

Chapter 12

The Future of Respiratory Bioinformatics

Rahul Kumar

 <https://orcid.org/0009-0000-1323-2220>

Department of Microbiology, Graphic Era University, Dehradun, India

Rachan Karmakar

 <https://orcid.org/0000-0002-3220-6287>

Department of Environmental Science, Graphic Era University, Dehradun, India

B. E. Guerra Sierra

Exactas Naturales y Agropecuarias, University de Santander, Bucaramanga, Colombia

Snežana Andjelković

 <https://orcid.org/0000-0003-0436-3530>

Institute for Forage Crops, Bulgaria

ABSTRACT

Respiratory bioinformatics is a fast-developing field that provides revolutionary information on the molecular mechanisms, pathogenesis, and individualized management of respiratory conditions. This chapter explores the potential future of respiratory bioinformatics, discussing innovations in the integration of data, artificial intelligence (AI), machine learning (ML), and multi-omics analysis to decipher intricate networks of respiratory diseases. From early diagnosis and predictive modeling to precision medicine and targeted therapies, bioinformatics has revolutionized the clinical and research paradigms of respiratory health. This chapter highlights the state-of-the-art advancements in big data analytics, high-throughput sequencing, and

DOI: 10.4018/979-8-3373-4923-7.ch012

Copyright © 2026, IGI Global Scientific Publishing. Copying or distributing in print or electronic forms without written permission of IGI Global Scientific Publishing is prohibited. Use of this chapter to train generative artificial intelligence (AI) technologies is expressly prohibited. The publisher reserves all rights to license its use for generative AI training and machine learning model development.

systems biology methodologies for the discovery of new biomarkers, drug targets, and disease signatures. It also covers imminent challenges, including data standardization, interoperability, and ethical aspects of bioinformatics-based research.

INTRODUCTION

Respiratory infections remain a staggering global health burden, with both communicable and non-communicable infections contributing significantly to morbidity and mortality, (Coates et al., 2020). Respiratory infections are among the leading causes of mortality globally, with over 2.6 million deaths recorded every year, as per the Global Burden of Disease (GBD) 2019 estimates, (Momtazmanesh et al., 2023; Viegi et al., 2020). Concurrently, long-term respiratory diseases like chronic obstructive pulmonary disease (COPD), asthma, and interstitial lung disease afflict more than half a billion individuals worldwide, with unequal burdens in low- and middle-income countries (LMICs). The international response to the COVID-19 pandemic has highlighted the critical need for swift and accurate diagnostics, real-time monitoring, and personalized therapeutic approaches, (Li et al., 2025). These requirements highlight the increasing importance of bioinformatics in cross-disciplinary science that utilizes computational methods and high-throughput data analysis to revolutionize respiratory medicine and research. Respiratory bioinformatics involves the use of computational biology, data analysis, and AI to better understand the etiology, diagnosis, treatment, and prevention of lung diseases, (Zhang et al., 2023).

This discipline combines information from an array of platforms, such as genomics, transcriptomics, proteomics, metabolomics, microbiomics, and epigenomics, to produce global insights into disease processes. The facilitating the interrogation of large and complicated datasets from patient samples, environmental exposures, imaging scans, and pathogen genomes, bioinformatics enables the identification of biomarkers, discovery of therapeutic targets, and deployment of precision medicine approaches, (Zalli et al., 2023). Over the past few years, the incorporation of multi-omics strategies in respiratory research has transformed our knowledge of the pulmonary pathophysiology. Genomic and transcriptomic profiling have revealed certain genetic variants and expression signatures implicated in asthma susceptibility, COPD phenotypes, and varying immune responses to respiratory pathogens, such as *Mycobacterium tuberculosis*, *Streptococcus pneumoniae*, and SARS-CoV-2, (Pandolfo et al., 2025). Moreover, epigenetic processes, such as DNA methylation and histone modification, have been reported to mediate gene-environment interactions that affect disease susceptibility. For instance, it has been reported that prolonged exposure to particulate matter (PM_{2.5}) and tobacco smoke can cause long-lasting changes in DNA methylation patterns, which may predispose individuals to airway

38 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/the-future-of-respiratory-bioinformatics/393268

Related Content

A Haplotype Analysis System for Genes Discovery of Common Diseases

Takashi Kido (2006). *Advanced Data Mining Technologies in Bioinformatics* (pp. 214-230).

www.irma-international.org/chapter/haplotype-analysis-system-genes-discovery/4253

K-NN Based Outlier Detection Technique on Intrusion Dataset

Santosh Kumar Sahu, Sanjay Kumar Jena and Manish Verma (2017). *International Journal of Knowledge Discovery in Bioinformatics* (pp. 58-70).

www.irma-international.org/article/k-nn-based-outlier-detection-technique-on-intrusion-dataset/178607

Interaction of Nucleic Acids: Hidden Order of Interaction

Gennadiy Vladimirovich Zhizhin (2021). *International Journal of Applied Research in Bioinformatics* (pp. 1-8).

www.irma-international.org/article/interaction-of-nucleic-acids/278747

Home Telecare, Medical Implant, and Mobile Technology: Evolutions in Geriatric Care

Vishaya Naidoo and Yedishtra Naidoo (2014). *Research Perspectives on the Role of Informatics in Health Policy and Management* (pp. 222-237).

www.irma-international.org/chapter/home-telecare-medical-implant-and-mobile-technology/78699

Genetic Diagnosis of Cancer by Evolutionary Fuzzy-Rough based Neural-Network Ensemble

Sujata Dash and Bichitrananda Patra (2016). *International Journal of Knowledge Discovery in Bioinformatics* (pp. 1-16).

www.irma-international.org/article/genetic-diagnosis-of-cancer-by-evolutionary-fuzzy-rough-based-neural-network-ensemble/171415