

Computer Science Seminar

User Interfaces for BioInformatics

*Bear Hall Room 206,
Wednesday January 15 , 2003,
12:00-1:00pm*

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So long as the practice of bioinformatics requires writing code, only a few biologists will use its tools, and many of those who do will not be as productive as they perhaps could be.

OpenDX and similar packages provided a graphical dataflow interface to visualization tools that successfully changed scientific visualization from a discipline practiced by specialist programmers to one accessible to non-programmers. I will review several projects, both closed- and open source, that are attempting to do the same for the analysis of biological data. Automatically composing analysis tools and tracking their use is key to progress for the field of bioinformatics. Specific questions examined include:

What are the differences between these projects? Are there any shortcomings they all share? Are there niches left for other groups to address? Why shouldn't biologists – and everybody else – have to learn to code? Is there any interesting work to do, or is it just lots of glue?