NCI Launches Cancer Molecular Analysis Portal with the Cancer Genome Atlas Glioblastoma Multiforme is First Data Set

The National Cancer Institute (NCI) is pleased to announce the public beta release of a new online resource for the broad scientific and medical communities. The Cancer Molecular Analysis (CMA) portal, a component of NCI?s cancer Biomedical Informatics Grid (caBIG?), is now online and available for use. The CMA portal enables researchers to use a single interface to integrate, visualize, and explore clinical and genomic characterization data from translational research studies, such as The Cancer Genome Atlas (TCGA) pilot project supported by the NCI and the National Human Genome Research Institute (NHGRI), as well as NCI?s REMBRANDT (Repository of Molecular Brain Neoplasia Data), which will be added by the end of 2008.

The current version of the CMA portal provides web access to tools for the analysis and visualization of gene expression, gene copy number, SNP data, methylation data and DNA sequence. The molecular data can be analyzed within the context of clinical information, including treatment history, pathology status, tumor site and surgical history. The CMA homepage provides a feedback link to encourage user input on functionality and ease of use. Enhancements and refinements to the CMA will be ongoing. In the future, CMA will include data from other vital cancer projects, as well as improvements in analytical tools and functionality.

One of the first data sets available on CMA is the data generated by TCGA on the brain tumor, glioblastoma multiforme (GBM). TCGA?s large data collection has unprecedented integrative power which is allowing a multi-dimensional, network view of common genetic alterations in the GBM genome. This data can be analyzed using GenePattern, Principal Component Analysis and the Cancer Genome Workbench analysis tools via the CMA. It also can be accessed through TCGA Data Access Matrix via the TCGA Data Portal, which provides advanced tools for selecting subsets of data from TCGA for download based on user-selected settings. Data on lung and ovarian tumors also will be made available as they are generated by the TCGA pilot.

To learn more about The Cancer Genome Atlas Project, please go to http://cancergenome.nih.gov/.