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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