S15 Developing Toxicogenomics Knowledge Base for Genotoxicity and Carcinogenecity Evaluation. Ju Han Kim, M.D., Ph.D., M.S. *Seoul National University Biomedical Informatics (SNUBI) http://www.snubi.org/.*

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. Postgenome informatics, powered by high throughput technologies and genomic-scale databases, is likely to transform our biomedical understanding forever much the same way that biochemistry did a generation ago. In this talk, I will describe how these technologies will impact toxicology research, introducing recent advances in databasing gene expression profiles with the emphasis on the necessity of tight integration of private and public databases and intelligent analysis toolkits. I will introduce some of our research efforts for toxicogenomics knowlege base. Xperanto (Expressionist's Esperanto in XML) integrates major data models for DNA microarray, tissue microarray and array CGH data with extended clinical and histo-pathological information models and supports analysis tools in an effort to establish a comprehensive knowledge base for toxicogenomics research. Each step will be given with real examples from ongoing research activities in the context of clinical relevance.

S16 Interpretation of aCGH Data. Su Young Kim. *The Catholic University of Korea.*

Most of malignant tumors, if they are not all, have a set of alterations in genetic information. This can be manifested as changes in DNA, RNA or protein. Considering the fact that genetic information is conveyed from DNA to protein via RNA, changes of genomic DNA might be a initial starting point in the propagation. Carcinogenesis usually involves combination of changes in several genes. To understand perspective changes which occur in genomic DNA, we need robust, high throughput modality scanning whole genome. Comparative genomic hybridization (CGH) has given perspective views of tumor genomes. As a result of effort to increase the resolution of CGH, new CGH method using microarray was developed. This method investigate copy number alterations in genome. Due to the size and complexity of human genome, microarray-based CGH (aCGH) experiment gives huge matrix of numbers which is beyond the limit of manual calculation or intuitive power. Raw aCGH data should be preprocessed and analyzed by statistical manner to get applicable biological information. Because analysis tools for aCGH data are generally provided by microarray manufacturers, most of them are platformspecific and expensive. R, which is free software for statistical computing, is a good option to choose to analyze aCGH data. In addition to R, FileMaker may be a good companion to build aCGH database for researchers who don't have sound IT infrastructure.