dcAncestralMP

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dcAncestralMP   *Function to reconstruct ancestral discrete states using maximum parsimony algorithm*

Description

dcAncestralMP is supposed to reconstruct ancestral discrete states using a maximum parsimony-modified Fitch algorithm. In a from-tip-to-root manner, ancestral state for an internal node is determined if a state is shared in a majority by all its children. If two or more states in a majority are equally shared, this internal node is temporarily marked as an unknown tie, which is further resolved in a from-root-to-tip manner: always being the same state as its direct parent holds. If the ties also occur at the root, the state at the root is set to the last state in ties (for example, usually being 'present' for 'present'-'absent' two states).

Usage

```
dcAncestralMP(x, phy, verbose = T)
```

Arguments

x   a vector of discrete states in the tips. It can be an unnamed vector; in this case, assumedly it has the same order as in the tree tips. More wisely, it is a named vector, whose names can be matched to the tip labels of the tree. The names of this input vector can be more than found in the tree labels, and they should contain all those in the tree labels

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 list of architectures, containing three components for "transition", "states" and "relative":

- transition: a posterior transition matrix between states
- states: a named vector storing states (extant and ancestral states)
- relative: a matrix of nodes X states, storing relative probability

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Note

This maximum parsimony algorithm for ancestral discrete state reconstruction is attributable to the basic idea as described in http://sysbio.oxfordjournals.org/content/20/4/406.short

See Also

dcAncestralML

Examples

```
# provide the tree and states in the tips
tree <-
"(((((t10:5,t2:5):2,(t9:4,t5:4):3):2,(t3:4,t7:4):6):2,((t6:4,t1:4):2,(t8:2,t4:2):4):6);"
phy <- ape::read.tree(text=paste(tree, collapse=""))
x <- c(0, rep(1,4), rep(0,5))

# reconstruct ancestral states
res <- dcAncestralMP(x, phy)
res

# visualise the tree with ancestral states and their conditional probability
Ntip <- ape::Ntip(phy)
Nnode <- ape::Nnode(phy)
color <- c("white","gray")
## visualise main tree
ape::plot.phylo(phy, type="p", use.edge.length=TRUE, label.offset=1,
show.tip.label=TRUE, show.node.label=FALSE)
## visualise tips (state 1 in gray, state 0 in white)
ape::tiplabels(pch=22, bg=color[as.numeric(x)+1], cex=2, adj=1)
## visualise internal nodes
### thermo bar to illustrate relative probability (state 1 in gray, state 0 in white)
ape::nodelabels(thermo=res$relative[Ntip+1:Nnode,2:1],
piecol=color[2:1], cex=0.75)
### labeling reconstructed ancestral states
ape::nodelabels(text=res$states[Ntip+1:Nnode], node=Ntip+1:Nnode,
frame="none", col="red", bg="transparent", cex=0.75)
```