

Developing Bioinformatic Tools for Analyzing Genomic Data for Chemical Risk Assessment

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Microarray technology has been widely accepted as an efficient and reproducible way to explore the gene expression changes involved in the regulation of biological processes. In toxicology, the ability to examine thousands of genes allows a broad survey of gene expression changes following chemical exposure. Despite the potential utility of the technology, the application of microarray data to risk assessment has been limited, in part, due to the lack of rigorous analysis methods and software tools. In this project, we will develop bioinformatic tools to analyze dose-response and cross-species microarray data. The combination of microarray technology with these software tools will result in a unique set of risk assessment tools that will allow exploration and analysis of the cross-species conservation and dose-response behavior of potential key events in the mode-of-action for a chemical.

Implications: Two of the fundamental challenges in chemical risk assessment are predicting the responses to chemicals at low doses and determining whether an adverse response will be conserved across species. For both challenges, microarray-based gene expression measurements can provide a broad survey of transcriptional changes following chemical exposure that allow a comprehensive examination of potential key events in the mode-of-action for a chemical. When performed in dose-response or across multiple species, the genomic data can provide reference doses at which these key events occur and help determine whether these key events are likely to be conserved across species. This project provides the software tools for analyzing dose-response and cross-species microarray data in a risk assessment context.

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