



Software Application for Re-annotating and Analyzing Gene Expression Data

Client Overview

The client is one of the largest academic and research institutes working to solve problems relevant to genomic medicine by developing new methodologies in translational bioinformatics.

Challenges

The client was interested in harnessing the publicly available molecular measurement data from gene expression microarrays to generate new knowledge and answer significant clinical questions pertaining to disease genetics. For this, the client needed a software application development partner who understood both the informatics as well as domain specific requirements of such a translational bioinformatics tool. Given the complexity of the project and the domain expertise it demanded, the client was challenged to find a competent Life Science informatics organization with multidisciplinary expertise in the field of genomics. Clearly, a highly skilled and specialized partner was needed to address the client's challenges. Optra with its deep domain expertise and experience in providing life science research solutions and multifunctional team of Subject matter experts, software architects and skilled bioinformatics scientists, was a perfect partner for this venture.

Solution

- Optra developed a software system to automatically extract gene expression microarray data from the public microarray repositories, and build two web servers, to enable scientists without computer skills to reuse millions of microarray data sets in the public domain.
- First, Optra collected all gene identifiers from Entrez Gene and UniGene and built a Universal Gene Identifier Table (UGIT).
- Each column of every GEO platform was then matched with UGIT to find the best matching column and type of external identifier, and annotated each probe ID with Entrez Gene IDs.
- The server offered four functions to help users re-annotate platforms.
- Platform annotation could add the latest annotations to any uploaded result file.
- Cross-species mapping could enable mapping platform annotations to other species.
- Platform comparison provided comparing of any two platforms to find corresponding probes mapping to the same gene.
- Gene Search could find deposited platforms and samples in GEO for any list of genes.
- Further Optra built a web server that enabled biologists and clinicians without bioinformatics skills to easily identify biological and clinical conditions in which a gene or set of genes was differentially expressed.
- The functionalities of this web server allowed the user to performs all group versus group comparisons, identify all experimental conditions where the expression levels of a gene or set of genes is significantly changed, and display them graphically with statistical comparisons and sort/filter functions.
- Further it also provided access to the original studies.

Technology Environment

- PHP
- Perl Scripting
- R-Script (Statistical Analysis Tool)
- MySQL
- Core Java, Swing
- Java Web Start
- RMI

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Benefits

- Seamless data integration solution for raw microarray data sets facilitated largest publically available re-annotated cross species gene identifier data
- It enabled reutilization of experimental data to answer new questions
- The easy to use functionalities allowed sophisticated statistical testing and multiple comparisons
- It was possible to elucidate information on function, transcriptional regulation, drug-response and clinical implications for genes of interest

About Optra Health

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