

John Maynard Smith - How much recombination is there?

Penicillin resistance

- penicillin binding sites
- recombination event required to acquire resistance

what are nucleotide substitutions in newly acquired segment

How show recombination?

- alignments + statistics
- linkage disequilibrium (Feldman)

$$D_A = \frac{V_k}{\sum (V_k)^{-1}}$$

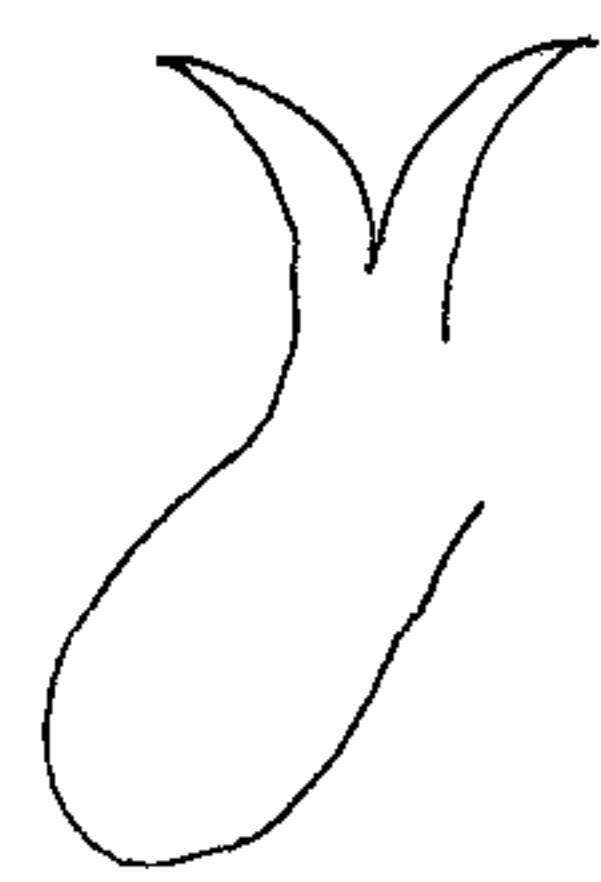
Nei gen 0.04 +/- 0.04 (indicated recomb ↑)

Sale typ 3.11 +/- 0.09 " " "

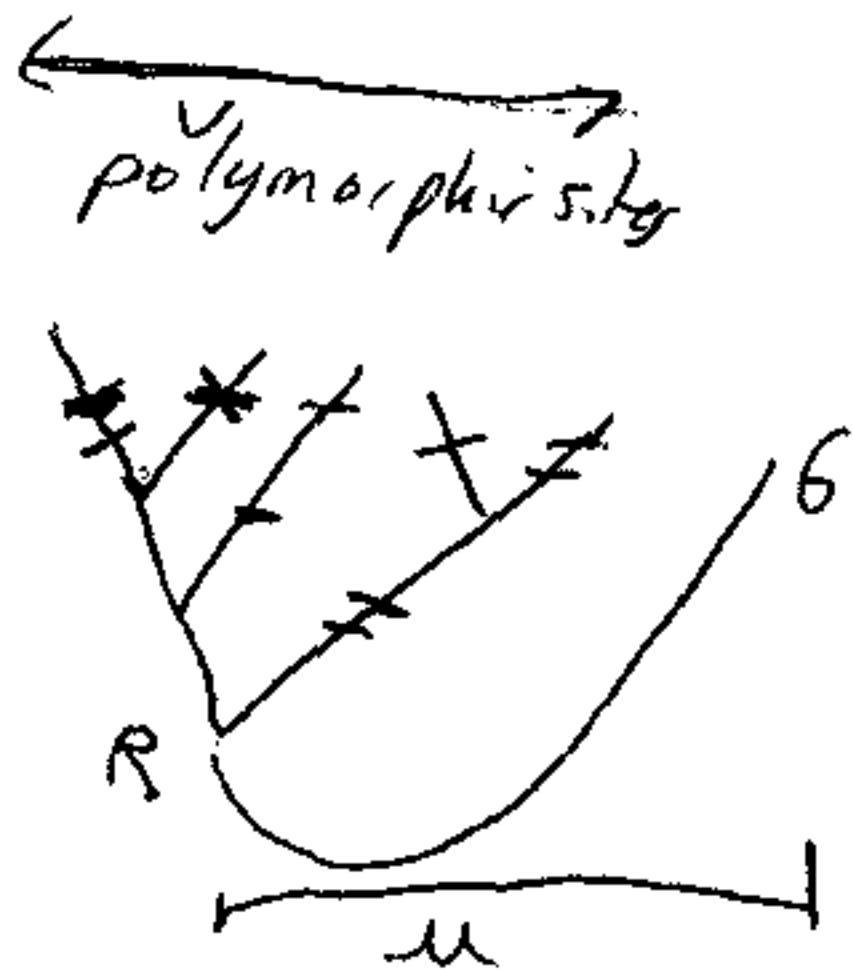
but probably due to separate subpopulations

parallel trees of same gene

argF } similar phylogenies
 rcaA }
 adk - different than argF, rcaA



But we ignore selection agst transfer of certain genes



How calculate expectation for recombining strands?

- h = steps - v = # of homoplasies
- if no recomb., no mutatn. then h=0
- can calculate effective site # using outgroup

can you apply this to Hillis + Bull?

If no recombination then whole genome works as a unit and selection on one works on all.
 But if there is recombination, the gene fitness can be different than genome.
 why transform?

Homoplasy Ratio

$$= \frac{H_{obs} - H_{clonal}}{H_{obs} - H_{clonal}}$$

