

Review

Recent Web Platforms for Multi-Omics Integration Unlocking Biological Complexity

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Abstract: The rapid advancement of high-throughput technologies has led to the generation of vast amounts of omics data, including genomics, epigenomics, and metabolomics. Integrating these diverse datasets has become essential for gaining comprehensive insights into complex biological systems and enhancing personalized healthcare solutions. This critical review examines the current state of multi-omics data integration platforms, highlighting both the strengths and limitations of existing tools. By evaluating the latest digital platforms, such as GraphOmics, OmicsAnalyst, and others, the paper explores how they support seamless integration and analysis of omics data in healthcare applications. Special attention is given to their role in clinical decision-making, disease prediction, and personalized medicine, with a focus on their interoperability, scalability, and usability. The review also discusses the challenges these platforms face, such as data complexity, standardization issues, and the need for improved machine learning and AI-based analytics. Finally, the paper proposes directions for future research and development, emphasizing the importance of more advanced, user-friendly, and secure platforms that can better serve comprehensive healthcare needs.



Academic Editor: José Machado

Received: 21 November 2024

Revised: 20 December 2024

Accepted: 27 December 2024

Published: 31 December 2024

Citation: Papadaki, E.; Kakkos, I.; Vlamos, P.; Petropoulou, O.; Miloulis, S.T.; Palamas, S.; Vrahatis, A.G. Recent Web Platforms for Multi-Omics Integration Unlocking Biological Complexity. *Appl. Sci.* **2025**, *15*, 329. <https://doi.org/10.3390/app15010329>

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Keywords: multi-omics data integration; digital healthcare platforms; genomics; epigenomics; metabolomics; personalized medicine; AI in healthcare; comprehensive healthcare; omics inter-operability; digital tools in healthcare; data standardization; machine learning in omics

1. Introduction

The field of omics research has been revolutionized by the rapid advancement of powerful and efficient technologies, enabling the generation of huge and complex datasets in various areas of omics, including genomics, epigenomics, proteomics, transcriptomics, and metabolomics. These molecular biology data provide unprecedented opportunities to uncover the complicated biological mechanisms underlying health, disease, and response to treatment [1]. Unlike other types of biological data (such as imaging or clinical phenotype data), molecular biology data directly reflect the cellular and molecular processes driving these mechanisms. By capturing the molecular makeup of biological systems—whether through genetic sequences, protein abundance, or metabolite concentrations—omics datasets provide deeper insights into the functional state of cells and tissues.

This allows researchers to move beyond descriptive phenotypes to understanding the mechanistic basis of diseases, pinpointing the molecular drivers of health conditions and responses to treatments [2,3]. However, the huge volume and heterogeneity of omics data have introduced significant challenges, particularly in the context of data integration. To fully realize the potential of these datasets, it has become necessary to develop computational platforms capable of integrating multiple omics, which allows a more complete view of biological systems.

In recent years, the field of omics has experienced an exponential increase in the amount of data generated, driven by technological advancements in high-throughput sequencing and mass spectrometry techniques. A major contributor to this surge is the development of single-cell sequencing technologies, which allow the study of individual cells at unprecedented resolution [4]. These advances have not only provided more detailed insights into cellular heterogeneity but also expanded the complexity of data, requiring more sophisticated tools for integration and analysis. With the ability to profile thousands of cells across multiple omics layers in a single experiment, the demand for platforms that can efficiently handle this data explosion has intensified [5].

Multi-omics data integration refers to the process of combining datasets from different levels of omics (such as genomics and proteomics) to reveal new biological insights that are not possible through single-omics analysis [6]. While individual omics approaches, such as transcriptomics or proteomics, can provide valuable information, they are often insufficient on their own. For instance, transcriptomics can reveal gene expression patterns, but this data alone does not reflect post-transcriptional modifications or protein activity, which are critical for understanding functional outcomes in cells [7]. Multi-omics approaches address this limitation by allowing researchers to explore how different omics layers interact and contribute to a systemic view of biological processes. By capturing these complex interactions across multiple layers, multi-omics approaches provide a more robust, comprehensive understanding of disease mechanisms, enabling the identification of biomarkers that would not be evident from a single-omics perspective [8]. This innovative approach is particularly valuable in areas such as personalized medicine, clinical decision-making, and disease prediction, where the complex interactions between genes, proteins, metabolites, and epigenetic modifications play a critical role in health outcomes. Molecular biology data, in particular, offer the granularity and specificity needed to identify these complex interactions. Unlike environmental or lifestyle data, molecular data directly represent the cellular activities and molecular modifications driving health and disease [9,10]. This makes them invaluable for revealing biomarkers and understanding pathways involved in disease onset, progression, and therapeutic response. By integrating multiple layers of omics, a better understanding of the underlying molecular mechanisms of disease, the identification of potential biomarkers for early detection, and the ability to tailor treatments can be achieved more effectively.

In recent years, various digital platforms have been developed to facilitate the integration and analysis of multi-omics data [11]. Platforms such as GraphOmics and OmicsAnalyst are specifically designed to address the complexity of multi-omics datasets. GraphOmics, for instance, excels in network-based visualizations, enabling researchers to explore molecular interactions and pathways through interactive clustering and enrichment analysis. Similarly, OmicsAnalyst focuses on user accessibility, offering an intuitive web-based interface that combines multi-omics integration with machine learning tools for predictive modeling and biomarker discovery. These tools not only handle data visualization but also cater to users with varying levels of computational expertise, enhancing accessibility and usability for a broader audience. By providing user-friendly interfaces,

they allow access to complex data analysis for clinicians, biologists, and researchers who may not have extensive computational expertise [12].

This accessibility speeds up the process of data interpretation and discovery, empowering healthcare professionals and biological researchers to make data-driven decisions more quickly. Furthermore, platforms democratize multi-omics analysis, making it available to a wider audience, not just specialists with high technical skills. This ensures that discoveries and analyses are not limited to a select group, promoting inclusivity in the scientific and healthcare communities. These platforms allow the exploration of the relationships between different types of omics, providing deeper insights into disease pathways and molecular networks. Moreover, they hold great promise in clinical applications, from diagnosis to personalized treatment strategies, supporting healthcare professionals in making more evidence-based decisions through integrated data analysis.

Despite these advances, significant challenges remain in the area of multi-omics integration [13]. Issues related to data normalization, interoperability between platforms, and the handling of large, complex datasets continue to constrain progress. In addition, the increasing dependency on machine learning (ML)-based analytics and artificial intelligence (AI) in healthcare underscores the need for platforms that can seamlessly integrate these advanced computational techniques. As the demand for more powerful and user-friendly tools grows, there is an urgent need for further development of platforms that provide both advanced analytics and give priority to security and accessibility for users with different levels of technical expertise.

This review presents a comprehensive analysis of such digital platforms, exploring their capabilities to address the complexities of multi-omics data. In this review, we evaluate how these platforms facilitate the integration of multi-omics data to reveal innovative biological insights, while offering ease of use to a broad range of researchers. Additionally, the review will highlight how these platforms contribute to improved clinical decision-making and personalized medicine by enabling more accurate and data-driven analysis. Our work examines the strengths and limitations of tools mentioned in these studies, particularly in the areas of data visualization, scalability, and accessibility for non-expert users. By summarizing the main features and functionalities of these platforms, we aim to provide a clear overview of their role in current omics research and healthcare. Furthermore, the review will examine the major challenges facing these platforms, including the need for standardization, improved ML/AI-based analysis, and enhanced utility. Finally, this work will suggest future directions for the development of more advanced, secure, and user-friendly platforms that can better address the ongoing demands of healthcare research and related clinical applications and services.

2. Methods

This review focuses on platforms that allow the integration of multi-omics data for a variety of research applications. The platforms (Table 1) selected for analysis were chosen based on their ability to integrate at least two types of omics data (e.g., genomics, transcriptomics, proteomics) (Table 2) and their relevance for fundamental biological and clinical applications such as disease-specific research, pathway analysis, and high-throughput omics integration. The search relied on a comprehensive literature review through scientific databases and research articles that discuss or feature digital platforms for multi-omics integration. The goal was to capture platforms that represent current trends and emerging tools in multi-omics research, mainly those that offer web interfaces or desktop applications to support the analysis and visualization of omics data. The search covered platforms published in major journals and online repositories in the last years.

The platforms were grouped based on their primary focus areas to facilitate a clearer comparison (Figure 1). The criteria used to compare the platforms included the types of omics integrated, the availability of a web interface, the computational tools employed for multi-omics analysis, the scalability and performance of the platform, as well as its strengths and limitations. This approach provides a comprehensive yet flexible examination of multi-omics platforms focusing on relevance and breadth in tool development.

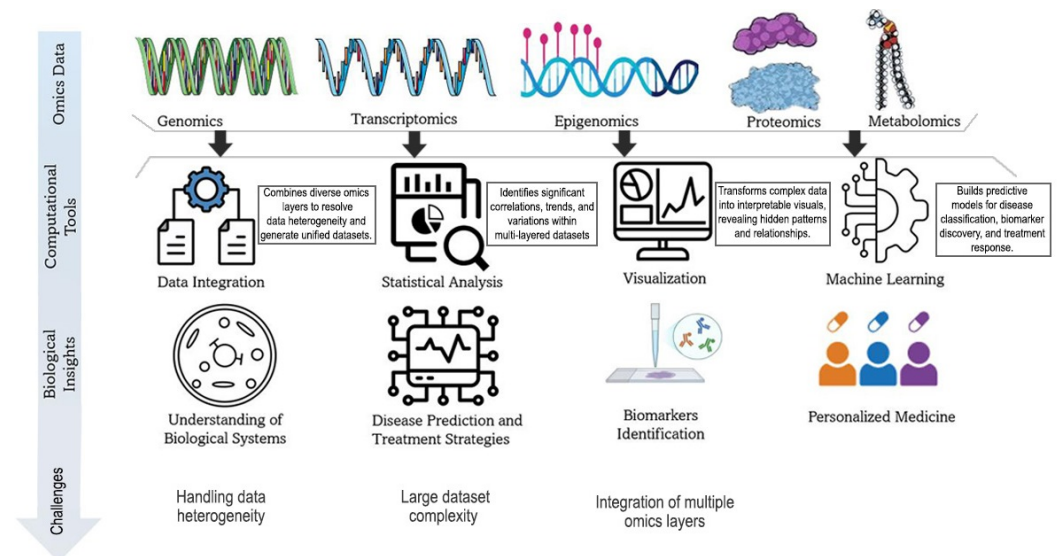


Figure 1. Tools and Data in Web Platforms for Multi-Omics Integration. This figure illustrates the integration of various omics data types—such as genomics, transcriptomics, epigenomics, proteomics, and metabolomics—within web platforms designed for multi-omics research. These platforms utilize several computational tools to enable the comprehensive analysis of biological systems. Data Integration tools combine different omics layers, allowing platforms to present a unified view of biological processes. Statistical Analysis is used to evaluate relationships between datasets, identify patterns, and highlight significant changes in molecular expression across conditions. Visualization techniques, such as heatmaps and network diagrams, aid in exploring these relationships interactively. Additionally, Machine Learning tools are employed to predict disease outcomes, identify biomarkers, and support personalized medicine by leveraging large-scale omics data. These computational tools lead to Biological Insights, including a deeper Understanding of Biological Systems, Disease Prediction and Treatment Strategies, Biomarker Identification, and the development of Personalized Medicine Approaches. They also address challenges, including handling data heterogeneity, large dataset complexity, and the integration of multiple omics layers.

2.1. Platforms for Disease-Specific Research and Drug Discovery

This section will focus on platforms specifically designed to support disease-specific research and drug discovery by integrating multi-omics data. These platforms typically aim to identify biomarkers, discover drug targets, and improve clinical decision-making by analyzing data from different omics layers.

2.1.1. AlzGPS: A Platform for Alzheimer's Drug Discovery Using Multi-Omics

By integrating genomics, transcriptomics, and proteomics data, AlzGPS focuses on Alzheimer's drug discovery [14]. Through its web-based interface, disease-associated gene-protein interactions and drug-target networks can be visualized, enabling researchers to map multi-omics data within the context of Alzheimer's disease (AD). The integration of genetic variants and gene expression data with protein interactions helps identify potential drug targets, utilizing network proximity analysis to uncover these connections.

Network proximity analysis reveals relationships between genes, proteins, and drug targets, offering insights into disease mechanisms and potential therapeutic interventions. With its emphasis on Alzheimer's drug discovery, the platform serves as a specialized tool for AD researchers. By linking omics data with known drug compounds, drug repurposing efforts are supported, enhancing the efficiency of identifying therapeutic candidates. However, the platform's narrow focus on Alzheimer's disease may reduce its utility for researchers working on other conditions. Additionally, the computational demands of network proximity analysis could limit accessibility for smaller research groups lacking the necessary resources.

2.1.2. PALMO: A Tool for Longitudinal Multi-Omics Analysis Across Diverse Diseases

In contrast to AlzGPS's Alzheimer's-focused network analysis, PALMO offers a more flexible approach by concentrating on longitudinal studies across multiple diseases. PALMO integrates transcriptomics and proteomics data, focusing on longitudinal studies. Unlike AlzGPS, it does not provide a web-based interface, but is available as an open-source software package [15]. PALMO enables longitudinal tracking of gene expression and protein abundance over time, helping researchers understand dynamic changes in diseases such as lymphoma and diabetes. Its Stability Pattern Evaluation (SPECT) and Outlier Detection Analysis (ODA) help detect abnormal molecular trends in disease progression. However, the absence of a user-friendly interface may limit its accessibility to non-experts, and its reliance on high-quality multi-time-point datasets poses challenges for smaller labs.

The platform tracks changes in gene expression and protein levels over multiple time points, making it useful for studies on diseases such as COVID-19, diabetes, and lymphoma. It uses variance decomposition and time-course analysis to analyze longitudinal datasets, identifying stable patterns or outliers in gene expression and protein abundance over time. PALMO's ability to track longitudinal changes makes it ideal for understanding dynamic biological processes and disease progression. Its open-source nature allows for flexibility and customization in a research setting. The absence of a web interface means that users must be comfortable with running the platform locally using R or Python, which may limit its accessibility to non-expert users. Longitudinal studies require multiple time-point data, which can be challenging to collect and analyze, especially for smaller labs.

2.1.3. Aging Bank: A Specialized Platform for Aging and Age-Related Disease Research

Taking this exploration of disease progression further, Aging Bank adds a specialized focus on the molecular mechanisms underlying aging and age-related diseases. Aging Bank is a specialized platform designed to integrate and analyze multi-omic data related to the biological processes of aging and age-related diseases. The platform focuses on providing researchers with tools to investigate the molecular mechanisms that contribute to aging, as well as to model age-affected diseases such as Alzheimer's, Parkinson's and other neurodegenerative diseases. By integrating data from various levels of omics, including genomics, transcriptomics and epigenomics, Aging Bank enables the elucidation of the complex regulatory pathways underlying the aging process [16]. An important advantage of the Aging Bank is its ability to facilitate the study of age-related molecular changes, helping in understanding how these changes increase susceptibility to diseases that commonly occur in older populations. The platform allows users to explore the relationships between gene expression, epigenetic modifications and genetic variations associated with both the normal aging process and aging-related pathologies.

Aging Bank facilitates aging research by integrating DNA methylation, histone modification, and other epigenomics data to uncover cancer-aging links. For example, its differential expression analysis and functional annotation tools have identified aging-

related susceptibility genes in Alzheimer's disease. However, its aging-specific focus limits its utility for non-age-related conditions, and it lacks integration of spatial or single-cell omics. By offering tools for pathway analysis, gene network construction and biomarker discovery, the platform helps with the identification of essential molecular signatures that can predict disease onset or progression in aging populations. While the platform is highly specialized for aging research, its narrow focus may limit its utility for other diseases that are not primarily age-related or for those requiring a broader multi-omics perspective beyond aging and it may not offer direct clinical decision-making tools outside the context of age-related disease modeling.

2.1.4. iODA: A Cancer-Focused Platform for Multi-Omics Pathway Analysis

For researchers looking into cancer, a more specialized platform like iODA provides essential tools for multi-omics cancer pathway analysis. iODA (integrative Omics Data Analysis) is a platform designed to facilitate the analysis of multi-omics data in cancer research. The tool integrates genomics, transcriptomics (mRNA and miRNA), and protein-DNA interaction data from ChIP-Seq experiments to help researchers explore the molecular mechanisms driving cancer progression. iODA excels in cross-level omics consistency analysis, combining ChIP-Seq and mRNA data to uncover transcription factor regulatory mechanisms in cancer. For example, its applications in breast cancer research have identified transcriptional regulators of therapy resistance. Despite these capabilities, iODA does not currently support metabolomics or single-cell data integration, which may limit its use in highly heterogeneous cancers [17].

iODA is particularly valuable in cancer studies due to its ability to handle heterogeneous multi-omics data, providing statistical tools for differential analysis and pathway enrichment. The platform supports the discovery of dysfunctional genes, miRNAs, and DNA-binding proteins across different data levels, making it an essential tool for exploring cancer heterogeneity and developing personalized medicine strategies. Although iODA is effective for transcriptomics and ChIP-Seq data, it does not currently integrate other types of omics data like metabolomics or epigenomics.

2.1.5. Summary and Comparative Insights

In summary, the platforms discussed—AlzGPS, PALMO, Aging Bank, and iODA—demonstrate distinct strengths and applications tailored to specific research objectives. AlzGPS excels in Alzheimer's research with its network proximity analysis for identifying drug targets and repurposing opportunities, making it uniquely tailored for AD-related studies. PALMO offers flexibility through longitudinal analysis tools, such as Stability Pattern Evaluation (SPECT), enabling the exploration of temporal changes across diseases like COVID-19 and lymphoma and making it ideal for understanding disease progression and treatment response in diverse conditions. Aging Bank specializes in integrating multi-omics data, particularly epigenomics, to study aging-related diseases and cancer-aging links. iODA focuses on cancer research, offering robust tools for cross-level omics analysis of transcriptional regulation and pathway-level biomarkers. While these platforms excel in their respective domains, they also present certain limitations, such as the narrow disease focus of AlzGPS and Aging Bank or the computational demands and technical expertise required by iODA and PALMO. Selecting the most suitable platform depends on the specific research goals, disease focus, and available resources, ensuring that the chosen tool aligns with the needs of the study.

2.2. Platforms for Multi-Omics Visualization and Pathway Exploration

This section reviews platforms designed to help the visualisation and exploration of the connections between different types of omics data within biological pathways. These platforms are commonly used to understand how changes in gene expression, protein abundance, or other molecular features are related between omics levels, which can help identify fundamental regulatory elements and molecular interactions that drive biological processes.

2.2.1. multiSLIDE: A Real-Time Visualization Tool for Transcriptomics and Proteomics Pathways

By integrating transcriptomics and proteomics data, multiSLIDE is designed for pathway-level analysis, with heatmap visualizations that reveal inter-omics relationships [18]. For example, its clustering tools have been used to correlate gene expression with proteomic changes in signaling pathways during breast cancer progression. However, its limitation to transcriptomics and proteomics may reduce its utility for more comprehensive omics integration. The visualization of heatmaps and clustered data facilitates the analysis of how gene expression changes correspond to protein abundance across different pathways. Real-time manipulation of data enables filtering, reordering, and clustering of omics-related information, allowing for the discovery of patterns and interactions within biological pathways.

Clustering algorithms and heatmaps are leveraged to group molecular features based on expression or abundance patterns, aiding researchers in identifying meaningful molecular relationships across various omics layers. The real-time interaction and manipulation of data enhance user accessibility, even for those without advanced bioinformatics expertise. The platform's strength lies in enabling real-time visualization and interaction, making it a highly accessible option for researchers focused on transcriptomics and proteomics within a pathway context. However, its limitation to two omics types may reduce its usefulness for researchers aiming to integrate additional layers, such as epigenomics or metabolomics.

2.2.2. MVP: A Multi-Omics Visualization Platform Supporting Genomics to Metabolomics

Expanding on the multi-omics visualization capabilities seen in ExpressVis, MVP (Multi-omics Visualization Platform) takes integration further by offering support for multiple omics layers, including genomics, proteomics, transcriptomics, and metabolomics. MVP is a comprehensive tool designed for the visualization and exploration of multi-omics data, allowing the integration and visualization of relationships between different omics layers, such as genomics, proteomics, transcriptomics, and metabolomics. The platform helps users investigate how various molecular entities interact within biological pathways and regulatory networks, making it particularly valuable for researchers studying complex diseases or molecular interactions [19]. MVP offers a variety of interactive visualizations, including network diagrams, heatmaps and scatter plots, which help the visual exploration of data and the identification of the relationships between genes, proteins and metabolites. This allows the understanding of how molecular changes at one level of omics affect other levels, providing a pivotal insight into biological processes.

A core feature of MVP is its ability to support multi-omics integration, which allows users to overlay multiple datasets and explore their combined effects on biological pathways. This can be particularly useful to the investigation of the molecular basis of disease, as it provides insights into how different levels of omics contribute to disease development or progression. While MVP is highly effective at visualizing multi-omics data, it may not offer as many advanced analytical tools for in-depth statistical analysis or machine learning-based predictive modeling. However, integrating MVP with platforms

that provide statistical analysis and machine learning capabilities, or combining it with clinical datasets (e.g., patient outcome data), could enhance its utility for clinical decision-making. Such an approach would allow MVP to leverage its robust visualization outputs for identifying clinically relevant biomarkers or predicting treatment responses.

2.2.3. VDJView: A Specialized Platform for Immune Repertoire Analysis Through VDJ Recombination Visualization

In contrast, VDJView offers a more specialised focus, targeting immune repertoire sequencing data with an emphasis on VDJ recombination in immune cells. VDJView is a specialized platform designed for the visualization and analysis of immune repertoire sequencing data, focusing on VDJ recombination in T-cell and B-cell receptors. VDJ recombination plays a significant role in generating immune diversity, and understanding this process is critical for research into immune responses in diseases such as cancer, autoimmune disorders, and infectious diseases [20]. The platform provides tools to explore immune clonality, immune receptor diversity, and the dynamics of VDJ recombination events.

By integrating and visualizing immune repertoire data, VDJView provides pseudo-time analysis and immune receptor diversity metrics to analyze adaptive immunity in cancer and autoimmune diseases. For example, it has been used to track T-cell clonotype expansion in melanoma patients undergoing immunotherapy. However, its narrow focus on immune repertoire data limits its applicability for broader multi-omics studies. VDJView allows users to generate interactive visualizations that display clonotype distributions, repertoire diversity, and other metrics important for immune system research. This makes it a valuable tool for those seeking to explore immune dynamics and diversity in various biological contexts. On the other hand, this focus on VDJ recombination means it may not be broadly applicable for researchers needing general multi-omics integration or those outside the field of immunology.

2.2.4. ProteomicsDB: A Platform Dedicated to Large-Scale Protein Expression and Interaction Data

Finally, ProteomicsDB shifts the focus to proteomics, offering large-scale data integration and visualization, much like MVP but with a more specific focus on protein expression. ProteomicsDB is a powerful platform designed for the integration, analysis, and visualization of proteomics data. The platform allows researchers to explore large-scale protein expression datasets across a wide range of tissues, organisms, and experimental conditions. ProteomicsDB enables users to visualize protein abundance, examine protein-protein interactions, and link proteomic data to biological functions and molecular pathways, making it a valuable resource for systems biology and functional genomics research [21]. The platform supports the exploration of protein expression profiles, providing insights into how proteins are regulated in different tissues and under various conditions. By connecting protein expression data with biological pathways, ProteomicsDB aids understanding the molecular mechanisms underlying biological processes and disease states.

ProteomicsDB offers users a range of visualization tools, including heatmaps, bar charts, and protein network maps, allowing for intuitive exploration of complex proteomics data. Researchers can also query specific proteins or pathways, making it easier to identify potential biomarkers or targets for therapeutic intervention. Being this platform specialized for proteomics data, users looking for broader multi-omics integration may need to supplement it with additional tools for transcriptomics, metabolomics, or genomics data. Additionally, the platform does not directly support clinical decision-making applications without additional layers of data integration. To bridge this gap, ProteomicsDB could be combined with complementary tools that enable network-based analysis, biomarker discovery, and the integration of transcriptomics or metabolomics data. By overlaying proteomics

data with other omics layers and incorporating clinical patient data, ProteomicsDB could provide deeper insights into disease progression, therapeutic targets, and personalized treatment strategies.

2.2.5. PaintOmics 3: A Web-Based Pathway-Centric Tool for Multi-Omics Visualization

PaintOmics 3 is a versatile web-based platform designed to facilitate pathway-level analysis and visualization of multi-omics data, integrating various omics layers such as transcriptomics, proteomics, metabolomics, and epigenomics. By allowing users to map omics data onto biological pathways, PaintOmics 3 helps researchers explore the complex interactions between molecular entities across different biological processes, making it particularly valuable for studies that require a pathway-centered analysis of omics data [22].

One of the strengths of PaintOmics 3 lies in its interactive and customizable interface, which enables users to overlay different omics layers onto known pathways and dynamically visualize how molecular interactions unfold in response to experimental conditions. Users can explore enrichment, differential expression, and pathway consistency analyses, providing a comprehensive perspective on how alterations in one omics layer may affect others within the same pathway. This functionality makes PaintOmics 3 especially valuable for identifying potential regulatory elements and interactions that may not be detectable through single-omics approaches alone.

Through PaintOmics 3, researchers without extensive bioinformatics expertise can access tools to visualize and interpret multi-omics data, thanks to the platform's user-friendly web interface and pathway-centric visualizations. While highly effective for exploring the relationships between multiple omics types within pathways, PaintOmics 3's focus on pathway visualization may limit its suitability for projects requiring in-depth statistical analysis or direct clinical decision-making. However, as a pathway-based visualization tool, it complements platforms like multiSLIDE and MVP by offering an accessible and intuitive approach to multi-omics exploration within known biological contexts.

2.2.6. Argonaut: A Collaborative Multi-Omics Platform with Real-Time Statistical and Interactive Visualization Tools

Argonaut is a collaborative, web-based platform that enables interactive exploration of multi-omic data through an intuitive and user-friendly interface. Designed for ease of use, Argonaut allows researchers to create customized data portals that can be securely shared and explored globally, making it a powerful tool for collaborative studies in multi-omics research [23]. By providing real-time statistical analyses and interactive visualizations such as volcano plots, PCA, and condition-correlation matrices, Argonaut supports efficient data exploration across multiple layers of omics without requiring advanced programming skills.

A notable feature of Argonaut is its focus on accessibility and collaboration, which allows researchers from diverse backgrounds to interact with and interpret complex datasets. The platform's use of Docker containers ensures seamless setup and reproducibility, while its permission-based sharing system enhances collaborative workflows. Furthermore, Argonaut is designed to have a minimal learning curve, enabling users without bioinformatics expertise to quickly gain proficiency. The platform offers comprehensive documentation, user tutorials, and a supportive community to assist new users in navigating its features. These resources are particularly valuable for interdisciplinary teams, ensuring that researchers from various fields can utilize Argonaut effectively with minimal technical barriers.

However, Argonaut's primary focus on data visualization and exploration may limit its application for users needing in-depth statistical analyses or pathway-centric tools. Nonetheless, Argonaut represents a significant advancement in making multi-omic data

accessible to a broader scientific community, particularly for collaborative and interdisciplinary research environments.

2.2.7. Summary and Comparative Insights

In conclusion, the platforms reviewed in this section—multiSLIDE, MVP, VDJView, ProteomicsDB, PaintOmics 3, and Argonaut—highlight the diverse approaches available for multi-omics visualization and pathway exploration. MultiSLIDE provides real-time, pathway-centric visualizations for transcriptomics and proteomics, ideal for researchers requiring interactive clustering tools, while PaintOmics 3 integrates multiple omics layers for dynamic pathway mapping. MVP extends visualization to include genomics and metabolomics, supporting complex disease studies through integrative pathway analysis. VDJView specializes in immune repertoire sequencing, offering clonotype diversity metrics that are valuable for immunotherapy research. ProteomicsDB excels in protein expression and interaction analysis, particularly in large-scale proteomics datasets. Lastly, Argonaut emphasizes accessibility and collaboration, offering real-time statistical and visualization tools suitable for interdisciplinary research. While each platform caters to specific needs, selecting the right tool depends on the research focus, the type of omics data being analyzed, and the intended depth of exploration.

2.3. Platforms for High-Throughput and Spatial Multi-Omics Integration

This section focuses on platforms that are designed to handle large datasets or specialize in the integration of spatial multi-omics data. These platforms are particularly useful for studies involving tissue-specific molecular activities, such as cancer research or neurobiology, where it is essential to understand how molecular features are organized within tissues.

2.3.1. SM-Omics: Automating High-Performance Spatial Transcriptomics and Proteomics Data Analysis

Designed to process high-throughput spatial multi-omics data, M-Omics integrates spatial transcriptomics and antibody-based proteomics to reveal molecular heterogeneity across tissue regions [24]. For instance, it has been applied in glioblastoma research to map gene expression in tumor microenvironments. However, its command-line nature may pose accessibility challenges for smaller labs with limited bioinformatics expertise. Rather than offering a web-based interface, SM-Omics relies on automated pipelines to handle large-scale datasets. Through the integration of spatial transcriptomics with antibody-based proteomics, gene expression and protein abundance can be mapped within tissue samples, offering insights into the molecular heterogeneity of complex biological systems such as tumors or brain tissue. This spatial integration provides a deeper understanding of tissue-specific biological processes by revealing how molecular features vary across different regions.

A basic advantage of SM-Omics lies in its ability to manage high-performance data through automated workflows. By using tools like Snakemake and Nextflow, multi-step processes for large datasets are automated, minimizing manual intervention and making the platform scalable and efficient for labs equipped with high-performance computing resources. The reliance on automated pipelines makes the platform well-suited for large-scale spatial multi-omics data processing. However, the absence of a user-friendly web interface means the platform is best suited for researchers with bioinformatics expertise comfortable with command-line tools. Moreover, the high computational demands for processing such data require substantial resources, potentially limiting accessibility for smaller research groups without dedicated infrastructure.

2.3.2. OmicsSuite: A GUI-Based High-Throughput Multi-Omics Integration Platform

In contrast to SM-Omics's command-line nature, OmicsSuite provides a more accessible approach by offering a graphical user interface (GUI) while maintaining its capacity for high-throughput multi-omics integration. OmicsSuite is a desktop-based application that supports high-throughput multi-omics integration across various omics types, including genomics, proteomics, transcriptomics, metabolomics, and single-cell data. It is built to assist experimental biologists who lack advanced computational skills by offering a graphical user interface (GUI) [25]. OmicsSuite is equipped with 175 sub-applications across different omics categories and offers pipelines for data integration, statistical analysis, and visualization tools such as heatmaps, PCA, and dimensionality reduction techniques like tSNE and UMAP. This makes the platform highly versatile for large-scale omics projects. Although it does not have a web interface, its comprehensive nature and GUI make it more accessible than command-line tools like SM-Omics. One limitation is that it requires local installation, which might be challenging for users without sufficient computational resources or technical expertise.

2.3.3. Single-Platform Multi-Omic Profiling: Concurrent Proteomics and Metabolomics Integration

Another approach within high-throughput multi-omics is the Single-Platform Multi-Omic Profiling system, which represents an advancement in integrating proteomics and metabolomics on a unified mass spectrometry platform. Traditionally, proteomics and metabolomics required separate workflows, often resulting in increased variability and larger sample requirements. The Single-Platform Multi-Omic Profiling system reduces variability by combining metabolomics and proteomics in a single workflow [26]. Its high-resolution mass spectrometry has been applied to identify biomarkers in rare disease research. However, its focus on mass spectrometry limits its integration with other omics types, such as epigenomics or transcriptomics.

At the core of this platform is high-resolution nano-LC-MS (liquid chromatography-mass spectrometry) technology, providing high sensitivity for concurrent measurements across proteomic and metabolomic layers. This setup enables researchers to map protein and metabolite levels in parallel, offering improved insight into real-time cellular dynamics and pathway interactions. This increased sensitivity is particularly beneficial for studying diseases where molecular information at multiple biological levels is critical, such as rare diseases and cancer.

The Single-Platform Multi-Omic Profiling system further supports robust data processing workflows, including normalization, alignment, and multi-omics data fusion, which are crucial for managing complex datasets. By aligning proteomic and metabolomic data, researchers can explore interactions between metabolic pathways and protein expression changes, revealing novel insights into disease mechanisms.

2.3.4. CHOmics: Optimizing CHO Cells for Biopharmaceutical Production Through Multi-Omics Integration

Moving from a broad multi-omics focus to a more specialized application, CHOmics addresses the unique challenges in optimizing Chinese Hamster Ovary (CHO) cells for biopharmaceutical production. CHOmics is a specialized multi-omics platform designed to integrate genomics, transcriptomics, proteomics, and metabolomics data for the optimization of Chinese Hamster Ovary (CHO) cells, which are widely used in the biopharmaceutical industry for the production of therapeutic proteins. The platform aims to provide insights into the molecular mechanisms that govern CHO cell behavior, helping the improvement of the efficiency and yield of protein production [27]. CHO cells are a cornerstone of biological drug production, and CHOmics facilitates the integration of multi-omics data to optimize

cellular processes, such as gene expression regulation, protein synthesis, and metabolic pathways. By analyzing data across multiple omics layers, CHOmics helps identify significant genetic and molecular factors that can be modified to enhance cell growth, stability, and protein yield.

The platform provides tools for pathway analysis, gene regulatory network exploration, and metabolic optimization, allowing a comprehensive understanding of how different molecular layers interact in CHO cells. This is crucial for fine-tuning cellular processes and optimizing production outcomes in high-throughput industrial settings. While CHOmics offers extensive benefits for the biotechnology industry, its applicability remains more limited for broader multi-omics studies. CHOmics, additionally, provides extensive tutorials, pre-configured pipelines, and interactive visualizations, enabling researchers to become proficient relatively quickly. These resources, combined with web-based deployment and community engagement opportunities, ensure accessibility for interdisciplinary teams with varying computational expertise.

2.3.5. Majorbio Cloud: A Cloud-Based Suite for Large-Scale Multi-Omics Research

Majorbio Cloud is a comprehensive, cloud-based platform designed to support large-scale multi-omics studies by providing a centralized suite of bioinformatics tools and workflows for integrating genomics, transcriptomics, proteomics, metabolomics, and metagenomics data. With its focus on ease of access and broad analytical capabilities, Majorbio Cloud caters to high-throughput demands by offering pre-configured pipelines that facilitate data processing, analysis, and visualization across multiple omics types [28].

The platform's cloud-based architecture allows researchers to manage and analyze substantial datasets without needing dedicated local infrastructure, thereby supporting institutions of varying scales. Majorbio Cloud incorporates over 300 distinct analysis tools, enabling users to perform complex analyses like differential expression, clustering, pathway enrichment, and gene interaction mapping within a single environment. These capabilities make it particularly suited for projects in areas such as cancer research, where examining interactions across various biological layers is crucial.

A key feature of Majorbio Cloud is its user-friendly web interface, which allows for customizable data exploration through interactive visualizations, such as heatmaps, PCA plots, and condition-correlation matrices. This interactive environment aids researchers in identifying molecular relationships and pathway dynamics, contributing to the in-depth study of disease mechanisms and tissue-specific molecular activities. Furthermore, Majorbio Cloud emphasizes collaborative workflows, enabling researchers to share data and results across teams, thus fostering interdisciplinary research efforts in multi-omics.

2.3.6. Summary and Comparative Insights

In summary, the platforms discussed—SM-Omics, OmicsSuite, Single-Platform Multi-Omic Profiling, CHOmics, and Majorbio Cloud—address the challenges of high-throughput and spatial multi-omics integration in unique ways. SM-Omics stands out for its automated workflows in spatial transcriptomics and proteomics, revealing tissue-specific heterogeneity in complex systems like tumors. OmicsSuite offers a GUI-based alternative for multi-omics integration, enabling users without advanced programming expertise to analyze large datasets. The Single-Platform Multi-Omic Profiling system unifies proteomics and metabolomics workflows, enhancing reproducibility for rare disease studies. CHOmics addresses the biopharmaceutical industry's needs, optimizing CHO cells for protein production using multi-omics approaches. Lastly, Majorbio Cloud offers a comprehensive, cloud-based solution for managing and analyzing multi-omics data, with an emphasis on collaboration and scalability. While each platform excels in specific applications, their

varying levels of accessibility, specialization, and computational requirements should guide in selecting the most appropriate tool for study needs.

2.4. Platforms for Clinical Decision-Making and Personalized Medicine

This section covers platforms that integrate multi-omics data to support clinical decision-making, disease prediction, and personalized medicine. These platforms often focus on applying omics data in clinical settings to tailor treatments to individual patients.

2.4.1. GraphOmics: A Network-Based Approach to Multi-Omics Data for Disease Biomarker Identification

Designed for multi-omics network-based analysis, GraphOmics leverages Reactome pathways to identify disease biomarkers, with its clustering and pathway enrichment tools applied in metabolic syndrome research to identify novel therapeutic targets [29]. However, the platform's computational demands limit its accessibility for smaller clinical research teams. By integrating data from genomics, proteomics, and metabolomics, interaction networks are created, revealing how molecular elements are connected in the context of disease. Clinical decision-making is supported through the identification of disease-associated pathways and molecular signatures, which can be leveraged to predict treatment responses. Network-based analyses enable researchers and clinicians to explore the relationships between molecular factors and their impact on disease outcomes.

The ability to handle large, multi-dimensional datasets while providing detailed network visualizations is one of the platform's essential strengths. However, significant computational resources and advanced expertise in network biology are required for effective use, making GraphOmics less accessible to non-expert users.

Although GraphOmics offers a powerful means of analyzing large, multi-dimensional datasets, it requires significant computational resources and expertise in network biology, limiting its accessibility for non-expert users. To address this challenge, platforms like OmicsAnalyst aim to provide a more user-friendly interface for clinical research, enabling a broader range of researchers to explore multi-omics data.

2.4.2. OmicsAnalyst: A User-Friendly Web Platform for Clinical and Personalized Medicine Research

OmicsAnalyst is a user-friendly, web-based platform designed for the integration and analysis of multi-omics data, with a strong focus on applications in clinical research and personalized medicine. The platform allows the combination of genomics, transcriptomics, proteomics, metabolomics, and other omics data types to gain insights into biomarkers, pathway analysis, and disease prediction [30]. One of the main advantages of OmicsAnalyst is its intuitive web interface, which makes it accessible to users who may not have extensive computing experience. The platform offers a variety of data analysis tools tailored for clinical applications, including statistical analysis, pathway enrichment and biomarker discovery. In addition, machine learning algorithms are built into the platform, supporting predictive modeling for disease classification and biomarker identification, which are essential to personalized treatment strategies.

OmicsAnalyst's integration of machine learning algorithms enables predictive biomarker discovery, demonstrated in its application to classify subtypes of breast cancer. Its focus on user-friendly workflows makes it accessible to clinical researchers, though its lack of support for spatial omics limits its use in advanced tissue-specific studies. The platform's capacity to combine different omics types enables the exploration of molecular pathways and identify connections between various biological layers, such as gene expression, protein levels, and metabolite concentrations. This makes it especially useful for disease research where understanding the molecular interactions and drivers of dis-

ease is crucial for personalized therapeutic approaches. A feature of OmicsAnalyst is its interactivity, allowing the exploration of data in depth through customizable visualizations such as heatmaps, PCA plots and network analysis. These visual tools assist the quick identification of relevant molecular patterns and the gain of actionable insights for clinical decision making. While OmicsAnalyst offers broad multi-omics integration capabilities, its primary focus on clinical research might limit its use in certain basic research fields or in areas where highly specialized omics types, such as epigenomics or spatial omics, are required.

2.4.3. OmicsNet 2.0: A Platform for Network Visualization and Multi-Omics Interaction Mapping

Building on the web-based, user-friendly approach of OmicsAnalyst, OmicsNet 2.0 takes multi-omics integration a step further by focusing on network visualization and molecular interaction mapping. OmicsNet 2.0 is a web-based platform designed for network-based multi-omics data integration and visualization. The platform allows users to construct and analyze molecular interaction networks by integrating diverse omics data, including genomics, transcriptomics, proteomics, metabolomics, and microbiomics. OmicsNet 2.0 is particularly valuable in clinical research and personalized medicine due to its ability to map disease-associated molecular networks and facilitate biomarker discovery [31]. The strength of the platform lies in its ability to visualise complex molecular networks, allowing the understanding of the relationships between different molecular entities such as genes, proteins and metabolites. By integrating multi-omics data into biological networks, OmicsNet 2.0 helps the identification of critical pathways and molecular interactions associated with disease development and progression.

A major attribute of OmicsNet 2.0 is its user-friendly web interface, which simplifies the construction and visualization of networks for users without advanced bioinformatics experience. The platform also offers tools for functional enrichment analysis and pathway exploration, making it particularly relevant for those seeking to understand the functional implications of molecular interactions identified through network analysis. While the web interface is easy to use, handling large datasets and complex network analysis may still require significant computational resources, which could limit its use in resource-constrained environments. Also, despite being powerful for network-based insights, OmicsNet 2.0's focus on network visualization may not be appropriate for all multi-omics research scenarios, where non-network-based approaches are preferred.

2.4.4. Summary and Comparative Insights

In summary, the platforms discussed—GraphOmics, OmicsAnalyst, and OmicsNet 2.0—offer powerful tools for integrating multi-omics data into clinical decision-making and personalized medicine. GraphOmics employs network-based analyses to uncover disease biomarkers and therapeutic targets, particularly in metabolic syndrome and cancer pathways. OmicsAnalyst integrates machine learning algorithms for predictive biomarker discovery, demonstrated in breast cancer subtype classification studies. However, its focus on clinical applications may limit its use in basic research or for omics types like epigenomics or spatial omics. OmicsNet 2.0 enables multi-omics network visualization, helping researchers map gene-protein interactions in clinical settings. While it excels in visualizing complex molecular relationships, its computational demands and focus on network-based methods may restrict its application in resource-limited environments or scenarios where alternative analytical approaches are preferred. Collectively, these platforms provide robust solutions for multi-omics integration in clinical settings, with their suitability dependent on the specific research objectives and resources available.

Table 1. Overview of Multi-Omics Integration Platforms (Part 1).

Platform/Paper	Programming Languages/Tools	Processes/Analysis Performed
AlzGPS [14]	Django, HTML, CSS, JavaScript, Cytoscape.js, NetworkX	Network-based drug repurposing, AD-related gene and protein network analysis, Mechanism of action (MOA) analysis, Network proximity analysis
PALMO [15]	R, Python, ArchR, Seurat, variancePartition	Variance Decomposition Analysis (VDA), Coefficient of Variation Profiling (CVP), Stability Pattern Evaluation (SPECT), Outlier Detection Analysis (ODA), Time Course Analysis (TCA)
Aging Bank [16]	Web-based platform using tools like Differential Expression Analyzer, Co-Expression Network, Functional Annotation Analyzer	Multi-omics data integration, differential expression analysis, co-expression network analysis, functional annotation, cancer-aging associations
iODA [17]	Java, R, MACS, PeakAnalyzer, Perl	Differential gene/mRNA expression analysis, pathway enrichment analysis, ChIP-Seq data analysis, cross-level omics consistency analysis
multiSLIDE [18]	Java (backend), Python (computation), Angular (frontend), MongoDB, SVG (visualization)	Heatmap visualization of multi-omics data, pathway and GO term-based queries, hierarchical clustering, network visualization of inter-omics relationships, differential expression analysis, FDR control
MVP [19]	HTML, JavaScript, CSS, SQLite, IGV.js, Lorikeet	Proteogenomics data integration, visualization of peptides, MS/MS spectra visualization, protein-genome alignment, variant annotation analysis
VDJView [20]	R, Shiny, dplyr, Seurat, tcr, Rcircos	Gene expression and clonotype analysis, clustering, dimensionality reduction (PCA, t-SNE, UMAP), pseudo-time analysis, immune receptor gene analysis
ProteomicsDB [21]	SAP HANA (database), JavaScript, R, Docker, Prosit (deep learning), Python	Mass spectrometry-based proteomics, transcriptomics-proteomics integration, drug sensitivity prediction, protein-protein interaction analysis, missing value imputation, biochemical assay analysis
PaintOmics 3 [22]	Python, R, MongoDB, JavaScript, HTML5	Pathway enrichment, multi-layer feature matching, network analysis, interactive visualization, KEGG-based pathway mapping, heatmaps, trend analysis, integration of regulatory data
Argonaut [23]	Docker, HTML, JavaScript (D3.js), MySQL, PHP, Bootstrap, Angular	Real-time statistical analysis, interactive data visualization (e.g., volcano plots, PCA, GO enrichment), batch control, missing value imputation, outlier analysis, secure data sharing
SM-Omics [24]	Python, Image registration tools (SpoTteR)	High-throughput spatial transcriptomics, multiplex protein detection, image registration
OmicsSuite [25]	Java, R, Shiny, JavaFX, BioJava, Bioconductor	Multi-omics integration, differential expression analysis, PPI network construction, enrichment analysis, single-cell RNA-Seq, spatial transcriptomics workflows
Single-Platform Multi-Omic Profiling system [26]	LC-MS, nLC-MS, computational workflows for proteomics and metabolomics integration	Simultaneous proteomics and metabolomics data acquisition, network-based integrative framework, sample preparation techniques, high-sensitivity analysis, pathway and network analysis, mass spectrometry optimization

Table 1. *Cont.*

Platform/Paper	Programming Languages/Tools	Processes/Analysis Performed
CHOmics [27]	PHP, R, JavaScript, Limma, Subread, Voom, KEGG pathways	RNA-Seq processing, Differential expression (DE) analysis, PCA, pathway enrichment, meta-analysis, visualization of gene expression and pathway diagrams across multiple omics
Majorbio Cloud [28]	Django, HTML, CSS, JavaScript, MongoDB, Ceph, MySQL, D3	One-stop multi-omics data integration, gene expression analysis, gene set and structure analysis, metagenomics, differential expression analysis, taxonomic and functional analysis, correlation, model predictive analysis, visualization through Sanger-Charts, interactive analysis reports, and cloud storage.
GraphOmics [29]	Python, JavaScript, Django, Plotly, D3, SQLite, Neo4j	Horizontal omics integration using Reactome pathways, differential expression analysis, PCA, pathway enrichment analysis, interactive clustering, heatmaps, gene ontology analysis, multi-omics integration, linked data exploration across tables
OmicsAnalyst [30]	Java, R, JavaServer Faces (JSF), PrimeFaces, sigma.js, three.js	Correlation network analysis, cluster heatmap analysis, dimension reduction analysis, multi-view clustering, interactive 2D/3D visual analytics, PCA, DIABLO, feature correlation, enrichment analysis
OmicsNet 2.0 [31]	Python, R, JavaScript, Rcpp, Cytoscape, Rgraphviz	Multi-omics network creation, SNP and peak annotation, microbiome interaction network analysis, 2D and 3D network visualization, random walk with restart algorithm for disease gene prediction, network refinement using graph algorithms (PCSF), enrichment analysis

Table 2. Overview of Multi-Omics Integration Platforms (Part 2/Omics Integrated).

Platform/Paper	Genome	Transcriptome	Proteome	Metabolome	Epigenome
AlzGPS [14]	Yes	Yes	Yes	Yes	No
PALMO [15]	Yes	Yes	Yes	No	Yes
Aging Bank [16]	Yes	Yes	No	No	Yes
iODA [17]	Yes	Yes	No	No	Yes
multiSLIDE [18]	Yes	Yes	Yes	Yes	No
MVP [19]	Yes	Yes	Yes	No	No
VDJView [20]	No	Yes	No	No	No
ProteomicsDB [21]	No	Yes	Yes	No	No
PaintOmics 3 [22]	No	Yes	Yes	Yes	Yes
Argonaut [23]	No	No	Yes	Yes	No
SM-Omics [24]	No	Yes	No	No	No
OmicsSuite [25]	Yes	Yes	Yes	Yes	No
Single-Platform					
Multi-Omic Profiling system [26]	No	No	Yes	Yes	No
CHOmics [27]	No	Yes	Yes	No	No
Majorbio Cloud [28]	Yes	Yes	Yes	Yes	No
GraphOmics [29]	No	Yes	Yes	Yes	No
OmicsAnalyst [30]	Yes	Yes	Yes	Yes	No
OmicsNet 2.0 [31]	Yes	Yes	Yes	Yes	No

3. Discussion

The rapid development of multi-omics platforms has introduced a new era of integrative biology, enabling deeper insights into complex biological systems and diseases [6]. The platforms discussed in this review have been instrumental in advancing research across

diverse fields, from Alzheimer's drug discovery to plant-specific trait development. By integrating data from genomics, transcriptomics, proteomics, metabolomics, and other omics layers, these platforms allow for a more systemic view of biological processes, thereby facilitating the identification of biomarkers, drug targets, and pathways that would otherwise remain hidden in single-omics analysis [32].

3.1. Case Studies in Multi-Omics Platforms

The practical utility of multi-omics platforms is best demonstrated through specific case studies spanning clinical research, agriculture, and disease-specific investigations. These examples highlight how platforms have driven significant advancements in understanding complex systems and tailoring interventions.

3.1.1. Clinical Research Applications

Platforms like AlzGPS have been instrumental in Alzheimer's research. For instance, AlzGPS facilitated the identification of potential therapeutic targets by mapping intricate gene-protein interactions linked to Alzheimer's disease. This has accelerated drug repurposing efforts, enabling researchers to identify candidate compounds such as donepezil and memantine for further investigation.

PALMO has shown great promise in longitudinal studies by tracking disease progression and treatment response in conditions such as diabetes and COVID-19. For example, PALMO was used in a longitudinal analysis of diabetic patients, revealing stable molecular signatures associated with treatment resistance. Similarly, its time-course analysis capabilities were pivotal in identifying temporal patterns of immune response during COVID-19 progression.

OmicsAnalyst has advanced personalized medicine by integrating diverse omics data types to identify disease biomarkers. In one notable study, the platform's ML tools enabled the stratification of breast cancer subtypes based on transcriptomic and proteomic data, leading to improved treatment recommendations tailored to molecular profiles.

3.1.2. Disease-Specific Insights

iODA has become a cornerstone in cancer research. A recent study utilized iODA to analyze the molecular drivers of therapy resistance in lung cancer, revealing miRNA-protein interactions that contribute to tumor heterogeneity. This insight has guided the development of personalized therapeutic strategies targeting specific pathways.

In aging research, Aging Bank has enabled the study of molecular mechanisms underlying age-related diseases. By integrating epigenomics and transcriptomics data, the platform has facilitated the discovery of biomarkers predictive of neurodegenerative diseases like Parkinson's, providing a foundation for early diagnostics.

3.1.3. Emerging Applications

Beyond established platforms, newer tools such as Argonaut and Majorbio Cloud have supported interdisciplinary research. Argonaut's collaborative features enabled the integration of lipidomics and proteomics to study metabolic disorders, while Majorbio Cloud facilitated the identification of microbial biomarkers for gut health in a metagenomic study of inflammatory bowel disease (IBD).

3.2. Limitations of Current Platforms

Despite their successes, there are several limitations and gaps that remain in current multi-omics platforms [33]. One of the most pressing issues is the need for greater data integration. While many platforms support multiple omics types, the integration of additional layers—such as epigenomics, spatial omics, and microbiomics—is still lacking in several

tools [34]. This restricts the ability to capture the full complexity of biological systems. Moreover, interoperability between platforms remains a challenge. The lack of standardized data formats and integration protocols can hinder the seamless exchange of data between different tools, reducing their overall utility in multi-disciplinary research settings.

Another critical limitation is the reliance on static datasets [35]. Many platforms operate on fixed datasets that may not be frequently updated or connected to real-time data sources. This is particularly problematic in clinical settings, where dynamic and real-time data integration is essential for timely decision-making and personalized treatment strategies. For example, clinical applications require platforms that can continuously update data based on patient outcomes and incorporate new discoveries from ongoing research. Additionally, while some platforms have integrated machine learning (ML) and AI-based tools, the full potential of these technologies has not yet been realized [36]. Many platforms still rely on traditional statistical approaches, which may not be sufficient to handle the growing volume and complexity of multi-omics data. The incorporation of more advanced AI tools, including deep learning models and smart algorithms, is essential for extracting actionable insights from multi-omics datasets.

While platforms such as multiSLIDE offer user-friendly, web-based interfaces that reduce barriers to entry for researchers without advanced programming skills, the learning curve for new users remains a consideration. Features like keyword-driven queries, real-time data filtering, and interactive heatmap-based visualization simplify multi-omics data exploration without requiring coding expertise. Additionally, accessible resources such as GitHub repositories, example datasets, and platform-specific documentation can support less experienced users in becoming proficient. However, formal training or familiarity with omics data analysis is still beneficial for fully leveraging these tools, particularly in interdisciplinary research settings.

3.3. Essential Improvements for Future Platforms

To fully harness the potential of multi-omics data, several improvements are essential in the development of future platforms [37]. Dynamic and real-time data integration should be prioritized, particularly for clinical applications, where the ability to update and analyze patient data in real time can significantly improve decision-making processes. Platforms should be able to integrate data from diverse sources, including electronic health records, wearable devices, and ongoing clinical trials, ensuring that the data remains current and relevant.

Furthermore, platforms must become more user-friendly and accessible to a broader audience [38]. While platforms like VDJView are designed to be accessible to users without profound bioinformatics expertise, the learning curve for such tools can still vary depending on a researcher's familiarity with omics data. Platforms such as OmicsAnalyst provide extensive support through FAQs, case studies, and step-by-step tutorials to guide users through complex workflows. These resources can help new users become proficient within a few days to weeks, depending on dataset complexity and prior experience. Incorporating similar features, such as video tutorials or interactive onboarding tools, would further reduce barriers to entry. Incorporating similar features, such as video tutorials or interactive onboarding tools, would further reduce barriers to entry, particularly for interdisciplinary teams with varying levels of computational expertise. The development of more intuitive interfaces and automation of complex analyses will be crucial to broadening the user base and facilitating access to multi-omics analysis. Incorporating similar features, such as video tutorials or interactive onboarding tools, would further reduce barriers to entry, particularly for interdisciplinary teams with varying levels of computational expertise. The development of more intuitive interfaces and automation of complex analyses will

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In addition, future platforms must focus on interoperability and standardization [39]. By adopting standardized data formats and protocols, platforms can ensure seamless integration and collaboration between different research groups and tools. This would not only facilitate multi-disciplinary research but also reduce the time and effort required to manually convert and format data between platforms.

4. Future Directions: AI and ML Tools in Multi-Omics Platforms

Looking ahead, the future of multi-omics platforms will undoubtedly be shaped by the growing integration of artificial intelligence (AI) and machine learning tools [40]. AI has the potential to revolutionize the analysis of multi-omics data by automating complex tasks such as feature selection, pattern recognition, and predictive modeling. Future platforms are likely to incorporate deep learning models that can identify subtle patterns and interactions across omics layers, enabling more accurate predictions of disease outcomes and treatment responses.

In addition to AI-driven analysis, the future will likely see platforms that are self-updating and capable of continuous learning. As more data becomes available, platforms will need to automatically integrate new findings and adapt their predictive models accordingly. This will ensure that they are always working with the most up-to-date information, leading to better decision-making and more personalized treatment strategies.

Moreover, the integration of smart tools such as natural language processing (NLP) could further enhance the usability of these platforms [41]. By enabling users to query datasets and interpret results using everyday language, platforms will become more intuitive and accessible to a wider range of users. This will not only speed up the research process but also facilitate collaboration between users from different fields.

Finally, cloud-based solutions and distributed computing will play a vital role in addressing the computational challenges posed by large-scale multi-omics data [42]. By leveraging cloud infrastructure, future platforms will be able to scale their resources dynamically, enabling the processing and analysis of massive datasets without the need for expensive local hardware.

5. Conclusions

In conclusion, multi-omics platforms have already made significant contributions to biological research and clinical applications, providing a more comprehensive understanding of complex diseases and traits. However, to fully realize the potential of these platforms, several improvements are necessary. Future platforms must prioritize dynamic data integration, interoperability, and the incorporation of advanced AI-driven tools. By embracing these advancements, multi-omics platforms will continue to drive innovation in personalized medicine, disease prediction, and fundamental biological research, shaping the future of healthcare and biology.

Author Contributions: E.P. conceptualized the study, conducted the methodology, performed the formal analysis, investigated the data, curated the data, wrote the original draft, visualized the results, and administered the project. I.K. supported the writing and interpretation of the results. P.V. provided writing support. O.P. and S.T.M. assisted in data validation, methodology refinement, and supported project administration. S.P. involved in data analysis, validation, and provided critical feedback on the methodology. A.G.V. supervised the project, contributed to the conceptualization, and secured funding. All authors have read and agreed to the published version of the manuscript.

Funding: This research received no external funding.

Conflicts of Interest: The authors declare no conflicts of interest.

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