Sophic
Integrated Life Science Solutions

Press Release

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Sophic Systems Alliance Receives Award from National Cancer Institute to Complete the Cancer Gene Index Project

June 23, 2008: Today, Sophic announced the launch of a 12-month, $1.3M project funded by the National Cancer Institute (NCI), to complete the first comprehensive index of 6,610 cancer-related genes found in Medline abstracts, with manually annotated gene-disease and gene-compound relationships. Over the past four years, Sophic has teamed with NCI and Biomax Informatics AG in Munich, Germany, to build this highly curated, standardized, computable cancer knowledge base. When complete, the cancer community will have access to a comprehensive compendium of cancer information. The 4,658 cancer genes annotated in previous phases of this project are already publically available at the NCI website at http://ncicb.nci.nih.gov/NCICB/projects/cgdcp.

Dr. David Steffen, Director of the Baylor College of Medicine Bioinformatics Research Center, said: "I had an opportunity to attend a caBIG™ briefing on this knowledge base and it's clear that this project will be a great asset for the entire cancer research and biomedical community."

"The Cancer Gene Index is a unique knowledge base, and is used as the foundation for the Biomax BioXM Knowledge Management Environment configuration used daily to support research at NCI's Center for Cancer Research," said Pat Blake, CEO of Sophic and Program Manager for the Project. "BioXM provides integration across traditional data silos and the Cancer Gene Index is the backbone used to map disparate information from various types of experiments."

Dr. Klaus Heumann, CEO of Biomax said, "This project is unique, based on the volume of the material to review and the complexity of the information derived, organized and presented to the scientist. We developed a "factory assembly line" methodology that allows the automated text mining results to be fed to the scientific team who curate and annotate the information in an efficient, quality-controlled, work-flow process. There are approximately 1M sentences to be manually annotated within the scope of the project to identify role codes and evidence codes for each of the 1,952 genes. This includes gene-disease and gene – compound relationships for 310 of the most highly studied and published genes such as BRACA1, P-53, MYC, etc. It is very rewarding for the team to have the NCI recognize the value of this information and fund subsequent phases of the project."

"This knowledge base is the foundation for reliable, accurate cancer research for all types of cancer diseases, clinical trials, biomarkers and much more. Sophic and Biomax appreciate the opportunity to provide the cancer community with this asset," said Pat Blake.

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About Sophic: Sophic Systems Alliance Inc. (Falmouth, MA and Rockville, MD.) was founded in 1993 and is a life science software and services integrator. The company provides a broad range of software and services to research scientists and MDs in government, commercial and medical sectors. Sophic is focused on supporting the fight to cure complex diseases and is actively involved in cancer research at the National Cancer Institute. Sophic's strategy is to expand the use of our software and services to fight other complex diseases such as cardiovascular, diabetes, Alzheimer's and HIV. Additional information about Sophic can be found on the World Wide Web at www.sophicalliance.com.

About Biomax: Biomax Informatics AG (Martinsried, Germany), a leader in the development of customized bioinformatics solutions, was founded in 1997 as a spin-off of the GSF-MIPS academic research group, now the German Research Center for Environment and Health-Institute for Bioinformatics (GSF-IBI). Founded by Dr. D. Frishman, Dr. K. Heumann and Prof. Dr. H. W. Mewes, Biomax developed the well-known BioXM™ Knowledge Management Environment, the BioRS™ Integration and Retrieval System, and the BioLT™ Linguistic Tool and other computational solutions that support better decision making and knowledge management in the life science industry. Additional information about Biomax can be found at the company's site on the World Wide Web at *www.biomax.com*.

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Fact Sheet and History of the Cancer Gene Index Project

The Pilot Phase of the Cancer Gene Index Project began in June 2004 with the goal of mining 8.8 million Medline abstracts to identify "suspect" cancer genes, manually verify "true" cancer genes, and manually annotate role codes and evidence codes for 1,000 cancer genes selected by NCI. Scientists identified 8,000 "suspect" cancer genes and then manually verified 4,685 "true" cancer genes. NCI's Thesaurus was leveraged by Biomax's BioLT Linguistic Tool to create extended dictionaries used to mine the literature. Scientist curators have manually verified all "true" cancer genes and have used controlled vocabularies to annotate and assign role codes and evidence codes to each gene. One thousand of the "true" cancer genes selected by NCI were manually annotated and delivered to NCI in October 2004.

From 2005 to 2007, three additional phases of the project were performed, each building on results and lessons learned in previous phases. The overall project strategy has been to ensure that "nothing is missed" and that all cancer genes, all types of cancer diseases, and all compounds and treatments related to cancer genes reported in the literature are found.