

HBIcloud: A comprehensive, user-centric platform for integrative multi-omics analysis

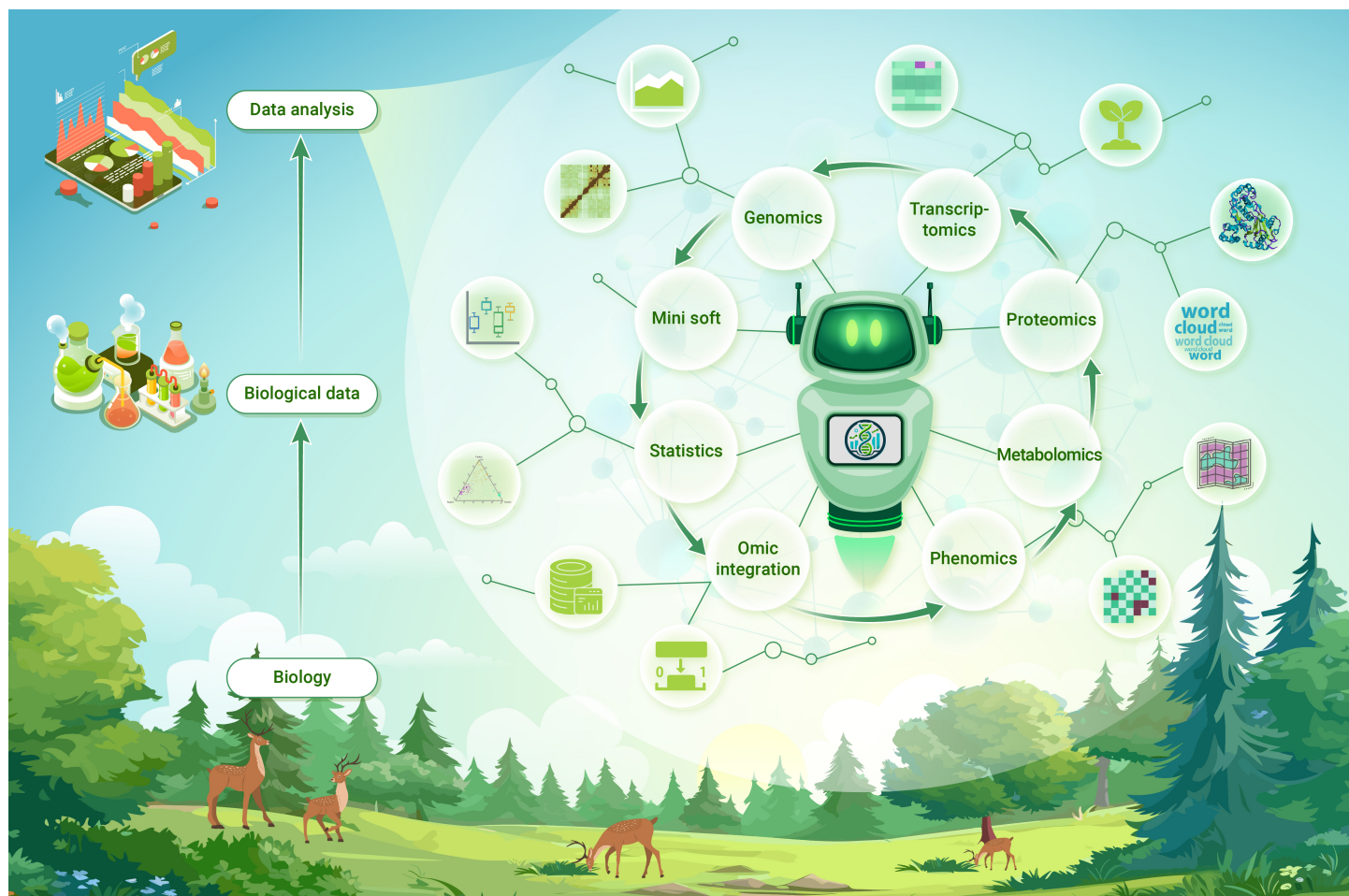
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GRAPHICAL ABSTRACT



PUBLIC SUMMARY

- HBIcloud is an online platform that integrates multi-dimensional omics tools.
- It enables users to perform analyses without requiring advanced programming skills.
- It offers over 100 tools through a simple, one-stop operation, catering to a wide range of needs.
- HBIcloud streamlines data preprocessing, normalization, and integration to aid research.

HBcloud: A comprehensive, user-centric platform for integrative multi-omics analysis

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The rapid expansion of multi-omics data has revolutionized biological research but introduced significant challenges in data integration and analysis, particularly for researchers without advanced computational expertise. HBcloud addresses this gap by offering a centralized, user-friendly online platform integrating 103 tools across genomics, transcriptomics, proteomics, metabolomics, phenomics, and multi-omics integration. Through standardized workflows, extensive parameter customization, and detailed documentation, HBcloud enables researchers to conduct high-quality, reproducible analyses without programming skills. The platform streamlines data preprocessing, normalization, and integration, empowering users to explore complex biological systems and drive innovation in multi-omics research. Furthermore, we discuss the prospects of HBcloud, including planned enhancements and its potential for high citation impact within the scientific community. By providing a robust and versatile platform, HBcloud aims to accelerate discovery and innovation in the field of multi-omics, fostering collaborative research and expanding the boundaries of biological understanding. The official website of HBcloud is <https://bioinformatics.hainanu.edu.cn/hbcloud/>.

INTRODUCTION

The rapid advancement of omics technologies has ushered in a new paradigm in biological research,¹ enabling investigators to systematically dissect the multi-layered regulatory networks of life activities with unprecedented resolution. As the origin of biological information flow, genomics deciphers the genetic blueprint of species,² providing a molecular foundation for understanding genetic variation patterns and evolutionary mechanisms. Building upon this, transcriptomics captures gene expression dynamics in real time,³ elucidating the precise regulatory mechanisms governing DNA to RNA transitions. Following the central dogma, proteomics further reveals post-translational modifications and protein-protein interaction networks,⁴ delineating the functional executors of biological processes. Meanwhile, metabolomics focuses on spatiotemporal variations of small-molecule metabolites,⁵ reflecting metabolic pathways and their dynamics. Notably, phenomics bridges genotypic variations with observable traits through high-throughput phenotyping technologies.⁶

Despite remarkable progress in single-omics studies, emergent properties of living systems often arise from multi-level synergistic regulation. This biological imperative has driven the development of multi-omics integration approaches—a framework that systematically combines multidimensional data (genomic variants, transcriptional regulation, protein interactions, and metabolic networks) to uncover regulatory hubs inaccessible to conventional single-omics analyses. Representative studies demonstrate that genome-transcriptome integration can precisely map expression quantitative trait loci (eQTLs),⁷ while protein-metabolite network reconstruction identifies rate-limiting nodes within disease-associated pathways.⁸ Such integrative strategies not only offer novel insights into complex trait formation but also pave new avenues for biomarker discovery and precision medicine.

Nevertheless, multi-omics integration presents a series of significant challenges.^{9,10} The inherent heterogeneity of omics data, including variations in data types, scales, and dimensionalities, complicates the integration process substantially. Differences in data quality, batch effects, and missing values further exacerbate this complexity. Furthermore, the computational and statistical methods required for effective integration are often sophisticated, demanding extensive domain expertise and substantial computational

resources.¹¹ Contemporary integration approaches, such as multimodal deep learning and graph neural networks, impose considerable requirements in terms of computational power and bioinformatics proficiency, thereby limiting their broader adoption. These barriers are particularly pronounced for researchers without advanced bioinformatics skills or access to high-performance computing infrastructure.

To address these challenges, the development of HBcloud was initially motivated by the need to democratize access to multi-omics data analysis tools. Our objective was to establish a platform that not only supports the integration of diverse omics data types but also offers an intuitive interface and comprehensive support, thereby empowering researchers from a wide range of backgrounds. HBcloud is specifically designed to enable wet lab scientists to concentrate on biological questions rather than technical intricacies.

Compared to the single visualization form of Majorbio's heatmaps tool in biodiversity analysis,¹² HBcloud offers a broader spectrum of heatmap presentation modes. Furthermore, HBcloud integrates advanced functionalities such as sequence editing, gene editing, and data transformation, providing more comprehensive capabilities than Hplot.¹³ The "Density peak plot" tool extends beyond traditional peak density maps generated using R language by incorporating chromatographic mapping and advancing visualization from two-dimensional to three-dimensional data representation,¹⁴ thereby significantly enriching the information displayed. This function also supports adjustable peak spacing. In proteomics analysis, HBcloud's "DNA2Protein" tool surpasses conventional DNA translation platforms through the inclusion of a Genetic Codes parameter option that encompasses 26 encoding methods and provides three alternative starting translation sites. Its versatile translation modes allow researchers to explore protein sequence characteristics with greater efficiency. Additionally, the integration of three-dimensional protein structure visualization enables multi-dimensional analysis of protein structures. Compared to BioLadder,¹⁵ HBcloud not only diversifies analytical parameters but also incorporates multiple algorithms. Moreover, HBcloud has implemented seed and seedling recognition image processing functionality, which is rarely found in most cloud platforms or software currently available on the market. HBcloud simplifies the entire analysis workflow, from data preprocessing and normalization through integration and visualization, ensuring that researchers from various backgrounds can achieve biologically significant and highly reproducible results without requiring extensive programming knowledge.

MATERIALS AND METHODS

Java (version 17.0.10), jQuery (version 3.2.1), Python (version 3.8) and R (version 4.3.1) serve as the primary technologies for developing the platform. The front-end interface development consists of HTML, CSS, Javascript and JAVA languages, combining the Thymeleaf framework (version 3.0.12) and Bootstrap (version 5.3.0). These tools facilitate data submission by researchers and customization of result presentation. SpringBoot (version 2.4.4) functions as the backend web framework, managing the data and parameters submitted by researchers. The analytical outcomes are then relayed to the front-end for researchers to review, with the option to download result files. In the realm of data visualization, HBcloud leverages ggplot2 (version 3.5.1), matplotlib (version 3.7.5), and seaborn (version 0.13.2). By harnessing the analytical and visualization capabilities of these libraries, researchers can delve into data exploration and analysis intuitively.

Collectively, the amalgamation of SpringBoot, Thymeleaf, jQuery, Bootstrap, ggplot2, matplotlib, and seaborn empowers HBcloud to seamlessly amalgamate backend functionalities, front-end development, and dynamic data



Figure 1. Overview of the 103 tools integrated in HBICloud All these tools are classified according to the different omics, including genomics, transcriptomics, proteomics, metabolomics, phenomics, omic integration, as well as statistics and mini-soft.

analysis and visualization.

RESULTS

HBICloud offers a suite of 103 tools covering various omics disciplines (Figure 1). For genomics, it includes tools for sequence alignment,¹⁶ variant calling,¹⁷ genome assembly, and annotation.^{18,19} In the realm of transcriptomics, it provides tools for differential gene expression analysis, transcript assembly, and functional annotation. Proteomics tools facilitate protein identification, quantification, and functional analysis, while metabolomics tools aid in metabolite identification, quantification, and pathway analysis.^{20,21} For phenomics, HBICloud offers tools for phenotype data analysis and visualization. Furthermore, the platform includes tools for multi-omics integration, such as clustering, dimensionality reduction, and network analysis.²²⁻²⁴ Additionally, a

collection of mini tools for specific tasks enhances the flexibility of the platform.

The HBICloud platform was designed with a user-centric approach, incorporating features that ensure a seamless experience (Figure 2). Its tool interface integrates a comprehensive and intuitive workflow system, along with a one-click analysis function that minimizes user interaction requirements (Figure 3). The step-by-step operational workflow of the HBICloud platform is designed to be intuitive and user-friendly, enabling researchers to perform complex analyses with ease. The procedure involves the following steps: (1) select the desired analytical tool; (2) review the Demo section, which provides an overview of the tool along with examples of input and output file formats; (3) input data manually or upload the corresponding file; (4) configure the analysis parameters as needed; (5) initiate the analysis by clicking the "Run"

HBICLOUD SOLUTIONS OF BIOLOGICAL DATA ANALYSIS | SINCE 2021

Home Genomics Transcriptomics Proteomics Metabolomics Phenomics Omic integration Statistics Mini soft

Algorithm

Data

	Sample1	Sample2	Sample3	Sample4
gene1	295.7	0.8	351.7	204.9
gene2	83.0	72.9	222.1	177.3
gene3	182.4	32.8	17.9	24.7
gene4	27.5	48.2	6.8	7.1
gene5	135.6	60.6	39.0	89.2
gene6	137.1	116.2	218.8	68.3
gene7	113.7	49.5	45.0	56.4
gene8	124.4	90.6	87.7	119.0
gene9	0.6	9.1	1.0	5.0
gene10	42.8	69.3	44.2	71.3

Preprocessing

Standard

$$D_{mn} = \frac{D - \bar{D}}{\sqrt{\frac{1}{N} \sum_{i=1}^n (D - \bar{D})^2}}$$

Z-score

$$D_{str} = \frac{D - D_{min}}{D_{max}}$$

MICE

$$\hat{X}_{ij} = f_j(X_{i, -j}) + \epsilon_{ij}$$

KNN

$$\hat{y} = mode\{y_i : i \in N_k(x)\}$$
$$\hat{y} = \frac{1}{k} \sum_{i \in N_k(x)} y_i$$

ComBat

$$Z_{ij} = \frac{Y_{ij} - \hat{\mu}_i}{\hat{\sigma}_i}$$
$$Y_{ij}^* = \gamma_j + \delta_j \cdot Z_{ij}$$
$$Y_{ij}^{abj} = \hat{\mu}_i + \hat{\sigma}_j \cdot Y_{ij}^*$$

Integration

iCluster

$$X_j = \Lambda_j Z + \epsilon_j \rightarrow \min_{\Lambda_j Z} \sum_j \|X_j - \Lambda_j Z\|^2 + \lambda \|Z\|_1$$



Tutorial



FAQ



Conferences



Lab



External links

AI conversations window

Total tools



Total:103

- Genomics
- Transcriptomics
- Proteomics
- Metabolomics
- Phenomics
- Omic integration
- Statistics
- Mini soft

Highlights



Comprehensive support for multi-omics analysis



Use chromatography to represent data of different sizes



Use multiple algorithms to facilitate data analysis



Add multiple innovative tools



Zero-code advanced analysis, fast generation



Encryption ensures data security

Updates

Welcome to send your suggestions or comments to us.

- ▼ (09-05-2025) Update the tutorial.
- ▼ (02-05-2025) Update 1 function (e.g. Sequence statistics).
- ▼ (21-02-2025) Update 1 function (e.g. Gene cluster prediction).
- ▼ (15-01-2025) Update 1 function (e.g. Maintain some functions of the website).
- ▼ (10-09-2024) Update 1 function (e.g. GSEA).
- ▼ (09-30-2024) Update 1 function (e.g. Kmens).

more+

About us

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Our users

Visits

Figure 2. The online homepage of HBICloud.

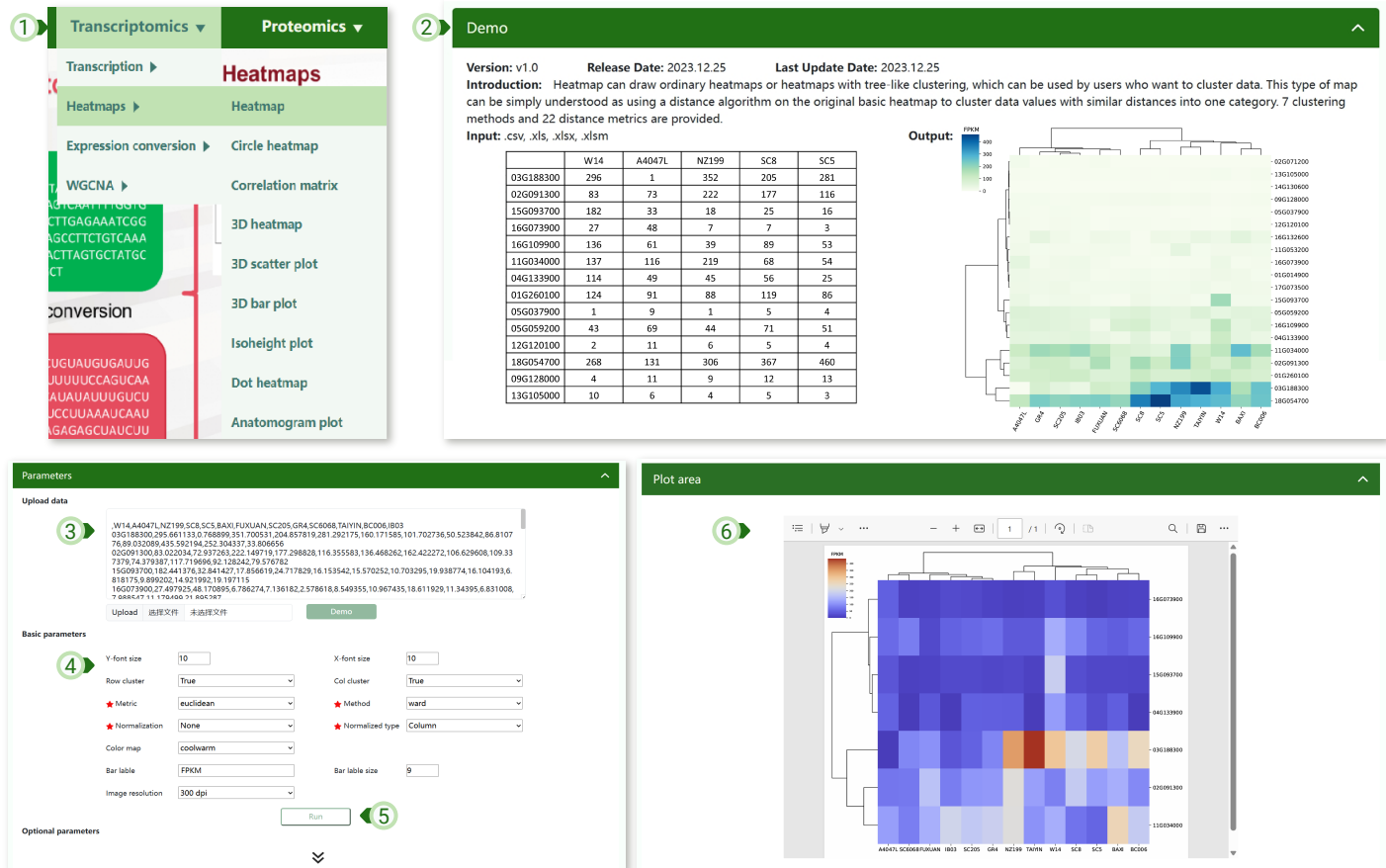


Figure 3. Schematic representation of HBIcloud tool usage The tool interface of HBIcloud is systematically organized into six primary sections, with each functionally distinct component indicated by numerically labeled circles.

button; and (6) visualize the resulting figures in the Plot Area. Standardized workflows for common analyses reduce the learning curve for new users, while extensive parameter options allow advanced users to fine-tune their analyses. The platform's graphical user interface eliminates the need for coding skills, making it accessible to researchers from diverse backgrounds. Comprehensive tutorials and a detailed FAQ section assist users at every step, ensuring they can effectively utilize the platform's capabilities. Moreover, HBIcloud supports various output formats, including publication-quality figures with various formats, and is compatible with multiple input file types, facilitating data import from various sources. The platform also offers instant access to all tools without registration, promoting ease of use and accessibility.

Applications and impact. HBIcloud offers comprehensive support for diverse applications in multi-omics research. The platform facilitates rigorous data analysis through advanced tools for dataset normalization and harmonization, thereby ensuring robust data comparability and enhanced reproducibility. Notably, its integrative analysis framework enables systematic combination of multiple omics layers, permitting elucidation of complex biological interactions and underlying regulatory mechanisms.²⁵⁻²⁷ Furthermore, the platform incorporates sophisticated visualization modules that transform analytical results into interpretable, publication-quality graphical representations, significantly enhancing researchers' capacity to effectively disseminate scientific findings.

In the field of multi-omics research, the comprehensive toolkit offered by the HBIcloud platform plays a crucial role in deciphering the complexity of biological systems. It supports the integration of multidimensional datasets, the analysis of statistical associations, and the automation of analytical workflows. The genomics toolkit is structured using a hierarchical modular framework, encompassing a series of core analytical components that enable sequential data processing (Figure 4). These components include sequence statistics, gene structure analysis, evolutionary inference, functional prediction, and gene editing, all arranged in a logically progressive analytical

pipeline. Particularly significant are specialized modules such as Hi-C plot, Chr. circle plot, and GuideRNA design, which provide key insights into the relationship between chromosomal architecture and gene function. The Hi-C technology captures genome-wide three-dimensional chromatin conformations, revealing spatial interactions within genomic domains and offering critical perspectives on gene regulation. The Chr. circle plot tool visualizes chromatin conformation data, helping researchers identify functional chromatin loops and elucidate their roles in transcriptional regulation. The GuideRNA design module enables precise targeting sequence design for CRISPR-Cas9 genome editing, facilitating both genome manipulation and functional verification.

In transcriptomics research, analytical tools such as diverse heatmap visualizations and Weighted Gene Co-expression Network Analysis (WGCNA) related plotting functions have substantially advanced our understanding of gene expression dynamics and their functional relevance (Figure 5). The HBIcloud platform provides a comprehensive suite of heatmap tools, including circular, isoheight, three-dimensional (3D), and dot heatmaps, all equipped with enhanced visualization capabilities. These tools support a variety of clustering options, encompassing seven distinct clustering algorithms and twenty-two distance metrics, thereby offering flexible and robust approaches to explore gene expression patterns. The heatmaps utilize intuitive color gradients to represent expression variability, allowing for rapid identification of expression shifts and their potential correlations with specific biological traits. The "Anatomogram plot" tool visualizes the expression patterns of various tissues from animals or plants in a color-coded format across the entire anatomical structure, thereby facilitating the identification of differences between tissues. Notably, the Module-Trait Analysis function within the WGCNA framework is instrumental in elucidating gene regulatory architecture by associating gene co-expression modules with phenotypic traits. This integrative analysis provides a systematic and biologically meaningful framework for interpreting transcriptomic data and uncovering regulatory mechanisms underlying complex biological processes.

HBIcloud provides a suite of essential proteomics tools, including protein analysis, protein domain annotation, and a 3D structure plot that are critical

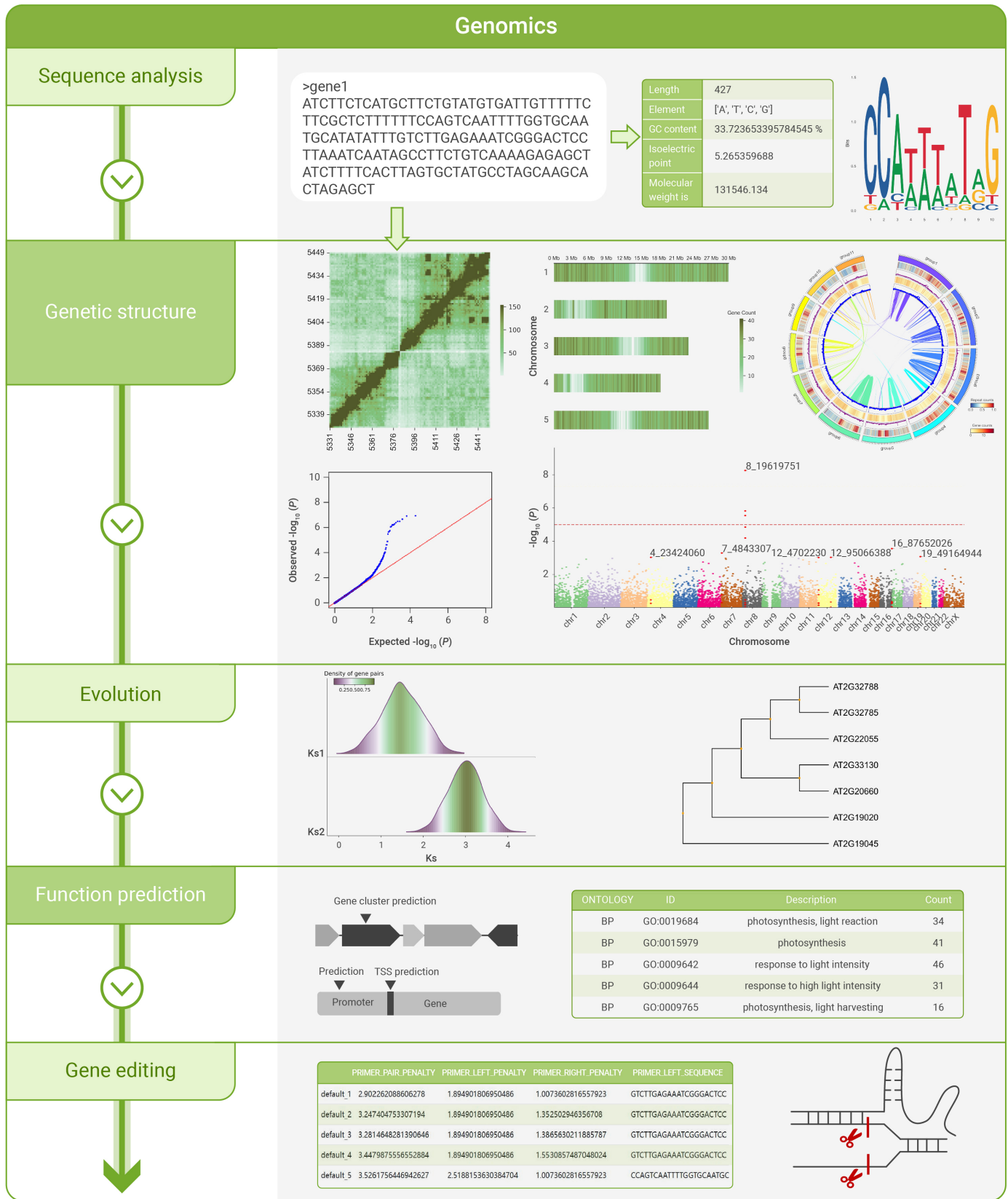


Figure 4. Representative genomic tools in HBIcloud These include tools for sequence analysis, genomic analysis, genetic analysis, and evolutionary analysis.

for elucidating protein function and molecular interactions (Figure 6). The Protein analysis tool offers a comprehensive set of physicochemical parameters, such as amino acid composition, molecular weight, aromaticity, instability index, isoelectric point, and molar extinction coefficient. These metrics facilitate functional characterization and interaction profiling of proteins in diverse biological contexts. The Protein domain analysis tool identifies conserved functional domains, thereby elucidating modular architectures that underpin specific biological activities and signaling mechanisms. The 3D structure plot

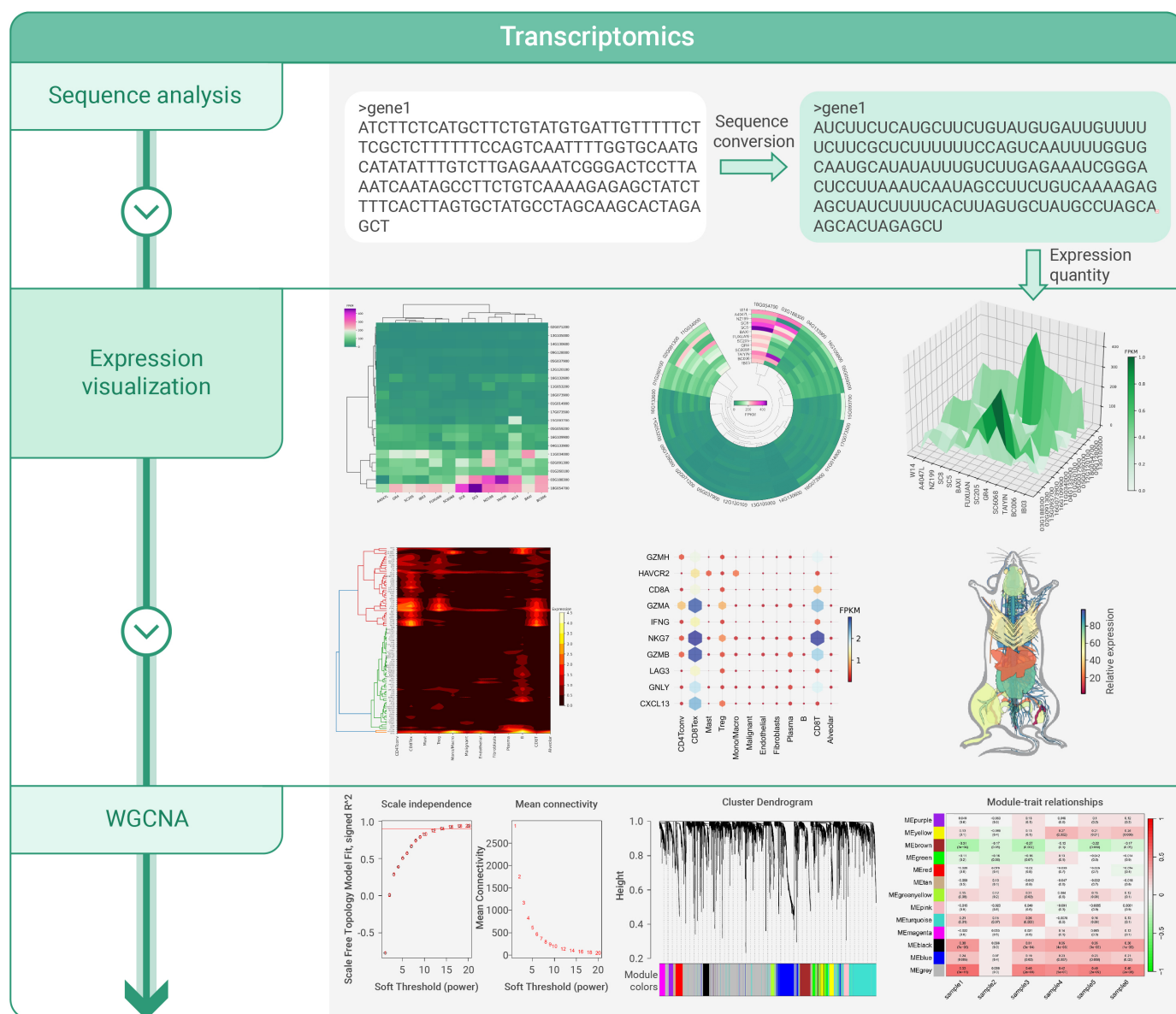


Figure 5. Representative transcriptomic tools in HBIcloud These include tools for sequence analysis, expressional analysis, and correlation analysis.

tool enables the modeling and rendering of protein spatial conformations, allowing researchers to examine structural features and potential interaction interfaces with ligands or other macromolecules. This supports in-depth structural functional analyses and aids in the identification of novel therapeutic targets.

In metabolomics, HBIcloud integrates pivotal tools such as metabolic Network plot, Volcano plot, and Corplot, which collectively enhance the interpretation of metabolic pathways and metabolite associations (Figure S1). The Network plot tool visually maps complex metabolite interactions, highlighting key nodes and regulatory hubs within metabolic networks. Volcano plot presents fold-change against statistical significance, enabling the identification of significantly altered metabolites with potential biomarker value. Corplot displays pairwise correlation matrices among metabolites, uncovering synergistic interactions and coordinated metabolic shifts, thus providing valuable insights into regulatory dynamics in metabolic systems.

In phenomics, specialized tools such as Seed recognition and Seedling recognition contribute to high-throughput phenotypic analysis (Figure 7). The Seed recognition tool processes seed imagery to assess morphological diversity and its association with environmental adaptability. The Seedling recognition tool quantifies developmental traits in emerging seedlings, offering insights into early growth performance. Additionally, the Geographic map tool, a geospatial heatmap visualization, presents phenotypic or distributional data across diverse geographic regions, facilitating the exploration of spatial

patterns in crop variety distribution and agronomic adaptation.

In multi-omics data integration, tools such as Z-score normalization, ComBat, and iCluster are fundamental for harmonizing and jointly analyzing heterogeneous omics datasets. Z-score normalization standardizes data across platforms, facilitating more intuitive and accurate cross-omics comparisons by mitigating discrepancies in data scales. The ComBat algorithm addresses batch effects arising from technical variations between experimental runs, thereby enhancing the reliability and reproducibility of integrated analyses. iCluster, a Bayesian-based integrative model, simultaneously incorporates multiple omics layers to uncover latent structures and inter-omics correlations, offering deeper insights into complex biological systems.

Within HBIcloud's statistical omics analysis framework, visualization tools such as Boxplot, Beeswarm plot, and Sankey plot support both exploratory data analysis and the interpretation of complex relationships. The Boxplot succinctly represent the distribution of quantitative data, highlighting medians, interquartile ranges, and potential outliers. The Beeswarm plot display individual data points in a non-overlapping manner, effectively conveying data density and variation, particularly advantageous for small-sample studies. The Sankey plot visualizes flow-like relationships between variables, enabling researchers to trace multi-factorial associations and interaction pathways, and is particularly useful in metabolic and pathway analysis as

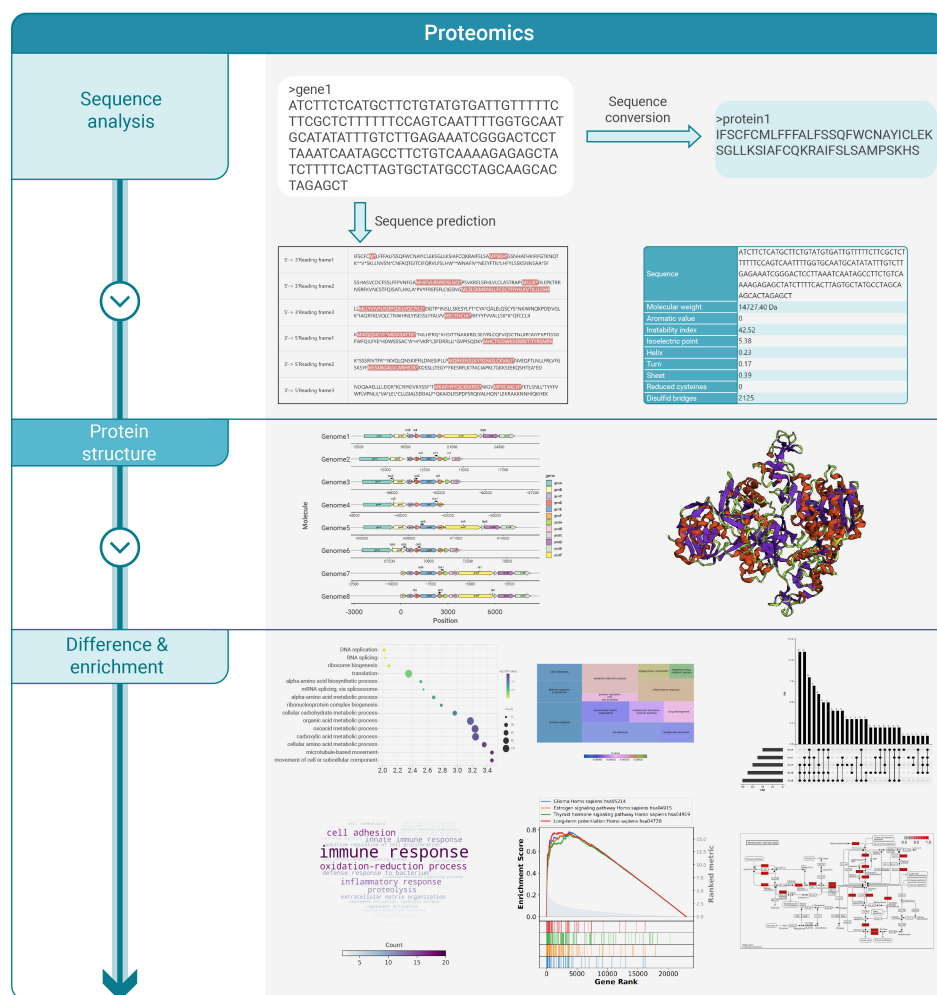


Figure 6. Representative proteomic tools in HBIcloud These include tools for sequence analysis, annotation, difference and enrichment analysis.

studies across different omics layers, driving the advancement of multi-omics research through diverse omics visualization and analysis, multidimensional data integration, and statistical analysis. They not only enhance data processing capabilities but also provide richer analytical dimensions and technical support for multi-omics research, fostering a more comprehensive understanding of biological systems.

The combination of comprehensive tools, user-friendly features, and robust documentation makes HBIcloud an invaluable resource for researchers. Its ability to facilitate high-quality, reproducible multi-omics analysis positions it as a highly citable platform in the scientific community.

FUTURE PROSPECTS

Looking ahead, HBIcloud aims to continuously expand its suite of tools by integrating emerging technologies and methodologies, including single-cell omics,²⁸ spatial omics,²⁹ and advanced machine learning algorithms for integrative analysis.³⁰ By staying at the forefront of technological innovation, HBIcloud ensures its continued relevance and adaptability to the evolving needs of the research community.

Enhancing user experience is another key priority in HBIcloud's future development. Efforts will focus on improving interface design to make it more intuitive and responsive. Incorporating user feedback will guide regular updates, ensuring that the platform aligns with users' needs and preferences. The

well as in tracking sample or resource allocation.

HBIcloud also provides a set of lightweight utility modules that enhance routine data management and sharing. For instance, the QR Code Generator rapidly encodes data or hyperlinks into QR formats, streamlining digital communication and data accessibility. The MD5 checksum tool ensures file integrity by generating a unique digital fingerprint for each file, enabling verification of data authenticity during transmission and storage. These auxiliary tools serve as important components of a secure and efficient data analysis workflow.

HBIcloud enables comprehensive multi-omics integration through synergistic tool interoperability, exemplified by its transcriptome-metabolome joint analysis pipeline. The platform first employs the Scatter and PCA plot tool of metabolomics to establish sample correlations via principal component analysis (PCA) (Figure S2A), while the Volcano plot tool of transcriptomics identifies differentially expressed genes (Figure S2B). Subsequent WGCNA analysis pinpoints phenotype-associated key regulatory genes (Figures S2C-F), whose expression patterns are visualized through heatmap (Figure S3A). Functional enrichment analysis, leveraging genomics-derived KEGG/GO pathways (Figure S3B), is then performed and visualized using the Enrichment bar plot (Figure S3C) and Bubble plot (Figure S3D) tools of proteomics to elucidate candidate gene functions. This integrated workflow systematically reveals gene-metabolite interaction networks, identifies critical regulatory nodes, and deciphers underlying biological mechanisms. Furthermore, HBIcloud supports spatiotemporal dynamics analysis through the Calendar plot tool (Figure S4A) of phenomics and the Anatomogram plot tool (Figure S4B) of transcriptomics, enabling temporal tracking of Sorghum expression profiles and tissue-specific visualization. The platform's heatmap matrix function subsequently highlights dynamic expression patterns of screened key genes (Figure S4C), establishing a robust framework for investigating developmental or environmentally responsive regulatory networks.

These tools play a unique role in their respective fields, enabling not only in-depth single-omics analysis but also facilitating multidimensional correlation

development of automated workflows will further simplify complex analyses, minimize manual intervention, and enhance overall efficiency.

Collaborative features are also planned for future releases. These capabilities will enable researchers to share datasets, workflows, and results directly within the platform, fostering collaboration and knowledge exchange across the scientific community. This collaborative approach will help build a more robust and interconnected research ecosystem, accelerating collective progress in multi-omics studies.

To support the research community further, HBIcloud plans to offer online courses, webinars, and workshops on multi-omics data analysis using the platform (Figure S5). These educational initiatives will promote the adoption and effective use of HBIcloud, ensuring researchers can fully leverage its capabilities for their studies.

HBIcloud has made significant advances in the field of multi-omics data analysis by providing a comprehensive, user-friendly, and powerful toolkit. With its diverse array of omics tools, HBIcloud supports the systematic elucidation of gene regulatory networks and the intricate relationships between chromatin structure and function. Through the visualization of gene expression patterns and their association with phenotypes, it reveals the dynamic architecture of gene regulation and offers spatiotemporal insights into biological systems. By clarifying the roles of genes in molecular interactions and life processes, HBIcloud facilitates novel discoveries and the development of therapeutic strategies. Its comprehensive functionality, ease of use, and commitment to continuous improvement position HBIcloud as a leading platform in multi-omics research. Through high-quality integrative analyses, HBIcloud holds significant potential for scholarly impact and scientific advancement, serving as a critical resource for deepening our understanding of complex biological systems.

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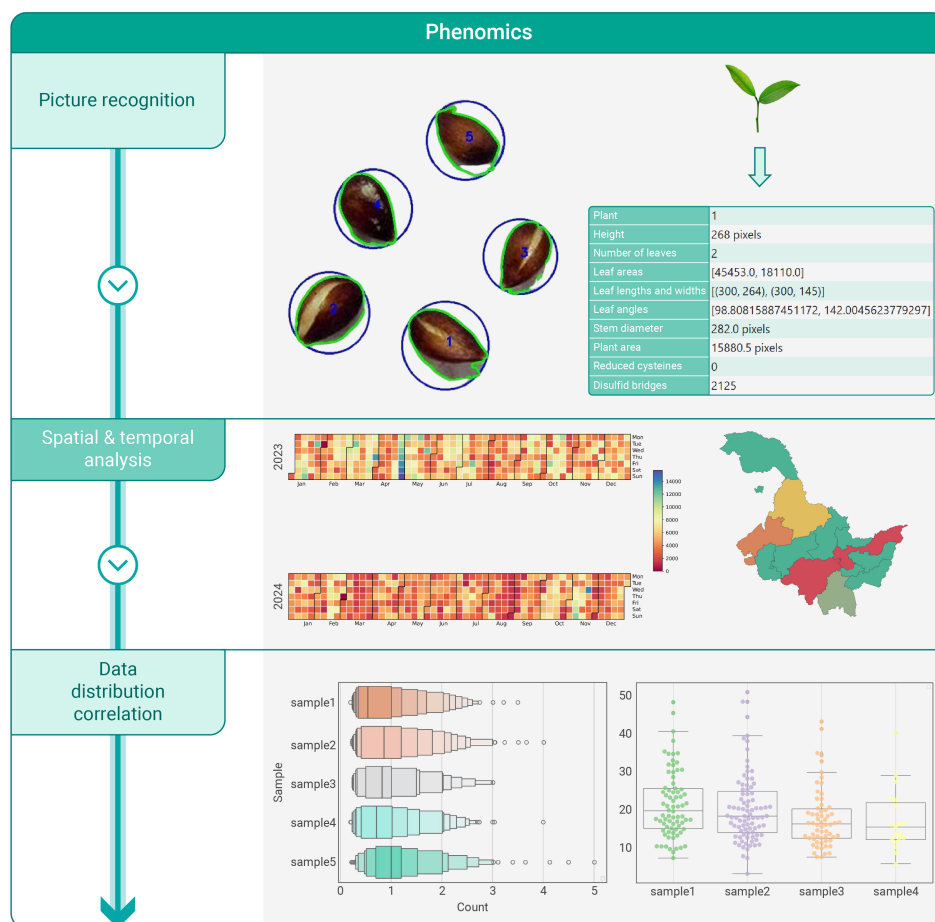


Figure 7. The HBICloud platform contains representative phenomics tools These include tools for Picture Recognition, Spatial & Temporal Analysis, and Data Distribution Correlation.

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AUTHOR CONTRIBUTIONS

Fei Chen and Ming Luo conceived the study. Fei Chen, Ming Luo and Wenquan Wang supervised the study. Yunqing Luo implemented the computational pipeline. Shuang He and Wei Dong performed the data analysis and visualization. Fei Chen and Shuang He wrote the manuscript. All authors reviewed and approved the manuscript.

DECLARATION OF INTERESTS

The authors declare no competing interests.

ETHICAL STATEMENT AND PATIENT CONSENT

Not applicable.

DATA AND CODE AVAILABILITY

All the data generated or analyzed during this research period are included in the Hbicloud platform (<https://bioinformatics.hainanu.edu.cn/hbicloud/>). Some of the data is from public data.

SUPPLEMENTAL INFORMATION

It can be found online at <https://doi.org/10.59717/j.xinn-life.2025.100157>