

**BRIDGING DISCIPLINES
WITH ARTIFICIAL
INTELLIGENCE**

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Foreword

It is with great pride and satisfaction that I present this edited book titled “Bridging Disciplines with Artificial Intelligence” to the readers from diverse disciplines, professional and intellectual backgrounds. This book has been envisioned with the belief that Artificial Intelligence (AI) is not merely a technological innovation but a life-changing force that is reshaping every human activity. The book reflects the rapidly expanding role of AI in transforming not only scientific and technological domains but also the fields of humanities, commerce and management. AI is no longer confined to computer science laboratories; rather it has become an interdisciplinary force integrating scientific innovation with human understanding, economic systems and managerial practices. The title of this book was deliberately chosen to emphasize the integrative and transformative nature of AI across multiple domains of knowledge. We are living in an era where the boundaries between disciplines are becoming increasingly interconnected. AI stands at the centre of this convergence, offering unprecedented opportunities while also presenting complex challenges that require multidisciplinary understanding.

The chapters included in this volume explore a broad spectrum of themes that demonstrate the multidimensional applications of AI. Several contributions examine the role of artificial intelligence in biological sciences, biotechnology, chemistry, physics, mathematics and environmental sustainability. These chapters highlight how AI-driven technologies are accelerating scientific discovery, improving diagnostics, enhancing computational modeling, and supporting sustainable solutions for global challenges. At the same time, the book also reflects the growing significance of AI in humanities and social sciences. The chapters discussing artificial intelligence in art and creativity, governance, public policy and societal transformation provide meaningful insights into the ethical, cultural and social implications of intelligent technologies. These discussions are especially relevant in an era where technological advancement must remain aligned with human values and responsible innovation. The volume further addresses the increasing integration of AI into commerce, banking, accounting, marketing, and human resource management. Artificial intelligence is reshaping organizational decision-making, consumer engagement, financial systems, cybersecurity and workplace dynamics.

This edited book aims to provide readers with a comprehensive understanding of the opportunities, challenges, ethical concerns, and future

prospects associated with artificial intelligence. As editor, I believe that the future of AI will not be determined solely by technological capability but by our collective wisdom in applying it responsibly, ethically and inclusively. The true promise of artificial intelligence lies not in replacing human intelligence but in augmenting it thus enhancing our ability to solve complex problems, generate new knowledge, foster innovation and improve the quality of life for individuals and communities around the world.

I extend my sincere gratitude to all contributors, reviewers, and collaborators whose dedication and expertise have made this work possible. Their commitment to interdisciplinary scholarship reflects the very spirit of this book. I also thank the readers who have chosen to engage with this important subject and contribute to the ongoing dialogue about the future of intelligent technologies. It is my hope that this volume will inspire thoughtful inquiry, encourage cross-disciplinary collaboration, and promote a deeper understanding of how artificial intelligence can serve humanity while advancing scientific, economic, cultural, and managerial development.

Editors:**Dr. Aanchal Arora^a**

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Chapter 1

AI-DRIVEN BIOINFORMATICS: TRANSFORMING DISEASE DISCOVERY, DIAGNOSIS AND THERAPY

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Abstract

The introduction of Artificial Intelligence (AI) in the field of Bioinformatics has completely changed disease discovery, diagnosis and treatments. High-throughput technology generates large amounts of genomic, transcriptomic, proteomic and clinical data that are challenging to analyze using conventional statistical analyses alone. Machine learning and deep learning techniques have enabled scientists and clinicians to quickly identify and extract biologically relevant features from large volumes of complex datasets, thereby allowing them to make quicker and more accurate conclusions regarding disease-causing genes, pathways and molecular fingerprints. We use clustering and predictive modelling methods and classify a disease into very specific biological categories that allows for earlier diagnoses and the ability to predict the risk of developing a disease. This method is especially advantageous in the areas of cancer, neurological disorders and rare inherited disorders. Using AI for applications in bioinformatics has revolutionized the drug discovery process by accelerating many key biochemical processes, including target identification, Protein Structure Prediction, Virtual Screening and Drug-Protein Interaction Modelling. These new capabilities allow researchers to develop therapeutics faster and with lower costs. This chapter reviews recent advances in AI-driven bioinformatics and highlights

how intelligent computational models are transforming disease research from a slow, trial-and-error process into a fast, predictive and data-driven scientific discipline.

Keywords: Artificial intelligence, bioinformatics, disease discovery, drug discovery, precision medicine

1.1 Introduction

Artificial Intelligence (AI)'s integration into bioinformatics constitutes one of the most impressive paradigm shifts in contemporary biomedical research over the last two decades. High-throughput technology advancements have brought about an explosion of biological data through next-generation sequencing, single-cell RNA sequencing, proteomics, metabolomics and large-scale clinical data systems. These tools allow researchers to better explore how molecular mechanisms cause disease; but at the same time, they generate such complex, high-dimensional data that it exceeds the ability of standard statistical methodologies to analyze them. Conventional approaches often find it difficult to facilitate modeling for non-linear relationships and multilayered dependencies that are common in multi-omics and clinical datasets (Wekesa and Achieng, 2023).

Bioinformatics has changed from a discipline concentrated on the alignment and annotation of sequences to an integrated, systems-level science. Disease biology today recognises that the majority of disease states arise due to dynamic interactions between genes, regulatory networks, cellular states and environmental influences rather than as a result of independent genetic mutations. Developing adequate methods to represent this complexity requires computational frameworks that can learn hierarchically from biological data at many scales. Modern algorithms for machine learning and deep learning provide scalable methods for discovering hidden structures in large datasets, while new foundation models will enhance the capability to generalise biological knowledge across various situations (Cui et al., 2024).

AI-based bioinformatics is changing the way of identifying diseases. The implementation of deep neural networks has led to better interpretations of pathogenic variants and improved gene prioritization

in rare inherited disorders, helping to minimize the uncertainty associated with missense variant analysis (Cheng et al., 2023). In addition, systems-level foundational models like Gene former have provided the ability to recreate gene regulatory networks, providing mechanistic insights of cardiovascular diseases, such as cardio myopathy (Theodoris et al., 2023). Integration of multiple omics data via AI-generated approaches has improved classification of subtypes of tumors and identification of biomarkers in cancer, with improved prognostic stratification (Sartori et al., 2025).

In addition to discovery and diagnosis, AI has accelerated the development of new therapies. The ability to utilize advancements in protein structure predictions and protein-protein and protein-DNA interaction modeling through the large-scale implementation of alphaFold has allowed protein structure-based drug development and improved drug target validation (Varadi et al., 2024). The use of a combination of genomic, transcriptomic, proteomic, structural and clinical data within predictive computational systems is changing biomedical research into a much more rapid and data-based process and is being carried out in a precision-based manner. This chapter reviews the foundations of the data, methodological advances and translation of the application of AI as a means of advancing the process of disease discovery, diagnosis and therapy.

1.2 Biological and Clinical Data Foundations For AI-Driven Disease Research

AI-powered bioinformatics relies heavily on high-quality and diverse biological datasets for effective analysis and interpretation. Modern disease research relies on the integration of multiple data sources to understand disease mechanisms, diagnosis and therapeutic development. This combined information supports the development of AI procedures to help researchers and clinicians in exploring human disease. Whole genome and whole exome sequencing provide in excess of millions of mutations in every individual. AI-assisted variant detection can improve the reliability of variant detection across sequencing platforms (Wekesa and Achieng, 2023), enabling the researchers to better understand the pathophysiology and cause of rare diseases (Cheng et al., 2023).

Transcriptomic data provides functional insight into gene activity, while bulk RNA sequencing provides tissue-level expression changes and single-cell RNA sequencing provides high-resolution mapping of cellular heterogeneity. Methods such as scGPT and Geneformer create foundation models that learn generalizable representations of gene expression patterns that aid in cell type annotation and in discovering disease subtypes (Cui et al., 2024). These approaches are particularly beneficial for cancer and immune-related diseases in which the diversity of the cellular populations influences disease progression (Theodoris et al., 2023). Proteomics and structural biology expand the analysis of the molecular level and include the study of protein structure. Recently developed AI-based structural prediction tools, including alphaFold and others, are transforming protein structure modeling and predicting interactions between biomolecules (Varadi et al., 2024). Lastly, clinical datasets, such as electronic health records and medical imaging, provide phenotypic information. Integration of multi-omics can give powerful insight but harmonizing or validating any external data is important to provide replicable evidence and decrease bias in predictions. More recently, multimodal AI models have integrated both molecular and clinical data to facilitate decision-making for discovery, diagnosis and treatment of a disease (Ding et al., 2025).

1.3 Artificial Intelligence Methodologies In Disease Modeling

The main methodologies of AI in disease research today are classified into three areas: machine learning, deep learning and advanced foundation learning models that can identify complex, non-linear relationships within high-dimensional datasets. The conventional statistical machine learning techniques, including support vector machines (SVMs), random forests, and gradient boosting, are still very useful for research involving the life sciences. All these methods work well when feature sets are well-defined, and sample sizes are moderate to large. These methods also have an advantage over other methodologies such as explanatory models because they can provide a degree of interpretability i.e. produce an understandable output from the data and relatively stable performance from test to test.

Deep learning allows for even further automation of feature representation extraction through hierarchical learning on unpro-