Articles

HiOmics 2.0: An All-in-One Intelligent Cloud Platform for Multi-Omics Analysis in Biomedical Research

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Rapid advances in high-throughput sequencing and mass spectrometry have introduced substantial challenges for multi-omics data analysis, including fragmented workflows, slow interactive responsiveness, and limited reproducibility of results. To address these issues, we present HiOmics 2.0 (https://henbio.com), a substantially upgraded cloud platform. The core innovation is a hierarchical task-scheduling system that decouples lightweight interactive tasks from compute-intensive analytical pipelines and enables real-time responses via a dedicated API cluster. This redesign reduces the generation time of common analytical plots from over 30 seconds to below 5 seconds (an improvement exceeding 80%), delivering responsiveness comparable to local desktop software. Building on this foundation, the platform adds modules for single-cell transcriptomics, proteomics, metabolomics, pathogen detection, and Mendelian randomization. Accordingly, HiOmics has evolved from a collection of discrete tools into an integrated infrastructure that supports systematic life science research. The unified platform enables users to complete an end-to-end research workflow—from data preprocessing and multi-omics mining to model development and visualization. As of November 2025, HiOmics 2.0 integrates 453 analytical tools, has recorded 112,957 visits from users worldwide, and has completed 36,726 analytical tasks. Representative case studies demonstrate its utility in both basic research and clinical translation. Overall, through architectural innovation and functional integration, HiOmics 2.0 provides an efficient, user-friendly, and reproducible all-in-one solution for life science research.

Introduction

Recent advances in high-throughput sequencing and mass spectrometry have accelerated the generation and accumulation of multi-dimensional omics data across multiple biological layers, including genomics, transcriptomics, proteomics, and metabolomics. These massive, heterogeneous datasets offer unprecedented opportunities to systematically elucidate the complex mechanisms underlying biological processes[1]. However, effectively leveraging these data remains challenging, particularly with respect to data integration, workflow standardization, and result reproducibility[2]. Specifically, the high heterogeneity of multi-omics data[3-5] has contributed to fragmented tool ecosystems and inconsistent processing standards. This fragmentation reduces analytical efficiency, weakens the linkage between visualization and interpretation, and ultimately hampers independent verification and replication of research findings.

Several bioinformatics platforms and tools have been developed to address specific aspects of these challenges. For example, Galaxy[6,7] supports the construction of standardized workflows across diverse data types, whereas ImageGP2[8,9] focuses on omics data visualization. However, these resources are often limited in scope and deployed as standalone solutions, which makes it difficult to support end-to-end multi-omics research needs—from data processing to knowledge discovery—in a unified manner. Consequently, a unified, user-friendly, and extensible workflow platform for integrated multi-omics analysis remains lacking. First, many methods (e.g., the mmMOI multi-omics integration model proposed by Li et al.[10]) are primarily distributed as source code. This distribution mode places substantial demands on users' programming and modeling expertise, limiting accessibility for researchers without strong computational backgrounds. Second, existing solutions often exhibit gaps in functional coverage. Few platforms provide a fully integrated pipeline that supports the complete process, from raw data preprocessing and integrative multi-omics mining to advanced statistical or machine learning modeling and publication-quality visualization. This fragmentation hinders researchers from conducting multilevel translational analyses—from basic discovery to clinical applications —within a single, coherent environment.

To address these challenges and incorporate ongoing feedback from the user community, we developed and released HiOmics 2.0 (https://henbio.com), a substantially upgraded platform. With the goals of lowering technical barriers, improving analytical efficiency, and enhancing reproducibility, we redesigned the platform to incorporate an updated task-scheduling system and strengthened real-time interactive capabilities. Building on existing functionality, HiOmics 2.0 introduces modules for single-cell transcriptomics, proteomics, metabolomics, rapid pathogen detection, and Mendelian randomization. Collectively, these additions provide an end-to-end workflow encompassing data preprocessing, single- and multi-omics integrative analysis, model development, and result visualization and sharing. The platform adopts a decoupled front-end/back-end architecture and leverages Docker containerization[11], the WDL[12]/Cromwell[13] workflow engine, and cloud-native compute and storage services. This design improves reliability and traceability while increasing the efficiency of large-scale data processing and enhancing the overall user experience.

Since its launch in 2022, HiOmics has supported an active user

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community and a wide range of application scenarios. This upgrade aims to build a cloud platform that systematically transforms raw data into interpretable knowledge and ultimately actionable scientific insights. In doing so, it is intended to improve the efficiency, reproducibility, and clinical translational potential of multi-omics research. We aim to provide life science researchers with an integrated, low-barrier, high-performance infrastructure for omics analysis. In addition, this release integrates our previously published HPD-Kit algorithm for metagenomic pathogen detection[14] as a cloud-based service, thereby expanding the platform's utility for clinical infectious disease diagnosis.

Methods

In HiOmics 2.0, we implemented major upgrades to the system architecture and task-scheduling mechanisms to improve user experience and processing efficiency. The platform adopts a decoupled front-end/back-end architecture. The front end is implemented with Vue.js[15] and the Element Plus component library[16] to deliver an intuitive and responsive user interface. The back end is implemented with ThinkPHP[17]and exposes modular RESTful API services; a MySQL database is used for centralized management of users, tasks, and analysis metadata.

To improve responsiveness and resource utilization, we implemented a hierarchical task-scheduling strategy. This strategy decouples short-lived interactive tasks (e.g., plotting) from long-running analytical workflows (e.g., multi-step omics pipelines) and routes them to dedicated execution backends. For computing and storage resources, HiOmics 2.0 uses Docker containerization to encapsulate analysis environments, improving dependency consistency and reproducibility. The platform is integrated with Alibaba Cloud Object Storage Service (OSS) and Batch Compute, enabling elastic storage and distributed computing for multi-user and large-scale processing scenarios, while supporting reliable management and efficient processing of large datasets. In summary, building on the previous version, HiOmics 2.0 lowers barriers to complex multi-omics analysis through refined task scheduling and continuous front-end/back-end optimization. The platform is designed as an efficient and reliable all-in-one solution for data analysis and visualization.

Results

Core Architectural Innovation: Hierarchical Task Scheduling System

A key component of the HiOmics 2.0 upgrade is a redesigned task-scheduling architecture that addresses a major bottleneck in interactive data exploration. In the earlier version, all tasks—from complex, multi-step omics pipelines to simple statistical plots—were submitted to a single queue managed by a unified workflow engine (e.g., Cromwell). As a result, rapid visualization and exploratory analysis tasks could experience delays of tens of seconds, disrupting analytical continuity.

To address this issue, we designed and implemented a hierarchical task scheduling system (Figure 1). The core idea is to route tasks to distinct execution backends according to computational demand and responsiveness requirements, as follows:

- **Real-time interactive channel:** For lightweight, high-concurrency tasks (e.g., statistical lotting and simple data transformations), we deployed a dedicated API cluster based on the R RestRserve framework [18]. When initiated from the front end, requests are processed by this cluster and typically return rendered results within 5 seconds, providing an experience comparable to desktop software.

- **Batch analysis channel:** For complex, standardized omics workflows (e.g., RNA-seq and single-cell RNA-seq analysis), tasks are managed and scheduled by the WDL/Cromwell workflow engine, supporting reliability, traceability, and fault tolerance.

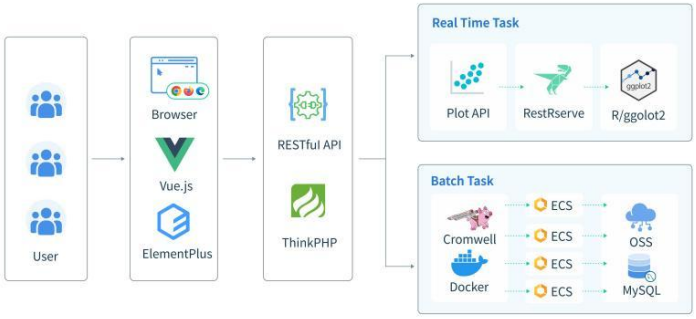

Figure 1. Architecture of the hierarchical task scheduling system in HiOmics 2.0. The system dynamically routes tasks to dedicated backends based on computational profiles and responsiveness requirements. The real-time interaction channel handles lightweight, high-concurrency tasks (e.g., statistical plotting) through a dedicated high-performance API cluster built on the RestRserve framework, typically returning rendered results within 5 seconds to support desktop-like interaction. The batch analysis channel executes complex, standardized omics workflows (e.g., RNA-seq and single-cell analysis) via the WDL/Cromwell workflow engine, improving reliability, traceability, and fault tolerance.

This architecture decouples exploratory analysis from batch computation, reducing response times for interactive tasks from tens of seconds to a few seconds and providing a technical basis for iterative scientific discovery.

Platform Functional Architecture and Scale

The hierarchical scheduling system provides a technical foundation for a comprehensive multi-omics analysis ecosystem. Building on this foundation, HiOmics 2.0 integrates and expands its functional architecture to support an end-to-end workflow from raw data to biological insight. Platform functionality is organized into three pillars—Analytical Workflows, Professional Applications, and Resource Support—encompassing 21 core analytical modules (Figure 2). The Analytical Workflows pillar provides standardized pipelines spanning major omics types, including genomics, transcriptomics (including single-cell transcriptomics), proteomics, metabolomics, metagenomics, and phenomics. The Professional Applications pillar integrates tools for in-depth analyses, including advanced statistical analysis, prognostic modeling with immune-infiltration assessment, machine-learning/AI modeling, and rapid pathogen detection based on the published HPD-Kit[14]. The Resource Support pillar integrates data preprocessing, interactive visualization, and access to biomedical databases and software resources, supporting workflow completeness and result interpretability.

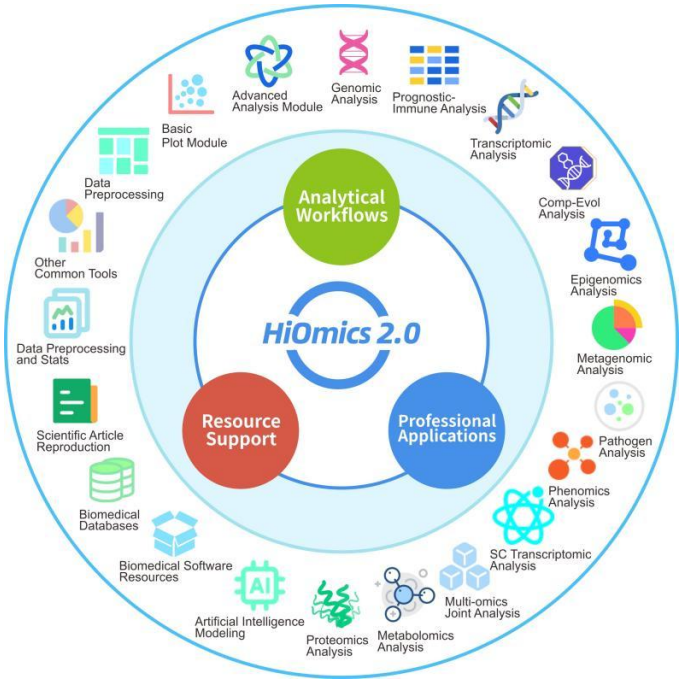

Figure 2. Functional architecture of the HiOmics 2.0 platform. The platform is organized into three layers. The outer ring represents three foundational components: Analytical Workflows (standardized pipelines across omics types), Professional Applications (advanced and specialized analysis tools), and Resource Support (data preprocessing, visualization, and knowledge bases). Together, these components comprise 21 core analytical modules and support integrated, modular analysis.

As of November 2025, the platform integrates 453 core analytical tools and provides direct links to 1,121 external resources. Since its launch in 2022, HiOmics has received 112,957 visits from users worldwide and completed 36,726 analytical tasks. Together, these metrics indicate broad usage and sustained adoption of the platform. This architecture reflects the evolution of HiOmics from a collection of discrete tools into an integrated infrastructure for life science research. Users can complete an end-to-end analysis cycle—from data preprocessing and multi-omics mining to model development and publication-ready visualization—within a unified platform. In terms of functionality, this release extends several core modules: (i) visualization, with improved real-time interaction and publication-quality customization; (ii) data processing, with streamlined preprocessing supported by a validation engine; and (iii) multi-omics analysis and causal inference (e.g., Mendelian randomization), including single-cell transcriptomics, proteomics, and metabolomic analyses. Together, these updates improve both coverage and analytical depth for addressing a range of current research questions.

Application Case Studies

To illustrate the analytical performance and application scope of core HiOmics 2.0 modules, we present three representative case studies. The case studies address three scenarios: (1) high-resolution single-cell exploratory analysis; (2) phenotype interpretation from a metabolomic perspective; and (3) rapid metagenomic pathogen identification and source tracing with clinical relevance. Collectively, they span stages from discovery-oriented exploration and mechanistic interpretation to application-oriented analysis, highlighting the platform's ability to support integrated analyses for complex biological questions.

Case study 1: Single-Cell Transcriptomics Analysis

Single-cell RNA sequencing (scRNA-seq) enables high-resolution profiling of gene expression in individual cells, supporting studies of cellular heterogeneity, cell-state transitions, and tissue microenvironments. To lower technical barriers, HiOmics 2.0 integrates 20 tools spanning the scRNA-seq analysis workflow, providing a standardized path from raw sequencing data to biological interpretation (Figure. 3A). The module supports key steps including cell quantification and quality control, clustering and visualization, differential expression analysis, cell type annotation, cell–cell communication analysis, and immune repertoire profiling.

To demonstrate module functionality, we analyzed the 10x Genomics peripheral blood mononuclear cell (PBMC) scRNA-seq dataset[19] using HiOmics 2.0. We first performed filtering, normalization, dimensionality reduction, and unsupervised clustering using the Single-Cell Quality-Control and Clustering tool, and visualized the resulting clusters (Figure. 3B). We then performed differential expression analysis for each cluster. Using the manual annotation feature in the Cell Annotation tool, together with known marker genes identified by differential expression (effect size and statistical significance), we annotated major immune populations, including B cells, T cells, NK cells, and monocytes (Figure. 3C). We visualized expression patterns of selected genes using Single-Cell Gene Expression Density Plots and Single-Cell Gene Expression Bubble Plots (Figure. 3D, E). Finally, we inferred ligand – receptor interaction networks between cell types using the Cell Communication Analysis tool, and assessed associated signaling pathway activity (Figure. 3F) and communication strength (Figure. 3G, H), generating hypotheses about intercellular crosstalk.

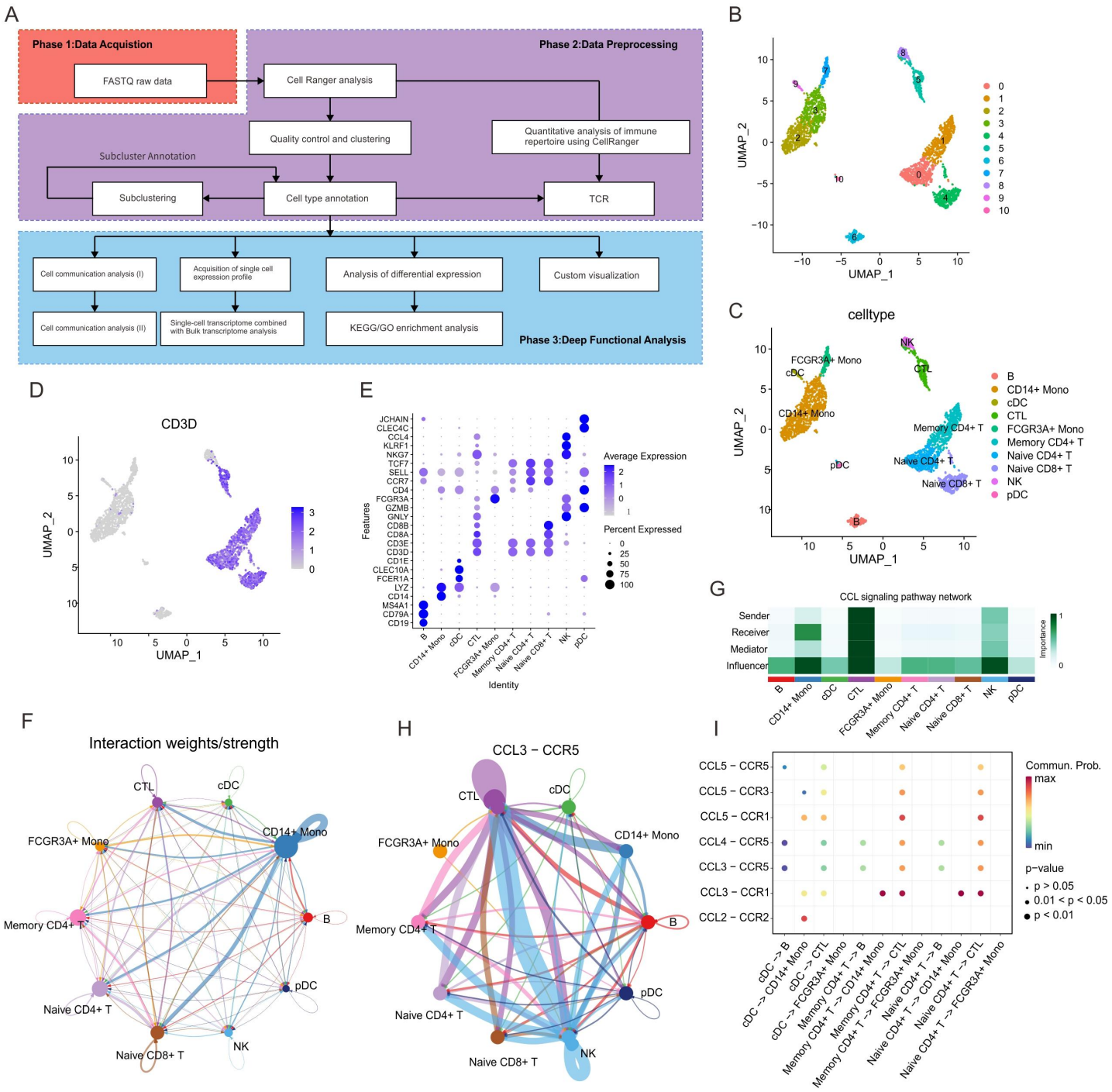

Figure 3. scRNA-seq workflow and representative visualizations in HiOmics 2.0. (A) Overview of the standardized single-cell RNA sequencing (scRNA-seq) analysis pipeline. (B) Uniform Manifold Approximation and Projection (UMAP) showing unsupervised clustering of peripheral blood mononuclear cells (PBMCs) after quality control, normalization, and dimensionality reduction. (C) Cell type annotation based on marker-gene expression. (D) Density plots of key-gene expression distributions across cell subpopulations. (E) Bubble plot showing average expression of signature genes and the fraction of expressing cells per cluster. (F) Schematic of the cell – cell communication network inferred from ligand – receptor interactions. (G) Heatmap of inferred centrality scores. (H, I) Network and bubble plots showing inferred communication strength between cell types and ligand – receptor pairs, respectively.

This case study shows that the single-cell module supports an end-to-end exploratory workflow from raw data to biological hypotheses with minimal programming requirements. The module is designed to improve standardization and reproducibility and to facilitate biological interpretation of scRNA-seq results.

Case study 2: Metabolomics Profiling and Analysis

Metabolomics captures downstream biochemical changes and is often used to characterize functional phenotypes of biological

systems. To support mechanistic interpretation from raw data, HiOmics 2.0 provides a dedicated metabolomics analysis module. The module provides an integrated workflow for mass-spectrometry data preprocessing, metabolite annotation, multivariate statistical analysis, and pathway enrichment.

To demonstrate module functionality, we analyzed a publicly available whole-blood metabolomics dataset in mzML format[20]. We first used the built-in Metabolomics MS Identification and Preprocessing tool to perform peak picking, alignment, normalization, and metabolite annotation. Quality control indicated consistent total ion chromatograms (Figure. 4A) and balanced cross-sample intensity distributions after log transformation (Figure. 4B); within-group reproducibility was supported by a sample-correlation heatmap (Figure. 4C). We then performed principal component analysis (PCA) and orthogonal partial least squares discriminant analysis (OPLS-DA) using the Multivariate Statistical Analysis tool (Figure. 4D, E). Differential metabolites were identified based on statistical testing (Figure. 4F). In addition, users can invoke MetaboAnalyst 6.0 or use the built-in Basic Plot Module for differential-metabolite analysis and customized visualization.

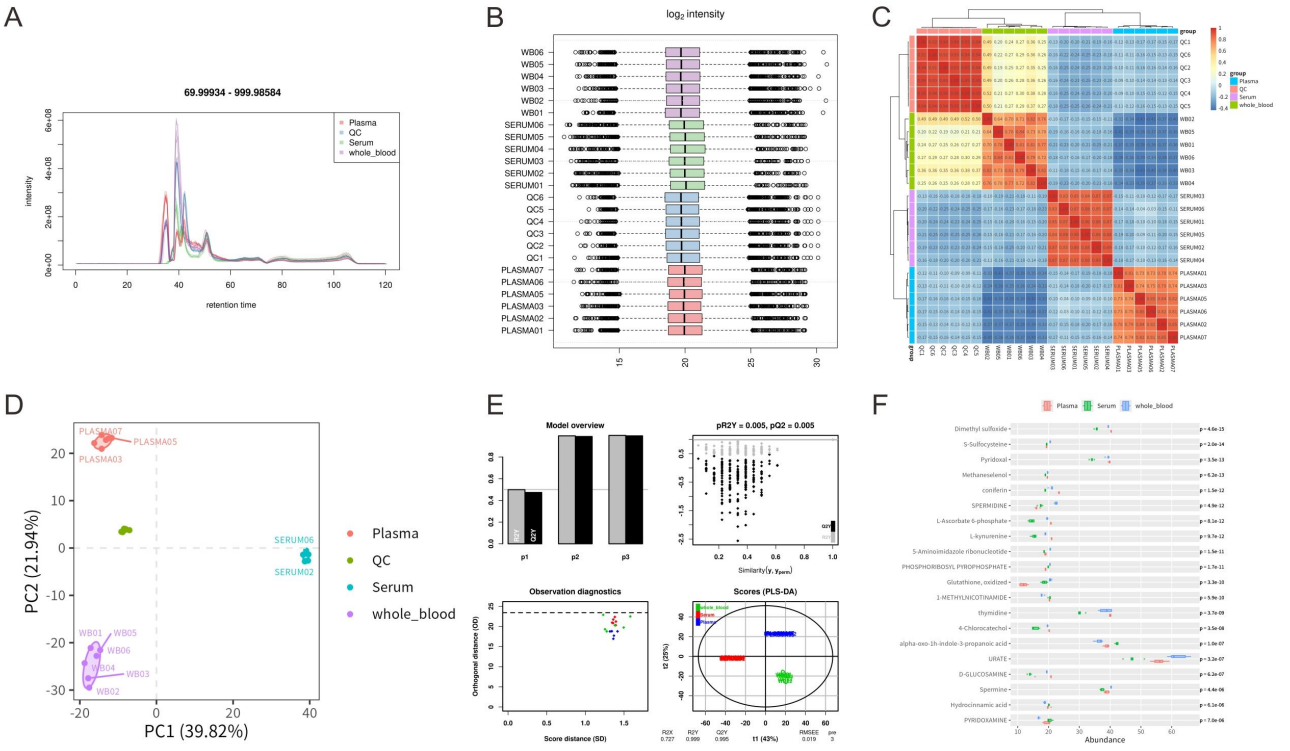

Figure 4. Representative visualizations from the HiOmics 2.0 metabolomics module. (A) Total ion chromatogram (TIC) from raw liquid chromatography – mass spectrometry (LC – MS) data. (B) Box plot of log-transformed signal intensities across samples. (C) Sample-by-sample Pearson correlation heatmap. (D) Principal component analysis (PCA) score plot. (E) Orthogonal partial least squares discriminant analysis (OPLS-DA) permutation test. (F) Differential metabolite analysis between groups.

This case study shows that the metabolomics module supports an end-to-end workflow ― from raw data processing to hypothesis generation―reducing the need to switch across multiple software tools.

Case study 3: Pathogen Detection and Analysis

Clinical metagenomic next-generation sequencing (mNGS) remains challenging due to complex workflows, abundant host-derived background reads, and the difficulty of confidently identifying pathogenic organisms. To address these challenges, HiOmics 2.0 includes a dedicated Pathogen Analysis module. The module is built around our previously published HPD-Kit toolkit[14], for which performance evaluation and benchmarking have been reported previously; HiOmics 2.0 integrates HPD-Kit into an automated web-based workflow from raw data upload to report generation (Figure. 5).

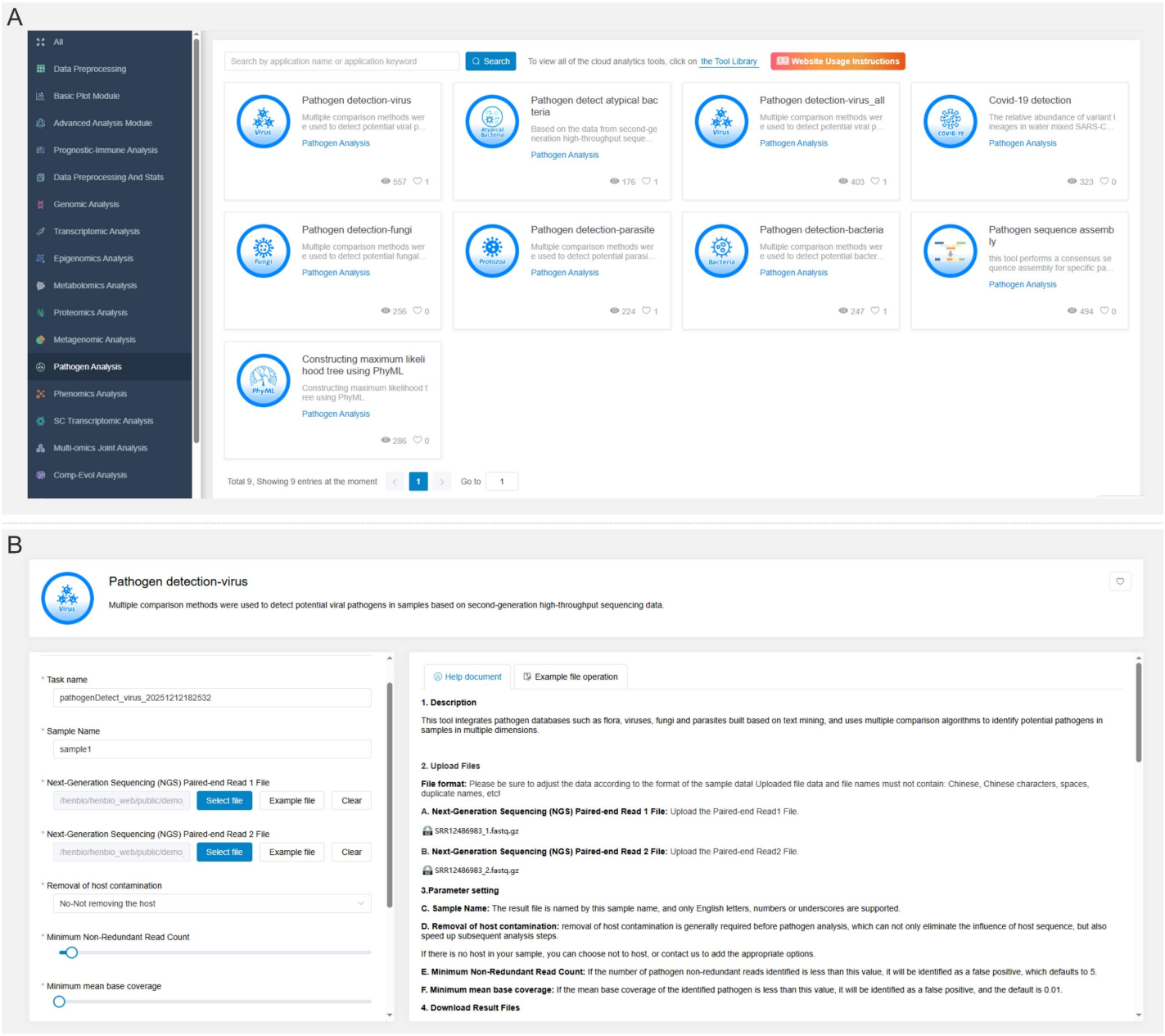

Figure 5. Interface of the Pathogen Analysis module in HiOmics 2.0. (A) Main interface of the Pathogen Analysis module. Users access detection workflows via the central panel and navigate using the left-side menu. (B) Interface of the Pathogen Analysis plug-in. The parameter configuration panel is on the left, and the results/summary panel is on the right.

The module supports detection of major pathogen groups (viruses, bacteria, fungi, and parasites) and includes targeted identification of clinically important atypical bacteria (e.g., *Chlamydia*, *Mycoplasma*, *Rickettsia*, and *Spirochaeta*). The platform also supports pathogen genome assembly and maximum-likelihood phylogenetic tree construction using PhyML, enabling source tracing and evolutionary analysis. Together, these features provide an end-to-end pipeline from pathogen identification to downstream evolutionary analysis. Users upload raw sequencing data (e.g., respiratory, cerebrospinal fluid, blood, or stool samples) and select the appropriate pipeline. The platform then executes: (1) host-read removal and quality control; (2) multi-algorithm pathogen identification, reporting species abundance, genome coverage, and the novel Normalized Pathogen Abundance Score (NPAS) (developed in this study); and (3) assembly of detected pathogen genomes followed by phylogenetic tree construction for source tracing and variant analysis. This workflow consolidates steps that typically require command-line tools into a web-based service, lowering the technical barrier for routine use.

This case study shows that the Pathogen Analysis module operationalizes HPD-Kit as an accessible service for clinical and research use, supporting time-sensitive metagenomic analyses.

Integrated Performance and User Experience

To evaluate the practical impact of the upgrade, we benchmarked the hierarchical task-scheduling system. The benchmark results indicate improved interactive responsiveness under the new architecture. For example, the end-to-end time to generate a standard differential-expression volcano plot decreased from over 30 seconds to below 5 seconds (an improvement exceeding 80%).

For interaction design, the platform uses a synchronized two-panel interface: users set parameters and submit tasks on the left, and results are rendered on the right in real time. This

design reduces frequent page switching between task submission, result viewing, and file downloads in conventional workflows. The platform also enables common statistical plots (e.g., heatmaps and box plots) to be rendered within seconds, facilitating interactive data exploration and iterative analysis.

To lower the barrier to adoption, we provide a support framework with three components: (i) a user manual covering platform overview, registration, tool usage, and data management, with guidance from introductory to advanced operations; (ii) video tutorials organized by typical use cases, with 16 videos covering bulk and single-cell transcriptomics, prognostic model construction, publication-quality figure generation, and Mendelian randomization; and (iii) an in-platform feedback mechanism with a one-click error report in the task-management interface, where reports automatically include task logs, environment metadata, and operation context to support troubleshooting and issue resolution.

Together with the platform ' s high-performance computing backend, these components provide a cloud-based environment for efficient processing and user-oriented interaction, lowering the technical barrier for multi-omics analysis and shortening the operational path from data to results. This allows researchers to focus on scientific questions while routine analysis and troubleshooting are handled within the platform.

Discussion

This study presents HiOmics 2.0, addressing challenges in multi-omics data analysis related to platform integration, interactive responsiveness, and analytical accessibility. HiOmics 2.0 introduces hierarchical task scheduling and integrates modules for single-cell transcriptomics, metabolomics, and clinical pathogen detection, enabling an end-to-end workflow from data processing to downstream interpretation. Benchmarking showed that interactive response times were reduced by over 80% for representative plotting tasks. Case studies illustrate the platform ' s use in diverse scenarios, inclu- ding constructing high-resolution cell atlases, investigating metabolic regulation, and supporting rapid pathogen iden- tification. Together, these advances move HiOmics from a collection of discrete tools toward a cloud-based research environment that supports integrated multi-omics analysis with improved efficiency and reproducibility.

Compared with general-purpose workflow platforms (e.g., Galaxy) or standalone tools, HiOmics 2.0 emphasizes a tightly integrated, closed-loop user workflow from task submission to visualization and reporting. The upgrade contributes in three aspects. First, hierarchical task scheduling reduces latency during exploratory analysis and supports interactive, iterative workflows. Second, HiOmics 2.0 integrates advanced modules across single-cell omics, metabolomics, and pathogen detection, including HPD-Kit previously published and evaluated in our prior work[14], providing a consolidated environment spanning basic research and translational settings. Third, documentation, video tutorials, and an in-platform one-click error-reporting mechanism improve accessibility by simplifying onboarding and troubleshooting. Collectively, these improvements provide a more responsive and integrated environment for modern multi-omics workflows.

Looking ahead, we will focus on platform intelligence, interactive experience, and ecosystem openness. Planned work includes exploring AI-agent assistance for workflow recommendations and preliminary result summaries, optimizing real-time interaction and visual feedback, and enabling connectivity with external resources through open APIs. Our goal is to develop HiOmics into an intelligent, open, and trustworthy next-generation life-science analysis platform.

Conclusion

Through architectural and functional upgrades, HiOmics 2.0 advances toward an integrated cloud platform for large-scale multi-omics analysis. A key contribution is hierarchical task scheduling, which reduces latency in interactive analysis and improves responsiveness during exploratory workflows. By integrating advanced analytical modules and providing standardized, containerized workflows, HiOmics 2.0 lowers the operational barrier to running end-to-end analyses while improving reproducibility and traceability. Overall, HiOmics 2.0 provides a responsive and integrated analysis environment for life-science research.

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Author Contributions

Zhining Zhang: Writing-original manuscript, Methodology, Supervision, Software. Yuanyuan Tang: Writing-original manuscript. Yunlin He: Single-cell data analysis. Yong Xu: Metabolomics data analysis. Zhiwei Lu: Visualization, Figure preparation. Kangming He: Software. Hong Qiu: Investigation, Resources. Yongjian Huang, Juan Huang and Honghong Pu: Validation. Yanling Hu: Supervision, Project administration, Funding acquisition. All authors have read the final manuscript and approved it for publication.

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Ethics Statement

This study utilized publicly available, de-identified human data for platform demonstration. Ethical compliance for data generation was ensured by the original studies, and secondary analysis here is exempt from additional approval.

Conflict of interest statement

Yanling Hu hold the position of Editor-in-Chief for iCell and was blinded from peer review and decision-making for the manuscript.

Data availability statement

The website can be freely accessed at https://henbio.com. Furthermore, the available open-source code of the website is located at https://github.com/yongkangning/HiOmics.