



Contact: Julie Bryant
VP Business Development and Marketing
GeneGo, Inc.
(858) 756 7996
julie@genego.com

**FOR THE FIRST TIME, SIGNALING AND METABOLIC NETWORKS CAN NOW BE
MERGED WITH GENEGO'S METACORE VERSION 3.0**

St. Joseph, Michigan, October 31st, 2005. GeneGo, Inc., a leading provider of software and databases for systems biology, announced today the major new release of its flagship data mining platform MetaCore 3.0. In the new version, scientists can for the first time build combined signaling/metabolic networks from virtually any kind of experimental data. This breakthrough may provide a quantum leap in the resolution of functional analysis of gene expression, proteomics, metabolomics, high content screening (HCS), siRNA and other types of experimental data. MetaCore 3.0 also features a unique parser for visualizing metabolomics data in the context of pathways with seamless connectivity between networks, canonical pathways, cellular processes and human diseases. The new version also adds a sophisticated enterprise-wide data management and user access system and disease specific networks.

“We believe that in this new version, we solved a major problem in functional data analysis – namely the uncoupling between signaling and effector networks in complex systems,” said Dr. Tatiana Nikolskaya, Chief Scientific Officer, President and Founder of GeneGo. “A living cell reacts to stimuli largely by changing its core biochemistry, and many metabolites serve as signaling molecules and mediators. Genome-wide formalization of the whole process from receptor-ligand interactions to activation of certain metabolic pathways is key in the understanding of complex conditions such as diseases or drug effects. Yet, signaling and metabolic pathways so far were largely not connectible even for the best studied yeast. Now, we have completed this project for human and other mammals. With integration of metabolic and signaling networks, as well as receptor-ligand interactions, the spectrum of resolution in MetaCore covers all levels from cellular processes to individual proteins small molecules interactions.”

“In practical terms, this means that our customers can now analyze in one system multiple datasets which would be incompatible in any other environment, for instance mass spec metabolic data from human blood generated in clinical trials with pre-clinical rat expression arrays and cell culture siRNA experiments”, said Julie Bryant, VP of business development at GeneGo. “Think about cross-validation of metabolic biomarkers and drug

mode of action studied in animal systems and screening data. MetaCore 3.0 is a common environment for both biologists and chemists throughout the whole drug discovery pipeline. We have also addressed sharing of experiments, knowledge and analysis with a sophisticated enterprise account and experiment management system with hierarchical access to shared accounts, data and results exchange and annotation through e-notes.”

About GeneGo

GeneGo develops systems biology technology for life science research. The original computational platform allows an integration and expert analysis of different kinds of experimental data (mRNA expression, proteomics, metabolomics, siRNA and other phenotypic data) and relevant bioactive chemistry (metabolites, drugs, other xenobiotics) within the framework of curated biological pathways and networks. GeneGo’s flagship product, MetaCore, assists pharmaceutical scientists in the areas of target selection and validation, identification of biomarkers for disease states and toxicology. The second product, MetaDrugTM is designed for prediction of human metabolism, toxicity and biological effects for novel small molecules compounds. MetaBaseTM represents the knowledge base for MetaCore. For more information, please visit the company's web site at www.genego.com.

MetaCoreTM, MetaBaseTM and MetaDrugTM are trademarks of GeneGo, Inc.