

dcSubtreeTips

December 23, 2014

| | |
|---------------|---|
| dcSubtreeTips | <i>Function to extract a tip-induced subtree from a phylo-formatted phylogenetic tree</i> |
|---------------|---|

Description

dcSubtreeTips is supposed to extract a tip-induced subtree from a phylo-formatted phylogenetic tree. In addition to the tree in subject, another input is a vector containing tip labels of interest. From valid tip labels, there are two types of subtree to extract. One is first induce clade (an internal node) from tip labels, and then the subtree is extracted under the induced clade. Another type is to extract a subtree only containing given tip labels; in this situation, some internal nodes perhaps need to further trimmed. The resulting subtree is also represented as an object of class 'phylo'.

Usage

```
dcSubtreeTips(phy, choose.tip.labels = NULL, subtree.type = c("clade",  
"tips_only"), verbose = T)
```

Arguments

| | |
|-------------------|--|
| phy | an object of class 'phylo' |
| choose.tip.labels | a character specifying which tips are chosen |
| subtree.type | a character specifying how to extract subtree from given tips. It can be 'clade' or 'tips_only'. The former is first induce clade (an internal node) from tip labels, and then to extract the subtree under the induced clade. The latter is to directly extract the subtree only containing given tip labels, (if necessary), after trimming out unnecessary internal nodes |
| verbose | logical to indicate whether the messages will be displayed in the screen. By default, it sets to TRUE for display |

Value

an object of class 'phylo'

Note

nonde

See Also

[dcTreeConnectivity](#), [dcSubtreeClade](#)

Examples

```
# 1) with internal node labels
tree <- "(((t1:5,t2:5)i3:2,(t3:4,t4:4)i4:3)i2:2,(t5:4,t6:4)i5:6)i1;"
phy <- ape::read.tree(text=tree)
ape::plot.phylo(phy, type="p", use.edge.length=TRUE,
show.node.label=TRUE)

# 2) tip labels of interest
choose.tip.labels <- c(t1,t2,t3)
# 2a) extract subtree via an induced clade
subphy <- dcSubtreeTips(phy, choose.tip.labels, subtree.type="clade")
ape::plot.phylo(subphy, type="p", use.edge.length=TRUE,
show.node.label=TRUE)
# 2b) extract subtree containing only tips
subphy <- dcSubtreeTips(phy, choose.tip.labels,
subtree.type="tips_only")
ape::plot.phylo(subphy, type="p", use.edge.length=TRUE,
show.node.label=TRUE)
```