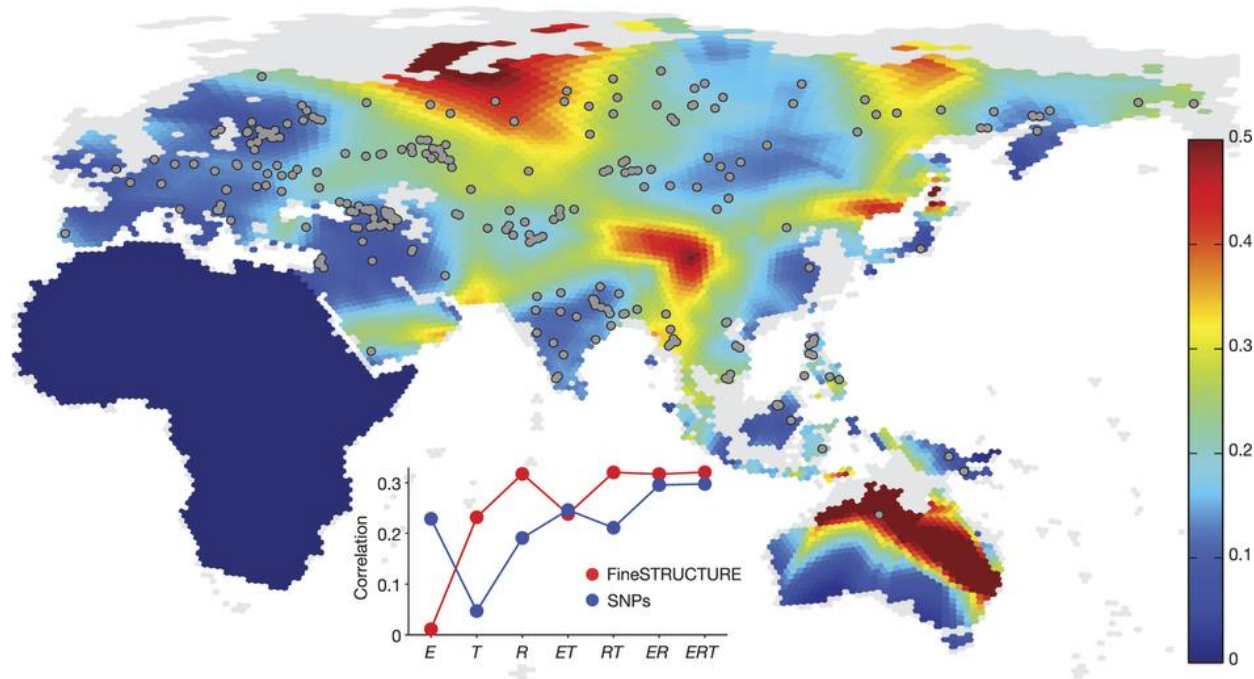


# Quantifying relationships among populations: Many populations



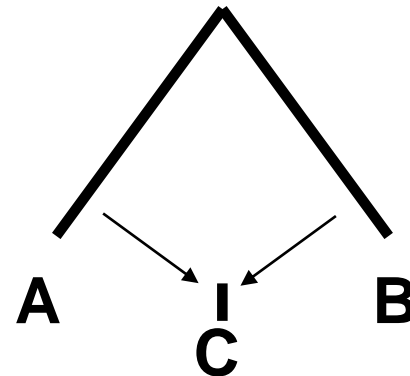
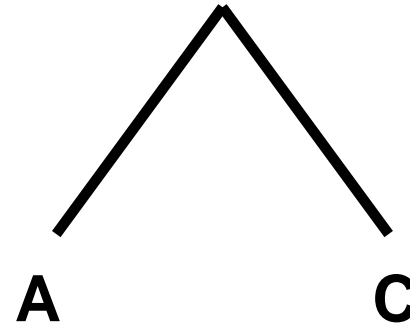
Andrea Manica



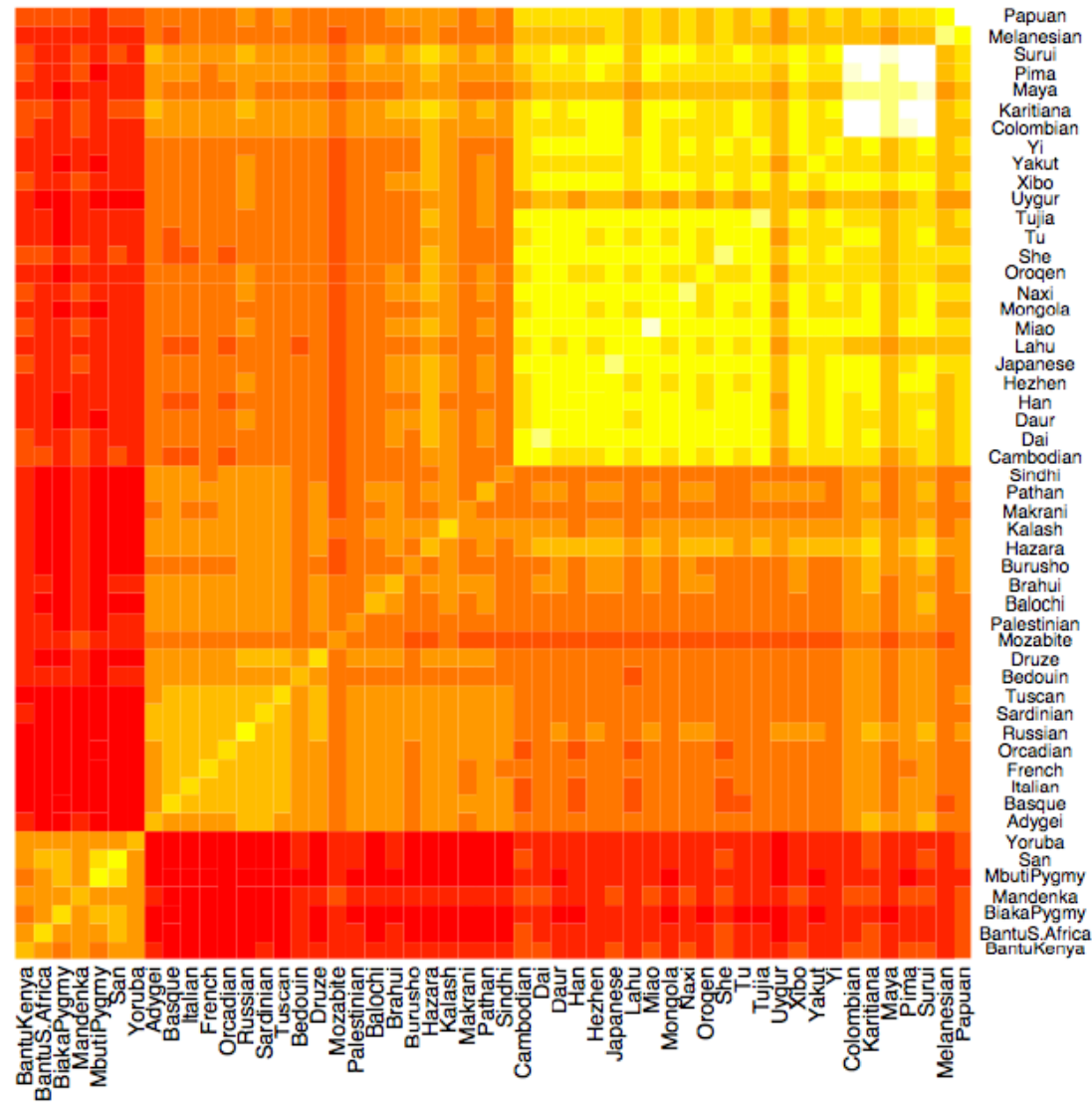
UNIVERSITY OF  
CAMBRIDGE

# Outline

- Quantifying distances between populations
- Building trees
- Admixture Graphs
- Some spatial statistics



# Quantifying distances among populations



## Quantifying distances among populations

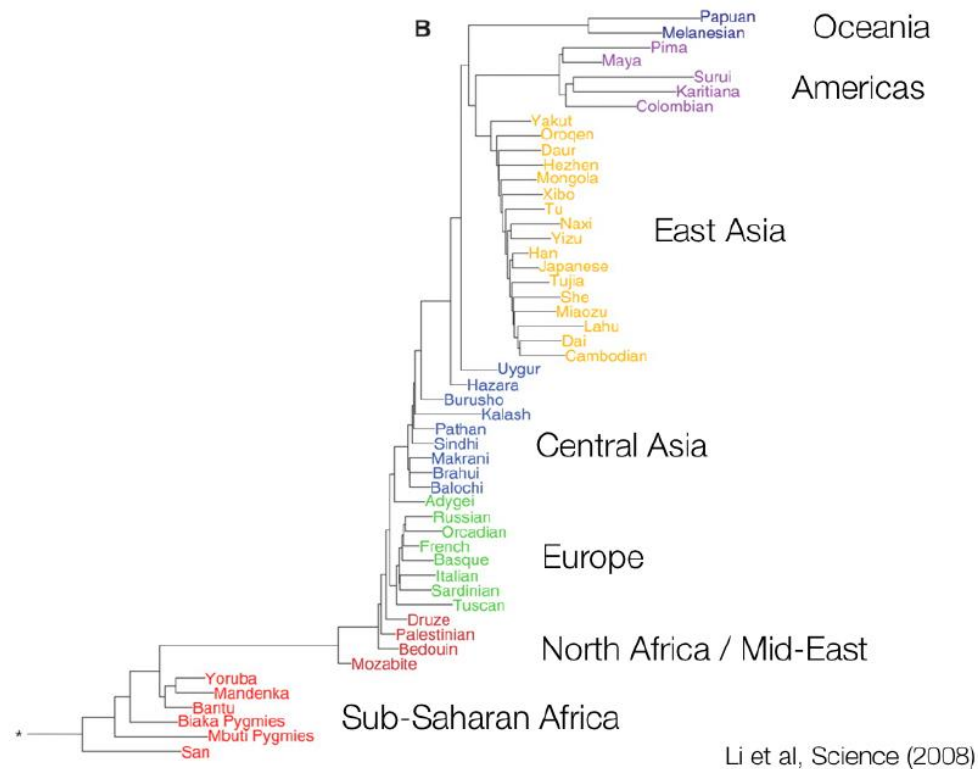
$$F_2(A,B) = E[(p_A - p_B)^2]$$

$$\hat{F}_2(P_1, P_2) = \pi_{12} - \frac{\pi_{11} + \pi_{22}}{2}.$$

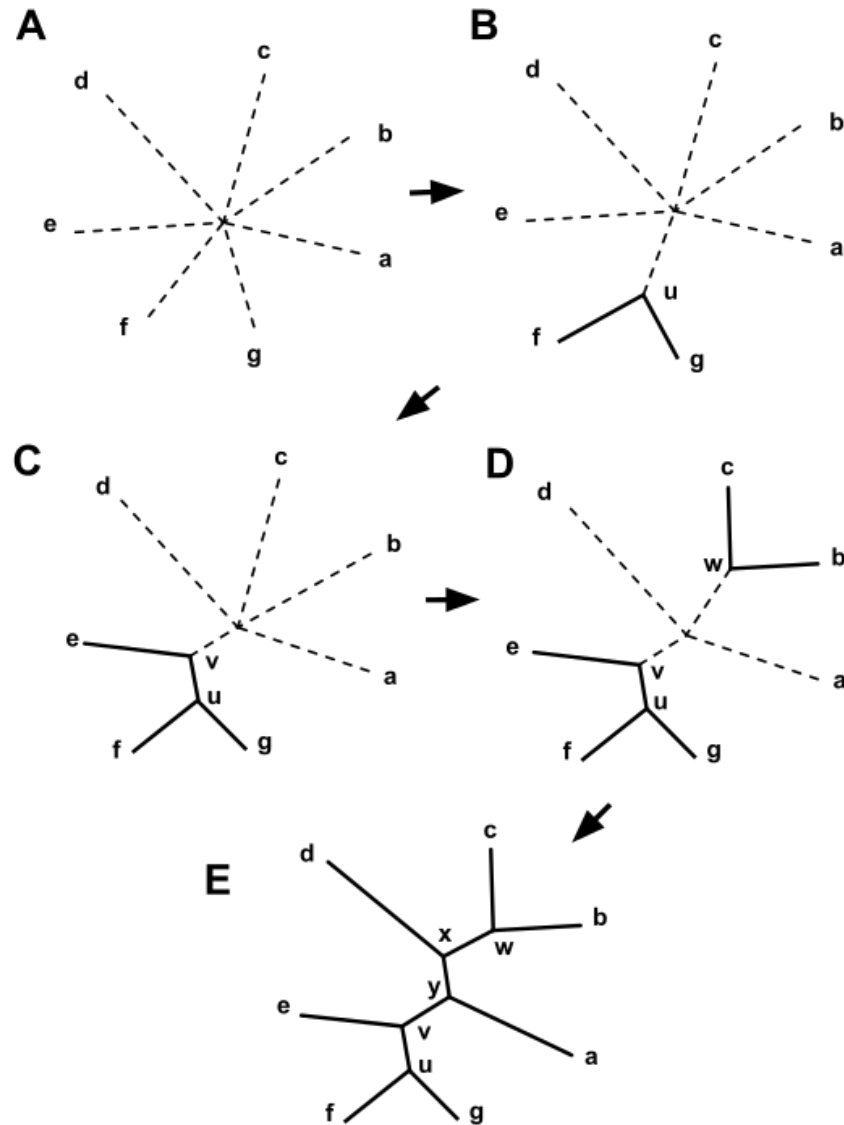
$$F_2(P_1, P_2) = \frac{1}{2} F_{ST} \mathbb{E} H_{\text{exp}}.$$

$$F_2(P_1, P_2) = 2\mathbb{E} T_{12} - \mathbb{E} T_{11} - \mathbb{E} T_{22}$$

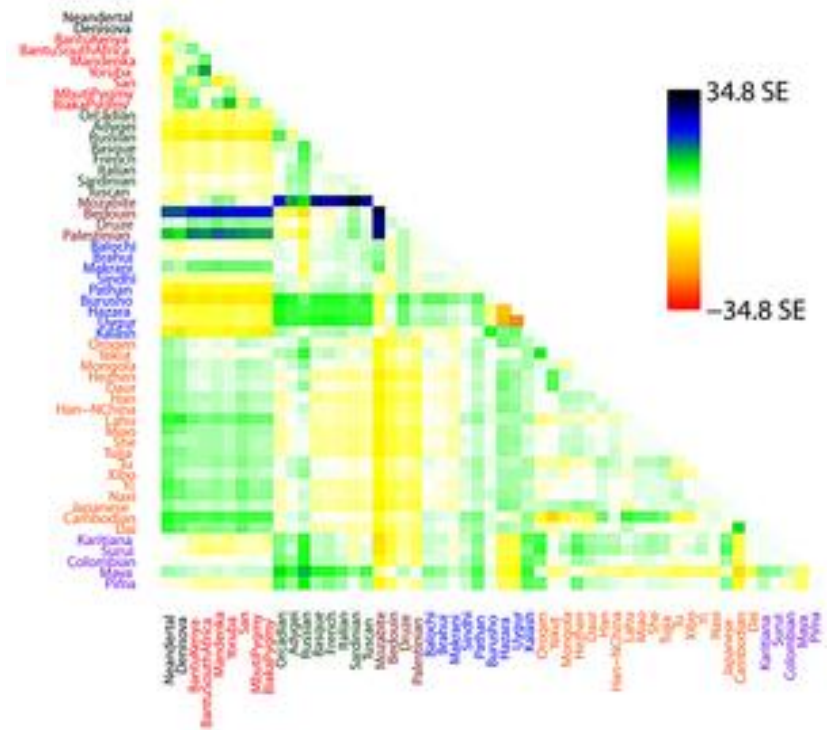
# Quantifying distances among populations



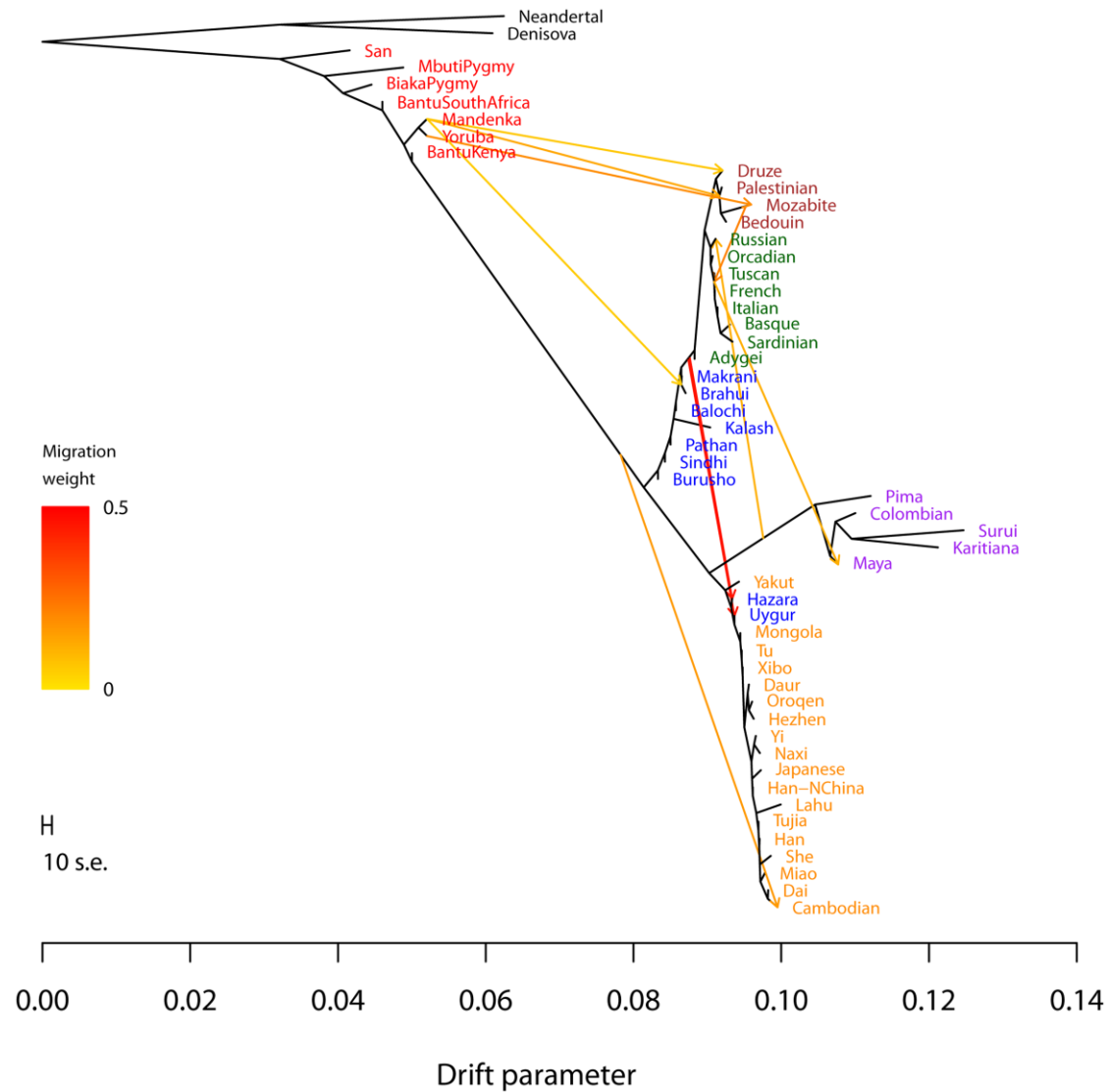
# Neighbour Joining trees



## A

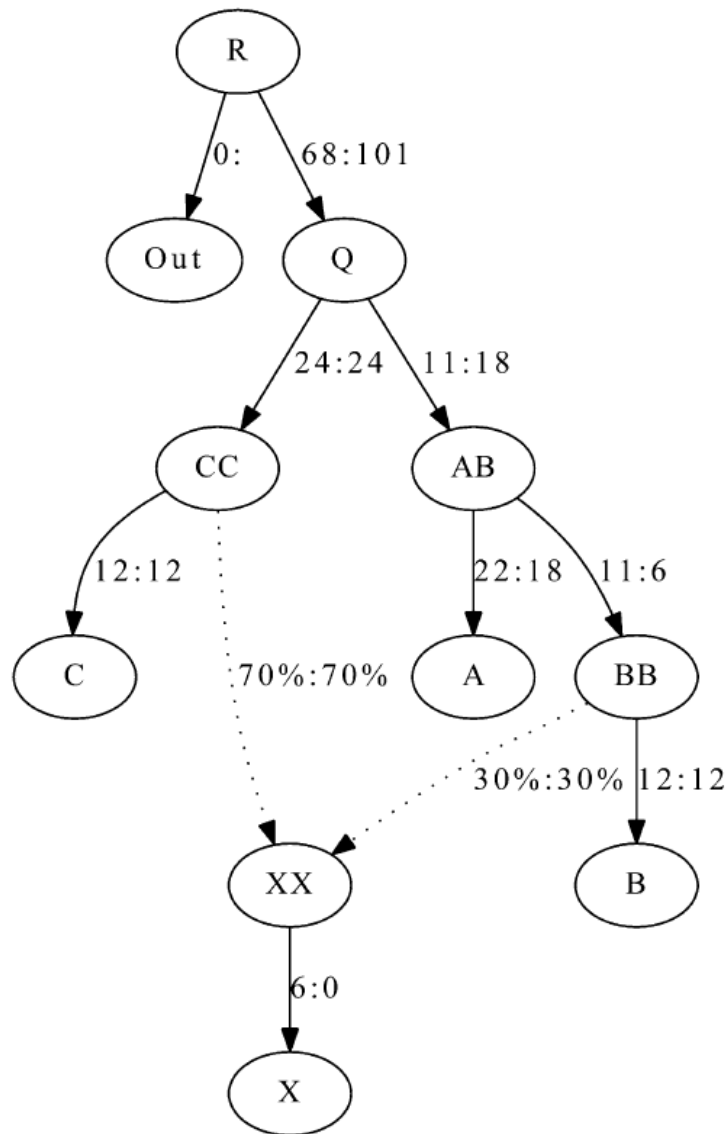


# Treemix





# qpGraph



Fitted on  $F_2$

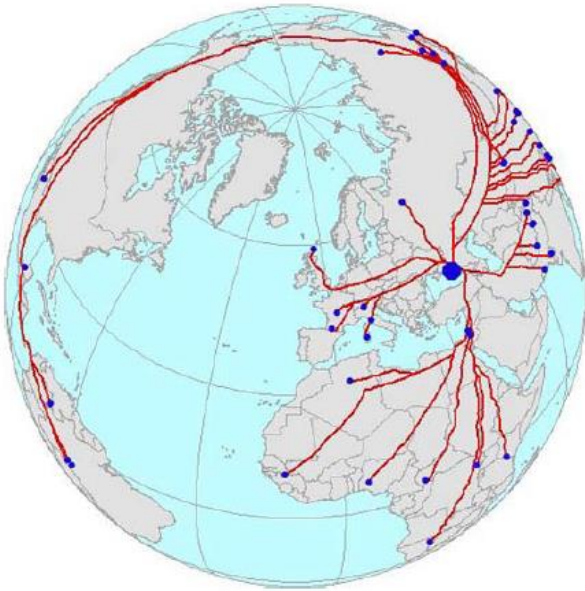
First fit unadmixed skeleton

Then test admixture  
scenarios

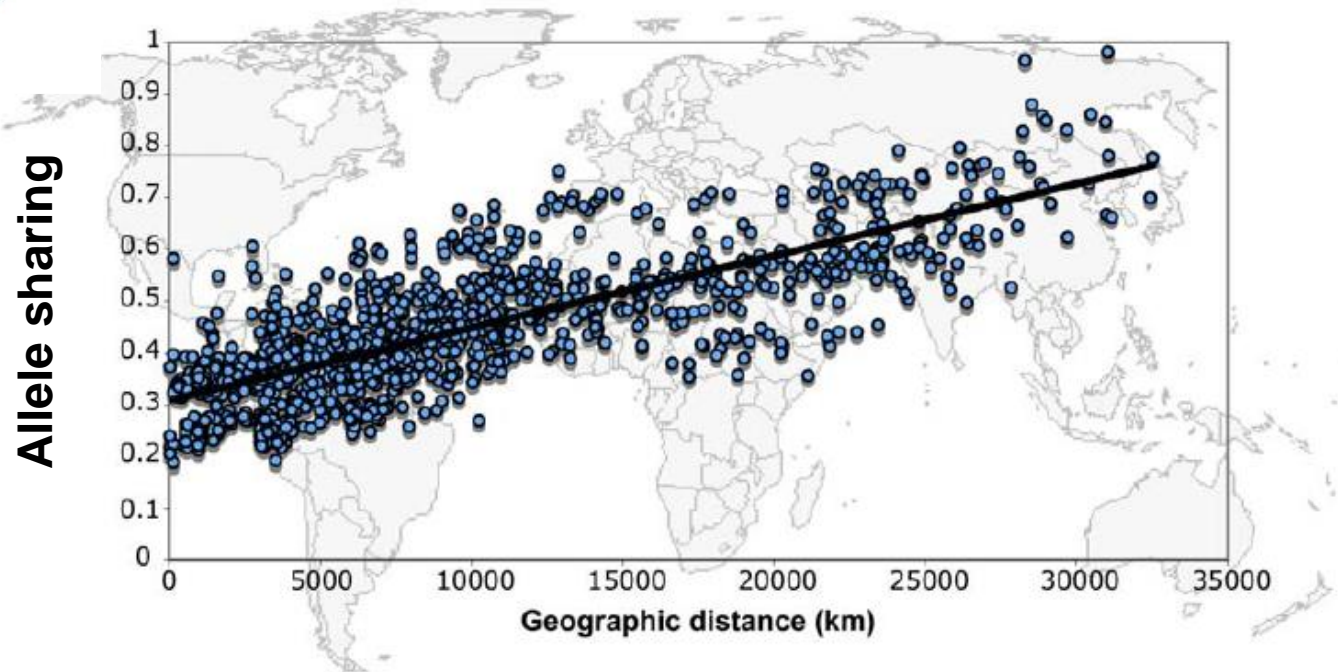
Check for mismatches in  
predicted vs observed  $F_3$   
and  $F_4$

Not exhaustive, multiple  
graphs might fit data  
equally

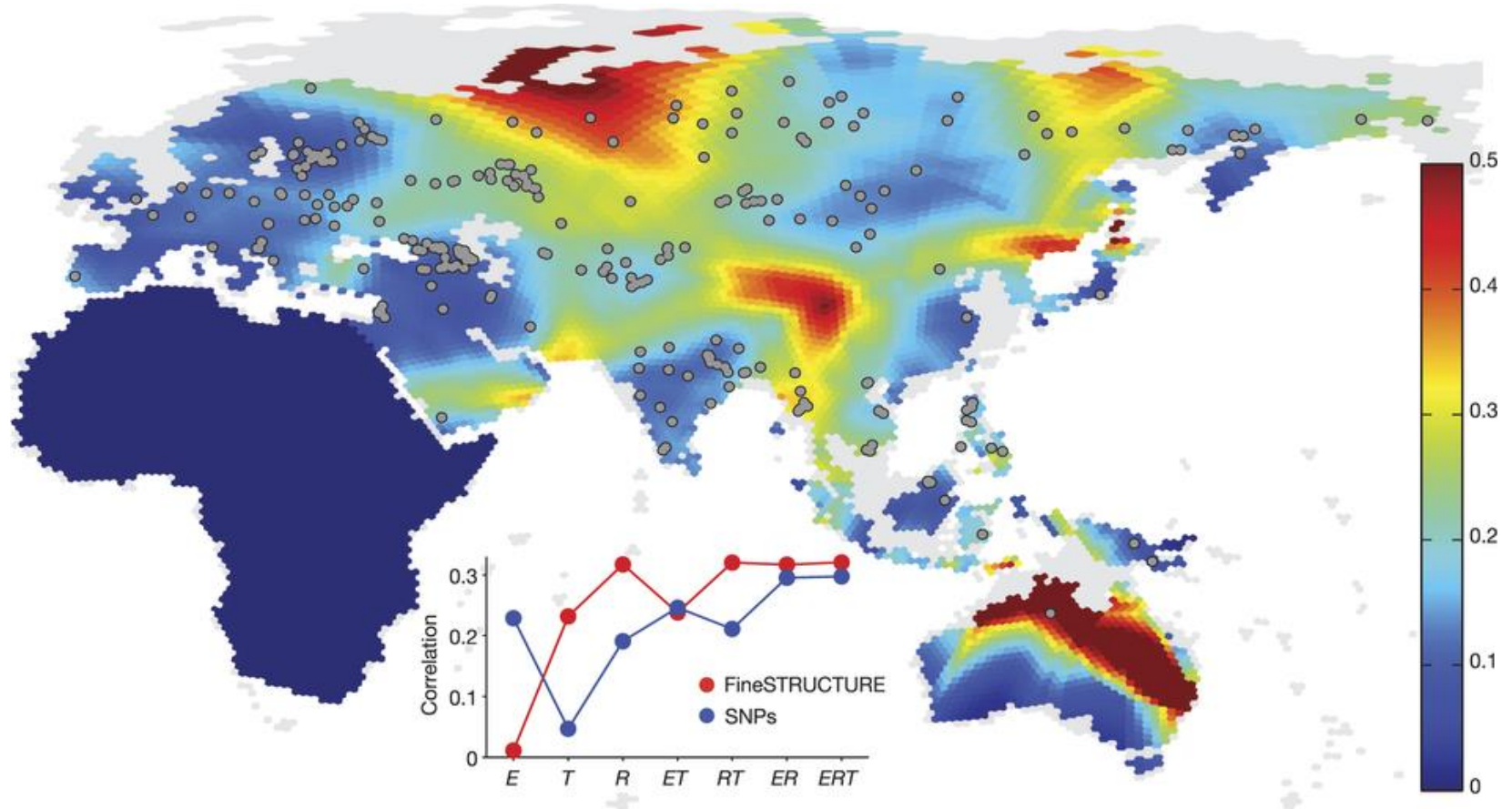
# Using space to model many populations



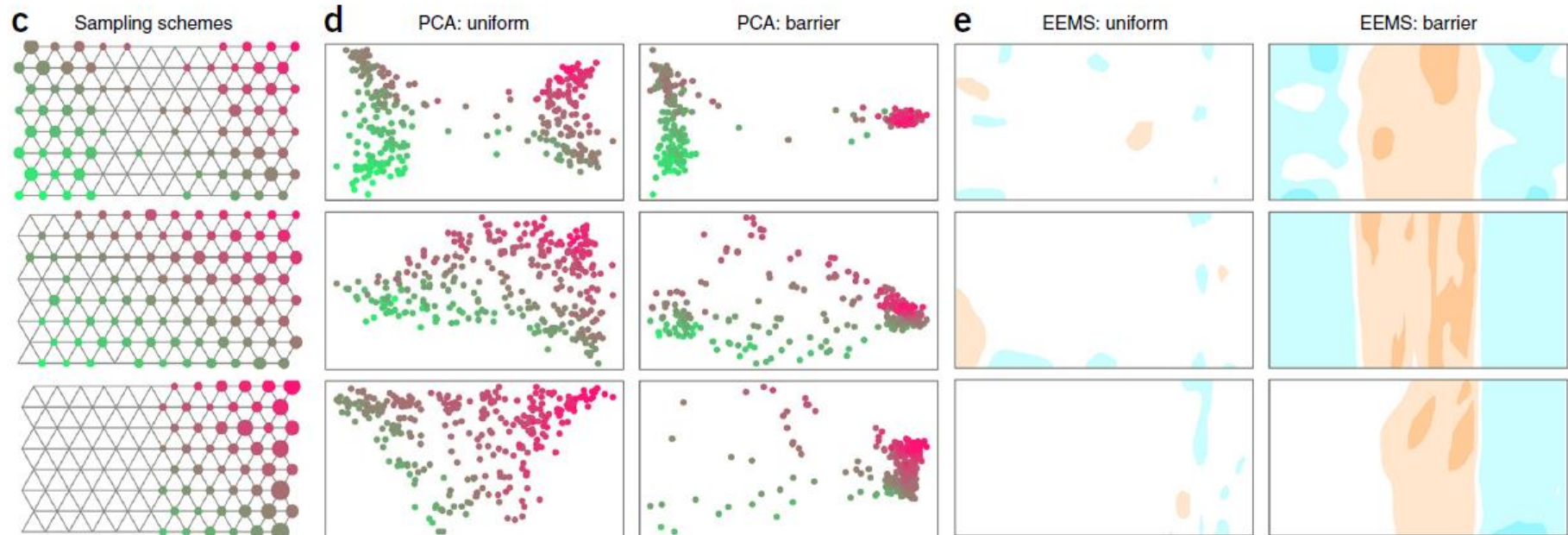
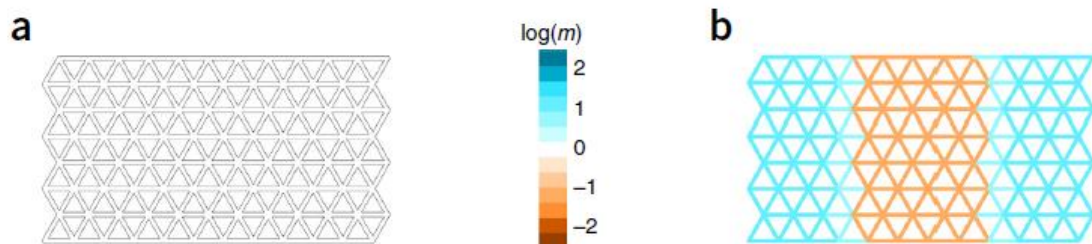
Isolation by distance can explain a lot of differences



# Barriers for human movement

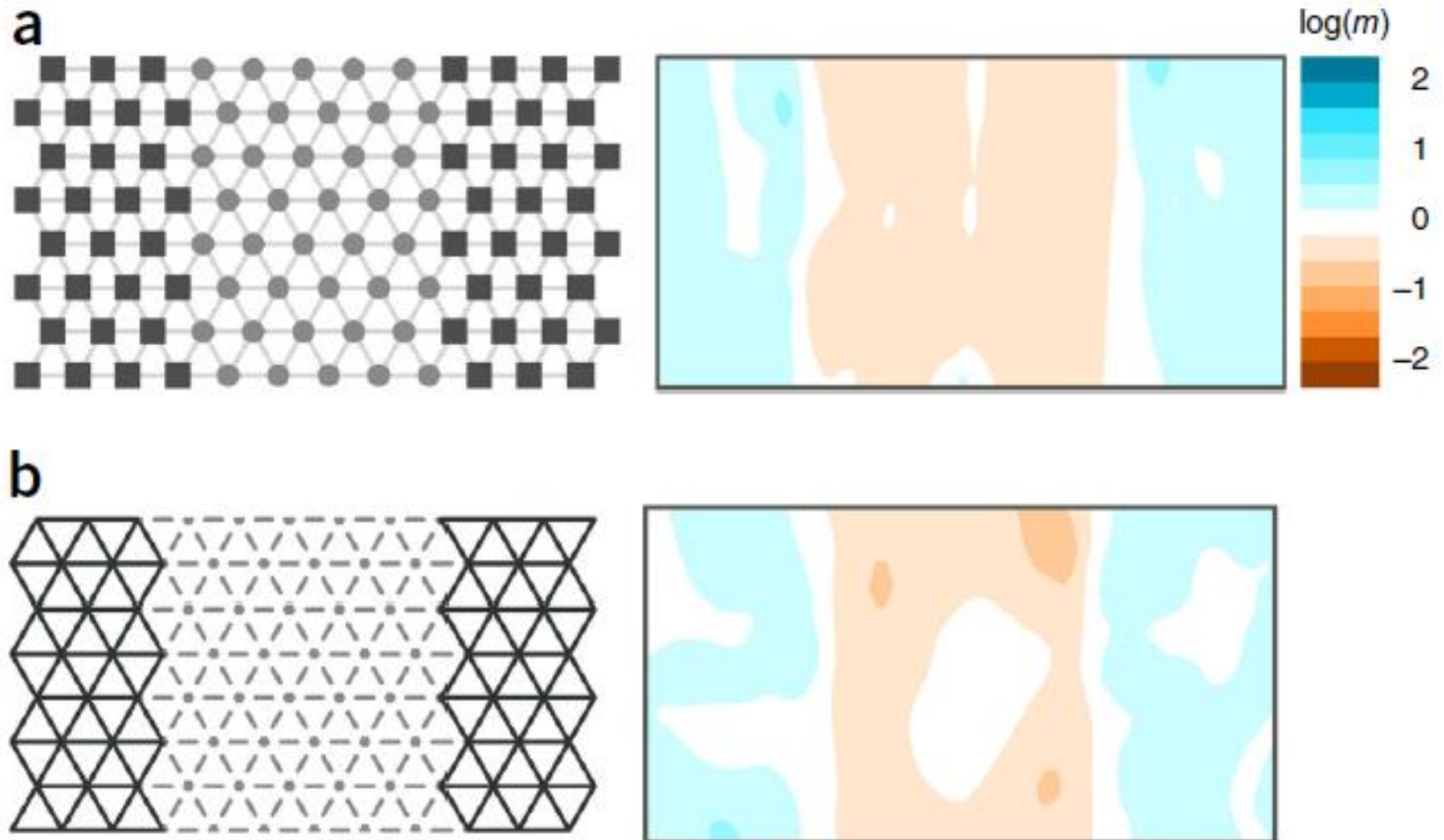


# EMMS



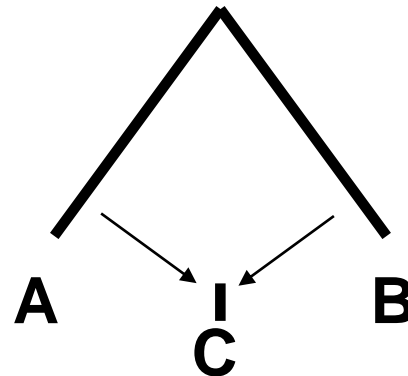
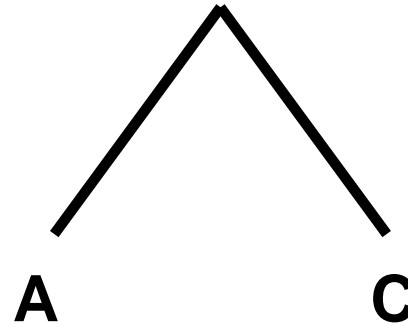


# EMMS – migration vs population size



# Summary

- Quantifying distances between populations
- Building trees
- Admixture Graphs
- Spatial statistics



# Practical

- Use Admixtools to fit admixture graph
- Human dataset with modern and ancient

## qpGraph input file

root    R

label   Name   NameInDataset

label   Mbuti   Mbuti

edge   Name                      Source Destination

edge   R\_Mbuti                  R                  Mbuti

Admix Target Source1                  Source2                  Prop1   Prop2

admix pLBK    X1                  BE                  80                  20