INFORMATICS

BRIEFS

Perceptive Informatics forges alliance with Biospective

BOSTON—Perceptive Informatics, an e-clinical solutions provider and subsidiary of PAREXEL International Corp., (Nasdaq: PRXL), announced in July that it has partnered with Biospective Inc., a medical imaging process and analysis software provider, to enhance its capabilities with respect to processing and analysis of medical images for central nervous system- (CNS) and oncology-related clinical trials. Biospective will provide software solutions tailored for CNS and oncology studies, including specialized Magnetic Resonance Imaging (MRI) and Positron Emission Tomography (PET) techniques. This will enable Perceptive Informatics to support independent reviews of imaging data for both exploratory and large-scale, multi-center studies. Financial terms of the deal were not disclosed.

Optibrium acquires software platform from BioFocus DPI

CAMBRIDGE, England—Optibrium Ltd. is pleased to announce its acquisition of the StarDrop business from BioFocus DPI, a sub-

Search for pathway-level biomarkers

Agilent Foundation awards grant to UCSD to develop system for analyzing proteomics data and identifying protein-network cancer biomarkers

BY AMY SWINDERMAN

LA JOLLA, Calif.—In a collaboration that will produce a system for analyzing proteomics data to map pathways, the Agilent Foundation, the philanthropic arm of Agilent Technologies Inc., announced in July that it will support leukemia research efforts at the University of California, San Diego's (UCSD) Ideker Laboratory, a unit in the school's medicine and bioengineering departments that uses genome-scale measurements to construct computer-aided models of cellular processes and disease.

Under the agreement, Agilent will provide scientific and financial support to the lab, led by principal investigator Dr. Trey Ideker, associate professor of bioengineering, adjunct professor of computer science and member of the Moores UCSD Cancer Center. Agilent's sponsorship will give the lab the resources it needs to investigate the relationships between genetic variations and proteins in the search for better methods of analyzing cancer, including a new approach for recognizing the mechanism that triggers leukemia using multiple scientific disciplines.

Ultimately, the lab hopes to develop a system for analyzing proteomics data to map path-
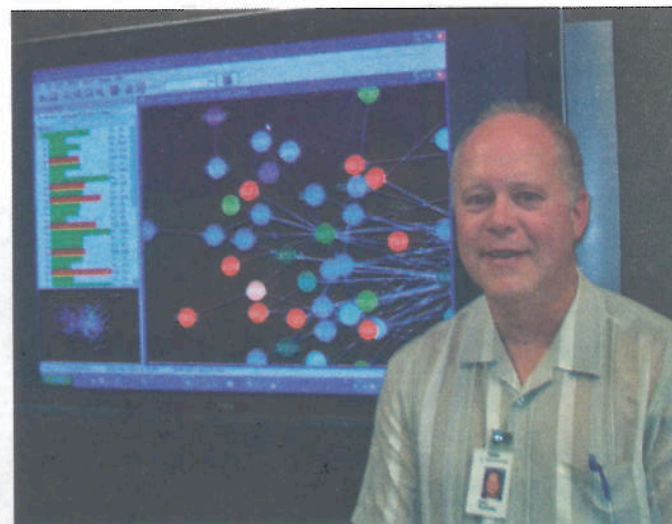
Allan Kuchinsky, principal project scientist at Agilent, says Trey Ideker's lab at UCSD is doing a lot of biomedical research in addition to applying software analysis techniques to the study of chronic lymphocytic leukemia.

ways, and for finding protein-network biomarkers of cancer. Specific financial details on the grant were not disclosed, but the project is expected to last nearly a year.

Agilent and UCSD are no strangers to each other, as the two parties have a longstanding

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collaboration in the network biology space. In 2002, Agilent and Ideker, among many other collaborators, co-developed and released Cytoscape, an open-source bioinformatics software platform for visualizing molecular interaction networks and biological pathways and integrating these networks with annotations, gene expression profiles and other state data.

Although Cytoscape was originally designed for biological research, now it is a general platform for complex network analysis and visualization. The project was funded by a federal grant from the National Institute of General Medical Sciences (NIGMS) of the National Institutes of Health (NIH) and the National Science Foundation (NSF). Corporate funding was provided through a contract from Unilever PLC.

According to Allan Kuchinksy, principal project scientist at Agilent, "Trey Ideker's lab is a lot bigger than just Cytoscape," which led Agilent to help the Ideker lab to develop a protein network visualization application for Cytoscape to study leukemia. Considered a pioneer in using genome-scale measurements to construct network models of cellular processes and disease, Ideker has developed software and algorithms for protein network analysis, network-level comparison of pathogens and genome-scale models of the response to DNA-damaging agents. His work has been featured recently in *The Scientist, Technology Review*, the *San Diego Union Tribune* and *Forbes* magazine. Ideker is also the recipient of the 2009 Overton Prize, awarded each year to an early-to-mid-career scientist making a significant contribution to the field of computational biology.

Ideker's lab has received funding to study protein interaction networks from the NIGMS, the NSF, the National Institute of Environmental Health Sciences (NIEHS), the National Institute of Mental Health (NIMH), Microsoft, Pfizer and Unilever.

"Trey Ideker's lab is doing a lot of biomedical research in addition to applying the software's analysis techniques to chronic lymphocytic leukemia (CLL)," Kuchinsky says.

"We saw that as very strategic to Agilent's direction, and we wanted to fund that research as a separate collaboration from the Cytoscape project, although we will use some of those analysis techniques as Cytoscape plug-ins."

Cytoscape's plug-ins are available for network and molecular profiling analyses, new layouts, additional file format support, scripting and connection with databases. Plug-ins may be developed by anyone using the Cytoscape open API based on Java technology, and plug-in community development is encouraged. Most are freely available.

The new plug-ins planned for Cytoscape will modularize the visualization platform, allowing it to be accessed through scripting languages and reorganizing all libraries and plug-ins so users can more easily locate them.

"This is an important strategic area for Agilent because we see open-source software as something that enables people to interpret their data," Kuchinsky says. "We're providers of measurement equipment, reagents and consumables, but people aren't really interested in our instruments as much as the information that comes out of them and how it answers biological questions. One of the big challenges in this area is how to analyze different types of data across different platforms in concert and manage it. The challenge is not so much how you are storing and retrieving the data, but how you are interpreting it. These tools are a start for us in helping people use our different platforms in concert to solve a problem."

Ideker says his lab's research efforts, coupled with the data analysis capabilities created by Cytoscape, represent a new paradigm shift in genomics research.

"I think the field needs to stop thinking about biomarkers as individual markers," Ideker says. "It's like saying, 'my engine died, and I think it is this screw,' when the problem is actually the alternator. All the little parts form bigger parts, and it's the bigger parts that are the problem. If you look at the 1990s, it was all about genomics—how do you sequence the genome, process DNA, etc. But in the 2000s, we haven't really done much to build on that. It is all well and good to know that we have 30,000 genes, but we need to know how proteins interact with those genes."

The goal of this collaboration is to try to elevate biomarkers from individual proteins to entire pathways of proteins, Ideker says.

"There is currently no tool out there for discovering pathway-level biomarkers," he says. "How you aggregate proteins into pathways and show how predictive a disease or drug toxicity is going to be has always been a bottleneck. What is exciting and daunting at the same time is that we have no clue how to analyze that data. There are numerous technical issues and challenges involved with figuring out how to aggregate proteins together into a pathway-level biomarker. It's these issues that are going to have to be worked out."

The Agilent Foundation recently announced $1.3 million in new grants for the second half of its fiscal year 2009. DDN

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> —Dr. Trey Ideker, associate professor of bioengineering and adjunct professor of computer science, University of California, San Diego