S6-03

Bioinformatics and DNA Microarray Applications in Cancer Research

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Bioinformatics is a rapidly emerging field of biomedical research. A flood of large-scale genomic and postgenomic data means that many of the challenges in biomedical research are now challenges in computational sciences. The revolutions both in bioinformatics and high throughput genomics using DNA microarray will eventually transform the current practice of cancer management, including diagnostics, therapeutics, and prognostics. In this talk, I will describe how the high throughput technologies combined with computational sciences will impact cancer research and clinical care, emphasizing recent advances in biochip-based functional genomics and proteomics. Basic data preprocessing with normalization and filtering, primary pattern analysis, and machine learning algorithms will be presented. Use of integrative DNA microarray informatics technologies including multivariate data projection, gene-expression-metabolic-pathway mapping, automated biomolecular annotation, text mining of factual and literature databases, and integrated management of biomolecular databases will be discussed. Each step will be given with real examples from ongoing research activities in the context of clinical relevance. Issues of creating standard-based cancer genomics databases and cancer informatics infrastructure will be discussed.

S6-04

Comprehensive Analysis of Gene Expression Profiles in the Methylotrophic Yeast Hansenula polymorpha by a Whole-genome cDNA Microarray

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A whole-genome cDNA microarray for the methylotrophic yeast Hansenula polymorpha was developed and used to investigate systematically how gene expression in this yeast is fine-tuned in response to various environmental changes. We analyzed the temporal changes of gene expression accompanying carbon source shift from glucose to methanol and glucose consumption. The obtained information on the metabolic fate of glucose and methanol will be usefully applied for pathway engineering and process optimization in exploiting H. polymorpha as a cell factory. We also analyzed global transcriptional responses of H. polymorpha to heavy metal stress caused by cadmium and oxidative stress caused by menadione. The gene expression profiles allowed us to identify novel H. polymorpha genes, which could be usefully exploited for the development of yeast whole-cell sensing system of environmental pollutants.