will provide important new search parameters for expression data. Extensive interconnections with sequence databases and with databases from other species further extend GXD's utility for analysis of gene expression information.

Robinson, Alan

Data mining and visualisation of microarray gene expression data

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DNA microarray technology is one of the most important recent breakthroughs in experimental molecular biology. With evermore laboratories acquiring this high-throughput technology, the amounts of data being generated are growing extremely rapidly, and the informatics necessary for handling and analysing these data is becoming a major bottleneck. The EBI is working on the development of applications to promote and further the development of the informatics and analysis of microarray data and that is integrated with other biological resources in order to better understand the results of gene expression experiments. We are exploring the development of new techniques as well as technology transfer from marketing and telecommunications domains, e.g. application of visualisation, data mining and statistical analysis. Currently, the EBI is assessing the suitability of different data mining algorithms to microarray gene expression data, e.g. neural networks, classification trees, market basket analysis, clustering, classification, etc. As well developing Internet tools that will allow users to browse and query microarray data stored in a database, the EBI is investigating techniques and technologies that will allow direct access to the microarray information in a database over computer networks, for example CORBA and JDBC. This technology will allow developers at other sites to develop and write their own novel software tools that can perform queries and analyses on microarray data that is pulled over the Internet from the EBI microarray database.

Rose, Stanley

A versatile system enabling analysis of slide-based, high-density microarrays with a variety of alternative chemistries

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It is now becoming generally recognized that microarray technology will be a fundamental tool used in future genomics research. As the technology becomes more widely accessible, larger numbers of biologists will be able to shift their focus from the study of individual events to the analysis of complex systems and pathways. To help drive this transition, we have used novel tools for creating and reading high-density microarrays of spotted DNAs to investigate whether conventional chemistries (for example, Southern, northern and western blots) might be applied to microarray analysis. It had previously been assumed that these well-documented methodologies could not be used for microarray analysis because: (i) spotting instruments could not produce arrays on membranes such as nitrocellulose or nylon; and (ii) these membranes were thought to produce levels of fluorescence which would make analysis impossible. We will show data developed using a Pin-and-Ring™ spotting system (the GMS 417 Arrayer) and an epi-fluorescent confocal laser microscope that employs Flying Objective™ scanning technology (the GMS 418 Array Scanner), demonstrating that conventional chemistries can be used for microarray analysis. We believe that demonstration of the feasibility of this approach will facilitate the migration of more biologists toward the use of microarray technology, as they will now be able to use commercially available instrumentation and familiar methodologies for highly parallel genomic analysis. These novel instrument systems also provide enhanced performance (for example, consistency of spotting, speed and sensitivity of scanning) with biochemical methodologies developed specifically for microarray analysis, so that scientists can obtain the same degree of analytical power independent of the biochemistry they choose to employ.

Sahay, Nisha

The reproducibility factor in differential gene expression analysis by microarray technology

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DNA microarray technology is a powerful tool to investigate the expression pattern of a high number of genes in parallel. A major experimental challenge of this emerging technology is establishing the reproducibility of data sets. For differential expression measurements, total RNA from human adult and fetal brain was reverse transcribed and labelled with Cy3 and Cy5 fluors respectively, to obtain single-stranded cDNA probes. The labelled cDNA probes were used for competitive hybridisation on a microarray chip containing 768 genes, each gene spotted by the Flexys™ robot five times in an 8X8, 32 grid pattern. Potential errors in hybridisation efficiency were minimised by the use of the GeneTAC™ Hybridisation Station. The slides were imaged in the GeneTAC™ 1000 Biochip Analyser, a high-throughput imager equipped to handle up to four fluors simultaneously. Images were analysed using the GeneTAC™ Integrator software. Genes showing threefold and higher change in expression were targeted to determine a percent variation in reproducibility. First, an intra-array reproducibility study was performed where a change exhibited by a gene was compared with its duplicates within a single array. In addition, an inter-array experiment was done to determine the variation in numerical values of genes between ten separate 384-gene chips, each independently hybridised with identical sets of probes.

Sampas, Nick

Feature extraction and clustering tools for analysing gene expression data from DNA microarrays

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To extract useful biological information from DNA microarray experiments, it is necessary to accurately quantify the measured expression levels and to systemat-