

Phylogenetic trees

Branch confidence

Genome 559: Introduction to Statistical and
Computational Genomics

Elhanan Borenstein

A quick review

- The parsimony principle:

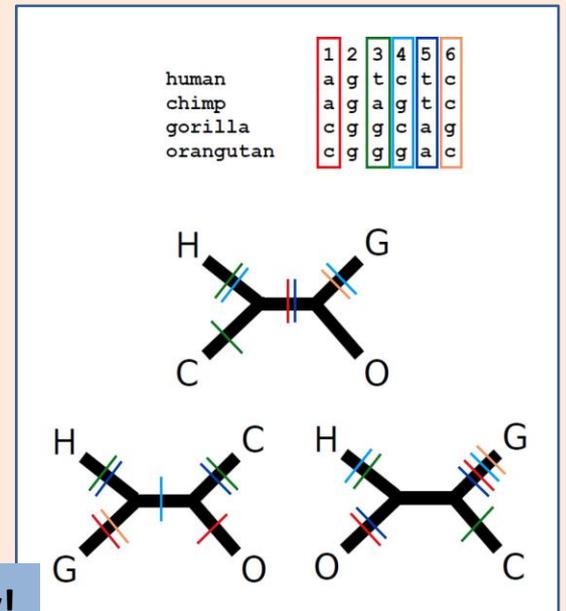
- Find the tree that requires the fewest evolutionary changes!

- A fundamentally different method:

- Search rather than reconstruct

- Parsimony algorithm

1. Construct all possible trees — Too many!
2. For each site in the alignment and for each tree count the minimal number of changes required — The small parsimony problem
3. Add sites to obtain the total number of changes required for each tree
4. Pick the tree with the lowest score

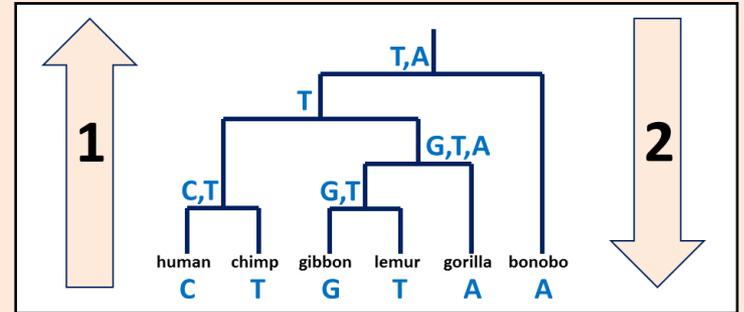


A quick review – cont'

- Small vs. large parsimony

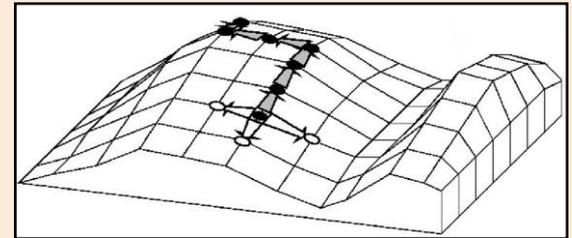
- Fitch's algorithm:

1. **Bottom-up phase:** Determine the set of possible states
2. **Top-down phase:** Pick a state for each internal node



- Searching the tree space:

- Exhaustive search, branch and bound
- Hill climbing with Nearest-Neighbor Interchange



- Extensions

Phylogenetic trees: Summary

Parsimony Trees:

- 1) Construct all possible trees **or search the space of possible trees**
- 2) For each site in the alignment and for each tree count the minimal number of changes required **using Fitch's algorithm**
- 3) Add all sites up to obtain the total number of changes for each tree
- 4) Pick the tree with the lowest score

Distance Trees:

- 1) Compute pairwise corrected distances.
- 2) Build tree by sequential clustering algorithm (UPGMA or Neighbor-Joining).
- 3) These algorithms don't consider all tree topologies, so they are very fast, even for large trees.

Maximum-Likelihood Trees:

- 1) Tree evaluated for likelihood of data given tree.
- 2) Uses a specific model for evolutionary rates (such as Jukes-Cantor).
- 3) Like parsimony, must search tree space.
- 4) Usually most accurate method but slow.

Branch confidence

How certain are we that this is the correct tree?

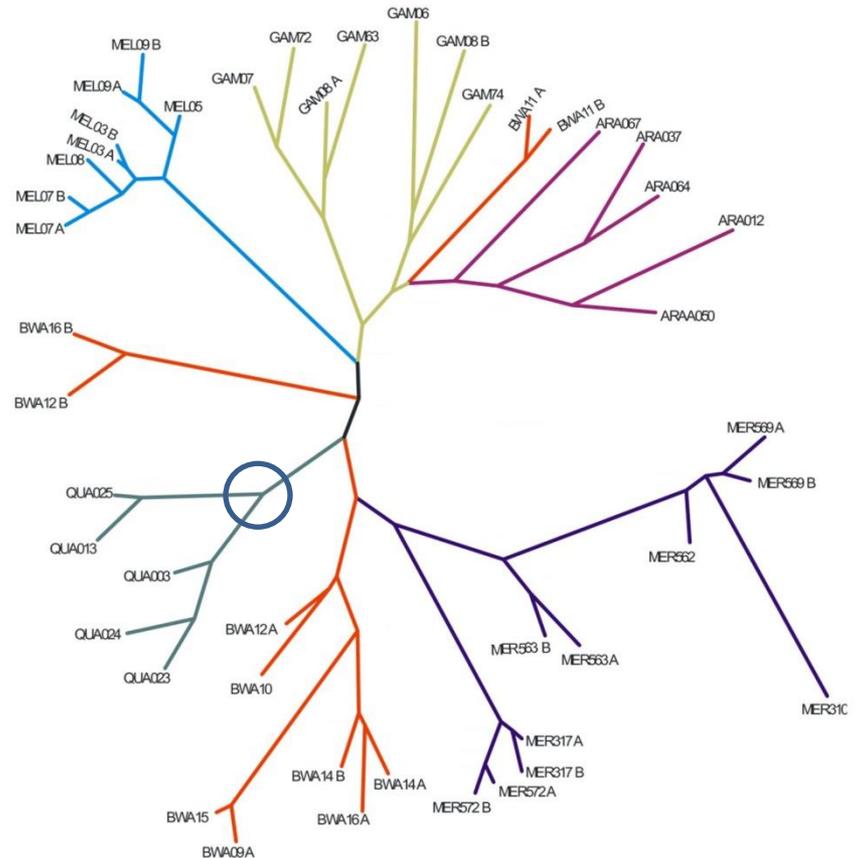
Can be reduced to many simpler questions - how certain are we that each **branch point** is correct?

For example, at the circled branch point, how certain are we that the three subtrees have the correct content:

subtree1 - QUA025, QUA013

subtree2 - QUA003, QUA024, QUA023

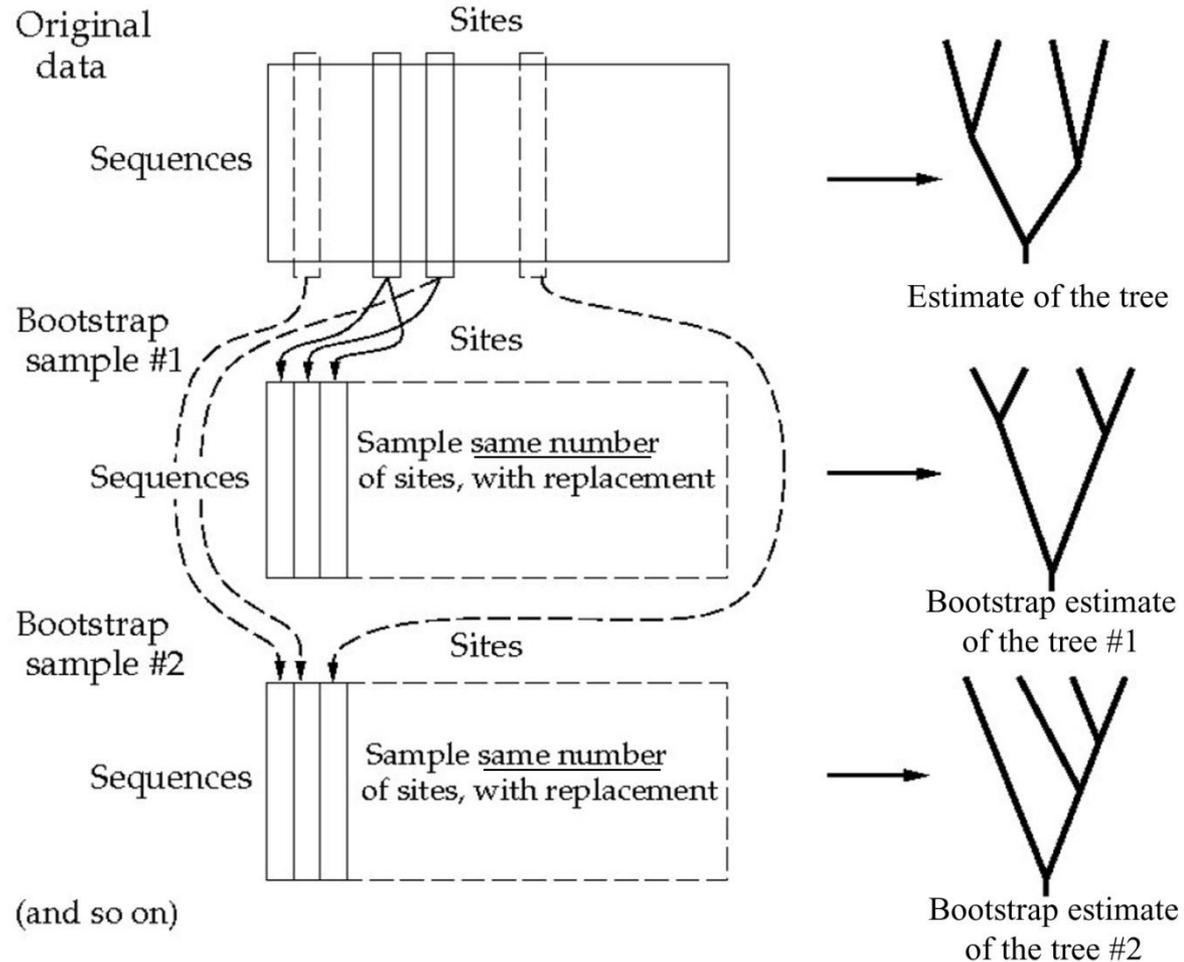
subtree3 - everything else



Bootstrap support

Most commonly used branch support test:

1. *Randomly sample alignment sites.*
2. *Use sample to estimate the tree.*
3. *Repeat many times.*



(sample with replacement means that a sampled site remains in the source data after each sampling, so that some sites will be sampled more than once)

Bootstrap support

For each branch point on the computed tree, count what fraction of the bootstrap trees have the same subtree partitions (regardless of topology within the subtrees).

For example at the circled branch point, what fraction of the bootstrap trees have a branch point where the three subtrees include:

- subtree1 - QUA025, QUA013
- subtree2 - QUA003, QUA024, QUA023
- subtree3 - everything else

This fraction is the **bootstrap support** for that branch.

