

Tree visualisation

Last Updated Tuesday, 24 April 2007

A useful way of classifying phylogenetic tree visualization software is according to the size of the trees they are able to handle. I would define three main categories:

- small trees (hundreds of nodes)
 - large trees (thousands of nodes)
 - huge trees (tens to hundreds of thousands of nodes)
- Visualising small phylogenetic trees - 2D euclidean space
The majority of tree visualization tools fall within this category. Some of the most used tools are:

- DRAWTREE
- TREEVIEW

- ATV These tools lay out the trees in a 2D euclidean space and are successful at visualising trees of up to a few hundred nodes. However, with more than a few hundred nodes, it is no longer possible to visualise the whole tree on one screen without increasing the level of clutter to the point where the display is unreadable. It is possible to focus in on one area of the tree, but the user then loses a sense of the context since the parts of the tree that are not in focus disappear off screen. However, although these tree visualisation tools are only able to handle a limited number of nodes, they are able to display trees with rich information content (branch lengths, bootstrap values, etc).

Visualising large phylogenetic trees - 2D hyperbolic space Some software tools aimed at visualising large trees exploit the properties of 2D hyperbolic space to provide a focus+context view i.e. the possibility to zoom in on a particular subset of data while keeping the broader picture in view:

- HYPERTREE (a 2D hyperbolic viewer that reads phylogenetic tree file formats)
- TREEBOLIC (a general 2D hyperbolic viewer) In hyperbolic space (as opposed to euclidean space), circumference and area increase exponentially instead of geometrically. Thus, there is enough room to allocate the same amount of space to every node, regardless of the size of the tree. Although hyperbolic space is infinite, it can be projected into a finite volume of euclidean space for a focus+context view. The result of the projection is a disc where points within the disc are magnified according to their radial distance from the center with the amount of magnification decreasing continuously and at an accelerating rate from the center to the boundary. By bringing different parts of a tree to the magnified central region, the user can examine every part of the tree in detail while retaining a sense of the context.

Visualising huge phylogenetic trees - 3D hyperbolic space By visualising in 3D rather than 2D hyperbolic space so that the trees are rendered inside a sphere rather than a disc and by using specifically developed layout algorithms, some tools are able to interactively visualise trees with several hundred thousand nodes:

- H3VIEWER (the original 3D hyperbolic viewer for which many of the underlying ideas and techniques of 3D hyperbolic viewing of trees were developed)
- WALRUS (a Java based 3D hyperbolic viewer) The problem with the 3D hyperbolic viewers is that they do not read standard phylogenetic tree file formats but a conversion program does exist for converting the standard phylogenetic tree format to LibSea which is the format read by Walrus. This makes it possible to visualise huge trees e.g. the whole NCBI taxonomy database which currently contains approx. 180,000 nodes (which is as close as one can get to a tree of life at the moment).

Visualisation of the NCBI "Tree of Life" in Walrus

(larger picture and details)

Visualization of the Eutheria (Placentals) in Walrus

(larger picture and details)

Some references
Modernizing the Tree of Life, E. Pennisi, Science, Vol 300, June 2003

US "Assembling tree of life" program (www.nsf.gov/bio/progdes/bioatol.htm)

European "Assembling the tree of life" expression of interest to sixth framework program (eoi.cordis.lu/dsp_details.cfm?ID=31692)

Felsenstein, J (1993) PHYLIP: Phylogeny Inference Package, Version 3.6. University of Washington, Seattle, WA (<http://www.evolution.genetics.washington.edu/phylip.html>)

Page, R. D. M. (1996) TREEVIEW: an application to display phylogenetic trees on personal computers. Comput. Appl. Biosci., 12, 357-358.

ATV: display and manipulation of annotated phylogenetic trees, C. M. Zmasek and S. R. Eddy, Bioinformatics, Vol 17-4, 2001, pages 383-384.

Visualizing large hierarchical clusters in hyperbolic space, J. Bingham and S. Sudarsanam, Bioinformatics, Vol 16-7, 2000, pages 660-661.

H3: laying out large directed graphs in 3D hyperbolic space, T. Munzner, Proceedings of the 1997 IEEE Symposium on Information Visualization, October 20-21 1997, Phoenix, AZ, pp 2-10, 1997.

<http://www.caida.org/tools/visualization/walrus>, Y. Hyun

Exploring large graphs in 3D hyperbolic space, Tamara Munzner, IEEE Computer Graphics and Applications, Vol. 18, No. 4, pp 18-23, July/August 1998

Drawing large graphs with H3Viewer and Site Manager, T. Munzner, Pulished in the Lecture Notes in Computer Science series GD'98: Symposium on Graph Drawing, Montreal, Canada, August 1998

An initial examination of ease of use for 2D and 3D information visualizations of web content, K. Ridsen, M. P. Czerwinski, T. Munzner, D.B. Cook, International Journal of Human-Computer Studies, (2000) 53, 695-714