


Chapter 14

Conclusion for Next- Generation Bioinformatics for Pulmonary Disease Research

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ABSTRACT

This book explores computational approaches revolutionizing pulmonary disease studies through AI, machine learning, and multi-omics. Chapters cover AI-driven respiratory data analysis, single-cell approaches, and integrative omics for lung disease outcomes. Key areas include tuberculosis, severe asthma, idiopathic pulmonary fibrosis, and non-small cell lung cancer, integrating genomic, proteomic, and epigenomic data. Novel methods like Sequential Attribute Designator for feature

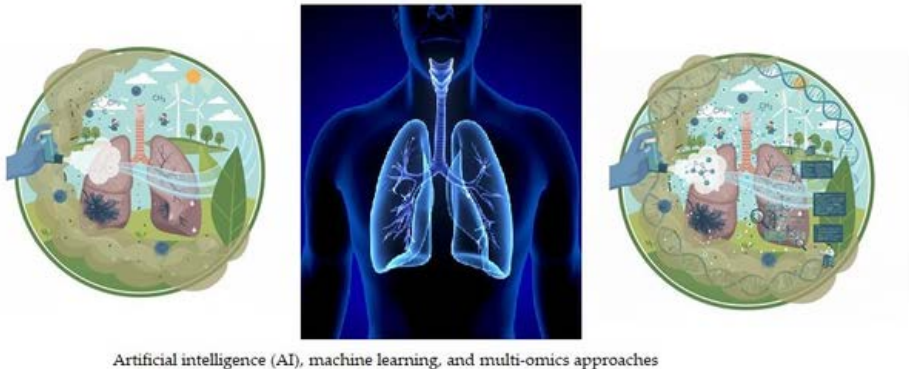
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selection and deep learning models for lung disease diagnosis via chest X-rays are introduced. The book addresses lung microbiome, metagenomic tools, and environmental exposure effects. By connecting translational bioinformatics with clinical applications, it highlights precision pulmonology's future through advanced omics and machine learning, advancing disease diagnosis, treatment, and research.

INTRODUCTION

The rapid advancement of bioinformatics has significantly transformed biomedical research, providing unprecedented opportunities to elucidate the complexities of pulmonary diseases, (Casotti et al., 2023). “*Next-Generation Bioinformatics for Pulmonary Disease Research*” offers a comprehensive examination of computational methodologies that are redefining the study, diagnosis, and treatment of respiratory conditions. As pulmonary diseases ranging from tuberculosis and asthma to idiopathic pulmonary fibrosis and non-small cell lung cancer continue to present substantial global health challenges, the integration of advanced computational tools with biological data is essential, (Chen et al., 2025). This book seeks to bridge the gap between cutting-edge bioinformatics and clinical applications, highlighting the role of artificial intelligence (AI), machine learning, and multiomics approaches in advancing precision pulmonology (Figure 1).

Figure 1. Pulmonary disease research



The field of pulmonary bioinformatics is extensive, incorporating genomic, transcriptomic, proteomic, and epigenomic data to elucidate the molecular foundations of lung diseases. With the emergence of high-throughput sequencing and single-cell technologies, researchers are now able to examine cellular heterogeneity

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