BayesTrees V1.3

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Key Features:
        Compute strict / non-strict majority rule consensus tree
        Tag, highlight and trace clades within a sample
        Root samples of trees
        Compact trees to retain unique topologies and their frequencies
        Compare distribution of topologies under different models
        Shadow trees, alternative trees to the consensus
        Delete taxa, prune or retain clades
        5 Tree balance metrics, $I_c, \overline{N}, \sigma_N^2, B_1, B_2$
        Compare trees within a sample
        Export trees as graphics, png, bmp, tiff, gif, emf, exif, wfm
        Alter branch or clade lengths
        Print and export manipulated trees
        Animate samples of trees for display purposes
        Display trees from models that have multiple branches per node
        Filter samples of trees.

Introduction

BayesTrees is a program designed to visually interact with samples of trees, in particular Bayesian samples. Please e-mail the author any suggestions for additional features or the support for additional tree files formats.

Requirements

Windows

BayesTrees is written in C# and requires the .NET framework version 2 or higher. It is compatible with Windows 2000, XP, Vista and Windows 7. The .Net framework is freely available from the Microsoft site. BayesTrees is available in two versions, 32-bit and 64-bit.

OS X and Linux

A early beta version of BayesTrees 1.1 is available for Linux and OS X. It requires mono version 2.6.7 (http://www.mono-project.com/), not 2.8. To print trees CUPS (http://www.cups.org/) must be installed

Running

Extract the BayesTrees.1.3 folder to a location on your computer.

Windows: Double click on "BayesTrees.exe"
Linux: Double click on "BayesTrees.sh"
OS X: Double click on "BayesTrees.command"

Input Files

BayesTrees reads files in nexus format. The file must have a translate block, linking taxa names to unique numbers. A number of example input files are included with the program. BayesTrees is designed to read input files generated by programmes such as MrBayes, PAUP and BayesPhylogenies, additional formats and variances are supported via the converter program.

BayesTreesConverter

Tree file formats are notoriously problematic. A separate program "BayesTreesConverter" is shipped with BayesTrees to convert trees in Phylip and various other nexus formats, so they can be read in BayesTrees, these include Beast, Mesquite and FigTree files. Examples of files that can be converted are in the "ConvertTrees" folder. BayesTrees and BayesTreesConverter are designed to read computer generated files, hand generated files may crash the program without any informative feedback.

Tips for inputting trees

1)   Read the error message that the tree file generates.
2)   Open the files in another program, such as PAUP, TreeView or FigTree, if the files do not read into these programs they will not be accepted by BayesTrees. If the trees are read successfully they can be saved and should load into BayesTrees or BayesTreesConverter.
3)   Check the format of the trees with the example file, files that are known to work and the example files with the converter.

The number of trees and taxa that can be used in BayesTrees is dependent on the amount of available memory. There are also limits on the amount of memory 32-bit system and program can address. The 64-bit version of BayesTrees can overcome these memory limitations but must be used with a 64 bit operating system. The error message "Exception of type 'System.OutOfMemoryException' was thrown." is displayed when out of memory. If you encounter this error message try reducing the number of trees in the sample or increase the amount of memory. The size of the file on the disk does not represent the amount of memory required to load the sample.

Consensus Trees

BayesTrees supports a number of different consensus tree methods, strict, semi-strict and majority rule. The consensus tree is displayed using button K, in Fig 1, different consensus trees can be selected using box L. In addition to the standard consensus tree methods, BayesTrees calculates shadow trees. Shadow trees, are a sample of trees constructed from the remaining partitions once the consensus tree has been built.

Figure 1 shows the main window of BayesTrees with the example tree file "Ruminants.trees" loaded.

A   Loads a tree file in nexus format. Files ending .trees, .tree, .nex, .nexus, .tre can also be dragged and dropped in the main window to load.

B   Save loaded trees. Trees can be saved in nexus, strict or relaxed phylip format. Trees are saved with the branches that are currently on view (see I). If the consensus tree is being viewed it is saved otherwise all trees in the sample are saved. To save formatting information and options use the BayesTrees format.

C   View the previous tree.

D   View the next tree.

E   Jump to a specific tree.

F   Start / Stop a slide show of trees, the delay between trees is shown in box G.

G   Time in seconds to pause between trees in the slide show, time may not be accurate and is dependent on system performance.

H   Selects how to ladderize the trees, left or right.

I   Selects the branch lengths to display.

User supplied	Branch lengths found in the nexus file, if present.
Mean	The mean branch for the partition is used.
Uniform	All branches are set to the same length.
Ultrametric	All taxa have the same root to tip path length.

K   Display the consensus tree.

L   Different types of consensus tree, including shadow and semi-strict.

M   Root the tree, clicking on the button then on the node defining the out-group, alternatively right click on the node. Trees that do not have the node are deleted. This can also be done by right clicking on a node and selecting root.

N   Identify the numbers and frequency of unique topologies in a sample by reducing the sample to unique topologies only. This function removes duplicate trees and records the number of times each topology occurs. Branch lengths are set to the mean value of the nodes if the topologies are identical. Trees are sorted in decreasing order of frequency. Box V indicates how often a topology occurred, if trees have been compacted.

O   Delete taxa from the sample. Right clicking on a node will also allow nodes to be deleted or cropped.

P   Add a tag to a node. Tags can be used to highlight nodes of interest and traced them through a sample. Tags can be added to a node by right clicking on a node selecting add tag

Q   Show tree metrics for the sample of trees, including tree length. Results can be copied to the clipboard.

R   Compare the partitions of two trees.

S   Simulates continuous data using the current tree.

T   Tools to generate commands to recreate nodes and most recent common ancestors (MRCA) in BayesTraits. By clicking on a node in the tree, the BayesTraits command to reconstruct the node is automatically generated and can be copied into BayesTraits or saved in a command file

U   Zoom level

V   BayesTrees options.

1   Scale

2   Tree name

3   Posterior probability of the partition, values in blue are greater than 50%

4   A clade highlighted in blue with a tag added. To highlight a clade, right click on a node and select "Add A Tag"

5   The tree length of the current tree.

6   Frequency of the current topology in the sample. The current topology occurs 21 time in the sample of 500 trees or 4.2%

7   Rank order of the topology, this topology is the 4th most common in the sample.

8   Tree number and total number of trees.

9   Posterior probability of a node, values in red are less than 50%

10   A unique (ish) number associated with the each topology

11   A highlighted taxa.

12   Location and percentage of mouse pointer in the same units as the scale, from the left side of the tree.

Menus

File

Load	Load a trees in Nexus format or BayesTrees format
Save	Save trees in Nexus format or BayesTrees format
Save Image	Save the current tree as an image file in png, bmp, tiff, gif, emf, exif or wfm format
Save All Tree (BMP)	Save all the trees as bitmap files in a directory, this can be used to make a animations of the samples. This can take some time.
Load Data	No Current function
Print	Print the current tree
Print Preview	Preview the output of the print command
Close	Close the current tree, freeing the memory
Exit	Quit the program

Tree

Root	Same as M
Consensus	Same as K
Compact	Same as N
Resolve trees	Resolve the sample of tree by adding a user defined branch length.
Delete trees	Remove trees from the sample.
Branch lengths	Same as J
Branch length info	Display information about branch lengths and partitions, for the current tree or for all trees in the sample. Showing information for all trees can be slow.
Squash trees	Not in use
Topology Info	Display information about the topologies in the sample, including position, frequency, probability and product of all partition probabilities in log base e.
Partition info	Show all partitions, including, taxa, posterior probability, mean and standard definition associated with the branch.
Reset taxa number	Reset taxa number so they are sequential
Colour Tree	Not in use
Select Taxa	Highlight one or more taxa in the sample
Options	Same as V

Node menu (right click on a node)

Add A Tag	Same as P
Delete Node	Delete all taxa in the selected node from all trees
Crop to Node	Delete all taxa in the tree except ones in the selected node
Root	Root the tree at the node, deleting trees in which the node is not

	present.
Highlight	Draw a red ring round the taxa name if the node is a tip
Change the branch length	Change the branch length of the node or all branch lengths in the clade.
Rotate node	Swap the order nodes are drawn in.

Keyboard Commands

Right Arrow	Next tree
Left Arrow	Previous tree
Up Arrow	Advance 10% of the sample
Down Arrow	Regress 10% of the sample
Page Up	Last tree in the sample
Page Down	First tree in the sample

Heterotachy

BayesTrees can be used to view results of heterotachy models, which support more than one branch length set per node. Two of these models are implemented in BayesPhylogenies, one which has a fixed number of branch length sets (BLS) per node and one which uses reverse jump to identify nodes within a tree that has signal for heterotachy. As these models produce trees with more than one branch per node they are non-standard nexus format.

Kiontke.trees is an example tree file that has been created using the reverse jump model allowing, potentially, 2 two branch per node. Values in green below branches represent the posterior probability of a second branch at each node. Only values above 0.1 are displayed on the tree, this can be changed in Options → Posterior → BLS Cut Probability. This is to make it easier to identify nodes that have multiple branches with low posterior likely to occur by chance.

By default the first branch length set is displayed, but different branch length sets can be selected by pressing the number keys.

Tips:

To save the sample of trees with tags, highlighted taxa and customised options, save the trees in the BayesTrees format.

A large number of formatting choices can be set in the options window, including font, branch length information, back ground colour and poster probability information.
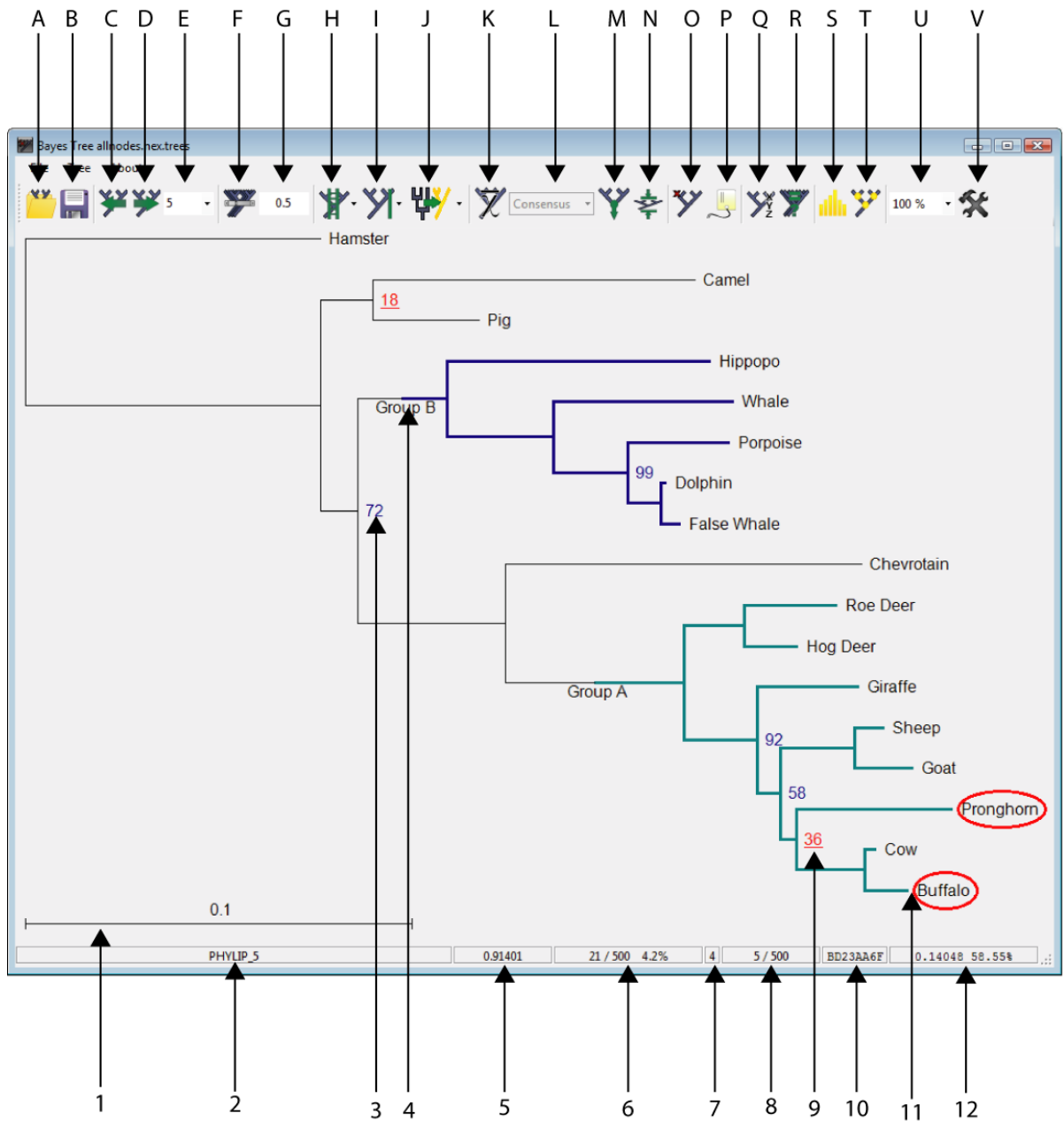
Figure 1. Screen shot of main window with the example tree file "Ruminants.trees" loaded.