

Splits Class

August 15, 2011

1 Overview

The class *splits* is used to model a set of weighted splits in R. The splits themselves are modelled using an array of bytes (raw type in R) in the following way. Suppose we have n taxa, and that we choose an arbitrary ordering on these taxa. Then we model a split on these taxa by using a bitmask of size n , where if bit i is set, taxon i belongs to one half of the split, and if it is not set it belongs to the other half of the split. Since often we will have more taxa than could be stored in a single byte, we will use an array of size $\lfloor n/8 \rfloor$ of bytes, which is basically a breakdown into "byte-sized chunks" of the entire set of bits which needs to be used. In the event that we have trailing bits which are not used, user code should make no assumptions of the values of these bits.

2 Fields

The class has the following fields:

- matrix of bytes. This is used to model the actual splits in the set. Column i is a vector of raw type which models a split (as described in the overview).
- an integer, n , representing the number of taxa
- an integer, m , representing the number of splits
- an array of size n of taxon labels
- an array of size m of split weights

3 Methods

Two methods have been written for this class:

- `iscompatible()`, which checks whether a given *splits* object is represents a compatible set of splits

- `treePop()`, which uses tree popping to produce a phylogenetic tree from a given *splits* object

The reader is referred to the documentation of each of these functions for more details.