

PHYLIP

[flp]

PHYLIP stands for PHYLogeny Inference Package. Phylip claims to be the most widely distributed and oldest (since 1980) package of programs for inferring phylogenetic trees. It is free software, written in C consisting of 30+ smaller programs that can be operated through a menu structure. It is platform independent and executable versions are available for the latest installments of Windows, Mac OS, and Linux. Like [PAUP](#) Phylip features maximum parsimony, maximum likelihood, and several [distance based approaches](#) to build phylogenetic trees, including [bootstrapping](#) and [consensus trees](#). Phylip uses a specific input and output file format.

References

- <http://evolution.genetics.washington.edu/phylip.html>. Accessed 9 October 2015.
- Felsenstein, Joseph. 1989. "PHYLIP – Phylogeny Inference Package (Version 3.2)." *Cladistics* 5: 164–166.

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