

## Phylogenetic Events Counting

1. For each pair of positions, start with root of phylogenetic tree
2. For each node
3. Compute the *equality set* for the node as the set of pair types having the maximum count among the child sequences at this node
4. If the node is an internal node,
  5. for each child node
  6. do co-evolutionary events counting for each child node
  7. add the positive and negative events count tag from child to current node respectively.
8. Sort each pair type into *pair\_list* based on the number of occurrence among sequences directly within this node if it is at least one.
9. Add any pair type from child equality sets that is not included in the *pair\_list* at the end of *pair\_list*
10. Move the head of *pair\_list* to the parent candidate set
11. For each pair type  $p$  in *pair\_list*
  12. if  $p$  is covary with parent set, move  $p$  into parent candidate set, and increase current `positive_event_count` by 1
  13. else increase current `negative_event_counts` by 1

**Definition of positive events:** Given a pair of positions in a set of aligned sequences under the same ancestral node on the phylogenetic tree, a positive event is counted when both positions changed from the ancestral sequence. The type of pair having positive events will be accounted as one of ancestral pair collection.

**Definition of negative events:** Given a pair of positions in a set of aligned sequences under the same ancestral node on the phylogenetic tree, a negative event is counted when only one position changed from the ancestral sequence.