BayesTrees V1.0

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Features:

- Compute strict / non-strict majority rule consensus tree
- Root samples of trees
- Compact trees to retain unique topologies and their frequencies
- Compare two trees
- Delete taxa, prune or retain clades
- Tree metrics ic, b1, b2 ect
- Export trees as graphics, png, bmp, tiff, gif, emf, exif, wfm
- Tag, highlight and trace clades within a sample
- Alter branch or clade lengths
- Print and export manipulated trees
- View samples of trees as a slide show
- Display trees from models that have multiple branches per node

Introduction

BayesTrees is a program designed to display, analyse and manipulate samples of trees, in particular Bayesian samples. Any comments, suggestions or features you would like added please contact the authors.

Requirements

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.

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.

Tips for inputting trees

1) Read the error message that the tree file generates in BayesTrees.
2) Try reading the files into another program that accepts trees, such as PAUP or TreeView, 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.
3) Check the format of the trees with the example file or files that are known to work.

The number and size of trees that can be used in BayesTrees is dependent on the amount of available memory. There are also limits on the amount of memory a 32-bit operating 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 it.

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

A Load 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.

C View the previous tree.

D View the next tree.

E Displays and selects the tree to view.

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.

J Display the consensus tree.

K Root the tree, clicking on the button then on a node will root the tree at the chosen node (click the end of the line, between the line and the root label). Trees that do not have the node are deleted. This can also be done by right clicking on a node and selecting root.

L Identify the numbers and frequency of unique topologies in a sample / compact sample. 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.

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

N Add a tag to a node. Tags can be used to highlight nodes of interest so they can be traced through a sample of trees. Tags can be added to a node by right clicking on a node selecting add tag

O Show tree metrics for the sample of trees, including tree length, M, O^2, Ic, B1 and B2. Clicking "copy" will copy the table to the clipboard.

P Compare the partitions of two trees.

Q	** DO NOT USE **. Simulates continuous data up a tree. This does not currently work and should not be used.
R	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.
S	BayesTrees options.
T	The current tree name.
U	The tree length
V	If the trees have been compacted (L) the number of times the toplogy appeared in the sample.
W	The tree number and the total number of trees in the sample.
X	Highlight a single taxa, making it easy to find and track.
Y	Posteriors are displayed on the trees. The clade consisting of Pronghorn, Cow and Buffalo occurred 36% of the time. Posteriors below 50% are in red, values greater than or equal to 50% are in blue. These values are arbitrary and can be set in the options menu (S) but help easily identify portions of the tree that have low support.
Z	A tag has been added to a clade called "Group B" and coloured green.

Menus

File

Open	Same as A
Load Data	No Current Use
Save	Same as B
Save Image	Save the current tree as an image 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 film of the sample
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 K
Consensus	Same as J
Compact	Same as L
Branch lengths	Same as I
Squash Trees	No function
Partition info	Display all partitions present in the sample
Get Branch lengths	Show all the branch lengths for the current tree
Options	Same as S

Node menu (right click on a node)

Add A Tag	Same as N
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.

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 BLS. 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.

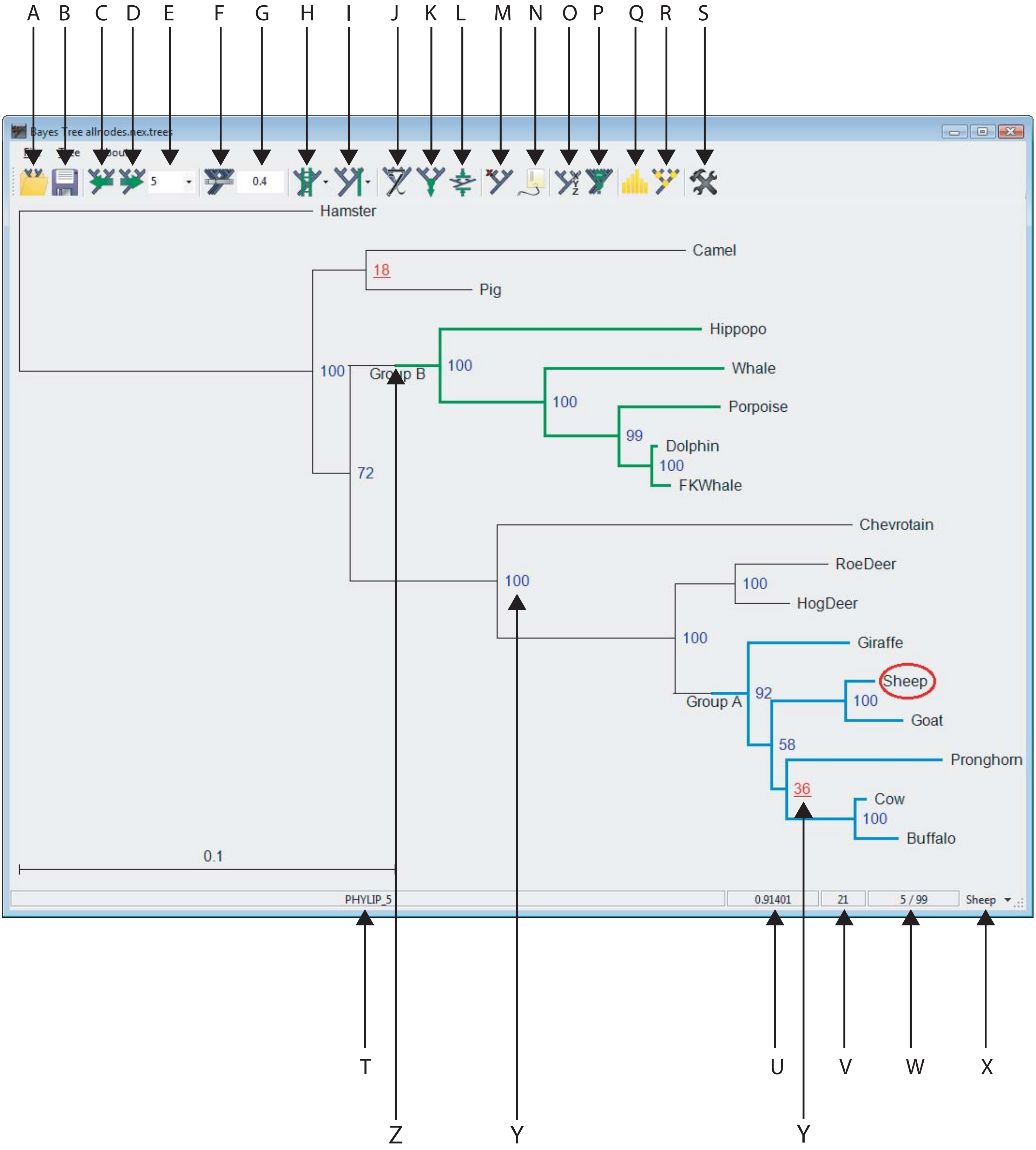

Figure 1. Screen shot of main window with the example tree file "Ruminants.trees" loaded.