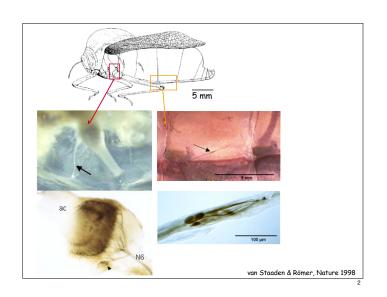
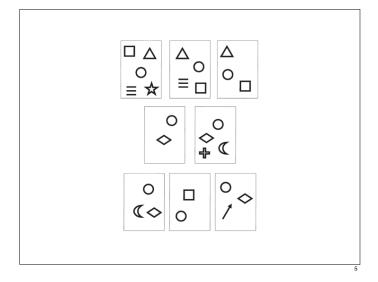
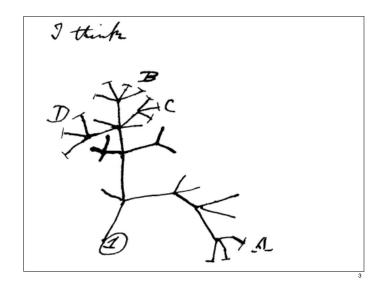
## Introduction to Phylogenetic Analysis









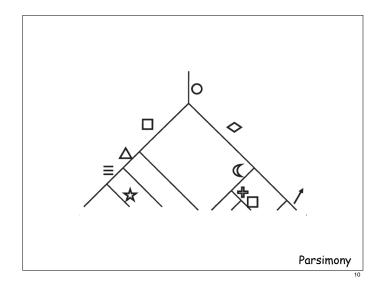


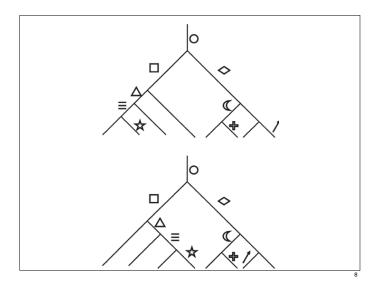


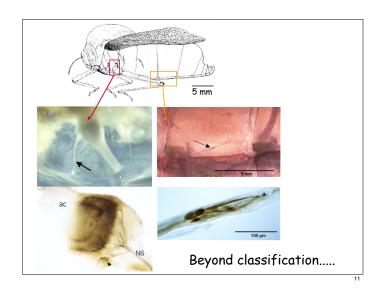
## Task:

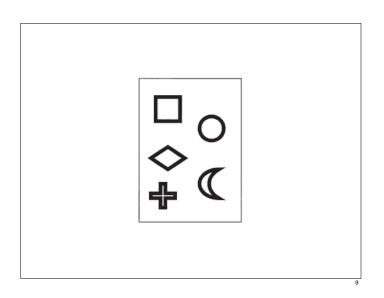
Draw a map of the racecourse, complete with check-in stations.

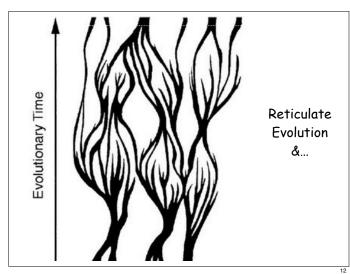
- 1. All runners  $\underline{\text{must}}$  complete the race.
- 2. Paths branch only into 2 new paths never more.
- 3. Two paths branched off from one another, can never reunite.
- 4. Check-in stations are located along straightaways between branching points.

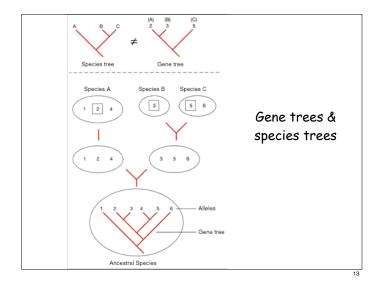


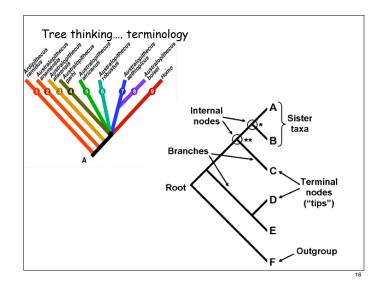


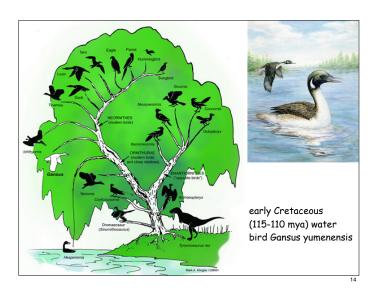


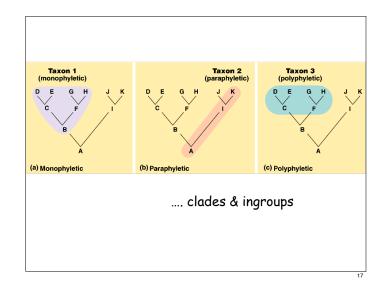




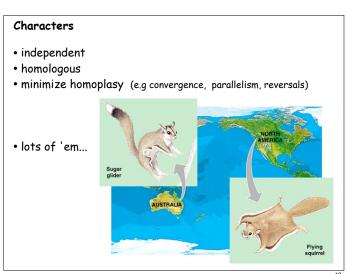








2000 - 1000 1000 2000 Yucatecan Branch Proto-Mayan Western Chuj Tojolab'al Branch Mamea Ixilear lxil Awakatek Eastern Branch





## Morphological

- homology across taxa
- · lack of independence
- higher measurement error & subjectivity
- 1 CCATCAGAGTCC homology & alignment 2 CCATCAGAGTCC across taxa ✓ Deletion independence of base 1 CCATCAGAGTCC substitutions 2 CCATCAGAGTCC G T A) Insertion talA CTITICAAGG AGTATITCCT ATGAACGAGT TAGACGGCAC BYGA CATTGCAAAG GGAATAATCT ATGAACGCAA TAATTATTGA ypdl CATTTTCAGG ATAACTTTCT ATGAAAGTAA ACTTAATACT ypdl nirB GAAAAGAAAT CGAGGCAAAA ATGAGCAAAG TCAGACTCGC hmpA TGCAAAAAAA GGAAGACCAT ATGCTTGACG CTCAAACCAT TTTTTGTGGA GAAGACGCGT GTGATTGTTA narQ GTTATTAAGG ATATGTTCAT ATGTTTTCA
  TACCCACCGG ATTTTTACCC ATGCTCACCG AAAAGAACCT TTAAGCAGAT gltF yIdF AATCAAAATG GAATAAAATC ATGCTACCAT CTATTTCAAT dsdX ATCACAGGGG AAGGTGAGAT ATGCACTCTC AAATCTGGGT suhB ACATCCAGTG AGAGAGACCG ATGCATCCGA TGCTGAACAT

Molecular 2048 2176 2304 AACTGTCTTTATTTAATATCTAAAATTTAACTTTTGAGTCAAAAGGGCTCAAATTTTTCTTTAGGACGATAAGGACCCTAATAGAGCTTAATA 140 150 160 170 180 190 200 210 220

