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## Cytoscape open-source bioinformatics platform symposium highlights a mushrooming user community

[November 9, 2007 Alto Marketing]

*Key scientists gather for major Systems Biology meeting*

AMSTERDAM, Netherlands, Nov. 9th, 2007

November 6-9 saw the largest ever annual Cytoscape® Public Symposium hosted for the first time in Europe by the Human Genetics Department of the Academic Medical Centre in Amsterdam. The Symposium attracted a great deal of interest in how Systems Biology is being conducted within leading laboratories worldwide through data analysis across a broad range of biological processes to understand the mechanisms of life.

As an open-source freely available network visualization and analysis tool, Cytoscape enables users to view, manipulate and analyze large networks of any type. The scale of the latest symposium reflects the growing Cytoscape global user base which is now utilizing the free software for a wealth of molecular life science applications. Since its inception at the Institute for Systems Biology in 2001 there have been over 40,000 free downloads, with over 20,000 in the last year alone.

"Now with over 2000 downloads a month and numerous citations in scientific literature, our Cytoscape user community is growing at a phenomenal rate," said Prof Trey Ideker, co-originator and President of the not-for-profit Cytoscape Consortium. "Over the past seven years, Cytoscape has grown to become an industry standard for Systems Biology data analysis that is integrating, visualizing, and modeling genome-scale data sets. In this regard, our annual meeting is of interest to two types of researchers: biologists looking to gain expertise in how Cytoscape is used, and software developers who are currently building software with the Cytoscape codebase."

The Annual Symposium provides a platform for users and developers to meet face to face and set new software development priorities and take responsibility for them. New directions are largely driven by the programmers themselves. "Although the Cytoscape Consortium project directors ensure their voices are heard too, the whole process has a very grass-roots feel about it," continued Prof Ideker. "Because Cytoscape is a distributed project, there are numerous developers involved from around the world, making the Symposium a real marketplace of ideas."

The variety of Cytoscape applications, such as signal transduction networks in cells through to similarity networks of proteins, was highlighted by the range of presentations given at the Annual Symposium entitled, "At the cutting edge of network analysis and biological data integration". These included invited talks by Ewan Birney (EBI), Peter Sorger (Harvard), Ruedi Aebersold (ETH), Andrew Hopkins (Pfizer), Jean-Daniel Fekete (INRIA, France), and Rogier Versteeg (Academic Medical Center, Amsterdam), as well as talks by Cytoscape Consortium members Leroy Hood, Trey Ideker, Benno Schwikowski, and Chris Sander.

"Cytoscape is a marvelous community project with important contributions from many

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different laboratories across the world," said Dr Leroy Hood, Institute for Systems Biology and Keynote Speaker at the Symposium. "We are now undertaking a systems approach to prion disease in mice. We use Cytoscape visualizations to illustrate how dynamically changing networks in the brain can explain much of the known pathophysiological behavior of this degenerative brain disease. Cytoscape also helps to illustrate how little we actually understand about many additional mechanisms that this disease employs."

Cytoscape has two parts, a Core and a set of Plug-ins, or extensions. Currently, there are over 35 plug-ins that provide Cytoscape with an extremely rich set of functions beyond its core network functionality. Many plug-ins have been written by third party developers across the world. For example, Agilent Technologies has developed two freely available plug-ins, the Agilent Literature Search Tool and the soon to be released Agilent VistaClara Tool. This new plug-in enables highly interactive visual analysis of gene and protein expression data that enables the user to view details and global context simultaneously.

"Agilent has found in its own work that it is important to be able to work across organizational boundaries, sharing emerging understanding in the form of models or networks," said Annette Adler, Project Manager, Agilent Technologies and Cytoscape Consortium member. "Cytoscape provides us with an extremely powerful prototyping tool to use in our own research with collaborators, allowing a full range of collaborations without license restrictions. We believe in supporting emerging standards such as Cytoscape since tools like this will make diagnostics and drug discovery and development more effective. We are very pleased to be able to actively contribute to this open-source community and assist in Systems Biology developments worldwide."

### About Cytoscape

Cytoscape is a publicly-available bioinformatics resource for integration, visualization, and query of biological networks to derive computational models. Its central organizing metaphor is a network graph, with genes or proteins represented as nodes and intermolecular interactions represented as links between nodes. The Cytoscape core is extended through a straightforward plug-in architecture, allowing rapid development of advanced computational analyses and features. At present, 35 Cytoscape plug-ins are actively supported and available at [www.cytoscape.org/plugins](http://www.cytoscape.org/plugins); numerous others exist as proprietary or experimental software. Importantly, the majority of plug-ins have been written by third-party developers not directly affiliated with the Cytoscape project, and approximately 15 plug-ins have themselves been published as stand-alone methods papers.

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