

# 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