Toxicogenomics Principles and Applications. Edited by H. K. Hamadeh and C. A. Afshari (Amgen, Inc.). Wiley-Liss, Hoboken. 2004. xii + 361 pp. 6 × 9½ in. $64.95. ISBN 0-471-43417-5.

Toxicogenomics characterizes the activity of a particular toxin or chemical substance on living tissue by profiling the agent's affect on genetic material. The term toxicogenomics, however, is a bit deceptive. This discipline is not the simple combination of toxicology and genomics, but instead a multifaceted field that also embraces molecular biology, chemistry, pathology, statistics, bioinformatics, and engineering. As no one person is an expert in all these areas, toxicogenomics calls for a team approach. Effective teamwork, as exemplified in sports, requires cross training. *Toxicogenomics Principles and Applications* provides this cross training for a broad audience. For students, the book reviews the fundamentals of toxicology and explains technologies and "omic" approaches used in this discipline. Experienced researchers will find it a useful resource to help evaluate emerging research and participate in new studies.

Users of the text will need to have some understanding of biology, chemistry, genetics, statistics, and bioinformatics. Even the most general material assumes an understanding of biological processes such as apoptosis, inflammation, and carcinogenesis; the chemistry of phase I and II metabolic reactions; the fundamentals of gene expression; the difference between parametric and nonparametric statistical analyses; and the basics of data management and knowledge-based systems.

Several chapters are dedicated to the technologies and experimental tools used in the "omic" approach to toxicology. These chapters include helpful discussions of microarrays and polymerase chain reaction (PCR) methodologies, scanners used to collect data, database management systems, and high-throughput technologies. Additional chapters focus on data analysis and interpretation. One such chapter is dedicated to the statistics of toxicogenomics. Unlike traditional toxicology that measures a few variables, toxicogenomics uses microarrays that allow measurement of thousands of variables. The large number of potential relationships between these variables requires thoughtful consideration to avoid faulty interpretations and false conclusions. Statistical concepts and techniques are illustrated using a typical experiment, and common pitfalls that contribute to data misinterpretation are discussed.

The book (and perhaps the field itself) is slightly mistitled, as it goes beyond genomics and also includes transcriptomics (the study of an entire population of transcripts in a cell population at a given time), proteomics (the study of all proteins expressed in a cell and how they interact), and metabolomics (the study of small molecules that specific cellular processes leave behind). All these -omics are integral to toxicogenomics. Toxicants interact with proteins, affecting protein signaling, transcription factors, and metabolite−protein interactions, which regulate the expression of genes as transcripts.

The last chapter of the book provides many useful web-based resources. In some cases, the URLs have changed (e.g., LocusLink has been reorganized as Entrez Gene) or no longer function (e.g., AMAD database system). The vast majority of resources, however, are reliable web sites that will help researchers keep abreast of programs, standards, tools, and databases that are key to the study of toxicogenomics.

The editors have assembled a useful guide for new and seasoned scientists exploring the relationships between genetic variation and toxic response.

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