

**Program for the 2nd International Biocuration Meeting
San Jose, California - October 25-28, 2007**

Thursday October 25, 2007

- 3:00-10:00 Arrival / Registration (Hayes Ballroom Foyer)
6:00-10:00 Reception (put up posters) (Hayes Ballroom Foyer)

Friday October 26, 2007

- 6:30-8:15 Breakfast
- 8:15-8:30 Sue Rhee, Carnegie Institution (Hayes Ballroom)
Welcome and Introductory Comments
- 8:30-9:30 **PLENARY SPEAKER (Hayes Ballroom)**
Judy Blake, Jackson Laboratories
Evidence and Inference: Paths of Curation
- 9:30-11:00 **SESSION #1 (Mary Schaeffer, Chair) (Hayes Ballroom)**
Literature Collection and Curation
- Toni Kazic, University of Missouri - *Quirky Searches: Annotation irregularities bias data for curation*
 - Bruce Schatz, University of Illinois - *Gene Summarizer: Software for automatically generating structured summaries from biomedical literature*
 - Allan Peter Davis, The Mount Desert Island Biological Laboratory - *Curation of the comparative toxicogenomics database: a knowledge environment for chemical-gene-disease associations*
 - Ramana Madupu, J Craig Venter Institute - *CHAR: A repository of experimentally characterized proteins*
- 11:00-11:30 Break
- 11:30-1:00 **SESSION #2 (Susan St. Pierre, Chair) (Hayes Ballroom)**
Genome Sequence Annotation and Comparative Genomics
- Manolis Kellis, MIT - *Systematic genome annotation using comparative genomics*
 - Charles Steward, Sanger Institute - *Genome annotation at WTSI*
 - Daniel Lawson, EMBL-EBI - *VectorBase: annotation of invertebrate vector genomes using both automated and manual procedures*
 - David Swarbreck, Carnegie Institution - *The challenge of genome annotation*
- 1:00-2:00 Lunch
- 2:30-5:30 **CONCURRENT WORKSHOPS**
- **WORKSHOP #1 (Doug Howe, Chair) (Monterey Room, Downstairs)**
Genome Annotation
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- Linda Hannick, J Craig Venter Institute - *Approaches to Genome Annotation: A Genome Center's Perspective*
- **WORKSHOP #2 (Petra Fey, Chair) (Hayes Ballroom)**
Curation Standards and Best Curation Practices
 - Petra Fey, Northwestern University - *Curation standards and best curation practices at dictyBase*
 - Michele Magrane, European Bioinformatics Institute - *UniProt Knowledgebase: ensuring accurate protein data*
 - Karen Christie, Stanford University - *Curation practices and standards at the Saccharomyces Genome Database*
 - P. Bryan Heidorn, University Illinois - *Biological information management from molecules to ecosystems*

6:00-7:00 Dinner

7:00-10:00 **POSTER SESSION #1 (Hayes Ballroom and Foyer, Refreshments)**

Saturday October 27, 2007

6:30-8:30 Breakfast

8:30-9:30 **PLENARY SPEAKER (Hayes Ballroom)**
Minoru Kanehisa, Kyoto University
Genomic and Chemical Annotations in KEGG

9:30-11:00 **SESSION #3 (Simon Twigger, Chair) (Hayes Ballroom)**
Ontology Development

- William Bug, Drexel University - *Semantically-driven integration of disparate, spatially qualified brain gene expression data sets using RDF and SPARQL*
- David Osumi-Sutherland, Cambridge University - *A system for representing developmental time*
- Cecilia Arighi, Georgetown University - *Protein ontology (PRO) framework and the building of the prototype for TGF-beta signaling proteins*
- Anne Maglia, University of Missouri-Rolla - *Development of the amphibian anatomical ontology*

11:00-11:30 Break

11:30-1:00 **SESSION #4 (Takashi Gojobori, Chair) (Hayes Ballroom)**
Functional Genomics Data Curation

- Tadashi Imanishi, National Institute of Advanced Industrial Science and Technology, Japan - *Annotation of human genes and alternative splicing variants in H-InvDB release 4*
- Ilene Mizrachi, National Center for Biotechnology Information - *Genome submissions to GenBank*

- Kim Pruitt, National Center for Biotechnology Information- *RefSeq and Entrez Gene: a nexus for functional genomics*
- Jeff Christiansen, Medical Research Council Human Genetics Unit - *EMAGE: casting off the shackles of text-based descriptions for 2D and 3D image-based biological data*
- Michael Livstone, Princeton University - *YFGdb: a functional genomics database containing large-scale data sets from genome-wide experiments in yeast*
- Sudhansu Dash, Iowa State University - *PLEXdb: plant and pathogen expression database and tools for comparative and functional genomics analysis*

1:00-2:00 Lunch

2:30-5:30 **CONCURRENT WORKSHOPS**

- **WORKSHOP #3 (Renate Kania, Chair) (Monterey Room, Downstairs)**
Collaboration Between Journal Publishers and Database Curators
 - Amos Bairoch, Swiss Institute of Bioinformatics - *To annotate is useful, to annotate well is better, to reannotate is essential!*
 - Lynn Fink, University of California at San Diego - *Revitalizing scientific literature for the electronic age*
 - Matt Day, Nature Publishing Group - *Nature databases and gateways: Collaborations to create online information resources*
 - Tanya Berardini, Carnegie Institution - *Eeny, meeny, miny, moe: prioritization in literature curation and how journals can get in on the act*
- **WORKSHOP #4 (David Hill, Chair) (Hayes Ballroom)**
Best Practices in Ontology Development
 - David Hill, Jackson Laboratories
 - Chris Mungall, Lawrence Berkeley National Laboratory
 - Ceri VanSlyke, University of Oregon
 - Nicole Washington, National Center for Biomedical Ontology, Lawrence Berkeley National Laboratory

6:00-7:00 Dinner

7:00-10:00 **POSTER SESSION #2 (Hayes Ballroom and Foyer, Refreshments)**

Sunday, October 28, 2007

6:30-8:30 Breakfast

8:30-9:30 **PLENARY SPEAKER (Hayes Ballroom)**
Helen Berman, Rutgers University
Curation of Biological Macromolecular Structure Data: The Protein Data Bank

- 9:30-11:00 **SESSION #5 (Owen White, Chair) (Hayes Ballroom)**
Community Curation
- Jim Hu, Texas A&M University - *EcoliWiki and GONUTS: Wiki-based community annotation and ontology usage systems*
 - Peifen Zhang, Stanford University - *Involving biochemistry and metabolism experts in improving the depth, breadth, and quality of plant metabolic pathway data in biological databases*
 - Gully Burns, Information Sciences Institute - *Using large-scale semi-automated information extraction for the biocuration of experimental observations: the million -paper challenge*
 - Astrid Terry, Joint Genome Institute - *Enabling community based genome annotation at the Joint Genome Institute*
- 11:00-11:30 Break
- 11:30-12:30 **MEETING EVALUATION AND OUTLOOK (Hayes Ballroom)**
- 1:00-2:00 Lunch & Adjourn
- 2:00-6:00 Cell Ontology Breakout Meeting (Melissa Haendel, Organizer) (Madrone Room, Downstairs)
Restructuring the cell ontology and coordination between CARO, GO and the CL