

# visTreeBootstrap

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visTreeBootstrap

*Function to build and visualise the bootstrapped tree*

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## Description

visTreeBootstrap is supposed to build the tree, perform bootstrap analysis and visualise the bootstrapped tree. It returns an object of class "phylo". For easy downstream analysis, the bootstrapped tree is rerooted either at the internal node with the minimum bootstrap/confidence value or at any customised internal node.

## Usage

```
visTreeBootstrap(data, algorithm = c("nj", "fastme.ols", "fastme.bal"),
metric = c("euclidean", "pearson", "spearman", "cos", "manhattan",
"kendall", "mi"), num.bootstrap = 100, consensus = FALSE,
consensus.majority = 0.5, reroot = "min.bootstrap",
plot.phylo.arg = NULL, nodelabels.arg = NULL, visTree = T,
verbose = T, ...)
```

## Arguments

data	an input data matrix used to build the tree. The built tree describes the relationships between rows of input matrix
algorithm	the tree-building algorithm. It can be one of "nj" for the neighbor-joining tree estimation, "fastme.ols" for the minimum evolution algorithm with ordinary least-squares (OLS) fitting of a metric to a tree structure, and "fastme.bal" for the minimum evolution algorithm under a balanced (BAL) weighting scheme
metric	distance metric used to calculate a distance matrix between rows of input matrix. It can be: "pearson" for pearson correlation, "spearman" for spearman rank correlation, "kendall" for kendall tau rank correlation, "euclidean" for euclidean distance, "manhattan" for cityblock distance, "cos" for cosine similarity, "mi" for mutual information
num.bootstrap	an integer specifying the number of bootstrap replicates
consensus	logical to indicate whether to return the consensus tree. By default, it sets to false for not doing so. Note: if true, there will be no visualisation of the bootstrapped tree

<code>consensus.majority</code>	a numeric value between 0.5 and 1 (or between 50 and 100) giving the proportion for a clade to be represented in the consensus tree
<code>reroot</code>	determines if and how the bootstrapped tree should be rerooted. By default, it is "min.bootstrap", which implies that the bootstrapped tree will be rerooted at the internal node with the minimum bootstrap/confidence value. If it is an integer between 1 and the number of internal nodes, the tree will be rerooted at the internal node with this index value
<code>plot.phylo.arg</code>	a list of main parameters used in the function "ape::plot.phylo" <a href="http://www.inside-r.org/packages/cran/ape/docs/plot.phylo">http://www.inside-r.org/packages/cran/ape/docs/plot.phylo</a> . See 'Note' below for details on the parameters
<code>node.labels.arg</code>	a list of main parameters used in the function "ape::node.labels" <a href="http://www.inside-r.org/packages/cran/ape/docs/node.labels">http://www.inside-r.org/packages/cran/ape/docs/node.labels</a> . See 'Note' below for details on the parameters
<code>visTree</code>	logical to indicate whether the bootstrap tree will be visualised. By default, it sets to true for display. Note, the consensus tree can not be enabled for visualisation
<code>verbose</code>	logical to indicate whether the messages will be displayed in the screen. By default, it sets to true for display
<code>...</code>	additional "ape::plot.phylo" parameters

## Value

an object of class "phylo". It can return a bootstrapped tree or a consensus tree (if enabled): When a bootstrapped tree is returned (also visualised by default), the "phylo" object has a list with following components:

- `Nnode`: the number of internal nodes
- `node.label`: the labels for internal nodes. Here, each internal node is associated with the bootstrap value
- `tip.label`: the labels for tip nodes. Tip labels come from the row names of the input matrix, but are not necessarily the same order as they appear in the input matrix
- `edge`: a two-column matrix describing the links between tree nodes (including internal and tip nodes)
- `edge.length`: a vector indicating the edge length in the 'edge'
- `Note`: the tree structure is indexed with  $1:Ntip$  for tip nodes, and  $(Ntip+1):(Ntip+Nnode)$  for internal nodes, where  $Ntip$  is the number of tip nodes and  $Nnode$  for the number of internal nodes. Moreover,  $nrow(data) = Ntip = Nnode - 2$ .

When a consensus tree is returned (no visualisation), the "phylo" object has a list with following components:

- `Nnode`: the number of internal nodes
- `tip.label`: the labels for tip nodes. Tip labels come from the row names of the input matrix, but are not necessarily the same order as they appear in the input matrix
- `edge`: a two-column matrix describing the links between tree nodes (including internal and tip nodes)

**Note**

A list of main parameters used in the function "ape::plot.phylo":

- "type": a character string specifying the type of phylogeny to be drawn; it must be one of "phylogram" (the default), "cladogram", "fan", "unrooted", "radial" or any unambiguous abbreviation of these
- "direction": a character string specifying the direction of the tree. Four values are possible: "rightwards" (the default), "leftwards", "upwards", and "downwards"
- "lab4ut": (= labels for unrooted trees) a character string specifying the display of tip labels for unrooted trees: either "horizontal" where all labels are horizontal (the default), or "axial" where the labels are displayed in the axis of the corresponding terminal branches. This option has an effect only if type = "unrooted"
- "edge.color": a vector of mode character giving the colours used to draw the branches of the plotted phylogeny. These are taken to be in the same order than the component edge of phy. If fewer colours are given than the length of edge, then the colours are recycled
- "edge.width": a numeric vector giving the width of the branches of the plotted phylogeny. These are taken to be in the same order than the component edge of phy. If fewer widths are given than the length of edge, then these are recycled
- "edge.lty": same than the previous argument but for line types; 1: plain, 2: dashed, 3: dotted, 4: dotdash, 5: longdash, 6: twodash
- "font": an integer specifying the type of font for the labels: 1 (plain text), 2 (bold), 3 (italic, the default), or 4 (bold italic)
- "cex": a numeric value giving the factor scaling of the tip and node labels (Character EXpansion). The default is to take the current value from the graphical parameters
- "adj": a numeric specifying the justification of the text strings of the labels: 0 (left-justification), 0.5 (centering), or 1 (right-justification). This option has no effect if type="unrooted". If NULL (the default) the value is set with respect of direction (see details)
- "srt": a numeric giving how much the labels are rotated in degrees (negative values are allowed resulting in clock-like rotation); the value has an effect respectively to the value of direction (see Examples). This option has no effect if type="unrooted"
- "no.margin": a logical. If TRUE, the margins are set to zero and the plot uses all the space of the device
- "label.offset": a numeric giving the space between the nodes and the tips of the phylogeny and their corresponding labels. This option has no effect if type="unrooted"
- "rotate.tree": for "fan", "unrooted", or "radial" trees: the rotation of the whole tree in degrees (negative values are accepted)

A list of main parameters used in the function "ape::nodelabels":

- "text": a vector of mode character giving the text to be printed. By default, the labels for internal nodes (see "node.label"), that is, the bootstrap values associated with internal nodes
- "node": a vector of mode numeric giving the numbers of the nodes where the text or the symbols are to be printed. By default, indexes for internal nodes, that is,  $(Ntip+1):(Ntip+Nnode)$ , where  $Ntip$  is the number of tip nodes and  $Nnode$  for the number of internal nodes
- "adj": one or two numeric values specifying the horizontal and vertical, respectively, justification of the text or symbols. By default, the text is centered horizontally and vertically. If a single value is given, this alters only the horizontal position of the text
- "frame": a character string specifying the kind of frame to be printed around the text. This must be one of "rect" (the default), "circle", "none", or any unambiguous abbreviation of these

- "cex": a numeric value giving the factor scaling of the tip and node labels (Character EXpansion). The default is to take the current value from the graphical parameters
- "font": an integer specifying the type of font for the labels: 1 (plain text), 2 (bold), 3 (italic, the default), or 4 (bold italic)
- "col": a character string giving the color to be used for the text or the plotting symbols; this is eventually recycled
- "bg": a character string giving the color to be used for the background of the text frames or of the plotting symbols if it applies; this is eventually recycled. It can be one of "jet" (jet colormap), "bwr" (blue-white-red colormap), "gbr" (green-black-red colormap), "wyr" (white-yellow-red colormap), "br" (black-red colormap), "yr" (yellow-red colormap), "wb" (white-black colormap), and "rainbow" (rainbow colormap, that is, red-yellow-green-cyan-blue-magenta). Alternatively, any hyphen-separated HTML color names, e.g. "blue-black-yellow", "royalblue-white-sandybrown", "darkgreen-white-darkviolet". A list of standard color names can be found in <http://html-color-codes.info/color-names>

### See Also

[visTreeBootstrap](#)

### Examples

```
# 1) generate an iid normal random matrix of 100x10
data <- matrix( rnorm(100*10,mean=0,sd=1), nrow=100, ncol=10)
colnames(data) <- paste(rep('S',10), seq(1:10), sep="")
data <- t(data)

# 2) build neighbor-joining tree with bootstrap values and visualise it by default
visTreeBootstrap(data)

# 3) only display those internal nodes with bootstrap values > 30
# 3a) generate the bootstrapped tree (without visualisation)
tree_bs <- visTreeBootstrap(data, visTree=FALSE)
# 3b) look at the bootstrap values and ordered row names of input matrix
# the bootstrap values
tree_bs$node.label
# ordered row names of input matrix
tree_bs$tip.label
# 3c) determine internal nodes that should be displayed
Ntip <- length(tree_bs$tip.label) # number of tip nodes
Nnode <- length(tree_bs$node.label) # number of internal nodes
flag <- as.numeric(tree_bs$node.label) > 30
text <- tree_bs$node.label[flag]
node <- Ntip + (1:Nnode)[flag]
visTreeBootstrap(data, nodelabels.arg=list(text=text,node=node))

# 4) obtain the consensus tree
tree_cons <- visTreeBootstrap(data, consensus=TRUE, num.bootstrap=10)
```