



Perspective

Future Prospects for Omics Sciences: Expanding the Boundaries of Systems Biology

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Abstract

High-throughput omics technologies have profoundly transformed our approach to studying biological systems, enabling system-level exploration of genomes, transcriptomes, proteomes, metabolomes, and beyond. Despite these advances, current omics approaches remain limited in capturing dynamic temporal changes, preserving spatial organization within tissues, and effectively integrating multi-layered datasets into coherent biological interpretations. The aim of this review is to provide a structured and critical overview of established, emerging, and conceptual omics sciences, and to propose a unifying framework that expands the boundaries of systems biology. This review organizes established and emerging omics into a structured framework, highlighting conceptual innovations such as adaptomics, resiliomics, chrono-adaptomics, and signalomics. We discuss technological advances, computational strategies, and potential applications for research and clinical practice.

Keywords: omics sciences; multi-omics integration; systems biology; adaptomics; resiliomics; signalomics; single-cell omics; spatial omics; emerging omics; integrative biology

1. Introduction

Omics sciences refer to a collection of high-throughput disciplines that aim to comprehensively characterize classes of biological molecules within a system. These include genomics (DNA), transcriptomics (RNA), proteomics (proteins), and metabolomics (metabolites), among others. Collectively, omics approaches enable system-level investigation of biological processes by capturing global molecular profiles rather than focusing on individual components.

Over the past two decades, omics technologies have transformed the life sciences by enabling comprehensive, systems-level characterization of biological molecules and processes. Historically rooted in genomics, high-throughput sequencing first allowed researchers to decode entire genomes, laying the foundation for subsequent global analyses of transcripts, proteins, and metabolites [1,2]. This progression from analyses focusing on individual molecular layers (e.g., genomics or transcriptomics alone) to integrated multi-omics approaches represents a paradigm shift in biological research, facilitating unprecedented insights into cellular heterogeneity, tissue architecture, and organismal complexity [2,3]. High-throughput omics now encompasses a wide range of molecular layers including genomics, transcriptomics, proteomics, metabolomics, and emerging spatial and single-cell modalities, each contributing uniquely to our understanding of living systems [2,4].



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Fundamental omics fields such as genomics, transcriptomics, proteomics, and metabolomics have been extensively applied across diverse disciplines—from plant-pathogen interactions to human disease [2]. For example, omics technologies have elucidated molecular mechanisms underlying plant immunity by profiling genomic, transcriptomic, proteomic, and metabolomic changes in response to pathogenic attack [2,5]. In biomedical contexts, transcriptomic and proteomic profiling has been crucial in unraveling the cellular heterogeneity of complex disorders such as osteoarthritis, where integration of multi-omics data has identified novel biomarkers and pathways [6–9]. For example, genomics has been widely applied in genome-wide association studies (GWAS) to identify disease-associated variants, transcriptomics has enabled the characterization of gene expression changes in cancer and developmental biology, and proteomics has been used to identify biomarkers and signaling pathways in complex diseases such as Alzheimer’s disease and cancer.

Advances in single-cell omics and spatial multi-omics have further refined our capacity to dissect biological systems with high resolution. Single-cell technologies enable the characterization of individual cellular states and rare populations, revealing heterogeneity that bulk analyses obscure [10]. Spatial omics maintains the positional context of molecular profiles within tissues, linking molecular signatures with architectural features and enhancing our understanding of cellular interactions within microenvironments [11]. Together, these innovations move omics research beyond static snapshots toward dynamic, context-aware views of complex living systems.

Despite these significant advancements, fundamental challenges remain. Integration of multi-omics datasets demands sophisticated computational tools and analytical strategies to manage heterogeneity in scale, dimensionality, and data modality. Narrative reviews highlight that while statistical approaches and machine learning techniques have enabled progress in data integration, issues such as missing values, dimensionality, and data quality complicate interpretation and cross-layer synthesis [12]. As a result, the next frontier of omics science will be defined not only by novel experimental technologies but also by frameworks that contextualize temporal dynamics, environmental responses, and regulatory complexity across biological scales [13,14].

In this review, we provide a structured and critical overview of both established omics disciplines and emerging conceptual omics layers. In this context, an ‘omics layer’ refers to a distinct level of biological information (e.g., genome, transcriptome, proteome, metabolome) that can be measured independently and integrated to provide a systems-level understanding. We organize these fields into thematic chapters—including regulatory, environmental, system-specific, and integrative omics—and evaluate their current status, limitations, and future prospects. We also explore increasingly speculative domains poised to extend the limits of systems biology, emphasizing how technological innovation and conceptual expansion together shape the future of omics sciences.

In addition to established omics disciplines, this review also introduces a series of emerging and conceptual omics layers that aim to extend the current boundaries of systems biology. These conceptual omics are proposed as theoretical frameworks rather than fully established experimental disciplines, reflecting both the rapid evolution of technologies and the need for new integrative paradigms.

This review adopts a cross-disciplinary systems biology perspective, using examples from plant, microbial, and biomedical systems to illustrate generalizable principles of omics integration. The proposed emerging and conceptual omics frameworks are not intended as fully independent experimental disciplines, but rather as integrative conceptual layers that extend existing multi-omics approaches.

2. Conceptual vs. Experimental Omics: Scope and Classification

To ensure conceptual clarity, it is important to distinguish between different levels of maturity within omics sciences. Established omics disciplines, such as genomics, transcriptomics, proteomics, and metabolomics, are supported by robust experimental methodologies and standardized analytical frameworks [15]. In contrast, emerging omics fields—including single-cell omics, spatial omics, and fluxomics—are rapidly evolving with ongoing technological advancements but still face limitations in scalability and integration [16].

Beyond these domains, this review introduces a series of conceptual omics, such as adaptomics, resiliomics, and signalomics, which aim to describe higher-order biological processes, including adaptation, robustness, and cellular decision-making. These conceptual omics are proposed as theoretical frameworks rather than fully established experimental disciplines, reflecting current technological limitations and the need for integrative models in systems biology. Finally, more speculative omics domains, such as vibratomics or conscienomics, are discussed as long-term perspectives that may guide future scientific exploration.

Figure 1 summarizes the hierarchical organization and evolution of omics sciences from fundamental to integrative layers. This figure illustrates the hierarchical organization of omics sciences, from established molecular layers (genomics, transcriptomics, proteomics, metabolomics) to emerging and conceptual frameworks. Each layer represents a distinct level of biological information, while arrows indicate integration pathways across layers. The figure highlights how multi-omics approaches combine these levels to enable systems-level understanding of biological processes.

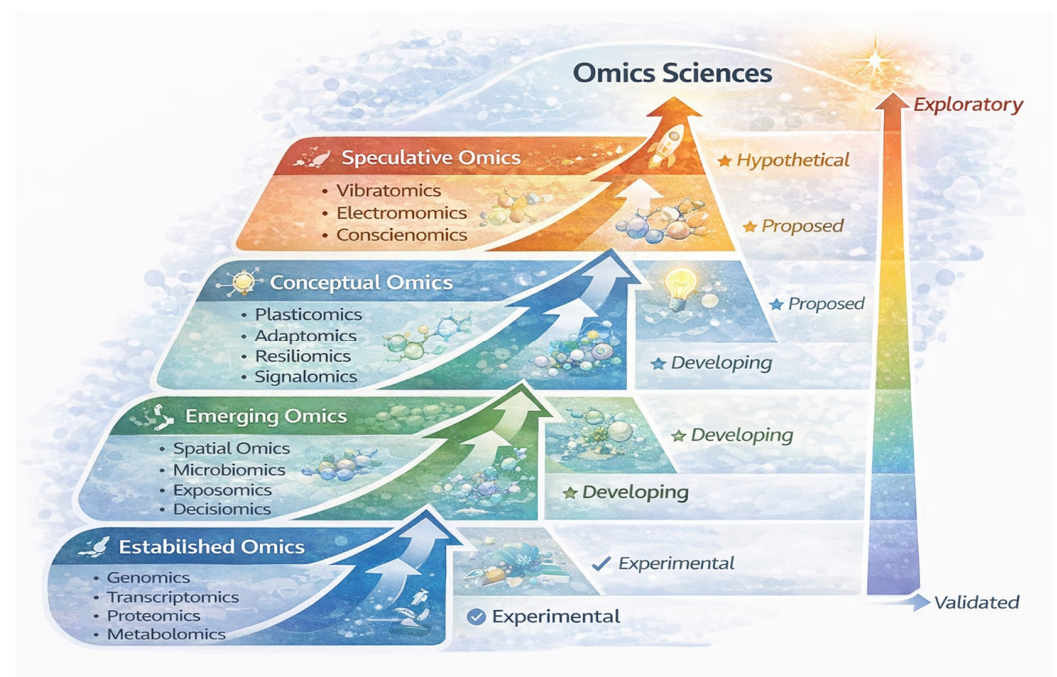


Figure 1. Future Prospects in Omics Sciences.

To avoid conceptual fragmentation, we categorize omics into four levels:

- (i) Established omics (experimentally mature),
- (ii) Emerging omics (technologically advancing),
- (iii) Conceptual omics (frameworks describing system-level processes), and
- (iv) Speculative omics (long-term perspectives).

Importantly, conceptual omics are not proposed as independent experimental layers, but as integrative abstractions that organize multi-omics data into biologically meaningful dimensions such as adaptation, resilience, and signaling.

3. Fundamental Omics (Core of Life Sciences)

The foundation of modern systems biology is built on a series of large-scale molecular profiling techniques collectively referred to as fundamental omics. These approaches aim to comprehensively catalog and quantify macromolecules—ranging from DNA to small metabolites—providing an essential framework for understanding organismal complexity. These fundamental omics layers serve as the basis upon which more specialized and integrative omics methods are developed [17,18].

3.1. Genomics

Genomics entails the systematic analysis of complete DNA sequences of organisms, capturing genetic information at the level of entire genomes [19,20]. The initial breakthrough in this field came with the sequencing of the human genome, which established a reference blueprint for human genetic variation [21]. Contemporary genomic studies extend this paradigm to diverse species, including agriculturally important plants and non-model organisms, elucidating both conserved and unique genomic features.

By identifying genetic variants such as single nucleotide polymorphisms (SNPs), copy number variations, and structural rearrangements, genomics enables researchers to link genotype with phenotype and disease susceptibility [22]. In plant sciences, comparative genomics has shed light on genomic diversity underlying stress tolerance and adaptation. For example, recent work demonstrates how integrative genomic analysis can reveal complex trait architectures in crops, highlighting genome-wide variation associated with valuable agronomic characteristics [23–26]. Such studies underscore the centrality of genomics in both basic and applied biological research [27–32].

3.2. Transcriptomics

While genomics provides the static blueprint of potential biological function, transcriptomics captures the dynamic expression of genes across time, tissues, and conditions by quantifying RNA molecules [33–35]. Transcriptomic profiling includes bulk RNA sequencing (RNA-seq), which measures average gene expression across populations of cells, and single-cell RNA-seq, which resolves gene expression at the resolution of individual cells. More recently, spatial transcriptomics technologies have emerged, preserving the spatial context of RNA expression within tissue architecture [36,37]. For instance, technologies such as 10× Genomics Visium and MERFISH enable spatially resolved gene expression profiling, allowing researchers to map transcriptional activity within tissue architecture. These approaches have been applied in tumor microenvironment studies and brain tissue organization.

Transcriptomics is widely used to map tissue heterogeneity, characterize disease microenvironments, and identify regulatory networks driving biological processes. For example, spatial mapping of transcripts in tumor tissues has advanced our understanding of cellular interactions in immuno-oncology, providing insight into microenvironmental influences on therapy response [38–42]. Emerging spatial methods further link transcript expression to histological features, enabling a more integrated view of tissue biology [42–45].

3.3. Proteomics

Whereas transcriptomics reflects the potential for protein synthesis, proteomics directly measures the expressed protein complement of a cell or tissue, including post-translational modifications (PTMs) that regulate protein activity, localization, and interactions. Mass

spectrometry (MS) has become the cornerstone of quantitative proteomics, offering high-throughput identification and quantification of thousands of proteins in complex biological samples [46–50].

Proteomic profiling facilitates functional annotation of genomes, identification of protein complexes, and discovery of biomarkers associated with physiological states and diseases. The development of advanced MS platforms with increased sensitivity and dynamic range has expanded proteomic depth, allowing detection of low-abundance proteins and diverse PTMs. Proteomics thus provides a critical functional layer, linking gene expression to biochemical activity [15,48].

3.4. Metabolomics

Completing the fundamental omics suite, metabolomics focuses on the comprehensive profiling of small molecules (metabolites) that represent the end products of cellular processes (Table 1). Because metabolites are directly tied to biochemical reactions and cellular physiology, metabolomic signatures provide a functional readout of metabolic activity and phenotypic state [51–54].

Table 1. Core Omics Overview.

Omics	Target Molecule	Technology	Output	Applications
Genomics	DNA	NGS	Variants	Evolution, breeding
Transcriptomics	RNA	RNA-seq	Expression	Regulation
Proteomics	Proteins	MS	Abundance/PTMs	Function
Metabolomics	Metabolites	LC-MS/NMR	Metabolic profile	Phenotype

Metabolomics employs technologies such as liquid chromatography-mass spectrometry (LC-MS) and nuclear magnetic resonance (NMR) spectroscopy to capture the diversity of metabolites within biological samples. These profiles can reveal disruptions in metabolic pathways associated with disease, stress responses, or environmental adaptation. Unlike genomic and transcriptomic measures, which reflect potential biological activity, metabolomics reflects realized biochemical function, making it a powerful tool for phenotype characterization and biomarker discovery [54–56].

This table summarizes major omics categories, their measurable biological features, associated technologies, and representative applications. The ‘Examples’ column provides real-world use cases illustrating how each omics approach has been applied in research and clinical contexts.

4. Functional and Structural Omics

While fundamental omics describe static inventories of molecules, functional and structural omics (Figure 2) aim to characterize how biomolecules interact, change conformation, and carry out coordinated functions within complex systems [18,54,57]. These layers provide insights into dynamic regulatory networks, post-translational modifications, and emergent properties that cannot be deduced from sequence alone. These approaches leverage advancements in interactomics, quantitative mass spectrometry, high-resolution structural biology, and emerging real-time imaging techniques to bridge genotype and phenotype at a mechanistic level [58,59].

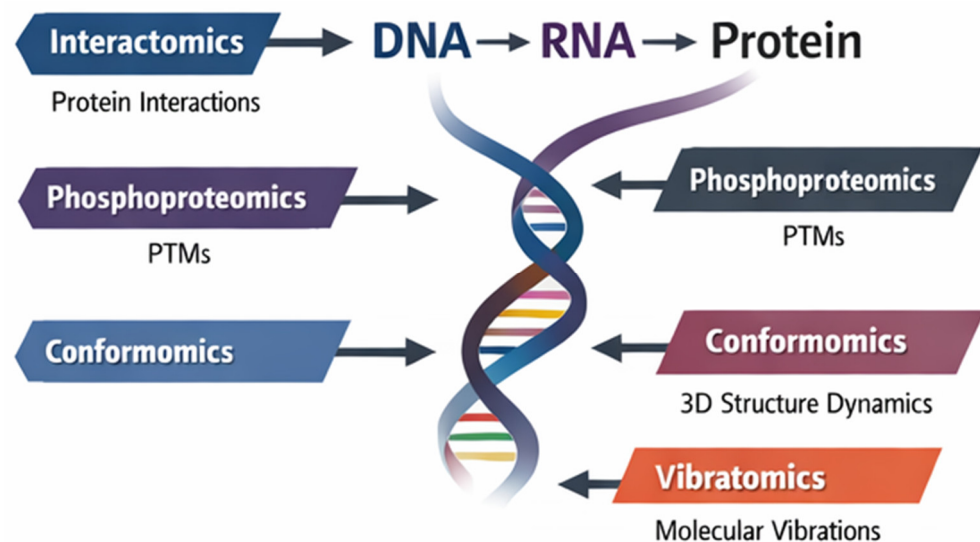


Figure 2. Functional Layers Beyond Central Dogma.

This figure illustrates the integration of multiple omics layers into a unified systems biology framework. Each layer represents a distinct biological dimension, while connecting arrows indicate interactions and data integration pathways. The figure emphasizes the transition from single-omics analysis to multi-omics and integrative modeling.

4.1. Interactomics

Interactomics encompasses the systematic mapping of molecular interactions, including protein–protein, protein–DNA, and protein–RNA networks. High-throughput affinity purification coupled to mass spectrometry (AP-MS), yeast two-hybrid screens, and cross-linking methods now enable large-scale reconstruction of interactomes, revealing how biomolecules assemble into functional complexes [60,61]. The unbiased characterization of interaction networks has shed light on cellular signaling crosstalk, the modular organization of pathways, and the rewiring of networks in disease states [62,63].

For example, integrated protein–protein and protein–RNA interactome maps have recently been used to dissect signaling networks involved in immune cell activation and differentiation, illustrating how perturbations in interactomes can underlie pathological phenotypes [64–66]. These network maps are increasingly used in systems biology modeling to predict functional dependencies and regulatory bottlenecks [64–66].

4.2. Phosphoproteomics & Glycomics

Post-translational modifications (PTMs) add an essential layer of functional regulation that cannot be inferred from genomic or transcriptomic data alone. Phosphoproteomics quantitatively profiles phosphorylation events across thousands of sites, enabling characterization of kinase activity and signaling cascades. Recent advancements in high-resolution mass spectrometry have improved phosphoproteome coverage, allowing temporal profiling of dynamic signaling responses, such as stress adaptation and drug responses in cancer cells [67–69].

In parallel, glycomics addresses the complex landscape of glycosylation patterns on proteins and lipids. Glycosylation modulates protein folding, stability, and cell–cell interactions, and its dysregulation is implicated in cancer progression, immunity, and developmental disorders. Recent analytical platforms combining liquid chromatography, lectin arrays, and advanced mass spectrometry have expanded glycan structural resolution, facilitating mapping of glycosylation signatures associated with disease [70–72].

4.3. Lipidomics

Lipidomics provides comprehensive characterization of lipid species, which play essential roles in membrane architecture, energy storage, and signaling. The lipidome comprises thousands of structurally diverse molecules, including glycerophospholipids, sphingolipids, sterols, and fatty acids. Advances in shotgun lipidomics and ion mobility mass spectrometry enable high-throughput quantification of lipid classes across tissues and conditions [73–75].

Recent lipidomic studies have revealed condition-specific lipid remodeling in metabolic diseases and during cellular stress responses, underscoring the role of lipids not only as structural components but also as bioactive mediators of inflammation and metabolic regulation [76–78].

4.4. Structural Omics

Structural omics extends traditional functional layers by examining the three-dimensional conformation and physical dynamics of biomolecules, thereby linking structure with function (Table 2).

Table 2. Functional vs. Structural Omics.

Category	Omics	Measured Feature	Status
Functional	Interactomics	Networks	Established
Functional	Phosphoproteomics	PTMs	Advanced
Structural	Conformomic	3D dynamics	Emerging
Speculative	Vibratomics	Vibrations	Hypothetical

4.4.1. Conformomics

Conformomic refers to the systematic characterization of dynamic conformational states of proteins and nucleic acids. Unlike traditional structural biology focused on static snapshots (e.g., X-ray crystallography), conformomics exploits techniques such as cryo-electron microscopy (cryo-EM), nuclear magnetic resonance (NMR), and hydrogen–deuterium exchange mass spectrometry (HDX-MS) to capture ensembles of conformations [79–83]. Recent computational tools like AlphaFold2 not only predict static structures with high accuracy but also facilitate exploration of conformational landscapes and folding intermediates, enabling deeper functional interpretation of proteomes [79–83].

4.4.2. Vibratomics (Speculative)

Vibratomic is a speculative conceptual model that seeks to characterize *biologically relevant molecular vibrations* at the quantum–biological interface. Emerging spectroscopic technologies (e.g., two-dimensional infrared spectroscopy) allow probing of vibrational modes associated with protein function and solvation dynamics. While still far from routine omics application, the idea of integrating vibrational signatures into systems biology could one day provide insight into energetics and conformational flexibility at a level beyond standard structural analyses [84,85].

4.4.3. Electromomics (Speculative)

Electromomic represents another forward-looking concept focused on intracellular electromagnetic fields as potential regulators of molecular communication. Living cells maintain ion gradients and electrical potentials that influence processes such as membrane transport and signal transduction. Although direct high-throughput measurement of intracellular electric fields remains technologically challenging, advances in nanoscale

sensors and voltage-sensitive probes may one day enable profiling of bioelectrical states as an integrated molecular layer [86,87].

Both vibratonic and electromomic remain speculative, but they underscore a growing interest in expanding omics beyond chemical inventories to include physical and biophysical dimensions of living systems.

Selected References for Functional and Structural Omics:

1. Interactomics:
 - Comprehensive interactome mapping in immune systems highlights functional network reorganization [62].
 - Protein–RNA interaction networks reveal signaling dependencies [88,89].
2. Phosphoproteomics/Glycomics:
 - Advances in phosphoproteomics reveal signaling dynamics in drug response [90–92].
 - Glycan structural profiling and disease associations [93,94].
3. Lipidomics:
 - Lipid remodeling in metabolic stress and disease [77].
 - High-throughput lipidomics and analytical innovation [95].
4. Structural Omics:
 - Cryo-EM and AlphaFold2 expand conformational landscape analysis [80].

5. Regulatory and Control Omics

Unlike classical omics that quantify molecular abundance, the following regulatory omics frameworks focus on dynamic system properties such as signaling, adaptation, and stability. These layers are derived from time-resolved and multi-omics datasets, rather than representing independent measurement technologies.

Regulatory and control omics encompass molecular layers that govern the dynamic regulation (Figure 3, Table 3), signaling processes, adaptive decision-making, and robustness of biological systems. Beyond static descriptions of molecular abundance, these omics aim to capture mechanisms by which cells interpret internal and external cues, modulate gene expression programs, and maintain functional integrity in response to perturbations [96,97]. Recent advances in high-resolution imaging, longitudinal sampling, and computational modeling enable the emergence of novel frameworks that expand the boundaries of traditional regulatory biology [98,99].

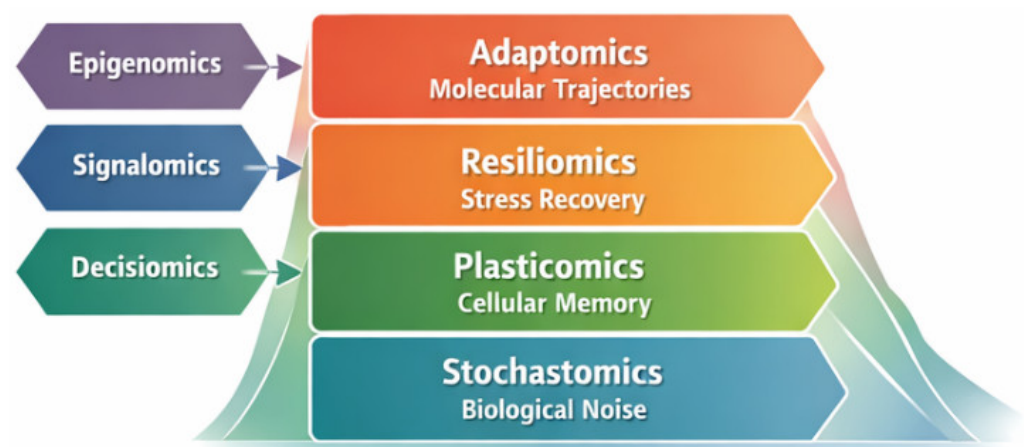


Figure 3. Regulatory Omics Framework.

Table 3. Emerging Regulatory Omics.

Omics	Measures	Type	Maturity	Key Application
Adaptomics	Trajectories	Dynamic	Emerging	Stress biology
Resiliomics	Recovery	System	Emerging	Robustness
Chrono-adaptomics	Time	Temporal	Emerging	Circadian
Plasticomics	Memory	Adaptive	Conceptual	Priming

5.1. Epigenomics

Epigenomics refers to the genome-wide profiling of heritable and dynamic regulatory modifications that impact gene expression without altering nucleotide sequence. Key epigenomic marks include DNA methylation, histone post-translational modifications (e.g., acetylation, methylation), and chromatin accessibility [100,101]. These layers collectively shape the regulatory landscape by determining how DNA is packaged and accessed by transcriptional machinery. Techniques such as bisulfite sequencing and ATAC-seq have enabled precise quantification of these features, revealing their pivotal roles in development, cellular differentiation, and disease pathogenesis [102,103]. Integrative epigenomic analyses have been especially impactful in cancer research, where aberrant methylation and chromatin states drive oncogenic programs [104,105].

5.2. Signalomics (Emerging)

Signalomics is an emerging conceptual omics layer that seeks to systematically characterize the dynamic signaling processes within cells. Unlike conventional omics focused on molecular abundance, signalomics encompasses the temporal patterns of intracellular signals mediated by second messengers such as Ca^{2+} , cAMP, diacylglycerol, and kinase cascade activation. With the advent of live-cell imaging, fluorescent biosensors, and high-throughput kinetic assays, it is now feasible to quantify signaling dynamics at high temporal resolution [106–108]. These data provide insights into how cells interpret gradients, stressors, and developmental cues. Because cellular decision-making is intimately tied to signaling dynamics, signalomics represents a critical frontier in understanding regulatory networks [109,110].

5.3. Decisiomics

Decisiomics focuses on the molecular and network processes that underlie cellular decision-making, such as lineage commitment, apoptosis, quiescence, and cell cycle transitions. Rather than cataloging expression levels, decisiomics investigates functional thresholds, bistability, and attractor states that govern phenotypic switches [111,112]. For example, the interplay between transcription factors and feedback loops can determine whether a hematopoietic progenitor differentiates along one lineage or another. Systems biology approaches integrating transcriptomic, proteomic, and dynamic modeling data are essential to capture these decision landscapes, and decisiomics formalizes this regulatory dimension [113–115].

5.4. Adaptomics

Adaptomics is proposed as a new omics framework for systematically characterizing molecular adaptation trajectories in response to dynamic environmental stress. Traditional omics often capture static states at single time points, limiting insights into adaptation processes that unfold over time [13]. Adaptomics addresses this by integrating longitudinal multi-omics profiles (transcriptomics, proteomics, metabolomics) collected across multiple perturbation phases. This approach allows the quantification of trajectory features, such as

the speed and direction of molecular response, decoupling transient stress responses from sustained adaptive changes.

- What it measures:

Adaptomics quantifies molecular trajectories: changes in gene expression, protein abundance, and metabolite levels as a function of environmental challenges (e.g., temperature shifts, nutrient limitations, pathogen attack). Such data can distinguish immediate stress responses from later adaptive states.

- Experimental approaches:

Adaptomic studies require controlled perturbations with multi-timepoint sampling, coupled with longitudinal multi-omics data acquisition. Computational modeling—such as trajectory inference, dynamic network reconstruction, and time-series clustering—is essential to extract adaptive features.

- Scientific value:

Adaptomics differentiates response vs. adaptation, offering insights into resilience, plasticity, and evolutionary strategies. It has broad relevance across plants (abiotic and biotic stress), microbial ecology (adaptation to changing environments), and disease (adaptive drug resistance).

We propose the concept of adaptomics as a system-level framework to characterize dynamic molecular trajectories underlying biological adaptation to environmental constraints.

Adaptomics builds on concepts from temporal multi-omics and dynamic systems biology to provide a temporal dimension often missing in conventional studies [116].

5.5. Resiliomics

Résiliomic expands regulatory omics by focusing on the ability of biological systems to absorb disturbances and return to functional equilibrium—a property often referred to as resilience. While traditional stress-response studies emphasize peak responses, resiliomics quantifies recovery kinetics, amplitude of perturbation effects, and network stability over time.

- What it measures:

Key metrics include time to baseline recovery, magnitude of deviation from homeostasis, and robustness of interaction networks under stress.

- Data sources:

Time-series transcriptomics, proteomics, and targeted metabolomics provide the core datasets. Network analysis and stability metrics (e.g., eigenvalues of interaction matrices) help assess resilience.

- Applications:

Resiliomics has implications for understanding tolerance mechanisms in plants (e.g., drought recovery), human health (recovery after inflammation or therapy), and ecological robustness.

Resiliomics provides a quantitative framework to assess biological robustness beyond classical stress-response analyses.

Conceptually, resiliomics synthesizes stress physiology and systems biology, offering quantitative resilience metrics previously explored in ecology and engineering disciplines [117].

5.6. Chrono-Adaptomics

Chrono-adaptomics bridges chronobiology and adaptomics by examining how temporal rhythms (e.g., circadian, ultradian, seasonal cycles) influence adaptive molecular responses. Circadian clocks orchestrate gene expression and metabolic fluxes, modulating a cell's capacity to perceive and react to environmental stressors. By combining timeline-based omics (e.g., sampling at defined circadian phases) with adaptive trajectories, chrono-adaptomics reveals how temporal gating impacts adaptive efficiency and outcome.

- What it measures:

Circadian clock outputs, phase-specific gene networks, time-dependent response amplitudes, and temporal plasticity metrics.

This emerging framework leverages developments in time-resolved omics and rhythmic biology to understand how biological clocks shape adaptation and resilience [118,119].

5.7. Plasticomics

Plasticomic refers to the global analysis of molecular plasticity—the capacity of a system to modify its state in response to repeated perturbations. While adaptomics focuses on single adaptation trajectories, plasticomics examines changes in responsiveness across repeated stimuli (e.g., priming, cellular memory). This includes comparing primary responses (first exposure) with secondary responses (subsequent exposures), revealing mechanisms of acclimation and molecular memory.

- Importance:

Plasticity underpins learning, immune training, stress tolerance, and developmental flexibility—domains where plasticomic profiling can yield mechanistic insights [120,121].

5.8. Stochastomics

Stochastomics addresses the random variability in gene expression and molecular processes, often framed as biological noise. Even genetically identical cells in identical environments can exhibit heterogeneous expression due to stochastic transcriptional bursting, variable promoter states, and noisy signaling pathways [122,123]. Quantifying this variability at scale—via single-cell transcriptomics and proteomics—provides insight into how noise influences phenotype, fate decisions, and population dynamics [124].

Regulatory and control omics extend beyond static molecular measurements to interrogate how biological systems respond, adapt, decide, and maintain stability under internal and external perturbations. Emerging frameworks such as signalomics, adaptomics, resiliomics, chrono-adaptomics, and plasticomics exemplify future directions poised to deepen our mechanistic understanding of regulatory dynamics.

5.9. Integration of Regulatory Omics into Multi-Omics Frameworks

The integration of regulatory omics into systems biology relies on combining longitudinal multi-omics datasets with computational modeling. Rather than generating independent datasets, frameworks such as adaptomics and resiliomics are derived from existing omics layers (transcriptomics, proteomics, metabolomics) through temporal and network-based analyses.

Key integration strategies include:

- Time-series modeling: capturing dynamic trajectories of molecular responses.
- Network inference: reconstructing regulatory and signaling interactions.
- Trajectory analysis: identifying adaptive pathways and system transitions.
- Machine learning approaches: integrating heterogeneous datasets across scales.

These approaches allow regulatory omics to act as higher-order descriptors of biological systems rather than standalone measurement layers.

The implementation of regulatory omics requires substantial computational resources, including high-performance computing, cloud-based infrastructures, and advanced machine learning algorithms. The analysis of longitudinal multi-omics datasets is computationally intensive due to high dimensionality, temporal complexity, and data heterogeneity. Current approaches rely on scalable architectures and optimized algorithms, while future developments will likely depend on artificial intelligence and distributed computing frameworks.

6. Environmental and Ecological Omics

Environmental and ecological omics are included to illustrate that systems biology principles extend beyond individual organisms to organism–environment interactions. These examples serve to demonstrate the scalability of omics frameworks rather than to shift the focus of the review.

The application of omics technologies has catalyzed a paradigm shift in how environmental and ecological processes are studied (Figure 4), enabling researchers to move beyond isolated variables and toward integrated, system-level understandings of organism–environment interactions [125–127]. Traditional ecological studies have long recognized the complexity of biotic and abiotic interactions, but multi-omics approaches now allow these relationships to be probed at molecular, cellular, and community scales simultaneously [128–130]. Such approaches have proven essential for unraveling the mechanisms by which organisms and ecosystems respond to climate variability, pollution, and human-induced habitat transformations [131,132].

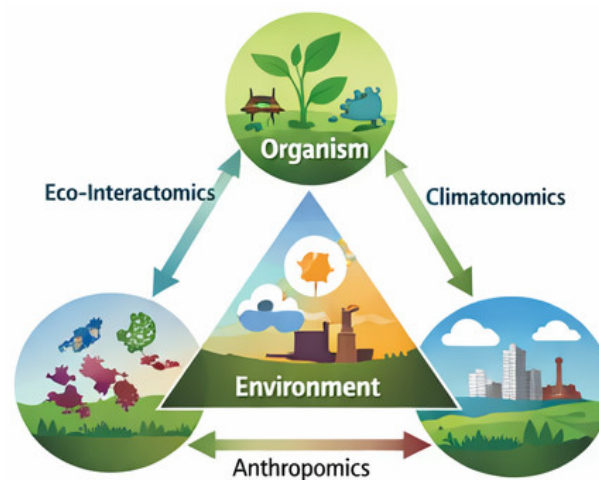


Figure 4. Organism–Environment Omics Interface.

This framework is conceptually aligned with the One Health paradigm, which integrates human, animal, and environmental health into a unified systems perspective.

6.1. Eco-Interactomics

Ecological systems are defined by intricate interactions among organisms, their associated microbiomes, and surrounding environmental matrices such as soil and climate [133]. Omics technologies—including metagenomics, metatranscriptomics, proteomics, and metabolomics—have revolutionized the study of such plant–microbe–soil networks, revealing complex interdependencies that underlie nutrient cycling, stress tolerance, and ecosystem function [33,134]. These tools facilitate simultaneous profiling of multiple bi-

ological domains, enabling holistic views of community structure and function across ecological gradients.

For example, multi-omics analyses have illuminated molecular dialogues between crop plants and beneficial microorganisms, linking microbial taxa and plant genes to enhanced nutrient uptake and stress resilience, with direct implications for sustainable agriculture and soil health [33,135]. Similar approaches have been used to dissect the biochemical influence of invasive species on soil microbiomes and ecosystem dynamics, enhancing predictive models of ecological responses to perturbations [136].

6.2. *Climatonomics*

Climate change represents a dominant driver of environmental stress across ecosystems, affecting organismal physiology, community assembly, and biogeochemical cycles [137]. Omics methods provide powerful means to quantify and interpret these changes at multiple biological levels. Recent research has shown that plant–microbiome interactions—critical for host adaptation under stress—are significantly modulated by climatic factors such as elevated CO₂, warming, and drought [138–140].

Moreover, omics technologies are increasingly applied to marine and terrestrial organisms to understand molecular adaptations to climate stress [141,142]. These include the identification of climate-tolerant genetic variants, stress-responsive metabolic pathways, and epigenetic modifications that enable phenotypic plasticity under rapid environmental change. Such multi-layered insights are fundamental for forecasting ecological outcomes under future climate scenarios and for designing strategies that enhance resilience in vulnerable species and communities [143–146].

6.3. *Anthropomics*

Human activities have dramatically reshaped ecosystems around the globe, with urbanization, industrialization, and agricultural intensification exerting profound impacts on biodiversity, habitat structure, and ecosystem services [147]. Anthropogenic stressors—from air and soil pollution to land-use change—influence organisms at molecular, physiological, and population levels. For example, urban air pollutants such as ozone, nitrogen oxides, and particulate matter trigger complex stress responses in plants that are increasingly being characterized through transcriptomic and metabolomic profiling [148].

Omics-based environmental assessments have also improved our understanding of how contaminants affect microbial community dynamics and the capacity of ecosystems to degrade pollutants through bioremediation processes. These insights not only reveal mechanistic responses to anthropogenic stressors but also inform risk assessment frameworks aimed at safeguarding ecological and human health [125].

At larger scales, anthropogenic land-use changes such as deforestation, urban sprawl, and agricultural expansion contribute to biodiversity loss, ecosystem fragmentation, and altered nutrient cycles, fundamentally altering ecosystem functioning [148]. These complex, multi-factorial impacts underscore the importance of integrative omics frameworks to disentangle organismal responses from broader environmental change and to support sustainable ecosystem management.

7. System-Specific Omics

While foundational and integrative omics approaches have provided broad insights into biological regulation (Table 4), a growing body of research focuses on system-specific omics, targeting particular biological systems or organismal interactions [58,149]. These specialized layers of omics science enable researchers to decode the molecular complexity inherent to specific physiological domains, from neural networks to microbial ecosystems.

Table 4. System-Specific Omics Domains.

Field	Biological System	Key Technologies	Applications
Neuro-omics	Brain	Spatial omics	Neurodegeneration
Immunomics	Immune system	RepSeq	Vaccines
Microbiomics	Microbiota	Metagenomics	Health
Mycomics	Fungi	Multi-omics	Biotechnology

7.1. *Neuro-Omics*

Neuro-omics encompasses the application of high-throughput omics techniques to the nervous system, integrating molecular profiles with structural and functional neural data [150–152]. Traditional genomics and transcriptomics have been complemented by proteomic, metabolomic, and spatial omics technologies to map molecular networks associated with brain function and disease. For example, multi-omic integration combined with imaging modalities such as MRI and PET has been used to construct multi-molecular brain maps, revealing molecular signatures that correlate with neurodegenerative processes and highlighting potential therapeutic targets for brain diseases [153]. This integrative approach demonstrates how omics technologies can elucidate complex neural mechanisms that would remain inaccessible via reductionist methodologies [154].

7.2. *Immunomics*

Immunomics refers to global profiling of the immune system, including the characterization of antibody and T-cell receptor repertoires, signaling networks, and functional responses of immune cells. High-throughput sequencing of adaptive immune receptors (Rep-Seq) has expanded our understanding of B and T cell diversity, enabling detailed mapping of immune repertoire landscapes that reflect host responses to infection, vaccination, and disease [155,156]. Comprehensive immune profiling through multi-omics integration—including transcriptomics, proteomics, and functional assays—provides insights into immune cell differentiation and function, as well as cell-type-specific regulatory networks [157]. These combined analyses are pivotal for advancing precision immunology and therapeutic development.

7.3. *Microbiomics and Viromics*

Microbiomics and viromics leverage omics technologies to characterize microbial communities and viral populations, respectively, in complex environments such as the gut, soil, and host tissues [158,159]. Microbiomics integrates metagenomics, metatranscriptomics, metaproteomics, and metabolomics to reveal both taxonomic composition and functional potential of microbial ecosystems [160–162]. Such integrated meta-omics approaches have been instrumental in linking microbiome dynamics with host phenotypes, metabolic activities, and disease states, often employing machine learning to extract clinically relevant patterns from high-dimensional data [163].

Similarly, viromics combines multi-omics and bioinformatics to study viral diversity, dynamics, and host interactions within ecosystems. In veterinary and infectious disease research, multi-omics strategies have enhanced understanding of viral pathogenesis and host responses, paving the way for novel antiviral interventions [164,165].

7.4. *Mycomics*

Mycomics applies omics technologies specifically to fungal biology, probing the functional roles and dynamics of fungal communities [166]. Fungi represent a diverse kingdom with key ecological, industrial, and clinical importance [167–169]. Omics approaches—spanning genomics, transcriptomics, proteomics, and metabolomics—enable comprehen-

sive characterization of fungal genomes, expression patterns, and metabolite profiles, thereby uncovering mechanisms of enzyme production, environmental adaptation, and symbiotic interactions [33,138,170]. These analyses facilitate both basic fungal biology and biotechnological applications, such as enzyme discovery and bio-product development. Although formal reviews on mycomics are less numerous than for bacterial microbiomes, emerging literature highlights the value of integrating multiple omic layers to unravel fungal complexity and functional contributions [171–174].

System-specific omics disciplines extend high-throughput molecular profiling into targeted biological domains, offering fine-grained insights that complement broader multi-omics frameworks. By dissecting the molecular infrastructure of neural networks, immune landscapes, microbial communities, and fungal ecosystems, these specialized omics approaches contribute to a deeper understanding of biological specificity and complexity, with translational potential across medicine, ecology, and biotechnology.

8. Advanced Molecular Omics

The following speculative omics are presented as conceptual extensions rather than fully defined disciplines, and their inclusion is intended to illustrate possible future directions rather than immediate research priorities. Recent advances in high-resolution measurement technologies have expanded the frontier of omics beyond population-level analyses, enabling interrogation of biological systems at unprecedented scales of resolution and complexity [6,13]. This section highlights the major developments in advanced molecular omics, spanning from single-cell profiling to speculative information-based frameworks that may guide the next generation of systems biology (Figure 5, Table 5).

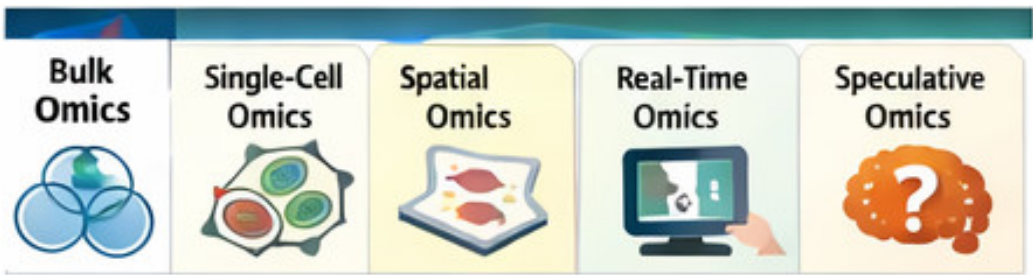


Figure 5. Resolution Scale in Omics.

Table 5. Advanced & Speculative Omics.

Omics	Dimension	Measurable Today?	Technology
Single-cell	Cellular	Yes	scRNA-seq
Spatial	Tissue	Yes	Visium
Fluxomics	Dynamic	Yes	Isotope tracing
Energomics	Energy	No	Future
Thermomics	Heat	No	Emerging
Bioenergetic omics	Energy integration	No (Emerging)	Future biosensors

8.1. Single-Cell Omics

Single-cell omics has revolutionized our understanding of cellular heterogeneity by enabling genomic, transcriptomic, proteomic, and epigenomic profiling at the level of individual cells [175–177]. Traditional bulk assays average signals over heterogeneous cell populations, masking critical variation among individual cells [175–178]. Single-cell transcriptomics, propelled by droplet-based and plate-based platforms, has unveiled rare cell states, lineage hierarchies, and dynamic cellular responses in development, immunity,

and disease [179–182]. More recently, single-cell multimodal approaches integrate gene expression with chromatin accessibility or protein abundance, providing richer, multi-layered insights into cellular state transitions [183,184]. These technologies have revealed, for example, regulatory programs underlying tumor heterogeneity and immune cell diversification in cancer and infection [183,184].

8.2. Spatial Omics

Spatial omics preserves the physical context of molecular measurements within tissues, maintaining the positional information that is essential for understanding cellular interactions and microenvironments [185]. Techniques such as spatial transcriptomics, imaging mass cytometry, and in situ sequencing enable localized mapping of RNA and protein distribution directly in tissue sections [186]. These advances integrate histological structure with molecular phenotypes, bridging molecular biology and tissue architecture [187]. Spatial omics has been transformative in neuroscience, cancer biology, and developmental biology by revealing how spatial context shapes gene regulation, cell–cell communication, and tissue organization [188].

8.3. Fluxomics

Fluxomics focuses on dynamic metabolic flux analysis—the rates at which metabolites are produced, consumed, and transformed within the cell—rather than static abundance measurements [189]. By using stable isotope tracers detected via mass spectrometry or NMR, fluxomics quantifies metabolic pathway activity, providing functional insight into the kinetic organization of metabolism [190,191]. This layer is important for understanding cellular energy allocation, metabolic adaptations to stress, and rewiring in disease states such as cancer and metabolic disorders. Fluxomics complements metabolomic snapshots by linking metabolite profiles to pathway dynamics and physiological responses [192,193].

8.4. Phenomics

Phenomics encompasses large-scale phenotypic mapping that links genotypes and molecular phenotypes to observable traits at organismal and cellular levels [194]. High-throughput phenotyping platforms measure complex traits including morphology, growth kinetics, physiology, and behavior across genetic populations or environmental conditions [195,196]. In agriculture, phenomics accelerates breeding by connecting genomic variation with drought tolerance, yield, and nutrient use efficiency. In biomedical research, phenomic profiling enables systematic characterization of drug responses, developmental defects, and disease progression [195,196]. The integration of phenomics with other omics layers enriches genotype–phenotype mapping and predictive modeling [197].

8.5. Energomics, Thermomics, Pressiomics and Bioenergetic Omics (Emerging)

At the frontier of speculative omics, energy-centric layers aim to quantify physical and biophysical constraints within cells:

Energomics seeks to characterize cellular energy fluxes and distributions of high-energy molecules (e.g., ATP, proton gradients) across physiological states [198].

Thermomics investigates micro-thermal fluctuations and thermodynamic gradients within cellular compartments, potentially linking metabolic activity with localized heat production [199,200].

Pressiomics contemplates mechanical pressures and forces at microscopic scales, such as membrane tension, intracellular crowding, and mechanotransductive stresses [201].

Bioenergetic omics is an emerging conceptual framework aimed at integrating cellular energy production, distribution, and utilization across biological systems. Unlike traditional metabolomics or fluxomics, which capture metabolic intermediates or path-

way dynamics, bioenergetic omics seeks to unify energetic processes—including ATP flux, mitochondrial function, redox balance, and thermodynamic constraints—into a coherent systems-level layer.

This framework has the potential to serve as an integrative axis linking multiple omics layers, as energy availability fundamentally constrains gene expression, protein activity, and metabolic fluxes. Advances in live-cell imaging, biosensors, and computational modeling may enable future quantification of bioenergetic states at high resolution.

Conceptually, bioenergetic omics complements emerging fields such as signalomics by providing a unifying energetic context for molecular decision-making and adaptation.

Although current technologies do not yet provide direct, multiplexed measurement frameworks for these physical parameters across entire cell populations, emerging methods in biophysics and live-cell imaging suggest that future advances may render these dimensions tractable. These speculative omics expand the conceptual space of biological measurement to include energy, heat, and force as dimensions of cellular systems.

8.6. Information-Based Omics

In parallel with molecular profiling, information-centred omics frameworks emphasize the organization, processing, and encoding of biological information beyond linear sequences:

Infomics focuses on the flow and processing of biological information within cellular networks, including signaling cascades, gene regulatory circuits, and feedback loops. This perspective aligns with information theory frameworks applied to transcriptional regulation and cellular decision-making [202].

Codomics extends the concept of biological codes beyond the genetic code to include epigenetic, histone modification, and glycan coding systems that influence molecular interactions and phenotypes [203].

Algorithmiomics proposes the study of intrinsic biological logic and computation—measuring the algorithmic or rule-based structures that govern dynamic processes such as differentiation, homeostasis, and adaptation [204].

While still conceptual, these layers illustrate a growing interest in framing biological systems as information processors, where data flow and code interpretation are central to understanding complexity. Tools from computational biology, network science, and machine learning are instrumental in operationalizing these frameworks.

9. Integrative Omics

Figure 6 Schematic representation of multi-omics integration workflows, illustrating data acquisition, preprocessing, integration strategies, and biological interpretation.

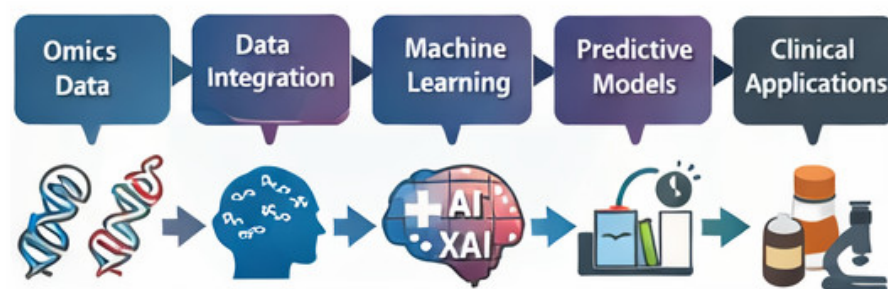


Figure 6. Multi-Omics Integration Pipeline.

Integration of multi-omics data is typically achieved through:

- (i) network-based approaches linking molecular interactions,
- (ii) statistical models integrating heterogeneous datasets, and

- (iii) machine learning frameworks capable of capturing nonlinear relationships across omics layers.

Increasingly, longitudinal and spatially resolved datasets are incorporated to enable dynamic systems modeling.

Integrative omics encompasses analytical strategies that combine multiple layers of biological data to achieve system-level insights into complex biological mechanisms [205]. Rather than analyzing individual omics layers in isolation, multi-omics integration leverages collectively the information contained in genomic, transcriptomic, proteomic, metabolomic, and other molecular profiles [206]. This holistic approach enables researchers to uncover intricate regulatory networks, characterize disease subtypes with higher resolution, and refine biomarker discovery beyond what single-omics analyses can achieve. Such integration has been particularly transformative in areas like nephrology, where machine learning frameworks applied to multi-omics data can reveal novel molecular signatures with clinical relevance for disease progression and prognosis [207].

A defining challenge of integrative omics lies in the interpretation of high-dimensional and heterogeneous datasets, which often exhibit complex interdependencies across molecular layers. Recent advances in artificial intelligence (AI) and machine learning (ML) have therefore become central to multi-omics data analysis [208]. Traditional statistical methods are increasingly complemented or replaced by data-driven approaches such as deep learning and graph neural networks, which can jointly model nonlinear relationships across omics modalities and improve predictive accuracy for disease classification and phenotype inference [207].

However, many AI methods suffer from limited interpretability—a barrier to clinical translation. To address this, explainable AI (xAI) strategies have been developed to make model decisions transparent and biologically meaningful. xAI frameworks can highlight key molecular features driving predictions, making complex models accessible to domain experts and enhancing trust in actionable insights for clinical and systems biology applications [209].

Predictive modeling represents another critical frontier in integrative omics. Here, machine learning models are trained not simply to describe data but to forecast biological outcomes, such as disease onset, progression, or treatment response [210,211]. Integration of multi-omics profiles with ML systems has demonstrated improved predictive performance in cancer survival analyses, personalized immunotherapy response predictions, and multi-scale genotype–phenotype modeling [212].

The future of integrative omics lies in scalable, interpretable, and AI-driven frameworks capable of assimilating complex multi-layer biological information while maintaining biological relevance and clinical utility. Continued innovation in explainable machine learning, coupled with rigorous experimental design and data harmonization standards, will be essential for translating multi-omics integration into robust predictive tools for biomedical, ecological, and biotechnological applications [213].

10. Limitations and Future Directions

Beyond technical challenges, economic feasibility represents a major limitation for large-scale omics integration. High-throughput sequencing, multi-omics profiling, and advanced computational infrastructure entail substantial costs, which may limit accessibility across research settings. The implementation of integrative omics frameworks will therefore depend on collaborative infrastructures, shared data platforms, and international research consortia. Over time, technological scaling and cost reduction—similar to trends observed in genome sequencing—may improve accessibility.

Despite remarkable progress in omics technologies and their applications across biology and medicine, several key limitations continue to constrain the full realization of a systems-level understanding of living organisms [13].

First, temporal and spatial resolution remain a significant challenge. Most traditional omics approaches capture static snapshots of molecular states, providing limited insight into the dynamic changes that occur over time or within the complex architecture of tissues [186]. Although single-cell and spatial omics methods have enhanced resolution, their temporal profiling capabilities are still emergent and often constrained by technical and analytical limitations (e.g., sampling throughput and live-cell compatibility) [6,214].

Second, integration across biological scales—from molecular to cellular to tissue levels—remains computationally challenging. Multi-omics datasets exhibit considerable heterogeneity in data types, distribution, and dimensionality, requiring advanced algorithms for harmonization. While machine learning and network-based integration methods have made strides, issues such as missing data, batch effects, and interpretability continue to impede robust cross-layer synthesis [215,216]. Furthermore, many integrative models prioritize predictive performance over mechanistic interpretability, limiting biological insight.

Third, a range of emerging and speculative omics concepts—including signalomics, conformomics, electromomics, and others—have been proposed, yet their experimental validation is largely absent. The practical implementation of these conceptual omics awaits technological innovations capable of capturing the relevant phenomena with sufficient sensitivity and resolution [13,216]. For example, experimentally characterizing intracellular electromagnetic fields or biologically meaningful vibrational states will require new sensing modalities beyond the current state of the art.

Finally, while the integration of multi-omics data offers transformative potential, conceptual expansion is essential to advance the field. Frameworks such as adaptomics, resiliomics, chrono-adaptomics, and plasticomics provide novel perspectives on biological adaptation, resilience, temporal modulation, and plasticity that extend beyond static measurement. These conceptual layers emphasize dynamic processes and system behavior, opening new avenues for understanding how organisms respond to environmental, developmental, and stochastic influences. However, realizing their potential will depend on developing appropriate experimental designs, longitudinal sampling strategies, and computational models capable of capturing dynamic trajectories [206,216].

In summary, although fundamental and advanced omics technologies have expanded our ability to observe and characterize life at multiple scales, significant methodological, computational, and conceptual challenges remain. Addressing these limitations will require interdisciplinary collaboration, sustained innovation in both experimental and computational domains, and a willingness to develop new theoretical frameworks that embrace complexity and dynamics.

It is important to emphasize that many conceptual omics frameworks described in this review represent long-term perspectives rather than immediately implementable technologies. Their value lies in guiding future research directions and providing integrative conceptual models for complex biological systems.

11. Conclusions

This review highlights that omics sciences are evolving from descriptive molecular cataloging toward dynamic, integrative, and predictive frameworks. A key conclusion is that future progress will depend not only on technological advancements but also on the development of conceptual models capable of integrating temporal dynamics, spatial organization, and system-level regulation.

Emerging frameworks such as adaptomics, resiliomics, signalomics, and bioenergetic omics illustrate a shift toward understanding biological systems as adaptive, energy-constrained, and information-processing entities. However, these concepts remain largely theoretical and require experimental validation.

Another major conclusion is that multi-omics integration, while powerful, remains limited by computational challenges, data heterogeneity, and lack of interpretability. Advances in explainable artificial intelligence and longitudinal experimental design will be essential to overcome these barriers.

Overall, the future of omics sciences lies in bridging molecular data with dynamic system behavior, enabling predictive and mechanistic insights across biological scales. A key priority for future research will be the operationalization of conceptual omics into measurable frameworks supported by experimental and computational advances.

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Abbreviations

AI	Artificial Intelligence
ATP	Adenosine Triphosphate
ChIP-seq	Chromatin Immunoprecipitation Sequencing
CO ₂	Carbon Dioxide
DNA	Deoxyribonucleic Acid
GC-MS	Gas Chromatography–Mass Spectrometry
LC-MS	Liquid Chromatography–Mass Spectrometry
mRNA	Messenger RNA
NGS	Next-Generation Sequencing
NMR	Nuclear Magnetic Resonance
PTMs	Post-Translational Modifications
RNA	Ribonucleic Acid
RNA-seq	RNA Sequencing
scRNA-seq	Single-Cell RNA Sequencing
Adaptomics (ADP)	Study of dynamic biological adaptation
Anthropomics (ANT)	Impact of human activities on biological systems
Chrono-adaptomics (CAD)	Temporal dynamics of adaptation
Climatonomics (CLM)	Biological responses to climate variables
Conformomics (CNF)	Biomolecular conformational dynamics
Decisiomics (DEC)	Cellular decision-making processes
Electromomics (ELM)	Intracellular electromagnetic fields (hypothetical)
Energomics (ENG)	Cellular energy fluxes (conceptual)
Fluxomics (FLX)	Metabolic flux analysis
Genomics (GEN)	Study of genomes
Interactomics (INT)	Molecular interaction networks
Metabolomics (MET)	Small molecule/metabolite profiling
Microbiomics (MIC)	Microbial community analysis

Plasticomics (PLA)	Molecular plasticity and cellular memory
Proteomics (PRO)	Protein profiling
Resiliomics (RES)	Biological resilience and recovery
Signalomics (SIG)	Cellular signaling dynamics
Spatial omics (SPO)	Spatially resolved molecular profiling
Stochastomics (STO)	Biological variability and noise
Transcriptomics (TRA)	RNA expression profiling
Vibratomics (VIB)	Molecular vibration analysis (speculative)

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