

## **C-eXpress: A Web-Based Analysis Platform for Comparative Functional Genomics and Proteomics in Human Cancer Cell Line, NCI-60 as an Example**

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**Abstract :** Background: Recent advances in high-throughput research technologies such as new-generation sequencing and multi-dimensional liquid chromatography makes it possible to dissect the complete transcriptome and proteome in a single run for the first time. However, it is almost impossible for many laboratories to handle and analysis these "BIG" data without the support from a bioinformatics team. We aimed to provide a web-based analysis platform for users with only limited knowledge on bio-computing to study the functional genomics and proteomics. Method: We use NCI-60 as an example dataset to demonstrate the power of the web-based analysis platform and data delivering system: C-eXpress takes a simple text file that contain the standard NCBI gene or protein ID and expression levels (rpkm or fold) as input file to generate a distribution map of gene/protein expression levels in a heatmap diagram organized by color gradients. The diagram is hyper-linked to a dynamic html table that allows the users to filter the datasets based on various gene features. A dynamic summary chart is generated automatically after each filtering process. Results: We implemented an integrated database that contain pre-defined annotations such as gene/protein properties (ID, name, length, MW, pI); pathways based on KEGG and GO biological process; subcellular localization based on GO cellular component; functional classification based on GO molecular function, kinase, peptidase and transporter. Multiple ways of sorting of column and rows is also provided for comparative analysis and visualization of multiple samples.

**Keywords :** cancer, visualization, database, functional annotation

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