Treeortho, an algorithm to identify orthologs in evolutionary trees

```
function parcourOrtho(Node node) :
if(duplication(node)){
        foreach child (enfantsD(node){
        parcourOrtho(child);
      }
}
else{
        children = children(node);
        // We traverse all possible pairs of children of 'node'
      for(i = 0 ; i < length(children) ; i++){
        for(j = i+1 ; j <= length(children) ; j++){
                // All the pairs of proteins are orthologous
                // Because there is no duplication
                foreach child1 ( leaves(children[$i]) ){
                        foreach child2(leaves(children[$j]) ){
                                print “ortho child1-child2]”;
                        }
                }
        }
      }
      foreach child (children){
        parcourOrtho(child);
      }
}

function duplication(Node node) :
// If the node is leaf, it's not a duplication
if(leaf(node)){
        return FALSE;
}

children = children(node);
intersect = FALSE;
// We traverse the direct children of node by pairs
for(i=0;i<length(children) && !$intersect;$i++){
        for(j=i+1;j<=length(children) && !$intersect;$j++){
                if(intersect(leaves(children[$i]),leaves(children[$j])){
                        $intersect = TRUE ;
```