

Mesquite's communication with other analysis tools

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Mesquite handles analyses and data management in evolutionary biology. It is extensible through modules, written in Java, and has an interactive graphical interface, although it can also be controlled via the command line and scripting. About 700 modules now provide diverse services and analyses including tree visualization and comparison, ancestral state reconstruction, phylogenetic tests of correlation and diversification, simulations & randomizations (including coalescence simulations), charting, and data management.

We demonstrate Mesquite's new and forthcoming integration with other tools, beginning with a workflow in which chromatograms are processed and sequences proofread (integration with phred-phrap), then sequences are aligned (integration with Opal), then trees are inferred (integration with RAxML and GARLI). We also demonstrate Mesquite used as a tree editor from R, and R functions used in Mesquite.

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