

NCI Center for Bioinformatics Informatics Seminar Series

Annotating Microarray Data with the MGED Ontology

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1:30 until 3:30 PM
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6120 Executive Blvd. (EPN), Conf. Room H

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Chris Stoeckert, PhD
Research Associate Professor
Department of Genetics
University of Pennsylvania

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Practical applications are needed for the acceptance and productive utilization of ontologies in functional genomics. These applications need to provide intuitive interaction with the ontology yet shield the user from the details of the structure. Furthermore, they must incorporate a mechanism for advancing the ontology through inclusion of new terms. The RAD Study-Annotator (RSA) is an application that addresses these needs for annotating microarray experiments. RAD (<http://www.cbil.upenn.edu/RAD>) is a gene expression database that incorporates the standards developed by the Microarray Gene Expression Data (MGED) society (<http://www.mged.org>). MGED has generated a set of guidelines as to the Minimum Amount of Information about a Microarray Experiment (MIAME), has developed a MicroArray Object Model (MAGE-OM) to represent this domain, and has created the MGED Ontology (MO) to provide the semantics for MIAME and MAGE. MO provides terms for the annotation of microarray experiments through classes, properties, and instances to describe the design, the biological materials, and the technical elements of a microarray experiment. MO also provides a framework to reference terms from external ontologies to take advantage of existing ontologies. In principle, MO can be extended to describe additional types of functional genomics experiments.

Dr. Stoeckert is a Research Associate Professor in the Department of Genetics (School of Medicine), a faculty member in the Center of Bioinformatics, and a member of the Penn Genomics Institute. His group, the Computational Biology and Informatics Laboratory (CBIL) has developed and maintains a number of public resources including Allgenes

(human and mouse ESTs and RNAs clustered and assembled into genes), PlasmoDB (a genomic resource for Plasmodia). Dr. Stoeckert is on the Board of Directors for the Microarray Gene Expression Data (MGED) Society and the leader of the MGED Ontology Working Group.

Following the presentation there will be an open discussion.