dcSubtreeClade

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dcSubtreeClade | *Function to extract a subtree under a given clade from a phylo-formatted phylogenetic tree*

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 interna 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.

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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)
```