

# dcTreeConnectivity

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dcTreeConnectivity	<i>Function to calculate the sparse connectivity matrix between parents and children from a phylo-formatted phylogenetic tree</i>
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## Description

dcTreeConnectivity is supposed to calculate the sparse connectivity matrix between parents and children from a phylo-formatted phylogenetic tree. The matrix has internal nodes (in rows) and tips plus internal nodes (in columns). For a row (an internal node; as a parent), the non-zeros indicate all its descendants/children.

## Usage

```
dcTreeConnectivity(phy, verbose = T)
```

## Arguments

phy	an object of class 'phylo'
verbose	logical to indicate whether the messages will be displayed in the screen. By default, it sets to TRUE for display

## Value

a sparse matrix of  $Nnode \times Ntip + Nnode$ , where  $Ntip$  and  $Nnode$  are the number of tips and internal nodes. A non-zero entry indicates a pair of a parent and its child.

## Note

None

## See Also

[dcTreeConnectivity](#)

**Examples**

```
# a newick tree
tree <- "(((t1:5,t2:5):2,(t3:4,t4:4):3):2,(t5:4,t6:4):6);"
phy <- ape::read.tree(text=tree)

# connectivity matrix
res <- dcTreeConnectivity(phy)
dim(res)
# convert to a full Matrix
as.matrix(res)
```