estimated Effective Migration Surfaces (EEMS)

- Complements PCA

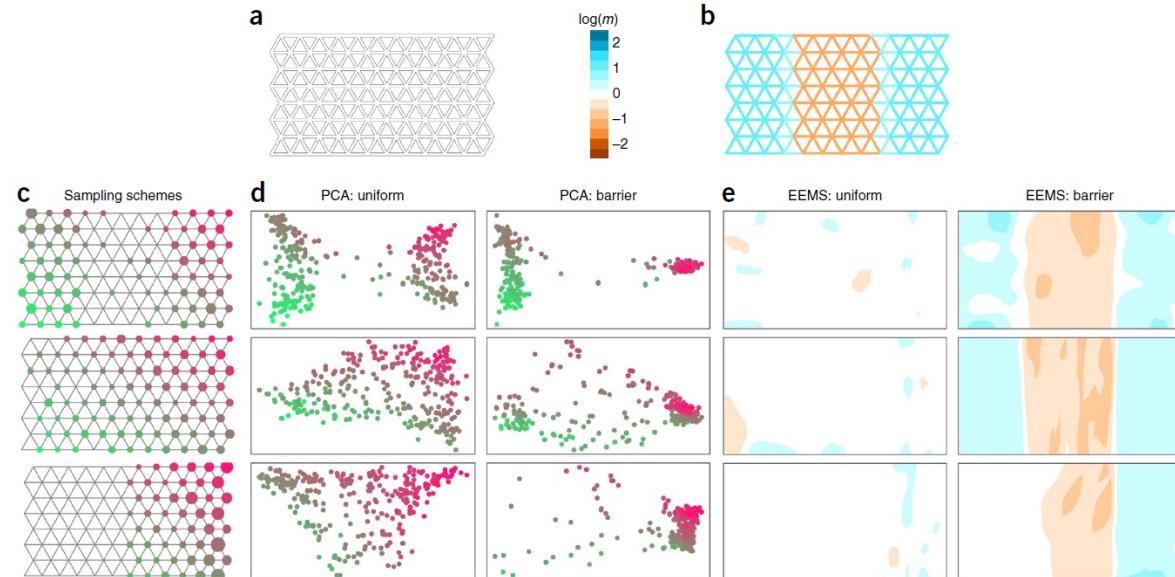


Figure 2 Simulations comparing EEMS and PCA. For each method, we show results for two migration scenarios—representing uniform migration and a barrier to migration—and three different sampling schemes. (a,b) The true underlying migration rates for the uniform (a) and barrier (b) scenarios; colors represent relative migration rates. (c) The three sampling schemes used; the size of the circle at each node is proportional to the number of individuals sampled at that location, and locations are color-coded to facilitate cross-referencing the EEMS and PCA results. (d) PCA results. (e) EEMS results. In contrast to PCA, EEMS is robust to sampling scheme and shows clear qualitative differences between the estimated effective migration rates under the two scenarios, reflecting the underlying simulation truth.

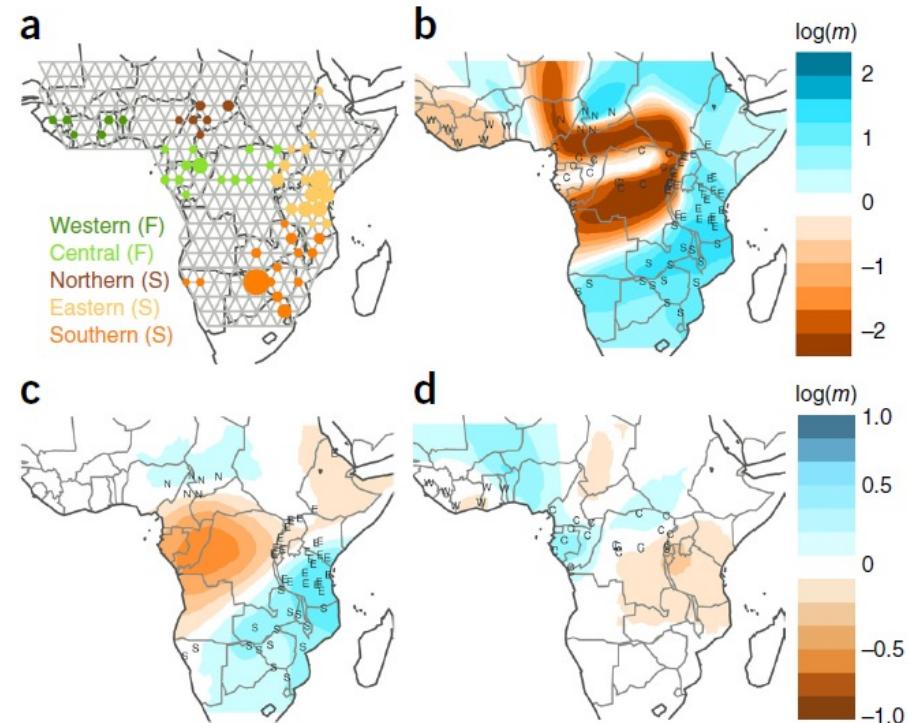
Estimated Effective Migration Surfaces (EEMS)

- Complements PCA

Figure 4 EEMS analysis of African elephant data. (a) African elephant samples are collected from two species in five biogeographic regions: the forest elephant (in green) inhabits the western and central regions, and the savanna elephant (in orange) inhabits the northern, eastern and southern regions. (b) Estimated effective migration rates for forest and savanna samples analyzed jointly. (c,d) Estimated effective migration rates for savanna (c) and forest (d) samples analyzed separately.

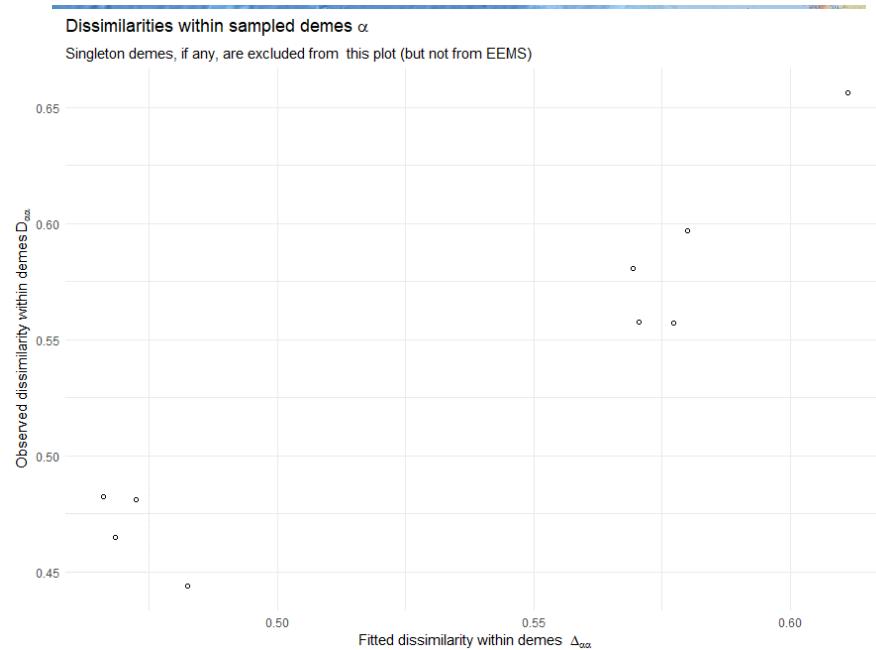
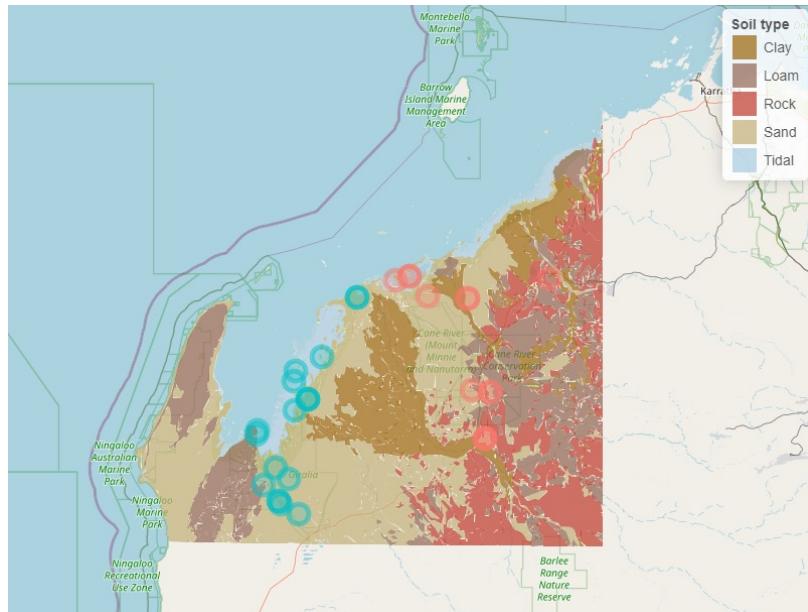
Visualizing spatial population structure with estimated effective migration surfaces

Desislava Petkova^{1,2}, John Novembre³ & Matthew Stephens^{1,3}



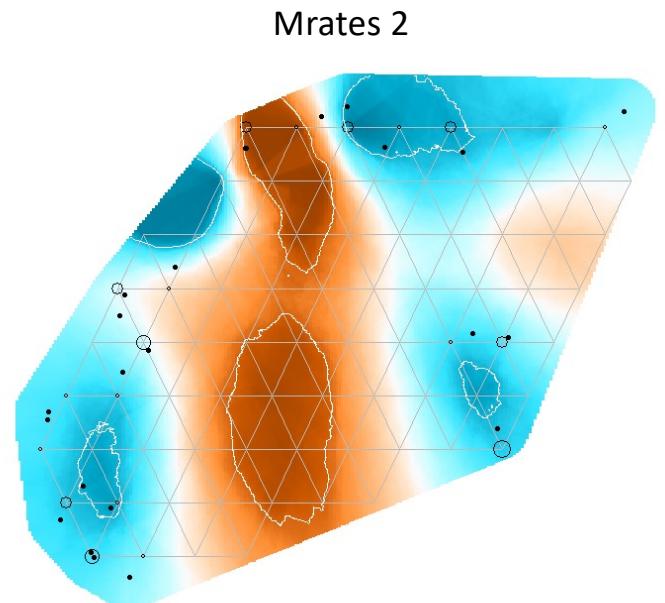
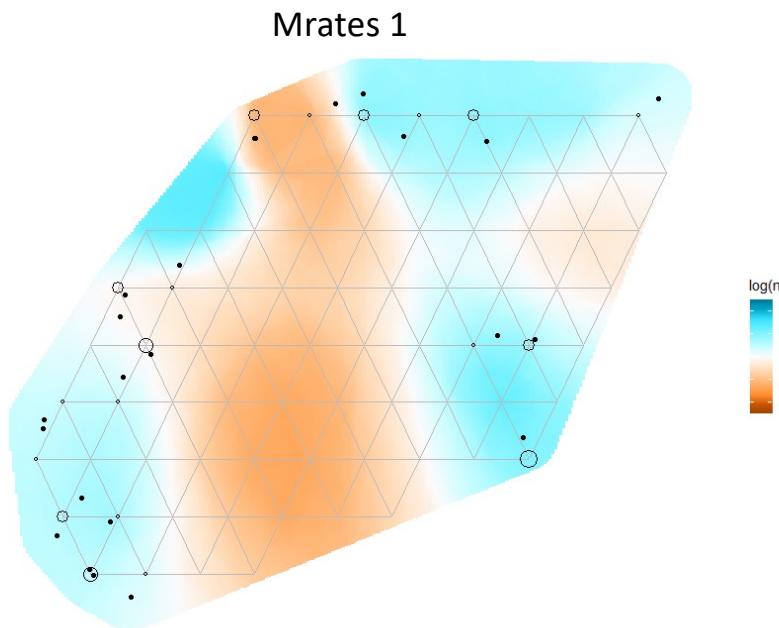
Example: Lesser hairy-footed dunnart

- The output of EEMS is a series of 8 plots.
- Once you ran the example we will discuss the output



Example: Lesser hairy-footed dunnart

- Migration surfaces

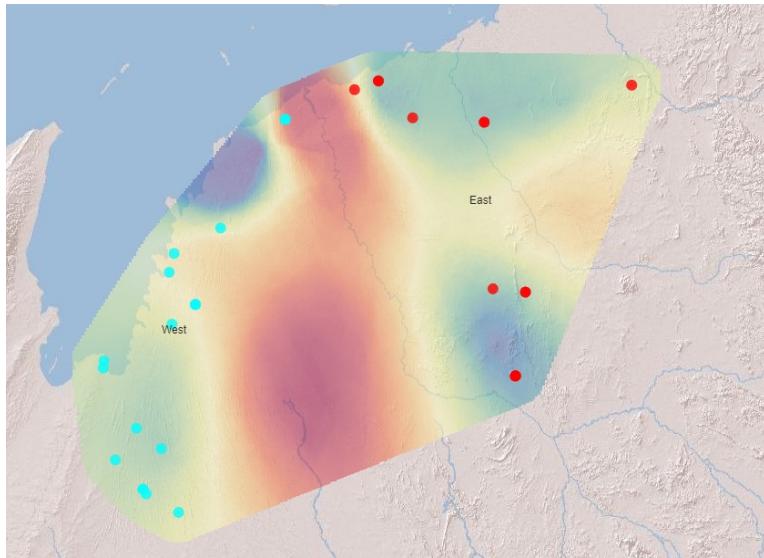


Example: Lesser hairy-footed dunnart

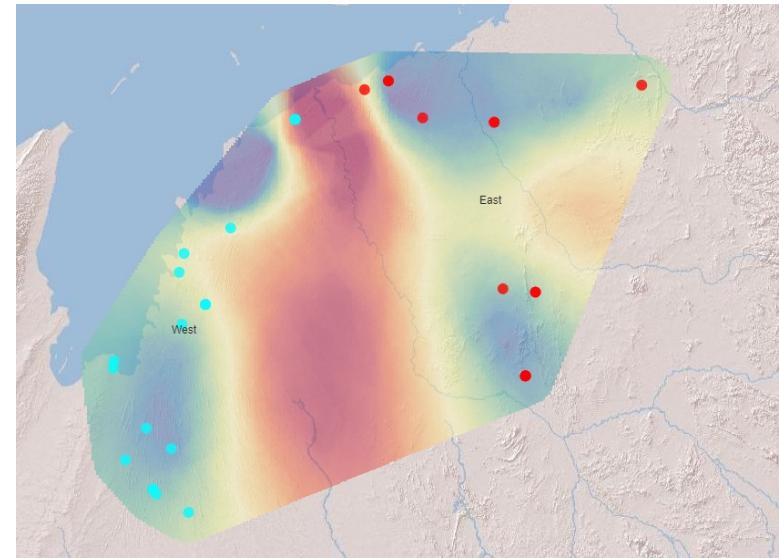


- Migration surfaces

Mrates 1



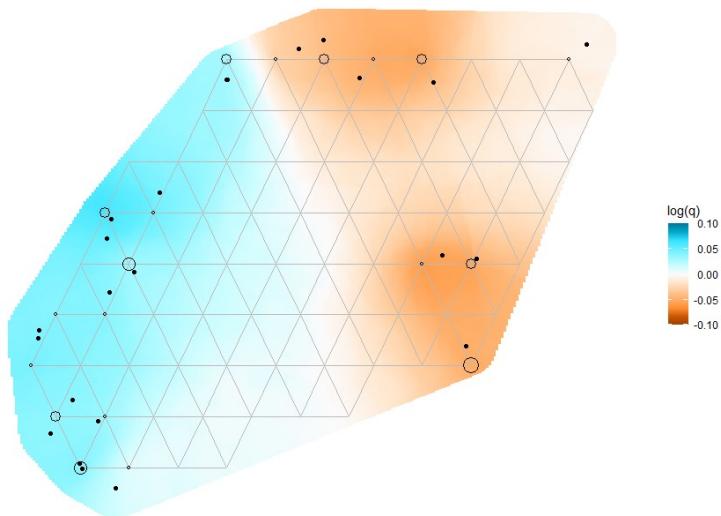
Mrates 2



Example: Lesser hairy-footed dunnart

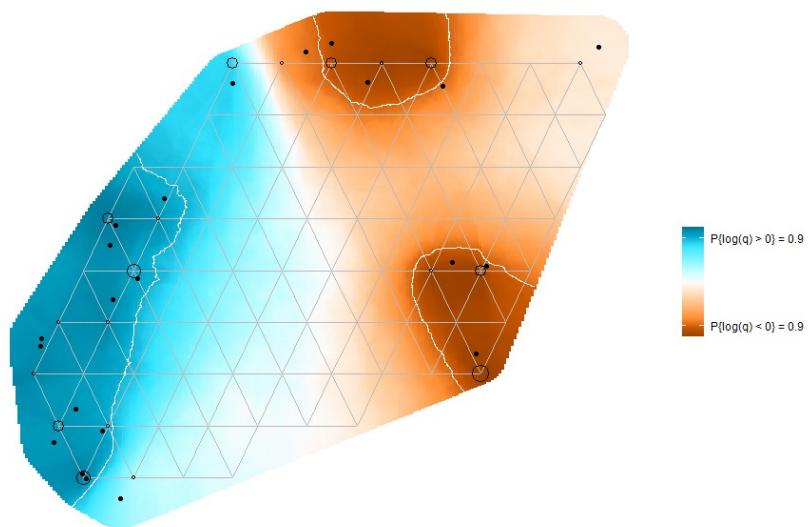


qrates 1



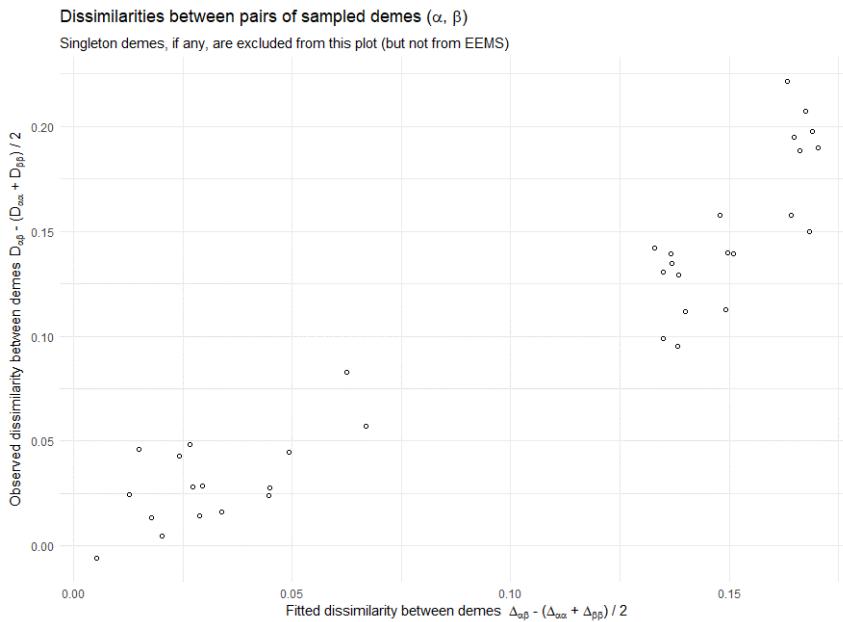
- Effective diversity surface

qrates 2



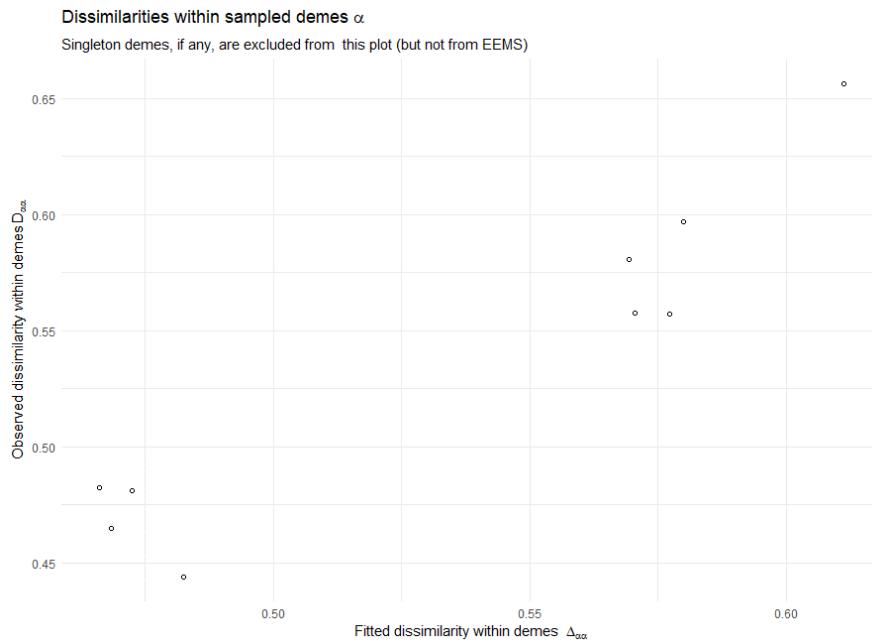
Example: Lesser hairy-footed dunnart

Between pairs of deemes



- Observed vs fitted

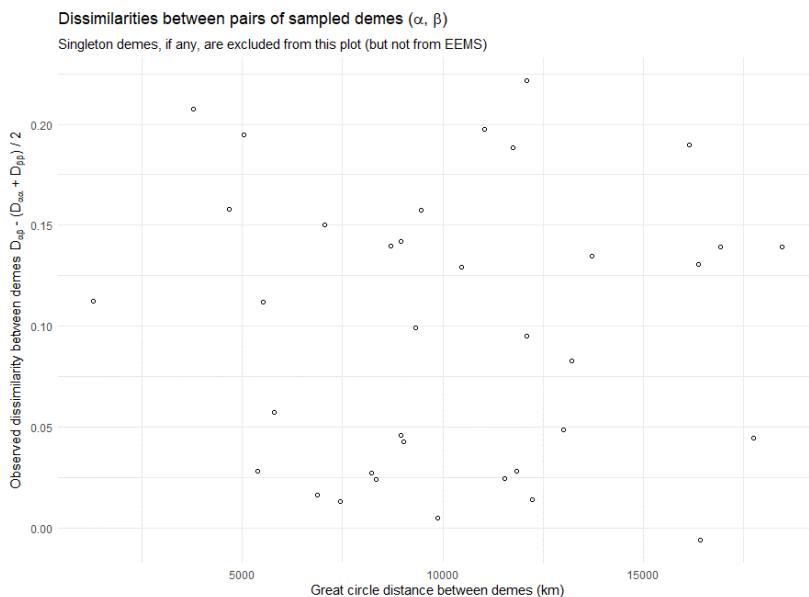
Within pairs of deemes



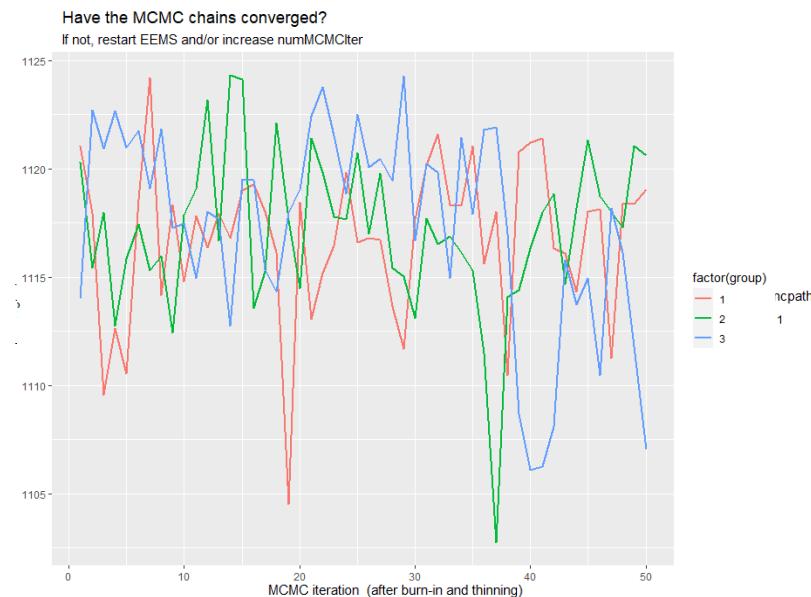
Example: Lesser hairy-footed dunnart

██████████

Dissimilarity by distance



Posterior trace





Overview

- What is a landscape genetic analysis based on resistance layers and how does it work?



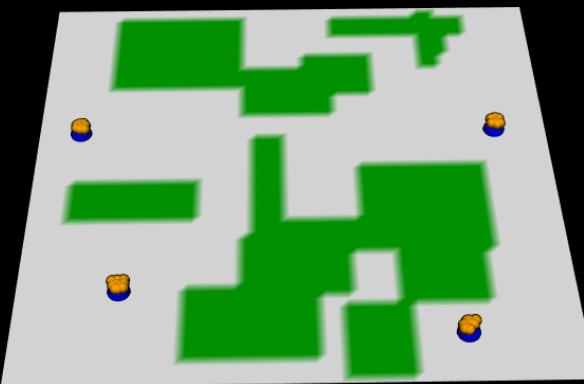
How does the approach work?

● populations



How does the approach work?

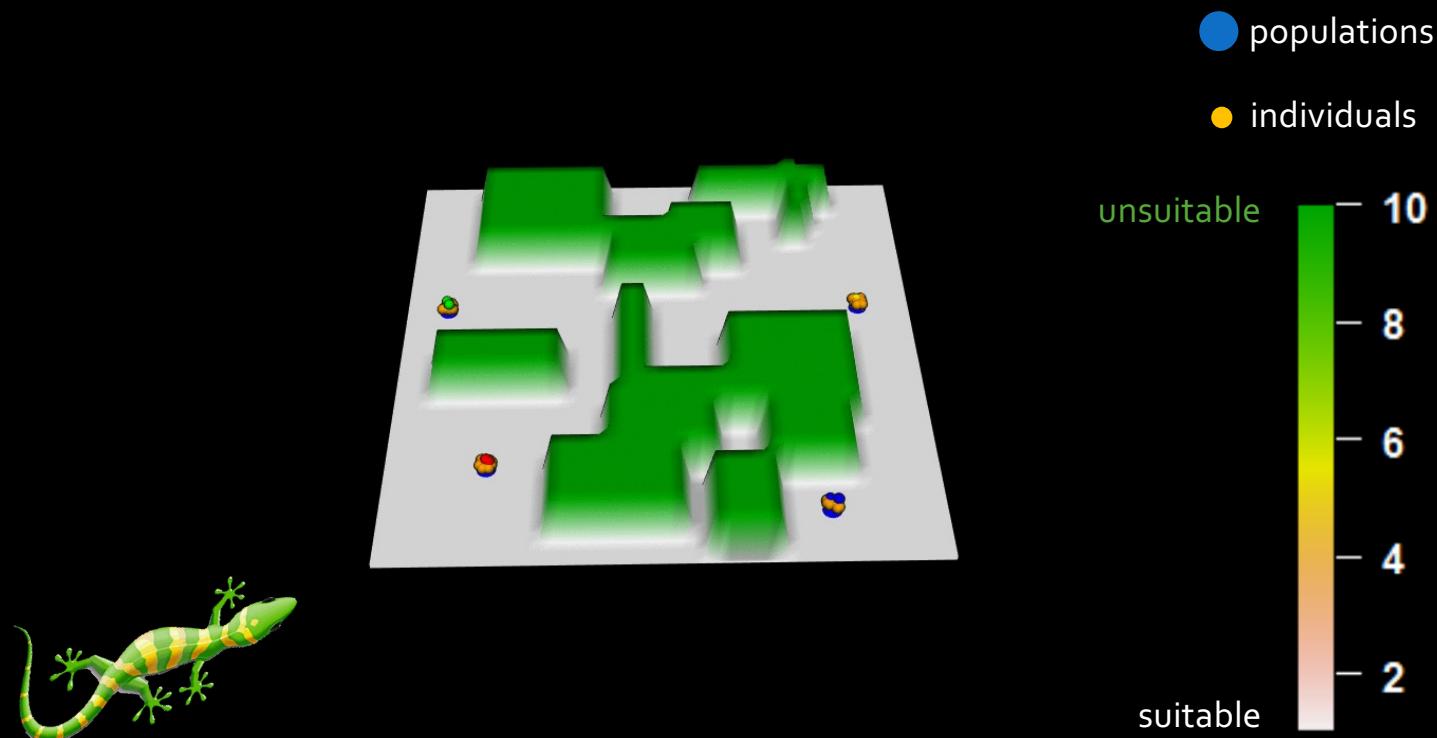
- populations
- individuals



How does the approach work?

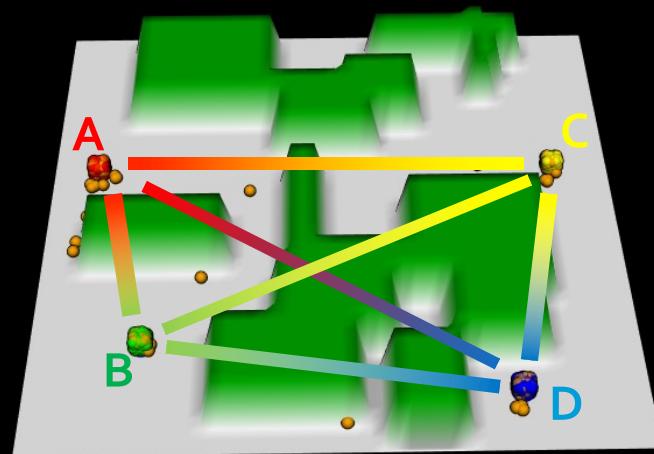


How does the approach work?



How does the approach work?

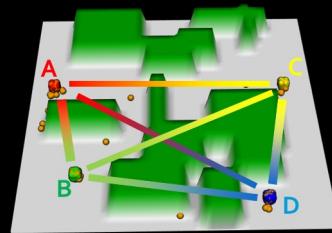
Pairwise Genetic Distances



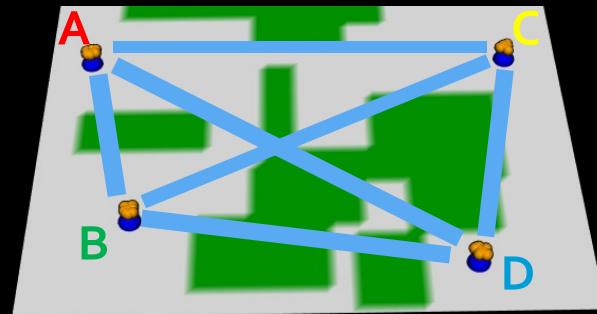
$G =$

	A	B	C	D
A	-	-	-	-
B	10	-	-	-
C	20	12	-	-
D	14	16	13	-

How does the approach work?


$$G =$$

	A	B	C	D
A	-	-	-	-
B	10	-	-	-
C	20	12	-	-
D	14	16	13	-



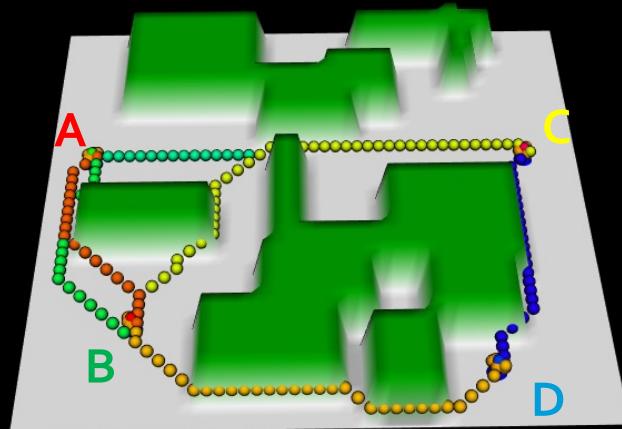
Pairwise Euclidean Distances

$E =$

	A	B	C	D
A	-	-	-	-
B	10	-	-	-
C	20	24	-	-
D	24	16	13	-

How does the approach work?

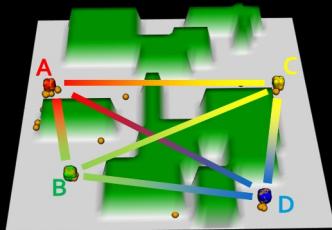
Pairwise Cost Distances



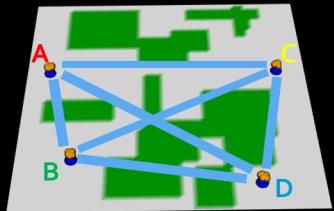
$C =$

A	B	C	D
B	15	-	-
C	12	6	-
D	8	9	13

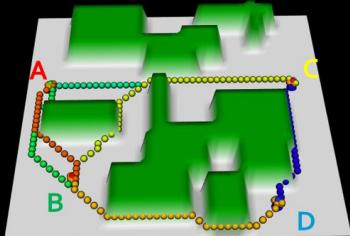
How does the approach work?



$$G = \begin{array}{c} \begin{matrix} & \text{A} & \text{B} & \text{C} & \text{D} \\ \text{A} & - & - & - & - \\ \text{B} & 10 & - & - & - \\ \text{C} & 20 & 12 & - & - \\ \text{D} & 14 & 16 & 13 & - \end{matrix} \end{array}$$



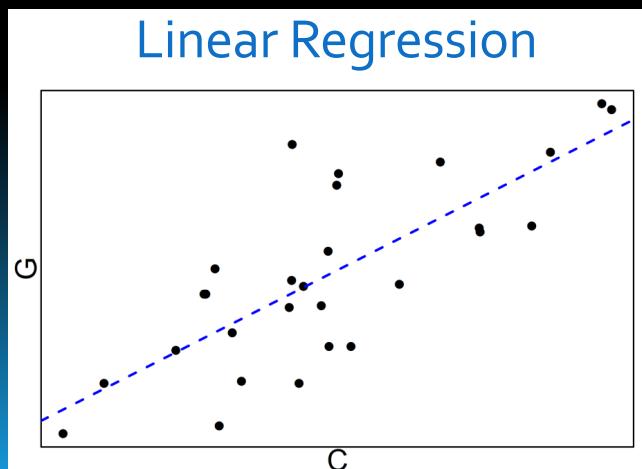
$$E = \begin{array}{c} \begin{matrix} & \text{A} & \text{B} & \text{C} & \text{D} \\ \text{A} & - & - & - & - \\ \text{B} & 10 & - & - & - \\ \text{C} & 20 & 12 & - & - \\ \text{D} & 14 & 16 & 13 & - \end{matrix} \end{array}$$



$$C = \begin{array}{c} \begin{matrix} & \text{A} & \text{B} & \text{C} & \text{D} \\ \text{A} & - & - & - & - \\ \text{B} & 10 & - & - & - \\ \text{C} & 20 & 12 & - & - \\ \text{D} & 14 & 16 & 13 & - \end{matrix} \end{array}$$

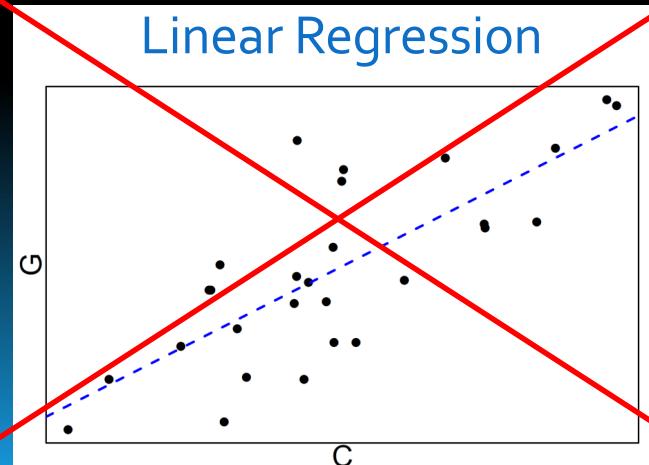
How does the approach work?

- Three pairwise distance matrices
 - G : Genetic Distance matrix
 - E : Euklidean Distance matrix
 - C : Least-Cost Path Distance Matrix
- Is there a correlation between $G \sim C$ (but not $G \sim E$) ??



How does the approach work?

- Three pairwise distance matrices
 - G : Genetic Distance matrix
 - E : Euclidean Distance matrix
 - C : Least-Cost Path Distance Matrix
- Is there a correlation between $G \sim C$ (but not $G \sim E$) ??

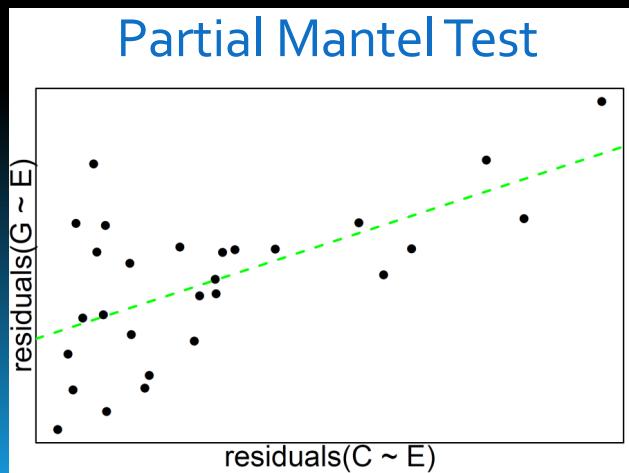


Not Good for two reasons:

- we ignore non independence
- we need to correct for E

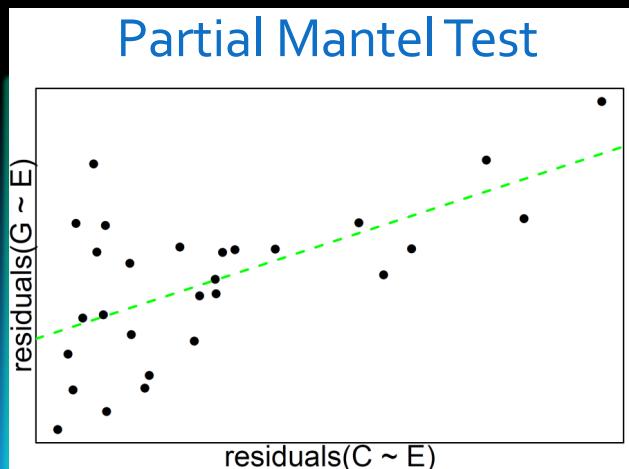
How does a landscape genetic approach work?

- Three pairwise distance matrices
 - G: Genetic Distance matrix
 - E: Euklidean Distance matrix
 - C: Least-Cost Path Distance Matrix
- Is there a correlation between $\text{resid}(G \sim E) \sim \text{resid}(C \sim E)$?



How does a landscape genetic approach work?

- Three pairwise distance matrices
 - G: Genetic Distance matrix
 - E: Euklidean Distance matrix
 - C: Least-Cost Path Distance Matrix
- Is there a correlation between $\text{resid}(G \sim E) \sim \text{resid}(C \sim E)$?



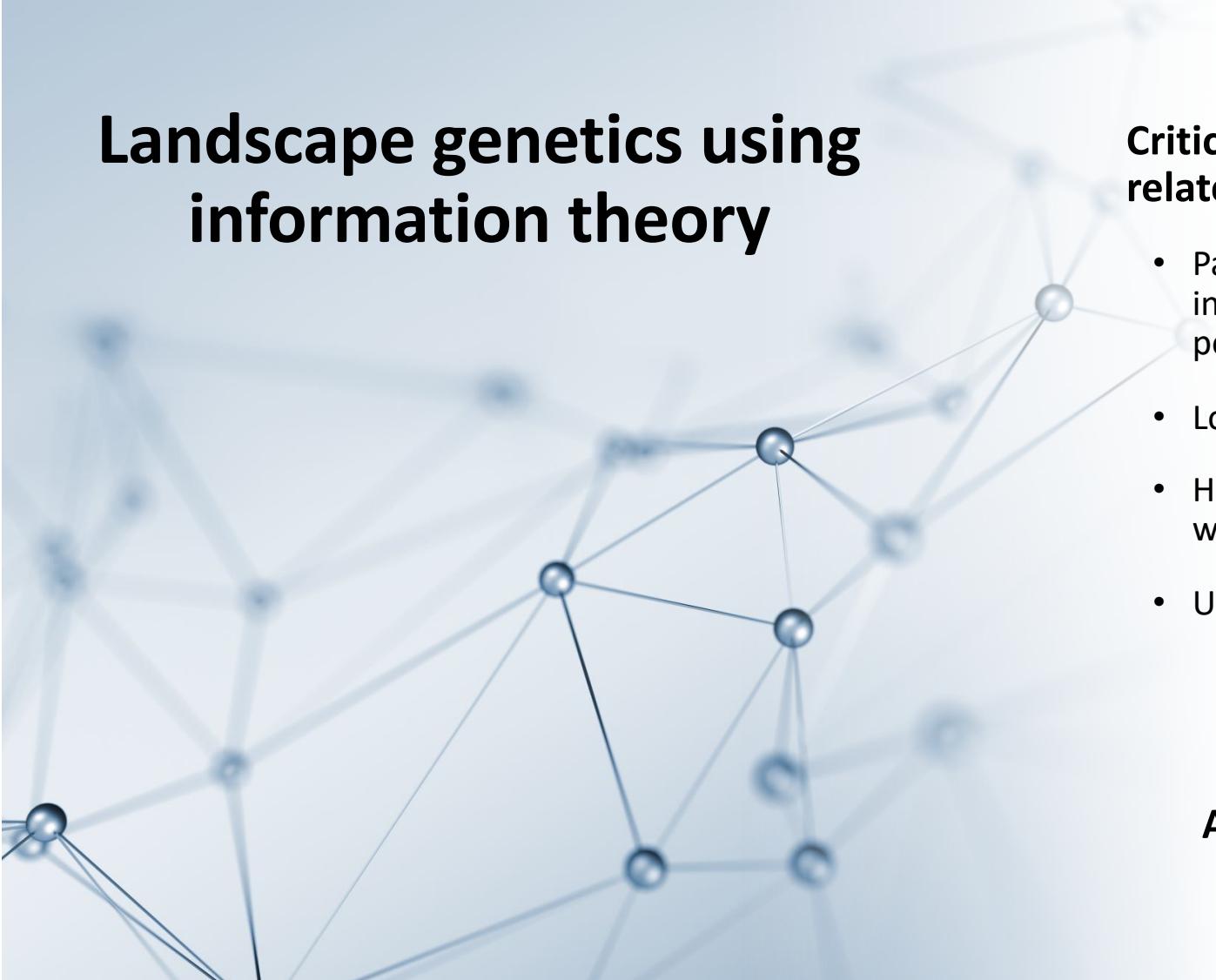
Good for two reasons:

- we treat non independence using a bootstrap approach
- we correct for E

How does a landscape genetic approach work?

- Three pairwise distance matrices
 - G: Genetic Distance matrix
 - E: Euclidean Distance matrix
 - C: Least-Cost Path Distance Matrix
- Approaches used to study the relationship:
 - (partial) mantel tests [Wasserman et al.]
 - MMRR (multiple matrix regression with randomisation) [Legendre et al., Wang]
 - Regression commonality analyses [Prunier et al.]
 - Generalised dissimilarity [Ferrier et al., Fitzpatrick & Kellner]
 - Bayesian approach [Sunder et al.]

Landscape genetics using information theory



Criticisms about Mantel tests and related methods:

- Pairwise data are not independent (can be corrected with permutation testing)
- Low statistical power
- Have inflated type 1 error rates when spatial autocorrelation present
- Usually one parameter at a time

Alternative approach: MLPE

Landscape genetics using information theory

MLPE:

- Maximum-likelihood population-effects mixed models (Clarke et al. 2002, Van Strien et al. 2012)
- "Mixed" because it includes both fixed effects (genetic/landscape distance) + random effects to account for pairwise data
- Spatial autocorrelation can be included in MLPE
- Can test different predictors and compare them using model selection

Important note:

- Recommendation: get parameter estimates using REML, get AIC or BIC using maximum likelihood

Best approach

- Identify a small, testable and ecologically plausible set of hypotheses
- Landscapes characteristics are often correlated – avoid including correlated variables in models
- Use model selection (i.e. ranks and weights) to make inferences about the likelihood of each model being true

And one more thing...

- Can combine and optimise to create a single resistance surface:

Received: 27 October 2017 | Accepted: 1 February 2018
DOI: 10.1111/2041-210X.12984

APPLICATION

ResistanceGA: An R package for the optimization of resistance surfaces using genetic algorithms

William E. Peterman

Methods in Ecology and Evolution  BRITISH ECOLOGICAL SOCIETY



Foxes, 3000 individuals, 29 microsatellites

