



Cytoscape Reloaded: Agilent Extends Collaboration with the Ideker Lab, Helps Re-Architect Platform

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Last week, the Agilent Foundation, the philanthropic arm of Agilent Technologies, announced it is collaborating with Trey Ideker of the University of California, San Diego, to apply network analysis methods to leukemia research.

Agilent said that the collaboration "includes scientific and financial support" but a spokesperson for the company declined to disclose financial details.

Allan Kuchinsky, principal project scientist at Agilent Laboratories, will work with the Ideker lab to help develop a protein network visualization application for Cytoscape to study leukemia.

Agilent is a member of the Cytoscape consortium along with UCSD and the Institute for Systems Biology. Other collaborators include Memorial Sloan Kettering Cancer Center, the National Center for Integrative Biomedical Informatics, Institut Pasteur, the University of Toronto, the University of California at San Francisco, and Unilever.

Separately, at the recent Intelligent Systems for Molecular Biology conference, Kuchinsky said that the Cytoscape development team is "re-architecting" the open source platform in preparation for the launch of Cytoscape 3.0.

There is no set schedule for Cytoscape 3.0 launch, Kuchinsky told *BioInform* this week, but he estimated it will be ready some time over the next year.

The effort to apply the current version of Cytoscape to leukemia research is separate from the re-architecting effort. "We have multiple ways of interacting with Trey Ideker's group," Kuchinsky said, adding that Agilent joined the development team in 2005.

For the re-architecting project, the plan is to not change Cytoscape's functionality, but to make it both easier to use and easier to extend, he said. The developers plan to make Cytoscape more modular, to separate the command layer from the application itself, to

allow users to define their own shapes and edges, to restructure the software so that all libraries and plug-ins can be more easily found, and to allow the Cytoscape API to be accessed through scripting languages.

Development of Cytoscape 3.0 can be followed [here](#).

Doing Good

Kuchinsky said that Agilent is involved with the open source software project "for strategic reasons."

As a firm that sells instrumentation such as DNA microarrays, mass spectrometers, and chromatography equipment, "we do sell software that goes with it," but mainly it is focused on hardware sales, he said. Users, meanwhile, are interested in the instruments but mainly in "the information that comes off them and how they can interpret them."

Agilent cannot manage all the software engineering on its own, Kuchinsky explained, but "we can align with leading software developers in this field," help with software development, and provide it to customers. "The end result is that [if] our customers can make measurements more easily, they make more measurements and they buy more microarrays and mass spectrometers," he said. This software development activity helps give Agilent "a foot in the door."

As Kuchinsky pointed out in his ISMB talk, the main motivation is to deal with Cytoscape's "growing pains" in a number of ways. With more than 5,000 classes in the public API, and little way for plug-ins to communicate, it has become difficult to "add a new feature to Cytoscape," he said. There is also a certain level of redundancy in the system. In the next version, it will be possible to deliver a "smaller set of functions" that users can call with a guaranteed level of performance and robustness.

For Cytoscape to grow, it must be easier to write plug-ins for it, he said. There are now close to 75 plug-ins for the platform, and "at some point it gets a little unwieldy," he said. For example, plug-ins can conflict with each other, "competing for mouse events."

Cytoscape was not designed to be such a large system, Kuchinsky explained. He said that in internal discussions thus far, developers have described the current platform as akin to a cottage to which floors and rooms have been added over time. "Eventually you have to jack it up and put in a new foundation," Kuchinsky said. That new foundation will facilitate writing plug-ins and extend the functionality of the platform to enable further growth.

Thinking About the Crowd

At its core, Cytoscape is a graph analysis package, Kuchinsky said. "The real biology is in the plug-ins, the extensions people write, and there is an army of people writing them," he said, adding that the developers intend to keep this large community in mind and at the forefront of planning.

Cytoscape has been downloaded nearly 60,000 times with a current rate of 2,500 downloads per month.

In keeping with that large, international circle of users and developers, the idea is not to

change the functionality of the system but rather to divide Cytoscape into tiers or modules that will be split up across core developers, Kuchinsky said.

In addition to the yearly Cytoscape retreat for the community involved in developing the software, the core development team is meeting every three months for two-day sessions on Cytoscape 3.0, he said.

The team is still in the process of divvying up the labor, but Kuchinsky said Agilent is taking on the task of editing networks in Cytoscape. "Milestones are set by the developers in conjunction with the board," he said. The layer discussions include Cytoscape's basic model, which is the software's core graphic model; a view model representation; its I/O, which includes web services and databases; the presentation, which renders the view models; and the higher-level functions such as creating a network and creating a layout.

At the ISMB session, one of the main questions from developers was whether they should wait for version 3.0 before developing new plug-ins. "We have been advising people to develop on [version 2.6]," which will be supported for at least a year, he said.

Kuchinsky acknowledged there is also some uneasiness among developers and users about migrating plug-ins developed for older systems to Cytoscape 3.0. "They will be migratable," he said. He said that the development team will be looking "most critically" at the most popular plug-ins. "We will make it our business that the core plug-ins get ported," he said.

The tool suites that the developers will be using include the Open Services Gateway Initiative, OSGi, and the Spring Dynamic Modules Framework.

OSGi is a non-profit consortium promoting standards and specifications that define a Java dynamic component system with applications composed of reusable parts and interoperable middleware.

The framework supports a set of services in which a plug-in can call a set of services and "not worry how those services are implemented," Kuchinsky said, enforcing a kind of modularity to the software.

Right now Cytoscape exists as a standalone desktop application. By introducing modularity, users who do not want the user interface and just seek to call the network analysis tools from their own platforms can do so.

This modularity will enable varying uses of Cytoscape, for example in "headless mode" or alternatively headed modes, he said. "It will also make it easier for people to build web interfaces," he said.

Spring is a programming model for Java applications and helps with tracking and managing of OSGi services, Kuchinsky said, and makes it easier to sign up for services via interfaces. "It becomes easier for you to re-wire your application in different ways, swap in a different database, and also enables plug-ins written in another language besides Java," he said.

The Cytoscape developers will be switching from Java build tool Apache Ant to Apache

Maven to manage the software development lifecycle, Kuchinsky said. "It helps us manage dependencies for our development as a distributed software team," Kuchinsky said.

Kuchinsky stressed that biologists and -omics researchers will be part of the Cytoscape re-architecting effort, and that usability engineering will be part of the process, as well. For example, University of Michigan researchers have been doing usability studies on the Michigan Molecular Integrating Protein interaction database, or MIMI, Cytoscape plug-in [*BioInform*, March 27, 2009].

Genomeweb system

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Issue Order: 1

