

# MULTI-OMICS INTEGRATION: A SYSTEMS BIOLOGY PERSPECTIVE ON HEALTH, AGRICULTURE AND THE ENVIRONMENT

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## ABSTRACT

The integration of high-throughput omics technologies with advanced bioinformatics has transformed modern biological and applied sciences. Multi-omics approaches, which combine genomics, transcriptomics, proteomics, metabolomics, epigenomics, and microbiomics, provide a holistic view of biological systems that cannot be achieved through single-omics analyses. Bioinformatics plays a critical role in managing, analyzing, and integrating these complex datasets, enabling systems-level insights into molecular mechanisms, disease pathways, and environmental interactions. This review highlights the applications of multi-omics and bioinformatics across biological sciences, medicine, agriculture, pharmaceuticals, food industries, environmental sciences, forensics, climate change research, and other applied fields. Current advancements, challenges, and future perspectives are discussed, emphasizing the importance of integrative omics in addressing global scientific and societal challenges.

**Key words:** Bioinformatics, Proteomics, Metabolomics, Metagenomics, Artificial Intelligence, Applications

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## INTRODUCTION

The rapid development of next-generation sequencing, mass spectrometry, and high-resolution analytical platforms has revolutionized life science research over the past two decades. These technologies have enabled large-scale characterization of biological molecules, leading to the emergence of omics sciences such as genomics, transcriptomics, proteomics, and metabolomics (Hasin *et al.*, 2017). However, biological systems are inherently complex, and single-omics approaches often fail to capture the dynamic interactions between different molecular layers. Multi-omics strategies aim to integrate multiple omics datasets to provide a comprehensive understanding of biological functions, regulatory networks, and phenotypic outcomes (Karczewski and Snyder, 2018). Bioinformatics and computational biology are indispensable in this context, offering tools for data integration, modeling, and interpretation.

### 1. Multi-Omics and Bioinformatics Framework

Multi-omics involves the combined analysis of multiple molecular layers within a biological system (Fig. 1). Genomics provides information about genetic variation, transcriptomics reveals gene expression patterns, proteomics identifies functional proteins, and metabolomics reflects cellular metabolic states (Misra *et al.*, 2019). Epigenomics adds another regulatory dimension by capturing heritable changes that do not alter DNA sequence, while microbiomics focuses on microbial communities and their functional roles. Bioinformatics facilitates these analyses through sequence alignment, functional annotation, pathway enrichment, network analysis, and machine-learning-based prediction models. Integration strategies such as data-driven, model-based, and network-based approaches are widely used to interpret multi-omics datasets (Subramanian *et al.*, 2020).

Multi-omics refers to the integrative study of multiple molecular layers that collectively define the structure, function, and dynamics of biological systems. Each omics field provides distinct yet complementary information, and their combined analysis enables a systems-level understanding of biological complexity (Hasin *et al.*, 2017; Karczewski and Snyder, 2018).

#### 1.1 Genomics

Genomics is the foundational omics field that focuses on the complete DNA content of an organism, including genes, regulatory elements, and structural variations. Genomic analyses involve whole-genome sequencing, exome sequencing, and genome-wide association studies to identify genetic variations linked to traits and diseases. Genomics has wide applications in evolutionary biology, disease genetics, crop improvement, and forensic identification (Metzker, 2010).

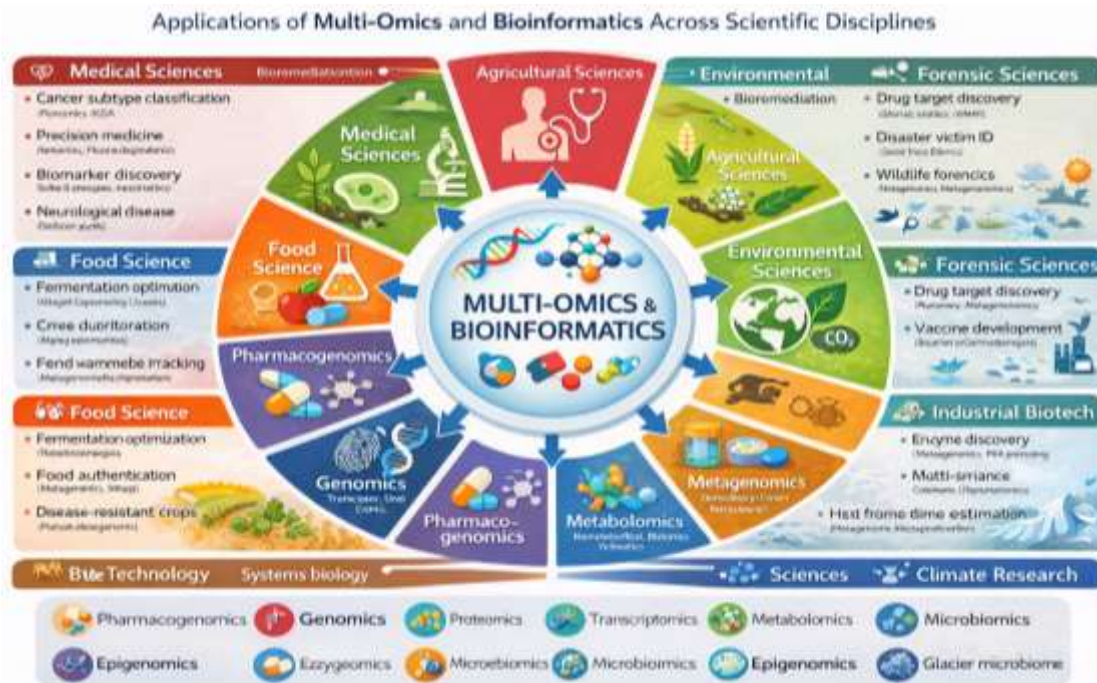


Figure 1. Overview of Omics

## 1.2 Transcriptomics

Transcriptomics examines the complete set of RNA transcripts produced by the genome under specific conditions or developmental stages. By analyzing messenger RNA and non-coding RNAs, transcriptomics provides insights into gene expression regulation and cellular responses to internal and external stimuli. RNA sequencing has become the dominant transcriptomic technique due to its high sensitivity and accuracy (Wang *et al.*, 2009).

### 1.3 Proteomics

Proteomics focuses on the large-scale study of proteins, which are the primary functional molecules in cells. It investigates protein expression levels, structures, interactions, and post-translational modifications. Since proteins directly execute biological functions, proteomics bridges the gap between genotype and phenotype (Aebersold and Mann, 2016).

### 1.4 Metabolomics

Metabolomics is the systematic analysis of small-molecule metabolites that represent the end products of cellular processes. It reflects the physiological and biochemical state of cells, tissues, or organisms. Metabolomics is widely used in disease biomarker discovery, nutritional studies, and environmental monitoring (Nicholson *et al.*, 2012).

### 1.5 Epigenomics

Epigenomics studies heritable changes in gene regulation that occur without alterations in DNA sequence. These include DNA methylation, histone modifications, and chromatin remodeling. Epigenomic modifications play critical roles in development, disease progression, aging, and environmental adaptation (Bird, 2007).

### 1.6 Microbiomics and Metagenomics

Microbiomics involves the analysis of microbial communities inhabiting various environments, including the human body, soil, water, and plants. Techniques such as 16S rRNA sequencing and shotgun metagenomics are used to study microbial diversity, composition, and function. Microbiomics has reshaped understanding of host–microbe interactions and ecosystem functioning (Turnbaugh *et al.*, 2007; Maitlo *et al.*, 2024 a).

Other emerging omics fields include lipidomics, which focuses on lipid species and signaling pathways; glycomics, which studies carbohydrate structures and functions; phenomics, which quantitatively analyzes phenotypes; and exposomics, which assesses environmental exposures throughout the lifespan. Integration of these diverse omics layers enhances predictive biology and translational research (Wishart, 2016). Based on data acquisition and integration strategies, multi-omics can be broadly categorized into horizontal multi-omics, where the same omics layer is analyzed across different conditions or species, and vertical multi-omics, where multiple omics layers are analyzed within the same biological system. Time-series and single-cell multi-omics represent advanced types that capture dynamic and cell-specific biological processes (Stuart and Satija, 2019).

## 2. Applications of Multi -omics and bioinformatics

Multi –omics and bioinformatics are widely used in different disciplines from biological sciences to environment (Fig 2). Different applications in multiple fields, related omics tools, are discussed in table 1. Some Major application across multiple fields are discussed under

### 2.1 Applications of Multi -omics in Biological Sciences

In basic biological research, multi-omics has significantly enhanced understanding of cellular organization, gene regulation, and evolutionary processes. Integrative omics studies have elucidated complex signaling pathways, transcriptional networks, and metabolic fluxes underlying development and differentiation in plants and animals (Joyce and Palsson, 2006). In microbiology, metagenomics and metatranscriptomics have revealed the structure and function of microbial communities in diverse ecosystems, shedding light on symbiosis, pathogenicity, and nutrient cycling (Handelsman, 2004; Jatt *et al.*, 2023). These approaches support systems biology by enabling predictive modeling of biological behavior.

### 2.2 Medical and Clinical Applications

The application of multi-omics in medicine has laid the foundation for precision and personalized healthcare. By integrating genomic, transcriptomic, proteomic, and metabolomic data, clinicians can stratify patients based on molecular profiles rather than clinical symptoms alone (Ashley, 2016). Multi-omics has been particularly impactful in cancer research, where tumor heterogeneity and drug resistance are major challenges. Integrative analyses have led to the identification of novel biomarkers, therapeutic targets, and prognostic signatures (Chakraborty *et al.*, 2018). In infectious diseases, genomic epidemiology and metagenomics enable rapid pathogen identification, outbreak tracking, and antimicrobial resistance surveillance.



Figure 2. Applications of Omics and Bioinformatics

### 2.3 Pharmaceutical and Drug Discovery Applications

In pharmaceutical sciences, bioinformatics and multi-omics have accelerated drug discovery and development processes. Genomics-based target identification, proteomics-guided mechanism-of-action studies, and metabolomics-driven toxicity assessments reduce attrition rates in clinical trials (Zhang *et al.*, 2021). Systems pharmacology integrates omics data with computational modeling to predict drug efficacy and adverse effects, supporting rational drug design and repurposing strategies.

### 2.4 Agricultural Sciences

Multi-omics approaches are increasingly used to improve crop productivity, resilience, and nutritional quality. Genomics-assisted breeding and transcriptomics-based stress response studies have enabled the development of crops tolerant to drought, salinity, and pests (Varshney *et al.*, 2021; Maitlo *et al.*, 2025a). In livestock and aquaculture, integrative omics enhances genetic selection, disease resistance, and feed efficiency. Microbiome analysis further supports sustainable agriculture by improving soil health and nutrient availability.

### 2.5 Food Science and Technology

In food science, multi-omics contributes to food safety, quality control, and innovation. Metabolomics and proteomics are used to detect food adulteration, allergens, and contaminants, while microbiome studies optimize fermentation processes and shelf-life stability (Cifuentes, 2020). Nutrigenomics links dietary components to gene expression and metabolic responses, facilitating the development of functional and personalized foods.

### 2.6 Industrial Biotechnology and Applied Sciences

Industrial biotechnology leverages multi-omics for metabolic engineering and synthetic biology applications. Integrated omics analyses enable optimization of microbial cell factories for the production of biofuels, enzymes, pharmaceuticals, and bioplastics (Nielsen and Keasling, 2016; Maitlo *et al.*, 2024b). Bioinformatics-driven pathway reconstruction and flux balance analysis improve process efficiency and sustainability across industrial sectors.

### 2.7 Environmental Sciences and Climate Change

Environmental applications of multi-omics include ecosystem monitoring, biodiversity assessment, and bioremediation. Metagenomics and metaproteomics identify pollutant-degrading microorganisms and assess ecosystem responses to environmental stressors (Gilbert and Dupont, 2011). In climate change research, omics approaches elucidate microbial roles in carbon and nitrogen cycling and reveal adaptive mechanisms of plants and microbes under changing climatic conditions (Trivedi *et al.*, 2020; Maitlo *et al.*, 2025b).

## 2.8 Forensic Sciences

Bioinformatics and genomics play an expanding role in forensic investigations. DNA profiling, ancestry inference, microbial forensics, and wildlife crime analysis rely heavily on computational tools (Kayser and Schneider, 2009). Epigenetic markers and transcriptomic signatures are increasingly explored for age estimation, tissue identification, and time-since-death analysis.

Table 1. Applications of Omics in different disciplines.

| Discipline      | Application                  | Related Omics / Tools   | Key Role of Multi-Omics               | References                           |
|-----------------|------------------------------|-------------------------|---------------------------------------|--------------------------------------|
| Agriculture     | Crop yield improvement       | Genomics, GWAS          | Trait-associated gene discovery       | Varshney <i>et al.</i> , 2021        |
|                 | Drought tolerance            | Transcriptomics         | Stress-responsive gene identification | Trivedi <i>et al.</i> , 2020         |
|                 | Salinity tolerance           | Ionomics, Genomics      | Adaptive trait mapping                | Munns <i>et al.</i> , 2020           |
|                 | Disease-resistant crops      | Genomics, Proteomics    | Resistance gene discovery             | Dangl <i>et al.</i> , 2013           |
|                 | Soil health assessment       | Metagenomics            | Microbial diversity profiling         | Handelsman, 2004                     |
|                 | Plant–microbe interactions   | Metatranscriptomics     | Rhizosphere functional analysis       | Mendes <i>et al.</i> , 2013          |
|                 | Livestock genomics           | Whole-genome sequencing | Genetic improvement                   | Georges <i>et al.</i> , 2019         |
|                 | Feed efficiency              | Metabolomics            | Nutrient utilization optimization     | Karisa <i>et al.</i> , 2014          |
|                 | Pest resistance              | Transcriptomics         | Defense mechanism analysis            | Hogehout <i>et al.</i> , 2018        |
|                 | Climate-smart crops          | Multi-omics integration | Yield stability under stress          | Varshney <i>et al.</i> , 2021        |
| Applied Biology | Systems biology modeling     | Multi-omics integration | Network-based biological insights     | Kitano, 2002                         |
|                 | Functional genomics          | CRISPR, RNA-seq         | Gene function annotation              | Shendure <i>et al.</i> , 2017        |
|                 | Protein–protein interactions | Proteomics              | Cellular pathway mapping              | Vidal <i>et al.</i> , 2011           |
|                 | Epigenetic regulation        | Epigenomics             | Gene expression control               | Roadmap Epigenomics Consortium, 2015 |
|                 | Single-cell biology          | scRNA-seq               | Cellular heterogeneity analysis       | Tang <i>et al.</i> , 2009            |
| Climate         | Carbon cycling               | Metagenomics            | Climate feedback modeling             | Falkowski <i>et al.</i> , 2008       |
|                 | Methane emissions            | Metatranscriptomics     | Greenhouse gas mitigation             | Conrad, 2009                         |
|                 | Permafrost thaw analysis     | Metabolomics            | Climate change impact assessment      | Mackelprang <i>et al.</i> , 2011     |
|                 | Ocean acidification          | Proteomics              | Marine ecosystem response             | Hofmann <i>et al.</i> , 2010         |
|                 | Crop resilience modeling     | Multi-omics             | Food security planning                | Varshney <i>et al.</i> , 2021        |
|                 | Plant adaptation studies     | Transcriptomics         | Climate resilience breeding           | Varshney <i>et al.</i> , 2021        |
|                 | Microbial climate feedback   | Metagenomics            | Greenhouse gas modeling               | Falkowski <i>et al.</i> , 2008       |
|                 | Ocean warming effects        | Proteomics              | Marine stress response                | Hofmann <i>et al.</i> , 2010         |

|                        |                                   |                     |                                    |                                 |
|------------------------|-----------------------------------|---------------------|------------------------------------|---------------------------------|
|                        | Desertification studies           | Multi-omics         | Ecosystem degradation assessment   | Maestre <i>et al.</i> , 2015    |
|                        | Glacier microbiomes               | Metagenomics        | Climate indicators                 | Edwards <i>et al.</i> , 2011    |
| Computational Biology  | AI-driven omics analysis          | Machine learning    | Pattern recognition                | Libbrecht and Noble, 2015       |
|                        | Network biology                   | Systems biology     | Disease module detection           | Barabási <i>et al.</i> , 2011   |
|                        | Multi-omics integration platforms | Galaxy, Cytoscape   | Data harmonization                 | Shannon <i>et al.</i> , 2003    |
|                        | Predictive modeling               | Bioinformatics      | Risk and outcome prediction        | Kreeger and Lauffenburger, 2010 |
|                        | Digital twin biology              | Multi-omics + AI    | Personalized simulations           | Viceconti <i>et al.</i> , 2016  |
|                        |                                   | Bioremediation      | Metagenomics                       | Pollutant-degrading microbes    |
| Environmental Sciences | Biodiversity monitoring           | eDNA                | Ecosystem health assessment        | Thomsen and Willerslev, 2015    |
|                        | Water quality analysis            | Metagenomics        | Pathogen detection                 | Newton <i>et al.</i> , 2015     |
|                        | Soil carbon cycling               | Metabolomics        | Climate impact modeling            | Trivedi <i>et al.</i> , 2020    |
|                        | Oil spill assessment              | Metaproteomics      | Functional microbial response      | Mason <i>et al.</i> , 2014      |
|                        | Air microbiome monitoring         | Metagenomics        | Pollution exposure assessment      | Bowers <i>et al.</i> , 2013     |
|                        | Marine microbiology               | Metagenomics        | Ocean ecosystem functioning        | Sunagawa <i>et al.</i> , 2015   |
|                        | Freshwater ecosystems             | Metatranscriptomics | Nutrient cycling analysis          | Newton <i>et al.</i> , 2011     |
|                        | Soil contamination                | Metabolomics        | Toxicity assessment                | Bundy <i>et al.</i> , 2009      |
|                        | Forest ecosystem health           | Multi-omics         | Climate resilience evaluation      | Trivedi <i>et al.</i> , 2020    |
|                        |                                   | Food authentication | Proteomics, Metabolomics           | Adulteration detection          |
| Food                   | Fermentation optimization         | Microbiomics        | Flavor and safety enhancement      | Xia <i>et al.</i> , 2015        |
|                        | Shelf-life prediction             | Metabolomics        | Spoilage monitoring                | Ellis <i>et al.</i> , 2012      |
|                        | Probiotic characterization        | Genomics            | Functional strain selection        | Marco <i>et al.</i> , 2017      |
|                        | Nutritional profiling             | Metabolomics        | Bioactive compound analysis        | Wishart, 2016                   |
|                        | Functional food development       | Nutri-genomics      | Health-promoting diet design       | Ferguson, 2009                  |
|                        | Personalized nutrition            | Metabolomics        | Individual dietary recommendations | Zeevi <i>et al.</i> , 2015      |
|                        | Foodborne pathogen tracking       | Pathogen genomics   | Food safety surveillance           | Allard <i>et al.</i> , 2016     |
|                        | Milk quality assessment           | Proteomics          | Dairy authentication               | Bendixen <i>et al.</i> , 2011   |
|                        | Meat traceability                 | DNA barcoding       | Species identification             | Ballin <i>et al.</i> , 2009     |
|                        | Forensics                         | Human               | STR genomics                       | Criminal identification         |

|                          |                                    |                                             |                                            |                                   |
|--------------------------|------------------------------------|---------------------------------------------|--------------------------------------------|-----------------------------------|
|                          | identification                     |                                             |                                            | 2009                              |
|                          | Disaster victim identification     | Genomics                                    | Mass casualty identification               | Budowle <i>et al.</i> , 2011      |
|                          | Wildlife forensics                 | DNA barcoding                               | Species identification                     | Hebert <i>et al.</i> , 2003       |
|                          | Ancestry inference                 | Population genomics                         | Biogeographical origin                     | Jobling and Gill, 2004            |
|                          | Microbial forensics                | Metagenomics                                | Source tracking                            | Budowle <i>et al.</i> , 2014      |
|                          | Microbial time-of-death estimation | Thanatobiome                                | Postmortem interval prediction             | Metcalf <i>et al.</i> , 2013      |
|                          | Soil trace evidence                | Metagenomics                                | Crime scene linkage                        | Habtom <i>et al.</i> , 2019       |
|                          | Illegal logging detection          | DNA barcoding                               | Timber origin tracing                      | Dormontt <i>et al.</i> , 2015     |
|                          | Wildlife population assignment     | Population genomics                         | Conservation law enforcement               | Ogden and Linacre, 2015           |
|                          | Bioterrorism detection             | Pathogen genomics                           | Threat identification                      | Budowle <i>et al.</i> , 2014      |
| Industrial Biotechnology | Biofuel production                 | Genomics, Metabolic modeling                | Optimization of microbial fuel pathways    | Nielsen and Keasling, 2016        |
|                          | Enzyme discovery                   | Metagenomics                                | Identification of novel biocatalysts       | Handelsman, 2004                  |
|                          | Bioplastic synthesis               | Systems biology                             | Sustainable polymer production             | Chen and Patel, 2012              |
|                          | Industrial fermentation            | Metabolomics                                | Yield and process optimization             | Villas-Bôas <i>et al.</i> , 2005  |
|                          | Synthetic biology circuits         | Genomics, Transcriptomics                   | Design of engineered organisms             | Kitano, 2002                      |
|                          | Wastewater treatment               | Metagenomics                                | Microbial community optimization           | Ju <i>et al.</i> , 2014           |
|                          | Mining biotechnology               | Metaproteomics                              | Metal bioleaching efficiency               | Rawlings, 2005                    |
|                          | Paper and pulp processing          | Enzymomics                                  | Reduction of chemical usage                | Singh <i>et al.</i> , 2017        |
|                          | Textile biotechnology              | Proteomics                                  | Eco-friendly dye degradation               | Verma <i>et al.</i> , 2021        |
|                          | Industrial probiotics              | Genomics                                    | Strain improvement                         | Marco <i>et al.</i> , 2017        |
| Medical Sciences         | Cancer subtype classification      | Genomics, Transcriptomics, Proteomics; TCGA | Tumor stratification and precision therapy | Hasin <i>et al.</i> , 2017        |
|                          | Precision medicine                 | Genomics, Pharmacogenomics                  | Personalized drug selection                | Ashley, 2016                      |
|                          | Biomarker discovery                | Proteomics, Metabolomics                    | Early disease diagnosis                    | Zhang <i>et al.</i> , 2021        |
|                          | Rare disease diagnosis             | Whole-genome sequencing                     | Identification of pathogenic variants      | Boycott <i>et al.</i> , 2013      |
|                          | Infectious disease surveillance    | Pathogen genomics, Metagenomics             | Outbreak detection and control             | Ritchie <i>et al.</i> , 2015      |
|                          | Antimicrobial resistance tracking  | Resistomics                                 | AMR gene monitoring                        | Laxminarayan <i>et al.</i> , 2013 |

|                         |                                |                              |                                            |                                         |
|-------------------------|--------------------------------|------------------------------|--------------------------------------------|-----------------------------------------|
|                         | Host–pathogen interaction      | Dual RNA-seq                 | Infection mechanism elucidation            | Westermann <i>et al.</i> , 2017         |
|                         | Autoimmune disease profiling   | Transcriptomics, Epigenomics | Immune pathway identification              | Karczewski and Snyder, 2018             |
|                         | Neurological disorder studies  | Proteomics, Metabolomics     | Molecular pathology mapping                | Johnson <i>et al.</i> , 2020            |
|                         | Cardiometabolic disease        | Metabolomics                 | Risk prediction and stratification         | Wishart, 2016                           |
| Pharmaceutical Sciences | Drug target discovery          | Proteomics                   | Identification of therapeutic targets      | Zhang <i>et al.</i> , 2021              |
|                         | Drug toxicity prediction       | Metabolomics                 | Safety assessment                          | Wishart, 2016                           |
|                         | Vaccine development            | Immunogenomics               | Antigen identification                     | Rappuoli, 2018                          |
|                         | Drug repurposing               | Systems biology              | Cost-effective therapy discovery           | Pushpakom <i>et al.</i> , 2019          |
|                         | Clinical trial stratification  | Genomics                     | Patient subgroup identification            | Ashley, 2016                            |
|                         | Biomarker validation           | Proteogenomics               | Clinical translation                       | Zhang <i>et al.</i> , 2014              |
|                         | Precision oncology             | Multi-omics                  | Personalized cancer therapy                | Hasin <i>et al.</i> , 2017              |
|                         | Drug resistance mechanisms     | Transcriptomics              | Therapy optimization                       | Holohan <i>et al.</i> , 2013            |
|                         | Nanomedicine design            | Systems biology              | Targeted drug delivery                     | Mura <i>et al.</i> , 2013               |
|                         | Pharmacometabolomics           | Metabolomics                 | Drug efficacy prediction                   | Clayton <i>et al.</i> , 2006            |
| Public Health           | Population genomics            | GWAS                         | Disease risk assessment                    | Visscher <i>et al.</i> , 2017           |
|                         | Pandemic preparedness          | Pathogen genomics            | Early warning systems                      | Gardy and Loman, 2018                   |
|                         | Microbiome epidemiology        | Metagenomics                 | Disease association mapping                | Gilbert <i>et al.</i> , 2018            |
|                         | Environmental exposure studies | Exposomics                   | Health risk evaluation                     | Wild, 2012                              |
| Space Biology           | Spaceflight omics              | Genomics, Metabolomics       | Astronaut health monitoring                | Garrett-Bakelman <i>et al.</i> , 2019   |
|                         | Microgravity adaptation        | Transcriptomics              | Cellular response analysis                 | Blaber <i>et al.</i> , 2014             |
| Translational Science   | Bench-to-bedside research      | Proteogenomics               | Clinical application                       | Rodriguez <i>et al.</i> , 2021          |
|                         | Companion diagnostics          | Genomics                     | Therapy selection                          | Ashley, 2016                            |
|                         | Precision agriculture          | Agri-omics                   | Yield optimization                         | Varshney <i>et al.</i> , 2021           |
|                         | One Health approach            | Multi-omics                  | Integrated human animal environment health | Destoumieux-Garzón <i>et al.</i> , 2018 |

### 3. Artificial Intelligence and Omics

Artificial intelligence (AI) has emerged as a critical component of modern omics research by enabling the analysis and integration of large-scale, high-dimensional datasets generated from genomics, transcriptomics, proteomics, metabolomics, and other omics platforms (Hasin *et al.*, 2017; Karczewski and Snyder, 2018). Machine

learning and deep learning approaches facilitate feature selection, pattern recognition, and multi-omics data fusion, allowing researchers to uncover complex, nonlinear relationships between molecular layers and phenotypic outcomes that are not detectable using conventional statistical methods (Ritchie *et al.*, 2015; Nam *et al.*, 2024).

Recent studies (2021–2026) demonstrate that AI-driven multi-omics frameworks significantly enhance biomarker discovery, disease risk prediction, and patient stratification in precision medicine, particularly in oncology and complex multifactorial diseases (Zhang *et al.*, 2025). Furthermore, the development of explainable AI models has improved biological interpretability by linking omics-derived signatures to regulatory networks and functional pathways, thereby supporting translational and clinical applications (Karczewski and Snyder, 2018; Nam *et al.*, 2024).

Beyond biomedical research, AI-assisted omics analyses are increasingly applied in agriculture, environmental monitoring, and microbiome studies to improve crop resilience, ecosystem modeling, and climate-related risk assessment, underscoring the broad interdisciplinary impact of AI-integrated omics approaches (Hasin *et al.*, 2017; Zhang *et al.*, 2025).

#### 4. Challenges and Future Perspectives

Despite their transformative impact, multi-omics and bioinformatics face challenges related to data integration, standardization, reproducibility, and ethical considerations. The high dimensionality of omics data demands advanced computational infrastructure and interdisciplinary expertise (Ritchie *et al.*, 2015). Future developments in artificial intelligence, single-cell and spatial omics, and cloud-based analytics are expected to further enhance integrative biological research.

#### 5. Conclusion

Multi-omics and bioinformatics have revolutionized biological, medical, agricultural, environmental, and applied sciences by enabling systems-level understanding of complex phenomena. Their broad applicability underscores their importance in addressing global challenges related to health, food security, sustainability, and climate change. Continued technological and computational advancements will further expand their impact across scientific disciplines.

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