

# PAUP

PAUP (Phylogenetic Analysis Using Parsimony) is a proprietary, and thus commercial, non-free software package for constructing and interpreting [phylogenetic trees](#). It is able to apply a [maximum parsimony](#) method, but also various other methods (that may, however, be less suitable to stemmatological analysis). It offers a rich set of settings to tune the behaviour of various methods, and to adapt the lay-out of computed trees. PAUP uses the [Nexus](#) file format which is shared by several bioinformatics software packages. Different versions for various platforms are available with slight variations in available functionality. PAUP can both be used as a command line tool or through a graphical interface. However, given lack or incomplete support for current platform GUIs such as Windows 8 and Max OS X, usage as a command line tool is advised.

## References

- <http://paup.csit.fsu.edu/>
- Swofford, David L., 2002. PAUP\*: Phylogenetic Analysis Using Parsimony (\* and Other Methods). Version 4, beta version. Sunderland: Sinauer Associates. Available at <http://www.tsu.edu/PDFFiles/CBER/Miranda/PAUP%20Manual.pdf>. Accessed 6 June 2014, but no longer accessible 27 October 2015.

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