MMHCC Newsletter March 2008

MouseLine

The Open Biomedical Ontologies (OBO) Foundry in 2008

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The Open Biomedical Ontologies (OBO) Consortium was created in 2001 by Michael Ashburner and Suzanna Lewis as an umbrella body for developers of ontologies in the domain of the life sciences. OBO ontologies were required to accept certain key principles which were seen as underlying the success of the Gene Ontology (GO) [Ashburner et al. 2003], above all that they be *open for use without restriction, instantiated in a well-specified syntax, and such as to employ a common space of identifiers.* The OBO library now comprises over 60 ontologies, and its role as an ontology information resource is being supported and extended by the National Center for Biomedical Ontology (NCBO) through its BioPortal [Rubin et al. 2006, http://www.bioontology.org/bioportal.html].

In 2005, the developers of a subset of OBO ontologies initiated the OBO Foundry, a collaborative experiment based on the acceptance of an enlarged and incrementally evolving set of principles (see http://obofoundry.org), designed to provide enhanced guidelines for those new to ontology development and to maximize the degree to which life science ontologies can work together in such a way as to support the needs of working scientists [Smith et al. 2007].

Candidate Foundry ontologies can be divided into two groups. First are those which pre-existed the Foundry and are now undergoing reform, including the GO, the Cell Ontology (CL), the Foundational Model of Anatomy Ontology (FMA) [Rosse and Mejino 2007], the Phenotypic Quality Ontology (PaTO), and the Sequence Ontology (SO). Second are ontologies being created *ab initio* following Foundry principles, including the Common Anatomy Reference Ontology (CARO), the Environment Ontology (EnvO), the Ontology for Biomedical Investigations (OBI), and the Protein Ontology (PRO).

Starting in 2008, each candidate Foundry ontology will be subject to a process of peer review managed by *Coordinating Editors*, whose primary responsibility is harmonizing interactions between the Foundry's constituent ontology development projects. Reviews will be carried out by the Foundry's *Associate Editors*, nominated by the ontologies already accepted for inclusion within the Foundry, who will work together with specialist reviewers who have expertise in the relevant biological domain. Currently, the Foundry's Coordinating Editors are Michael Ashburner (University of Cambridge), Suzanna Lewis and Chris Mungall (Berkeley/NCBO), Alan Ruttenberg (Science Commons), Richard Scheuermann (University of Texas Southwestern Medical Center), and Barry Smith (Buffalo/NCBO).

As with traditional journal submissions, peer review is expected to be an iterative process. Reviews and recommendations for revision will be addressed in successive versions of the reviewed ontologies until a stage is reached where the latter are deemed suitable for inclusion in the Foundry. Thereafter, the ontology will be subject to successive updates in tandem with the advance of scientific knowledge.

One long-term goal of the Foundry is that, for each domain of relevance for biomedical research, there should be convergence upon a single ontology that is recommended for use by those involved with the Foundry initiative. This does not imply that we believe that all ontology development in the biomedical field should take place within the OBO Foundry. Indeed, we are fully aware that scientific advance rests on the existence of a plurality of hypotheses and research paradigms and on the constant to-and-fro of criticism and exchange between the representatives of competing strategies. Foundry collaborators thus welcome the recent inauguration by the NCI Enterprise Vocabulary Services of the Biomedical Grid Terminology (http://www.biomedgt.org/) project to create an open, federated ontology covering translational research, in the hope that this and other parallel initiatives will serve to advance the principles and practice of evidence-based ontology development.

References

[Ashburner et al. 2003] M. Ashburner, C. Mungall and S. Lewis, Ontologies for Biologists: A Community Model for the Annotation of Genomic Data, Cold Spring Harbor Symposia on Quantitative Biology 68 (2003), pp. 227-236.

[Rosse and Mejino 2007] Rosse C. and JLV Mejino Jr., The Foundational Model of Anatomy Ontology. In A. Burger, D. Davidson, and R. Baldock, eds. Anatomy Ontologies for Bioinformatics. Springer, 2007, pp. 59-117.

[Rubin et al. 2006] Rubin DL, Lewis SE, Mungall CJ, Misra S, Westerfield M, Ashburner M, Sim I, Chute CG, Solbrig H, Storey MA, Smith B, Richter JD, Noy NF and Musen MA The National Center for Biomedical Ontology: Advancing Biomedicine through Structured Organization of Scientific Knowledge, OMICS 10 (2006), pp. 185-198.

[Smith et al. 2007] B, Ashburner M, Rosse C, Bard J, Bug W, Ceusters W, Goldberg LJ, Eilbeck K, Ireland A, Mungall CJ; OBI Consortium, Leontis N, Rocca-Serra P, Ruttenberg A, Sansone SA, Scheuermann RH, Shah N, Whetzel PL, Lewis S, The OBO Foundry: Coordinated Evolution of Ontologies to Support Biomedical Data Integration, Nature Biotechnology 25 (2007), pp. 1251-1255.

Special AACR Meeting Information

AACR Meeting San Diego, April 12-16, 2008

NCI/NIH-Sponsored Session
Monday, April 14, 10:30 am - 12:00 pm, Room 10

The Cancer Biomedical Informatics Grid™ (caBIG™) in action: a real-time demonstration of interoperable cancer research tools.

The Cancer Biomedical Informatics Grid™ (caBIG™) is a virtual informatics infrastructure that connects data, research tools, scientists and institutions to leverage the combined strengths and expertise in an open environment with common standards.
We will start with an introduction to the caBIG™ program, followed by a live demonstration of the current generation of caBIG™ tools and infrastructure. The demonstration will show caBIG™ supporting molecular medicine. It will feature tools to support translational research, integrating information across different research areas and institutions.

caBIG™ Learning Center
Monday, April 14, 1:00 pm – 5:00 pm, Room 15B

Demonstrations of the following caBIG™ Tools:

caArray
- A standards based data management system for array based expression, CGH and SNP data.
- MIAME compliant annotation of experiments.
- Connect to analytical tools: geWorkbench, GenePattern, BioConductor.

cancer Genome Wide Association Studies, caGWAS
- Access to SNP association findings, populations frequency, genotype, and phenotype data.
- Allows researchers to access and analyze clinical and experimental data across multiple studies.

cancer Models Database, caMOD
- Provides information about rodent and other animal models for human cancer to the research community.

caTissue
- Tissue banking tool for biospecimen inventory, tracking and annotation.
- Track the collection, storage, annotation, quality assurance and distribution of specimens.
- Find and request specimens with specific characteristics.

geWorkbench
- Enables integrated view of genomics data: gene expression, sequence, pathways.
- Genomic data integration with visualization tools, external databases, and computational services.

National Cancer Imaging Archive, NCIA
- Searchable, national repository integrating in vivo cancer images with clinical and genomic data.
- Public access to DICOM images, image markup, annotations and metadata.

Pathway Interaction Database, PID
- Curated collection of information about known biomolecular interactions and key cellular processes assembled into signaling pathways.

Notices and Funding Opportunities

Comparative Systems Genetics Studies - (RFA-CA-08-017)
The NCI and the NIEHS announce the availability of a Funding Opportunity to support Comparative Systems Genetics studies. This announcement solicits grant applications for research projects focused on the development and application of comparative (cross-species) systems genetics approaches to address key cancer-relevant problems. Use of systems genetics approaches should enhance the understanding of the mechanisms that underlie: (i) human cancer susceptibility and (ii) heterogeneity of human tumors. The proposed projects will likely involve appropriate interdisciplinary collaborations providing expertise in such areas as human genetics, statistical genetics, model organism genetics, systems biology, mathematical or computational modeling of biological processes, and computer sciences. All applicants must propose to use two species, one of which must be human.
Information about the RFA is available at: http://grants.nih.gov/grants/guide/rfa-files/RFA-CA-08-017.html.
The R01 applications are due by electronic submission no later than C.O.B. May 14, 2008.

Administrative supplements for making knockout mice
The NIH and the Knockout Mouse Project (KOMP) re-announce the opportunity for investigators to apply for administrative supplements to have mouse knockouts made from existing mutant ES cell resources. The goal of this program is to support use of existing resources and to ensure that ES cell lines are converted into frozen embryos that are available from a repository. With up to $13,125 (direct costs) from the NIH, you can get started quickly on generating the knockout you need for your research project.

See the recent NIH notice at http://grants.nih.gov/grants/guide/notice-files/NOT-HG-08-002.html.
There are two receipt dates in fiscal year 2008: April 1, 2008 and June 1, 2008.

National Animal Welfare Education Program Workshops and Conferences for 2008
NOT-OD-08-043
National Institutes of Health
http://grants.nih.gov/grants/guide/notice-files/NOT-OD-08-043.html

March IACUC 101 Workshop and PRIM&R 2008 Annual IACUC Conference in Atlanta, Georgia
NOT-OD-08-044
National Institutes of Health
http://grants.nih.gov/grants/guide/notice-files/NOT-OD-08-044.html

April IACUC 101 Workshop in Galveston, Texas
NOT-OD-08-045
National Institutes of Health
http://grants.nih.gov/grants/guide/notice-files/NOT-OD-08-045.html

Notices and Funding Opportunities cont.

Update of Sample Animal Welfare Assurance
NOT-OD-08-049
National Institutes of Health
http://grants.nih.gov/grants/guide/notice-files/NOT-OD-08-049.html

National Cancer Institute (NCI) Initiatives for Support of Basic and Translational Tumor Stem Cell Research
NOT-CA-08-010
National Cancer Institute
http://grants.nih.gov/grants/guide/notice-files/NOT-CA-08-010.html

Request for Information. Agents to be tested for Preclinical Efficacy in Prevention or Reversal of Type 1 Diabetes in Rodent Models. Type 1 Diabetes Preclinical Testing Program (T1D-PTP)
NOT-DK-08-012
National Institute of Diabetes and Digestive and Kidney Diseases
http://grants.nih.gov/grants/guide/notice-files/NOT-DK-08-012.html

Administrative Supplements for Making Knockout Mice
NOT-HG-08-002
Multiple Institutes
http://grants.nih.gov/grants/guide/notice-files/NOT-HG-08-002.html

Tumor Stem Cells in Cancer Biology, Prevention, and Therapy (R01)
RFA-CA-08-019
National Cancer Institute
http://grants.nih.gov/grants/guide/rfa-files/RFA-CA-08-019.html

Leiomyomata Uteri: Basic Science, Translational and Clinical Research (R01)
PAR-08-102
National Institute of Child Health and Human Development
National Institute of Environmental Health Sciences
Office of Research on Women's Health
http://grants.nih.gov/grants/guide/pa-files/PAR-08-102.html

Repository News

The MMHCC Mouse Repository is an NCI-supported resource for the distribution of mouse cancer models and associated strains. The Repository makes strains available to all members of the scientific community. Up to 3 breeder pairs of each available strain may be ordered.

Newly accepted strains
The following strains have recently been accepted into the MMHCC Repository and are available for distribution (*please click on the specific link, below, for additional information*):

1. B6;129-Gt(ROSA)26Sor $^{tm1(cre/Esr1)Tyj}$
   http://mouse.ncifcrf.gov/details.asp?ID=01XAB
2. B6;CBA-Tg(tetO-EGFR*L858R)56Hev (EGFR-L858R)
   http://mouse.ncifcrf.gov/details.asp?ID=01XEA

More information can be found on the Mouse Repository's website: http://mouse.ncifcrf.gov