

Centers for Integrated Genomics

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The Center for Integrated Genomics was established to insure that CIIT-LRI research programs would take advantage of contemporary toxicogenomics methods by providing genomic expertise and resources for use in toxicology and risk assessment studies throughout CIIT Centers for Health Research. Researchers affiliated with the Center are using genomic technology for the improved understanding of basic biological systems, gene-environmental interactions, and risks to human health from exposure to chemicals and other substances. A major function of the Center is to develop genomic competencies and technologies that facilitate LRI-sponsored research at CIIT. The Center provides training in genomics and bioinformatics to students, postdoctoral fellows, senior staff, and visiting scientists. Within the Center for Integrated Genomics, the CIIT Gene Expression Core provides researchers with “state of the art” technologies for assessing transcriptional changes and bioinformatics support for analyzing and interpreting those changes. The technologies for measuring gene expression changes include an Affymetrix microarray system for assessing transcriptional changes across thousands of genes in a single experiment, Applied Biosystems Real Time reverse transcriptase-polymerase chain reaction (RT-PCR) instruments for measuring or validating transcriptional changes in only a few genes at a time, an Arcturus laser capture microdissection instrument for obtaining tissue and ribonucleic acid (RNA) samples from a small number of cells in a tissue of interest, and additional instrumentation for checking the quality of samples given to the Core. Apart from the instrumentation, a comprehensive laboratory information management system for microarray gene expression analysis compiles the results and data associated with each experiment and stores the information in a relational database. Individual investigators can retrieve the information from the database and perform visualization and statistical analysis using a number of different software programs.

Start and end date: January 1998 – December 2002

Presentations:

Liu, D. and Gaido, K. W. (2006). Modeling effect of nucleotide compositions on expression levels of probes due to non-specific binding on AffyChips. Presentation at 2006 Summer Program on Multiplicity and Reproducibility in Scientific Studies Workshop, Research Triangle Park, NC, July 10–12, 2006.

Liu, D., Page, T., Chu, Z., Gaido, K., Wolfinger, R., and Thomas, R. (2006). Estimating transcription and degradation rates of mRNA in HeLa cells following heat shock. Poster presentation at Keystone Symposia: Systems and Biology jointly with Bioinformatics and Proteomics, Keystone, CO, April 8–12, 2006.

Peer-reviewed publications:

Liu, D., Peddada, S. D., Li, L., and Weinberg, C. R. (2006). Phase analysis of circadian-related genes in two tissues. *BMC Bioinformatics* 7: 87.

Liu, D., Gaido, K. W., and Wolfinger, R. (2005). Analysis of variation of amplitudes in cell cycle gene expression. *Theor. Biol. Med. Model* 2: 47.

Other publication(s): None to date.

Sponsors in addition to the LRI: None.

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