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DABS (DATA AND BIOINFORMATION STUFF) VOLUME 1 ISSUE 6: PHYLOGENETIC TREES

Posted on February 12, 2021 - [https://www2.hshsl.umaryland.edu/hslupdates/?p=4665] by J-P Courneya - [https://www2.hshsl.umaryland.edu/hslupdates/?author=16]

The Center for Data and Bioinformation Services (CDABS) is the University of Maryland Health Sciences and Human Services Library hub for data and bioinformation learning, services, resources, and communication.

This week (Feb 8-12) we celebrated Love Data Week and the official launch of CDABS. Check out our center, a virtual center, at our homepage: https://www2.hshsl.umaryland.edu/cdabs/ - [https://www2.hshsl.umaryland.edu/cdabs/]

Our topic in this edition is all about phylogenetic trees! A key concept to understanding the evolution of organisms and molecules. A phylogeny, or evolutionary tree, represents the evolutionary relationships among a set of organisms or groups of organisms, called taxa (singular: taxon). The tips of the tree represent groups of descendent taxa (often species) and the nodes on the tree represent the common ancestors of those descendants. Two descendants that split from the same node are called sister groups. This weeks links will guide you to repositories of reference molecular data to build trees as well as some software for building trees that is open source. Happy reading!

1. Berkley's Understanding Evolution team is a starting point to get an overview of phylogenetic systematics. In the tutorial, they cover how to read an evolutionary tree, how to classify organisms based on evolutionary trees, how to reconstruct an evolutionary tree, and how evolutionary trees are used. (5–minute read) https://evolution.berkeley.edu/evolibrary/article/0_0_0/phylogenetics_01 - [https://evolution.berkeley.edu/evolibrary/article/0_0_0/phylogenetics_01]

2. Finding high quality, reliable data is fundamental to building phylogenetic trees that are reliable. GeneCards is a searchable, integrative database that provides comprehensive, user-friendly information on all annotated and predicted human genes. The knowledgebase automatically integrates gene-centric data from ~150 web sources, including genomic, transcriptomic, proteomic, genetic, clinical and functional information. (5-minute overview & Infinite time exploring) https://www.genecards.org/ - [https://www.genecards.org/]

3. To build a molecular phylogenetic tree you will need to run a multiple sequence alignment and use the p hylogenetic tree output. One of the fundamental molecular biology tools for doing so is Clustal Omeg a "The last alignment program you'll ever need". Clustal Omega can be downloaded and run on your co mputer or you can also access a webserver to perform your alignment. (5-minute overview) http://www.c lustal.org/omega/ - [http://www.clustal.org/omega/]

4. Evolview is an interactive tree visualization tool designed to help researchers in visualizing phylogenetic trees and in annotating these with additional information. It offers the user with a platform to upload tree s in most common tree formats, such as Newick/Phylip, Nexus, Nhx and PhyloXML, and provides a ran ge of visualization options, using fifteen types of custom annotation datasets. (5-minute overview) www. evolgenius.info/evolview/ - [https://www.evolgenius.info/evolview/#login]

5. Cytoscape is an open source software platform for visualizing molecular interaction networks and biolog ical pathways and integrating these networks with annotations, gene expression profiles and other state data. In addition it is a tool for building phylogenetic trees. (5-minute overview) https://cytoscape.org - [ht tps://cytoscape.org/index.html]

6. There is an R package RCy3 that can be leveraged for creating phylogenetic trees in R and visualizing t hem in Cytoscape. This vignette will show you how to work the popular Newick format for phylogenetic t rees in Cytoscape by conversion to igraph and import via RCy3. (5-minute overview) http://cytoscape.or g/cytoscape-automation/for-scripters/R/notebooks/Phylogenetic-trees.nb.html - [http://cytoscape.org/cytosc ape-automation/for-scripters/R/notebooks/Phylogenetic-trees.nb.html]

Questions?

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