

dcSubtreeClade

November 26, 2014

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| dcSubtreeClade | <i>Function to extract a subtree under a given clade from a phylo-formatted phylogenetic tree</i> |
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Description

dcSubtreeClade is supposed to extract a subtree under a given clade from a phylo-formatted phylogenetic tree. In addition to the tree in subject, another input is a built-in integer specifying an internal node/clade of interest. Alternatively, the internal node of interest can be given by its label (if there are internal node labels). As a result, a subtree under a given clade is also represented as an object of class 'phylo'.

Usage

```
dcSubtreeClade(phy, choose.node = NULL, choose.node.label = NULL,  
verbose = T)
```

Arguments

| | |
|-------------------|---|
| phy | an object of class 'phylo' |
| choose.node | an integer specifying which internal node is chosen. For an object of class 'phylo', the tree has built-in ID for internal nodes, ranging from $Ntip + 1$ to $Ntip + Nnode$, where $Ntip$ and $Nnode$ are the number of tips and internal nodes. Internal nodes are indexed in a pre-ordered manner. The subtree under the given internal node will be extracted |
| choose.node.label | a character specifying which internal node is chosen. For the tree with internal node labels, the extraction of subtree can be done in this way |
| 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

If a valid 'choose.node' is given, then 'choose.node.label' will be ignored.

See Also[dcTreeConnectivity](#)**Examples**

```
# 1) a newick tree without internal node labels
tree <- "(((t1:5,t2:5):2,(t3:4,t4:4):3):2,(t5:4,t6:4):6);"
phy <- ape::read.tree(text=tree)
phy
Ntip <- ape::Ntip(phy)
Nnode <- ape::Nnode(phy)
ape::plot.phylo(phy, type="p", use.edge.length=TRUE)
ape::nodelabels(node=Ntip+1:Nnode, col="red", bg="white")
# a subtree specified via a built-in internal node ID
subphy <- dcSubtreeClade(phy, choose.node=Ntip+2)
subphy
ape::plot.phylo(subphy, type="p", use.edge.length=TRUE)

# 2) a newick tree 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)
phy
ape::plot.phylo(phy, type="p", use.edge.length=TRUE,
show.node.label=TRUE)
# a subtree specified via an internal node label
subphy <- dcSubtreeClade(phy, choose.node.label=i2)
subphy
ape::plot.phylo(subphy, type="p", use.edge.length=TRUE,
show.node.label=TRUE)
```