Chapter 1

Introduction:
The Landscape of Pulmonary Bioinformatics

Rahul Kumar
https://orcid.org/0009-0000-1323-2220
Department of Microbiology, Graphic Era University, Dehradun, India

Devvret Verma
Department of Biotechnology, Graphic Era University, Dehradun, India

Bahman Khoshru
University of Tabriz, Tabriz, Iran

Adeyemi Nurudeen Olatunbosun
Federal University of Agriculture, Abeokuta, Nigeria

ABSTRACT

Pulmonary bioinformatics is an area that is rapidly developing as a blend of computational biology, data science, and respiratory medicine to improve the understanding, diagnosis, and treatment of lung disorders. With high-throughput omics technologies and large-scale clinical datasets, bioinformatics methods have become critical for the discovery of molecular signatures of chronic obstructive pulmonary disease (COPD), asthma, pulmonary fibrosis, lung cancer, and infectious diseases, such as tuberculosis and COVID-19. Using genomics, transcriptomics, proteomics, and metabolomics, together with artificial intelligence and systems biology, pulmonary bioinformatics provides a multidimensional understanding of disease mechanisms and tailored therapeutic approaches. Public databases, biobanks, and electronic health records are important resources, although there are still issues with data

DOI: 10.4018/979-8-3373-4923-7.ch001

integration, standardization, and ethics. Advances in precision medicine, machine learning, and multi-omics integration will revolutionize respiratory health and make pulmonary bioinformatics care.

INTRODUCTION

Pulmonary bioinformatics is a groundbreaking discipline that integrates respiratory medicine, computational biology, and systems-level research to investigate lung structure, function, and pathology at molecular, cellular, and clinical levels, (Meira et al., 2024). This field offers unprecedented evidence regarding the mechanisms underlying lung health and disease, thereby enabling personalized medicine, drug discovery, biomarker identification, and predictive diagnostics. The evolution of pulmonary bioinformatics mirrors the general trajectory of computer-based methods in medicine, (Zosa, 2021). During the first few decades of respiratory research, investigations of pulmonary physiology and pathology relied heavily on descriptive anatomy, histopathology, and epidemiology. In the mid-20th century, imaging technologies such as chest X-rays, spirometry, and computed tomography (CT) allowed for quantitative analysis in diagnostic practice, (Senek et al., 2024). Molecular biology in the 1970s and the 1980s brought about genetic and protein-level alterations in lung disease, but these investigations were mainly reductionists targeting single genes or proteins, (Egan & Sharples, 2023). The 1990s Human Genome Project initiated the incorporation of genomics into pulmonary research to allow large-scale studies of genetic susceptibility to asthma, COPD, cystic fibrosis, and lung cancer, (Shrine et al., 2019). In the early 21st century, the advent of high-throughput sequencing, microarray, and proteomic technologies produced enormous amounts of data, creating the need for computational platforms to integrate, process, and analyze such information, (Liu & Zhang, 2024). This shift saw the emergence of pulmonary bioinformatics as a distinct subdiscipline, where computational methods began to play a critical role not only in data analysis but also in hypothesis generation and systems-level modeling.

The evolution of computational methods in pulmonary medicine has been characterized by a series of discrete milestones. Initially, statistical modeling and biostatistics were used to examine clinical trial results and population-level respiratory health surveys. With the expansion of bioinformatics databases during the 1990s and the 2000s, scientists were able to cross-reference gene expression information from diseased and healthy lung tissues to identify new biomarkers for pulmonary disease, (Li et al., 2020). In recent years, machine learning (ML) and artificial intelligence (AI) have transformed this discipline by making it possible to build predictive models for disease progression, image analysis of CT and MRI scans,

34 more pages are available in the full version of this document, which may be purchased using the "Add to Cart" button on the publisher's webpage: www.igi-global.com/chapter/introduction/393257

Related Content

Digital Model for Diagnosis of Postoperative Complications in Medicine Using Bioinformatics: Evaluate and Predict the Patient's Condition
Vladimir Gorbachenko (2019). *International Journal of Applied Research in Bioinformatics (pp. 1-23).*
www.irma-international.org/article/digital-model-for-diagnosis-of-postoperative-complications-in-medicine-using-bioinformatics/237197

Data Stewards, Curators, and Experts: Library Data Engagement at Samuel J. Wood Library at Weil Cornell Medicine
Peter R. Oxley, Sarah Ben Maamarand Terrie Wheeler (2024). *Research Anthology on Bioinformatics, Genomics, and Computational Biology (pp. 566-583).*
www.irma-international.org/chapter/data-stewards-curators-experts/342544

Combinatorial Optimization Algorithms for Metabolic Networks Alignments and Their Applications
Qiong Chengand Alexander Zelikovsky (2011). *International Journal of Knowledge Discovery in Bioinformatics (pp. 1-23).*
www.irma-international.org/article/combinatorial-optimization-algorithms-metabolic-networks/52768

Heart Sounds Human Identification and Verification Approaches using Vector Quantization and Gaussian Mixture Models
Neveen I. Ghali, Rasha Wahidand Aboul Ella Hassanien (2012). *International Journal of Systems Biology and Biomedical Technologies (pp. 74-87).*
www.irma-international.org/article/heart-sounds-human-identification-verification/75155

BioTextRetriever: A Tool to Retrieve Relevant Papers
Célia Talma Gonçalves, Rui Camachoand Eugénio Oliveira (2011). *International Journal of Knowledge Discovery in Bioinformatics (pp. 21-36).*
www.irma-international.org/article/biotextretriever-tool-retrieve-relevant-papers/63615