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Prepping for Future Demand, SAS Adds JMP Genomic Tools to Its Drug Development Suite

As part of a strategy to align with the long-term goals of its pharmaceutical customers, SAS this week said that it has added genomic and proteomic analysis capabilities to its SAS Drug Development software platform, which is primarily targeted to clinical development.

Laurie Rose, director of global health and life science for SAS, said that the integrated system is geared toward researchers who are "breaking down the walls between discovery and development" to bring biomarker and molecular information into their clinical analysis.

Rose conceded, however, that this target market is still fairly small and that the company has not yet implemented the integrated platform at any customer sites.

"There are probably more people who are talking about that as the direction they want to go than are doing it, so the demand is at the lower end of the curve right now," she said. Nevertheless, she noted, "there are people out there that we've been working with either on the SAS Drug Development side or the genomic analysis side who have really driven us to bring those two platforms together."

SAS Drug Development is a centralized repository for clinical research data that is validatable under the US Food and Drug Administration's 21 CFR Part 11 regulations for electronic signatures.

"There are probably more people who are talking about that as the direction they want to go than are doing it, so the demand is at the lower end of the curve right now."

The company's genomics software, meanwhile, was originally developed as part of SAS Scientific Discovery Solutions, an enterprise-scale system that included a centralized data repository called SAS Research Data Management, along with SAS Microarray, SAS Genetic Marker, and SAS Proteomics.

In March, SAS relaunched the genomics tools through its JMP business unit, which specializes in data visualization and user-friendly desktop implementations of analytical software tools [[BioInform 03-24-06](#)].

The products were rebranded JMP Genetics, JMP Microarray, and JMP Proteomics, while the remaining components of SAS Scientific Discovery were rolled into SAS Drug Development.

Now, SAS is giving customers the option to bring these two platforms together in order to analyze molecular information in a CFR 11-compliant environment.

Researchers using the JMP tools in the desktop environment have the flexibility of an interactive environment for discovery, "but once it is in that SAS Drug Development environment, everything is tracked," Rose said.

One driver for bringing the two software families together was the FDA's Critical Path Opportunities List, released in March [[BioInform 03-24-06](#)], which highlighted biomarker identification as one of its primary focus areas.

Rose said that SAS had already "started going down the path" toward integrating molecular data with its clinical research infrastructure, but added that the Critical Path has "influenced" the company's development strategy. "We were very interested in seeing what the opportunity areas were when they came out, and the fact that that whole first section was about biomarker qualification and different areas where they're looking

for the industry to start making more sense of that information and applying it on the clinical side — that was a perfect fit for that direction that we had already decided we wanted to go in," she said.

While the market for this integrated platform is still not defined, "it is growing and we're seeing it growing," Rose said.

Certainly, SAS is not the first to ensure that its bioinformatics tools work in a CFR 11-compliant environment. A number of microarray-analysis firms, including Rosetta Biosoftware, Genedata, and Affymetrix, have enabled their software to be validated in 21 CFR 11-compliant environments.

In addition, Insightful, a SAS competitor in the clinical research market, has its own microarray analysis tools as well as a nascent effort underway to develop biomarker-analysis software [[BioInform 05-19-06](#)].

Michael O'Connell, director of life science solutions for Insightful, said that even though the company is not yet seeing a great deal of demand for its ArrayAnalyzer software in the later stages of drug development, some of its pharma customers are using microarray data alongside clinical information in discovery. "We've seen more of the adoption of the combination of clinical microarray data in the early phase — people wanting to see if there are genes that affect drug absorption or drug bioavailability," he said. "In the early-phase stuff, we've seen a lot of traction, but it's been a little more exploratory."

While characterizing the FDA's Critical Path focus on biomarkers as a "megatrend" that should have a long-term impact on the industry, O'Connell said, "We haven't seen it translate into the market so much yet."

O'Connell noted that even though Insightful doesn't have "a formal product line" that integrates its genomics software with its clinical trial analysis tools, he said that ArrayAnalyzer is already integrated with the company's S-Plus platform, which can be validated under CFR 11.

Rose said that the SAS platform is one of the first integrated systems for merging genomic data with an FDA-compliant clinical research infrastructure. "There aren't a lot of solutions out there that provide that level of integration," she said, so researchers within pharmaceutical firms who are trying to exploit genomic data in clinical trials "have to do it themselves."

Rose noted that one barrier to adoption is likely to be the organizational "silos" that currently divide discovery from development within pharmaceutical firms. "They all have their walls up and they all just want to be very possessive with their data and what they're doing," she said. "We feel like even though there are still cultural barriers that exist, we have that technology platform to enable that sharing of research information, and I think that's going to become hugely important as people really start to better understand some of the implications of that genetic data and how it can affect the safety and efficacy of a drug as it moves downstream in the process."

— *Bernadette Toner* (btoner@genomeweb.com)

Software Developers Nudge Structure-Based Drug Design Forward with Improved Methods

Pharmaceutical firms are demanding better tools for computational drug design, and presentations during last week's Structure-Based Drug Design conference indicate that software developers in the academic and private sectors are eager to deliver.

As *BioInform* reported last week [[BioInform 06-16-06](#)], pharmaceutical researchers are seeing positive results from virtual screening, molecular modeling, and other computational methods, but are outspoken in describing the current shortcomings of the field. In particular, pharma is seeking improved methods for sampling the conformational space of ligands, better ways of accounting for protein and ligand flexibility, and more accurate scoring functions.

In response, a number of software vendors and academic developers discussed ways in which they are addressing those issues. One such effort is a collaboration between Schrödinger and William Jorgensen's computational chemistry team at Yale University and involves an improved version of the OPLS (Optimized Potential for Liquid Simulations) force field for molecular modeling.

Woody Sherman, application scientist at Schrödinger, said that the current version of the force field, OPLS 2005, includes 1,780 torsion types — many more than some other popular force fields, such as MMFF (Merck Molecular Force Field), which includes 918 torsion types. However, Sherman noted, in a study of commercially available compounds, the company found that there are approximately 7,000 additional torsion types that could be added that would greatly improve the performance of the force field.

Sherman said that Schrödinger has purchased a compute cluster in order to run "quantum mechanical torsional scans" on these compounds as it works on developing the next version of the force field, OPLS 2007.

Jorgensen, the original developer of OPLS, said that Schrödinger's work in expanding torsion types is "very important" for the field. His lab, meanwhile, is developing software for designing inhibitors for a given target binding site by "growing" molecules. The program, called BOMB (biochemical and organic model builder), begins with a "core" fragment in the binding site, and then builds a combinatorial library of compounds by adding substituents from a list of more than 600 drug fragments.

Jorgensen said that there are 100 possible cores, and up to four positions where substituents can be added, resulting in a virtual library of up to 10 trillion possible molecules.

Hans Briem, senior scientist in the compound design and computational chemistry group at Schering, noted that these large combinatorial libraries require extremely fast docking algorithms, but said that drugmakers also require methods that consider pharmacophore restraints while docking. This is a "difficult problem," he said.

Briem said that Schering has been working with BioSolveIT to combine the software company's FlexXc program for docking combinatorial libraries with its FlexX-Pharm program for docking with pharmacophore constraints.

The new module, called FlexXc-Pharm, has shown promising results so far, Briem said. In a study involving a combinatorial library of 22.4 million compounds built upon the core scaffold for Gleevec, FlexXc-Pharm docked around 70,000 in 3 hours on a 20-node cluster. The closest Gleevec analog was ranked No. 124, placing it in the top 0.001 percent of all the compounds, Briem said.

A BioSolveIT representative at the meeting said that the FlexXc-Pharm module will be available in FlexX 2.1, which is due out in the late fall.

Another company that is addressing the challenge of pharmacophore modeling is Tripos. Bob Clark, senior director of software research at the company, discussed the module, called GALAHAD (Genetic Algorithm with Linear Assignment for Hypermolecule Alignment of Datasets), which Tripos added to its Sybyl molecular modeling environment last year [[BioInform 08-15-06](#)].

Clark said that GALAHAD also helps address the challenge of binding site flexibility, which varies greatly between proteins. The method first builds a set of low-energy conformations, which are run through a "multi-objective" genetic algorithm that looks for conformers with minimal energy, maximum steric overlap, and maximum pharmacophore concordance, Clark said.

While the genetic algorithm did a good job of finding the best conformers, Clark said it fell short when it came to alignment, so Tripos has incorporated a version of the LAMDA (Linear Assignment Method for Database Alignment) algorithm developed at the University of Sheffield into the method.

— *Bernadette Toner* (btoner@genomeweb.com)

SAFE Moves from 'Create' to 'Do,' but Paperless FDA Filings Are a Bit Farther Off



Mollie Shields Uehling,
president and CEO of
the SAFE-BioPharma
Association

Two years ago, a consortium of major pharmaceutical firms began developing an electronic signature standard called SAFE (Secure Access for Everyone). The standard, maintained by the non-profit SAFE-Biopharma Association, consists of operating procedures and technical specifications for distributing identity credentials among collaborators and with regulatory agencies.

This week, Mollie Shields Uehling, president and CEO of SAFE-BioPharma, chaired a session on digital signatures and identity management at the Drug Information Association's annual meeting in Philadelphia. *BioInform* caught up with Shields Uehling by phone to get caught up on the status of the SAFE initiative and the standard.

I spoke to Guy Tallent about SAFE last year [[BioInform 06-27-05](#)]. Can you provide a general overview of the initiative's progress over the last year?

There's been a great deal accomplished over the last year. Right before DIA last year, SAFE was still a standard in early development, and since that time, we've further refined the standard and made some very pragmatic changes to it; we have created a legal entity of the SAFE-Biopharma Association; we have hired staff; we have done an FDA auditor-familiarization and -training program jointly with the FDA in which we jointly developed a manual — an inspection manual — and then a training program; [and] we've done a [standard operating procedure] for members so they know what to do.

At that time I believe we had almost completed a technical pilot with the National Cancer Institute. Well, that was completed, and we are now initiating an operational pilot, which will credential up to a couple hundred of NCI's principal investigators. The initial application is the [Food and Drug Administration's] 1572 [form], which is the investigator statement. It includes the clinical trial protocol, the CV of the investigator, the IRB, all of the key sub-investigators, and the financial statement of the investigator. It is the most redundant and most frequently submitted form to the FDA every year. Some 200,000 to 240,000 of these are submitted every year to the FDA. And this will be the first instance in which industry and the NCI are collaborating so the investigators will create this form in a secure, shared environment, they'll make all changes online, they'll sign it, and they'll submit it to NCI sponsor firms, which in turn will submit it electronically to the FDA, and it will be reviewed by the FDA digitally. So it will be a paperless transaction for the SAFE pilot.

So it's very collaborative and a real example of the direction we're all headed in, in terms of collaborative R&D.

With the European Medicines Evaluation Agency, we are now running a pilot, which is a technical pilot to show how it works and that it works, and it involves EMEA, Organon, Pfizer, GlaxoSmithKline. The European Commission has already found that the SAFE digital signature meets the EU digital signature directive, and it's looking at affirming as to whether there are any legal issues within the member states. We do not believe there are, but it will be an official communication from the commission in that regard.

Also the EMEA is looking at the auditability of the SAFE digital signature. So, much of the work that we developed for the FDA will be reconfigured and applied in a way that's appropriate for the European environment.

In the last year the FDA has accepted SAFE-signed 1572s, and it has indicated to a couple of members that it would accept INDs and NDAs that are SAFE-signed. So we have a couple members who are working on those submissions, but they have not been submitted yet.

We have a number of member companies that are doing proofs of concept and pilots in various areas. One area is e-sampling, where doctors are getting the SAFE identity credential, and will order online and sign for samples using the SAFE identity and digital signature. Other companies are doing pilots in clinical as well as in [the US Securities and Exchange Commission's] Sarbanes-Oxley [financial-reporting] requirements, particularly where signatures are required, to replace the wet signatures with digital signatures.

In these pilot projects, are you finding that this technology is replacing piles of paper, or are the early adopters still using it in parallel with paper submissions?

They're still doing them both in parallel. One of the reasons for SAFE in the first place is because of the unique nature of the industry, in that there is the regulatory environment, the need to meet regulatory standards, and the need for legal enforceability, and certainly the risk management. So when you change from paper-based processes, which are regulatory, you have to align everyone in the organization. So you need legal, you need IT, you need clinical, you need regulatory. If it's marketing, you need marketing, and a whole host of others. So you have to align the whole organization around it, develop new SOPs, show that it works, and then sort of build confidence within the organization that this works. So, initially it's an investment, and your savings aren't right in the offing. They're a year or two away from the companies who right now have these back-up paper-based processes.

What about on the regulatory side? How much openness are you seeing from the FDA in terms of adopting this?

They are accepting digital signatures, electronic signatures, right now. It's here. Certainly with the joint inspection manual and the training program, we're ramping that up and doing a more intensive set of training with the FDA in July.

So it's moving. Is it here? Is it normal practice? No. But SAFE is not sexy, new technology. It's not a silver bullet. What's neat about SAFE is the high standard of identity assurance, the digital signature that you can validate at the time of signing, and 10 years later, it's sort of all of these elements, and all of these have the potential to be transformational in the industry. But it's step by step by step, and we're still in the early phases. Although we're in the "do" phase rather than the "create" phase right now.

Also, one of the things our member companies want is off-the-shelf applications. So we have been working with a number of vendors to SAFE-enable their applications. So, for example, Adobe, Cybertrust, Arcot — a number of companies are SAFE-enabling applications.

In addition, one of our member companies, Pfizer, created something called the Universal SAFE Signing Interface, and this is like a server you can put out there and people from within your company or elsewhere can put a document out there, you can sign it, and then you're notified when it's signed and you can take it down off the server.

They've made that open source, so we have a number of vendors who are using that to SAFE-enable their applications, and we have companies who are creating their own internal servers to find documents.

Is that available through the SAFE-Biopharma website?

It has just gone open source. If it's not on the website now, it will be.

It's unusual for pharmaceutical companies to be willing to share technology like that.

That's what's been so unique about SAFE. SAFE-Biopharma consists of a bunch of companies that are really early adopters and have this vision of a paperless industry. So they're motivated. A rising tide lifts all boats. So it's been very interesting, because member companies, as they do pilots and implementations, are inviting other companies over to learn from them. Not across the boards, but certainly in clinical, some of the regulatory. It's been very interesting and very, very collaborative.

Are you seeing any use of this technology in early discovery, or is it really still in the regulatory and clinical trials phase of the pipeline?

It's not in the discovery phase yet, but certainly there are potential applications for it — toxicology, lab work, that kind of thing. It has the potential. It's not being used there and we don't have pilots that we know of in that area yet.

I guess the same kind of pressure isn't there.

Yet. But the pressure is on the industry to become more efficient, more productive. That's one of the funny things about the industry, in that it's one of the biggest users of informatics in the world, except in its business practices. And there, it's got one of the lowest penetration rates of any sector. So Wall Street and others have been saying, 'Hey, you've got to fix the infrastructure cost as well as the efficiency.' The industry is just a million collaborators — deals, alliances, joint ventures, co-marketing, outsourcing — and all of that requires the ability to know with high assurance that the other person at the end of the Internet is who he or she says he is, and secondly, that they can sign a document that will have the same force in law as a notarized wet signature. So it's coming. It just doesn't happen overnight.

What are your short-and long-term goals going forward? Have you passed the most difficult hurdles now that you're in the 'do' phase? Now that people have started to adopt this, do you see it building critical mass in the next year or so?

Yes, I think over the next year or so that we'll see a critical mass, particularly in the clinical area, because that is where many companies are focused. What we have out there are a whole host of investigators who do clinical research or clinical trials for a variety of sponsors, and so that is one of the first areas that we're focused on.

What we have now are lots and lots of operational pilots, and I think what we'll be seeing over the next year is more and more project implementation. For example, with e-sampling — you'll see that rolled out with hundreds of doctors. Then you'll see the NCI, after we finish the operational pilot of a couple hundred investigators, over the next few years, we'll be issuing credentials to 13,500 principal investigators. And others. [At] one of our member companies we have issued credentials to a couple hundred clinical investigators. So I think you'll see more and more operational-level [projects], and then it's going to take a couple of years before you see really widespread adoption.

Again, change doesn't take place overnight.

The NCI application is really interesting because NCI has a memo of understanding with SAFE and a memo of understanding with the FDA to allow all of this to transpire. So as we move through the operational pilot and into full production, I think that is going to be an example for the industry of a collaborative digital environment in which investigators, companies, the research arm of the government, and the regulatory arm of the government, can operate efficiently and in a collaborative manner that works for the benefit of all the enterprises involved.

What's the timeline for the NCI project?

The operational pilot will be completed this fall, and then we'll start rolling out the full project. So by the end of this year.

Funding Update

NSF Bioinformatics Grants, May 14 — June 17 2006

Computational Studies of Dynamic Molecular Search Mechanisms. Start date: June 15, 2006. Expires: May 31, 2007. Expected total amount: \$538,624. Principal investigator: Aaron Dinner. Sponsor: University of Chicago.

Funds development of computational tools for characterizing the dynamics of molecular recognition, which will be applied to the human protein O6-alkylguanine-DNA alkyltransferase (AGT). The research will "promote application of state-of-the-art methods for studying activated dynamics to biomolecular systems, and their use to treat the dynamics of AGT and DNA will provide atomic-level insight into the kinetic strategies molecules use to control their interactions," according to the grant abstract.

Computational Methods for Exploring the Geometry of Large Data Sets. Start date: June 1, 2006. May 31, 2009. Expected total amount: \$212,855. Principal investigator: Gilad Lerman. Sponsor: University of Minnesota, Twin Cities.

Funds development of a computational and theoretical framework to analyze large data sets with low-dimensional intrinsic structure. Applications include the identification of protein-binding genomic regions and quantitative exploration of the functional domain in the gene ontology and its relation with structural properties.

Computational Biology Facility for Western Massachusetts. Start date: June 1, 2006. Expires: May 31, 2007. Expected total amount: \$185,015. Principal investigator: Oliver Brock. Sponsor: University of Massachusetts, Amherst.

Supports the acquisition of a computer cluster for research in bioinformatics and computational biology.

Characterization of the Tomato Secretome Using Integrated Functional and Computational Strategies. Start date: June 1, 2006. Expires: May 31, 2007. Expected total amount: \$3,627,035. Principal investigator: Jocelyn Rose. Sponsor: Cornell University.

Funds an integrated project to catalog the tomato "secretome" — the composition and dynamic properties of the cell wall proteome. The project will combine a suite of new functional screens with sequencing of purified wall protein extracts, bioinformatic tools, and computational prediction. A publicly accessible tomato secretome database, called SecreTom, will be developed to house the project data, to provide access to all associated computational tools, and to act as a hub for plant wall proteome research.

WebFusion — Autonomous Data Integration Tools for Biotechnology. Start date: July 1, 2006. Expires: Dec. 31, 2006. Expected total amount: \$99,992. Principal investigator: Khaled Jababo. Sponsor: OishiiTech.

Phase I SBIR supports development of a graphical front-end database interface that will allow biologists to manage data on a local computer as well as remotely. The proposed product, called WebFusion, will provide

"faster and more accurate data management tools to fully exploit the large commercial and public databases available online and through other sources," according to the grant abstract.

Machine Learning Software for Viral Sequence Analysis and Diagnostics. Start date: July 1, 2006. Expires: Dec. 31, 2006. Expected total amount: \$100,000. Principal investigator: Gary Fogel. Sponsor: Natural Selection.

Phase I SBIR funds development of computational tools for viral sequence analysis that can be used to understand the relationship between sequence variations and phenotypic behavior and or response. The software will help predict the effect of viral mutations on infectivity and efficacy of the virus as well as aid in the development of antivirals and predict the effect of treatments.

Developing a Bioinformatics Database for Stoichioproteomics. Start date: July 1, 2006. Expires: June 30, 2007. Expected total amount: \$1,027,900. Principal investigator: William Fagan. Sponsor: University of Maryland, College Park.

Supports the exploration of how the availability of nutrients in the environment affects proteins by modulating their amino acid composition. To do so, the project will create a bioinformatics database, the Genomics Resource Access for Stoichio-Proteomics (GRASP), which will contain an integrated ecological dataset for insect species and a database of protein composition.

MultiMedia Information Retrieval for Biological Research. Start date: July 1, 2006. Expires: June 30, 2007. Expected total amount: \$1,198,998. Principal investigator: Linda Shapiro. Sponsor: University of Washington.

Supports development of a "unified methodology" for the organization and retrieval of biological data, particularly image data and related measurements from scientific experiments. The grantees will develop a probabilistic query framework for multimedia data that will provide users with a unified way to access multiple types of data.

Characterization, Quantification, and Management of Sequence-Alignment Errors with Emphasis on Molecular Phylogenetic Reconstructions. Start date: July 1, 2006. Expires: June 30, 2007. Expected total amount: \$723,859. Principal investigator: Dan Graur. Sponsor: University of Houston.

Supports a project that will classify errors in multiple sequence alignment and develop tools and protocols through which alignment errors and uncertainties can be accounted for and properly managed. "The practical effects of alignment-error management will be assessed on real databases and real phylogenetic problems," according to the grant abstract. All software, data, and protocols will be made freely available.

Bioinformatics Tools Enabling Large-Scale DNA Barcoding. Start date: July 1, 2006. Expires: June 30, 2009. Expected total amount: \$399,602. Principal investigator: Ion Mandoiu. Sponsor: University of Connecticut.

Proposal to develop bioinformatics tools and design methodologies that will enable large-scale species identification based on universal DNA arrays. The work will include efficient combinatorial algorithms for optimization problems in the design of large-scale identification assays.

Computational Methods and Software for Structured Multiscale Models of Tumor Invasion. Start date: Aug. 1, 2006. Expires: July 31, 2008. Expected total amount: \$120,641. Principal investigator: Bruce Ayati. Sponsor: Southern Methodist University.

Proposal to develop computational methods and software to solve systems of partial differential equations in multiscale models of tumor invasion. The software will be developed with cancer biologists at Vanderbilt University and will handle "the complicated situation where the different genetic profiles of the multitudes of individual cells within a tumor, and the different stages in the cell-division cycle of each of these cells, are linked to the physically larger complete tumor," according to the grant abstract. This is expected to be useful in studying the effects of chemotherapy when using drugs that affect cells differently depending on their genetic type or what part of the cell-division cycle they are in.

Automated Annotation of Function in Protein Structures from Evolutionary-based 3D-Templates. Start date: Sept. 1, 2006. Expires: Aug. 31, 2007. Expected total amount: \$1,288,463. Principal investigator: Olivier Lichtarge. Sponsor: Baylor College of Medicine.

Project will develop automated algorithms to identify functional sites in protein structures and to characterize protein function on a genome scale. The approach will build on the Evolutionary Trace method to locate functional sites in structures.

Bioinformatics Briefs

Gene Logic Genomics Revenue 'Significantly Lower' Than Expected for Q2 and 2005

Gene Logic said this week that revenue for its genomics division will be "significantly lower" than anticipated for both the second quarter and the full year of 2006, and it is withdrawing its financial guidance for 2006 and 2007 as a result.

The company has not provided specific guidance for either fiscal year, but said in February that it expected to reach profitability in 2007 [[BioInform 02-24-06](#)].

The company said it is performing a review of the genomics division's strategy, and it expects to announce those results within 90 days. The performance of Gene Logic's drug-repositioning division and its preclinical division will not deviate significantly from estimates, the company said.

Dennis Rossi, Gene Logic's senior vice president and general manager of genomics, has resigned for "personal reasons and to pursue other career opportunities," the company said.

Boehringer Ingelheim to Use MetaCore Software for Toxicogenomics

GeneGo said this week that Boehringer Ingelheim has licensed its MetaCore data-mining software, which it will primarily use in toxicogenomics research.

Julie Bryant, vice president of business development at GeneGo, said that toxicogenomics "is one of the main applications" of the platform, which includes "tools and workflows specifically for the analysis of toxicogenomics datasets."

Financial terms of the agreement were not provide.

Simulations Plus Sees 26 Percent Increase in Preliminary Q3 Revenues

Simulations Plus reported preliminary financial results for the third fiscal quarter of its 2006 fiscal year ended May 31 this week.

Revenues for the quarter increased 26 percent to \$1.8 million from \$1.4 million in the third quarter of fiscal year 2005.

The company said in a statement that this is a new record for third-quarter revenues.

Revenues from pharmaceutical software and services were \$1.1 million, an increase of 66 percent from \$662,000 in the third quarter of fiscal year 2005.

CTC Lab Systems to Distribute Pharsight Software in Japan

Japan's CTC Laboratory Systems will distribute Pharsight's software systems in the Japanese market,

Pharsight said this week.

CTC will distribute Pharsight Knowledgebase Server, PKS Reporter, PKS Validation Suite, and Pharsight Trial Simulator.

Downloads & Upgrades/People in the News

Downloads & Upgrades

BioWisdom has released **SRS 8.2**, the first SRS update since BioWisdom acquired **Lion Bioscience's** bioinformatics business in April. SRS 8.2 is twice as fast for common indexing and querying tasks as previous versions, according to the company. The new version also offers improved data sharing and a simplified start page. The standard SRS package now includes SRS Relational, which allows users to combine and analyze internally generated databases with the third-party information supplied via SRS.

Ingenuity Systems has launched **Ingenuity Pathways Analysis 4.0**, which includes enhanced search and reporting capabilities. IPA 4.0 enables users to conduct and save advanced searches for genes, proteins, or biological relationships; create reports on bibliographies of pathway information; and export high-resolution images for publication and presentations. IPA 4.0 also supports the Mac platform in addition to PCs. Ingenuity is offering trials of the software at <http://www.ingenuity.com/trial>.

Affymetrix has released version 4.38 of **IGB (Integrated Genome Browser)**, an application for visualizing genomes and annotations from multiple data sources, at http://www.affymetrix.com/support/developer/tools/download_igb.affx.

Spotfire has released analytic services for its **DecisionSite** software so that pharmaceutical scientists can visually analyze and interact with data from clinical trials. Features include integration with customer clinical data management and electronic data capture systems, support for SAS files and programs, and guided analyses for quality control and monitoring of clinical data.

Ensembl 39 is available at <http://www.ensembl.org>. The release includes new assemblies for mouse, zebrafish, opossum, and *Ciona savignyi* and other updates.

The Genome Bioinformatics Group at the **University of California, Santa Cruz**, has released version 4.1 of the *Xenopus tropicalis* assembly through the **UCSC Genome Browser** at <http://genome.jgi-psf.org/Xentr4/Xentr4.home.html> and a Genome Browser for the v3.4 *Rattus norvegicus* genome at <ftp://hgdownload.cse.ucsc.edu/goldenPath/rn4/> or <http://hgdownload.cse.ucsc.edu/downloads.html#rat>.

The **National Center for Biotechnology Information** has released **GenBank 154.0** at <ftp://ftp.ncbi.nih.gov/>. The release contains 63,412,609,711 base pairs and 58,890,345 entries. Uncompressed, the 154.0 flat files require about 222 GB for the sequence files only. The ASN.1 version requires around 192 GB. NCBI said that a new protein residue abbreviation for the 22nd amino acid, **pyrrolysine**, will become "legal" in GenBank protein sequences as of release 156.0, in October. "Because

several letters are assigned to represent different experimental ambiguities, the only letter still available for use is O (uppercase letter o)," NCBI said. For Blast and other sequence similarity search tools, NCBI said it will map pyrrolysine (O) to unknown (X), as it already does with selenocysteine (U), the 21st encoded amino acid. The 156.0 release will also include the residue abbreviation J for leucine/iso-leucine ambiguities in mass spectrometry experiments. "Although this abbreviation has been part of the IUPAC recommendations for some time, it has not previously appeared in protein sequences in the GenBank database," NCBI said.

EML Research and the **Virginia Bioinformatics Institute** have launched **COPASI (Complex Pathway Simulator)**, a software package that allows users to model, simulate, and analyze biochemical and systems biology networks, at <http://www.copasi.org>.

Unleashed Informatics has launched **DogBox Inside**, a remotely maintained data warehouse that is installed on the customer's in-house hardware and open to customer audit and compliance requirements. DogBox Inside includes hourly updated gene sequence and molecular interaction data from 18 sources, as well as pre-computed BlastP and RPS-Blast information for all protein sequences in NCBI's NR database. The service is priced at \$14,500 per year.

Tripes has released **Benchware Notebook 2.1**, an update of its enterprise electronic laboratory notebook. The new version includes a new page navigation toolbar and increased support for third-party chemical sketching applications.

People in the News

Dennis Rossi, has resigned as senior vice president and general manager of genomics at **Gene Logic** (*see [briefs, this issue](#)*). Rossi joined the company in 2004. Prior to that, he served as vice president of marketing for life sciences for **Accelrys** and was a partner for **Harvard Strategy Group**, a life sciences consulting firm. He also held several senior level management positions at **Digital Equipment Corporation**, which was acquired by **Compaq** (now **Hewlett-Packard**).

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