



Foundations of Systems Biology: Using Cell Illustrator and Pathway Databases (Computational Biology)

Masao Nagasaki, Ayumu Saito, Atsushi Doi, Hiroshi Matsuno, Satoru Miyano

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Today, as hundreds of genomes have been sequenced and thousands of proteins and more than ten thousand metabolites have been identified, navigating safely through this wealth of information without getting completely lost has become crucial for research in, and teaching of, molecular biology. Consequently, a considerable number of tools have been developed and put on the market in the last two decades that describe the multitude of potential/putative interactions between genes, proteins, metabolites, and other biologically relevant compounds in terms of metabolic, genetic, signaling, and other networks, their aim being to support all sorts of explorations through bio-data bases currently called Systems Biology. As a result, navigating safely through this wealth of information-processing tools has become equally crucial for successful work in molecular biology. To help perform such navigation tasks successfully, this book starts by providing an extremely useful overview of existing tools for finding (or designing) and investigating metabolic, genetic, signaling, and other network databases, addressing also user-relevant practical questions like • Is the database viewable through a web browser? • Is there a licensing fee? • What is the data type (metabolic, gene regulatory, signaling, etc.)? • Is the database developed/maintained by a curator or a computer? • Is there any software for editing pathways? • Is it possible to simulate the pathway? It then goes on to introduce a specific such tool, that is, the fabulous “Cell - lustrator 3. 0” tool developed by the authors.

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