Solving Research Problems: Perform Integrative Analysis of Clinical and Expression Data

Molecular Analysis Tools Knowledge Center

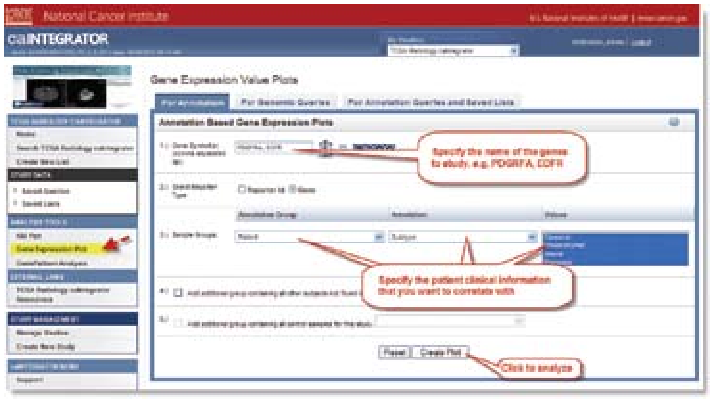
Molecular analysis tools provide powerful analytic capabilities for genomic data interpretation. Four key tools are supported by the Molecular Analysis Tools Knowledge Center: geWorkbench, which provides an innovative, open-source software platform for genomic data integration while bringing together analysis and visualization tools for gene expression, sequences, pathways and other biomedical data; GenePattern, which provides bioinformatics tools for gene expression, proteomic and SNP analysis; caArray, a system that supports the management and exchange of array data and annotations and caIntegrator, a novel translational informatics platform that allows researchers and bioinformaticians to access and analyze clinical and experimental data across multiple clinical trials and studies.

The Problem: Integrative Analysis of Clinical Data and Microarray Gene Expression Data

One of the critical challenges facing clinical oncology research is the ability to get a complete view of a patient's disease through the integration of different types of available data. An example of such a challenge is the integration of microarray gene expression data and patient clinical data to identify potential correlations.

The Solution: caIntegrator

caIntegrator, a web-based software application, is designed to address the challenge of the integrative data analysis. After importing data into the application, a researcher can explore the correlation between the patent clinical information and the gene expression level using the Gene Expression Plot function built in caIntegrator in as few as three steps, as illustrated in **Fig. 1**. The resulting plot reveals the correlations of the expression levels of the genes selected with the clinical information under the study, as illustrated in **Fig. 2**.

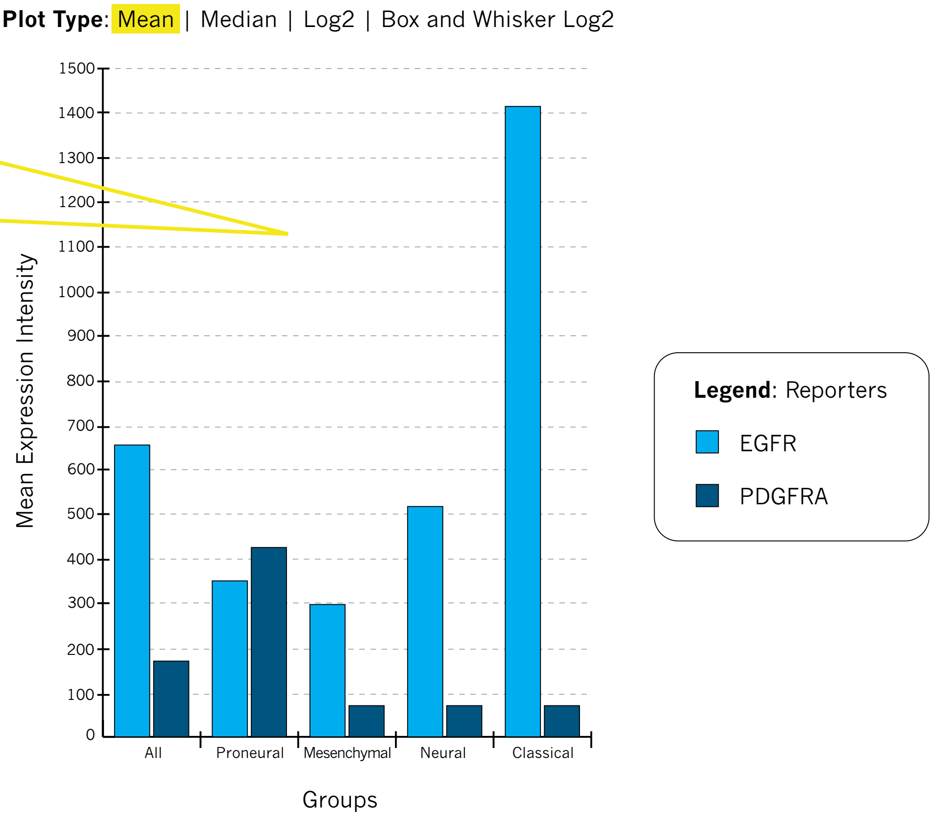


Specify the name of the genes to study, e.g. PDGRFA, EGFR

Specify the patient clinical information that you want to correlate with

Click to analyze

Fig. 1 Use of the Gene Expression Plot in caIntegrator.



The results showed the differential expression levels of EGRF and PDGFRA in four subtypes of Glioblastoma among the patients under study.

Fig. 2 The results of the Gene Expression Plot.

The Benefits:

With caIntegrator, cancer researchers can explore the correlation between the patent clinical information and gene expression data on one integrated platform.

Key Contributors:

caIntegrator development team
Molecular Analysis Tools Knowledge Center

For More Information:

Molecular Analysis Tools Knowledge Center: *https://cabig-kc.nci.nih.gov/Molecular/KC/index.php/Main_Page*

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