

Gene Ontology Users Meeting Schedule
La Paloma Resort, Cottonwood Room
Tucson, AZ
February 1, 2002

9:00-9:15	Welcome	
9:15-9:30	Michael Ashburner - Introduction	
9:30-10:45	<u>Development of Ontologies</u>	
	Midori Harris (GO Consortium) - Development of the Gene Ontologies	(15')
	P. Leszek Vincent (Maize Mapping Project, POC) - The Plant Ontology™ Consortium and Plant Ontologies.	(10')
	Peter E. Midford (University of Arizona) - Behavior: the ethogram as an ontology	(10')
	Pankaj Jaiswal (Cornell University) - Efforts on development and integration of controlled vocabulary at Gramene.	(10')
	Panel Discussion	(30')
10:45-11:0	BREAK	
11:00-12:00	<u>Ontology Mapping and Applications to the Annotation Pipeline</u>	
	Richard Belew (UCSD) - Reconciling Hierarchical Taxonomies	(10')
	Evelyn Camon (SWISS-PROT/TrEMBL/InterPro) - Integration & Application of GO Annotation at EBI	(10')
	Michelle Gwinn (TIGR) - TIGR's use of the GO system - an update	(10')
	Panel Discussion	(30')
12:00-1:00	LUNCH	

1:00-2:00	<u>The Annotation Pipeline: Use of sequence similarity methods</u>	
	Antonio Planchard (MGI)	(10')
	- Utilization of orthology relationships in curation	
	Jed Mathis (RGD)	(10')
	- Incorporation of GO annotations and future plans for GO within RGD	
	Matt Berriman (Pathogen Genomes, at Sanger)	(10')
	- GO for the primary annotation of genome sequencing projects	
	Panel Discussion	(30')
2:00-2:50	<u>The Annotation Trickle: Hand annotation of individual gene products</u>	
	Rebecca Foulger (FlyBase)	(10')
	- Assigning GO evidence codes in <i>Drosophila</i>	
	Karen Christie (SGD)	(10')
	- Curation of GO annotations for <i>Saccharomyces</i>	
	Panel Discussion	(30')
2:50-3:10	BREAK	
3:10-4:20	<u>Uses of GO and GO Annotations</u>	
	Elizabeth Nickerson (CSHL)	(10')
	- The Human Genome KnowledgeBase	
	Scott Doniger (Gladstone Institute, UCSF)	(10')
	- GenMAPP and Gene Ontology: Developing new tools for the organization and analysis of DNA microarray data	
	Michael Caudy (Cornell)	(10')
	- Using Gene Ontology databases for annotating functional DNA sequence motifs revealed by computational genome analysis	
	Christopher Hogue (Mt. Sinai Hospital Research Institute)	(10')
	- Large scale use of genome ontology for functional discovery in the Biomolecular Interaction Network Database	
	Hong Dang (Incellico)	(10')
	- Evaluation of the accuracy of Gene Ontology (GO) assignments to sequences and integration of GO in a cross-referencing database.	
	Panel Discussion	(30')
4:30-5:00	<u>Wrap up and final comments</u>	