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 ...

Nnode integer, number of nodes

tip.label character vector of tip labels

root.edge integer or NA, defining root edge

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`.

```
> library(ape)
```

2 To do/problems

- Warning on undocumented code objects: print, nNodes, nTips, ...