User Manual for Dendroscope V3.2.5

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Contents

1 Introduction

Type-setting conventions: In this manual we use e.g. `Edit→Find` to indicate the `Find` menu item in the `Edit` menu.

How to cite: If you publish results obtained in part by using Dendroscope , then we require that you acknowledge this by `citing the program` as follows:

- Daniel H. Huson and Celine Scornavacca. Dendroscope 3: An interactive tool for rooted phylogenetic trees and networks, Systematic Biology (2012), `http://sysbio.oxfordjournals.org/cgi/content/abstract/sys062?ijkey=ZCxPRbYt74aQJhR&keytype=ref`, software freely available from www.dendroscope.org.

This manual is based on the user manual for Dendroscope 1, which was written by Daniel H. Huson, Daniel C. Richter, Christian Rausch and Regula Rupp.

2 Program Overview

Dendroscope is a platform-independent software written in Java that enables conveniently to browse phylogenetic trees and networks with up to hundreds of thousands of taxa. Here is an overview of its features:

- There are 8 different tree views available, e.g. phylogram, cladogram or radial views.
- Its novel navigational features facilitate the analysis of large trees.
- It provides several tree manipulating functions like rerooting, subtree rotating, tree flipping and formatting features like renaming, coloring or resizing edges, nodes and labels.
- A comprehensive set of export formats for the generation of images is available.
- User formatted trees can be saved as a NeXML project file or as *.nexus*, or Newick tree files.
- Tree structures (single or multiple) can be loaded from *.tre* (Newick format) or *.nexus* files or entered manually.

- Rooted phylogenetic networks can be entered and visualized using the Extended Newick format [3].
- The program permits the computation of consensus trees from a set of input trees.
- The program also permits the computation of rooted phylogenetic networks (among others cluster networks [8], galled networks [9], minimum networks [20] and hybridization networks [?, 14]) from a set of input trees.
- It provides several tree manipulating functions like rerooting, subtree rotating, tree flipping and formatting features like renaming, coloring or resizing edges, nodes and labels.

3 Obtaining and Installing the Program

Dendroscope is written in Java and requires a Java runtime environment version 1.5 or later, freely available from www.java.org.

Dendroscope is installed using an installer program that is freely available from www.dendroscope.org. There are three different installers, targeting different operating systems:

- `Dendroscope_windows_3.2.5.exe` provides an installer for Windows.
- `Dendroscope_macos_3.2.5.dmg` provides an installer for MacOS.
- `Dendroscope_unix_3.2.5.sh` provides a shell installer for Linux and Unix.

Alternatively Dendroscope will be available as Java `Webstart application` from http://ab.inf.uni-tuebingen.de/data/software/dendroscope/webstart/. If you need information concerning Java Webstart, go to http://java.sun.com/products/javawebstart/.

4 Getting Started

This section describes how to get started and to do the first steps of analyses using Dendroscope .

First, download an installer for the program from www.dendroscope.org, see Section 3 for details.

Start the program and load any *.tre*, *.nexus*, *.nexml* or *.dendro* project file via `File→Open` . Alternatively, if the file was recently opened by the program, then it may be contained in the `File→Open Recent` submenu.
At startup, the tree will be scaled to fit to the window size.

Draw the tree differently by choosing one of the 8 provided views e.g. `Layout→Draw Rectangular Phylogram` , `Layout→Draw Rectangular Cladogram` , `Layout→Draw Slanted Cladogram` , `Layout→Draw Circular Phylogram` , `Layout→Draw Circular Cladogram` , `Layout→Draw Inner Circular Cladogram` , `Layout→Draw Radial Phylogram` , `Layout→Draw Radial Cladogram` . Try out the magnifier functions by clicking on `View→Use Magnifier` . Change any label font, size, color or edge/node size/width by opening the `Format Panel` via `Edit→Format` .

If you want to print the current image choose `File→Print` . In case you need a quality image of the tree, simply export it to several file formats via `File→Export Image` .

Finally, if you want to save the tree(s) and the formatting click `File→Save As` generating a *.nexml* project file. You can also export the tree(s) by clicking `File→Export` . Choose one of the export formats (newick or nexus).

Note that only by saving a formatted tree as a *.nexml* project file you can save the formatting with the tree.

5 Main Window

The `Main` window is used to display the taxonomy and to control the program via the main menus.

We now discuss all menus of the `Main` window.

5.1 File Menu

The `File` menu contains the following file-related items:

- The `File→New` item opens a new document. Any selected trees are put in it.
- The `File→Open` item provides an `Open File` dialog to open one or more files containing input data. The supported formats are *.nexml*, *.dendro*, *.tre*, *.nexus* (see Section 8). Note that the standard open dialog does not allow one to open more than one file under MacOS X. As a work-around, press the shift-key when selecting the `File→Open` menu item so as to obtain an alternative file open dialog that allows one to select more than one file for opening.
- The `File→Open Recent` can be used to re-open a recently opened file.
- The `File→Add From File` item adds trees or networks from a file to the current document.
- The `File→Enter Trees or Networks` item enters trees in Newick or networks in extended Newick format.
- The `File→Save` item saves the current document in NeXML format.
- The `File→Save As` item saves the current document under a new name.
- The `File→Export` item opens the `Choose output format` dialog which is used to export the current trees or networks in a number of file formats, see Section 8.
- The `File→Duplicate` item duplicates this document.
- The `File→Export Image` item opens the `Export Image` dialog which is used to save the current network in a number of different graphics formats, see Section 8.6.
- The `File→Page Setup` item setups the page for printing.

- The `File→Print` item prints the network.
- The `File→Close` item closes the current window. In case only one window is opened, the application exits.
- The `File→Quit` item quits the program (Windows and Linux only).

5.2 Edit Menu

The `Edit` menu contains the usual edit-related items:

- The `Edit→Copy` item is used to copy the current tree or network or all selected trees or networks.
- The `Edit→Copy Image` item is used to copy the current tree or network or all selected trees or networks as an image that can be pasted into another program, e.g. PowerPoint.
- The `Edit→Paste` item is used to paste the copied trees or networks to a new tab.
- The `Edit→Find` item opens the `Find` tool bar which can be used to search for taxa.
- The `Edit→Find Again` item finds the next occurrence of a search string.
- The `Edit→Replace` item opens the `Replace` tool bar which can be used to replace taxon names.
- The `Edit→Reroot` item reroots the tree or the network at the specified nodes or edge. If more than node is selected, all selected taxon labels are intepreted as *outgroup* taxa and the program determines the "tightest" rooting so that the outgroup appear together below the root. If several nodes share the same label, all these nodes are considered to determine the "tightest" rooting.
- The `Edit→Swap Subtrees` item swaps the order of subtrees (or subnetworks) below the specified node (or nodes).
- The `Edit→Rotate Subtrees` item rotates the order of the subtrees (or subnetworks) below the specified node(s).
- The `Edit→Reorder Subtrees` item opens the `Reorder subtrees` dialog that allows one to specific any type of reordering of the children of the specified node using "drag and drop'.
- The `Edit→Delete Taxa` item removes the selected taxa in the selected trees or networks
- The `Edit→Unlock Edge Lengths` item is used to "unlock edge lengths" so that the user is allowed to reshape trees or networks by dragging nodes or internal edge points.
- The `Edit→Format` item opens a `Format Panel` which provides several possibilities to change color, fonts, node and edge shapes and the positioning of the labels of the tree.

5.3 Select Menu

The `Select` menu contains items for selecting panels and different sets of substructures of trees or networks.

- The `Select→Advanced Selection` submenu contains a number of advanced selection menu items that are probably not of general interest.
- The `Select→All Panels` item selects all panels.
- The `Select→No Panels` item deselects all panels.
- The `Select→Invert Panels` item inverts the selection of all panels.
- The `Select→Select All` item is used to select all nodes and edges.
- The `Select→Select Nodes` item is used to select all nodes.
- The `Select→Select Edges` item is used to select all edges.
- The `Select→From Previous Window` item is used to apply the selection of the previous window to the active window.
- The `Select→Deselect All` item is used to deselect all nodes and edges that are currently selected.
- The `Select→Deselect Nodes` item is used to deselect all nodes that are currently selected.
- The `Select→Deselect Edges` item is used to deselect all edges that are currently selected.
- The `Select→Select Labeled Nodes` item is used to select all labeled nodes.
- The `Select→Select Leaves` item is used to select all leaves.
- The `Select→Select Root` item is used to select the root node of the tree.
- The `Select→Select Non-Terminal` item is used to select all non-terminal nodes and edges.
- The `Select→Select Special` item is used to select all edges leading to reticulation nodes in networks.
- The `Select→Invert Selection` item is used to invert the current selection.
- The `Select→Scroll to Selection` item is used to scroll to the current selection.
- The `Select→List Selected Taxa` item is used to list all selected taxa.

The advanced selection submenu contains the following items:

- The `Advanced Selection→Select Subnetwork` item is used to select the subtree or subnetwork below a selected inner node or edge..

- The `Advanced Selection→Select Induced Network` item is used to select a subtree or subnetwork induced by the set of currently selected nodes.
- The `Advanced Selection→Select LSA Induced Network` item is used to select the subtree or subnetwork rooted at the LSA of the selected nodes.
- The `Advanced Selection→Select Spanned Edges` item is used to select all edges spanned by the set of currently selected nodes.

5.4 Options Menu

The `Options` menu contains items for collapsing nodes and extracting subtrees.

- The `Options→Advanced Options` submenu contains some advanced options that are probably not of general interest.
- The `Options→Collapse` item enables to collapse subtrees or subnetworks below the specified nodes. The former subtrees or subnetworks are replaced by rectangles.
- The `Options→Uncollapse` item is used to uncollapse (expand) the selected, collapsed subtrees or subnetworks .
- The `Options→Uncollapse Subtree` item is used to uncollapse (expand) all collapsed subtrees or subnetworks below the specified nodes.
- The `Options→Collapse Complement` item is used to collapse all subtrees or subnetworks except the currently selected part of the tree or subnetwork
- The `Options→Collapse at Level` item is used to collapse all subtrees or subnetworks at the specified level from the root.
- The `Options→Load Taxon Images` item is used to specify a directory containing image files. Dendroscope tries to match taxon names to the names of images files and for each match found, Dendroscope shows the image near the node representing the given taxon (recognized formats: GIF, JPG, JPEG, BMP and PNG).
- The `Options→Set Image Size` item is used to set the size of the image for the currently selected nodes.
- The `Options→Image Position` submenu is used to determine the relative positions of images in relative to the corresponding nodes (North, South, East, West, Radial).
- The `Options→Next Tree` item moves to the next tree.
- The `Options→Previous Tree` item moves to the previous tree.
- The `Options→Go to Tree` item goes to a specific tree.
- The `Options→Set Tree Name` item sets the name of a tree or network.

The advanced options submenu contains the following items:

- The `Advanced Options→Extract Subnetwork` item is used to extract a subtree or subnetwork below a node or edge.
- The `Advanced Options→Extract Induced Network` item is used to extract a subtree or subnetwork induced by the selected nodes to a new file.
- The `Advanced Options→Extract LSA Induced Network` item is used to extract a subtree or subnetwork rooted at the LSA of the selected nodes to a new file.
- The `Advanced Options→Extract Induced Restriction` item is used to extract the restriction induced by the selected nodes to a new file.

5.5 Algorithms Menu

The `Algorithms` menu contains items for computing networks from trees and for comparing trees or networks.

- The `Algorithms→Advanced Algorithms` submenu contains additional advanced algorithms that are probably not of general interest.
- The `Algorithms→Strict Consensus` item is used to compute the *strict consensus* of a set of trees.
- The `Algorithms→Loose Consensus` item is used to compute the *loose consensus* of a set of trees.
- The `Algorithms→Majority Consensus` item is used to compute the *majority consensus* of a set of trees.
- The `Algorithms→LSA Consensus` item is used to compute the *LSA consensus* of a set of trees [10].
- The `Algorithms→Primodial Consensus` item is used to compute the *primodial consensus* of a set of trees [**?**].
- The `Algorithms→Network Consensus` item is used to compute a *rooted network consensus* of a set of trees.

  If the input set contains more than two trees, then the user can set a threshold that determines the percentage of input trees that a cluster must be contained in to make it into the output rooted network. The user can also decide whether the program should come a *cluster network* [8] that shows the clusters in a *hardwired representation* , a *galled network* [9] that represents the clusters in a topologically restricted *softwired representation* , or a *minimum network* that attempts to represent the clusters in a network of minimum *level* , as described in [20].
- The `Algorithms→Network for Multi-Labeled Tree` menu item is used to compute a rooted phylogenetic network for a multi-labeled tree such that the network contains each label (or taxon) exactly once. There are three methods available here: the *cluster-based method* extracts all the clusters in the tree and constructs a cluster network. The *exact method* computes the nested label for the root node of the tree and then constructs the

corresponding network for that label [6]. The *level-k-based* method extracts all clusters and then seeks to compute a level-k network of minimum level k for the clusters.

- The `Algorithms→Hybridization Network` item computes all minimum hybridization networks for two rooted phylogenetic trees, not necessarily binary, on overlapping taxon sets using the Autumn algorithm [14].
- The `Algorithms→Hybridization Network (Binary Trees)` item computes all minimum hybridization networks for two bifurcating trees on the same taxon set [**?**].
- The `Algorithms→Reroot By Hybridization Number` item determines a rooting that minimizes the hybridization number, given two rooted phylogenetic trees, not necessarily binary, on overlapping taxon sets, using the Autumn algorithm [14].
  item The `Algorithms→Tanglegram→i` tem is used to compute a *tanglegram* for two trees or networks using a NeighborNet-based heuristic [18].

Note that Dendroscope does not require that the trees all contain exactly the same set of taxa to be able to compute a consensus (unlike most other programs), as it uses the Z-closure method to merge partial data [13].

The advanced algorithms submenu contains the following items:

- the `Advanced Algorithms→Hybridization Number` item is used to compute the hybridization number for two rooted trees using the Autumn algorithm [14]. Trees need not be binary and need not have identical taxon sets.
- the `Advanced Algorithms→Hybridization Number (Binary Trees)` item is used to compute the hybridization number for two selected rooted binary trees on the same taxon set [**?**].
- the `Advanced Algorithms→rSPR Distance (Binary Trees)` item is used to compute the rSPR distance for two selected rooted binary trees on the same taxon set [21].
- the `Advanced Algorithms→DTL Reconciliation` item is used to calculate the DTL reconciliation between two binary trees [4].
- the `Advanced Algorithms→Hardwired Cluster Distance` item is used to calculate the *hardwired cluster distance* between two trees or networks [10].
- the `Advanced Algorithms→Softwired Cluster Distance` item is used to calculate the *softwired cluster distance* between two trees or networks [10].
- the `Advanced Algorithms→Displayed Trees Distance` item is used to calculate the *displayed trees distance* between two trees or networks [10].
- the `Advanced Algorithms→Tripartition Distance` item is used to calculate the *tripartition distance* between two trees or networks [15].
- the `Advanced Algorithms→Nested Labels Distance` item is used to calculate the *nested labels distance* between two trees or networks [2, 16].
- the `Advanced Algorithms→Path Multiplicity Distance` item is used to calculate the *path multiplicity distance* between two trees or networks [1].
- The `Advanced Algorithms→Simplistic` item computes a phylogenetic networks using the *simplistic algorithm* [19].
- The `Advanced Algorithms→Trees and Networks Simulator` item is used to create trees or networks data sets.

5.6 Layout Menu

The `Layout` menu contains items for different tree and network views [12].

- The `Layout→Draw Rectangular Phylogram` item is used to draw trees or networks as rectangular phylograms.
- The `Layout→Draw Rectangular Cladogram` item is used to draw trees or networks as rectangular cladograms.
- The `Layout→Draw Slanted Cladogram` item is used to draw trees or networks as slanted cladograms.
- The `Layout→Draw Circular Phylogram` item is used to drawtrees or networks as circular phylograms.
- The `Layout→Draw Circular Cladogram` item is used to draw as circular cladograms.
- The `Layout→Draw Inner Circular Cladogram` item is used to draw trees or networks as circular cladograms with leaves on the inside.
- The `Layout→Draw Radial Phylogram` item is used to draw trees or networks as radial phylograms.
- The `Layout→Draw Radial Cladogram` item is used to draw trees or networks as radial cladograms.
- The `Layout→Ladderize Left` item is used to order trees or networks so that the largest clades appear leftmost (uppermost in the view).
- The `Layout→Ladderize Right` item is used to order trees or networks so that the largest clades appear rightmost (lowermost in the view).
- The `Layout→Ladderize Random` item is used to order the clades randomly.
- The `Layout→Network Layout` item is used to choose the way the network embedding is computed. There are four methods available here. With *No Optimization* , we do not attempt to optimize the embedding of networks. The *2008 Algorithm* optimizes embedding of networks using the algorithm described in (Kloepper and Huson 2008). The *2009 Algorithm* optimizes embedding of networks using the algorithm described in (Huson 2009). The *2010 Algorithm* optimizes embedding of networks using a new algorithm developed by Huson and Scornavacca in 2010.
- The `Layout→Align Taxa` item: Attempts to align taxa in all selected trees or networks using an algorithm described in [18].
- The `Layout→Connect Taxa` item: Connect all taxa of the same name in different trees or networks.
- The `Layout→Disconnect All` item: Disconnect all nodes in different trees or networks.

5.7 View Menu

The `Views` menu contains items for setting the grid, scaling trees or networks, using the magnifier and showing/hiding labels.

- The `View→Set Grid` item is used to set the tree or network grid dimensions.
- The `View→Less Panels` item is used to lessen the number of panels in the grid.
- The `View→More Panels` item is used to increase the number of panels in the grid.
- The `View→Show Scroll Bars` item is used to show or hide scroll bars.
- The `View→Show Borders` item is used to show or hide borders.
- The `View→Show Scale Bar` item is used to show or hide scale bar.
- The `View→Zoom to Fit` item is used to scale the tree or network to fit the window.
- The `View→Fully Contract` item is used to contract the tree or network.
- The `View→Fully Expand` item is used to expand the whole tree or network.
- The `View→Use Magnifier` item is used to turn the magnifier functionality on and off.
- The `View→Magnify All Mode` item modifiers the magnification process so that the whole tree gets mapped into the magnifier.
- The `View→Show Node Labels` item is used to make all node labels visible or invisible.
- The `View→Show Edge Labels` item is used to make edge labels visible or invisible.
- The `View→Label Edges By Weights` item uses the edge weights as edge labels.
- The `View→Sparse Labels` item instructs the program to show only a subset of the taxon labels, thus avoiding overlapping labels.
- The `View→Radial Labels` item instructs the program to rotate leaf labels to match the orientation of the edges that lead to them.
- The `View→Reposition Labels` item sets all the labels to their original position.

5.8 Window Menu

The `Window` menu contains a number of window-related commands as well as a list of all currently open windows.

- The `Window→About` item opens a splash screen showing the program version. In MacOS, this can be found under `Dendroscope→About` .

- The `Window→How to Cite` item shows the citation info for this software which is: (1) Daniel H Huson, Daniel C Richter, Christian Rausch, Tobias Dezulian, Markus Franz and Regula Rupp. Dendroscope: An interactive viewer for large phylogenetic trees . BMC Bioinformatics 8:460, 2007. (2) Daniel H Huson and Celine Scornavacca. Dendroscope 3: a tool for drawing, modifying and computing rooted phylogenetic networks. In preparation.
- The `Window→Website` item is used to go to the program website.
- The `Window→Register` item is used to register the program for free.
- The `Window→Set Window Size` item is used to set the size of the `Main` window.
- The `Window→Command-line Syntax` item lists all commands supported by the program.
- The `Window→Command Input` item opens a window that can be used to enter a command (see command). tree or network manually in Newick Format.
- The `Window→Message Window` item is used to open the `Message` window.
- If several program windows are opened, they are listed at the end of the window menu.

5.9 Toolbar

For easier access of frequently used functions, a *Toolbar* is provided. The button images are self-explicative and a description appears when passing on the buttons with the mouse.

5.10 Context Menus

A right mouse click when the index finger of the hand icon is positioned on a node opens a context menu which allows to edit the node label, open the `Format Panel`, show or hide node labels, copy the node label, select the subtree starting from this node, and swap the subtree starting from this node.

A right mouse click when the index finger of the hand icon is positioned on an edge opens a context menu which allows to edit the edge label, open the `Format Panel`, show or hide edge labels, and copy the edge label.

A right mouse click beside the tree opens a context menu which allows to select or deselect all edges, nodes, and labels, to scale the tree or network to fit the window or finally to show or hide scroll bars and borders.

5.11 Status Line

The `Status Line` at the bottom of the program window shows the index of the current tree, the total number of trees, the number of nodes and edges and the available space of the reserved memory.

6 Additional Windows

6.1 Format Panel

The `Format Panel` can be opened via `Edit→Format` or by a right mouse click after selecting elements of the tree like edges, nodes or labels. You can format them as follows:

- Edges can have their edge width and edge width set.
- Edges can be assigned three types of shapes: straight edges, curved edges and angular edges, the effect of which depends on the current view.
- Nodes can be assigned certain shapes: square nodes, circle nodes or none. Square and circle node shapes can have their node size and node color set.
- If a selected node or edge has a label, then you can choose its font family, font style or font size.
- Labels can be switched on and off, and can be rotated to the left or right.

Configuration changes are applied immediately. The `Options→Save Font As Default` menu item can be used to set the default font, style and size used by the program.

6.2 Find and Replace Toolbars

The `Find` toolbar can be opened or closed using the `Edit→Find` menu item. Its purpose is to search labels in the displayed trees or networks. Enter a query specifying the text to find in the top text region. Use the following check boxes to configure the search:

- If the `Case sensitive` item is selected, then the case of letters is distinguished in comparisons.
- If the `Whole words only` item is selected, then only taxa or labels matching the complete query string will be returned.
- If the `Regular Expression` item is selected, the query is interpreted as a Java regular expression (see example further down).

The scope of the search can be `Global` or `Selection`. If a searched label is "hidden" inside a bounding box (black opaque area of tree or network) or in a collapsed branch, it will be selected.

Press the `Close`, `Find First`, `Find Next` or `Find All` buttons to close the toolbar, or find the first, or next occurrence of the query, respectively. Press `Unselect All` to unselect the highlighted occurrences.

The `Replace` toolbar can be opened or closed using the `Edit→Replace` menu item. Its purpose is to replace text in the displayed trees or networks. Enter a replacement text in the bottom text region.

Press the `Replace` or `Replace All` buttons to replace the next or all occurrences of the query with the text in the bottom text region, respectively.

Regular Expressions are powerful and flexible text-processing tools. They allow to specify complex patterns of text that can be discovered in an input string.

Example 1:

Each of the following represent valid regular expressions, and all will successfully match the character sequence "`Escherichia`":

- Escherichia
- E.*
- [eE]scherichia
- [eE]sch[aeiou][a-z]ichi.*

Example 2:

To select the five taxa simultaneously, e.g. Human, Mouse, Dog, Cat and Rat, use the following expression: `Human|Mouse|Dog|cat|Rat` and then press `Find All` .

For an extensive list of metacharacters and further explanations go to http://java.sun.com/j2se/1.5.0/docs/api/java/util/regex/Pattern.html

6.3 Message Window

The `Message` window is opened using the `Window→Message Window` item. The program writes all internal messages to this window. The window contains the usual File and Edit menu items.

6.4 Export Image Dialog

The `Export Image` dialog is opened using the `File→Export Image` item. This dialog is used to save an image of the current tree in a number of different formats, see Section 8.6.

The dialog permits to specify the file name and where to save the graphics file. The format is chosen from a menu. There are two radio buttons `Save whole image` to save the whole image, and `Save visible region` to save only the part of the image that is currently visible in the main viewer.

6.5 About Window

The `About` Window is opened using the `Window→About` submenu (`Dendroscope→About` in MacOS). It reports the version of the program and its authors.

7 Additional Features

7.1 Using the Mouse to Select

Nodes, edges and labels can also be selected by clicking on them with the index finger of the hand icon. If the left mouse click is press for 2 seconds or shift-clicking, an arrow appears: dragging the mouse, it is possible to perform a rubber-band selection in which all objects contained within a dragged rectangle are selected.

7.2 Magnifier Functionality

Dendroscope provides the user with a *magnifier functionality* that can be used to magnify portions of the tree.

Selecting the `View→Use Magnifier` item adds a magnifier layer to the view.

- *Magnifier band*: For all rooted views (rectangular and slanted view) a *magnifier band* is laid over the tree.
- *Magnifier disk*: For all unrooted views (radial and circular tree view) a *circular* magnifier is laid over the tree.

The magnifier can be pulled to a desired position by grabbing its frame with the mouse. The radius/width of the magnifier can be changed by dragging the rhomb at the magnifier's border line. The zoom factor of the magnifier can be changed via the [+,-] button.
Two magnifier modes are available depending on the current tree view.

7.3 Navigating trees with keys and mouse wheel

Dendroscope allows one to browse and analyze trees. `Navigating trees` is facilitated by some `key bindings` :

- *Scrolling:* Hold down the Shift button and use the mouse wheel to scroll top-down.
  Hold down the Alt and Shift buttons and use the mouse wheel to scroll right-left.
- *Zooming:* Use the mouse wheel to zoom the tree. Zooming is centered on the current mouse position. Press the shift key to zoom the graph in horizontal direction.
- *Rotating:* For circular and radial drawings, use the shift-key and left and right arrow keys to rotate the tree.

Alternatively, use the arrow keys to scroll the tree or network, or additionally press the shift key to zoom the graph in horizontal or vertical direction (zoom not available in this way for circular and radial drawings). Use the alt and control keys for acceleration.

8 File Formats

Dendroscope uses the NeXML file format to store the data of the modified and/or formatted tree or network. By convention, we use the suffix *.nexml* for NeXML files.

8.1 NeXML files

Dendroscope saves trees in a simple text-based format with the file extension `.nexml`. It contains the tree in Newick notation and additional (machine-readable) information on the view, selections, coloring etc. of the saved trees.

Trees can also be saved in Nexus and Newick format. However, when these formats are used, all information on the layout of the trees, fonts, colors, line widths etc are lost.

8.2 Old Dendroscope files

For backward compatibility, this version of Dendroscope can still open `.dendro` files (see the old version of this manual).

8.3 Nexus files

Dendroscope can read a Nexus file that contains a Nexus trees block and can export trees in this format.

8.4 Newick files

Dendroscope can read Newick files and can export trees in this format.

8.5 Extended Newick format and rooted phylogenetic networks

The *Extended Newick* format was designed as an extension of the Newick format to be able to describe rooted phylogenetic networks in bracket notation. Unfortunately, there is not just one such format, but a number of different ones. Dendroscope implements a version of the Extended-Newick proposed by [3].

In Dendroscope, a rooted phylogenetic network is described as a single line of extended-Newick format using brackets, as in the description of a rooted phylogenetic tree in the standard Newick format, with additional labels placed at the end of node labels. These special labels are of the form '#H1', '#H2', etc. When parsing an extended-Newick string, all nodes whose labels end on '#H1' are identified with each other, all nodes that end on '#H2' are identified, etc.

For example, to describe a rooted phylogenetic network with three leaves labeled 'a', 'b' and 'c', in which 'b' is to have a "reticulate" parent node that connects both above 'a' and above 'c', use the following extended-Newick string:

```
((a,(b)#H1),(c,#H1));
```

Copy and paste this string into a Dendroscope window to see the corresponding network.

In Dendroscope, quite everything that can be done with a rooted tree can also be done with a rooted phylogenetic network!

8.6 Graphics Formats

The following `graphics formats` are supported (how to open the `Export Image` dialog see 6.4):

- JPEG, "Joint Photographic Experts Group".
- GIF, "Graphics Interchange Format".
- SVG, "Scalable Vector Graphics".
- PNG, "Portable Network Graphics".
- BMP, "Bitmap".
- PDF, "Portable Document Format".

9 Using More Memory

The Dendroscope installer allows you to specify the amount of Dendroscope that the program can use.

To run Dendroscope with more than 400 MB under MacOS X on an intel Mac, edit the file ⟨installation-dir⟩/Dendroscope/Dendroscope.app/Contents/Info.plist as follows: Find the lines

```
<key>VMOptions</key>
<string>-server -Xmx400M</string><!-- I4J_INSERT_VMOPTIONS -->
```

and replace them by:

```
<key>VMOptions</key>
<string>-server -Xmx1000M </string><!--I4J_INSERT_VMOPTIONS -->
```

to run using 1 gigabyte, for example.

To run Dendroscope with more more than 400 Mb on a 64-bit unix/linux system, open the file ⟨installation-dir⟩/Dendroscope in a text editor. Find the current memory specification (e.g. -Xmx400M) and replace it by -d64 -Xmx100M to run with 1 gigabyte of memory, say. Note that the flag -d64 is necessary to specify 64-bit Java.

10 Commands

The program provides a command-interpreter to access all its functionalities. A *command* can be entered either using the `Window→Command Input` item or by starting the program in command-line mode and typing (or piping) commands to the program via the console.

The `Command input` window has a field for entering commands, a cancel button and two different apply buttons. The Apply button applies the entered command to the current tree or network, whereas the Apply to Every Tree in File button applies the entered command to all trees and networks in the current file, each one separately. Use this button with care.

To start Dendroscope in command-line mode use the option `+g`. For example under MacOS X type

```
⟨installation-dir⟩/Dendroscope/Dendroscope.app/Contents/MacOS/JavaApplicationStub +g
```

in a terminal shell. To make things easier, in the command line version only one file is opened at the time. When new trees or networks are computed, the file is emptied and filled with the newly computed trees and networks. To apply a set of commands to all trees and networks in the current file in the command line version, use the syntax:

```
apply-all-begin <command;> [<command>;..] apply-all-end;
```

Note that the Apply to All syntax should only be used for commands that change the trees (or networks), e.g. for computing the consensus network or changing the drawer for all trees in the file, and not for commands that change transient aspects of the visualization such as zoom factor, edges/nodes selection etc. Also, it is pointless to use a command such as open file or add file in this context.

Here is a summary of all available commands:

```
Opening and saving files:
        open file=filename [init=command] ;      Open the named file in the current window, if empty, otherwise in a new window,
                                                 and then optionally perform specified initial commands in new window
        save [format=value] file=filename ;      Save data to file in the specified format (possible formats: nexus newick nexml)
        exportimage file=filename [format={PNG|GIF|JPG|SVG|PDF}] [replace=bool] [textasshapes=bool] [title=title]  -
                                                 Export a picture of the current tree
        source file=filename ;                   Read commands (separated by semicolons) from the named file
        new ;                                    Open a new document. Any selected trees are put in it

Choosing tree and visualization:
        go tree={first,next,prev,last,<num>} ;   Go to the first, next, previous or last tree, or to a specific tree
        set drawer=drawer-name ;                 Set the drawer used to draw the tree (Possible values: RectangularPhylogram RectangularCladogram SlantedCladogram
                                                 RadialPhylogram RadialCladogram CircularPhylogram CircularCladogram InnerCircularCladogram)
        auxiliaryparameter change={increment|decrement};
                                                 Decrement|Increment the  auxiliary parameter used by some of the drawers


Customizing the layout of a tree:
        reroot ;                                 Reroot current tree using currently selected set of nodes (outgroups), node or edge
        ladderize=value ;                        Ladderize each displayed tree (possible values: left right random)
        rotatesubtree ;                          Rotate all children of all selected nodes
        swapsubtree ;                            Swap subtree below selected node(s)
        reset labelpositions ;                   Reset all node label positions
        center ;                                 Center the trees
        rotate angle=number ;                    Rotate the whole tree by the given angle (in radian)
        set hflip={false|true} ;                 Flip the tree horizontally?
        rotatelabels percent=<integer> ;         Rotate the labels of selected nodes

Adding, creating and modifying trees:
        add tree=newick-tree ;                   Add the specified trees or networks (in (extended) Newick format) to the list of trees
        add file=filename ;                      Add trees or networks from a file to the current document
        extract induced network ;                Extract subtree or subnetwork induced by selected nodes
        extract LSA induced network ;            Extract subtree or subnetwork rooted at the LSA of the selected nodes
        extract subnetwork ;                     Extract subtree or subnetwork below node or edge
        remove taxa={selected|names} ;           Remove all selected taxa, if taxa=selected, otherwise, remove named taxa
        set unlockedgelengths={true|false} ;     Allow user to reshape tree by dragging nodes or internal edge points
```

```
        edit edgelabels ;                       Edit the selected edge labels
        edit nodelabels ;                       Edit the selected node labels
        align trees=selected-or-all ;           Attempts to align taxa in all selected trees or networks
        set name=<name> [treeId=<tree-number>]; Set the name of a tree or network


Algorithms:
        compute mult2net method={HOLM|cluster|levelk} ;
                                                Compute a network from a multi-labeled tree
        compute consensus method={Strict|Majority|Loose|level-k-network threshold=<value> |cluster-network threshold=<value> |galled-network threshold=<value>|
        Distortion1|LSAtree} ;                  Compute a consensus tree or network of a set of trees
        compute tanglegram method={nnet} ;      Compute a tanglegram for two trees or networks using the NeighborNet-based heuristic
        compute triplets2network method=simplistic ;
                                                Compute a network using the simplistic algorithm
        compute hybridization-network method=Autumn;
                                                Compute minimum hybridization networks for two rooted phylogenetic trees using the Autumn algorithm (Huson and Linz, subm
        compute hybridization-network method=ASCH2011 [showdialog={false|true}] [numberOfThreads=number];
                                                Compute minimum hybridization networks for two bifurcating trees on the same taxon set using the
                                                Albrecht, Scornavacca, Cenci, and Huson (2011) algorithm
       compute hybridization-number method=Autumn;
                                                Compute the hybridization number for rooted phylogenetic trees using the Autumn algorithm (Huson and Linz, submitted)
       rerootby method=min-hybridization-number;  Reroot to trees so as to minimize their hybridization number using the Autumn algorithm (Huson and Linz, submitted)
       compute hybridization-number method=ASCH2011 [showdialog={false|true}] [numberOfThreads=number];
                                                Compute the hybridization number for two rooted binary trees on the same taxon set
        compute rspr-distance method=ASCH2011 [showdialog={false|true}] [numberOfThreads=number];
                                                Compute the rSPR distance for two rooted binary trees on the same taxon set
        compute distance method={hardwired|softwired|displayedTrees|tripartition|nestedLabels|pathMultiplicity} ;
                                                Calculate distances between two trees or networks
        compute DTL_reconciliation ;            Calculate DTL reconciliation between two binary trees
        run-simulator parameters=<parameters> ; Create simulated trees and networks data sets.

Selection and Deselection:
        select all ;                            Select all nodes and edges
        select nodes={all|none|leaves|labeled}; Select nodes
        select edges={all|none|short|long} [threshold=<number>];
                                                Select all or none edges, or all edges
                                                longer than or shorter than the given threshold
        select previous ;                       Select all labeled nodes as in previous window
        select labelednodes ;                   Select all labeled nodes
        select leaves ;                         Select all leaves
        select subnetwork ;                     Select subtree or subnetwork below node or edge
        select induced network ;                Select subtree or subnetwork induced by selected nodes
        select LSA induced network ;            Select subtree or subnetwork rooted at the LSA of the selected nodes
        select subpart ;                        Select parts of tree that are reachable from any selected node without crossing any reticulate edges
        select nonterminal ;                    Select all non-terminal nodes and egdes
        select spanned ;                        Select all edges that connect any two selected nodes
        select root ;                           Select root
        select special ;                        Select all ’special’ edges
        select invert ;                         Invert the current selection
        select panels=all;                      Select all panels
        select panels=invert;                   Invert the selection of all panels
        select panels=none;                     Deselect all panels
        deselect all ;                          Deselect all nodes and edges
        deselect nodes ;                        Deselect all nodes
        deselect edges ;                        Deselect all edges
        list taxa=selected ;                    List all currently selected taxa

Searching:
        show finddialog={true|false} ;          Show or hide find/replace dialog
        find searchtext=text target={Nodes|Edges} [all=bool] [regex=bool] [wholeword=bool] [respectcase=bool] -
                                                Find and select labels matching the given search text
        replace searchtext=text replacetext=text [target={Nodes|Edges}] [all=bool]  [regex=bool] [wholeword=bool] [respectcase=bool] ;
                                                Find and replace labels matching the given search text

Collapsing and uncollapsing nodes:
        collapse what={selected|complement} ;   Collapse all selected nodes or their complement
        collapse level=<integer> ;              Collapse all nodes at the given level (distance from root)
        uncollapse what={all|selected|subtree} ; Uncollapse all nodes, all selected nodes, or the whole subtree below each selected node

Visualization:
        set grid=rows x cols ;                  Set the tree grid dimensions
        set window [width=num][height=num][x=num][y=num] ;
                                                Set size and location of main window
        set layouter={Unoptimized|Algorithm2008|Algorithm2009|Algorithm2010|Algorithm2010Dist|AlgorithmLSA} ;
                                                Chooses the way the network embedding is computed.
        set font=name                           Set font by name
        set autolayoutlabels={true|false} ;     Set auto-layout of labels
        set margin [left=num][right=num][top=num][bottom=num] ;
                                                Set the margin around the tree
        set approxthreshold=int ;               Set minimum threshold for representing subtrees by approximate shapes
        show edgelabels={true|false} ;          Show or hide edge labels
        show edgeweights={true|false} ;         Use the edge weights as edge labels
        show nodelabels={true|false} ;          Show or hide node labels
        show boarders={true|false} ;            Show or hide borders
        show scalebar={true|false} ;            Show or hide scale bar
        show scrollbars={true|false} ;          Show or hide scroll bars
        set edgeshape=value ;                   Set the shape of selected edges (possible values: angular straight curved)
        set nodeshape=value ;                   Set the shape of selected nodes (possible values: rectangle oval none)
```

```
        set radiallabels={true|false} ;          Set radial layout of node labels
        set sparselabels={true|false} ;          Set sparse layout of node labels (in which labels that would overlap others are not shown)
        set color=r g b ;                        Set the color of all selected nodes and edges
        set fillcolor=r g b ;                    Set the fill color of selected nodes
        set labelcolor=r g b ;                   Set the label color of all selected nodes and edges
        set labelfillcolor=r g b ;               Set the label fill color of selected nodes and edges
        set edgewidth=num ;                      Set the line width of all selected edges
        set nodesize=num ;                       Set the size of all selected nodes

Scaling:
        contract direction=horizontal ;          Contract  horizontally
        contract direction=vertical ;            Contract  vertically
        expand direction=horizontal ;            Expand  horizontally
        expand direction=vertical ;              Expand  vertically
        zoom selection ;                         Zoom to current selection of nodes
        zoom what=<{contract|expand|fit}> ;      Fully contract, fully expand or zoom to fit the whole tree or network  in the window

Controlling the magnifier:
        set magnifier={true|false} ;             Turn magnifier on or off
        set magradius=<integer> ;                Set magnifier radius
        set magdisplacement=<float> ;            Set magnifier displacement (power)
        set magnifyallmode={true|false} ;        Set the magnifier all mode

Adding images to nodes:
        load imagedir=<directory-name>           Load image files from named directory. Images are placed next to taxa of same name (recognized formats: GIF,
                                                 JPG, JPEG, BMP and PNG)
        set imageheight=<integer> ;              Set the height of the images associated with all selected nodes
        set imagelayout=<value> ;                Set the layout used for images (possible values: north south east west radial)

Special purpose:
        update ;                                 Update the trees
        set dirty={true|false} ;                 Set the dirty status of a document
        set vint={true|false} ;                  Set show version-in-window-title mode
        set scalebar={true|false} ;              Set show scalebar mode
        set prop <name>=<value> ;                Set the boolean value of a named property
        tofront ;                                Bring window to front

Other:
        howtocite ;                              How to cite the program
        website ;                                Go to the program website
        version ;                                List version info
        help [keyword] ;                         List this help or list help on given keyword
        about ;                                  List information about Dendroscope
        close ;                                  Close the window
        quit ;                                   Quit the program
```

Here is an example:

```
open file=’⟨installation-dir⟩/Dendroscope/examples/trees.new’;
select taxa=AE007869;
set labelcolor=225 180 0; //to color the taxon AE007869 in the first tree
deselect nodes;
exportimage format=PDF file=’testExport.pdf’;
quit;
```

11 Examples

In this section we illustrate some of the features of Dendroscope.

11.1 Basic tree view

Figure 1 shows the eight views possible with Dendroscope for the same phylogenic tree of mammal species.

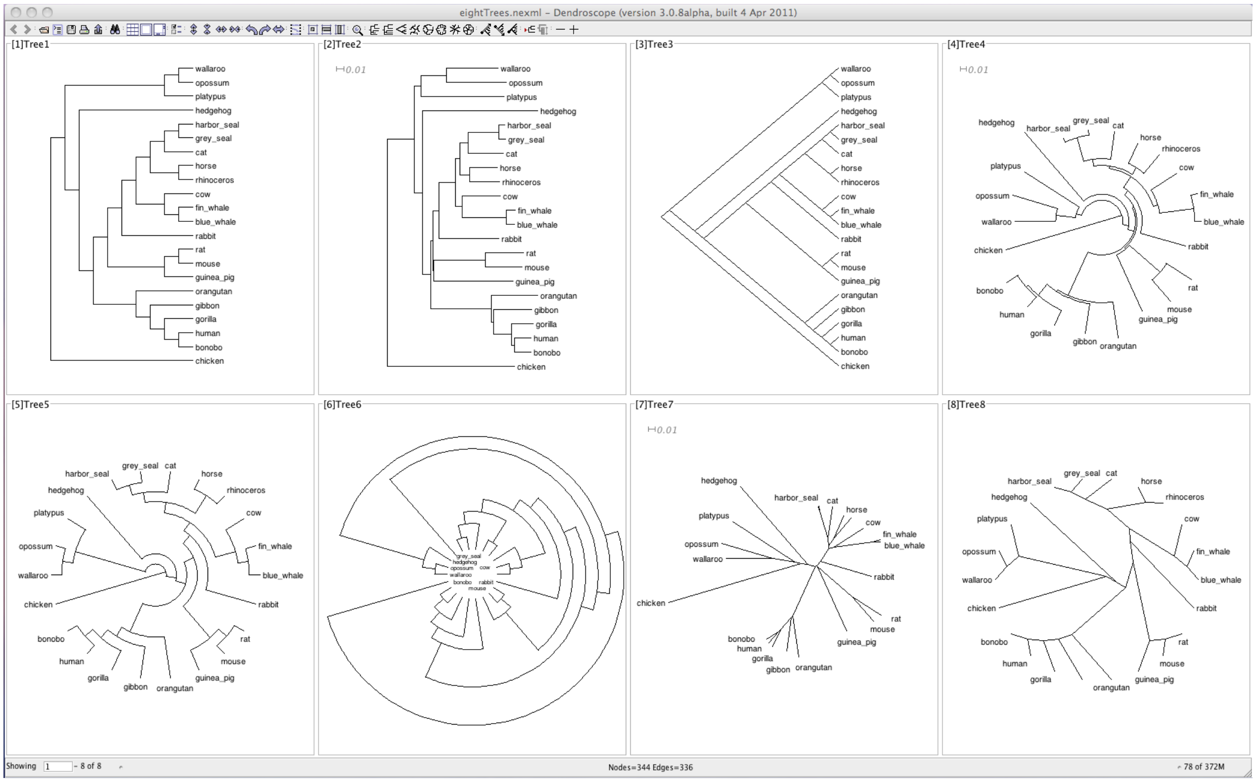

Figure 1: Illustration of the eight views possible with Dendroscope . Upper line: Rectangular Phylogram, Rectangular Cladogram, Slanted Cladogram, Circular Phylogram. Lower line: Circular Cladogram, Internal Circular Cladogram, Radial Phylogram, Radial Cladogram.

11.2 Additional tree view features

Figure 2 illustrates the action of the Magnifier on part of the NCBI taxonomy tree close to *Homo sapiens*.

11.3 Editing trees

Figure 3 demonstrates some of the editing possibilities present in Dendroscope.

11.4 Constructing rooted phylogenetic networks

Figure 4 depicts two phylogenetic trees from the Poaceae dataset from the Grass Phylogeny Working Group [5] and the 4 hybrid networks computed from these trees by the method presented in [?].

11.5 Tanglegram

Figure 5 shows a tanglegram between the first two networks in Figure 4(b).

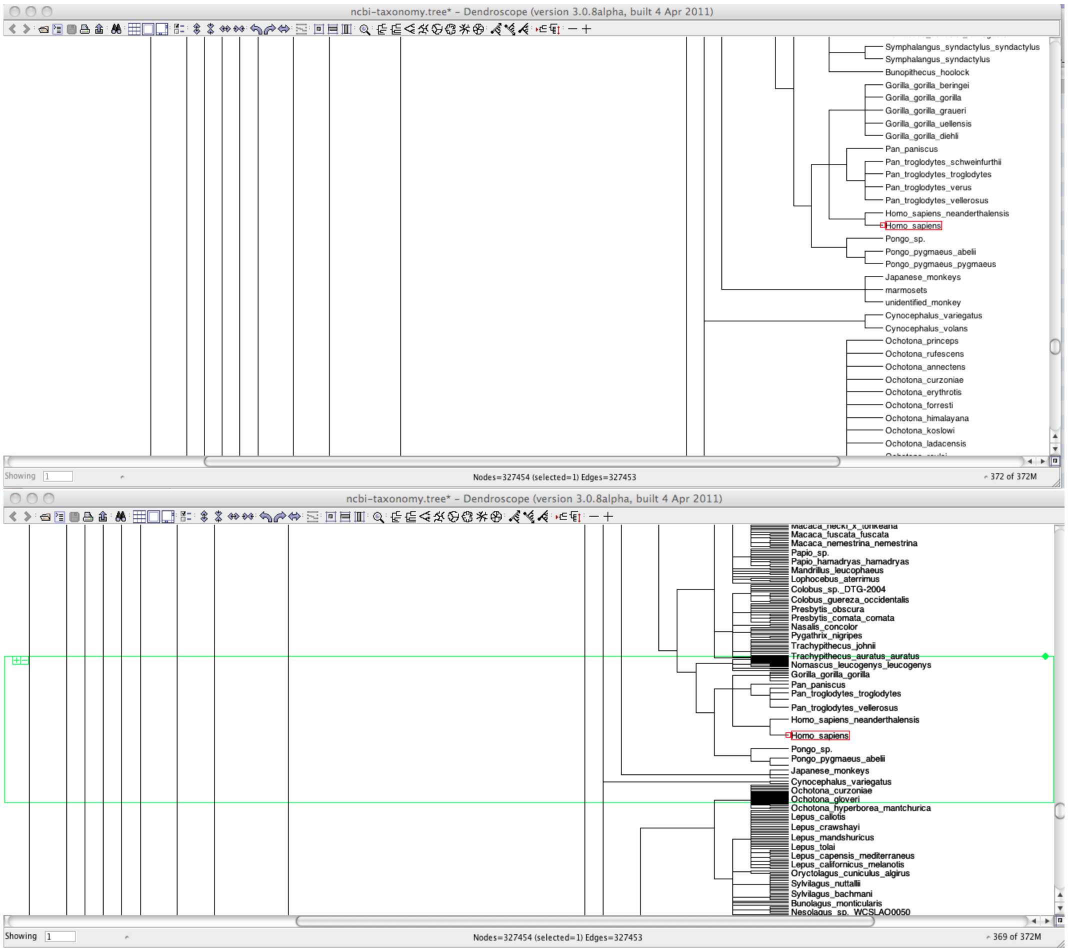

Figure 2: Part of the NCBI taxonomy showing *Homo sapiens* and his relatives without and with the magnifier turned on.

12 Acknowledgements

This program includes software developed by the Apache Software Foundation (`http://www.apache.org/`), namely the *Batik* library for generating image files. It also uses *MRJAdapter*, a Java package used to help construct user interfaces for the Apple Macintosh. This program uses Daniel Huson's unpublished `jloda` library, which is also used by SplitsTree4 (`http://www.splitstree.org`)[11, 7].

References

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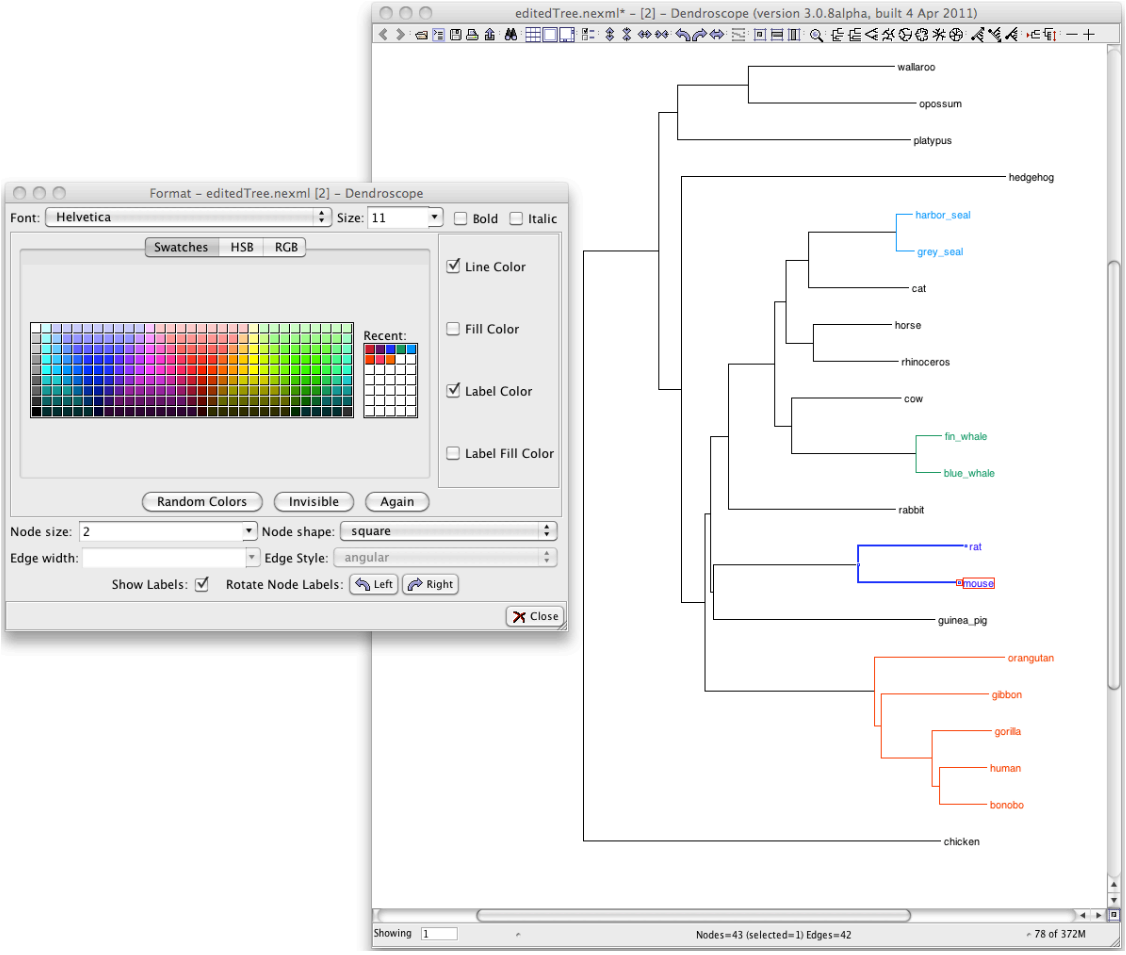

editedTree.nexml* – [2] – Dendroscope (version 3.0.8alpha, built 4 Apr 2011)

Format – editedTree.nexml [2] – Dendroscope

Font: Helvetica
Size: 11
☐ Bold
☐ Italic
☑ Line Color
☐ Fill Color
☑ Label Color
☐ Label Fill Color
Node size: 2
Node shape: square
Edge width:
Edge Style: angular
Show Labels: ☑

Showing 1
Nodes=43 (selected=1) Edges=42
78 of 372M

Figure 3: All labels and tree substructures can be easily edited.

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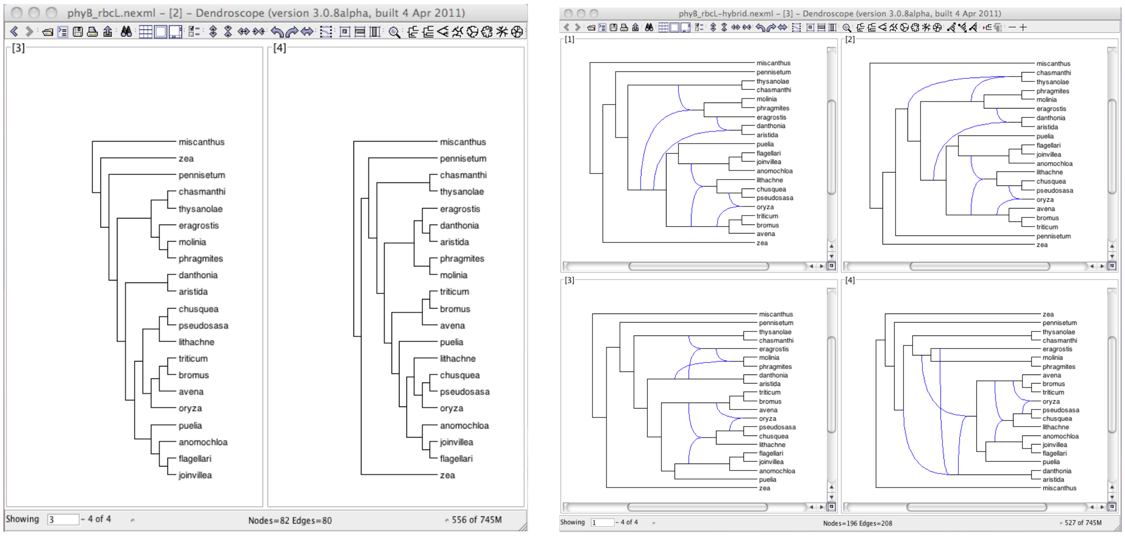

(a) (b)

Figure 4: (a) Two phylogenetic trees from the Poaceae dataset from the Grass Phylogeny Working Group [5]. The trees have been built from the loci *phytochrome B* (left) and *ribulose 1,5-biphosphate carboxylase/oxygenase, large subunit* (right) [17]. (b) The 4 hybrid networks for the trees in (a) reconstructed by the method presented in [?].

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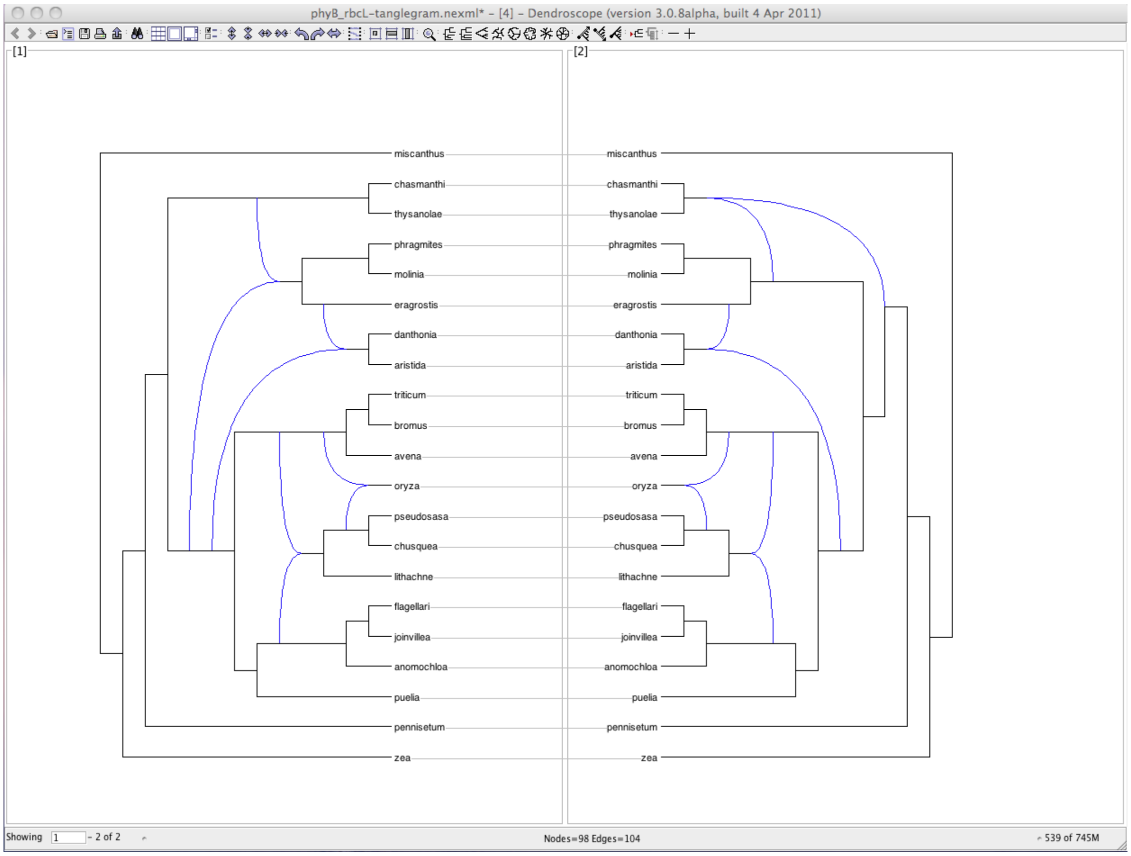

Figure 5: A tanglegram for two phylogenetic networks.

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