Testing a simple example for the inapplicability problem

Thomas Guillerme t.guillerme@imperial.ac.uk

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This vignette aims to test which algorithms will pick up the signal of a really simple matrix with a clear signal. We are going to test a simple 12 taxa matrix with a minimum parsimony of 18 steps and a "stairs" topology (i.e. (t1, (t2, (t3, etc.)));).

We are going to test with tnt inapplicable R package and phangorn R package.

1 Before starting

We are also going to need the IterativeAlgo "package" that contains some utilities functions.

```
if(!require(devtools)) install.packages("devtools")
install_github("TGuillerme/Parsimony_Inapplicable/IterativeAlgo")
```

These are the required packages in R.

```
library(IterativeAlgo)

## Warning in .doLoadActions(where, attach): trying to execute load actions without 'methods'
package

if(!require(ape)) install.packages("ape")
    if(!require(phangorn)) install.packages("phangorn")

## Loading required package: phangorn

if(!require(phyclust)) install.packages("phyclust")

## Loading required package: phyclust

if(!require(diversitree)) install.packages("diversitree")

## Loading required package: diversitree

if(!require(inapplicable)) install.packages("inapplicable")

## Loading required package: inapplicable

## Loading required package: parallel
```

2 Loading the data

The data is a simple 18 step matrix that should result in a ladderised tree. The matrix is available at this link https://github.com/TGuillerme/Parsimony_Inapplicable/blob/master/Simple_example/18step_matrix.csv.

```
## Reading in the matrix
matrix <- as.matrix(read.csv("18step_matrix.csv", header = F, row.names=1))

## Reading in the expected tree
expected_tree <- read.tree(
    text = "(t1,(t2,(t3,(t4,(t5,(t6,(t7,(t8,(t9,(t10,(t11,t12)))))))))))))))))</pre>
```

3 Setting up the data to be used by inapplicable

A couple of transformations have to be made in order to feed the data to the inapplicable package:

```
## Creating the contrast matrix (function from IterativeAlgo)
contrast_matrix <- get.contrast.matrix(matrix)</pre>
## Create the phyDat object
matrix_phyDat <- phyDat(matrix, type = 'USER', contrast = contrast_matrix)</pre>
## Optimise the data for the inapplicable package analysis
matrix_inap <- prepare.data(matrix_phyDat)</pre>
## Specify the names of the outgroup taxa
outgroup <- c('t1')</pre>
## Set random seed for generating the tree
set.seed(1)
## Generate a random tree
rand_tree <- rtree(nrow(matrix), tip.label = rownames(matrix), br = NULL)
## Generate a NJ tree (with 0 branch length)
nj_tree <- root(nj(dist.hamming(matrix_phyDat)), outgroup, resolve.root = TRUE)</pre>
nj_tree$edge.length <- NULL</pre>
## Generate a list of trees
trees <- list(expected_tree, rand_tree, expected_tree)</pre>
class(trees) <- "multiPhylo"</pre>
```

4 Calculating parsimony

We can then calculate the parsimony score using the simple Fitch algorithm from phytools and the one from inapplicable using the expected tree, the random one and the NJ calculated one.

We can also use the tree search algorithms from the inapplicable package. These functions do not seem to work properly (at least on the version of the inapplicable package I have, they crash R).

```
## Search for a better tree
better_tree <- tree.search(expected_tree, matrix_inap, outgroup)

## Try a sectorial search (Goloboff, 1999)
better_tree <- sectorial.search(rand_tree, matrix_inap)

## Try the parsimony ratchet (Nixon, 1999)
better_tree <- pratchet.inapp(expected_tree, matrix_inap, outgroup)</pre>
```