

# International Society for Biocuration



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### 2012 ISB Executive Committee Election Results

Following the recent ISB Executive Committee elections, this year's successful candidates have announced. Congratulations to Pascale Gaudet, J. Mike Cherry, Claire O'Donovan and Monica Munoz-Torres. They will join Alex Bateman, Chisato Yamasaki, Renate Kania, Teresa Attwood and Marc Robinson-Rechavi to complete the 2012/2013 ISB Executive Committee. The official handover date for the new committee will be November 1st. Many thanks to everyone, candidates and voters, who participated in this election!

## The New Image of ISB

We are delighted to share with you the new ISB Logo. Our new image combines the work of a graphic artist over some of the suggested logos submitted for the contest, depicting a modern take on elements from the original design. We would like to thank all those who submitted suggestions for this new design! As we move forward promoting the work and scholarly efforts of our members, we would like for everyone to adopt our renewed image. To request a copy of the new logo please contact us at intsocbio@gmail.com

### **Upcoming Conferences**

- The 2nd IEEE Symposium on Biological Data Visualization will take place on 14-15 October 2012 in Seattle, WA, USA. Read more at http://www.biovis.net
- The 2nd Joint Workshop on Knowledge Evolution and Ontology Dynamics will be collocated with the 11th International Semantic Web Conference (ISWC 2012), and will be held on November 11-12, 2012 in Boston, MA, USA. Details at http://bit.ly/MIZA9H
- Save the Date! Plan to join us at Churchill College in Cambridge, UK. The 6th International Biocuration Conference will be held on April 7-10, 2013.



The goal of the workshop was to engage researchers associated with major cultivated crops worldwide, increase their awareness, and showcase the latest developments in ontologies for plants. We concluded that there is a need for a broad, coordinated effort to create a semantic framework for meaningful cross-species queries using a Common Reference Ontology for Plants. This Reference Ontology will encompass all green plants and will facilitate queries for related gene expression and phenotype data from plant genomics, genetics experiments from the various species and clade-specific databases, and describe accessions in the various international crop germplasm collections. In addition to the presentations, participants engaged in hands-on activities, learning to use the ontology editor OBO-Edit and working in small groups to classify plant trait terms, which had been

# Crop Plant Trait Ontology Workshop

The Plant breeders, biologists and bioinformatics specialists from ten countries, seven US states and two plant agribusinesses firms gathered at Oregon State University in Corvallis, Oregon, September 13th-15th, 2012 for a Crop Plant Trait Ontology Workshop. The workshop was hosted by the Plant Ontology and the Trait Ontology, and coorganized by TransPlant, European Bioinformatics Institute, GARNet, Generation Challenge Program, Sol Genomics Network, and SoyBase.

Report by Dr. Laurel Cooper

submitted in advance. By creating a Common Reference Trait Ontology for Plants, we can achieve the goal of facilitating plant genetic and phenotypic data discovery and exchange. For further information, list of participants and sponsors, links to presentations and more details, please visit the workshop wiki page at http://tinyurl.com/Trait-Ontology.

Plant Ontology <a href="http://www.plantontology.org">http://www.plantontology.org</a> | Trait Ontology: <a href="http://transplantdb.eu">http://transplantdb.eu</a> | European Bioinformatics Institute: <a href="http://transplantdb.eu">http://transplantdb.eu</a> | European Bioinformatics Institute: <a href="http://www.generationcp.org">http://www.generationcp.org</a> | Sol Genomics Network: <a href="http://solgenomics.net">http://www.generationcp.org</a> | Sol Genomics Network: <a href="http://solgenomics.net">http://solgenomics.net</a> | SoyBase: <a href="http://soybase.org">http://soybase.org</a> | OBO-Edit; <a href="http://soboedit.org">http://soboedit.org</a>

### News from the ISB Community

Toxicogenomics Database Comparative released its MEDIC-Slim disease http://ctdbase.org) categories and a new filtering tool that adds functionality, reduces complexity of disease information, and eases data management. To annotate disease information at CTD, biocurators use MEDIC, a hierarchical disease controlled vocabulary that merges MeSH and OMIM disease terms into a single resource. CTD has now generated 'MEDIC-Slim', a high-level set of terms that organize all 9,700 MEDIC diseases into 36 generic categories. These mappings to MEDIC-Slim are available on all CTD "Disease" pages and can be downloaded from the MEDIC files, located at http://bit.ly/TfJF3m. Currently, CTD contains data for over 6,000 diseases, including more than 200,000 direct chemical-disease and gene-disease interactions, and 12 million inferred relationships (http://bit.ly/PVKNIG). To help manage this knowledge, users can now filter disease information using MEDIC-Slim categories. For example, the environmental chemical bisphenol A is associated with over 2,000 unique diseases at CTD (http://bit.ly/Rdg8V1).

The Comparative Toxicogenomics Database



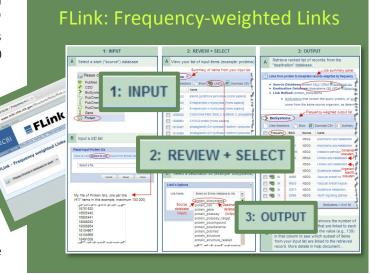
A pop-up chart conveniently shows the distribution of bisphenol A to the 36 disease categories. A user interested in exploring how this chemical is linked to cardiovascular diseases can select that category from either the graph directly (by clicking on the bar) or using the picklist in the "Disease Category" filter (below the chart) to retrieve the annotations relevant to that disease filter. MEDIC-Slim allows similar types of diseases to be grouped and analyzed for meta-analysis, provides better visualization opportunities, and facilitates knowledge management for users of CTD.



FLink is a tool that enables users to traverse from a group of records in an Entrez "source database" (e.g.: Proteins) to a ranked list of associated records in a "destination database" (e.g.: BioSystems). Developed at NCBI to handle large quantities

of input and output data, FLink can accept up to 100,000 identifiers from a database such as Entrez Gene, Protein, or PubChem as input. It can then retrieve up to 100,000 associated records from the desired destination database, such as BioSystems, ranking them by the number of items from the input list that are associated with each retrieved record. FLink can be accessed at <a href="http://1.usa.gov/en0GdX">http://1.usa.gov/en0GdX</a>. The <a href="http://1.usa.gov/bn0E8n">About FLink</a> site (<a href="http://1.usa.gov/bn0E8n">http://1.usa.gov/bn0E8n</a>) provides an illustration of an easy 1-2-3 step process to use the tool. The help document (<a href="http://1.usa.gov/WPLgkG">http://1.usa.gov/WPLgkG</a>) provides additional details about the proper formatting of the (1) input UID list, the

features of the (2) review + select display and (3) output display,



and a list of supported databases. FLink operates by mining the associations ("links") among data types stored in the Entrez search system back-end. The method by which associations are made depends on the source and destination databases and is displayed in the "Link method" line of the job summary panel, in the FLink output display (see <a href="http://l.usa.gov/PVQeYg">http://l.usa.gov/PVQeYg</a>). Initially developed as a companion tool for the NCBI BioSystems database (http://www.ncbi.nlm.nih.gov/biosystems/), FLink has been available since August 2010 and draws about 800 hits per day. The *How to* web page (<a href="http://l.usa.gov/hS2evZ">http://l.usa.gov/hS2evZ</a>) provides examples of the types of jobs that FLink is able to handle.



### **Databases Fighting Funding Cuts**

Last month Monya Baker wrote a piece for Nature News, on the topic of the unstable conditions of the financial support for online tools. Reporting on the consequences of funding cuts by the US National Library of Medicine (NLM), Baker considers the players on both side of the equation. To read about NLM's decision to put their funds into research and training, and the reactions from around our community, you can access the article at <a href="http://bit.ly/Q8RLiN">http://bit.ly/Q8RLiN</a>. At ISB, we do our best to constantly promote the work of biocurators and database developers, to help ensure that both researchers and funding agencies continue to recognize the value of this work.

### **Biocuration Job Openings**



- Postdoctoral Research Associate, microbial ontology. Department of Microbiology and Molecular Genetics, Michigan State University, East Lansing, MI, USA. Posted on Oct 7, 2012. Details are available at <a href="http://linkd.in/RfLLkv">http://linkd.in/RfLLkv</a>
- Scientific Curator Cancer Cell Type Ontology (OncoCL) Project, Jackson Laboratory, Bar Harbor Maine, USA. Posted September 16, 2012. For more information visit <a href="http://bit.ly/SRTCU2">http://bit.ly/SRTCU2</a>
- Postdoctoral position in the Genome Technology Branch (GTB) of the US National Human Genome Research Institute (NHGRI). Posted September 8, 2012. Details are available at <a href="http://bit.ly/NYu381">http://bit.ly/NYu381</a>
- ❖ Database and Semantic Web Developer, University of Colorado, Boulder, USA. Posted August 30, 2012. For more information visit <a href="http://t.co/C7dvQX9g">http://t.co/C7dvQX9g</a>

- NGS Bioinformatician, Montpellier, France. Posted August 30, 2012. Details on this position are available at <a href="http://bit.ly/QbQJRl">http://bit.ly/QbQJRl</a>
- Postdoctoral opportunity for Phenoscape at University of South Dakota, USA. Posted July 24, 2012. For more details, see <a href="http://bit.ly/OZd5SM">http://bit.ly/OZd5SM</a>
- Bioinformatics Analyst Fungal Genomics, US DOE Joint Genome Institute, Walnut Creek, CA. Posted July 8, 2012. For more details, please visit <a href="http://bit.ly/My7CVI">http://bit.ly/My7CVI</a>
- ♦ PhD position available in semantic web, biomedical ontologies, text mining, Montpellier, France . Posted July 8, 2012. Details are available at <a href="http://bit.ly/O9kRrX">http://bit.ly/O9kRrX</a>
- Data Wranglers for Saccharomyces Genome Database, Stanford University. Posted May 17, 2012. Details are available at: <a href="http://bit.ly/NcZhGR">http://bit.ly/NcZhGR</a>
- Web Engineers for Saccharomyces Genome Database, Stanford University. Posted May 17, 2012. Details are available at: <a href="http://bit.ly/JQcVid">http://bit.ly/JQcVid</a>





Kind regards, The ISB Executive Committee.

