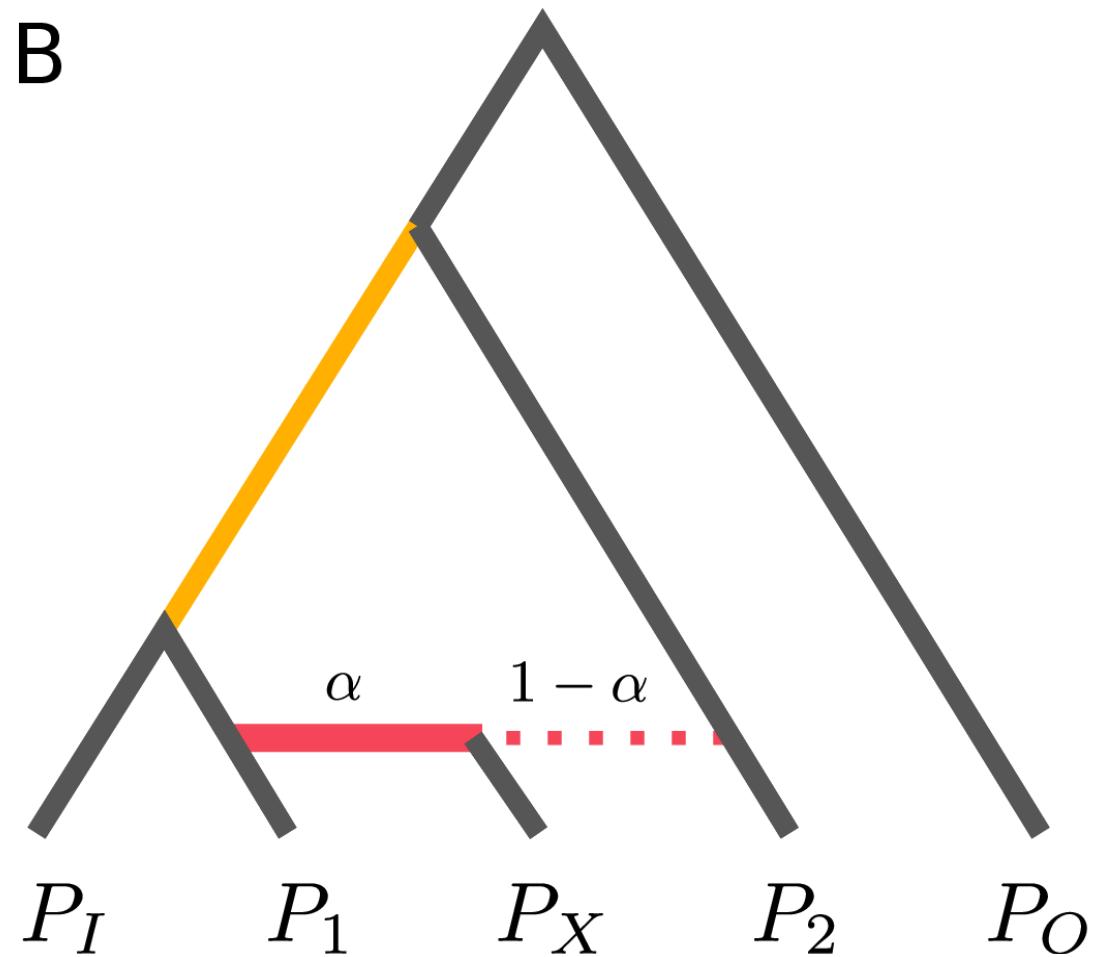
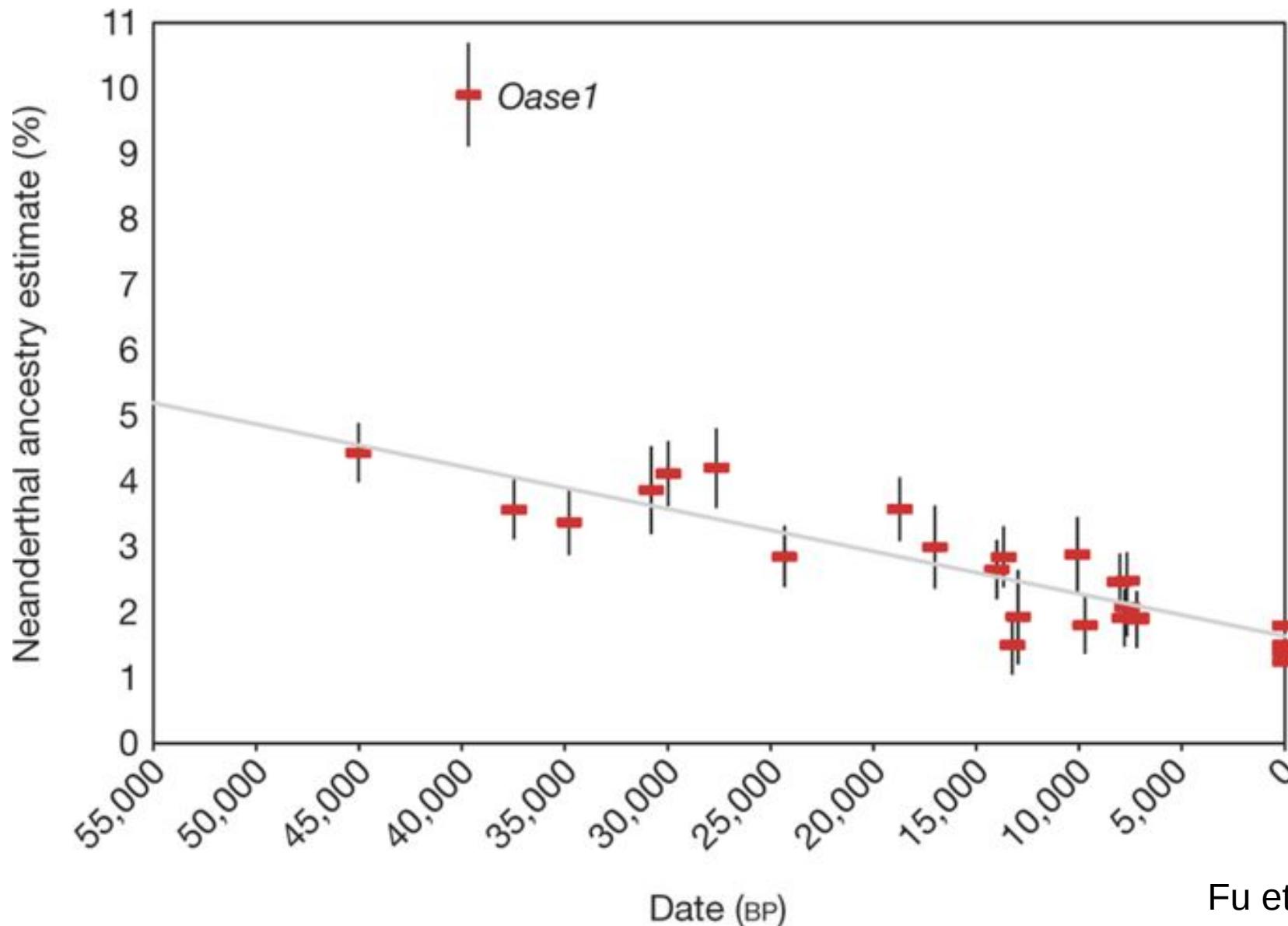


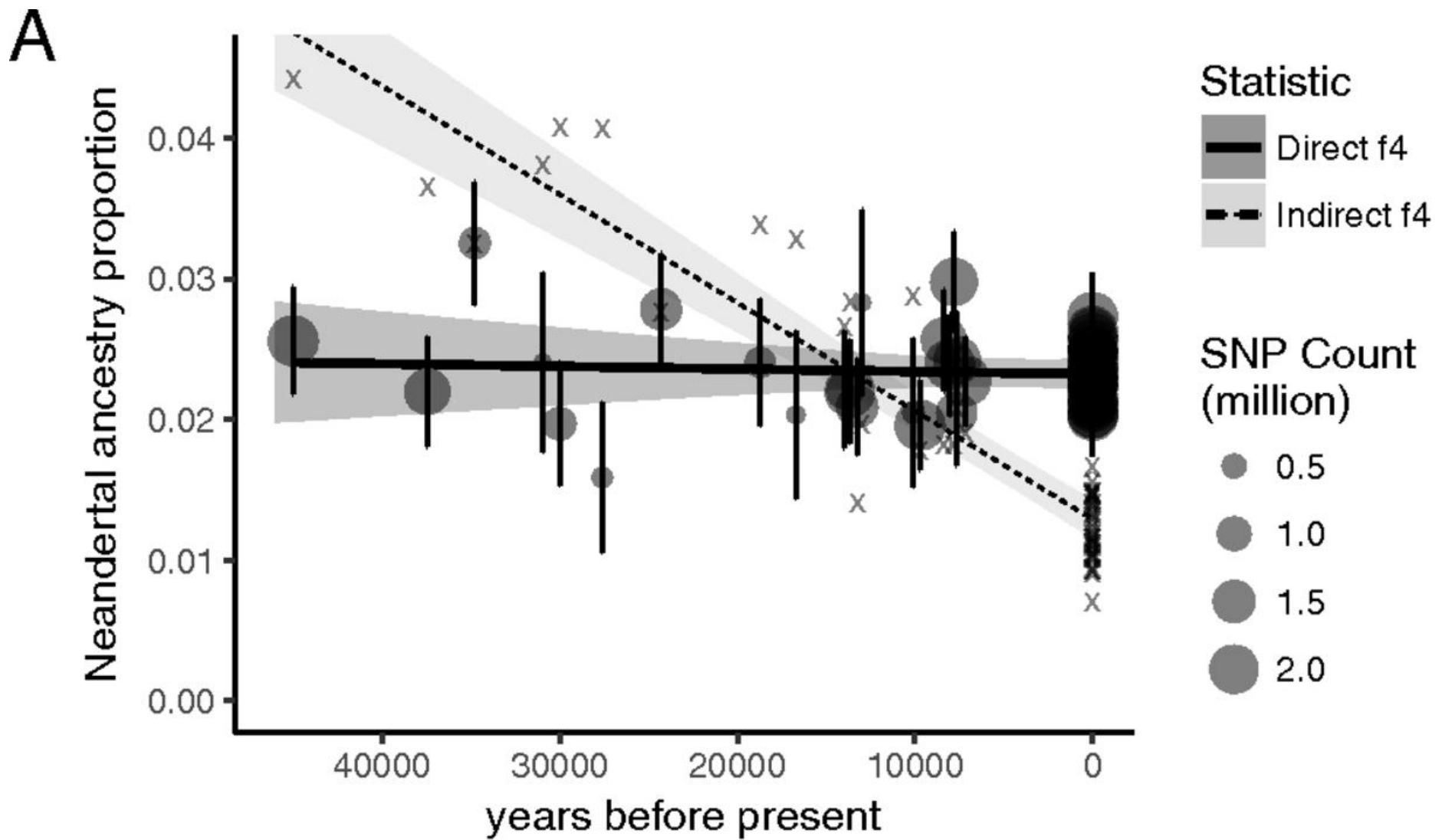
# F4-ratio

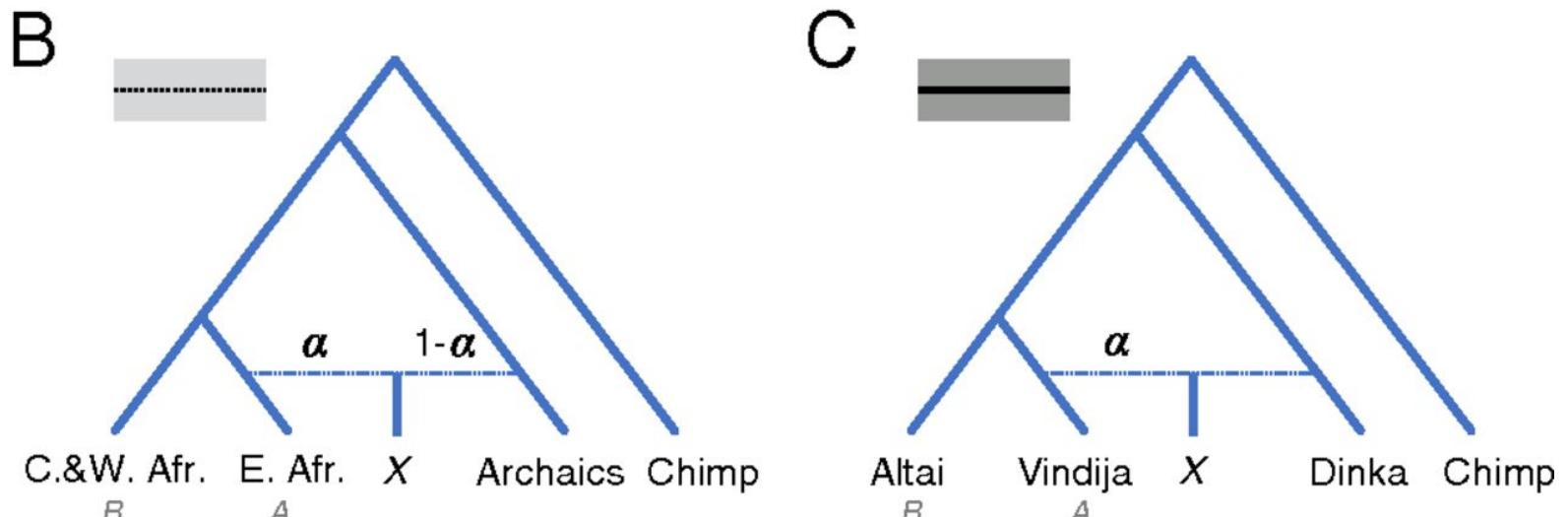
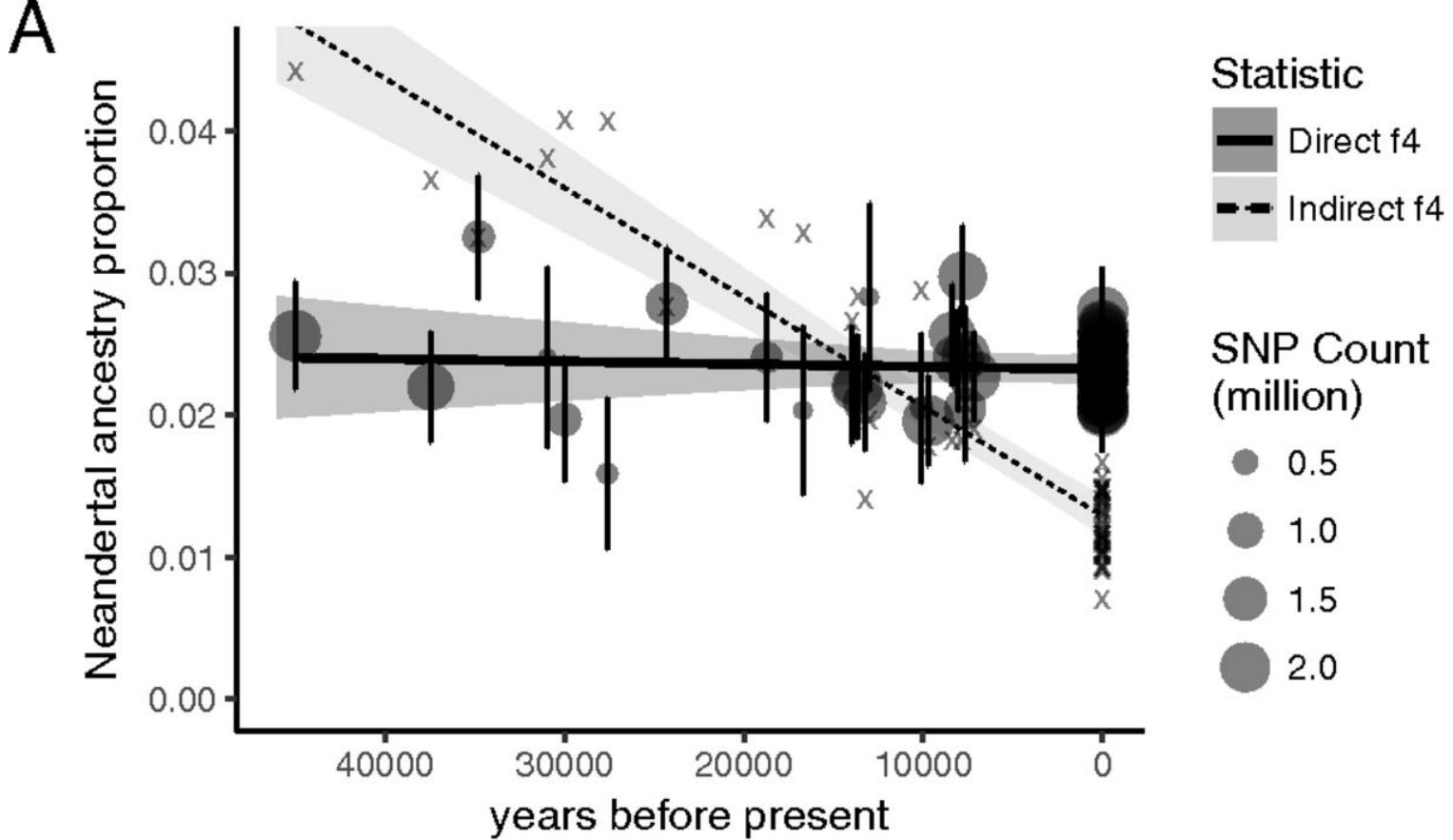


# Neandertal ancestry



Fu et al. 2016



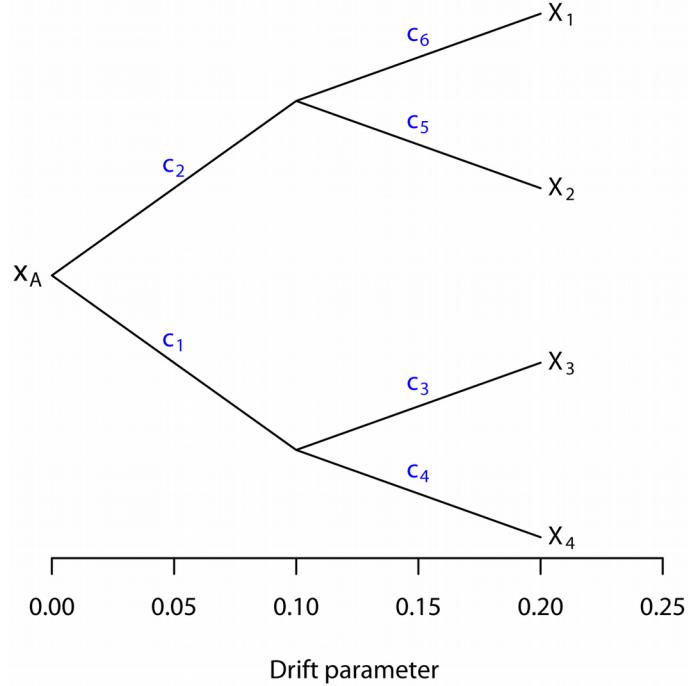


$$\alpha = \frac{f_4(\text{C. and W. Afr., Chimp}; X, \text{Archaics})}{f_4(\text{C. and W. Afr., Chimp}; \text{E. Afr., Archaics})}$$

$$\alpha = \frac{f_4(\text{Altai, Chimp}; X, \text{Dinka})}{f_4(\text{Altai, Chimp}; \text{Vindija, Dinka})}$$

# Admixture graphs

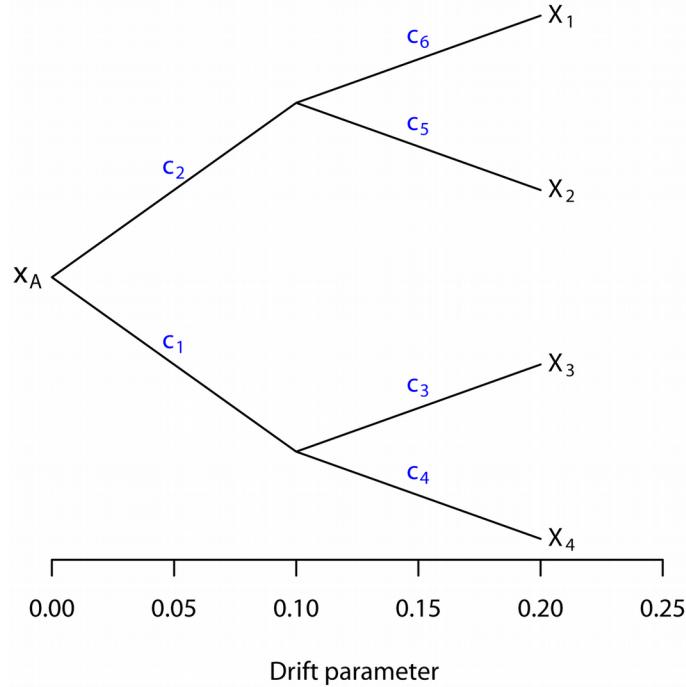
A. Example tree



B. Covariance matrix for tree in A.

$X_1$	$c_2 + c_6$	$c_2$	0	0
$X_2$	$c_2$	$c_2 + c_5$	0	0
$X_3$	0	0	$c_1 + c_3$	$c_1$
$X_4$	0	0	$c_1$	$c_1 + c_4$

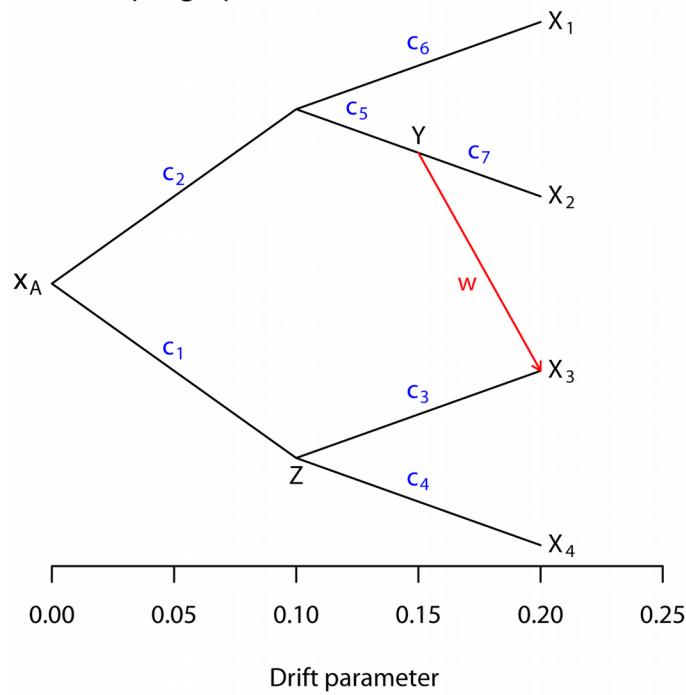
A. Example tree



B. Covariance matrix for tree in A.

$X_1$	$c_2 + c_6$	$c_2$	0	0
$X_2$	$c_2$	$c_2 + c_5$	0	0
$X_3$	0	0	$c_1 + c_3$	$c_1$
$X_4$	0	0	$c_1$	$c_1 + c_4$

C. Example graph



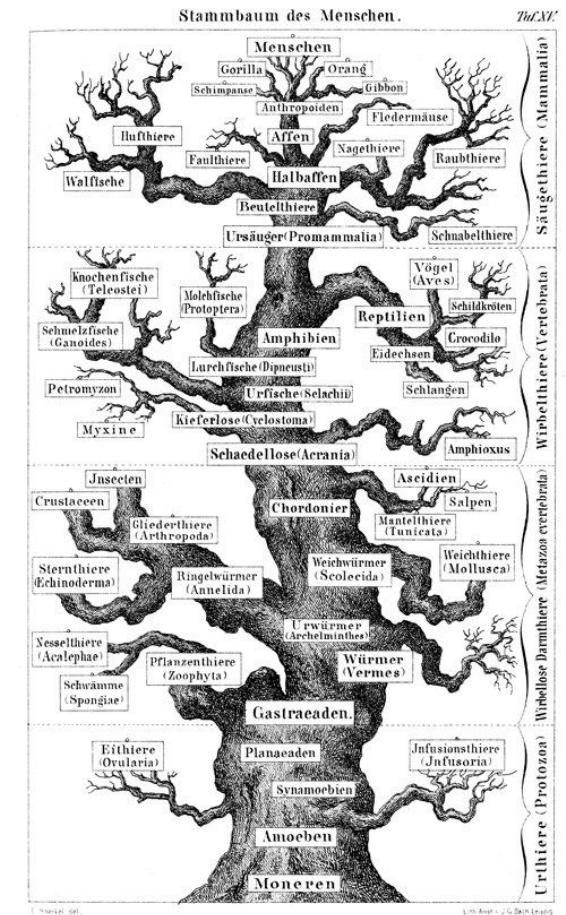
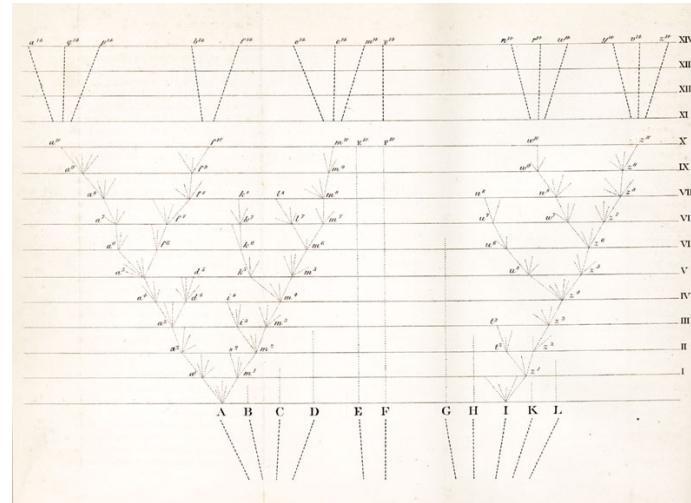
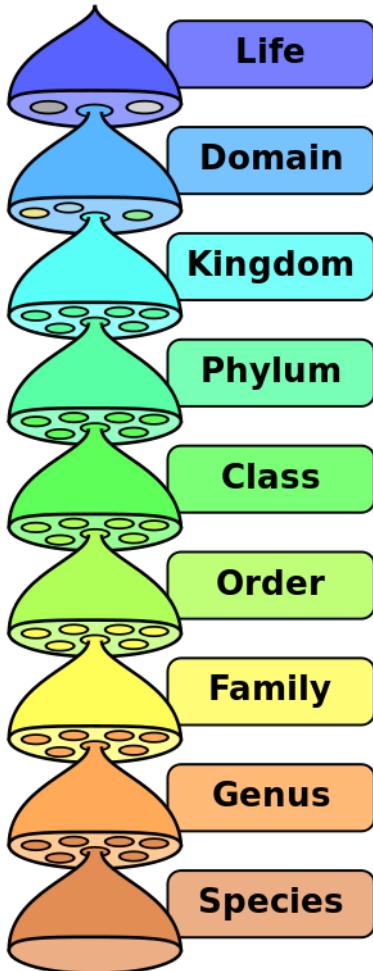
D. Covariance matrix for graph in C.

$X_1$	$c_2 + c_6$	$c_2$	$wc_2$	0
$X_2$	$c_2$	$c_2 + c_5 + c_7$	$w(c_2 + c_5)$	0
$X_3$	$wc_2$	$w(c_2 + c_5)$	$w^2(c_2 + c_5) + (1-w)^2(c_1 + c_3)$	$(1-w)c_1$
$X_4$	0	0	$(1-w)c_1$	$c_1 + c_4$

# Population structure models

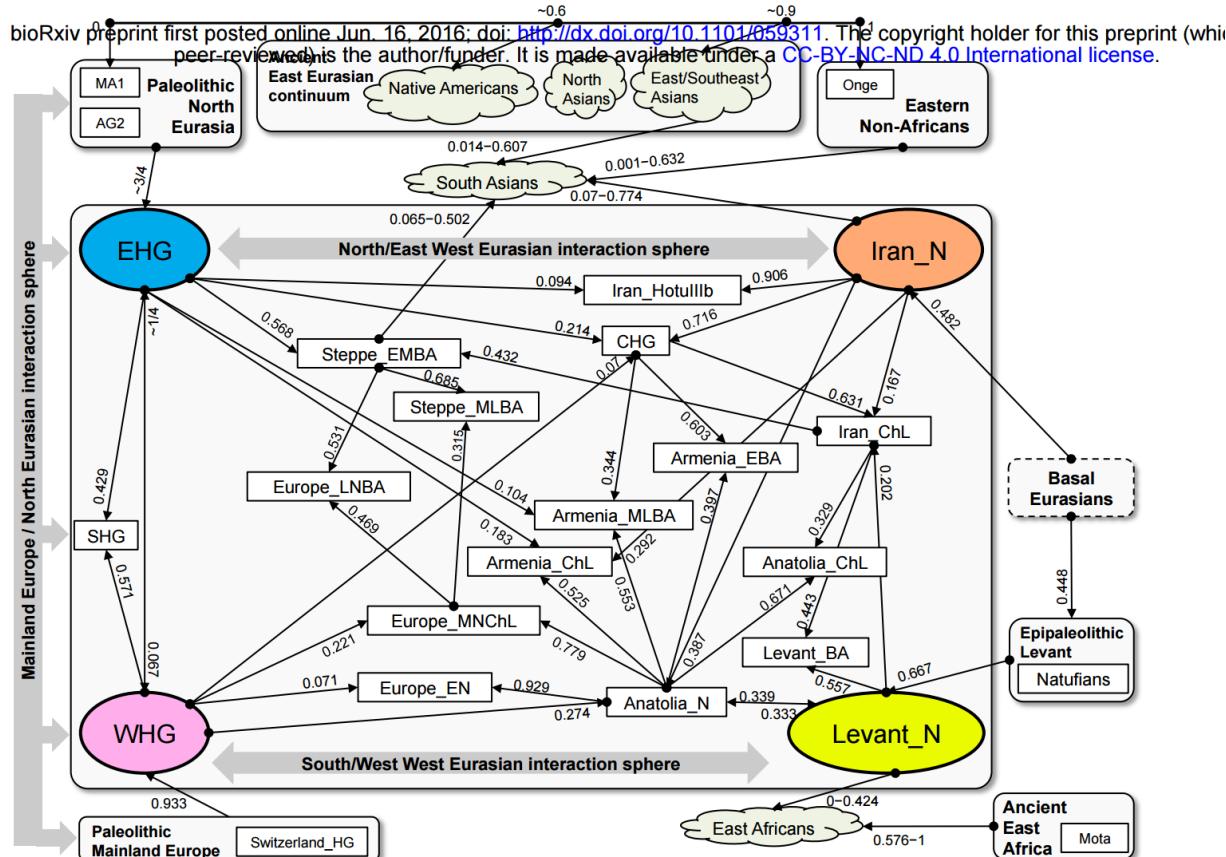
# Using trees to describe (human) population structure

# Trees are foundational to Systematics and Evolution



# Or really complicated

a



b

# Or (nearly) continuous

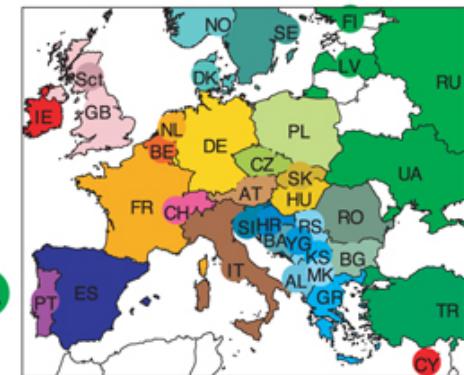
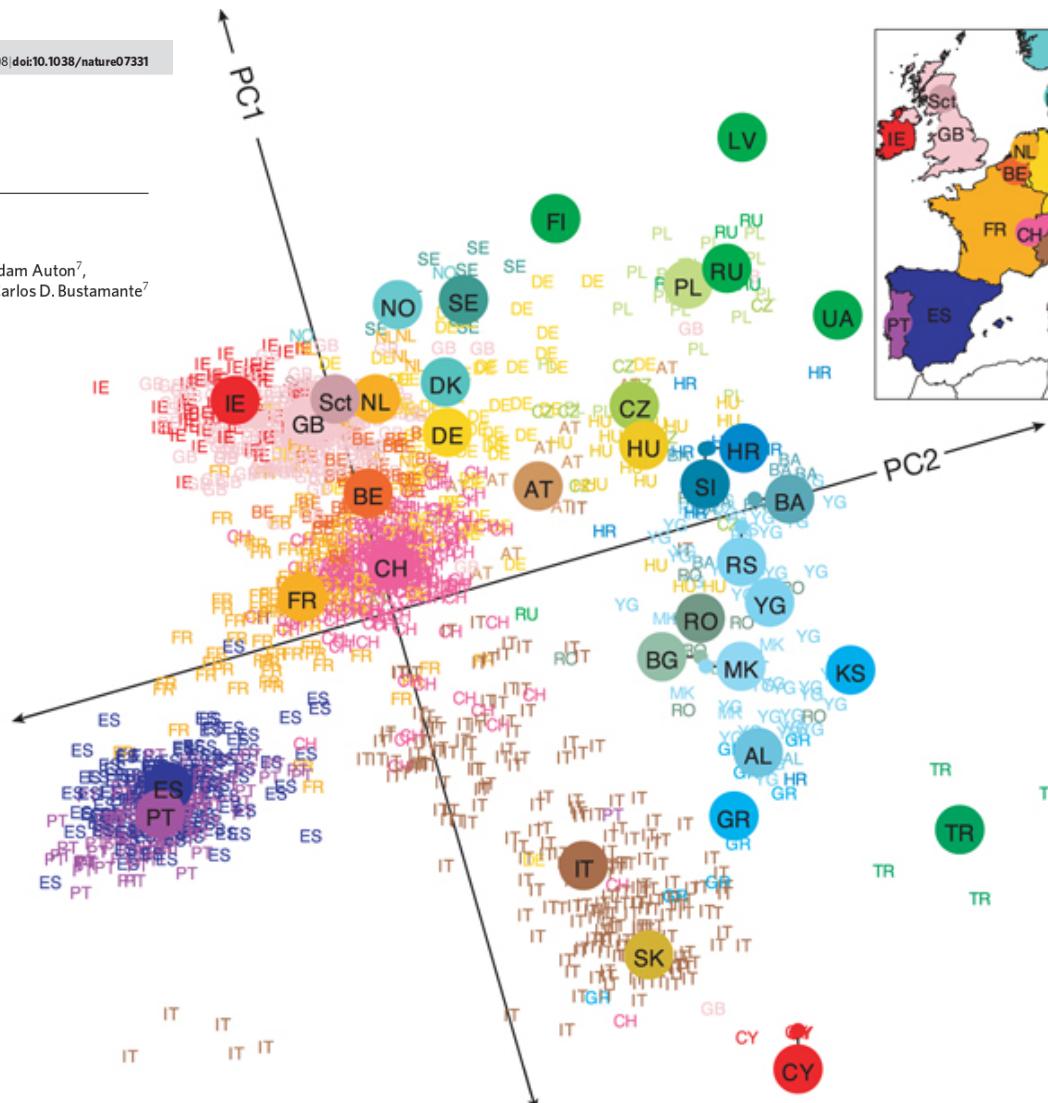
nature

Vol 456 | 6 November 2008 | doi:10.1038/nature07331

LETTERS

## **Genes mirror geography within Europe**

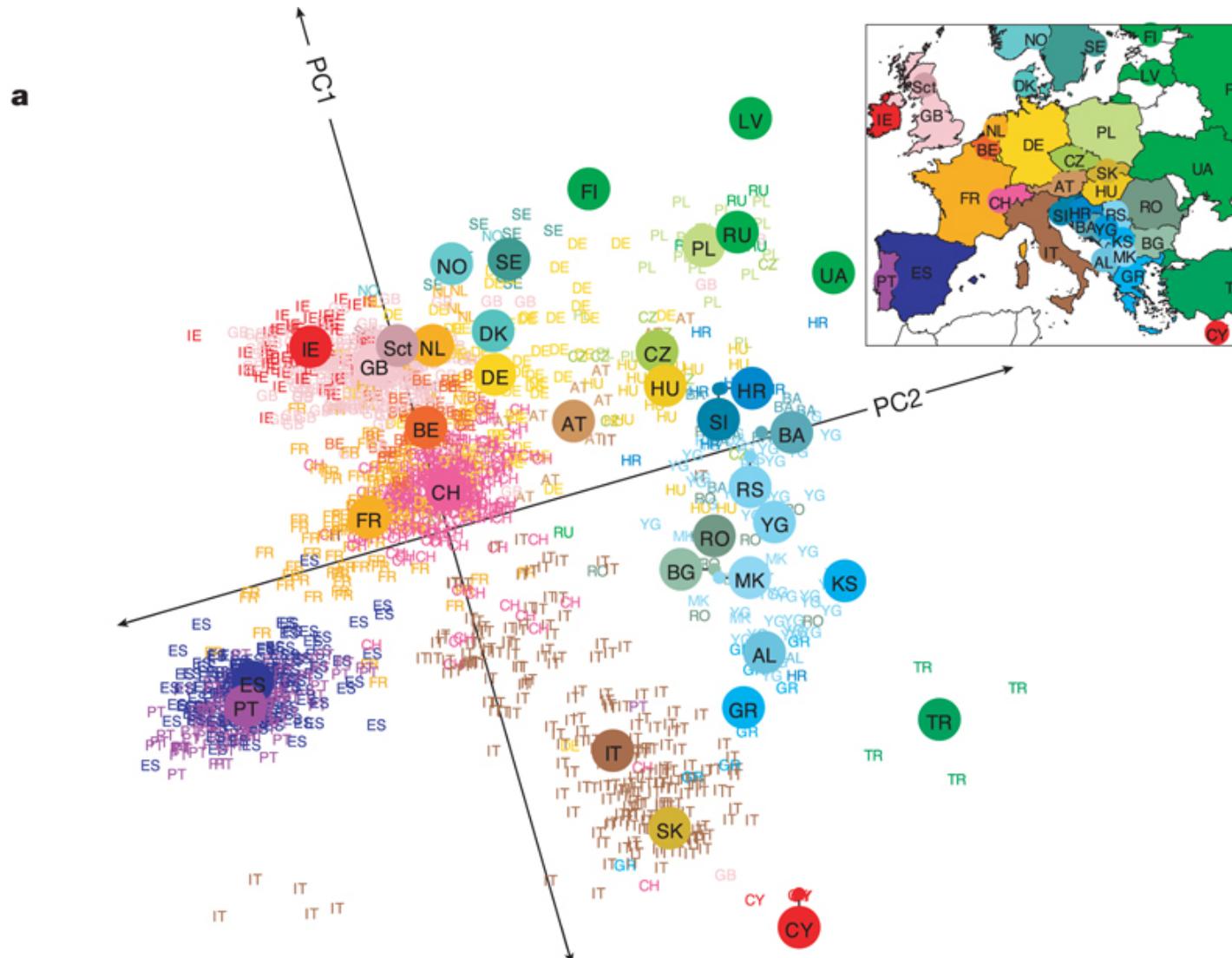
John Novembre<sup>1,2</sup>, Toby Johnson<sup>4,5,6</sup>, Katarzyna Bryc<sup>7</sup>, Zoltán Kutalik<sup>4,6</sup>, Adam R. Boyko<sup>7</sup>, Adam Auton<sup>7</sup>, Amit Indap<sup>7</sup>, Karen S. King<sup>8</sup>, Sven Bergmann<sup>4,6</sup>, Matthew R. Nelson<sup>8</sup>, Matthew Stephens<sup>2,3</sup> & Carlos D. Bustamante<sup>7</sup>



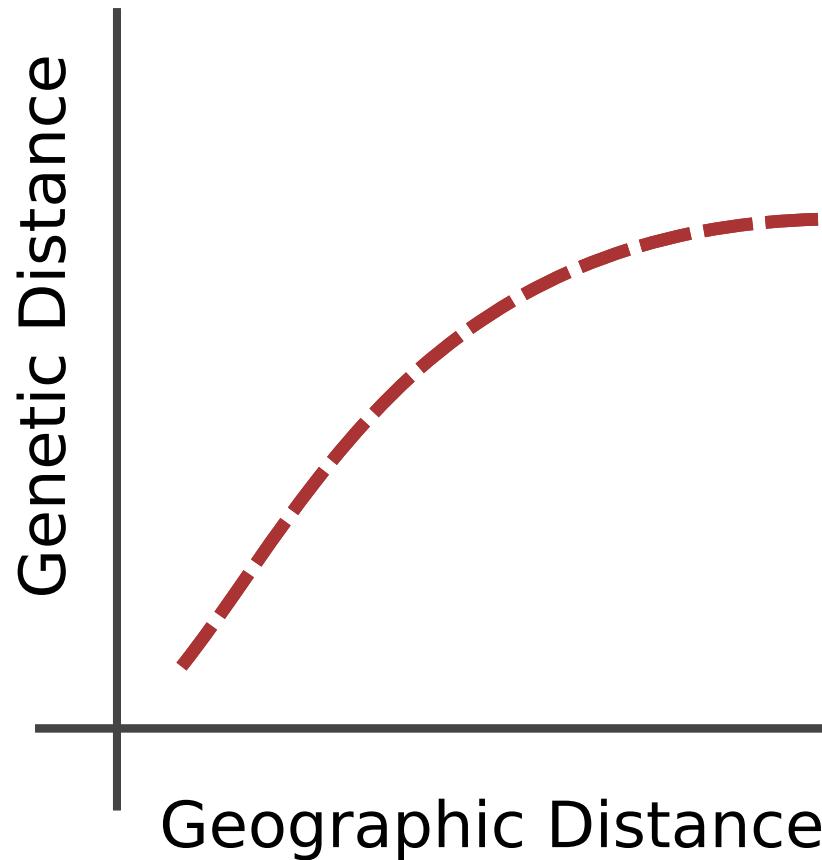
LETTERS

## **Genes mirror geography within Europe**

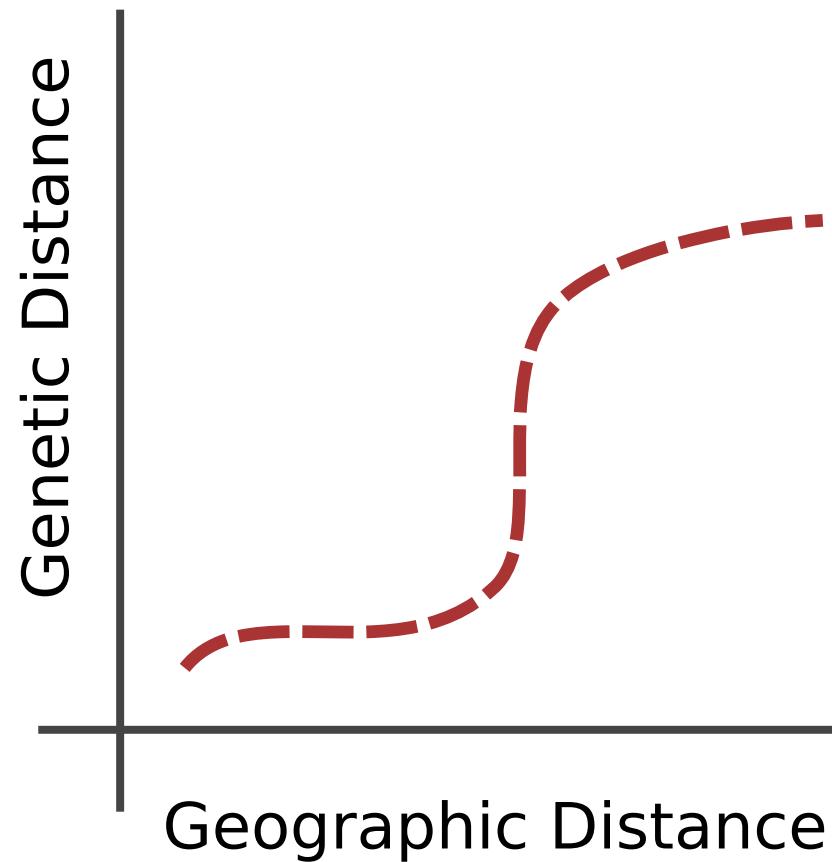
John Novembre<sup>1,2</sup>, Toby Johnson<sup>4,5,6</sup>, Katarzyna Bryc<sup>7</sup>, Zoltán Kutalik<sup>4,6</sup>, Adam R. Boyko<sup>7</sup>, Adam Auton<sup>7</sup>, Amit Indap<sup>7</sup>, Karen S. King<sup>8</sup>, Sven Bergmann<sup>4,6</sup>, Matthew R. Nelson<sup>8</sup>, Matthew Stephens<sup>2,3</sup> & Carlos D. Bustamante<sup>7</sup>



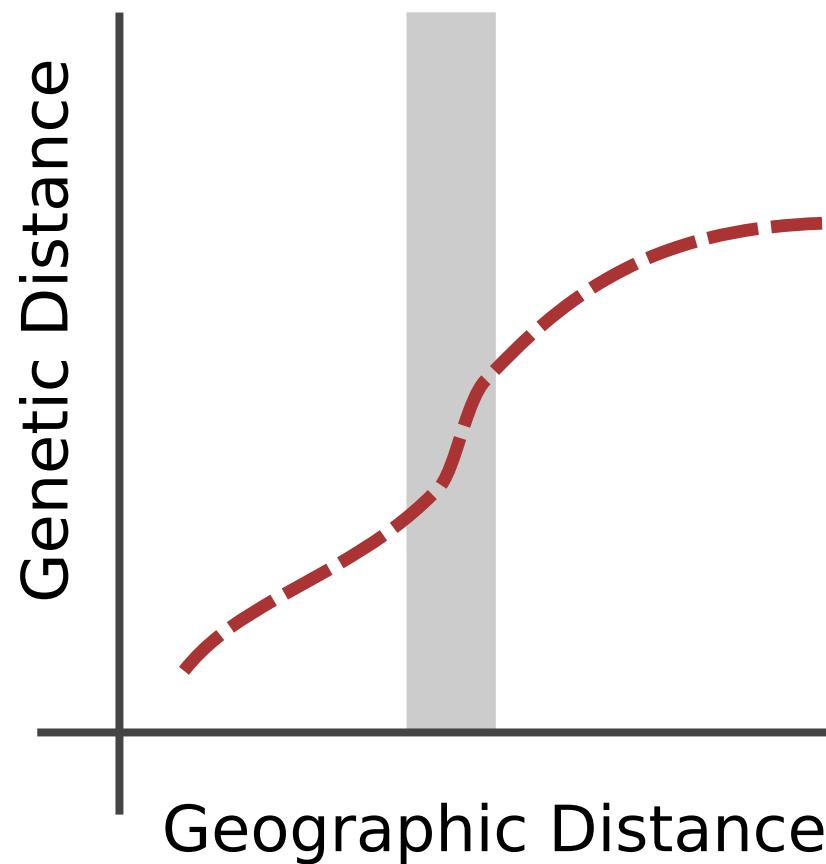
# Continuous structure



# Discrete structure

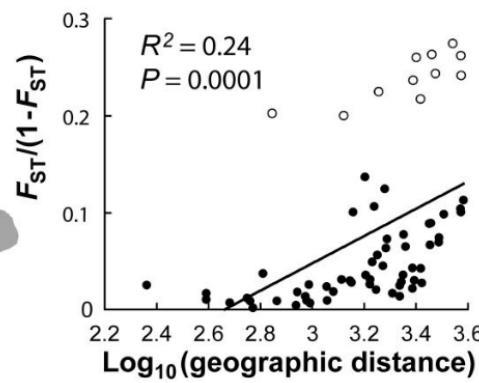
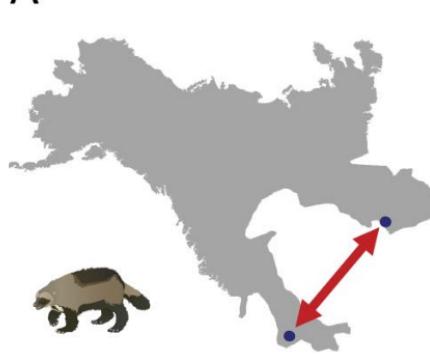


# Inferring discontinuities

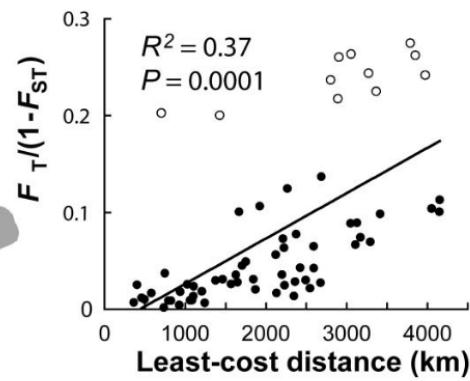
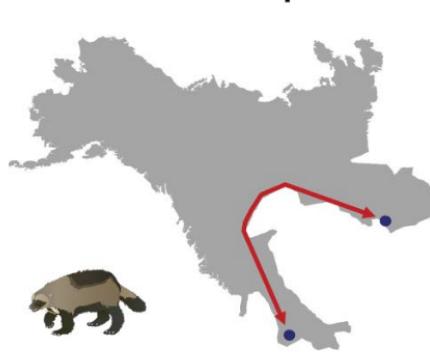


# Where do individuals move?

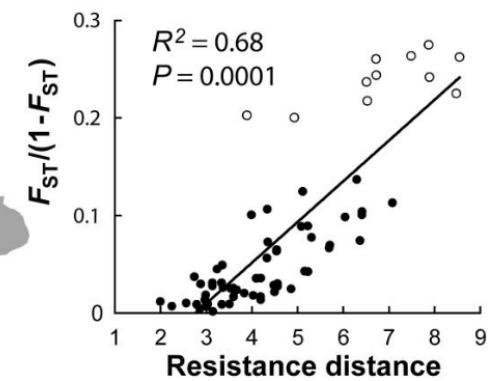
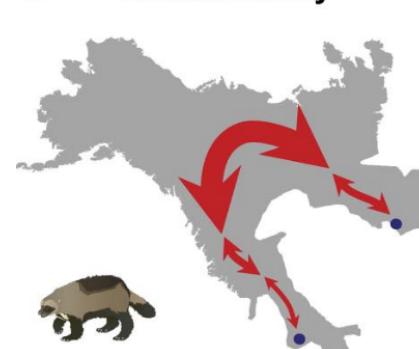
A 2-dimensional IBD



B Least-cost path



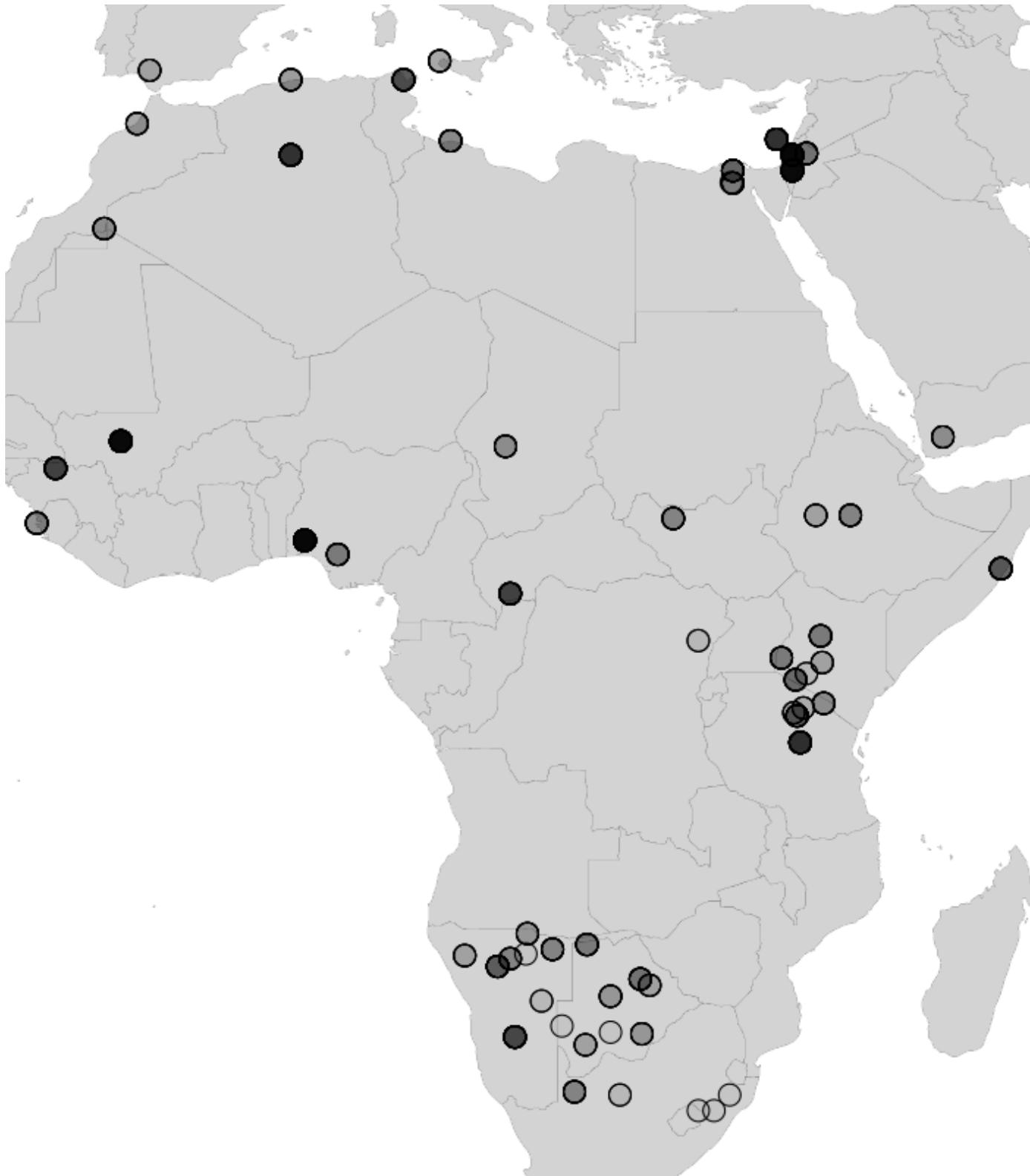
C Circuit theory

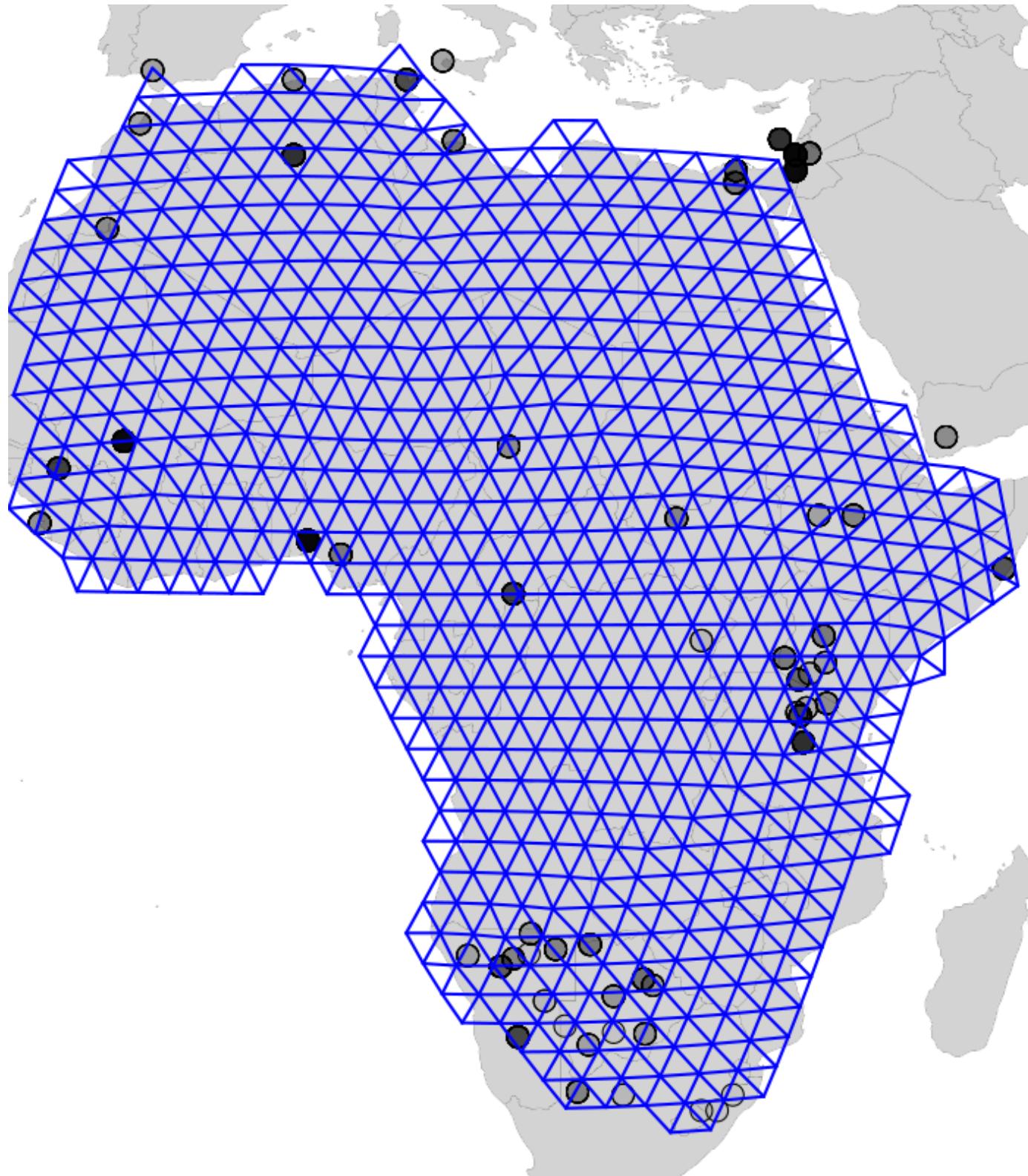


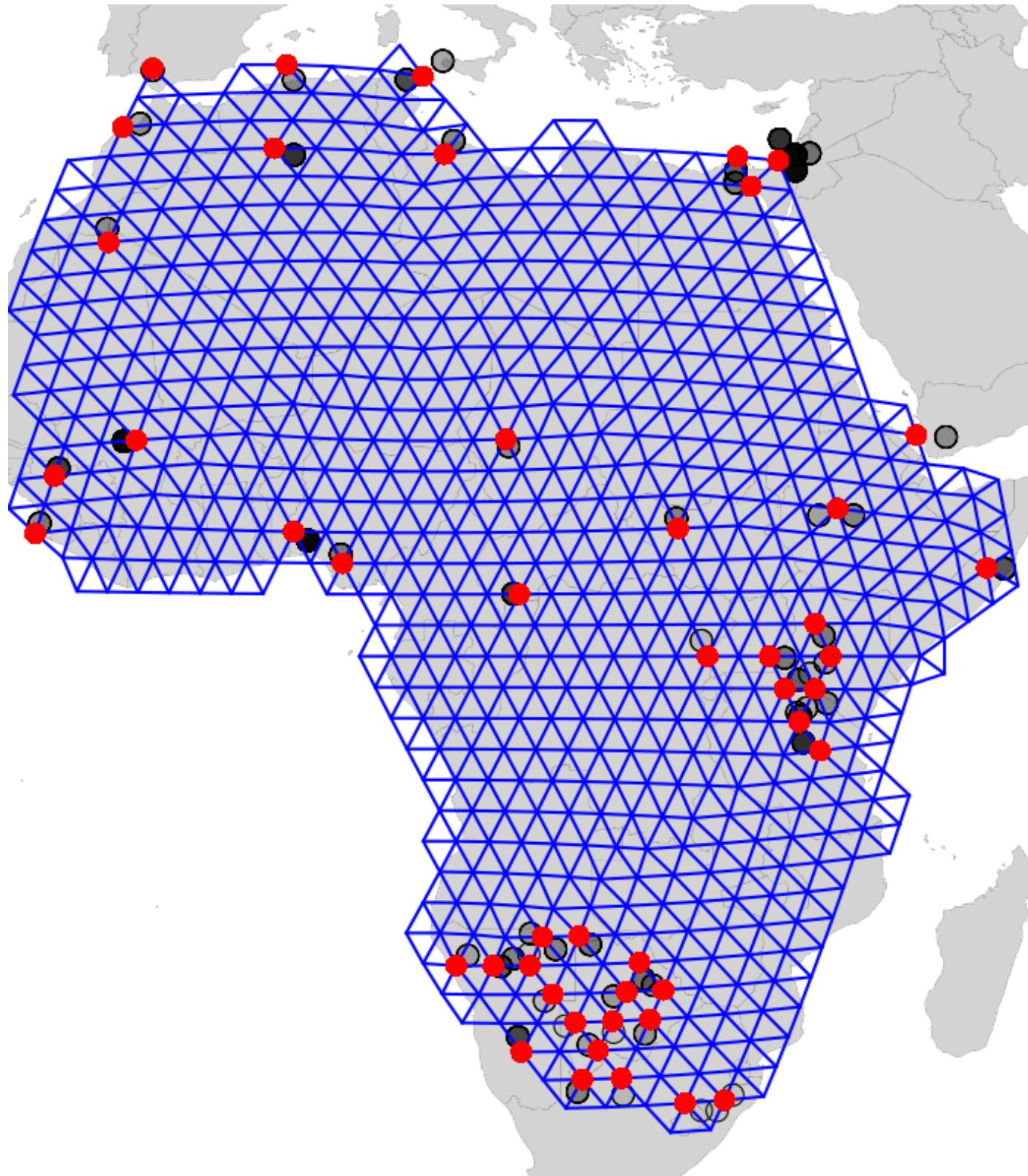
**Circuit theory resistance distances are proportional to commute times**  
( $T_{ij}$  = time to reach  $j$  and return to  $i$ )

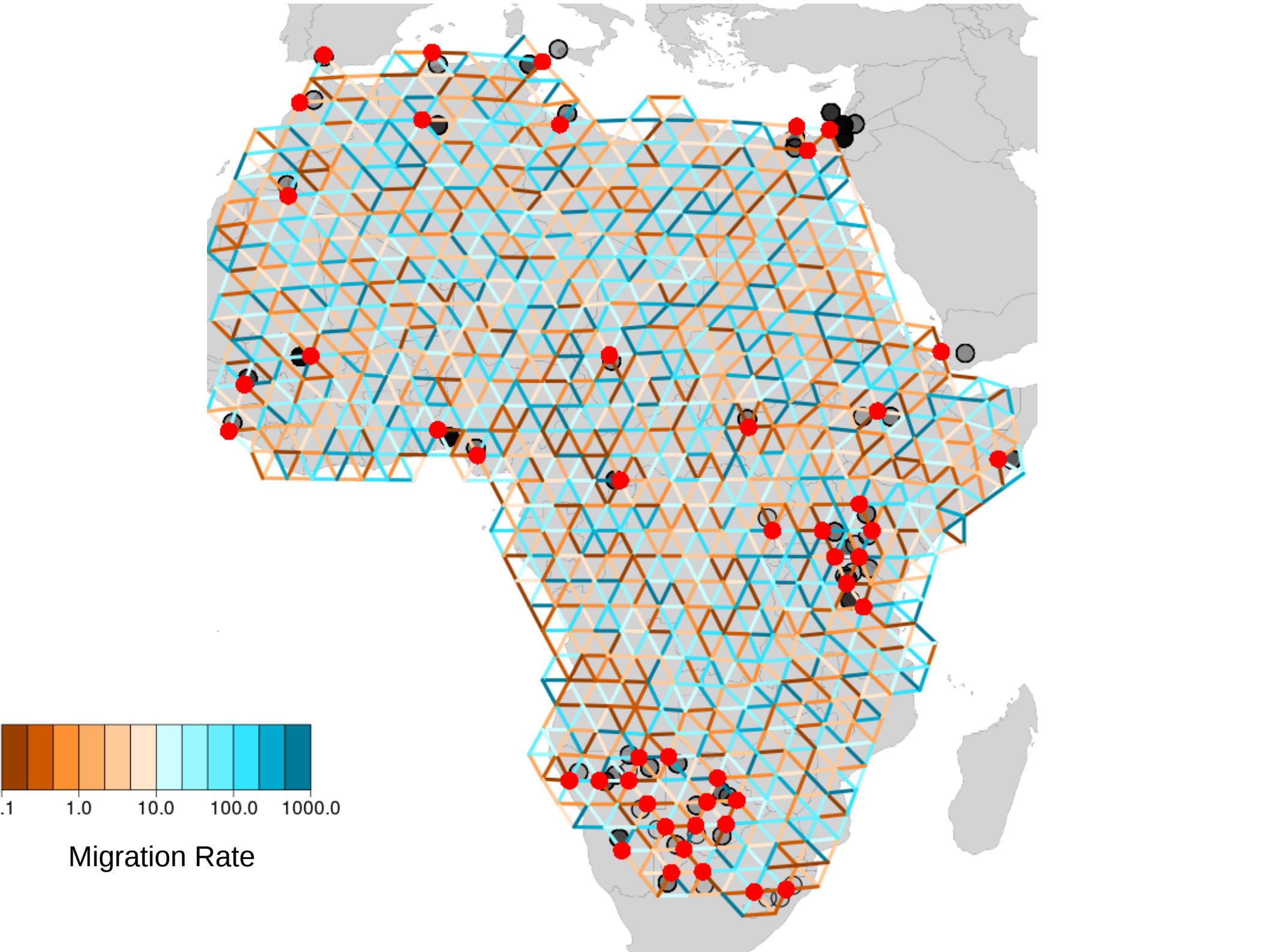
**Resistance distances approximate how genetic distance accumulates in populations**

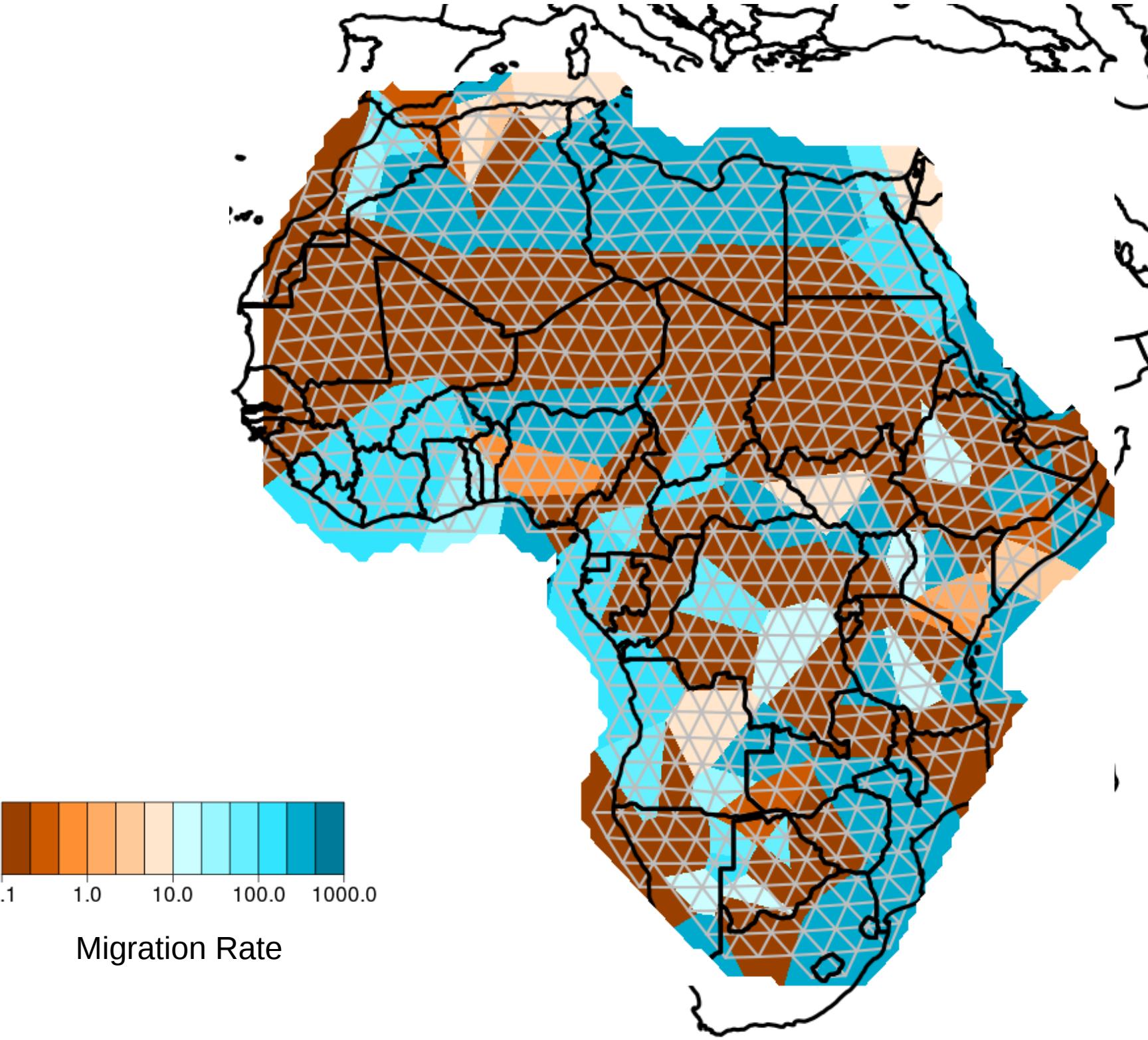


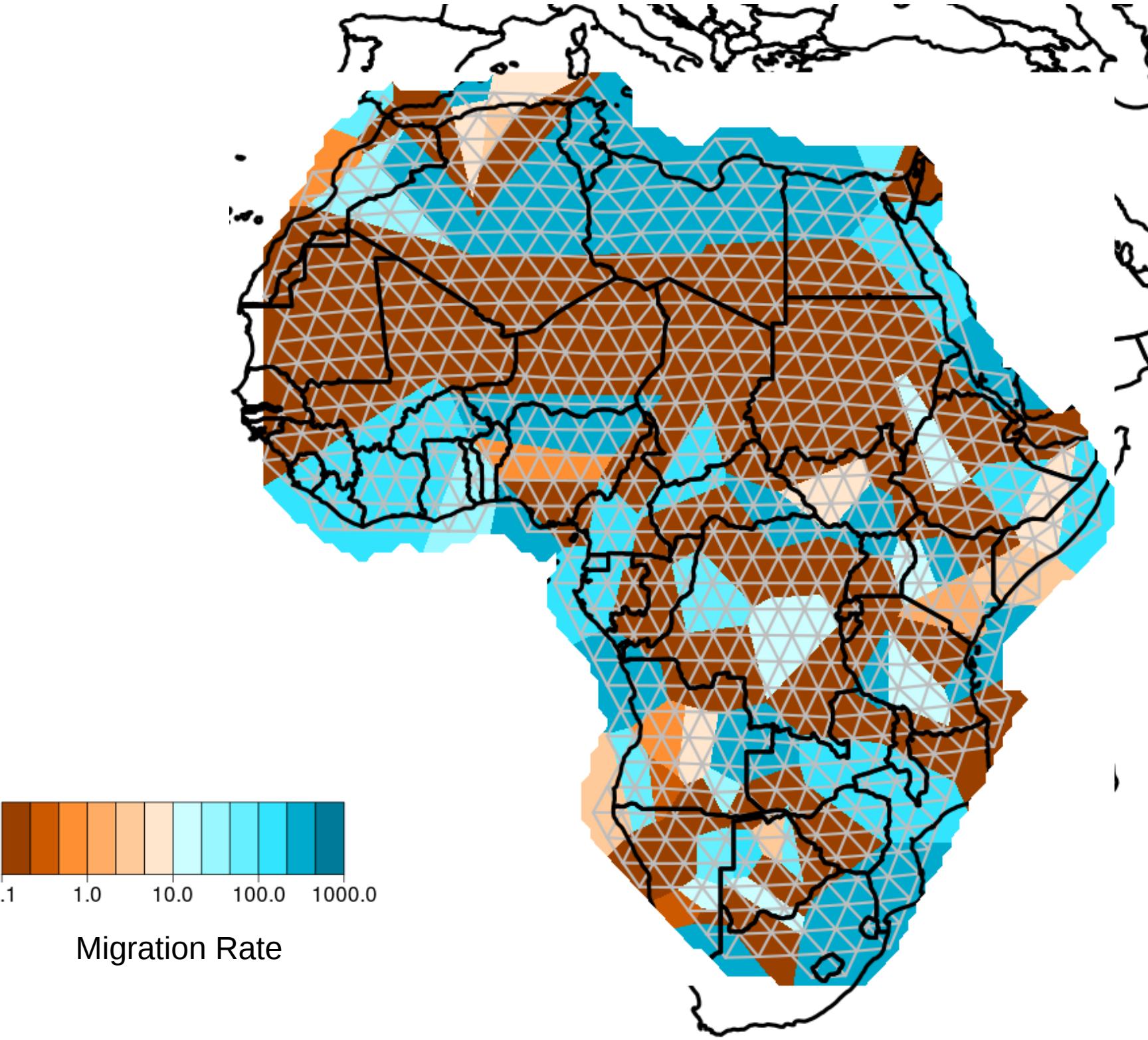


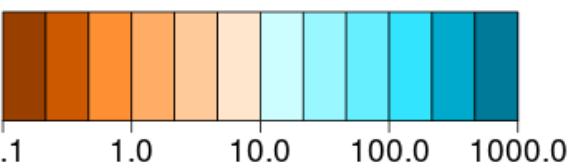
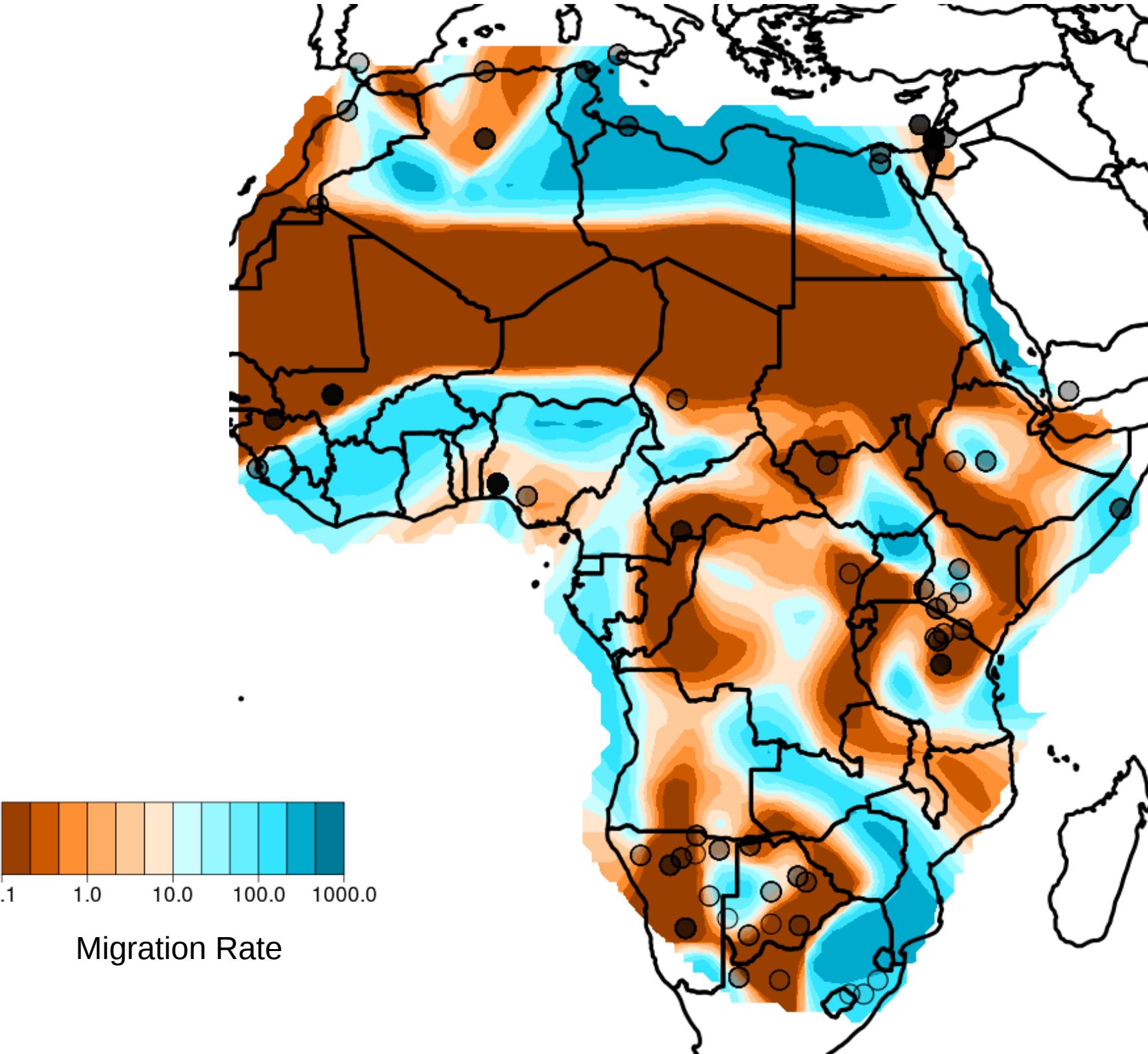




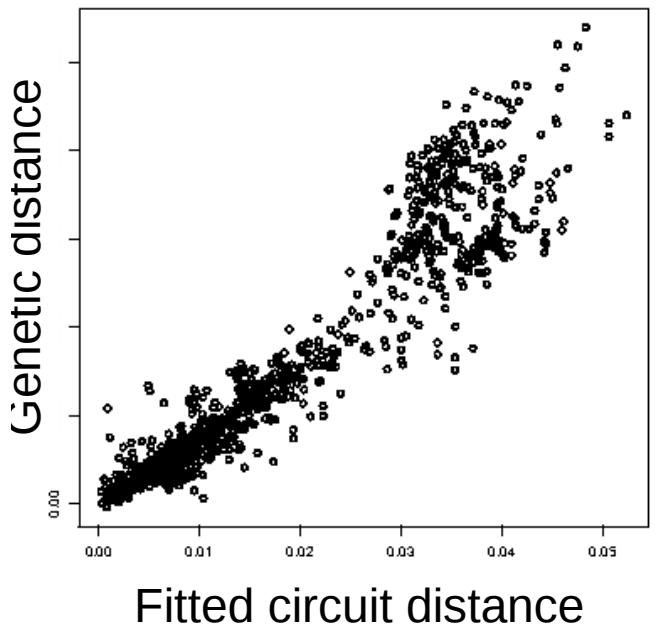
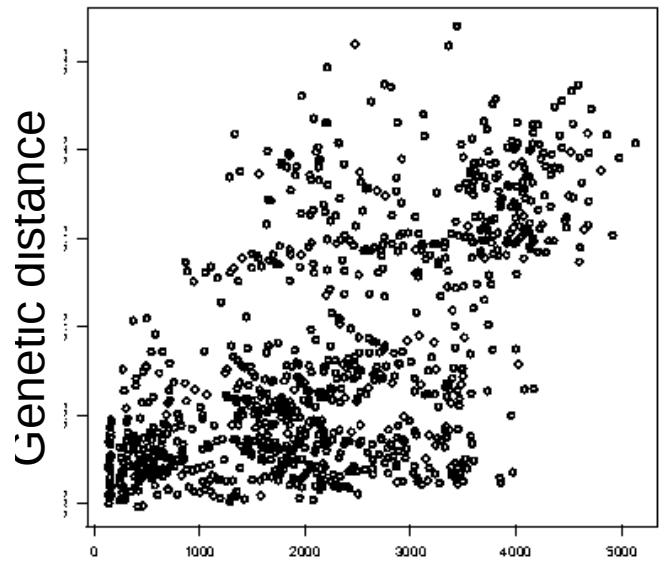
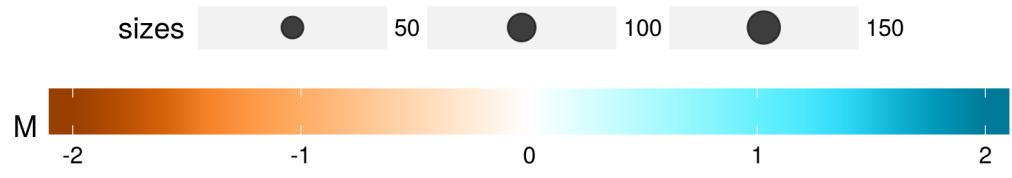
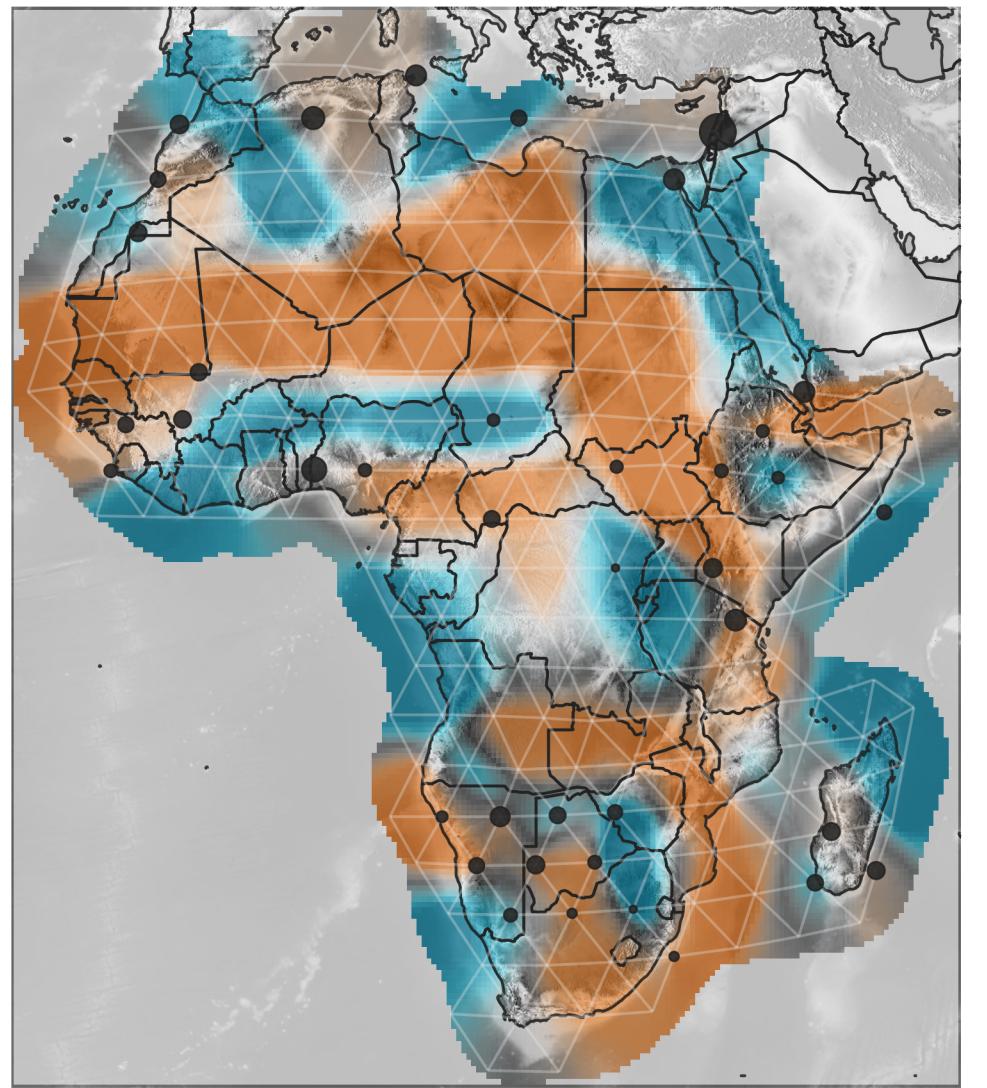




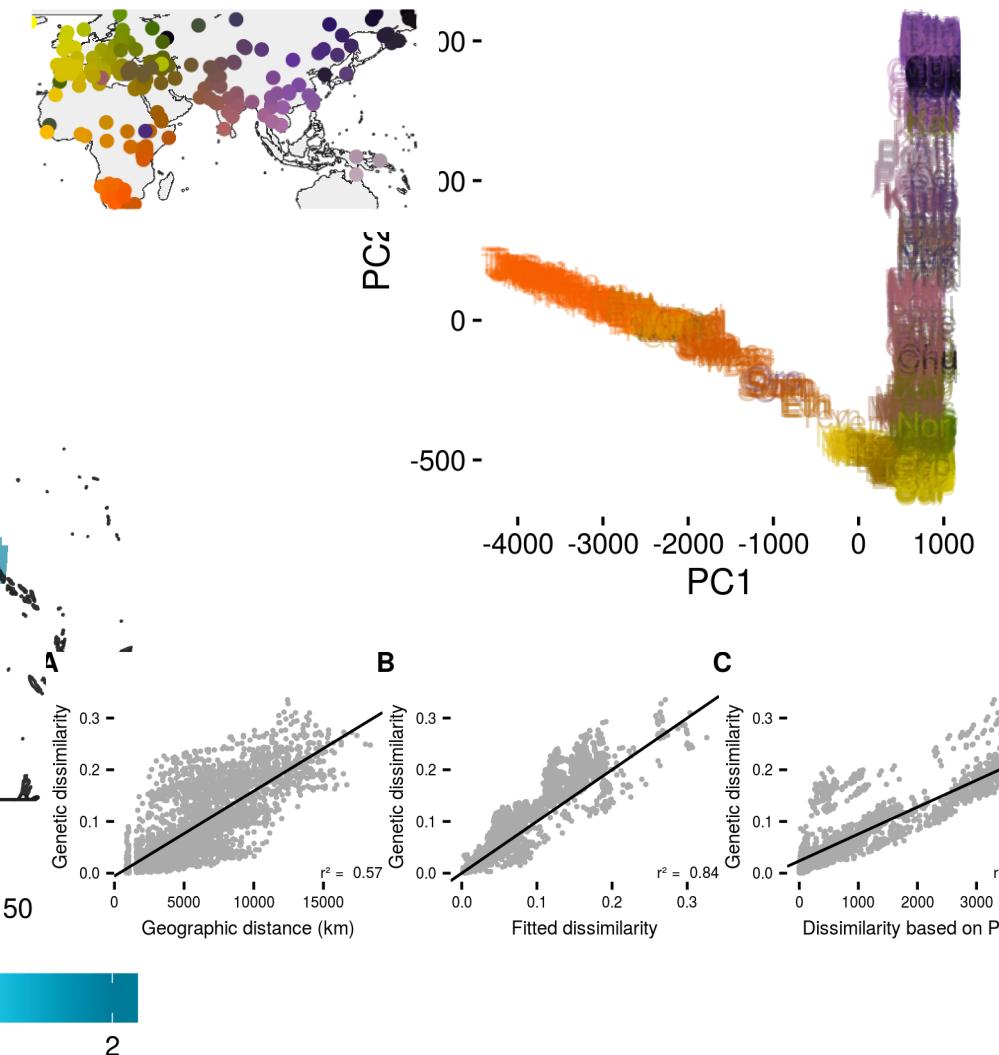
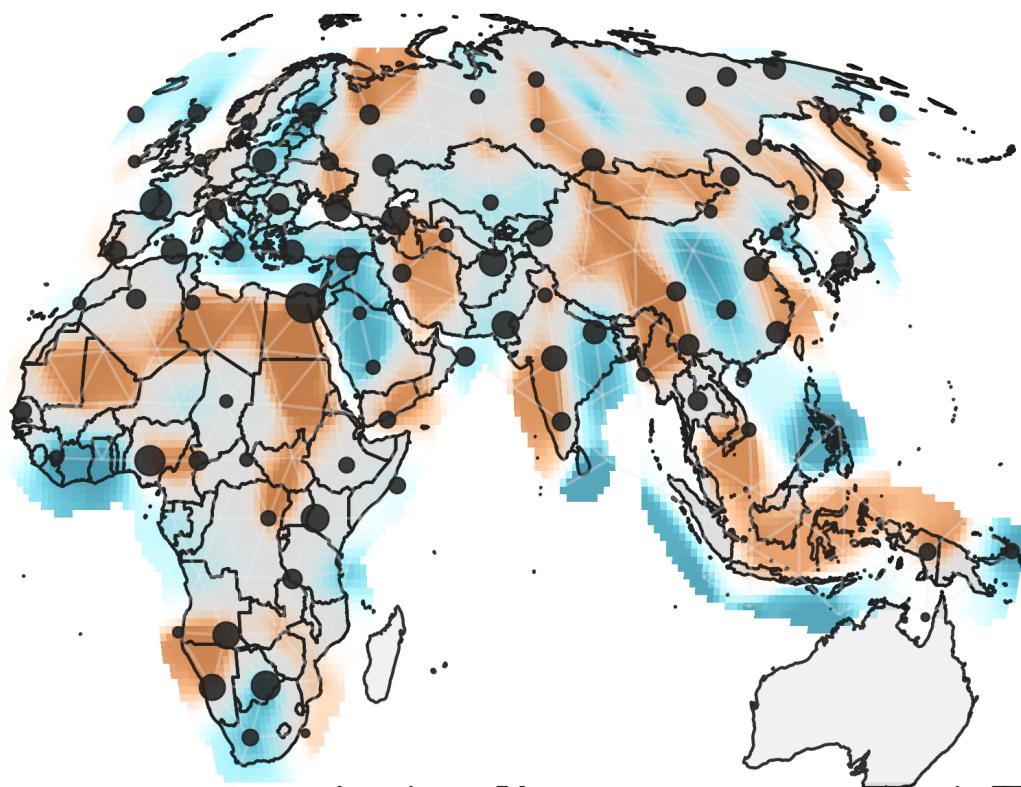




Migration Rate



# Global patterns



# Europe

