The visualization of hypothesized evolutionary processes is often shown through phylogenetic trees. Given evolutionary data presented in one of several widely accepted formats, software exists to render these data into a tree diagram. However, software packages commonly in use by biologists today often do not provide means to dynamically adjust and customize these diagrams for studying new hypothetical relationships, and for illustration and publication purposes. Even where these options are available, there can be a lack of intuitiveness and ease of use. The goal of our research is, thus, to investigate more natural and effective means of sensemaking of the data with different user input modalities.

To this end, we experimented with different input modalities, designing and running a series of formative studies, ultimately focusing our attention on pen-and-touch. Through several iterations of feedback and revision provided with the help of biology experts and students, we developed a pen-and-touch phylogenetic tree browsing and editing application called PhyloPen. This application expands on the capabilities of existing software with visualization techniques such as overview+detail, linked data views, and new interaction and manipulation techniques using pen-and-touch. To determine its impact on phylogenetic tree sensemaking, we conducted a within-subject comparative summative study against the most comparable and commonly used state-of-the-art mouse-based software system, Mesquite. Conducted with biology majors at the University of Central Florida, each used both software systems on a set number of exercise tasks of the same type. Determining effectiveness by several dependent measures, the results show PhyloPen was significantly better in terms of usefulness, satisfaction, ease of learning, ease of use, and cognitive load and relatively the same in variation of completion time. These results support an interaction paradigm that is superior to classic mouse-based interaction, which could have the potential to be applied to other communities that employ graph-based representations of their problem domains.

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The public is welcome to attend.