



MMHCC Newsletter March 2004

MouseLine

Please stop by the exhibit booth of the Mouse Models of Human Cancers Consortium (MMHCC) at the March meeting of the American Association of Cancer Research (AACR) in Orlando, Florida. Our [booth number is 549](#) – come meet us in person!



To learn more about the “Mouse Models of Human Cancers - Web-based Resources”, please attend Fei Xu’s presentation during the Cellular, Molecular and Tumor Biology (Bioinformatics and Cancer – Tools, Resources, and Biology) Minisymposium on Tuesday, March 30, 2004, 5:10 P.M. in Room W222.

Meetings

March 27-31, 2004

The AACR 95th Annual Meeting

Orlando, Florida

Meeting information: <http://www.aacr.org/2004AM/2004AM.asp>

April 20-24, 2003

9th International Congress on Hyperthermic Oncology

St. Louis, Missouri

Meeting information: <http://icho2004.org/>

April 26-27, 2004

- Cambridge Healthtech Institute’s 5th Annual **Microarrays in Medicine**

Meeting information: <http://www.healthtech.com/2004/mar/index.ASP>

- Cambridge Healthtech Institute’s 4th Annual **Genomic and Proteomic Sample Preparation**

Meeting information: <http://www.healthtech.com/2004/smp/index.asp>

April 28-30, 2004

- Cambridge Healthtech Institute’s 2nd Annual **Laser Capture Microdissection**

Meeting information: <http://www.healthtech.com/2004/mcr/index.ASP>

All meetings are to be held in Boston, Massachusetts





Funding Opportunities

Northwest Association for Biomedical Research IACUC Workshop in March

NOT-OD-04-021

National Institutes of Health (NIH)

<http://grants.nih.gov/grants/guide/notice-files/NOT-OD-04-021.html>

SCAW Advanced IACUC Workshop in Baltimore, March 2004

NOT-OD-04-022

National Institutes of Health (NIH)

<http://grants.nih.gov/grants/guide/notice-files/NOT-OD-04-022.html>

Bioinformatics

BIOgopher - <http://biogopher.nci.nih.gov/>

BIOgopher is a powerful ad hoc query and reporting tool that enables researchers to annotate entries in Microsoft Excel™ spreadsheets with data generated by the NCICB's Cancer Bioinformatics Infrastructure Objects. BIOgopher presents a web-based, graphical user interface with which a user can build complex queries incorporating data from any number of user-supplied local spreadsheets. The results of such queries are then delivered to the user as a new spreadsheet in which the originally submitted data and the caBIO data are merged.

As an example, suppose a scientist has a spreadsheet consisting of genomic sequence data, and that one of the columns in that spreadsheet contains the GenBank accession number for each row. A natural way of enhancing these data might be to incorporate the cellular pathway information associated with each of these accession numbers. In most environments, this would require visiting another web site such as BioCarta, entering appropriate queries consecutively, and cutting and pasting each response back into the spreadsheet. BIOgopher allows the user to accomplish this task with a single query by indicating which column contains the accession numbers and specifying what pathway information should be included. The resulting spreadsheet returned by BIOgopher will contain a new column specifying the selected pathway information for each gene, in conjunction with the original columns.

BIOgopher also allows users to build queries interactively without requiring any initial spreadsheets. The search query can be assembled using pull-down menus to select caBIO domain objects such as Clone, Disease, Gene etc., from the caBIO "object tree." After entering these query objects, the user then selects the desired data fields and values to be used in the query, and a spreadsheet containing the data extracted from the retrieved caBIO objects will be created. The caBIO domain objects provide an exhaustive model of the many biomedical and genomic entities commonly found in biomedical research today.

