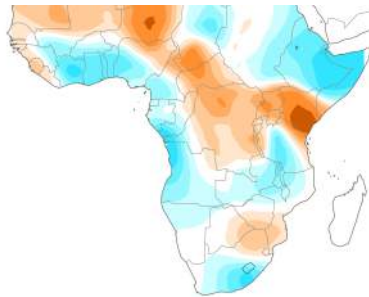
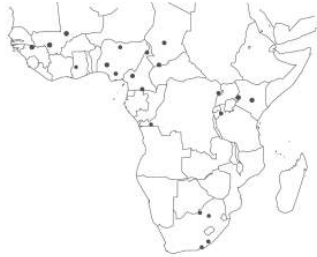


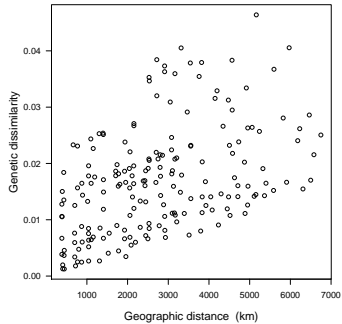


EEMS





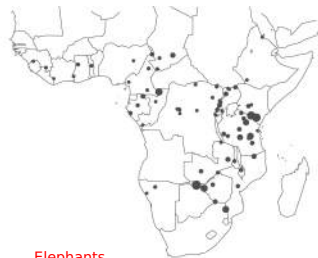
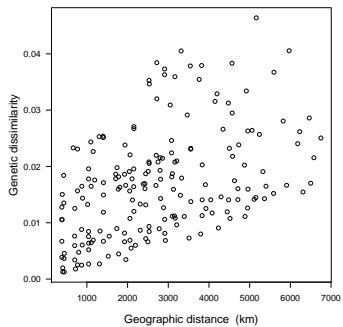
Spatially structured
population



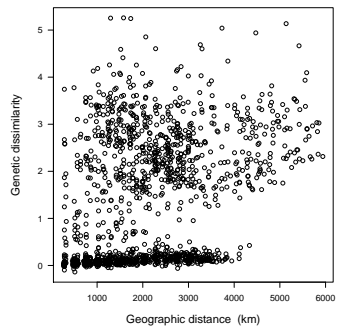
Isolation by distance

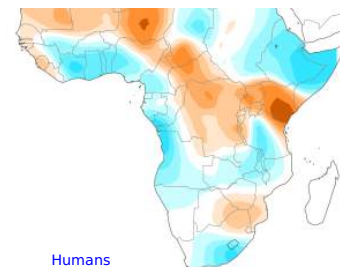


Humans

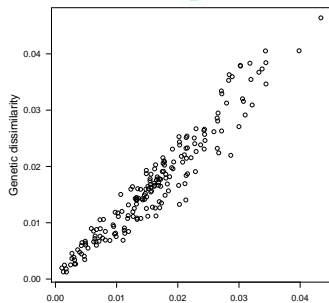


Elephants



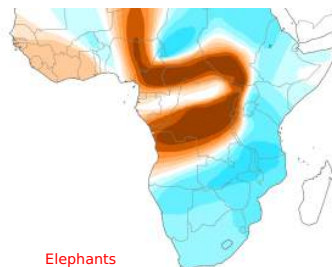
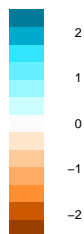


Humans

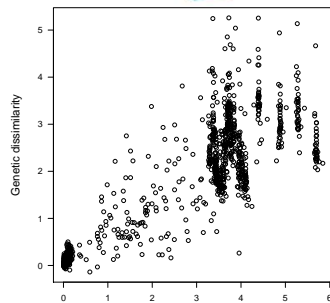


Human-specific distance

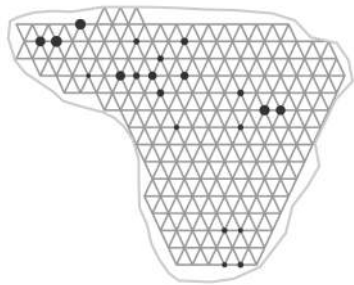
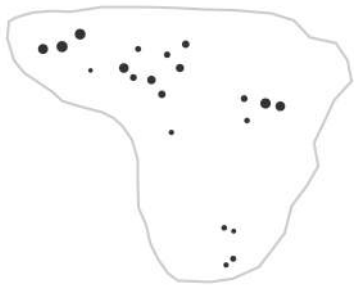
$\log(m)$



Elephants



Elephant-specific distance



$$D_{ij} = \frac{1}{p} \sum_{k=1}^p (z_{ik} - z_{jk})^2$$

i, j : samples, k : SNP

$$E\{D_{ij}\} = \Delta_{\delta(i)\delta(j)} = \Delta_{\alpha\beta}$$

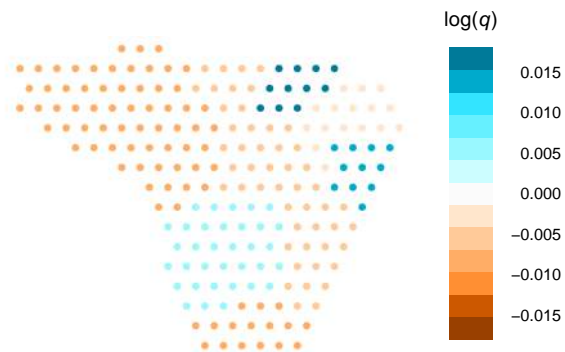
α, β : vertices

Model Δ :

$$\begin{aligned}\Delta_{\alpha\beta} &= \underbrace{\Delta_{\alpha\beta} - (\Delta_{\alpha\alpha} + \Delta_{\beta\beta})/2}_{\textcolor{red}{B(m)}_{\alpha\beta}} + \underbrace{(\Delta_{\alpha\alpha} + \Delta_{\beta\beta})/2}_{(\textcolor{blue}{W(q)}_{\alpha} + \textcolor{blue}{W(q)}_{\beta})/2} \\ &= \textcolor{red}{B(m)}_{\alpha\beta} + (\textcolor{blue}{W(q)}_{\alpha} + \textcolor{blue}{W(q)}_{\beta})/2\end{aligned}$$

Estimate m and q :

$$\Delta(m, q) \approx D$$

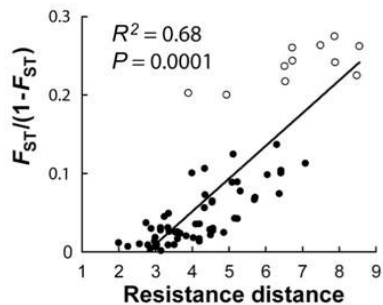
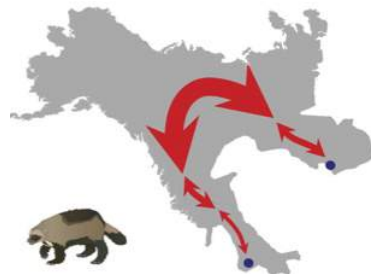
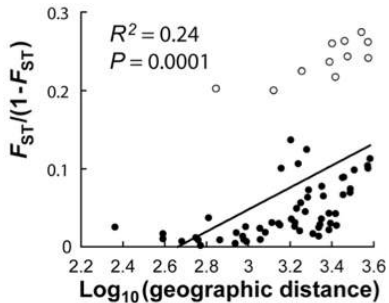
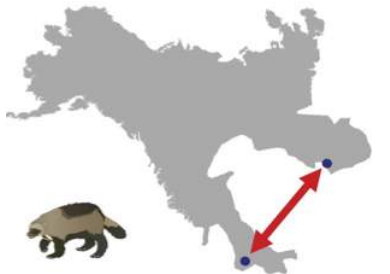


$$W(q) = \sigma^2 q$$

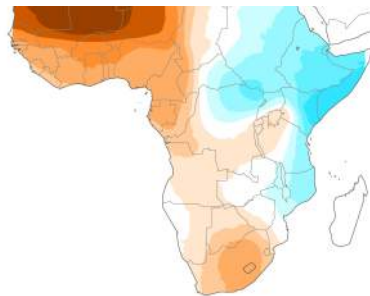


$$B(m) =$$

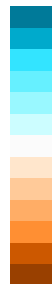
resistance distance



Isolation by resistance: McRae (2006), McRae & Beier (2007)



$\log(q)$



0.015

0.010

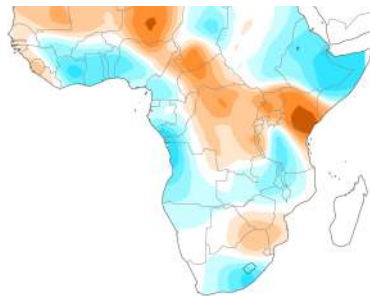
0.005

0.000

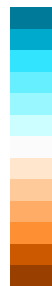
-0.005

-0.010

-0.015



$\log(m)$



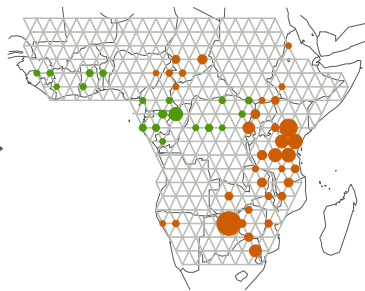
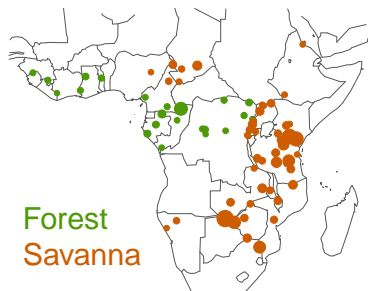
2

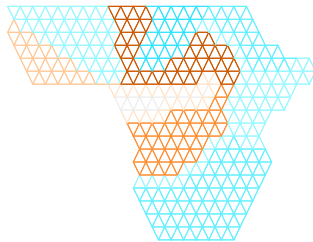
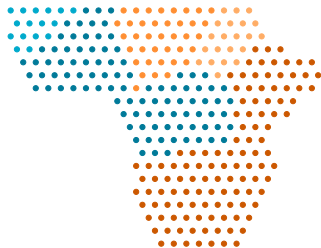
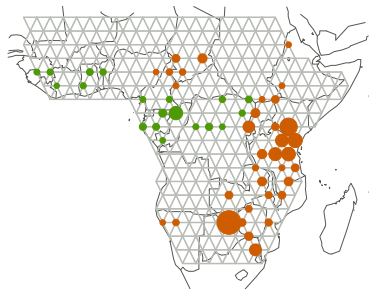
1

0

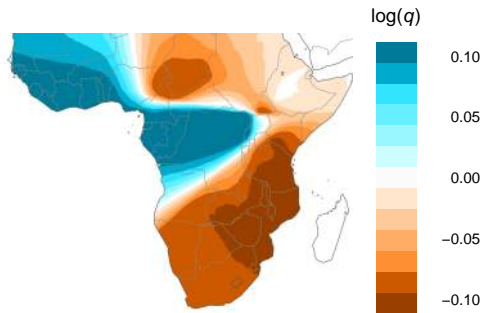
-1

-2

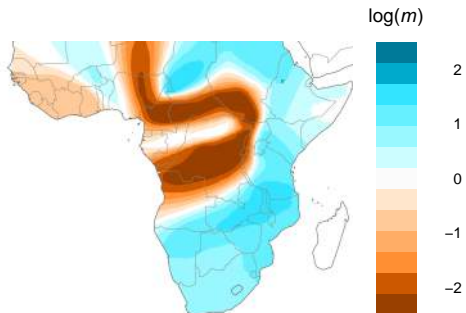




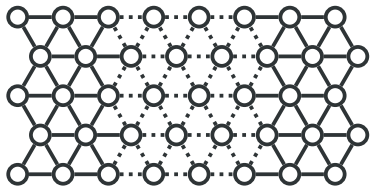
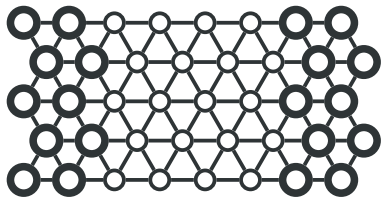
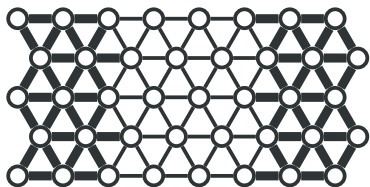
Effective migration is low
in regions where genetic
similarity decays quickly



W



B



EEMS: Petkova, Novembre & Stephens, bioRxiv 2014

The University of Chicago

Matthew Stephens

John Novembre

Hussein Al-Asadi

Benjamin Peter

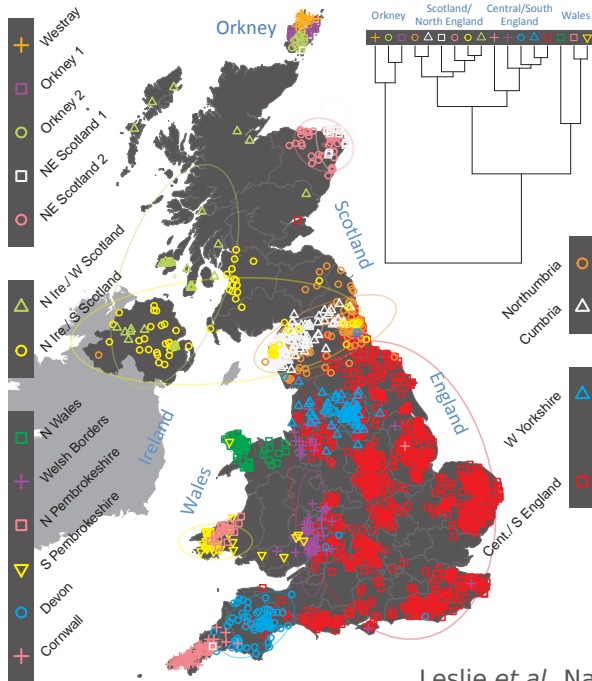
University of Washington

Samuel Wasser

University of Copenhagen

Ida Moltke

US National Institutes of Health
(NHGRI)



Leslie *et al.* Nature 2015

