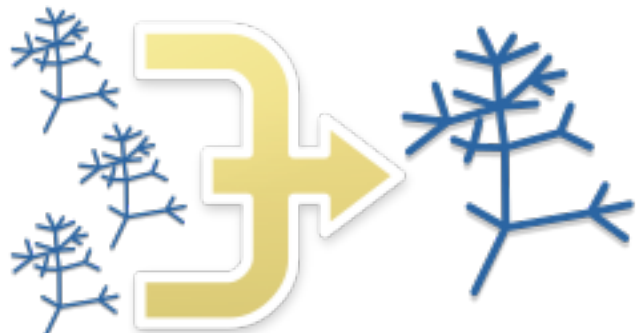# Consensus

Version 1.0.0, by Giorgio Bianchini

Description: Computes the consensus of multiple trees (or returns one of them).

Module type: Transformer

Module ID:
`32914d41-b182-461e-b7c6-5f0263cc1ccd`

This module computes a consensus tree out of all the trees contained in the selected file. Alternatively, it can return just one of the loaded trees.

The parameters for this module are only available if the selected tree file contains $n > 1$ trees. If $n = 1$, the tree is returned unchanged.

Parameters

Consensus tree

Control type: Check box

Default value: Checked if the trees all contain the same taxa; otherwise, unchecked

If this check box is checked, a consensus tree is computed. Otherwise, one of the trees from the file is returned.

Tree

Control type: Number spin box

Default value: 1

Range: [1, n]

If the Consensus tree check box is unchecked, this control is visible and determines which one of the trees from the file is returned. Otherwise, this control is hidden.

Branch lengths

Control type: Drop-down list

Default value: Median

Possible values:

- Mean
- Median

This parameter determines the algorithm used to compute the branch lengths of the consensus tree. If the value is `Mean`, the length of each branch in the consensus tree corresponds to the mean of the length of the corresponding branch in each tree. If the value is `Median`, the median of is instead used.

Threshold

Control type: Number spin box

Default value: 0.00

Range: [0.00, 1.00]

This parameter determines the threshold for the proportion of trees in which a split needs to appear to be included in the consensus tree. A value of `0.5` corresponds to a "majority-rule" consensus tree; a value of 1 corresponds to a strict consensus tree (only splits that are present in all of the trees are included); a value of 0 keeps all compatible splits in the tree.

Skip

Control type: Number spin box

Default value: 0

Range: [0, n]

This parameter determines the number of trees to skip before starting to consider trees for the consensus. This is useful e.g. to remove some trees as burn-in.

Every

Control type: Number spin box

Default value: 1

Range: [1, n]

This parameter determines how many trees are skipped between a sample and the following sample. If this is `1`, then all the trees are considered; if this is `2`, then one tree every 2 is used, and so on.

Until

Control type: Number spin box

Default value: n

Range: [1, n]

This parameter determines the last tree to be considered.

Recompute consensus

Control type: Button

This buttons applies changes to the other parameters and signals to the downstream modules that the tree has changed and everything needs to be computed again.

Further information

The consensus tree is computed as follows:

1. Each tree is transformed into a set of splits. Each split corresponds to a branch of the tree, and separates the taxa on either side of the branch. If the tree is not a clock-like tree, each split has an associated length (corresponding to the branch length). If the tree is a clock-like tree, each split has an age (corresponding to the age of the end node of the branch).

2. The splits from the various trees in the file are compared and sorted based on how many trees they appear in. Splits that appear in a proportion of trees lower than the Threshold are discarded.

3. Starting from the splits which appear in most trees, each split is tested to determine whether it is "compatible" with all preceding splits (i.e. whether there is a tree topology that can satisfy all the splits). If the split is compatible, it is kept; if it is incompatible, it is instead discarded.

4. The length or age of each of these compatible splits is computed using either the mean or the median of the length/age of the splits in the original trees (based on the value for Branch lengths.

5. This final set of splits (which are all compatible with each other) is transformed back into a (possibly multifurcating) tree, which corresponds to the consensus tree.