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A Web-based Workbench for Conducting "In-Silico" Experiments Using Microarray Data



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Short Abstract: The Colorado INIA Informatics website offers a suite of tools for sharing, analyzing, and interpreting microarray experiment data for worldwide collaborative research. The website allows users to combine gene expression data from an assortment of previously uploaded MIAME-compliant experiments to test novel hypotheses regarding gene expression and complex behaviors.

Long Abstract:

The Colorado INIA Informatics website offers a suite of tools for sharing, analyzing, and interpreting microarray experiment data for worldwide collaborative research. The website allows users to combine gene expression data from an assortment of previously uploaded MIAME-compliant experiments in order to test novel hypotheses regarding gene expression and complex behaviors.

The website serves three main purposes. First it provides access to a locally-maintained

repository where microarray experiment data can be uploaded in a MIAME-compliant format. The arrays are organized by organism, genetic variation, sex, and tissue and may be browsed by all visitors to the website. In contrast to other microarray data repositories, this website allows pre-approved, registered users to not only browse the available arrays, but also to use the data for "in-silico" experimentation. This investigation involves combining chips from multiple experiments, or subgroups of chips from within an experiment, to test novel hypotheses constructed from the collective objectives of the various experiments. As one would expect, the website enforces that the set of chips must first pass a series of quality control checks to ensure they are compatible for comparison. In addition to checking the integrity of the chips chosen, the quality control process also highlights particular conditions, such as probe intensity variance, where chips may not be comparable, and these results are displayed visually for the user.

The second main feature of the website is an intuitive, web-based interface for guiding the user through a series of steps to statistically analyze the "in-silico" experiment. This includes the ability to save the results from multiple normalization methods and to use different filtering options to restrict the genes used in statistical analysis. The user may conduct both parametric and non-parametric comparisons of chips divided into groups, and may choose from various adjustments for multiple comparisons. The resulting gene list may be saved at any point, and the parameters used for normalization, filtering, and statistics are saved with the gene list so the user may compare the results from using different combinations of parameters.

The final significant feature of the website is access to a suite of tools to aid in the interpretation of gene lists. Users can interpret the gene lists generated from the analysis of the "in-silico" experiments in addition to uploaded gene lists generated through other methods. Annotation tools translate gene identifiers between many different nomenclatures including gene symbols, RefSeq IDs, and probe names from both Affymetrix and CodeLink arrays. In fact, the website's translation tool can translate a gene list containing multiple identifier types and is also able to identify linkages between databases that are not directly linkable but are linked through a third database. Other options on the website allow the user to conduct literature searches and to do gene list comparisons. Promoter analysis using oPOSSUM methodology is also available and promoter sequences can be downloaded for input into other promoter analysis tools. Finally, expression QTL data on BxD recombinant inbred mice and HxB/BxH rats can be queried with respect to the user's gene lists.

As vendors release microarrays that are used for whole-genome mapping, SNP analysis, exon analysis, or methylation and transcript mapping, tools for managing the data sets from multiple experiments are required. In order to achieve the highest value from the next generation of microarray technology and to handle the lack of standardization in the current technology, biologists need tools for combining the data, testing for compatibility, and intuitively analyzing and interpreting the data. Not only does this website provide the foundation for doing such analysis, it also makes these tools available to a world-wide audience of researchers, ranging from departmental groups to large-scale consortiums.

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