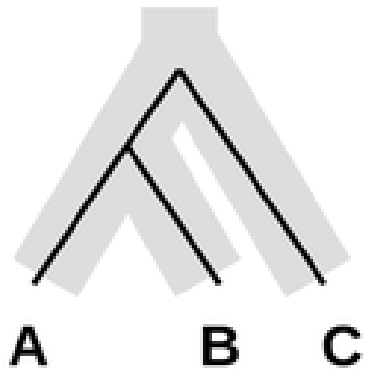


# **Detecting hybridisation with Dstatistics**

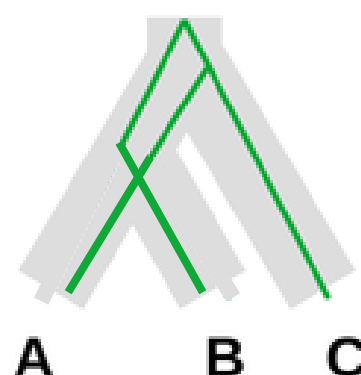
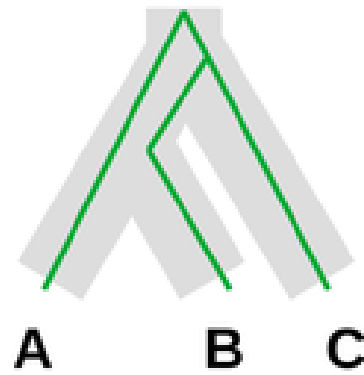
# Incomplete lineages sorting and introgression lead to gene tree that differ from the species tree

Gene tree is concordant/  
matching with species tree

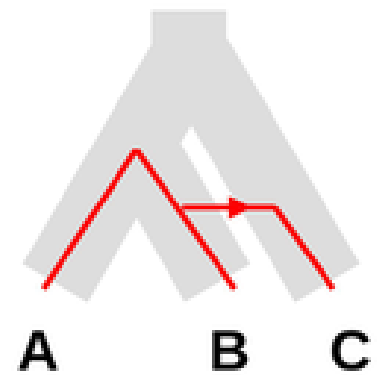


**Gene trees discordant/  
different from species tree**

Incomplete lineage sorting

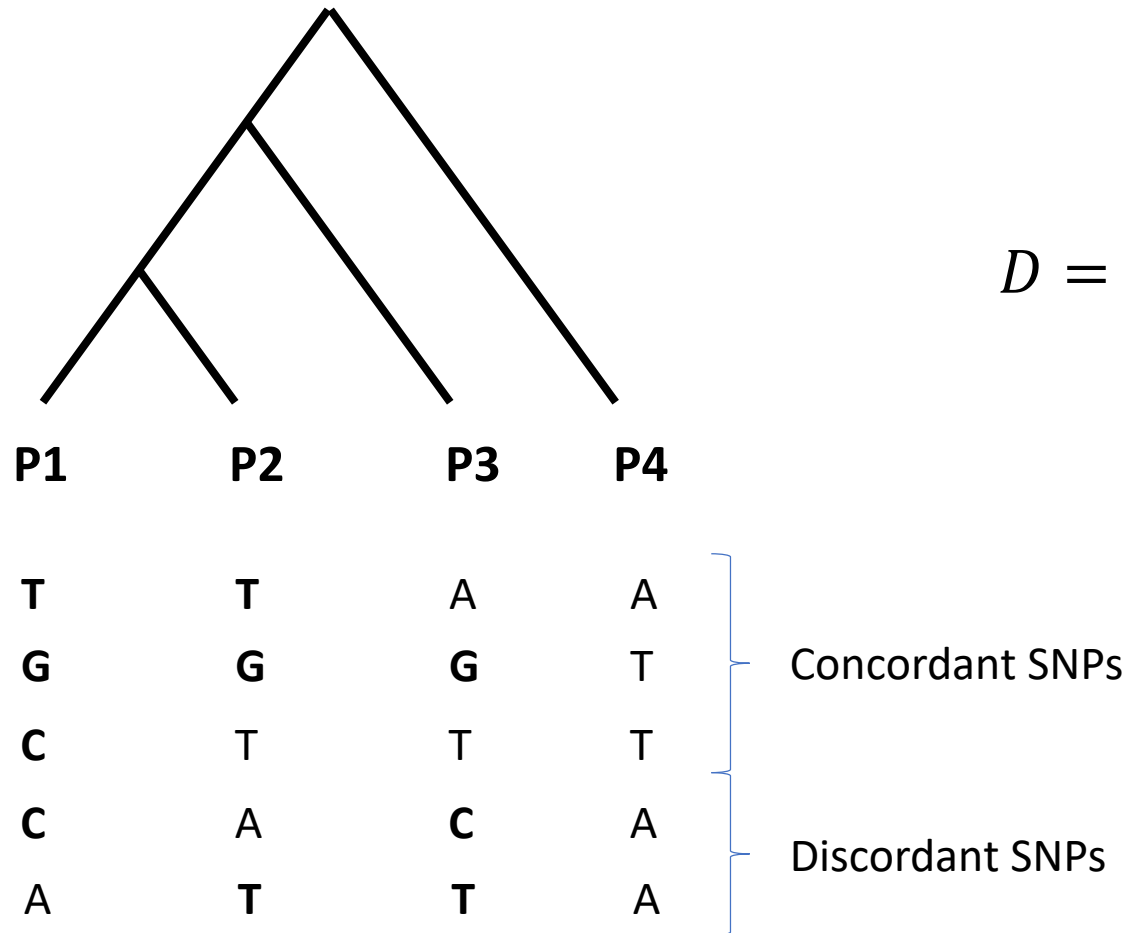


introgression



# Patterson's D statistics to identify hybridisation

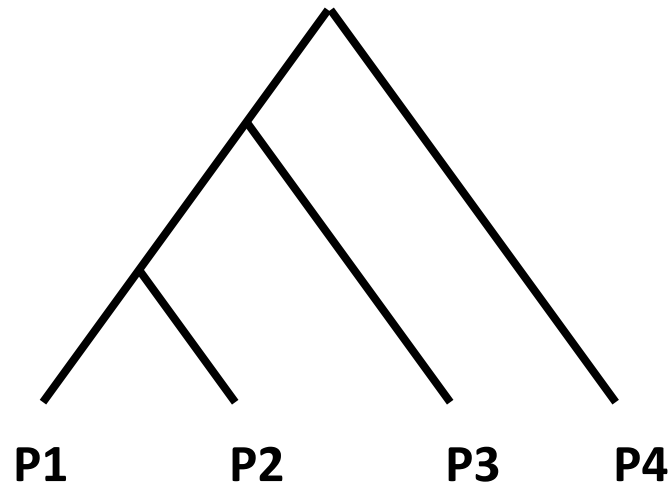
- Also called ABBA-BABA test:  $D = (ABBA - BABA) / (BABA + ABBA)$



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

# Patterson's D statistics to identify hybridisation

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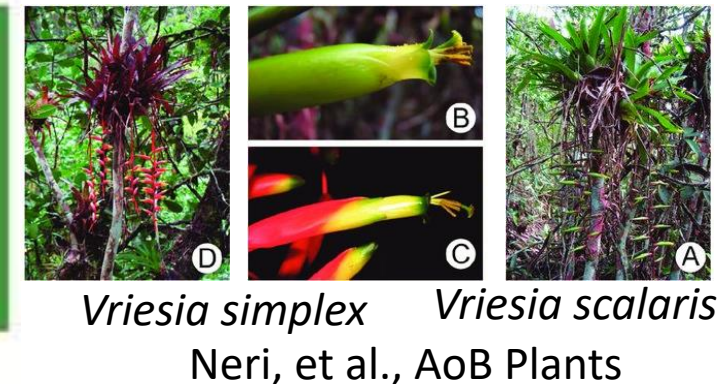
$$D = \frac{ABBA - BABA}{ABBA + BABA}$$

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

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

# Dstatistics

- Require 4 populations/species, whereby one is more introgressed than its sister population/species
- Cannot show the direction of introgression -> for that, we can use Dfoil (see tutorial) with five populations/species
- Do not show if introgression is ancestral to all individuals, or if it is still ongoing -> for that, we can use ADMIXTURE or STRUCTURE which will show if some individuals are more introgressed



# Testing for introgression between *Mechanitis nesaea* and *M. lysimnia*

