



Dendroscope 3: An Interactive Tool for Rooted Phylogenetic Trees and Networks

Daniel Huson, Celine Scornavacca

► To cite this version:

Daniel Huson, Celine Scornavacca. Dendroscope 3: An Interactive Tool for Rooted Phylogenetic Trees and Networks. *Systematic Biology*, 2012, 61 (6), pp.1061-1067. 10.1093/sysbio/sys062 . hal-02154987

HAL Id: hal-02154987

<https://hal.science/hal-02154987>

Submitted on 18 Dec 2019

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Dendroscope 3: An interactive tool for rooted phylogenetic trees and networks

DANIEL H. HUSON¹ AND CELINE SCORNAVACCA^{1,2}

¹ *Center for Bioinformatics (ZBIT), University of Tübingen, 72076, Tübingen, Germany;*

² *Institut des Sciences de l'Evolution Montpellier (ISEM), UMR 5554, Université Montpellier II, 34095 Montpellier, France*

Corresponding author: Daniel H. Huson, Center for Bioinformatics (ZBIT), University of Tübingen, Sand 14, 72076 Tübingen, Germany; E-mail: daniel.huson@uni-tuebingen.de.

Abstract.— Dendroscope 3 is a new program for working with rooted phylogenetic trees and networks. It provides a number of methods for drawing and comparing rooted phylogenetic networks, and for computing them from rooted trees. The program can be used interactively or in command-line mode. The program is written in Java, use of the software is free and installers for all three major operating systems can be downloaded from www.dendroscope.org.

(Keywords: Phylogenetic trees, phylogenetic networks, software)

The evolutionary history of a set of species or genes is usually represented by a phylogenetic tree, and many different methods exist for the computation of such trees (Felsenstein 2004). When reticulate events such as horizontal gene transfer, hybridization or recombination play a significant role in the history of a set of taxa, or when there are major incompatibilities in the given data, then a phylogenetic network may provide a more accurate evolutionary scenario (Sneath 1975; Doolittle 1999; Huson et al. 2010).

There are a number of established tools for computing unrooted phylogenetic networks. One popular program is SplitsTree (Huson and Bryant 2006), which contains implementations of a number of different methods for computing unrooted trees and networks, such as split decomposition (Bandelt and Dress 1992) and neighbor-net (Bryant and Moulton 2004). Another widely used method is median-joining (Bandelt et al. 1995), which is implemented in a program called Network, as well as in SplitsTree.

For rooted phylogenetic networks, the situation is slightly different. While much work has been done on developing concepts and theoretical methods for computing rooted phylogenetic networks (for an overview, see Huson and Scornavacca (2011)), the application of such ideas in biological studies has been hampered by the lack of robust and easy to use tools for their computation. While a number of tools for calculating rooted phylogenetic networks do exist, such as Lott et al. (2009); Than et al. (2008); Cardona et al. (2008b), they appear to be of limited utility for biologists.

In this paper we present a new user-friendly program for working with rooted phylogenetic trees and networks called Dendroscope 3, which is based on the popular tree drawing program Dendroscope 1 (Huson et al. 2007). The program provides numerous methods for drawing and comparing rooted phylogenetic networks, and for computing such networks (including hybridization networks) from rooted trees. With this new software, we hope to provide a standard tool for computing rooted phylogenetic networks.

Rooted phylogenetic trees and networks.—

The evolutionary history of a set of taxa (i.e. species or genes) is usually depicted as a rooted phylogenetic tree. Rooted phylogenetic networks provide a generalization of rooted phylogenetic trees that can be used to explicitly represent reticulate events or to visualize incompatibilities in a dataset. By definition, a *rooted phylogenetic network* is a directed acyclic graph in which each leaf is labeled by a unique taxon and that has precisely one node that is the ancestor of all other nodes, called the *root* (Huson et al. 2010). Any node with more than one parent is called a *reticulation* and the edges leading into such a node are called *reticulate* edges.

Rooted phylogenetic networks can be computed using a number of different methods. Here we briefly mention some of the approaches that build such networks from rooted phylogenetic trees or from the clusters that they contain. A cluster network is a rooted phylogenetic network that displays a given set of clusters, for example all clusters present in a set of rooted phylogenetic trees. Cluster networks are easy to compute (Huson and Rupp 2008). Similarly, a *level- k network* can be used to represent a set of clusters and aims at minimizing the number of reticulations in any biconnected component of the network (Choy et al. 2005; van Iersel et al. 2010) and a galled network can also be used to represent incompatible clusters (Huson et al. 2009). Given two rooted phylogenetic trees, a minimum *hybridization network* is a rooted phylogenetic network that contains both trees and has a minimum number of reticulations. The idea here is that reticulations correspond to speciation-by-hybridization events (Linder and Rieseberg 2004; Koblmüller et al. 2007). Such networks can be computed from bifurcating trees (Baroni et al. 2006; Bordewich et al. 2007; Chen and Wang 2010; Albrecht et al. 2011) or from multifurcating trees on unequal taxon sets (Linz and Semple 2009, Huson and Linz, unpublished). A rooted phylogenetic network may also be used to summarize a *multi-labeled* rooted phylogenetic tree (Huber et al. 2006).

Existing software.—

There exists a large number of programs for computing phylogenetic trees and for visualizing them (Felsenstein 2012). The original version of our program, Dendroscope 1 (Huson et al. 2007), was designed as a viewer for rooted phylogenetic trees and was based on a survey of existing programs in an attempt to provide all the most useful features in one program, in particular including the ability to draw large trees with up to one million nodes.

There has been much interest in recent years in developing methods for computing rooted phylogenetic networks and this has led to a number of software packages such as PhyloNet (Than et al. 2008), PADRE (Lott et al. 2009) or the Perl package Bio::PhyloNetwork (Cardona et al. 2008b). More detailed lists of existing software can be found in Huson et al. (2010) and Gambette (2012). While these programs contain some sophisticated algorithms, they do not appear to have been extensively engineered so as to provide robust, fast and GUI-based user-friendly tools.

Dendroscope 3.—

The aim of Dendroscope 3 is to provide a user-friendly tool for working with rooted phylogenetic trees and networks. To this end, all tree visualization and interactive manipulation methods of Dendroscope 1 (Huson et al. 2007) have been extended so as to also work for rooted networks. As a platform for computing rooted phylogenetic networks, our program provides a choice of algorithms for computing consensus trees and consensus networks, such as galled networks or hybridization networks, from rooted phylogenetic trees. To simplify multi-tree analyses, the program provides a number of distance calculations and can display a direct comparison of two trees or networks in terms of a tanglegram. Moreover, the program is able to show any number of trees and networks from the same dataset simultaneously in the same window and a find-and-replace tool is

provided that operates across all trees or networks that are shown in the same window. All features of the program are also accessible in command-line mode and the program can be run on a cluster or cloud as part of a larger analysis pipeline. The program is fully multi-threaded and a number of the computationally more demanding algorithms are implemented in a parallel fashion.

In Dendroscope 3, phylogenetic trees and networks can be loaded from a file in Newick format, in the case of trees, extended Newick format (Cardona et al. 2008a), in the case of networks, or in Nexus format. Moreover, an input dialog is provided for entering trees or networks by hand. The program uses the NeXML format (Vos et al. 2012) to save and reopen trees or networks that have been edited. In this case, the layout and formatting (colors, line width, fonts etc) is saved along with the trees or networks. Trees and networks can also be saved in other formats (Newick, extended Newick or Nexus) and can be exported in a number of different graphics formats.

The main window of Dendroscope 3 can be configured to show a grid of $n \times m$ trees or networks simultaneously, thus making it easier to work with datasets that contain multiple trees or networks, such as obtained from multiple genes, or by using multiple methods. Trees and networks can be displayed in a number of ways, namely as a circular, radial or rectangular phylograms or as (an internal or external) circular, radial, rectangular or slanted cladograms (Huson 2009) and a magnifier can be used to enlargen a part of a tree or of a network. Nodes, edges and labels of trees and networks can be interactively formatted and edited and the program supports operations such as reshaping, rerooting, subtree/subnetwork reordering or subtree/subnetwork extraction. One can attach images to taxa and these are then displayed next to the corresponding nodes.

As already mentioned, the program provides a choice of algorithms for computing consensus trees and consensus networks from rooted phylogenetic trees, such as the strict, majority and loose consensus (Bryant 2003), as well as the LSA consensus (Huson 2009). It

also provides implementations of algorithms for computing cluster networks (Huson and Rupp 2008), minimum galled networks (Huson et al. 2009) and level-k networks with small k (van Iersel et al. 2010). If the input trees are on overlapping, but non-identical taxon sets, then the program uses the *Z-closure* algorithm (Huson et al. 2004) to infer missing data. So, in particular, the program is able to compute the strict or majority consensus of a set of trees even if the trees do not all have the same taxon sets, although in the latter case the result may be a rooted phylogenetic network rather than a tree. Two recent methods are available for computing hybridization networks, the first can be applied to any two (possibly multifurcating) rooted phylogenetic trees with overlapping, but not necessarily identical taxon sets (Huson and Linz, unpublished), whereas the second method is optimized to run on a pair of bifurcating trees that contain exactly the same taxa (Albrecht et al. 2011, Scornavacca et al. unpublished). Dendroscope 3 provides two approaches to computing a single-labeled rooted phylogenetic network that represents a multi-labeled phylogenetic tree, namely one based on nested labels (Huber et al. 2006) and another that consists of extracting all clusters from the tree and then representing them by a cluster network (Huson et al. 2010, Section 11.7).

Dendroscope 3 provides a number of distance calculations for comparing two rooted phylogenetic trees or networks based on the contained clusters or trees and other concepts, such as the *hardwired cluster distance* (Huson et al. 2010), the *softwired cluster distance* (Huson et al. 2010), the *displayed trees distance* (Huson et al. 2010), the *tripartition distance* (Moret et al. 2004), the *nested labels distance* (Nakhleh 2009; Cardona et al. 2009) and the *path multiplicity distance* (Cardona et al. 2007). None of these measures is a proper metric because there exist cases in which they return a distance of zero for two distinct networks. Nevertheless they are useful in practice and some of them have been shown to be proper metrics on a suitably restricted set of networks. For two rooted phylogenetic trees on the same taxon set, another option is to compute their hybridization

distance (Bordewich et al. 2007; Albrecht et al. 2011, Huson and Linz unpublished) or their *rSPR distance*.

One way to visualize similarities and differences between two rooted phylogenetic trees or networks is to display a *tanglegram* in which the two trees or networks are drawn opposite each other and corresponding taxa are connected by lines, possibly changing the layout order of taxa in an attempt to minimize the number of line crossings.

Dendroscope 3 contains a very general algorithm that can compute a tanglegram for two rooted trees or networks that may contain multifurcations and may have different taxon sets (Scornavacca et al. 2011).

Examples.—

In Pirie et al. (2009), the authors explore the potential impact of conflicting gene trees on inferences of evolutionary history above the species level, in particular studying grasses and using both chloroplast DNA (cpDNA) and nuclear ribosomal DNA (ITS region). The authors argue that the contradictions can be explained by past hybridization events, which have linked gains of complex morphologies with unrelated chloroplast lineages and have erased evidence of dispersals from the nuclear genome.

In Figure 1 of Pirie et al. (2009), the authors show a tanglegram involving a rooted phylogenetic tree computed from cpDNA and one computed from ITS sequence data. The two trees can be downloaded from

<http://ab.inf.uni-tuebingen.de/software/dendroscope/data/Pirie2009-cpDNA-ITS.txt>.

While time-consuming to produce by hand, such a visualization is easily produced in Dendroscope 3 simply by loading the two trees and then selecting the “Tanglegram” menu item. The resulting tanglegram is shown in Figure 1 of our paper.

To go beyond the analyses performed in Pirie et al. (2009), one can take the two trees and use Dendroscope 3 to compute a minimum hybridization network for them. In

less than five seconds, the program establishes that the minimum number of reticulations is 12 and it returns a “representative set” of 486 such networks (Albrecht et al. 2011). This type of computation can form the basis of a more refined analysis. In Figure 2, we display the first network in the list.

In Figure 3(b) of Pirie et al. (2009), the authors show an unrooted hybridization network for two “combined gene trees”, computed using SplitsTree (Huson and Bryant 2006). Reportedly, the first input tree is based on ITS data, with the cpDNA data recoded as missing data, whereas the second input tree is based on cpDNA data with ITS recoded as missing data. The trees were computed using maximum parsimony and then subjected to a 70% bootstrap threshold. They can be downloaded from

<http://ab.inf.uni-tuebingen.de/software/dendroscope/data/Pirie2009-Matrix4-5.txt>.

A rooted version of that network is easily computed using Dendroscope 3. One must first load the two trees into the program and then select the “Hybridization Network” menu item. The resulting rooted phylogenetic network is shown in Figure 3 of our paper.

Availability.—

Dendroscope 3 is written in Java. Use of the software is free and installers for all three major operating systems (MacOS, Windows and Linux) are available from

<http://www.dendroscope.org>.

Acknowledgments.—

This publication is the contribution no. 2012-077 of the Institut des Sciences de l’Evolution de Montpellier (ISE-M, UMR 5554). This work has been partially funded by the ANCESTRUME project ANR-10-IABI-0-01.

We thank Michael D. Pirie for providing the trees used in the examples section.

*.—References

- Albrecht, B., C. Scornavacca, A. Cenci, and D. H. Huson. 2011. Fast computation of minimum hybridization networks. *Bioinformatics* 28:191–197.
- Bandelt, H.-J. and A. W. M. Dress. 1992. A canonical decomposition theory for metrics on a finite set. *Advances in Mathematics* 92:47–105.
- Bandelt, H.-J., P. Forster, B. C. Sykes, and M. B. Richards. 1995. Mitochondrial portraits of human population using median networks. *Genetics* 141:743–753.
- Baroni, M., C. Semple, and M. Steel. 2006. Hybrids in real time. *Systematic Biology* 55:46–56.
- Bordewich, M., S. Linz, K. St. John, and C. Semple. 2007. A reduction algorithm for computing the hybridization number of two trees. *Evolutionary Bioinformatics* 3:86–98.
- Bryant, D. 2003. A classification of consensus methods for phylogenies. Pages 163–184 *in* BioConsensus (M. Janowitz, F.-J. Lapointe, F. McMorris, B. Mirkin, and F. Roberts, eds.). AMS, DIMACS.
- Bryant, D. and V. Moulton. 2004. Neighbor-net: An agglomerative method for the construction of phylogenetic networks. *Molecular Biology and Evolution* 21:255–265.
- Cardona, G., M. Llabrés, F. Rosselló, and G. Valiente. 2009. On Nakhleh’s metric for reduced phylogenetic networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 6:629–638.
- Cardona, G., F. Rosselló, and G. Valiente. 2007. Comparison of tree-child phylogenetic networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 6:552–569.
- Cardona, G., F. Rosselló, and G. Valiente. 2008a. Extended Newick: It is time for a standard representation of phylogenetic networks. *BMC Bioinformatics* 9:532.

- Cardona, G., F. Rosselló, and G. Valiente. 2008b. A perl package and an alignment tool for phylogenetic networks. *BMC Bioinformatics* 9:175.
- Chen, Z.-Z. and L. Wang. 2010. HybridNET: a tool for constructing hybridization networks. *Bioinformatics* 26:2912–2913.
- Choy, C., J. Jansson, K. Sadakane, and W.-K. Sung. 2005. Computing the maximum agreement of phylogenetic networks. *Theoretical Computer Science* 335:93–107.
- Doolittle, W. F. 1999. Phylogenetic classification and the universal tree. *Science* 284:2124–2128.
- Felsenstein, J. 2004. *Inferring Phylogenies*. Sinauer Associates, Inc.
- Felsenstein, J. 2012. Tree software.
<http://evolution.genetics.washington.edu/phylip/software.html>.
- Gambette, P. 2012. Who is who in phylogenetic networks - articles, authors and programs.
<http://www.atgc-montpellier.fr/phylnet/programs>.
- Huber, K. T., B. Oxelman, M. Lott, and V. Moulton. 2006. Reconstructing the evolutionary history of polyploids from multilabeled trees. *Molecular Biology and Evolution* 23:1784–1791.
- Huson, D., T. DeZulian, T. Kloepper, and M. A. Steel. 2004. Phylogenetic super-networks from partial trees. *IEEE/ACM Transactions in Computational Biology and Bioinformatics* 1:151–158.
- Huson, D., D. Richter, C. Rausch, T. DeZulian, M. Franz, and R. Rupp. 2007. Dendroscope: An interactive viewer for large phylogenetic trees. *BMC Bioinformatics* 8:460doi:10.1186/1471-2105-8-460 software available from www.dendroscope.org.

- Huson, D. H. 2009. Drawing rooted phylogenetic networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 6:103–109.
- Huson, D. H. and D. Bryant. 2006. Application of phylogenetic networks in evolutionary studies. *Molecular Biology and Evolution* 23:254–267 software available from www.splitstree.org.
- Huson, D. H. and R. Rupp. 2008. Summarizing multiple gene trees using cluster networks. Pages 296–305 *in* Algorithms in Bioinformatics, WABI 2008 (K. Crandall and J. Lagergren, eds.) vol. 5251. Springer Berlin/Heidelberg.
- Huson, D. H., R. Rupp, V. Berry, P. Gambette, and C. Paul. 2009. Computing galled networks from real data. *Bioinformatics* 25.
- Huson, D. H., R. Rupp, and C. Scornavacca. 2010. *Phylogenetic Networks*. Cambridge University Press.
- Huson, D. H. and C. Scornavacca. 2011. A survey of combinatorial methods for phylogenetic networks. *Genome Biology and Evolution* 3:23–35.
- Koblmüller, S., N. Duftner, K. Sefc, M. Aibara, M. Stipacek, M. Blanc, B. Egger, and C. Sturmbauer. 2007. Reticulate phylogeny of gastropod-shell-breeding cichlids from lake tanganyika - the result of repeated introgressive hybridization. *BMC Evolutionary Biology* 7:7.
- Linder, C. R. and L. H. Rieseberg. 2004. Reconstructing patterns of reticulate evolution in plants. *American Journal of Botany* 91:1700–1708.
- Linz, S. and C. Semple. 2009. Hybridization in nonbinary trees. *IEEE/ACM Transactions in Computational Biology and Bioinformatics* 6:30–45.

- Lott, M., A. Spillner, K. T. Huber, and V. Moulton. 2009. Padre: A package for analyzing and displaying reticulate evolution. *Bioinformatics* 25:1199–1200.
- Moret, B. M. E., L. Nakhleh, T. Warnow, C. R. Linder, A. Tholse, A. Padolina, J. Sun, and R. Timme. 2004. Phylogenetic networks: Modeling, reconstructibility, and accuracy. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 1:13–23.
- Nakhleh, L. 2009. A metric on the space of reduced phylogenetic networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 99.
- Pirie, M. D., A. M. Humphreys, N. P. Barker, and H. P. Linder. 2009. Reticulation, data combination, and inferring evolutionary history: an example from *Danthonioideae* (Poaceae). *Syst Biol* 58:612–28.
- Scornavacca, C., F. Zickmann, and D. Huson. 2011. Tanglegrams for rooted phylogenetic trees and networks. *Bioinformatics* 27:i248–i256.
- Sneath, P. 1975. Cladistic representation of reticulate evolution. *Systematic Zoology* 24:360–368.
- Than, C., D. Ruths, and L. Nakhleh. 2008. PhyloNet: a software package for analyzing and reconstructing reticulate evolutionary relationships. *BMC Bioinformatics* 9:322.
- van Iersel, L., S. Kelk, R. Rupp, and D. H. Huson. 2010. Phylogenetic networks do not need to be complex: using fewer reticulations to represent conflicting clusters. *Bioinformatics* 26:i124–i131.
- Vos, R. A., J. P. Balhoff, J. A. Caravas, M. T. Holder, H. Lapp, W. P. Maddison, P. E. Midford, A. Priyam, J. Sukumaran, X. Xia, and A. Stoltzfus. 2012. Nexml: Rich, extensible, and verifiable representation of comparative data and metadata. *Systematic Biology* 61:675–689.

Figure Captions.—

Figure 1 A tanglegram computed by Dendroscope 3 for the cpDNA and ITS trees that are reported in Figure 1 of Pirie et al. (2009).

Figure 2 A minimum hybridization network computed by Dendroscope 3 for the cpDNA and ITS trees that are reported in Figure 1 of Pirie et al. (2009). It has 12 reticulations and is one of 486 networks calculated by the program.

Figure 3 A hybridization network computed from the two simplified trees that were used as input for Figure 3(b) of Pirie et al. (2009).