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## Machine learning for biological data analysis


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### Abstract

Automated machine learning is a hallmark of machine learning (ML). The focus is on creating data-driven predictions using programmed algorithms. ML has several application areas, including bioinformatics, the field of research and practice concerned with the application of computational deduction to obtain biological data. This includes collecting, retrieving, storing, manipulating, and modeling data for analysis or prediction using customized software. Comprehensive programming of bioinformatics algorithms for applications such as protein structure prediction has traditionally been a very tedious task. Algorithms using ML and deep learning (DL) have now increased the speed and efficiency of programming such algorithms. “Applications of Machine Learning and Deep Learning to Biological Data” explores the application of ML and DL to fields such as proteomics, genomics, microarrays, text mining, and systems biology. The main goal is to cover ML applications to biological science problems, with a focus on issues related to bioinformatics. This book describes current research topics and techniques in the field of ML as applied to the rapidly evolving field of bioinformatics. Applying ML and DL to biological and neuroimaging data opens new frontiers in biomedical engineering, for example to improve the understanding of complex diseases such as cancer, neurodegenerative diseases, and psychiatric disorders. Advances in this field could ultimately lead to the development of precision medicine and automated diagnostic tools that can tailor care to an individual's lifestyle, diversity, and environment. Machine learning has shown promise in the analysis of large-scale and complex biological data. However, in reality, successful applications require biological information in addition to machine learning.

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