A Flexible Phylogenetic Tree Viewer

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Abstract

As we determine the ancestry of various common mouse strains, a novel use for a phylogenetic tree viewer emerges. Such a viewer can be used to show relationships between strains on a small region of the genome, rather than across its entirety. Unfortunately, previous tree viewers could not handle the trees produced from this data, as the trees have numerous small-distance or zero-distance relationships between strains, making it impossible to read the displayed trees.

A new phylogenetic tree viewer is necessary to solve this problem. "Phylo" is a small, OpenGL driven tree viewer which can display trees in various forms, including an unrooted tree view with the option to "explode" the labels for clear reading. While this unrooted view is the most useful for the mouse strain ancestry project, rooted views are available for trees with a defined root (such as evolutionary trees).

Phylo will open any Newick format tree file, whether local or from the web. It was designed specifically to work with web browsers, thus allowing it to integrate with a genome browser or similar tool, joining the trees with the data as a whole. In the future, more options will be available to the user for control and customization of the tool.

Introduction

Phylo is a phylogenetic tree viewer capable of displaying any Newick format tree, including those with zero-distance members. This was a necessity due to the mouse ancestry project, which produced thousands of trees with the problematic zero-distance members.

Normally, such trees would be impossible to view, since the labels defining the members would inevitably intersect with each other when displayed, making them illegible. Since no pre-existing tree viewer could make these labels legible, it was necessary to create a new program that could.

Specifications

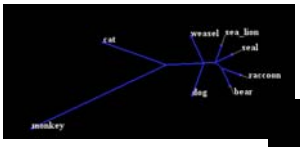
Phylo displays trees in three different views.

- An unrooted view, best used to show differences between genotypes. In this view, labels that are connected to shorter tree brances will "explode" outward to become more legible; the user can increase or decrease the distance of the labels as they choose.
- A rooted view, with the root on the far left side. This is a more classic tree view, with options for square, V-shape, and "European" style trees.
- A rooted, circular view, with the root being a small circle in the center. This is the same as the previous view in squared tree format, but in polar co-ordinates. The circle can change size as the user wishes.

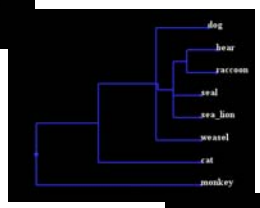
In all of these views, the user may *move, rotate,* and *zoom* in or out of the tree at any time. Pressing a single key will revert the tree to the default view, an overview of the entire tree.

Trees may be opened by dropping a tree file onto the program, or by opening the file through another program (such as a web browser). In this way, Phylo can be connected to a genome browser, such as GMOD's GBrowse.

Phylo In Action



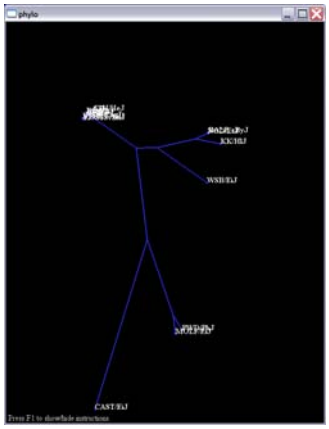
Phylo displays trees in unrooted…



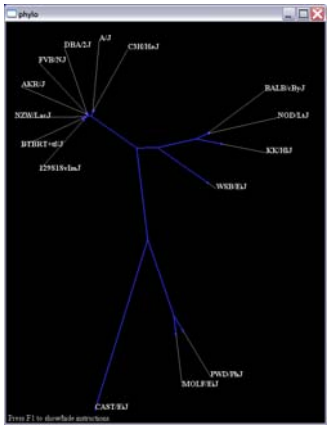
rooted…

and circular rooted views.

Phylo can be used in conjunction with other tools, such as the GMOD genome browser (Depicted below)



With labels directly at the nodes, trees may become illegible.



Phylo allows the labels to expand outward, making the tree easy to read.*

The Newick tree strings used in the above trees:

* (FVB/NJ:0.00256,AKR/J:0.00000,((NZW/LacJ:0.00256,BTBRT+tf/J:0.01962,129S1/SvImJ:0.02068):0.01231,(((CAST/EiJ:0.91302,(MOLF/EiJ:0.09557,PWD/PhJ:0.09045):0.41147):0.47446,(WSB/EiJ:0.31234,(KK/HlJ:0.11311,(NOD/LtJ:0.00512,BALB/cByJ:0.01024):0.06457):0.20162):0.10723):0.28323,(C3H/HeJ:0.00644,A/J:0.00000):0.02464):0.01515):0.00717,DBA/2J:0.01024)[0.1429];

† (((dog:22.90000,(((bear:13.60000,raccoon:13.00000):5.75000,seal:12.00000,sea_lion:12.00000):6.75000):1.00000,weasel:19.75000):3.15000):22.01667,cat:44.91667):27.22619,monkey:72.14286); (UPGMA tree for Sarich carnivore data, *Inferring Phylogenies*)

Links

The Newick format tree files used can be found:

- **http://cgd.jax.org/cgi-bin/dblocate?name=chr3%2B0320&opt=rawtree**
  This corresponds to the section between 32.0 Mbp and 32.1 Mbp in the mouse genome, as found at http://cgd.jax.org/cgi-bin/gbrowse/sample/
- **http://evolution.gs.washington.edu/book/sarichupgma.tre**
  Which must be edited slightly to correct errors (a missing left parenthesis at the beginning, carriage returns).

An existing use of the GMOD genome browser in conjunction with Phylo may be found at http://cgd.jax.org/gbrowse.html

Phylo may be downloaded from a link at the same location.

This is a production of the Center for Genome Dynamics (CGD), website http://www.genomedynamics.org

Implementation

Language: C.
Dependencies: OpenGL, freeglut, FreeType.
Platforms: Windows.
Future Platforms include Linux and Mac OS X via X11.

References

- **Hyuna Yang, Timothy A. Bell, Gary A. Churchill, Fernando Pardo-Manuel de Villena, "On the subspecific origin of the laboratory mouse," *Nature Genetics* (in press)**
- **Joseph Felsenstein, *Inferring Phylogenies,* Sinauer Associates, Inc., Sunderland, Mass. 2004**

Conclusions

- **The Phylo tree viewer meets its goals of displaying trees legibly and quickly, and of granting users a great amount of control over the image.**
- **Labels may be illegible at first, but properly "exploding" the labels allows them to be read with no trouble.**
- **The viewer can read any Newick tree it is given, not just those used in the current data set.**
- **There is still room for improvement in this program. In later versions, the user may be able to customize the displayed trees in many ways, including color, line weight, font choice, etc. It could then be used as a tool for publication in addition to interpretation of data.**