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WORKSHOP II: SHARING AND INTEGRATION OF GENOMIC AND PROTEOMIC
DATA

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Sequencing of the human genome has stimulated a new way of thinking in biology; however, our understanding of the sequence is limited by our ability to retrieve meaning from it. The human and other genome sequencing projects underscore an emerging dependence on computational and comparative biology techniques to analyze this data. They have highlighted the critical need for repositories and curated databases to manage and distribute biological data to the public. The quantity and annotation of sequence data has also made possible new technologies such as microarrays, which permit analysis of transcriptional states of thousands of genes in a single experiment. As sequence and experimental data sets continue to grow; however, interesting questions about mechanisms for sharing data, analyzing data, data ownership and standardization of techniques are emerging on a new scale. During this workshop these issues will be discussed and an overview of genomic and proteomic resources, curated databases, genomic annotation approaches and microarray standardization efforts will be provided.