Input: Phylogenetic trees and user-defined sorting parameters

Output: Sorted phylogenetic trees

for each tree in target directory do
  read tree

  if tree is in extended Newick format then
    convert into traditional Newick using convert.eNewick
  end if

  import tree using ape package

  if all taxa in tree are targets then
    the tree is “All Exclusive”
  end if

  for each rooted and unrooted node in tree do
    if node satisfies min.support, min.prop.target and
      node has ≥ 1 taxon from each member of target.groups then
      if all target taxa in the node then
        the tree is “Exclusive”
      else if node satisfies clade.exclusivity then
        the tree is “Non-Exclusive”
      end if
    end if
  end for
end for

Supplementary Figure S1. Tree-sorting algorithm in PhySortR.