🔧 Set up stochastic map

Version 1.0.1, by Giorgio Bianchini

Description: Parses the information from a stochastic mapping analysis.

Module type: FurtherTransformation

Module ID: `32858c9d-0247-497f-aeee-03f7bfe24158`

This module is used to set up the program to display the results of a stochastic mapping analysis. These can be plotted using the *Node states* (id `0512b822-044d-4c13-b3bb-bca494c51daa`) and the *Stochastic mapping branches* (id `f7a20f2f-94b2-4331-8bbf-4e0087da6fba`) Plot action modules.

To use this module, you should open a tree file containing the results of a stochastic mapping analysis, in the format produced by the *phytools* R package (Revell, 2012). A suitable tree file can be obtained e.g. by using the `write.tree` function from *phytools*, or by using the *Merge-sMap* utility from sMap (Bianchini & SÆnchez-Baracaldo, 2021).

This module will use the character histories from the file to sample the character states along each branch. The sampling strategy used is essentially the same as in sMap (see the Supporting Information for the sMap paper, lines 233 and following, for more details).

Parameters

Treat trees as clock-like

Control type: Check box

Default value: Checked

If this check box is checked, it is assumed that the trees are clock-like trees, i.e. that the most recent tips in the tree represent taxa whose age is the same across all sampled trees. This results in all trees being aligned "to the right". Otherwise, it is assumed that the root node has the same age in all sampled trees, which results in the trees being aligned "to the left". This setting has no effect if all the sampled trees have the same branch lengths.

Resolution

Control type: Number spin box

Default value: 0.01

Range: [0, +∞)

This parameter determines the resolution at which the character states are sampled. Increasing this parameter will yield a "smooother" plot, but it will increase the size of exported files and slow down the drawing process.

Resolution unit

Control type: Drop-down list

Default value: Total tree length

Possible values:

- Absolute
- Total tree length
- Branch length

This parameter determines the unit for the [Resolution](#) parameter. If this is `Absolute`, the resolution is given in absolute tree units. If this is `Total tree length`, the resolution is intended as a fraction of the total tree length; e.g. if you set the resolution at `0.01`, the tree will be sampled at 100 intervals from the root to the tips. If the selected value is `Branch length`, the resolution is given as a fraction of the length of each branch; in this case a value of `0.01` will result in each branch being sampled 100 times, regardless of its length.

Apply

Control type: Button

This button applies the changes to the other parameter values and signals that the tree needs to be redrawn.

References

Liam J. Revell, **phytools: an R package for phylogenetic comparative biology (and other things)**, Methods in Ecology and Evolution, 3: 217-223, 2012. https://doi.org/10.1111/j.2041-210X.2011.00169.x

Giorgio Bianchini, Patricia SÆnchez-Baracaldo, **sMap: Evolution of independent, dependent and conditioned discrete characters in a Bayesian framework**, Methods in Ecology and Evolution, 12: 479-486, 2021. https://doi.org/10.1111/2041-210X.13540