Sampling Aware Ancestral State Inference (SAASI)

Main functions
  1) The solver: sassi
  2) The solver, with cladogenetic speciation: sassi.clado
  3) The simulation: sim_bds_tree
  4) Speciation & Extinction rate estimations, given sampling rate: mle.lm
  5) Transition rate estimations, given sampling rate: mle.qij
  6) Testing the accuracy of the result: sassi.acc
  7) Plotting the figures: sassi.plot
  8) Plotting the alluvial plots: sassi.alluvial

Input & Output:

  1) sassi:

     inputs: phy - The phylogeny, it should contain character states
             params - Speciation, extinction and sampling rates
             qij - The transition rates
     outputs: A data.frame class that contains the ASR inferences at the nodes

  2) sassi.clado:

     inputs: phy - The phylogeny, it should contain character states
             params - Speciation, extinction and sampling rates
             qij - The transition rates

     outputs: A data.frame object that contains the ASR inferences at the nodes

  3) sim_bds_tree:

     inputs: params - speciation, extinction and sampling rates
             qij - The transition rates
             max.taxa - The number of taxa that we have
             max.time -The maximum running time
             present - TRUE/FALSE statement, if we sample all the tips at the present day
     outputs: a simulated phy object under the birth-death-sampling model

  4) mle.lm:

     inputs: phy - The phylogeny, it should contain the branch.length
             psi - The sampling rate that we know
     outputs: Gives you a maximum likelihood estimate of speciation and extinction rates

5) mle.qij:

   inputs: phy - The phylogeny, it should contain character states
        model - The model that we are going to use in `ace', should either be
           `ER', `SYM', or `ARD'.
        psi.ratio - The sampling ratio of the largest psi over the smallest psi
        zero - TRUE/FALSE statement, if we also adjust the transitions rates equal to 0
        using `ace'. We assign them to the largest qij values.

   outputs: the adjusted transition rate matrix

6) sassi.acc:

   inputs: asr - Our ancestral state inferences using any ASR methods
        true.states - The true states in the simulation
        tip.states - The tip states
   outputs: Absolute and probability accuracies

7) sassi.plot:

   inputs: phy - The phylogeny, it should contain character states

   outputs: A plot phylogeny. This is based on ggtree and should be able to use all the
   ggtree arguments.

8) sassi.alluvial:

   inputs: phy - The phylogeny, it should contain character states
        asr - The internal node inferences, using any ASR method

   outputs: An alluvial plot. This is based on ggalluvial and should be able to use all the
   ggalluvial arguments.