Using **ggphylo** and **ggplot** to visualize phylogenetic trees and alignments

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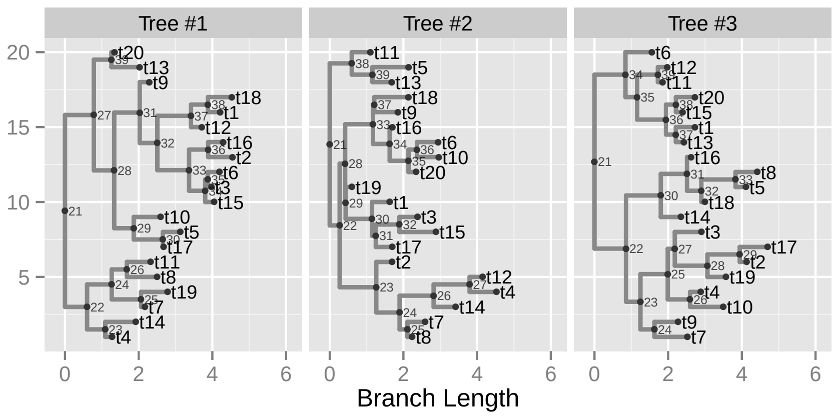
`ggphylo` is a package that provides convenient functions for manipulating `phylo` objects from R and plotting them using `ggplot`. External data can be attached to trees via NHX-format files, data frames or CSV files. These data can be mapped to visual elements of the tree or trees, allowing one to construct complex visualizations in a simple, flexible way.

1 For the impatient

1.1 Basic plots

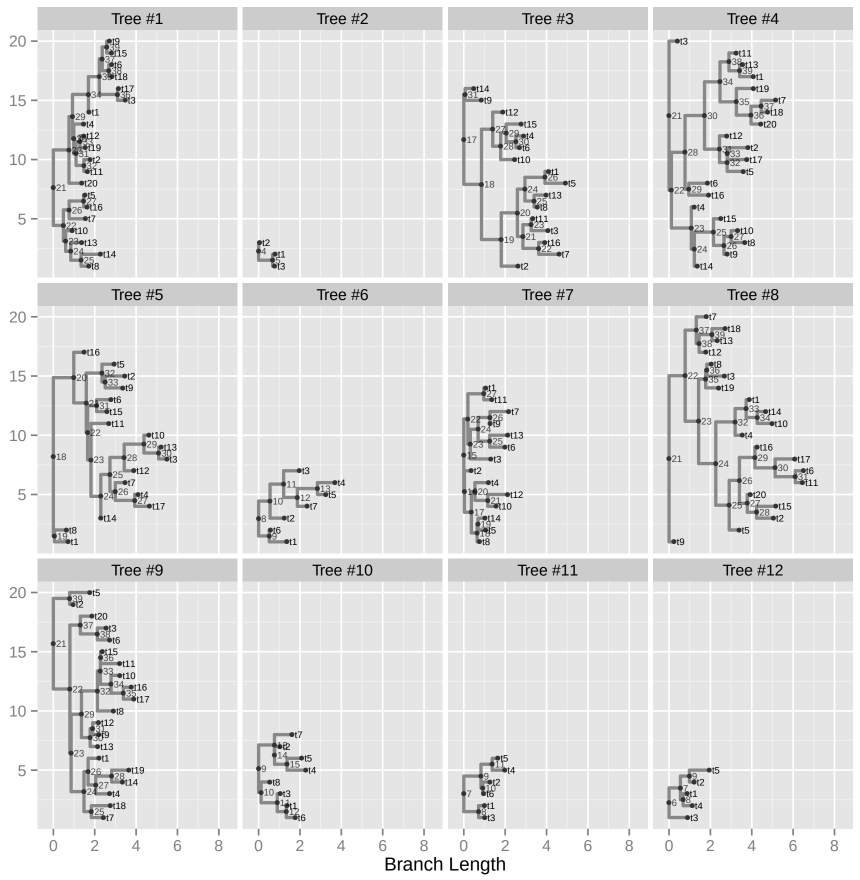
To get started, simply input a `phylo` object (or a list of `phylo` objects) and call the `ggphylo` function:

```
> tree.list <- list()
> for (i in 1:3) {
   x <- rtree(20)  # Random trees 20 leaves.
   tree.list[[i]] <- x
 }
> ggphylo(tree.list) # Plot the list of tres.
```



The result looks similar to the standard `plot.phylo` function from the `ape` package. It also scales well to several trees:

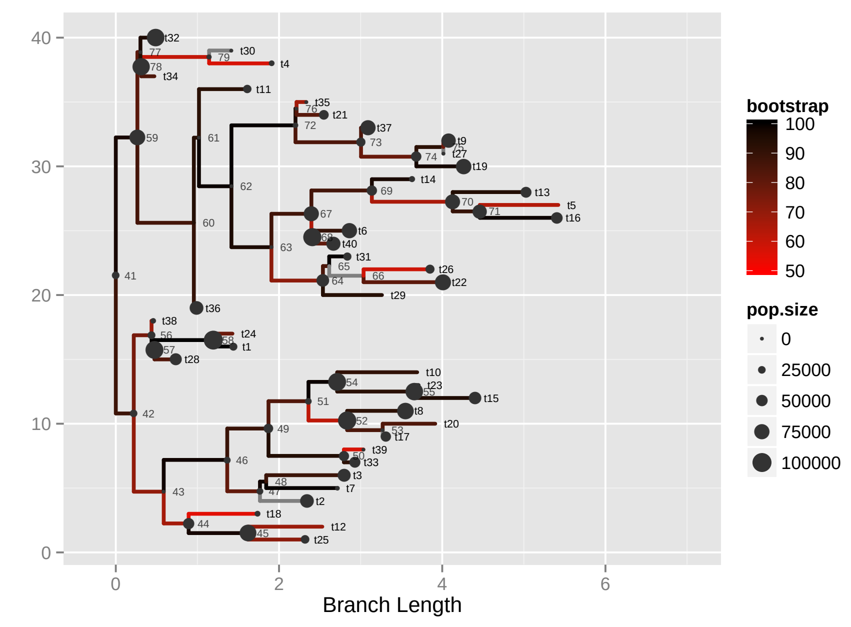
```
> n <- 12
> sizes <- sample(2:20, n, replace=T)
> for (i in 1:n) {
   tree.list[[i]] <- rtree(sizes[i])
 }
> ggphylo(tree.list, label.size=2) # Plot the list of trees.
```



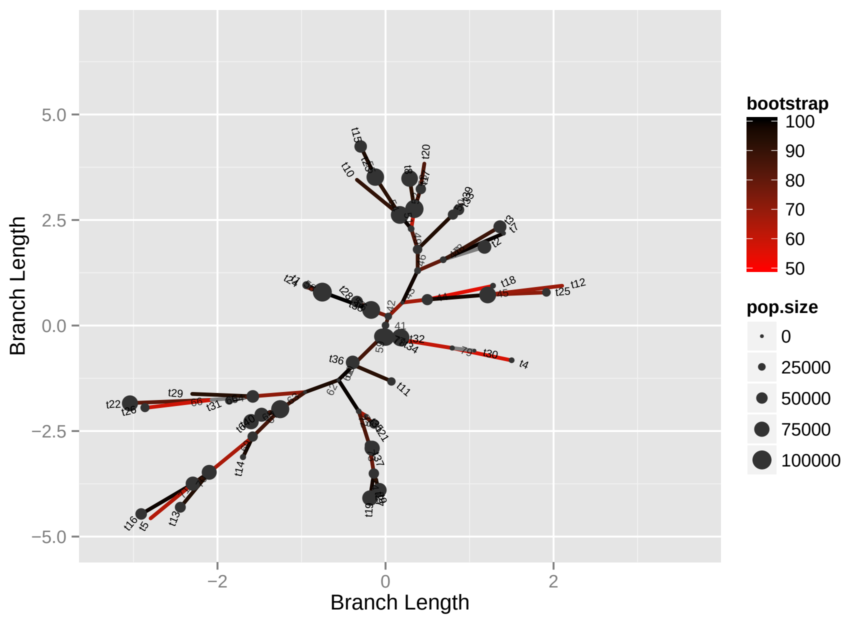
1.2 Plotting data along trees

The ggphylo package defines four visual entities (**lines, nodes, labels, and internal.labels**) and three visual properties (**color, alpha, size**) for visualizing data along a tree. Any combination of entity and property can be used: for example, the following code maps **bootstrap** values to **line color**, and **population size** values to **node size**:

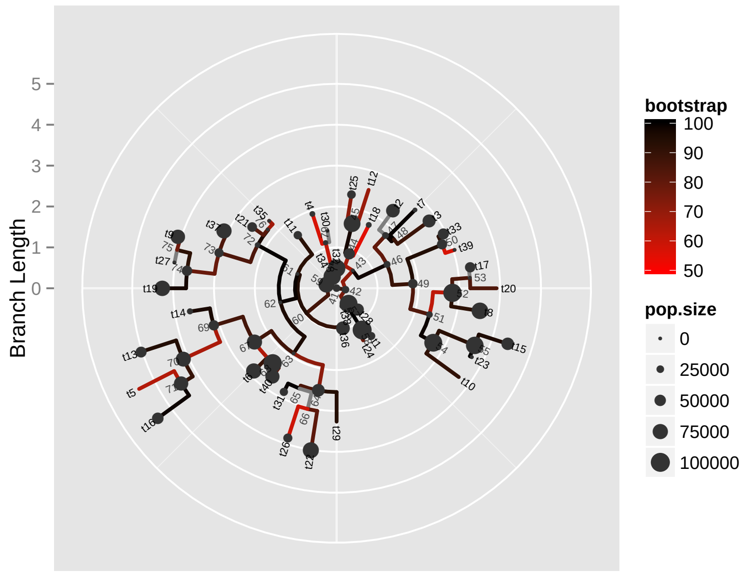
```
> n <- 40;  x <- rtree(n); n.nodes <- length(nodes(x))
> bootstraps <- 100 - rexp(n.nodes, rate=5) * 100
> pop.sizes <- pmax(0, rnorm(n.nodes, mean=50000, sd=50000))
> for (i in nodes(x)) {
   x <- tree.set.tag(x, i, 'bootstrap', bootstraps[i])
   x <- tree.set.tag(x, i, 'pop.size', pop.sizes[i])
 }
> plot.args <- list(
   x,
   line.color.by='bootstrap',
   line.color.scale=scale_colour_gradient(limits=c(50, 100), low='red', high='black'),
   node.size.by='pop.size',
   node.size.scale = scale_size_continuous(limits=c(0, 100000), range=c(1, 5)),
   label.size=2
 )
> do.call(ggphylo, plot.args)
```



```
> unrooted.args <- plot.args
> unrooted.args[['layout']] <- 'unrooted'
> do.call(ggphylo, unrooted.args)
```



```
> radial.args <- plot.args
> radial.args[['layout']] <- 'radial'
> do.call(ggphylo, radial.args)
```



Details of the above code will be explained in the remaining sections, but the general approach should be somewhat familiar to existing `ggplot` users. This introductory section was designed to merely give a brief overview of the main functionality exposed by `ggphylo`.

2 Using `ggphylo`

2.1 Attaching annotations to trees

To visualize data along a phylogeny, it must first be associated with nodes in the tree. `ggphylo` uses "tags" to store a set of key-value pairs with each node. (Internally, this is done by creating a list of lists, one per node, attached to the `phylo` object.) Data can be associated with nodes of a tree in three ways. Let's explore those methods by working with simple tree objects and attaching data in each of three ways:

- `tree.set.tag` This function allows a single key-value pair to be attached to a given node in the tree. The `phylo` object, node index, key and value are required arguments:

```
> tree <- tree.read('((a,b),c);')
> # Use the 'tree.find' method to return the node index given a label.
> b.node.index <- tree.find(tree, 'b')
> print(b.node.index)
```

```
[1] 2
```

```
> x <- tree.set.tag(tree, tree.find(tree, 'b'), 'foo', 'bar')
> print(as.character(x))
```

```
[1] "((a,b[&&NHX:foo=bar]),c);"
```

```
> print(as.data.frame(x, minimal.columns=TRUE))
```

```
  label node  foo
1     a    1 <NA>
5  <NA>    5 <NA>
2     b    2  bar
4  <NA>    4 <NA>
3     c    3 <NA>
```

Note that the above code uses a few of the convenience functions exposed by `ggphylo`: `tree.find` for finding the node index which has a given label, `as.character` which converts a tree into a Newick or NHX formatted string, and `as.data.frame` which converts a `phylo` object into a `data.frame` with one row per node. The `minimal.columns=T` option causes only the bare minimum information about each node to be included; a more detailed data frame can be produced by setting `minimal.columns=F`;

- `tree.read.nhx` The NHX format allows key-value pairs to be stored within a Newick-formatted tree string. `ggphylo` contains a tree.read.nhx function which extracts this data from a NHX string and stores it as tags in the returned `phylo` object:

```
> x <- tree.read.nhx('((a,b[&&NHX:foo=bar]),c[&&NHX:bizz=buzz]);')
> print(as.data.frame(x, minimal.columns=TRUE))
```

```
  label node  foo bizz
1     a    1 <NA> <NA>
5  <NA>    5 <NA> <NA>
2     b    2  bar <NA>
4  <NA>    4 <NA> <NA>
3     c    3 <NA> buzz
```

  It's useful to test how robust the tree parsing and writing functions are by performing round-trip tests:

```
> str <- '(((a[&&NHX:x=1],b[&&NHX:x=2])c[&&NHX:y=3],d[&&NHX:y=4])e,f)g;'
> x <- tree.read.nhx(str)
> print(as.character(x) == str)
```

```
[1] TRUE
```

- `tree.load.data` Sometimes the NHX format can be cumbersome for storing data when it is more easily available in row-based formats. In this case, a `data.frame` or CSV file can be used to add tags to a tree using the `tree.load.data` function. The only requirement is a 'label' column in the source data, which is used to match unique labels in the data and in the tree:

```
> tree <- tree.read('((a,b),c);')
> x <- data.frame(
   label=c('a', 'b', 'c'),
   xyz=c(1, 2, 3)
 )
> print(x)
```

```
  label xyz
1     a   1
2     b   2
3     c   3
```

```
> tree <- tree.load.data(tree, x)
> print(as.data.frame(tree, minimal.columns=TRUE))
```

```
  label node xyz
1     a    1   1
5  <NA>    5  NA
2     b    2   2
4  <NA>    4  NA
3     c    3   3
```

2.2 Controlling visual mappings