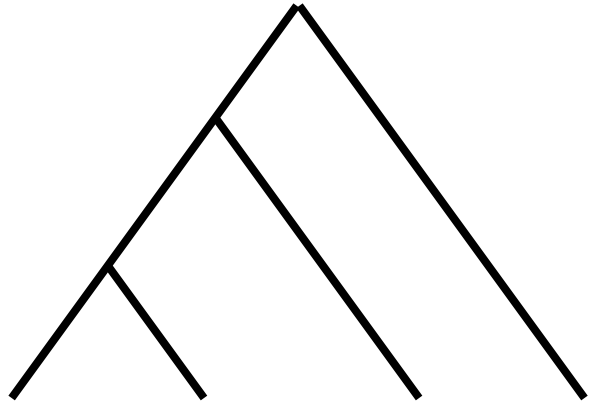
Detecting hybridization with ADMIXTOOLS

Patterson’s D statistics to identify hybridization

- Also called ABBA-BABA test: D=(ABBA-BABA)/(BABA+ABBA)



P1	P2	P3	P4	
T	**T**	A	A	
G	**G**	**G**	T	Concordant SNPs
C	T	T	T	
C	A	**C**	A	Discordant SNPs
A	**T**	**T**	A	

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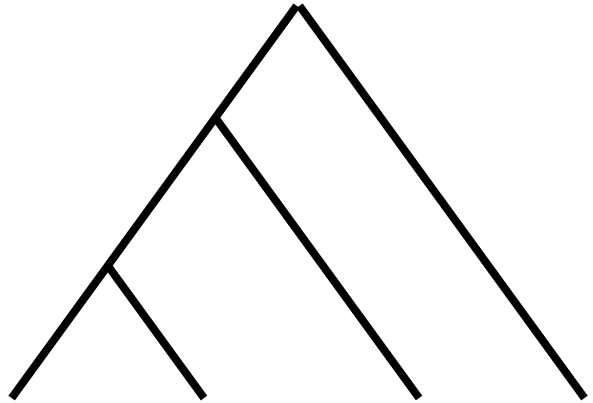
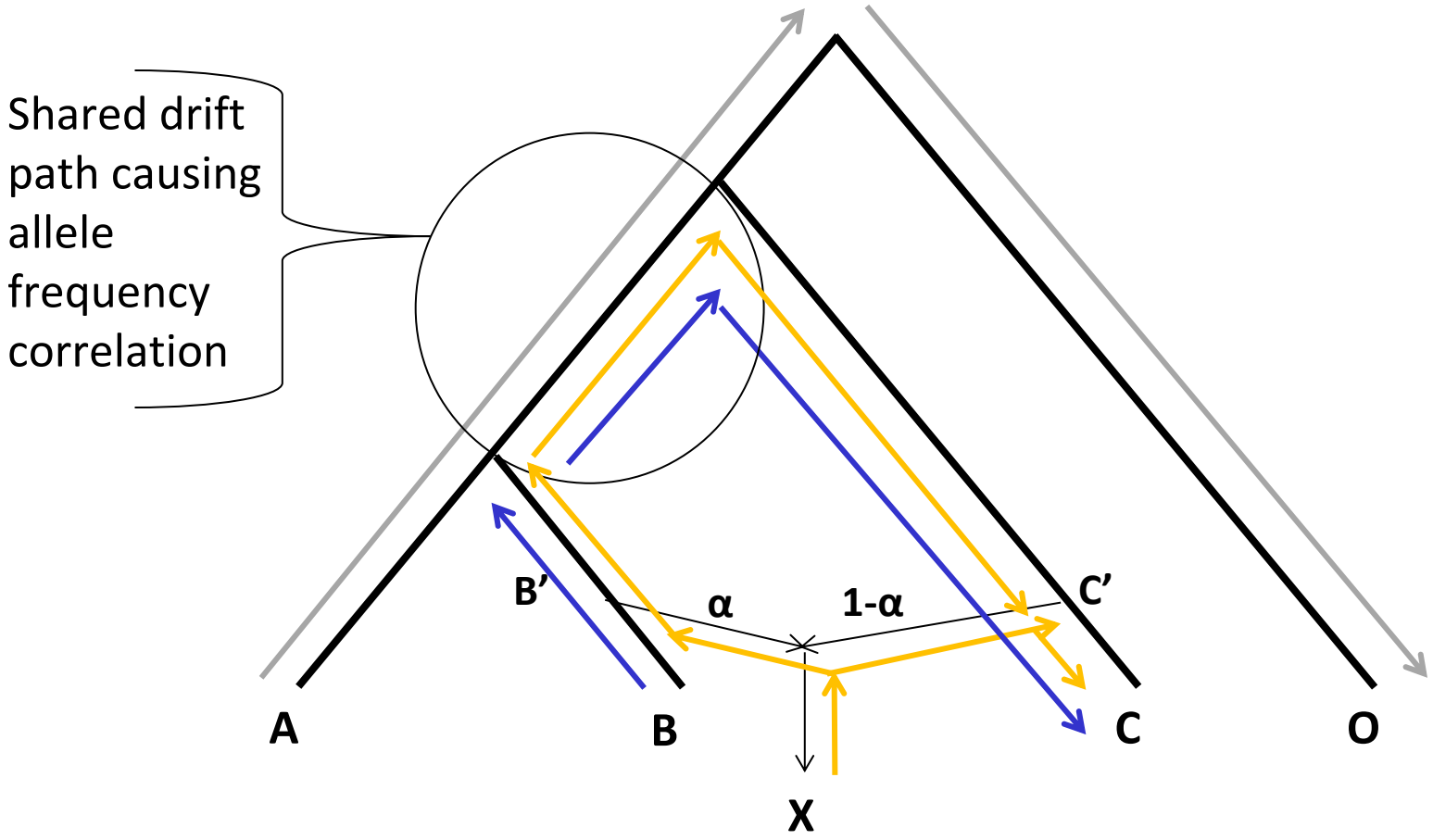


P1	P2	P3	P4	
T	**T**	A	A	
G	**G**	**G**	T	Concordant SNPs
C	T	T	T	
C	A	**C**	A	← BABA
A	**T**	**T**	A	← ABBA
C	**G**	**G**	C	← ABBA

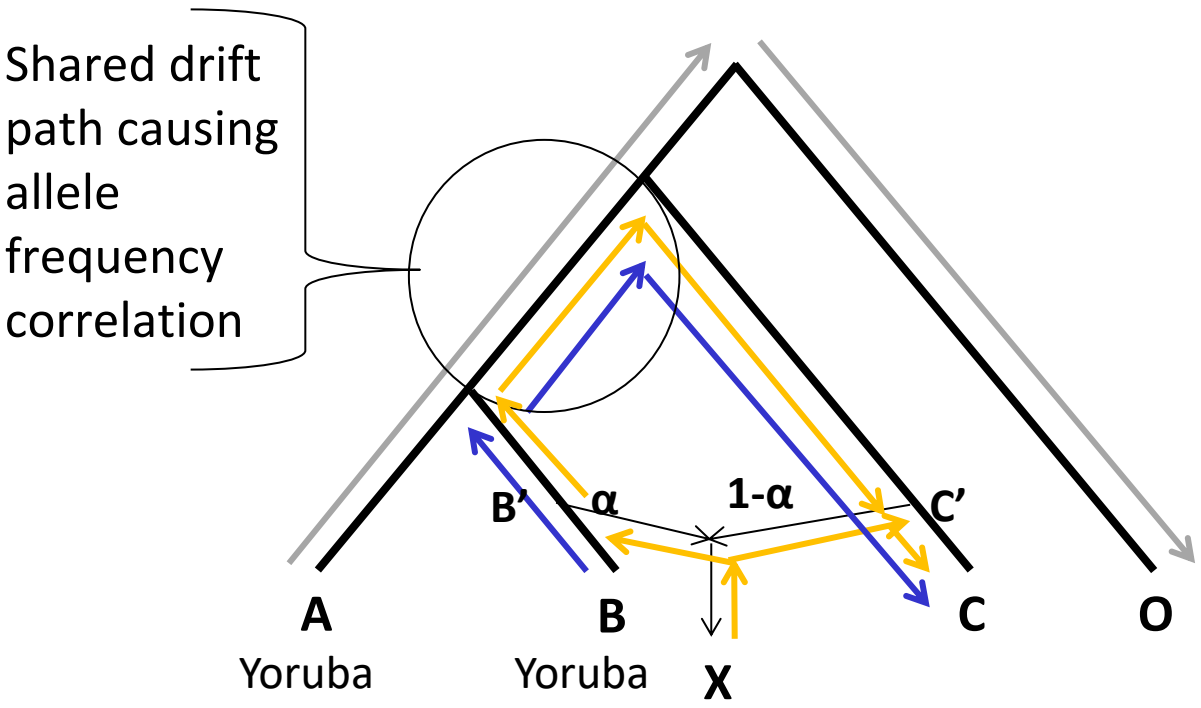
$$D = \frac{BABA - ABBA}{ABBA + BABA}$$

$$D = \frac{1-2}{2+1} = -1/3$$

f4 ratio test to infer the amount of admixture



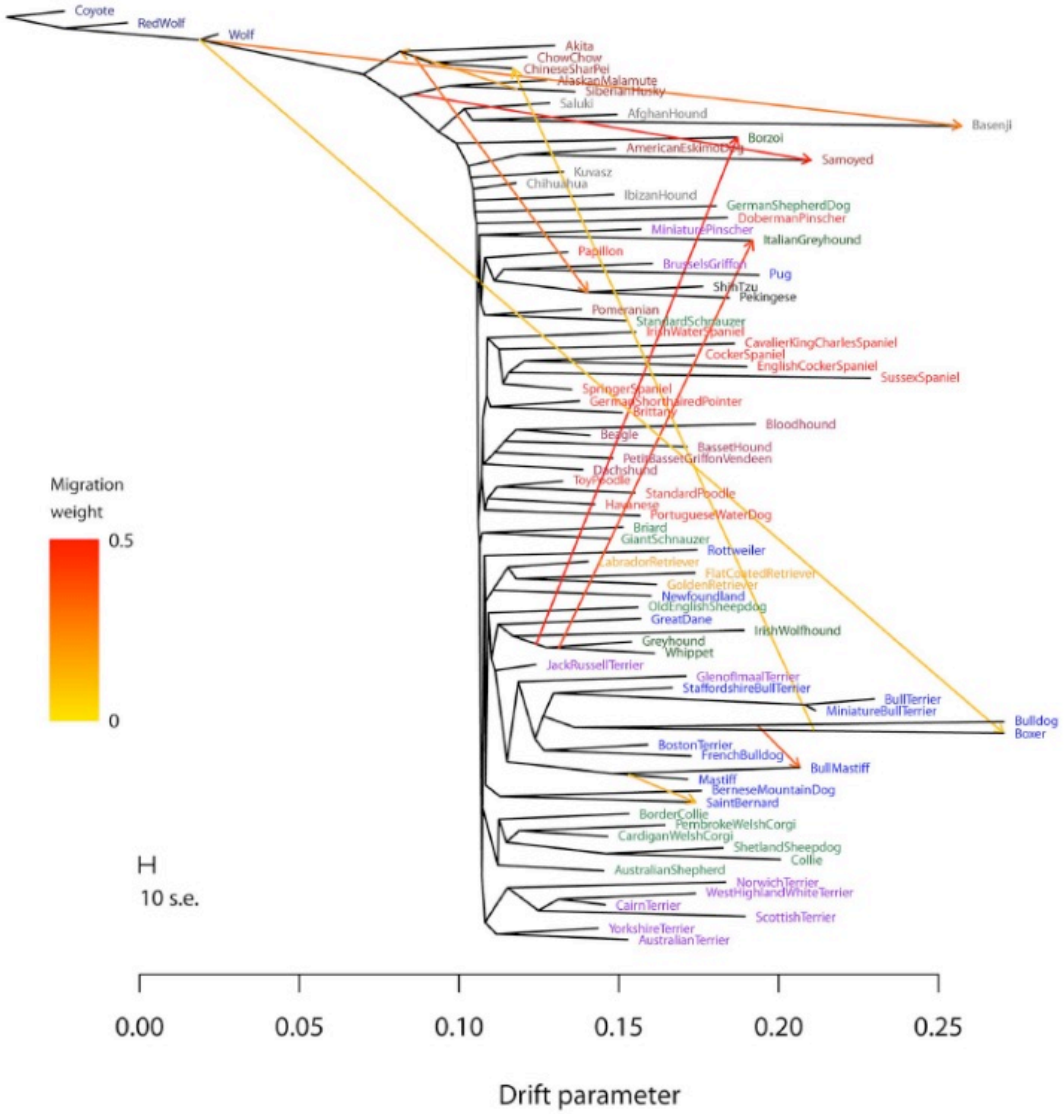
f4 ratio test to infer the amount of admixture



The shared drift path generates correlation between A-O and B-C. X-C share the same drift path by the proportion α.

$$\alpha = \frac{F_4(A,O;\,X,C)}{F_4(A,O;\,B,C)} = \frac{E[(a-o)(x-c)]}{E[(a-o)(b-c)]} = \frac{\text{Correlation of allele frequency difference between a-o and x-c}}{\text{Correlation of allele frequency difference between a-o and b-c}}$$

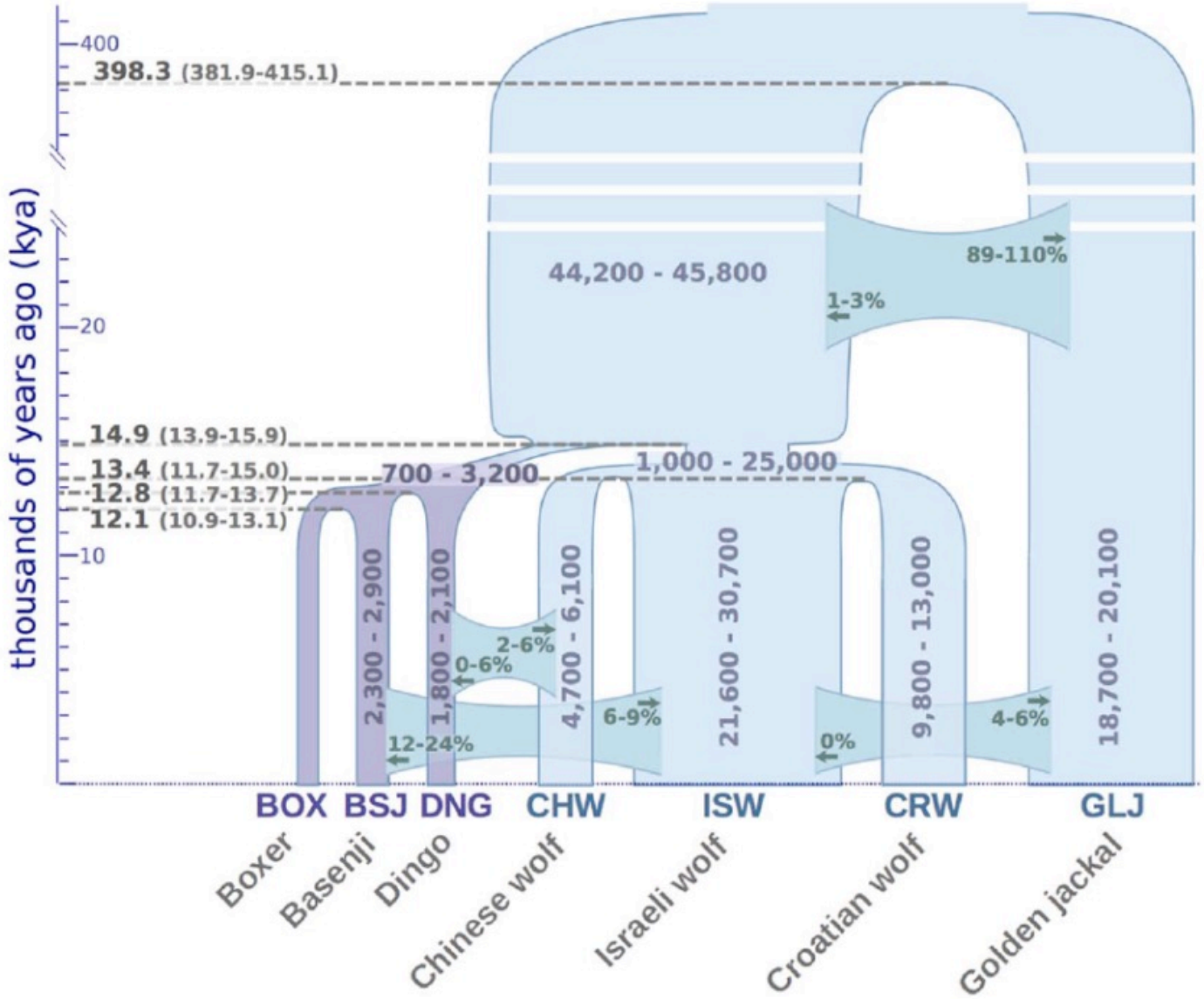
Treemix (Pickrell & Pritchard, 2012, Plos Genetics)

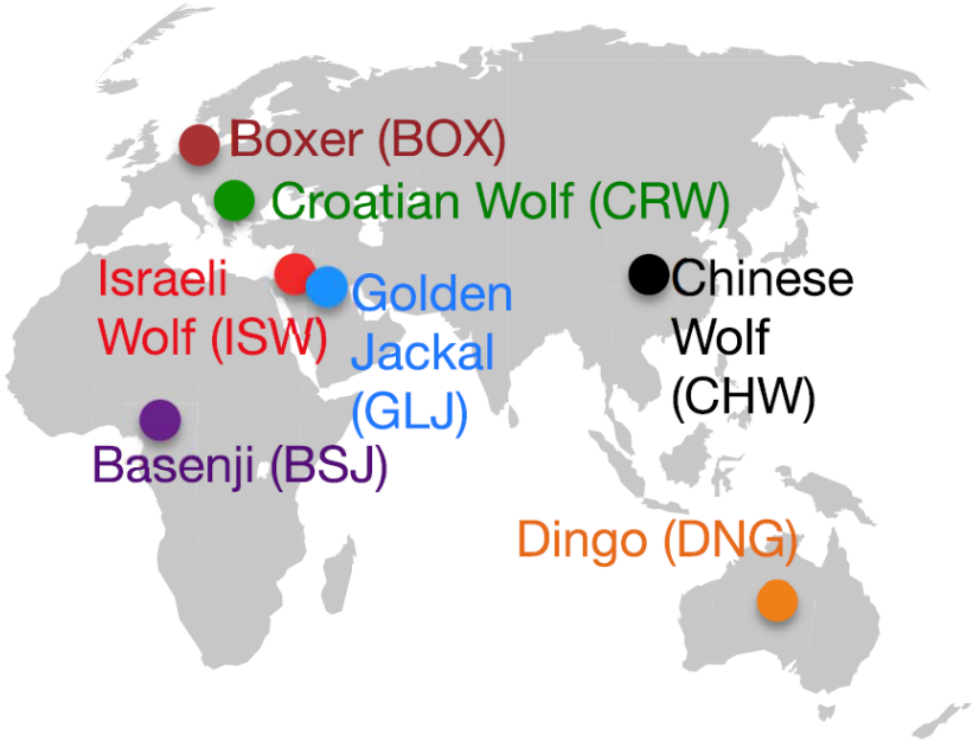


- Treemix uses covariances of allele frequencies to infer a maximum likely tree with a user-specified number of migration edges
- Gene flow edges are added sequentially to account for the greatest errors in the fit. This format makes TreeMix well-suited to handling very large trees: the entire fitting process is automated and can include arbitrarily many admixture events simultaneously.
- Treemix has most problems with inferring the direction of gene flow and sometimes places migration edges to taxa that are closely related but not involved in the hybridization event
- Treemix should not be used as only source of information and may sometimes not work at all…

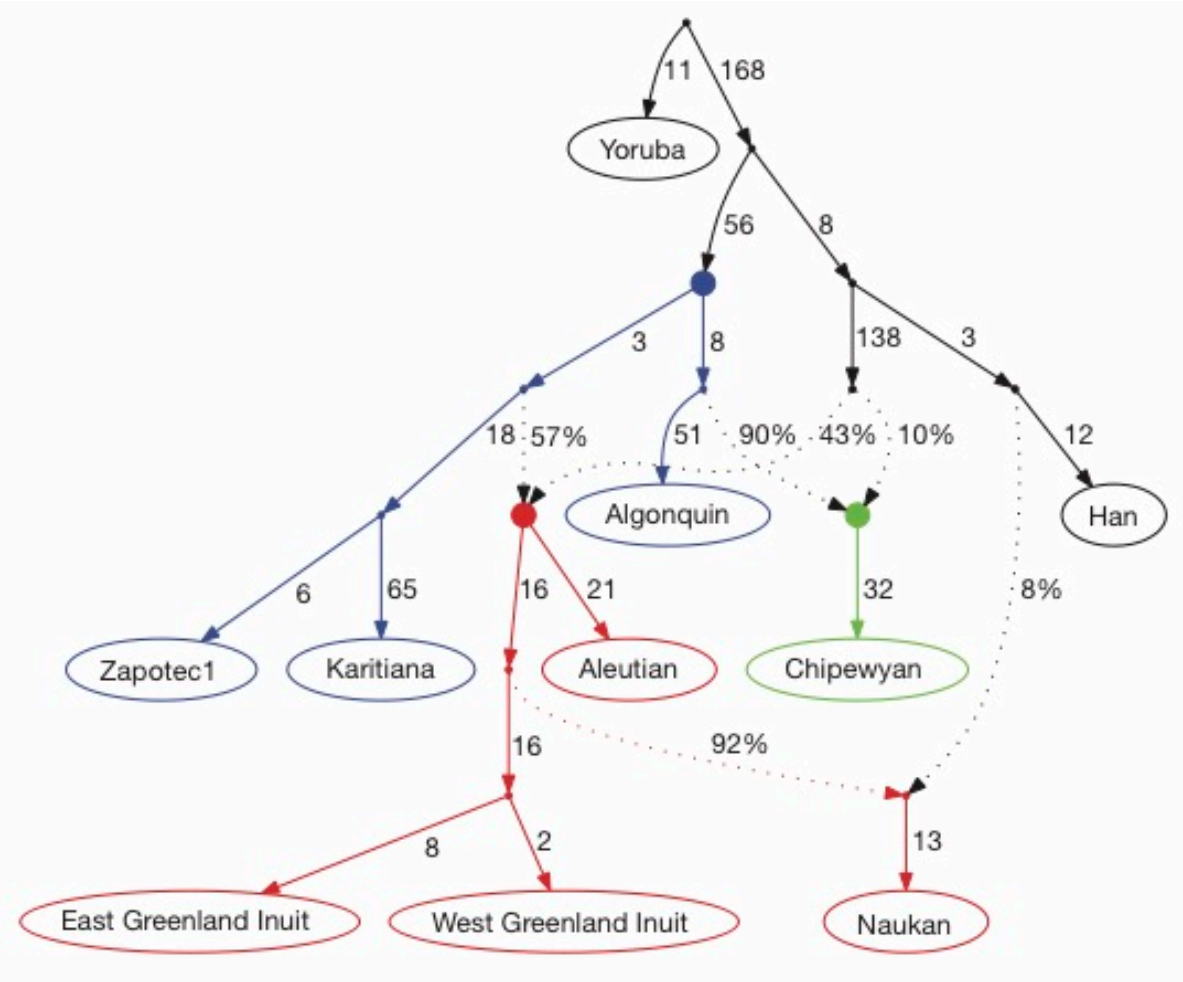
Freedman et al., 2014, PLoS Genetics: GPhoCS

Demographic modeling of population splits and gene flow «bands»





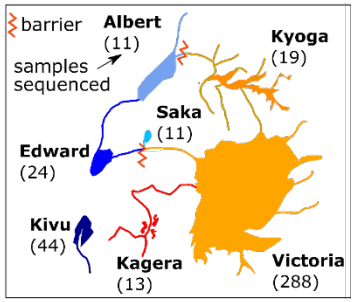
Admixture graphs (Reich et al. 2012)

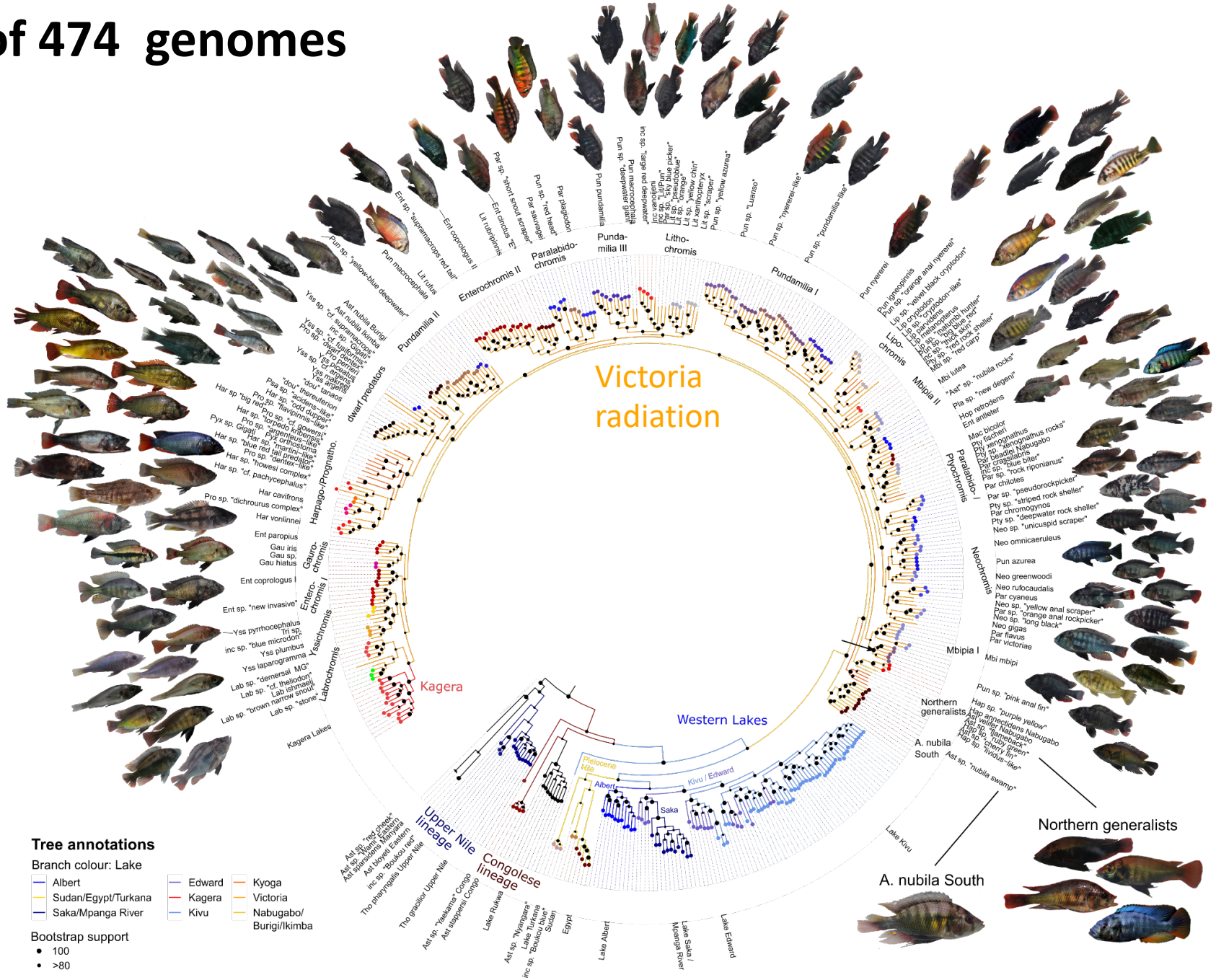


New admixtools R package has a good implementation of admixture graphs but it is still quite badly documented and has some bugs.

https://uqrmaie1.github.io/admixtools/articles/admixtools.html

Phylogeny of 474 genomes





Putative hybrid origin of pelagic dwarf predators

fineSTRUCTURE (genetic similarity matrix)