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GenoLogics, Institute for Systems Biology, LabKey Software, HUPO - Proteomics Standards Initiative, the University of Pennsylvania and the University of Manchester Collaborate on Support for Proteomics Data Standards

Victoria, B.C. Canada – GenoLogics Life Sciences Software Inc. (GenoLogics) announced today its commitment and support for the adoption of a proteomics data interchange standard. Proteomics projects increasingly involve researchers with diverse lab experiments and data exchanges can create compatibility issues affecting interpretation and reproducibility. To help overcome this challenge, GenoLogics is collaborating with a range of organizations and is involved in a number of initiatives to advance a common data standard and to foster the exchange of ideas among the commercial, open source and academic communities.

GenoLogics, the Institute for Systems Biology (ISB), HUPO - Proteomics Standards Initiative (PSI), the University of Pennsylvania - Institute for Translational Medicine and Therapeutics (ITMAT), the School of Computer Science at the University of Manchester and LabKey Software LLC, are teaming together to develop a demonstration model to showcase the benefits of proteomics data standards. A working example of a comprehensive suite of integrated software tools, lab information and data management and a proteomics data repository, all based on a common standard, will be showcased in Fall 2005. Data integrity and efficiency of data analysis are among the benefits that will be realized with a common standard.

The Institute for Systems Biology (ISB) is an internationally renowned non-profit research institute dedicated to unraveling the mysteries of human biology and identifying strategies for predicting and preventing diseases such as cancer, diabetes and AIDS. The driving force behind the innovative "systems" approach is the integration of biology, technology and computation. Further to its mission the ISB has developed a broad suite of open source software tools, many of which were developed in the laboratory of Dr. Ruedi Aebersold, co-founder of the ISB, to support the worldwide proteomics community. According to Dr. Aebersold, "Today it is common that proteomics research results obtained in different laboratories cannot be directly compared and are subject to varying interpretation. Researchers need to be able to consistently and transparently analyze and interpret proteomics data. This requires the availability of a common data standard and validated software tools for proteomics." All ISB software tools are accessible, as open source software, via its web site.

The HUPO – Proteomics Standard Initiative (PSI) has a mandate to define community standards for data representation in proteomics to facilitate data comparison, exchange and verification. With PSI's MIAPE (Minimum Information About a Proteomics Experiment) standard, the basic information required to be provided when reporting proteomic experiments benefits researchers and collaborators. GenoLogics is contributing to and supporting this and other PSI standards as they develop and become more widely adopted.

The University of Pennsylvania Institute for Translational Medicine and Therapeutics (ITMAT) and the University of Manchester are leading development of the FuGE-OM (Functional Genomics Experiment Object Model) that will provide a supporting structure for PSI's proteomics-focused position. Input from others has been incorporated to create a general standard to enable data sharing across mixed research domains for a systems biology approach. This ensures the emerging proteomics standards will integrate with other '-omics' disciplines such as genomics, transcriptomics and metabolomics in the long term.

Real life and implementable data standards, not theoretical standards are what organizations such as the Fred Hutchinson Cancer Research Center require to leverage the involvement of other regional cancer centers and facilitate the dissemination and sharing of data to advance discovery in cancer research. Labkey Software, working at the Computational Proteomics Laboratory at the Fred Hutchinson Cancer Research Center, has developed the 100 terabyte Comparative Proteomics Analysis System (CPAS) data repository, which will import a complete proteomics experiment archive (XAR) data file based on FuGE with proteomics extensions. This will enable better data quality, accuracy and speed associated with the transfer of data between laboratories and the sharing of results across organizations.

Michael Ball, CEO GenoLogics noted, "The adoption and implementation of standards across the industry will encourage sharing of results across disperse geographies and reap benefits in helping researchers better understand diseases and treatment of diseases. GenoLogics supports many open source analysis tools and the emerging proteomics data standards that help end users integrate and compare data from disparate software and hardware sources. This alleviates any "data silo" issues that can render expensive research projects ineffective. The result will be faster and more accurate biomarker identification and advancements in drug discovery and early disease detection." The GenoLogics lab and scientific data management system, *ProteusLIMS*[™] is a key component of the demonstration model. GenoLogics open systems approach and architecture is unique in the industry and the company is leading in the adoption of a common data standard.

GenoLogics also has other initiatives underway to support convergence of a common data standard. GenoLogics is partnering with PSI at HUPO in Munich and Geneva to sponsor meetings and participate in furthering the goal of defining community standards for data representation in proteomics to facilitate data comparison, exchange and verification. Furthermore, GenoLogics is spearheading a cross functional team of academic and commercial interests to continue moving forwards the alignment of PSI and FuGE standards.

The ISB and GenoLogics are collaborating to increase the widespread use of ISB's open source data analysis software tools. The two organizations have developed the roadmap to integrate the ISB tools and GenoLogics *ProteusLIMS*[™] to broaden the reach of the tools for a wider group of researchers. In addition, GenoLogics is working closely with the Fred Hutchinson Cancer Research Center to ensure that they have an extensible environment to share the data with other research centers of excellence.

About GenoLogics

GenoLogics develops bioinformatics solutions that help life science and pharmaceutical laboratories, specializing in the field of proteomics and systems biology research, to manage, integrate and analyze enormous volumes of scientific and lab data to advance health science research and drug discovery. More than a workflow solution, *ProteusLIMS*[™] is a comprehensive and integrated lab, instrument, and scientific data management system that transform the data management process into a sophisticated analytical system to aid research and scientific discovery. The Company is headquartered in Victoria, B.C., Canada. For more information, please visit www.genologics.com.

About the Other Organizations

For more information on the above mentioned organizations, please visit the following websites:

Institute for Systems Biology – www.systemsbiology.org

University of Pennsylvania - Institute for Translational Medicine and Therapeutics (ITMAT) -

http://www.uphs.upenn.edu/news/News_Releases/jan05/biomedinst.htm

School of Computer Science at the University of Manchester - <http://www.cs.man.ac.uk>

LabKey Software LLC – www.labkey.com

HUPO – Proteomics Standards Initiative - <http://psidev.sourceforge.net/>

FuGE – <http://fuge.sourceforge.net>

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