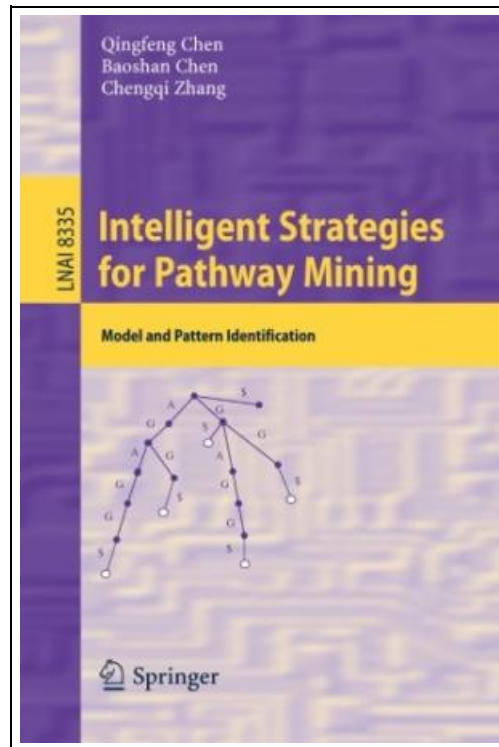# Intelligent Strategies for Pathway Mining: Model and Pattern Identification

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Reviews

This publication is definitely not simple to begin on studying but quite fun to see. It really is full of knowledge and wisdom I am just effortlessly can get a satisfaction of studying a created pdf.

(Alfreda Bradtke)

INTELLIGENT STRATEGIES FOR PATHWAY MINING: MODEL AND PATTERN IDENTIFICATION

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Springer International Publishing AG. Paperback. Condition: New. 299 pages. Dimensions: 9.2in. x 6.1in. x 0.7in.This book is organized into thirteen chapters that range over the relevant approaches and tools in data integration, modeling, analysis and knowledge discovery for signaling pathways. Having in mind that the book is also addressed for students, the contributors present the main results and techniques in an easily accessed and understood way together with many references and instances. Chapter 1 presents an introduction to signaling pathway, including motivations, background knowledge and relevant data mining techniques for pathway data analysis. Chapter 2 presents a variety of data sources and data analysis with respect to signaling pathway, including data integration and relevant data mining applications. Chapter 3 presents a framework to measure the inconsistency between heterogenous biological databases. A GO-based (genome ontology) strategy is proposed to associate different data sources. Chapter 4 presents identification of positive regulation of kinase pathways in terms of association rule mining. The results derived from this project could be used when predicting essential relationships and enable a comprehensive understanding of kinase pathway interaction. Chapter 5 presents graphical model-based methods to identify regulatory network of protein kinases. A framework using negative association rule mining is introduced in Chapter 6 to discover featured inhibitory regulation patterns and the relationships between involved regulation factors. It is necessary to not only detect the objects that exhibit a positive regulatory role in a kinase pathway but also to discover those objects that inhibit the regulation. Chapter 7 presents methods to model ncRNA secondary structure data in terms of stems, loops and marked labels, and illustrates how to find matched structure patterns for a given query. Chapter 8 shows an interval-based distance metric for computing the distance between conserved RNA secondary structures. Chapter 9 presents a framework to explore...

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