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in this issue

page 2
- People in the News
- Downloads & Upgrades

page 3
- Toolkit: Whitehead researchers ready an open source software system for cellular image analysis.

page 4
- *BioInform* lists recent NSF awards for bioinformatics projects.

page 7
- Bioinformatics Briefs: NHLBI to license SpringCore; Jubilant signs three database licenses; Vanderbilt to use FGT's EnTrust; USPTO OKs Health Discovery patent; OmniViz in development pact with Infocom; ADCRC awards contract to 5AM Solutions; GATC Biotech in EU study; Renovo licenses Partek software; Altana to use GeneGo's MetaCore.

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Biobase Acquires Incyte's Proteome Group To Expand Product Line and US Presence

INCYTE has jettisoned the last of its database holdings with the sale of its Proteome subsidiary to Biobase of Wolfenbüttel, Germany.

The deal effectively closes the door on Incyte's information business, but should open another one for Biobase, which gains access to Proteome's BioKnowledge Library and LifeSeq Foundation databases — along with an important foothold in the US market.

Financial terms for the acquisition were not disclosed, but Biobase said it financed the transaction through a fund managed by Avida, a private equity firm.

John Keller, Incyte's executive vice president and chief business officer, told *BioInform* that the Proteome group "was a small business in the context of our much broader, more intensive focus on drug discovery and development."

After a drastic restructuring last February in which Incyte gutted its Palo Alto genomics operations, the company retained the Proteome group for its "immediate potential to make a positive cash contribution to Incyte," Keller said at the time [*BioInform 02-09-04*]. However, he explained last week, it became clear to Incyte over the last year that Proteome would fit better with "an organization that was fully focused on this space and had complementary products."

Incyte has not yet begun generating income from its drug-discovery operations, so the data business has served as its primary source of revenue for the last several years. However, a company spokeswoman said that continued on page 4

Teranode Upgrades its Software Platform in Bid to Merge Workflow, Pathway Analysis

TAKING a page from Reese's peanut butter cups, Teranode of Seattle has combined two popular informatics technologies — workflow software and pathway analytics — into a single platform.

Whether the two approaches really do taste great together — or just represent the flavor of the month — will be up to the marketplace, but early signs indicate that Teranode is onto something. The company, founded in 2002, launched the first version of its software last February, and already claims 12 customers, including Amgen, AstraZeneca, Pfizer, and the NIH National Chemical Genomics Center.

This week, Teranode will release an upgraded version of its platform to advance what it calls "analytic design automation" — a term that describes its hybrid approach to computational workflow and model-based analysis.

The launch is two-pronged. The company is releasing Teranode Design Suite continued on page 6

PEOPLE IN THE NEWS

David Sankaran has joined **Accelrys** as CFO and senior vice president. He replaces **John Hanlon**, who will leave his post as CFO at the end of January. Sankaran joins the company from **Ocular Sciences**, a contact lens manufacturer, where he served as vice president and corporate controller. Prior to that, Sankaran held executive-level positions at **PeopleSoft, Affymetrix, Chiron**, **Raychem**, and **Arthur Andersen & Co**.

Lipomics, a company developing tools for lipid metabolite analysis, said last week that **Macdonald (Don) Morris** has joined the company as CTO and vice president of bioinformatics. Morris served as senior scientist at **Affymetrix** from 1993 to 1998, and then worked at **Incyte Genomics** from 1998 to 2002 as associate director, director, and senior director of bioinformatics. After Incyte, Morris joined **Expression Diagnostics** as vice president of informatics.

David Smith, who served as senior vice president and general counsel of **TissueInformatics** until its merger with **Icoria** last February, has joined law firm **Pepper Hamilton**'s intellectual property practice group in Pittsburgh, Pa.

DOWNLOADS & UPGRADES

Improved Outcomes Software has released **GeneLinker Gold** and **Platinum 4.6**. The new releases are focused primarily on importing and analyzing protein biomarker data. A protein biomarker package that previously required a separate installation is now included in the software, and the software's proteomics import scripts have also been improved. For gene expression data analysis, the company has added new data import scripts to handle Koadarray ratio and two-color data.

GeneGo has launched **MetaDrug 1.0**, a platform that combines software for predicting metabolites and over 40 ADME/tox properties with visualization and analysis of toxicogenomics and metabolomics data. MetaDrug can be used as a standalone product or together with **MetaCore**, GeneGo's analytical platform.

CueMol, a molecular structure visualization program that operates on Windows, is available at *http://cuemol.sourceforge.jp/en/*. CueMol supports molecular coordinates (PDB format), electron density (CCP4, CNS, and BRIX format), MSMS surface data, and GRASP electrostatic potential maps. It includes the QScript scripting language for batch operations.

Version 3.1.103 of the **E-Cell Simulation Environment** is available at *https://sourceforge.net/project/showfiles.php?group_id=72485&release_id=297582*. New features include an improved session monitor, a model editor with a pathway viewer, and support for differential-algebraic equations.

MWG Biotech has launched an improved **e-commerce website** (*http://www.the-mwg.com*), which includes new bioinformatics tools for designing primers, dual-labeled probes, and siRNAs. The website's DNA sequencing allows customers to download and view their data online, and provides **Phred** quality reports and **Blast** analysis.

Rescentris has released version 2.2.1 of its **CERF (Collaborative Electronic Research Framework)** knowledge management platform. CERF is based on Web Ontology Language ontologies, and can be customized for specific research workflows. CERF 2.2.1 is also integrated with the company's new **CERF-Notebook**, an electronic laboratory notebook module.

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Whitehead Plans Spring Launch for Open Source CellProfiler Software

AS HIGH-throughput cellular analysis methods become more commonplace in research labs, biologists are struggling to sort through thousands of images at a time. The problem, according to Anne Carpenter, a postdoc at the Whitehead Institute, is that the software tools for analyzing these images have not kept pace with the imaging platforms that are generating them.

In an effort to break this bottleneck, Carpenter is developing a software package called CellProfiler that will be released under a GPL license some time this spring, when a paper on the project is slated for publication. Carpenter and her collaborators, David Sabatini, Polina Gollard, and Thouis Jones, presented a poster on the project at the CSBi (Computational and Systems Biology) Symposium at MIT Jan. 13-14.

Carpenter said that when she joined Sabatini's lab just over a year ago, she conducted an "exhaustive survey" of commercial image analysis options to support the lab's research on cell growth regulation using high-throughput microscopy and cell microarrays. This research relies on "subtle" phenotypes that standard image analysis packages tend to miss, she said.

"Commercial software is mostly written for pharmaceutical companies," she said, "in which a defined visual output is measured. It was developed for phenotypes that are very straightforward and obvious to measure" — such as determining whether the cell had died or not, or identifying sharp changes in localization between the nucleus and cytoplasm, or even simply counting the number of cells.

But researchers at the Whitehead — and other academic labs — are increasingly trying to identify less obvious differences in cells, such as quantitative changes in particular proteins, or slight changes in localization, across thousands of images. This led Carpenter to develop CellProfiler, which can isolate individual objects, such as nuclei, from many images, while also providing several quantitative measurements for those objects.

One key to the software, according to a brochure about the project (available at *http://web.wi.mit.edu/sabatini/pub/AnneWeb/CPbrochure.pdf*), is an improved set of algorithms for segmenting objects — a stumbling block for many image analysis packages that have trouble separating clustered or overlapping images.

Once the objects — nuclei, cell boundaries, or components within the cytoplasm — are identified, CellProfiler offers several analysis modules for observing biological properties, including the number of objects, the size and shape of the objects, the intensity of the signal, and the texture of the objects. These properties, Carpenter said, allow researchers to measure many more types of phenotypes than currently available tools, "and not just answer yes-or-no questions."

Carpenter said that the software is still undergoing beta testing among "a small group of academic and commercial collaborators."

CellProfiler is envisioned as a complement to the software that is pre-packaged with imaging instruments, which is designed for "fast acquisition and fast image analysis, but the hangup is a lack of flexibility to analyze interesting phenotypes," Carpenter said. The software's open source license will enable labs to easily plug CellProfiler into their current image processing pipelines, she added.

Conversely, she said, the Whitehead team is offering commercial software providers the option to contribute modules for their packages as "plug-ins" to CellProfiler. These firms would still maintain the IP for their tools, she said, but the arrangement would give users access to a broader range of software options.

Once CellProfiler is released (at *http://www.cellprofiler.org*), Carpenter said she envisions the website serving as a repository for image analysis modules submitted by the community. "There are great algorithms and bits of software in the literature — in the computer vision research field, especially — that never make it to being used by real biologists," she said. The CellProfiler infrastructure could ultimately serve as a resource for biologists to find the best analysis modules for different image analysis tasks.

Carpenter and her colleagues are also collaborating with members of the Open Microscopy Environment (*http://www.openmicroscopy.org/*), a collaborative project to develop a system for storing image data, metadata, and analytical results. The OME developers are now looking into integrating analytical tools with the data management system, and Carpenter said that CellProfiler would be among the first of these tools included in the platform.

The two open source image informatics projects "are really complementary," she said, "and come at the perfect time for each other."

Further information about CellProfiler is available at *http://people.csail.mit.edu/u/a/anniebio/public_html/CellProfiler/*.

— BT

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BioInform's Funding Update: NSF Bioinformatics Awards to Jan. 15, 2004

Combined Computational and Experimental Approaches for the Design of Protein-Protein Interactions. Start date: Jan. 1, 2005. Expires: Dec. 31, 2009. Current year award amount: $199,015. Principal investigator: John Love. Sponsor: San Diego State University Foundation.

Project will use an inverse approach that combines computational docking methods with protein-design algorithms to drive the self-assembly of previously monomeric proteins. The proteins will be computationally docked together and then treated as one in which interfacial side chains are mutated and repacked in a manner analogous to the core of a well-folded protein. The goal is to select the specific amino acids that, upon mutation, will provide the physical chemical interactions that drive complex formation. Experimental techniques will also be used to screen combinatorial libraries of mutant candidate proteins for those that bind target proteins with high affinity.

Advancing Simulation Methods for Long Time-Scale Chemical and Biological Events. Start date: Jan. 15, 2005. Expires: Dec. 31, 2007. Current year award amount: $117,345. Principal investigator: Bin Chen Sponsor: Louisiana State University.

Supports development of an aggregation-volume-bias Monte Carlo (AVBMC) approach for research on a wide range of chemical and biological events. The AVBMC algorithm will be tailored to fit individual systems by adding histogram-reweighting and other techniques and by integrating AVBMC into an *ab initio* framework. The new simulation methods will be applied to the problem of protein crystallization in an effort to understand recent experimental studies.

Investigating Interactive Properties of Disordered Protein Regions. Start date: Feb. 1, 2005. Expires: Jan. 31, 2006. Awarded amount to date: $119,471. Principal investigator: Lilia Iakoucheva. Sponsor: Rockefeller University.

Project will test a hypothesis that proteins with multiple binding partners interact with their partners via natively disordered regions/domains. A combined approach using computational and experimental methods has been developed for the study. First, a computational analysis that includes disorder predictions on proteins with multiple interacting partners from the *C. elegans* interactome will be performed. In addition, the algorithm for predicting disorder-to-order transition mutations in these proteins will be developed. Second, prediction-guided and domain-guided approaches will be used to select the targets for experimental verification. Third, site-directed and deletion mutagenesis of predicted disordered regions followed by a high-throughput yeast two-hybrid screening using known binding partners will be carried out. Finally, a database that contains all *C. elegans* interaction domains together with their respective partners defined in the study will be assembled and disseminated.

Proteome ...

continued from page 1

the top-line impact from the sale of the subsidiary is not a concern.

"Revenue is not a metric that's meaningful for Incyte at this point," said Pam Murphy, vice president of investor relations. "We are a drug-discovery and -development company, and the revenues have not been meaningful in terms of Incyte's value as a drug discovery company."

Incyte has not yet reported its revenues for the 2004 fiscal year, but the company posted $15.2 million in sales for the first three quarters of 2004, a fall-off of nearly 60 percent compared to the same period in 2003, for which it posted $36.8 million in revenues.

Biobase now faces the challenge of turning the information business around financially.

As a privately held firm, Biobase does not disclose its own revenues, but CEO Michael Tysiak said that the company has been profitable for the last two years, despite the general downturn in the biological data market. Proteome, however, saw its sales decrease in 2004 compared to 2003 — a trend that Tysiak attributed to the unit's secondary role within Incyte. "That wasn't their focus," he said, "but I think because we're focused on it, we're confident that we can get that up again."

Tysiak said that Biobase intends to nudge Proteome into the black through cost-saving measures and increased sales of the BKL and LifeSeq products.

"We took over an operation that wasn't profitable, but it will be profitable this year," he said.

The acquisition nearly triples Biobase's headcount of 23 people. Tysiak said that there will be minimal staff reductions, however. "We will

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work on cost-efficient basis like we do in Germany, so there will be a few changes here, not only in headcount but generally in how we treat costs." Proteome's current US management team will be replaced with Biobase management, he said.

PRIVATE TO PUBLIC TO PRIVATE

The acquisition brings the Proteome subsidiary full circle. In 2000, Incyte acquired the privately held firm for $77 million in an effort to build out its information business. In the ensuing five years, as the market for genomics data took a dive and Incyte overhauled its business model to focus on drug discovery, the Proteome subsidiary stayed put at its Beverly, Mass., headquarters, operating very much as it did since it was founded in 1995.

Now, Proteome finds itself once again in the hands of a privately held firm — one that observers view as a better fit than Incyte.

Proteome co-founder James Garrels, who left the firm after it was acquired by Incyte, told *BioInform* that Biobase appears to be a "much better environment" for the group. Biobase "is a database company, they understand databases, and they already sell compatible databases to the academic and the pharmaceutical communities, so I think the products will mesh together well."

David Rubin, CEO of Cognia, which distributes Biobase's products in the US along with its own offerings, said that Proteome's databases complement those of Biobase with little or no overlap. "The key thing is how much strengthened [Biobase's] Transpath interaction databases are going to be, which makes a much more solid, competitive product immediately in the market," he said. "We sell Transpath and it's extremely high quality, but this adds a lot more content to it, and that's really one of the things that the customers want."

Rubin said that Cognia will maintain its distribution relationship with Biobase.

"The philosophy of [Proteome and Biobase] is pretty much the same," said Tysiak. "We concentrate on high-quality databases that are manually annotated in the biological area." Biobase is known primarily for its Transfac line of transcription factor databases. The company also sells Transpath, a database of signal transduction pathways, and BRENDA (the Braunschweig Enzyme Database), which it exclusively licensed from German firm Enzymeta in 2003.

"We took over an operation that wasn't profitable, but it will be profitable this year."

Proteome's BKL, which includes six separate volumes of annotated protein data, and LifeSeq, which includes human genomic sequence and gene-expression data, will be integrated with Biobase's products to improve ease of use for customers of both firms, Tysiak said.

Moving forward, he added, Biobase intends to continue expanding its product line, especially in the areas of interaction data and signal transduction. The company will expand further by acquiring additional databases "with a good name," Tysiak said, and through new internally developed products and new content for existing products.

"We always want to be ahead of the competition," he said. The Proteome acquisition, he added, will help position the firm as the "number-one supplier of biological databases."

HARSH ENVIRONMENT

But recent history — and a growing base of competitors — may stand in the way of Tysiak's goal. As Incyte's own decision to dump its information business proves, the commercial market for biological data has diminished considerably since it peaked during the Human Genome Project. Meanwhile, even as the overall market has waned, numerous vendors have emerged to meet demand for interaction data, pathway data, and other types of "post-genomic" information.

"The market is not easy," Tysiak conceded, "but customers are looking for high-quality products, and that's the niche that we are in."

Garrels agreed. "There's a definite market there," he said. "It's not like the genomic databases any more. These are heavily annotated databases, and that's a type of work that is intensive."

While publicly funded genomic and protein databases have rendered many commercial offerings all but obsolete, Garrels said that academic resources "haven't really filled the niche of ... high-quality databases generated from literature surveys."

Biobase is not alone in the annotated-database arena, however. Tysiak cited Ingenuity, Jubilant, and other pathway database firms as the primary competitors for its newly expanded business. Biobase's strategy for staying competitive, he said, will be "expanding the pathway database significantly."

Cognia's Rubin said that competition in the pathway database market isn't as fierce as it might seem from the growing number of players in the space. "It sounds like there's a lot," he said, "but when you go out and talk to customers, our sense is that no one's absolutely hit the sweet spot yet, and it's really wide open for competition."

— BT

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Teranode ...

continued from page 1

(TDS) 2.5 — a new version of its flagship desktop product for creating and visualizing biological models — as well as a new Pathway Analytics "template" that combines several of the company's offerings into a pre-configured product for pathway-based research.

"We see more and more groups being formed around either systems biology or pathway discovery … within large biotechs and pharmas," said Matthew Shanahan, chief marketing officer of Teranode. "What we're starting to see in the pathway analytics area is that people actually want to do experimental data management in conjunction with their pathway analysis, and that they need a way to manage the collaboration between the labs."

TDS 2.5 is the culmination of two development partnerships that Teranode announced in the fall, with the KEGG pathway database and The MathWorks [*BioInform 11-29-04*]. The new version of the software allows users to import more than 18,000 pathway models from KEGG, and merge these models with their own experimental data. This addresses one of the primary limitations of KEGG, according to Shanahan — the "read-only" aspect of the resource. With KEGG, Shanahan said, "you can look at the model, but you can't use it; you can't map your experimental data to it at all. It's great to look at the data in one window and the model in another window, but what you really want to do is match those together and see how your data is expressed in the model."

In addition, the new version of the company's software provides a drag-and-drop interface to The MathWorks' Matlab modeling language. Researchers can build biological models using a simple palette of icons, and the software automatically translates the visual model into a Matlab program that can be shared between — and understood by — both computational and bench biologists.

Shanahan said that this capability is already paying off at AstraZeneca. "The computational biologists kept publishing programs written in Matlab, and the laboratory biologists didn't understand them. So what they're using now is Teranode Design Suite to exchange model information back and forth and optimize what they were doing, and they dramatically reduced the number of experiments they had planned to do and really accelerated their overall research project as a result of that."

"We see more and more groups being formed around either systems biology or pathway discovery … within large biotechs and pharmas."

Shanahan was unable to provide details on the "actual numbers" behind AstraZeneca's productivity improvements, but said "the ROI was really substantial and has given us great traction inside the company."

Pricing for TDS 2.5 starts at $1,000.

In addition, the company is launching the second in a series of so-called Teranode Solutions, which combine the Teranode Design Suite, the Teranode Model Server, solution-specific protocol or biological models, and solution-specific equipment integration. The release of the Pathway Analytics Solution follows the launch of the company's Reagent Production Solution in December. Similar products targeted toward sample processing and high-throughput screening are planned for rollout later this year.

Pathway Analytics is configured for integration with in-house systems biology data and software, and also includes integration libraries for microarray and high-throughput screening data. Using TDS as a front end, researchers can view experimental data generated across the organization within the context of their biological models.

Pricing for Teranode Pathway Analytics begins at $75,000, with a 50-percent discount for non-profit groups and academic institutions.

Shanahan said that Teranode's platform addresses "the life cycle of experimentation." Scientists currently generate a hypothesis, plan their experiment, run the experiment, manage the protocol, analyze the data, and then assess how well this information supports their predictions. Based on these findings, most scientists tweak their hypotheses and start over again in an iterative pattern. The problem for many labs, Shanahan said, is that they must rely on a series of LIMS, statistical packages, visualization tools, databases, and modeling tools to bring the cycle full circle.

"We're focused on being one tool that's able to carry you through all of that," he said.

But with a goal this ambitious, is the 25-person company biting off more than it can chew? Shanahan acknowledged that it will be difficult to convince customers that Teranode's platform delivers on its broad promise. However, he said, as a 10-year veteran of Documentum, he's been through this before. "Documentum was coming out with document management software, and we had included in it some workflow, and some search and some configuration management. But at the time, every-

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body thought that was a separate product — you don't put that in with the library management. So we had the same challenge at that time, which was making sure that we identified application areas that we would sell to that actually required both."

In Teranode's case, he said, the company's marketing strategy relies on its solution configurations, which act as "templates that allow us to easily deploy this platform in specific solutions" — and thereby gain a foothold across several market segments. As an example, he said, the NIH Chemical Genomics Center and Pfizer signed on for the company's Reagent Production Solution, while Amgen, AstraZeneca, and MIT chose the Pathway Analytics product. But these specialized configurations act as entryways by which customers can access all the platform's capabilities, Shanahan said.

Teranode is marketing its platform as a new approach to pathway analysis — one that allows customers to manage the experimental data used to build biological pathways while also allowing them to build and share their own biological models.

"Most of the first-generation [pathway] tools … have been view-only tools of curated content, and what people are saying is that they're developing their own systems biology information and they need a system to manage that information," Shanahan said.

While admitting that "the first-generation solutions had the immediate traction," Shanahan said that Teranode ought to be able to catch up to the early movers in the pathway space. "Ingenuity probably has more customers than we do, but we would expect to see that change pretty dramatically over the next year," he said. — *BT*

BIOINFORMATICS BRIEFS

NHLBI TO TAKE SPRINGCORE LICENSE FROM AGILENT

The National Institutes of Health's National Heart, Lung, and Blood Institute has issued a presolicitation notice stating that it "intends to issue a purchase order on a noncompetitive basis" to Agilent Technologies for an annual SpringCore license.

The software will be installed at the NHLBI Bioinformatics Core Laboratory, according to the notice.

The SpringCore program, which Agilent subsidiary Silicon Genetics developed for core microarray labs, includes 100 seats for company's SigNet knowledge management software, a three-year license to the GeneSpring software, a license for a GeneSpring workstation, and training.

The NHLBI presolicitation notice did not include financial details for the licensing agreement.

SCHERING, BAYER, JAPANESE RESEARCH CENTER LICENSE JUBILANT DATABASES

Jubilant Biosys said last week that Schering has taken a global license to its Kinase ChemBiobase. Separately, Jubilant announced that it had licensed its PathArt pathway database to Bayer Healthcare and to Yasushi Okazaki, a professor at the Research Center for Genomic Medicine, Saitama Medical School, in Japan.

The Kinase ChemBiobase is a curated database of more than 250,000 known inhibitors to the kinase class of targets, and includes structural and functional, disease, pharmacokinetic and pharmacodynamic information and other family specific information.

PathArt includes more than 1,200 signaling, metabolic, and disease-specific pathways.

VANDERBILT TO USE FGT'S ENTRUST TO STUDY GENETICS OF DRUG SIDE EFFECTS

First Genetic Trust said last week that the Vanderbilt University Medical Center will use its EnTrust data management system to support a study on the genetics of drug-induced prolonged QT, a side effect for many different classes of drugs.

VUMC researchers will EnTrust's "distance enrollment" capabilities to recruit and enroll consenting participants who are referred through VUMC by other clinicians and clinical sites globally. The system will be used to collect and manage online informed consent, samples, and clinical and genetic data from study participants.

The system will also allow patients who sign a specific consent to be recontacted online by investigators for additional longitudinal data collection or to be reconsented for additional studies.

USPTO OKS HEALTH DISCOVERY'S SVM PATENT

Health Discovery said last week that it has received a notice of allowance from the United States Patent and Trademark Office for a patent application covering the use of recursive feature elimination in support vector machines.

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RFE is a process by which key features of input data can be identified as being more significant for use in classifying the data using a support vector machine, according to the company. The method is useful for reducing processor run time when analyzing the high volumes of data encountered with gene expression data and related information for discovery of biomarkers, Health Discovery said.

In addition to the allowed patent application, Health Discovery's SVM patent portfolio includes nine issued US and foreign patents covering applications of support vector machines for discovery of knowledge from large data sets.

Stephen Barnhill, chairman and CEO of Health Discovery, said, "We expect to generate significant near-term revenue from licensing and royalty fees received from our increasingly valuable patent portfolio, which contains state-of-the-art technology currently used by diagnostic and pharmaceutical companies worldwide for identifying novel diagnostic tests and new drug targets."

OMNIVIZ SIGNS DEVELOPMENT PACT WITH INFOCOM

Data-mining and visualization software firm OmniViz said last week that it has partnered with Tokyo-based Infocom to co-develop software for genetic network analysis.

OmniViz will integrate Infocom's Auto Net Finder software with its own OmniViz visualization software. Auto Net Finder extracts genetic networks directly from gene expression data.

According to OmniViz, Auto Net Finder will allow researchers to validate the relevance of pathways being studied. The software uses graphical Gaussian modeling to derive genetic networks from expression data, and the resulting network can then be compared to pathways of interest to ensure consistency with the experimental system.

As part of the arrangement, OmniViz will become a distributor of the integrated version of Auto Net Finder.

ADCRC AWARDS THREE-YEAR CONTRACT TO 5AM SOLUTIONS

5AM Solutions, a web solutions developer for life science research based in Phoenix, Az., said last week that it has been awarded a three-year contract totaling $300,000 from the Arizona Disease Control Research Commission to develop two life science informatics systems.

5AM will help develop the System for Collaborative Translational Research (SCTR) — a web-based application to support clinical research — and the Microarray Enterprise Manager (MEM) — a web-based information-management system for microarray core labs.

As part of the contract, 5AM will port the SCTR application to an IBM environment, enhance the software to meet the needs of researchers in Arizona, and provide access as an on-demand service available through *http://www.5amsolutions.com*.

SCTR will initially support two simultaneous studies: an Alzheimer's disease study led by the Translational Genomics Research Institute, and an Autism study led by the Southwest Autism Research and Resource Center.

5AM said it is "seeking other early adopters within Arizona who might benefit from the use of SCTR."

GATC BIOTECH TO DEVELOP BIOINFORMATICS TOOLS FOR EU STUDY

GATC Biotech, a provider of molecular biology services based in Constance, Germany, said last week that it will participate in an EU-funded research project to evaluate the safety of gene therapy in the treatment of monogenic inherited diseases.

The €13 million project will run through 2008, and includes 18 academic groups and three companies from nine countries.

GATC said that it will develop a bioinformatics platform "for comprehensive data storage and analysis of vector insertion sites in the genome, allowing for mechanistic studies of transgene/host interactions."

RENOVO LICENSES PARTEK SOFTWARE

Partek said last week that it has licensed its Partek software to Renovo, a biopharmaceutical company based in Manchester, UK.

The company purchased a site license for the software.

ALTANA LICENSES GENEGO'S METACORE

Altana Pharma has licensed GeneGo's MetaCore data analysis suite, GeneGo said last week.

Altana plans to use MetaCore to interpret genomics data and create new hypotheses for drug development.

MetaCore includes a database of human metabolism and signaling, network analysis software, and a toolkit for visualizing and managing high-throughput data.

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