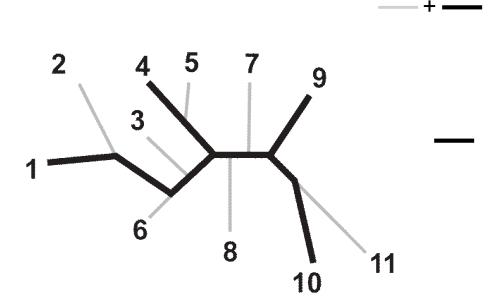
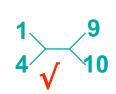
Bootstrap support values for embedded quartets

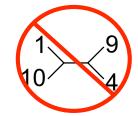


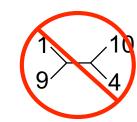
: tree calculated from one pseudosample generated by bootstraping from an alignment of one gene family present in 11 genomes

: embedded quartet for genomes 1, 4, 9, and 10.

This bootstrap sample supports the topology ((1,4),9,10).



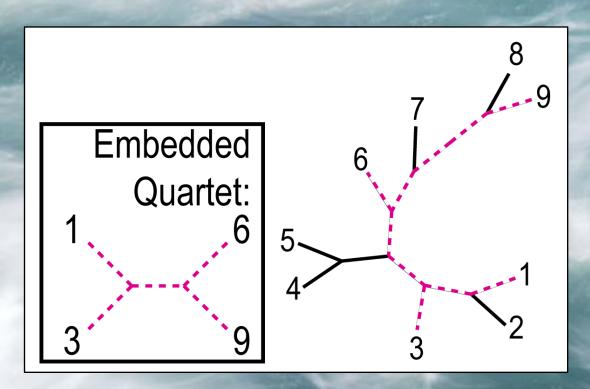




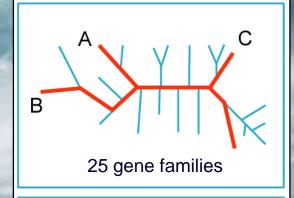
Quartet spectral analyses of genomes iterates over three loops:

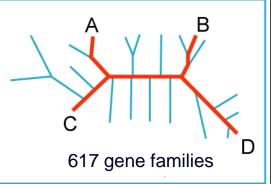
- > Repeat for all bootstrap samples.
- > Repeat for all possible embedded quartets.
- > Repeat for all gene families.

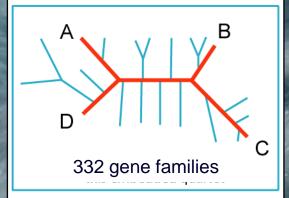
QUARTET DECOMPOSITION METHOD



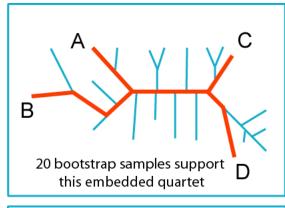
- Quartet is a smallest unit of phylogenetic information
- Each quartet is associated with only three unrooted tree topologies

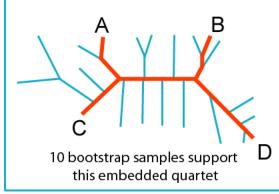


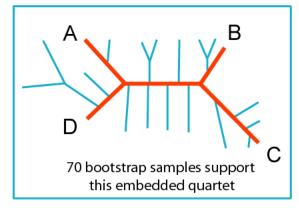




BOOTSTRAP SUPPORT
VALUE VECTOR:
(2.6, 63.3, 34.1)
974 gene families contain
this embedded quartet





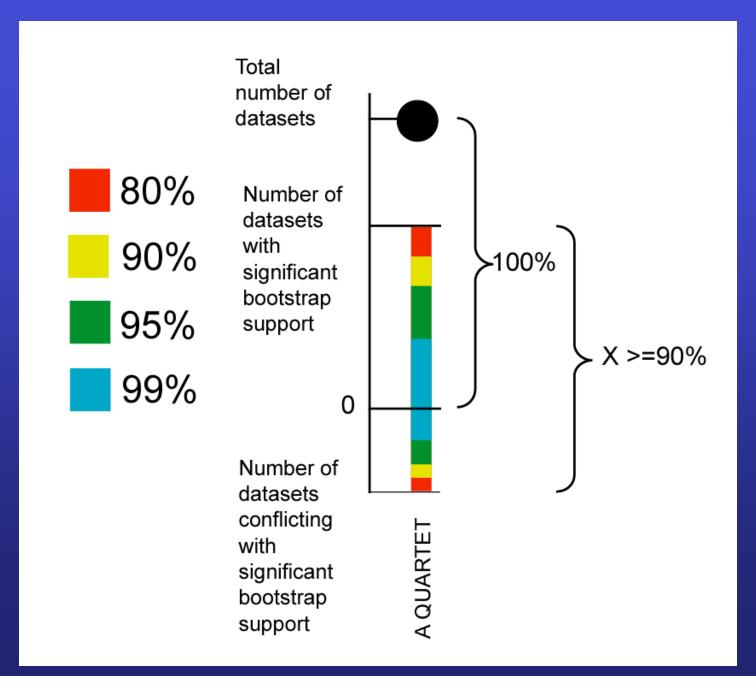


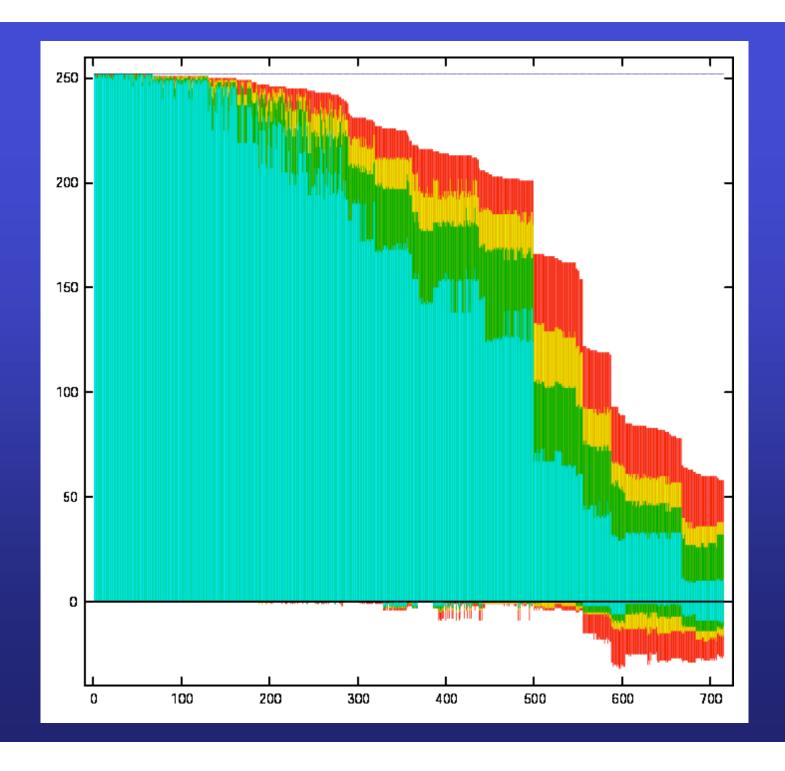
BOOTSTRAP SUPPORT VALUE VECTOR: (20,10,70)

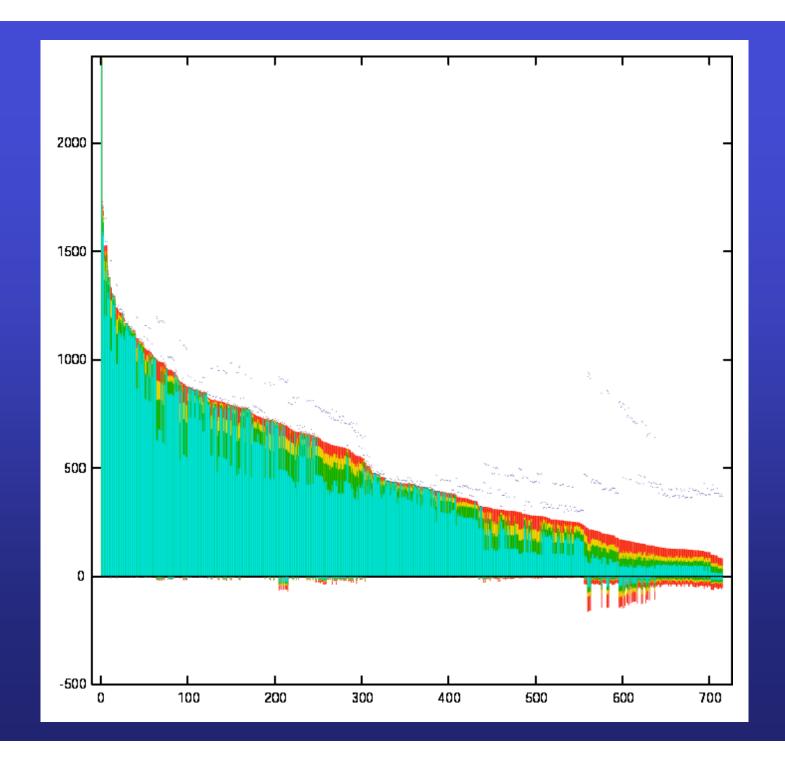
Calculation of bootstrap support vector for an embedded quartet

- Topology reconstructed from a bootstrap sample is examined for embedded topology of a quartet of interest.
- For a quartet, there are three possible unrooted tree topologies.
- Bootstrap support vector for a single gene family consists of percent of bootstrap samples supporting each of the three tree topologies.

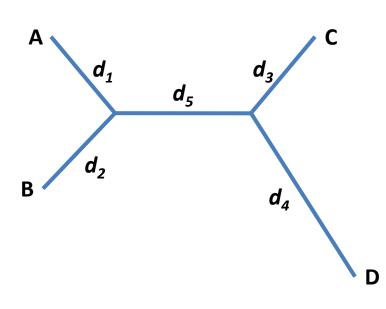
Illustration of a component of quartet spectral analyses







Quartet filters



- The quartet at the left is generated from a gene tree.
- d₁, d₂, d₃ and d₄ are lengths of external branches in the quartets for taxon A, B, C and D, respectively. d₅ is the length of the internal branch.
- Quartet filter 1: if d₅ ≤ 0.02 (or another user specified value), this quartet will not be counted.
- Quartet filter 2: if the longest external branch $(\mathbf{d_4} \text{ in the quartet})$ is too much longer than the internal branch, say, $\mathbf{d_4}/\mathbf{d_5} \ge 10$, this quartet will not be counted.
- Quartet filter 3: Since each quartet has a bootstrap support value in each gene family, the user can remove the quartets which are not well supported in most gene families. We suggest the user don't use this filter (or use 0,0 as thresholds). The user can try this filter with different thresholds after the job is done.