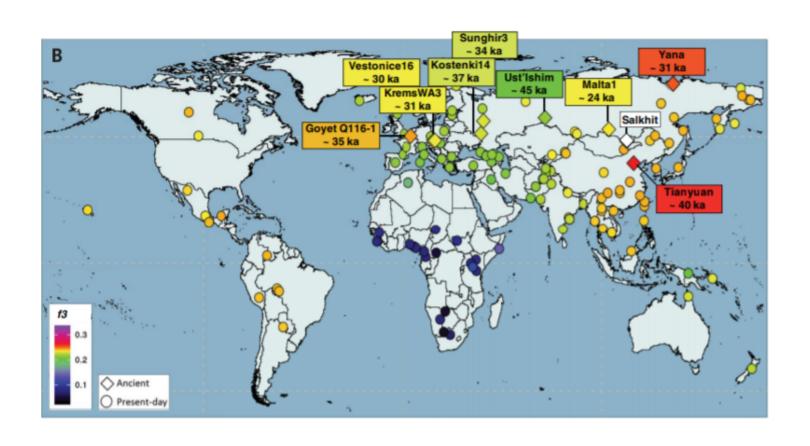
F-statistics and Population Structure

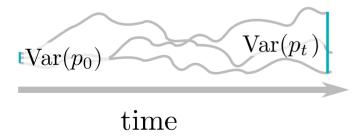
Motivation: Ancient DNA



Setup

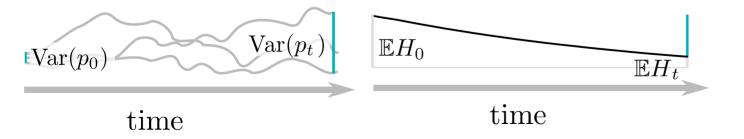
- Today: Theory of F-statistics and Computations
- Tomorrow: Using F-statistics to build more complex models

Decay of Heterozygosity



Decay of Heterozygosity

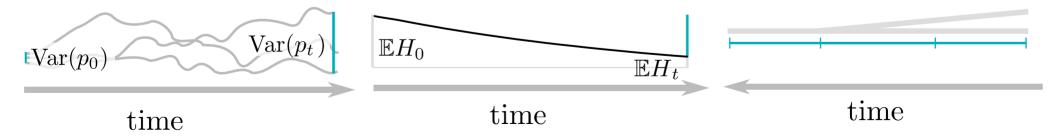
Change in Allele Frequency



Decay of Heterozygosity

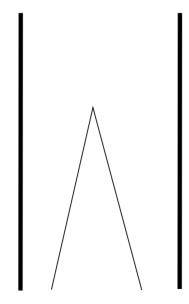
Change in Allele Frequency

Coalescence rates



Pairwise differences

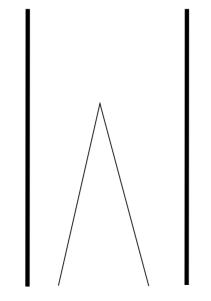
$$\mathbb{E}[\pi] = 4N\mu = \theta$$

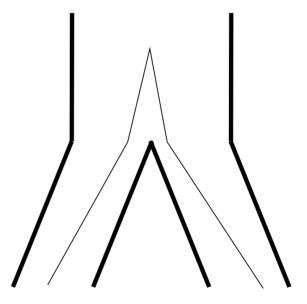


Pairwise differences

$$\mathbb{E}[\pi] = 4N\mu = \theta$$

$$\mathbb{E}[\pi_{12}] = t_{12} + 4N_{anc}\mu = \theta$$



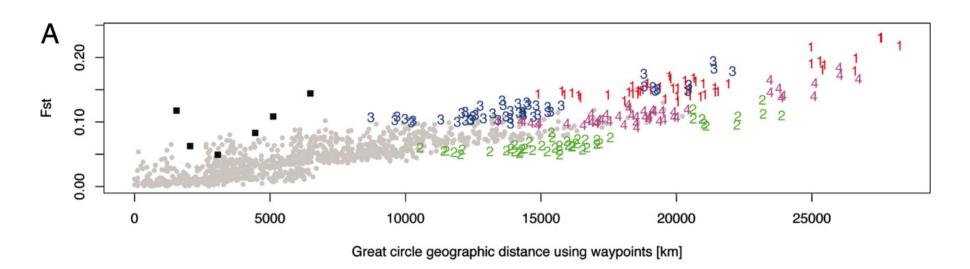


Fixation Index F_{ST}

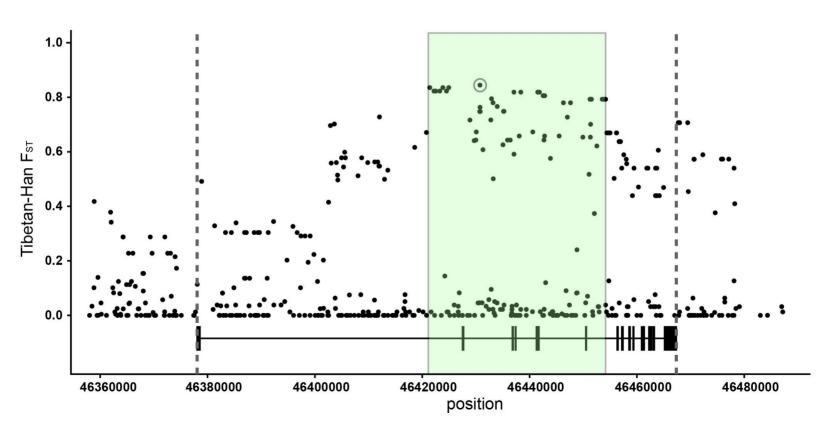
$$F_{ST}(P_1, P_2) = \frac{\pi_{12} - \frac{\pi_1 + \pi_2}{2}}{\pi_{12}}$$

- F_{ST} is a correlation coefficient
- Between 0 and 1
- Hierarchical partitioning (AMOVA)
- Many estimators exist
 - Hudson (1991)
 - Weir & Cockerham (1984)

Fixation Index $F_{\rm st}$



F_{ST} Outliers



Huerta-Sanchez et al. 2014

F_2 -statistic

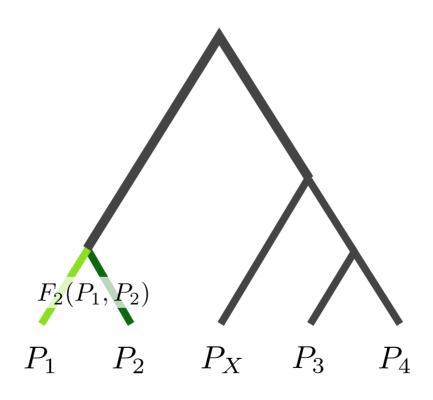
$$F_{ST}(P_1, P_2) = \frac{\pi_{12} - \frac{\pi_1 + \pi_2}{2}}{\pi_{12}}$$

- F_{ST} is a correlation coefficient
- Between 0 and 1
- Hierarchical partitioning (AMOVA)
- Many estimators exist
 - Hudson (1991)
 - Weir & Cockerham (1984)

$$F_2(P_1, P_2) = 2\pi_{12} - \pi_1 - \pi_2$$
$$= \sum_{l} (p_{1l} - p_{2l})^2$$

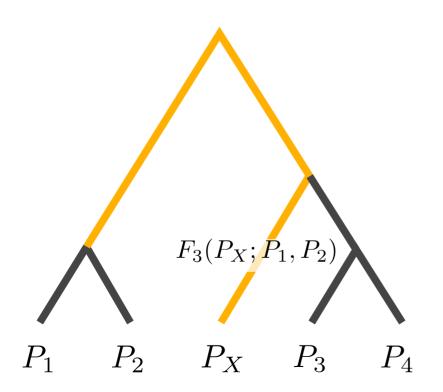
- F₂ is a covariance
- Bigger than 0
- Tree-additive
- Testing for treeness

Tree-additive



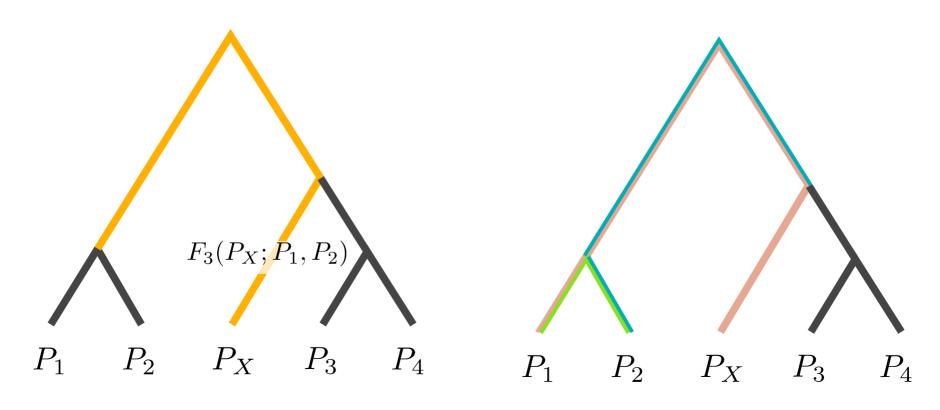
F_{3} -statistic

Given all F2-values, how can we calculate the yellow branch length?



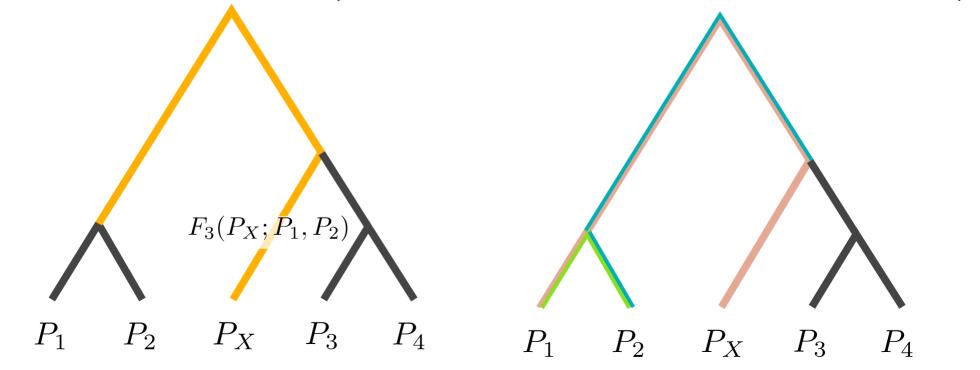
F_{3} -statistic

Given all F2-values, how can we calculate the yellow branch length?



F_{3} -statistic

$$F_3(P_X; P_1, P_2) = \frac{1}{2} \left(F_2(P_X, P_1) + F_2(P_X, P_2) - F_2(P_1, P_2) \right)$$



F_{3} -statistic equations

$$F_3(P_X; P_1, P_2) = \frac{1}{2} \left(F_2(P_X, P_1) + F_2(P_X, P_2) - F_2(P_1, P_2) \right)$$

$$F_3(P_X; P_1, P_2) = \sum_{l} (p_{xl} - p_{x1})(p_{xl} - p_{x2})$$

$$F_3(P_X; P_1, P_2) = \pi_{1x} + \pi_{2x} - \pi_{12} - \pi_x$$

(Branch)-F₄-statistic

$$F_4^{(B)}(P_1, P_2; P_3, P_4) = \frac{1}{2} \left(F_2(P_1, P_3) + F_2(P_2, P_4) - F_2(P_1, P_2) - F_2(P_3, P_4) \right)$$

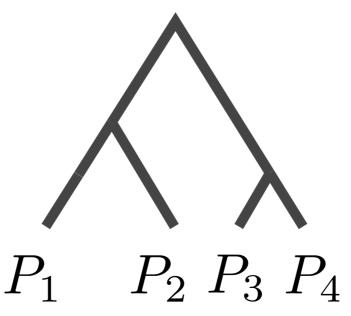


What if we reorder the arguments?

$$F_4^{(T)}(P_1, P_2; P_3, P_4) = F_4^{(B)}(P_1, P_4; P_3, P_2)$$

(Treeness)-F₄-statistic

$$F_4^{(T)}(P_1, P_2; P_3, P_4) = \frac{1}{2} \left(F_2(P_1, P_3) + F_2(P_2, P_4) - F_2(P_1, P_4) - F_2(P_2, P_3) \right)$$



F_{A} -statistic-equations

$$F_4^{(T)}(P_1, P_2; P_3, P_4) = \frac{1}{2} \left(F_2(P_1, P_3) + F_2(P_2, P_4) - F_2(P_1, P_4) - F_2(P_2, P_3) \right)$$

$$F_4^{(T)}(P_1, P_2; P_3, P_4) = \sum_{l} (p_{l1} - p_{l2})(p_{l3} - p_{l4})$$

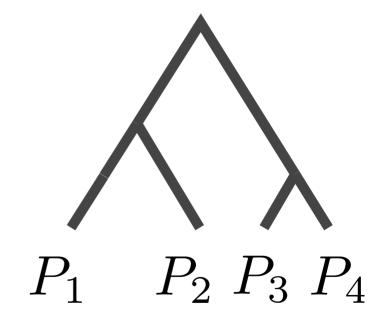
$$F_4^{(T)}(P_1, P_2; P_3, P_4) = \pi_{13} + \pi_{24} - \pi_{14} - \pi_{23}$$

Testing Treeness

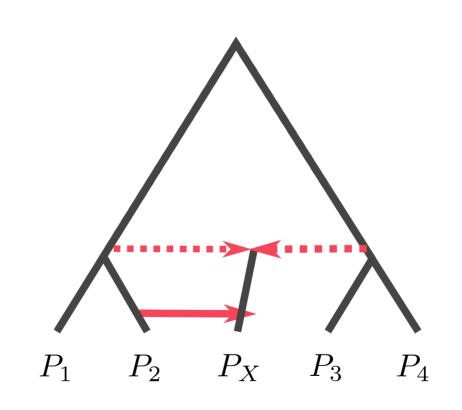
If data is generated from a tree:

$$F_3(P_3; P_1; P_2) \ge 0$$

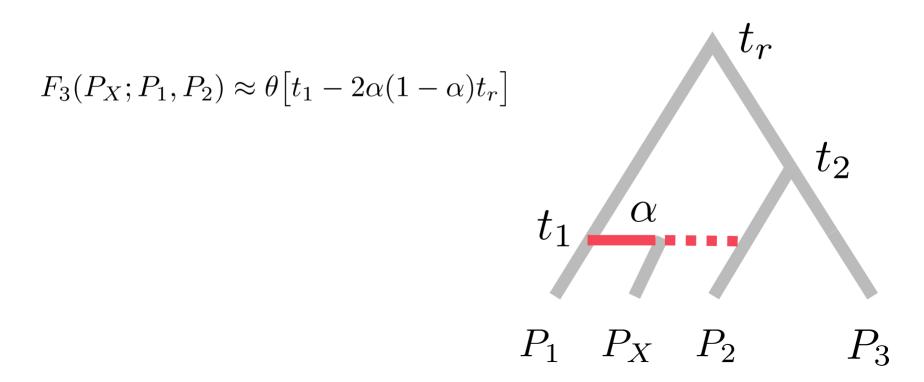
 $F_4^{(T)}(P_1, P_2; P_3, P_4) = 0$



Admixture Graphs



F3 in an admixture graph



F3 in an admixture graph

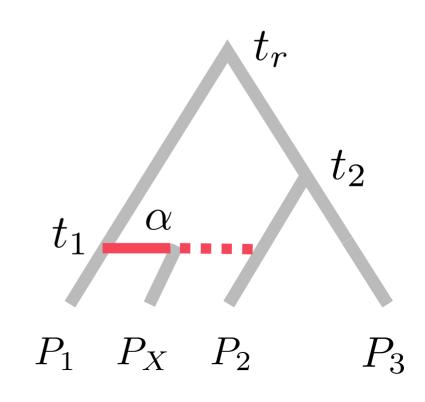
$$F_3(P_X; P_1, P_2) = \pi_{1x} + \pi_{2x} - \pi_{12} - \pi_x$$

$$F_3(P_X; P_1, P_2) \approx \theta \left[t_1 - 2\alpha(1 - \alpha)t_r\right]$$

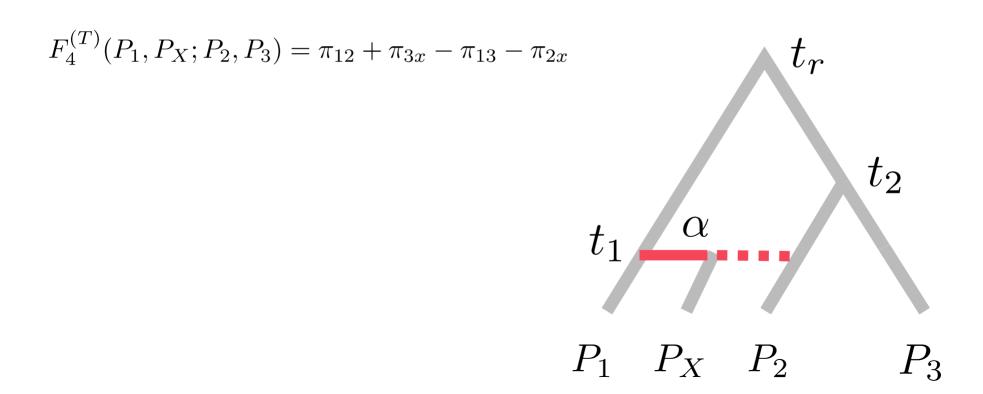
$$t_1 \qquad \qquad t_2$$

$$P_1 \qquad P_X \qquad P_2 \qquad P_3$$

F4 in an admixture graph



F4 in an admixture graph



F4 in an admixture graph

$$F_4^{(T)}(P_1, P_X; P_2, P_3) = \pi_{12} + \pi_{3x} - \pi_{13} - \pi_{2x}$$
 t_r

$$F_4^{(T)}(P_1, P_X; P_2, P_3) = (1 - \alpha)(t_2 - t_1) \neq 0$$

$$t_1 \qquad \alpha$$

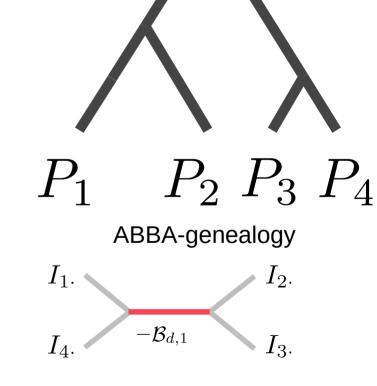
$$P_1 \quad P_X \quad P_2 \qquad P_3$$

D-statistic

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

D-statistic and F4 are closely related

$$F_4^{(T)}(P_1, P_2; P_3, P_4) = \pi_{13} + \pi_{24} - \pi_{14} - \pi_{23}$$



concordant BABA-genealogy
$$I_1$$
. I_3 . I_1 . I_2 . I_3 . I_4 . I_3 . I_4 . I_5 .

F4-ratio

$$\alpha = 1 - \frac{F_4^{(B)}(P_I, P_1; P_X, P_O)}{F_4^{(B)}(P_I, P_1; P_2, P_O)}$$

