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1  Input: Phylogenetic trees and user-defined sorting parameters
2  Output: Sorted phylogenetic trees
3  for each tree in target directory do
4      read tree
5      if tree is in extended Newick format then
6          |   convert into traditional Newick using convert.eNewick
7      end if
8      import tree using ape package
9      if all taxa in tree are targets then
10         |   the tree is "All Exclusive"
11     end if
12     for each rooted and unrooted node in tree do
13         |   if node satisfies min.support, min.prop.target and
14         |   |   node has  $\geq 1$  taxon from each member of target.groups then
15         |   |   |   if all target taxa in the node then
16         |   |   |   |   the tree is "Exclusive"
17         |   |   |   |   else if node satisfies clade.exclusivity then
18         |   |   |   |   |   the tree is "Non-Exclusive"
19         |   |   |   |   end if
20         |   |   |   end if
21         |   |   end if
22     end for

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Supplementary Figure S1. Tree-sorting algorithm in PhySortR.