

# Design decisions for the phylo4 class

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This document describes the design decisions associated with the new “phylo4” class, which is intended to provide some kind of unifying standard for phylogenetic data in R. It is closely modeled on the the `phylo` class in `ape`, which is the dominant data structure at the moment.

Like `phylo`, the main components of the `phylo4` class are:

**edge** an  $N \times 2$  matrix of integers, where the first column ...

**edge.length** numeric list of edge lengths (length  $N$  or empty)

**Nnode** integer, number of nodes

**tip.label** character vector of tip labels (required)

**node.label** character vector of node labels (maybe empty)

**root.edge** integer defining root edge (maybe NA)

Print method: add information about (ultrametric, scaled, polytomies (zero-length or structural))?

## 1 Hacks/backward compatibility

Hilmar Lapp very kindly showed a way to hack the `$` operator so that it would provide backward compatibility with code that is extracting internal elements of a `phylo4`. The basic recipe is:

```
> setMethod("$", "phylo4", function(x, name) {  
+   attr(x, name)  
+ })
```

but this has to be hacked slightly to intercept calls to elements that might be missing. For example, `ape` detects whether log-likelihood, root edges, node labels, etc. are missing by testing whether they are `NULL`, whereas missing items are represented in `phylo4` by zero-length vectors in the slots (or `NA` for the root edge) — so we need code like

```
> if (!hasNodeLabels(x)) NULL else x@node.label
```

to handle these cases.

```
> library(ape)
```

## 2 To do/problems

- Conflict with `nTips` if `ape` is loaded first: ask EP to get rid of this (obsolete?) function? (`Ntips` is the real `ape` function for getting the number of tips)
- basic tree manipulation: tip-dropping, `na.omit`, etc. — especially for multi-tree and tree-with-data cases
- tree-manipulation code: tree traversal (store current position as an attribute), pruning, etc.