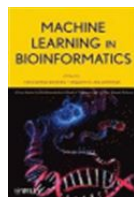


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Machine Learning in Bioinformatics

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An introduction to machine learning methods and their applications to problems in bioinformatics

Machine learning techniques are increasingly being used to address problems in computational biology and bioinformatics. Novel computational techniques to analyze high throughput data in the form of sequences, gene and protein expressions, pathways, and images are becoming vital for understanding diseases and future drug discovery. Machine learning techniques such as Markov models, support vector machines, neural networks, and graphical models have been successful in analyzing life science data because of their capabilities in handling randomness and uncertainty of data noise and in generalization.

From an internationally recognized panel of prominent researchers in the field, this book compiles recent approaches in machine learning methods and their applications in addressing contemporary problems in bioinformatics. Coverage includes: feature selection for genomic and proteomic data mining; comparing variable selection methods in gene selection and classification of microarray data; fuzzy gene mining; sequence-based prediction of residue-level properties in proteins; probabilistic methods for long-range features in biosequences; and much more.

This is an indispensable resource for computer scientists, engineers, biologists, mathematicians, researchers, clinicians, physicians, and medical informaticists. It is also a valuable reference text for computer science, engineering, and biology courses at the upper undergraduate and graduate levels.

Publication Year	2008
Edition	1st
Author/Editor	Zhang, Yanqing and Rajapakse, Jagath C.
Publisher	Wiley
ISBN	978-0-470-11662-3
Platform	Ovid
Product Type	Book
Speciality	Medical Genetics
Language	English
Pages	456
Illustrations	0