

SeekSoul Online: A user-friendly bioinformatics platform focused on single-cell multi-omics analysis

Xin Liu,^{1,3} Chenhua Wu,^{2,3} Lili Pan,¹ Jiaxin Wang,¹ Wanhai Chen,¹ Teng Gao,¹ Haifeng Guo,¹ Qun Ma,¹ Shaozhuo Jiao,¹ Zongwen Li,^{1,*} and Guangxin Zhang^{1,*}

*Correspondence: lizongwen@seekgene.com (Z.L.); zhangguangxin@seekgene.com (G.Z.)

Received: April 18, 2025; Accepted: August 19, 2025; Published Online: August 21, 2025; <https://doi.org/10.59717/j.xinn-life.2025.100156>

© 2025 The Author(s). This is an open access article under the CC BY license (<https://creativecommons.org/licenses/by/4.0/>).

GRAPHICAL ABSTRACT



PUBLIC SUMMARY

- SeekSoul Online supports the complete analysis process for scRNA, scTCR/BCR, and SeekSpace data.
- It provides a simple interface for manipulating, and visualising analysis to help users achieve efficient data analysis.
- The platform significantly improves the accuracy of cell-type annotation by high-quality reference sets and AI.
- It supports privilege management and multi-user collaborative analysis for cooperation and knowledge sharing.

SeekSoul Online: A user-friendly bioinformatics platform focused on single-cell multi-omics analysis

Xin Liu,^{1,3} Chenhua Wu,^{2,3} Lili Pan,¹ Jiaxin Wang,¹ Wanhai Chen,¹ Teng Gao,¹ Haifeng Guo,¹ Qun Ma,¹ Shaozhao Jiao,¹ Zongwen Li,^{1,*} and Guangxin Zhang^{1,*}

¹Beijing SeekGene BioSciences Co., Ltd, Beijing 102206, China

²Shandong Provincial Key Laboratory of Neuroimmune Interaction and Regulation; Department of Otorhinolaryngology, Head and Neck Surgery, Yantai Yuhuangding Hospital, Qingdao University; Shandong Provincial Clinical Research Center for Otorhinolaryngologic Diseases, Yantai 264000, China

³These authors contributed equally

*Correspondence: lizongwen@seekgene.com (Z.L.); zhangguangxin@seekgene.com (G.Z.)

Received: April 18, 2025; Accepted: August 19, 2025; Published Online: August 21, 2025; <https://doi.org/10.59717/j.xinn-life.2025.100156>

© 2025 The Author(s). This is an open access article under the CC BY license (<https://creativecommons.org/licenses/by/4.0/>).

Citation: Liu X., Wu C., Pan L., et al. (2025). SeekSoul Online: A user-friendly bioinformatics platform focused on single-cell multi-omics analysis. *The Innovation Life* 3:100156.

The rapid advancement of single-cell technologies has brought revolutionary progress in biology, medicine, and drug development. However, the sheer volume of data and the complexity of analysis methods often pose a significant challenge for researchers lacking programming skills. To address this problem, we developed SeekSoul Online (<https://seek soul.online/index.html#/login>), a comprehensive platform for single-cell multi-omics data analysis and interactive visualisation that requires no programming foundation. Designed with a user-friendly interface, the platform combines modular architecture and powerful computational capabilities to support the complete analysis process of single-cell transcriptome, single-cell immune repertoire data, and SeekSpace single-cell spatial transcriptome data. The platform achieves accurate cell type identification through self-constructed high-quality reference sets and artificial intelligence technology. In addition, SeekSoul Online offers interactive data analysis and report generation, allowing users to adjust analysis parameters in real time and generate analysis reports for communication. The platform also provides comprehensive project management and sharing functions to facilitate collaboration and knowledge sharing among research teams. With automated data processing workflows and an intuitive user interface, SeekSoul Online significantly enhances the convenience and efficiency of data analysis, allowing researchers to focus more on scientific discovery and accelerating research progress.

INTRODUCTION

Single-cell technology has been widely used in life science research, playing a crucial role in revealing cellular heterogeneity,^{1,2} exploring disease mechanisms,^{3,4} and drug development.^{5,6} Therefore, in-depth data analysis and mining based on bioinformatics has become an indispensable component of life science research. However, single-cell data analysis presents numerous challenges, such as massive data volumes, complex analytical processes, difficulties in integrating data from different tissue types, and high requirements for expertise and computational resources.⁷ Even if some researchers have programming ability or after specialised training, they still need to invest considerable time and effort in coding before completing their analyses. This not only increases the workload, but also leads to delays in research progress. Furthermore, traditional analysis tools tend to focus on the data analysis and usually lack project management and collaborative analysis features, which is not conducive to teamwork and knowledge sharing.

With no additional installation or preparation work required and no dependence on the user's programming skills or computing resources, online analysis platforms have emerged as the preferred choice for researchers.⁸⁻¹⁰ Users can easily upload their own data or select data provided by the platform for analysis and visualisation by simply accessing it via a browser.¹¹⁻¹³ This approach not only significantly reduces time spent on data analysis but also greatly enhances research efficiency, enabling investigators to reach their research goals more rapidly.

SeekSoul Online, the focus of this paper, is an integrated, modular and user-friendly single-cell multi-omics data analysis cloud platform designed to provide researchers with a comprehensive solution for data analysis. The platform supports a complete analytical pipeline from cell filtering, batch effect removal, clustering, cell annotation, differential genes expression

(DEGs) and enrichment analysis, to signature analysis, interactive visualisation of spatial transcriptome data, and a wide range of advanced analyses such as cell-cell communication,¹⁴⁻¹⁶ gene co-expression,¹⁷ tumor cell identification,^{18,19} and pseudotime analysis.^{20,21} The platform greatly improves the accuracy of cell annotations through reference sets created from published literature. Whilst its flexible metadata management capabilities meet researchers' individual needs of researchers for cell classification. SeekSoul Online also provides powerful interactive analysis and reporting capabilities, enabling users to independently perform in-depth data analysis and mining. Furthermore, its project management and collaborative analysis capabilities greatly facilitate project management efficiency and knowledge sharing. Thus, SeekSoul Online provides comprehensive and robust support for researchers in the field of single-cell multi-omics data analysis.

MATERIALS AND METHODS

System architecture

SeekSoul Online adopts a modern three-layer architecture design, including front-end, back-end, and bioinformatics, ensuring high performance, scalability, and reliability. It employs a user interface build the Vue.js framework, providing a responsive and interactive client-side experience. Users can upload data, manage analysis projects and tasks, and visualize results through a user-friendly web interface. The back-end of the platform employs a distributed file system (e.g., HDFS) and MySQL database to ensure data stability and rapid access.²² For data analysis, it is implemented based on container technology (Docker), and with analysis processes encapsulated in R and Python scripts. The computing service utilises cloud server that is stable, reliable, and elastically scalable, which can dynamically adjust computing resources according to the computing demand of the analysis tasks to ensure an efficient and smooth analysis process.²³ The platform dynamically allocates cloud server resources based on the scale of cellular data being processed.

Software

SeekSoul Online integrates a series of single-cell multi-omics analysis tools, such as Seurat for single-cell dimensionality reduction and clustering, SingleR for cell type identification, and clusterProfiler for gene function enrichment analysis.²⁴ In addition, the platform incorporates a variety of R packages specialised for statistical analysis and graphical presentation, enabling complex data processing and visualisation of results in single-cell genomics (Table S1). The parameters used in the analysis can be sourced from parameter templates or customised by users. For example, when clustering, the Louvain algorithm from Seurat is used, with a default resolution parameter of 0.5 (range of 0.1 to 3.0). When using CellPhoneDB, the threshold parameter is set at 0.1, and users can customise ligand-receptor cell pairs.

RESULTS

Streamlined usability for users without coding skills

SeekSoul Online provides a user-friendly web interface that greatly simplifies the entire process of single-cell multi-omics data analysis from data upload to result visualisation to downstream or advanced analysis. Users with no programming skills can easily complete complex data analysis tasks

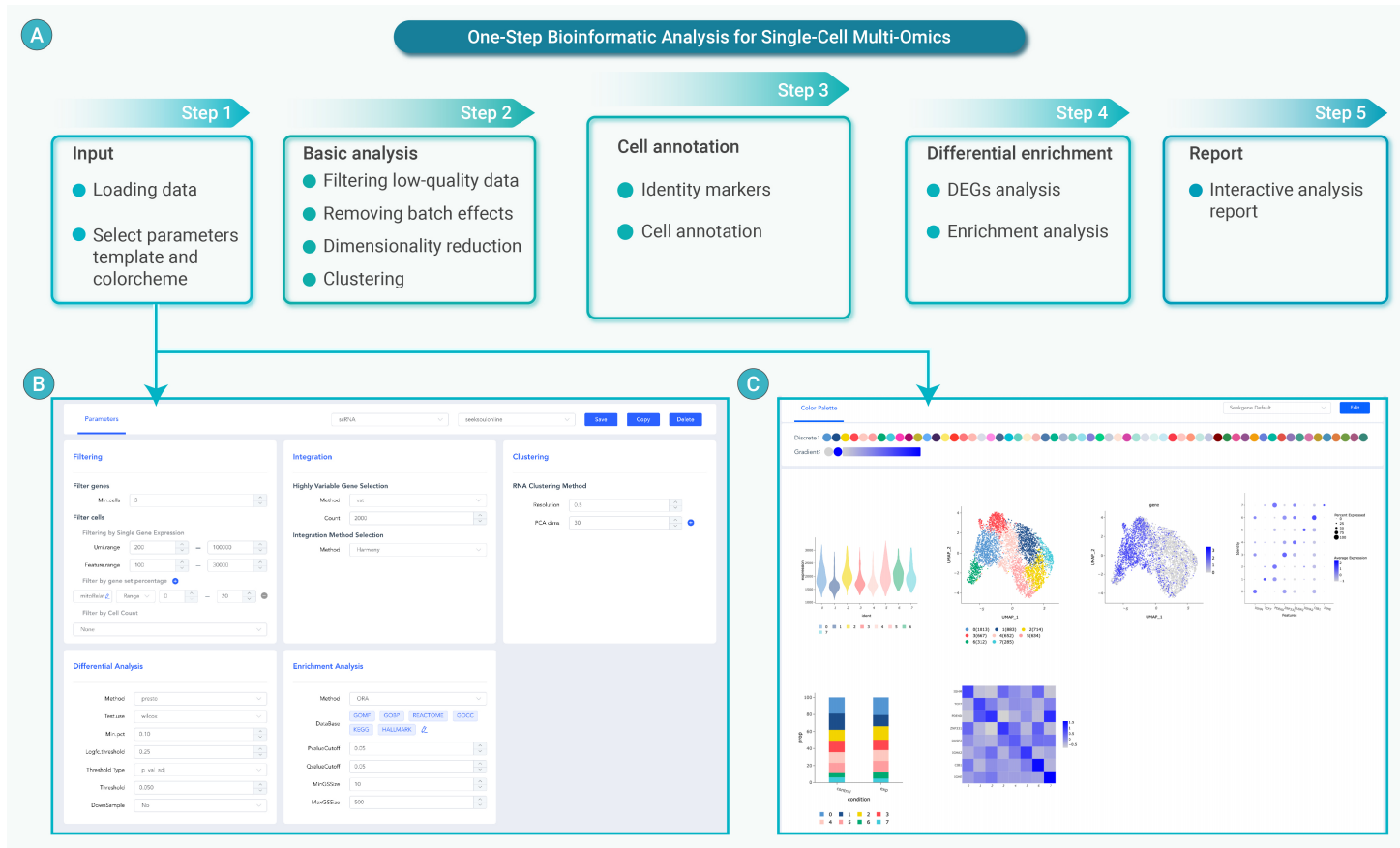


Figure 1. Workflow of one-step analysis for single-cell multi-omics data (A) The workflow includes five steps: (1) input, (2) basic analysis, (3) cell annotation, (4) differential genes expression analysis and enrichment analysis, (5) report. (B) Default parameters for analysis. (C) Color scheme.

through the intuitive interface. In order to ensure the accuracy of data analysis, we also provide parameter templates based on published articles and thousands of projects, as well as publishable color schemes to ensure that even beginners can quickly and accurately implement data analysis and mining. The platform also allows users to customise analysis parameters or color schemes according to individual needs or journal requirements. Based on the selected parameter templates and color schemes, the platform supports one-step completion of the whole process of analysis from data filtering, batch effect removal, dimensionality reduction and clustering to cell annotation, differential genes expressed and enrichment analysis (Figure 1). Additionally, the platform provides detailed user guide, descriptions of parameters, videos, Frequently Asked Questions (FAQs), and online customer service support to help users in obtaining the necessary help and support during the analysis process.

Complete single-cell multi-omics analysis process

SeekSoul Online provides a comprehensive workflow for single-cell transcriptome data, single-cell immune repertoire data, and SeekSpace single-cell spatial transcriptome data, covering all steps from data uploading to final report generation, ensuring that users can complete all analysis on a unified platform.²⁵ The process includes cell filtering, normalisation, batch effect removal,^{26,27} clustering, cell annotation, signature scoring, spatial location information analysis and differential genes expression and enrichment analysis, as well as advanced analysis such as cell-cell interaction, pseudotime, TCR, BCR, and report generation (Figure 2).

In order to realise the whole process of single-cell multi-omics analysis, SeekSoul Online adopts a modular design architecture, which divides the single-cell multi-omics data analysis process into multiple independent yet interconnected functional modules. These ten modules include **Basic Analysis**, **Cell Annotation**, **Visualisation**, **Module Score**, **Differential Enrichment**, **Interactive Analysis**, **Subset**, **Advanced Analysis**, **Metadata** and **Report**. Each module has independent functions, inputs and outputs. Users can flexibly

select and use different modules according to their specific research needs to build personalised data analysis processes. For example, when analysing SeekSpace spatial transcriptome data, users can first use the **Basic Analysis** module for quality control, then select the **Cell Annotation** module for cell type identification, and then select the **Interactive Analysis** module to visualise the spatial distribution of cells and gene expression (Table 1). Of course, the seamless connection and unified interface design between the modules ensure efficient data transfer and collaborative work between different modules, avoiding data loss and inconsistency problems. For example, users can score gene sets in the **Module Score** module and later visualise the scoring results in the **Visualisation** module and so on. This modular design not only simplifies the user's operation process, but also greatly enhances the scalability of the platform, allowing for rapid integration of emerging analysis tools and algorithms, thus becoming a powerful assistant for researchers in single-cell multi-omics data analysis (Figure 3).

Table 1. List of datasets used in SeekSoul Online as example datasets for single-cell transcriptome and SeekSpace spatial transcriptome.

Type	Name	Number of cells	Technology
scRNA-seq	Batch1 (PBMC)	15153	SeekOne® DD
	Batch 2 (PBMC)	11314	SeekOne® DD
SeekSpace	WTH1092(Brain)	32833	SeekSpace®

High confidence cell annotation

To improve the accuracy and reliability of single-cell data analysis, SeekSoul Online employs high-quality reference sets built in-house based on published articles and advanced artificial intelligence techniques for cell annotation. The reference sets, which have been subjected to stringent quality control and manual review, cover 57 human tissues and 46 mouse tissues (Table S2). Annotation is then performed based on these reference sets using

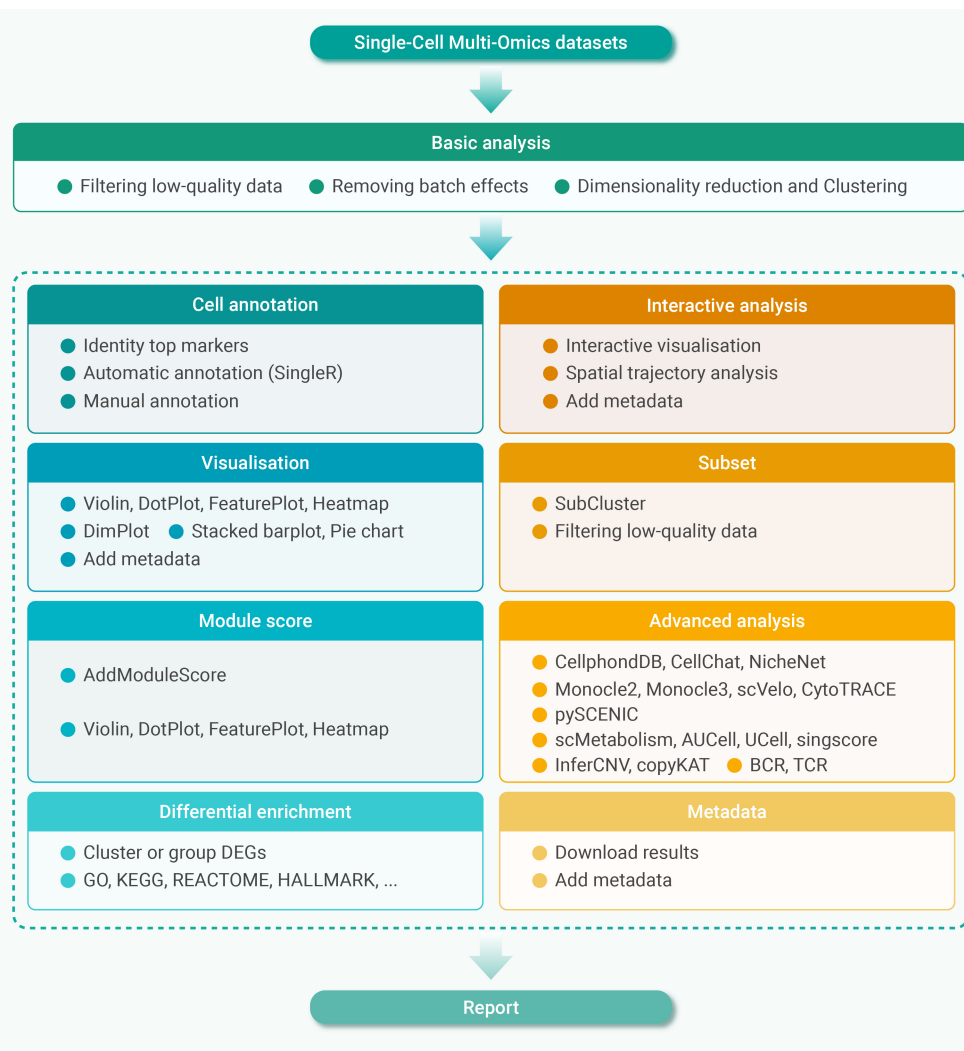


Figure 2. SeekSoul Online consists of ten modules for single-cell multi-omics analysis.

result summarisation and communication during the analysis process. At the data analysis stage, users can combine and compare multiple analysis results to visualise the impact of different analysis methods and parameter settings on the results. This flexible and efficient way of analysis helps users to understand the data more deeply and explore potential biological laws. The **Visualisation** module integrates a variety of dynamic charts and visualisation plots, including scatter plots, dot plots, violin plots, heatmaps, pie plots, and stacked bar plots. Users can adjust the plotting parameters, such as color and scale, in real time to generate high-quality images that meet the standards of academic publications. In addition, SeekSoul Online's interactive report-generation function allows users to summarise and organise analysis results to create personalised reports, which greatly facilitates the sharing and communication of findings. The integration of these features not only improves the transparency and interpretability of data analysis, but also facilitates collaboration and knowledge sharing among research teams, further promoting the development of single-cell multi-omics research.

Project management and multi-user collaborative analysis

SeekSoul Online also demonstrates significant advantages in project management and collaborative analysis. It supports efficient collaboration and data sharing among

SingleR,²⁸ ensuring the accuracy of automated annotation. In addition, the platform combines the classical cell markers database with artificial intelligence technology to automatically identify different cell types and their subtypes by analysing genes specifically expressed in each cluster.²⁹ This comprehensive approach not only improves the automation level of annotation but also effectively enhances the precision and accuracy of the results. Meanwhile, the platform allows users to conduct manual annotation based on marker expression after automated annotation (Figure 4 & Table S3).

Flexible metadata management and label customisation

SeekSoul Online demonstrates excellent metadata management capabilities in single-cell multi-omics analysis. The platform supports users in customising cell labels according to their individual needs. Additionally, it efficiently manages the metadata of single-cell data, allowing users to upload, edit, filter, merge and customise cell labels according to their research objectives or experimental design. For example, when performing tumor microenvironment analysis in SeekSpace, users can define specific cell types in the disease group or cells localised to a specific spatial region as new cell subtypes to achieve more precise analysis of disease characteristics and cell functions. Furthermore, we can also merge the annotation results of the main group and sub-groups to ensure data integrity, which enables downstream analyses such as cell-cell communication to be performed on a complete cellular atlas. This flexible and efficient metadata management capability not only improves the depth and accuracy of data analysis, but also significantly enhances the platform's adaptability and utility for diverse research needs.

Interactive analysis and shareable reports

SeekSoul Online's interactive analysis and report generation capabilities significantly enhance the convenience of real-time parameter adjustment,

research teams, effectively improving the efficiency and quality of research work. The platform provides an independent and structured management space for each project, allowing users to create and manage multiple analysis projects. Users can create, edit and store all kinds of information related to the project, such as sample details and data sources, ensuring the integrity and traceability of the project information. Moreover, it supports project leaders in assigning different user permissions to each project, ensuring the security and privacy of data and analysis processes. Through the project management function, team members can track project progress in real time, communicate and resolve analytical challenges promptly, and share results and research ideas. This efficient collaboration mechanism breaks down information silos in traditional scientific research and promotes close cooperation among team members and improved research outcomes.

Case study: Reproducing key findings in the human oesophageal squamous cell carcinoma microenvironment

The SeekSoul Online platform provides researchers with comprehensive support for various application scenarios. Users can complete cell type annotation, immune cell function assessment, interactive visualisation, and more with simple clicks. In order to demonstrate the value of the SeekSoul Online platform in real-world research, we used the esophageal squamous cell carcinoma (ESCC) microenvironmental study dataset published as an example. This demonstrates the ability of the SeekSoul Online platform to obtain analysis results comparable to those published in top journals without writing code.

Data downloading and processing. Users can download the matrix data from the accession number provided in the example article: GSE160269. In SeekSoul Online, the downloaded matrix files (including barcodes.tsv.gz, features.tsv.gz, and matrix.mtx.gz) are uploaded as a zip file through the

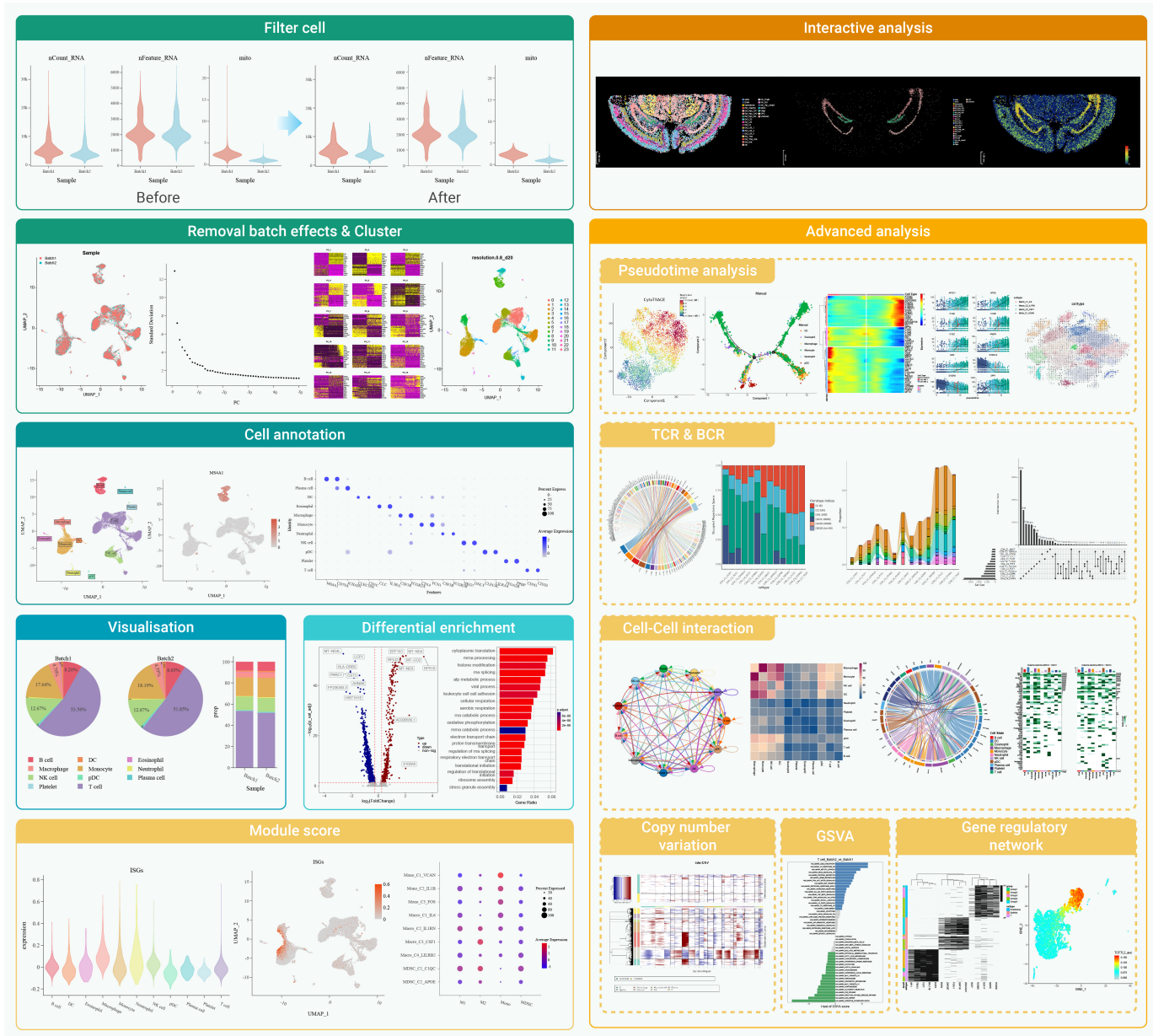


Figure 3. Outputs from each analysis module underpinning single-cell multi-omics analysis on SeekSoul Online.

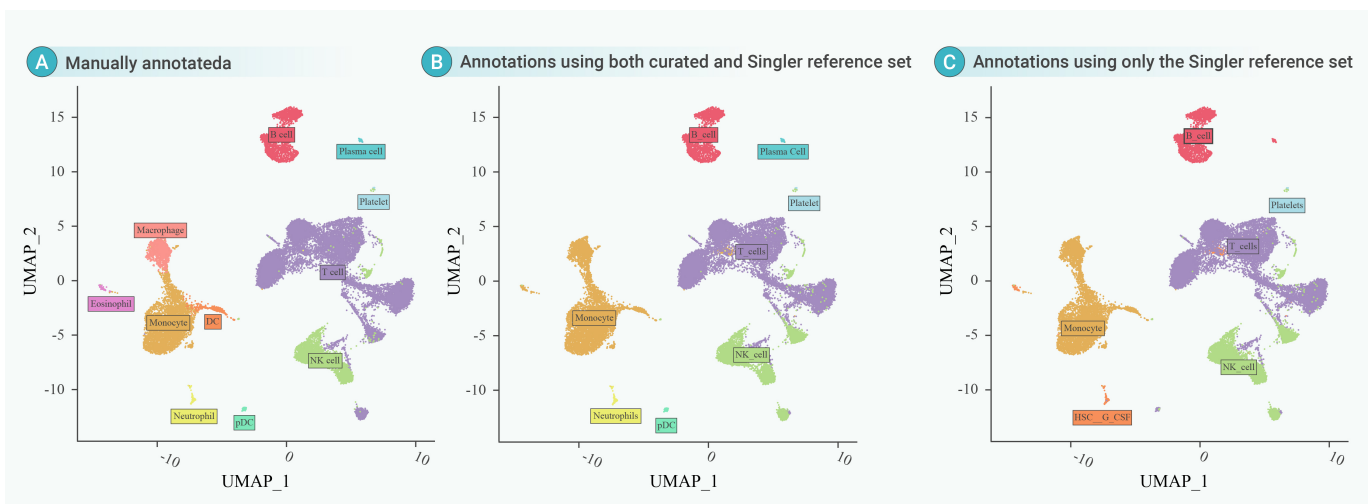


Figure 4. Higher-accuracy automated cell-type annotation using curated reference sets, with support for manual curation (A) Manual annotation. (B) Automatic annotation using both our and Singler reference sets. (C) Automatic annotation only using Singler reference set.

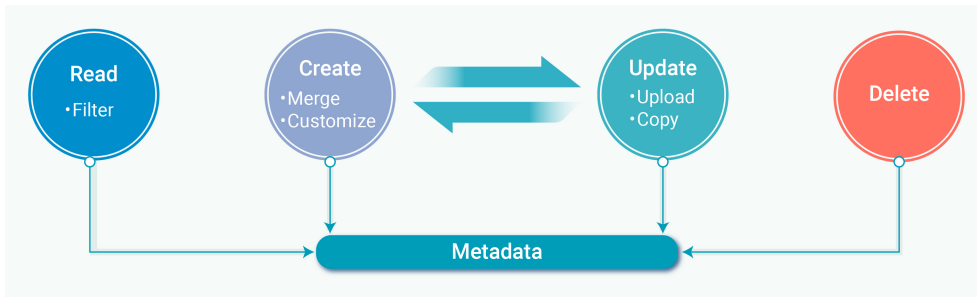


Figure 5. Free configuration and consolidation of cell labels to improve single-cell analysis.

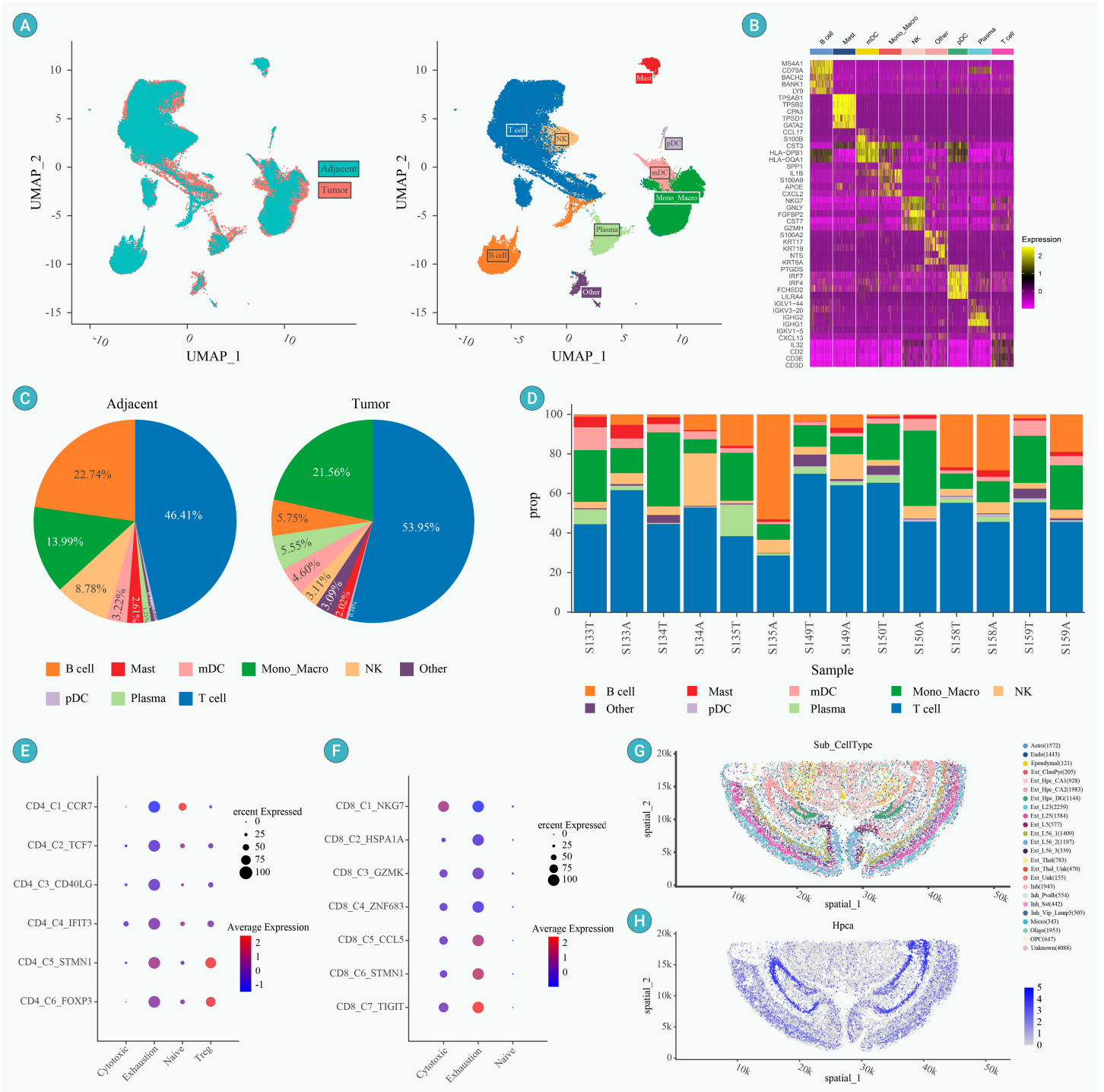


Figure 6. Oesophageal squamous cell carcinoma (ESCC) case study and spatial examples from SeekSpace data (A) UMAP plot of single cells colored by tissue and cell types. (B) Heatmap of the gene expression across cells. (C) Pie charts of cell-type fractions for tumor and adjacent tissues, colored by cell type. (D) The proportion of cells that contributed to cell types by each sample. (E) Dot plot of representative cytotoxic, exhaustive, naive, and Treg signatures in CD4 T cells. (F) Dot plot of representative cytotoxic, exhaustive, and naive signatures in CD8 T cells. (G) Visualisation of the spatial distribution of cell types in SeekSpace data. (H) Visualisation of the spatial distribution of gene expression in SeekSpace data.

Data Upload function. The platform automatically performs data format validation. To accommodate diverse user needs, the platform also supports HDF5 (.h5), SeuratObject (.rds), AnnData (.h5ad), and other data formats.

Analytical workflow. (1) Quality control and preprocessing: In the **Basic Analysis** module, set the filtering parameters (nFeature: 400-6000, mitochondrial gene ratio threshold: 10%) to remove low-quality cells. In the **Integration** section, select the top 2000 highly variable genes and use the Harmony method to remove batch effects (Figure 6A). After that, in the **Cluster** section, select top 20 principal components and set the resolution at 0.6 for cell clustering. (2) Cell type annotation: Based on the classical marker genes (e.g., *CD3D*, *CD19*, *IGHG1*, etc.) mentioned in the article, 8 major cell types including T cells, B cells, plasma cells, and others were identified through the **Cell Annotation** module (Figure 6B). (3) Visualisation: Using the **Visualisation** module, users can generate classic graphics such as dimension reduction plots, dot plots, heatmaps, etc. Pie plots, and stacked bar plots can also be drawn to compare the proportion of cell types in tumor and adjacent tissues (Figures 6C-D). (4) Subtypes analysis: Using the **'Subset'** module, T cells and NK cells can be selected for additional dimensionality reduction, clustering and annotation. Signature analysis can then be performed using the gene sets from the article to explore the functions and characteristics of cell subtypes (Figures 6E-F).

The results show that the platform successfully reproduces the main findings of the original article, including the compositional characteristics of cells in the human oesophageal squamous cell carcinoma microenvironment and their altered cellular states (Figure 6). Users can export the complete analysis report through the **'Report'** module to support further interpretation and sharing of the results. In addition, we can also display visualisation of the spatial distribution of gene expression and cell types in SeekSpace data (Figures 6G-H & Table 1).

DISCUSSION AND CONCLUSION

The SeekSoul Online platform is designed to enable researchers who are not proficient in coding to complete single-cell multi-omics data analysis independently. By integrating a comprehensive set of single-cell multi-omics data analysis tools and a user-friendly interface with modular design, the platform helps users complete single-cell transcriptome, single-cell immune repertoire data and SeekSpace single-cell spatial transcriptome data analysis in the form of graphics and videos. Moreover, the parameter templates and color schemes that we have compiled based on the literature and project experiences greatly facilitate one-step analysis, thus enabling even researchers without coding skills to quickly achieve autonomous analysis of single-cell multi-omics data.

The modular architecture of SeekSoul Online ensures both completeness and flexibility throughout the analysis process. Ten modules in total cover everything from data upload, preprocessing, including batch effect removal, dimensionality reduction and clustering, cell annotation to differential gene expression (DEGs) and enrichment analysis. It also includes advanced analysis such as cell-cell communication, gene co-expression, tumor cell identification, and pseudotime analysis. This one-step solution avoids the loss of data and inconsistency associated with switching between multiple platforms. In addition, SeekSoul Online's high-quality reference sets and advanced artificial intelligence technology, combined with SingleR and the classical marker databases, significantly improve the accuracy of cell annotation.

For data visualisation and report generation, SeekSoul Online provides a rich set of interactive visualisation tools and interactive report functions, which support users to adjust analysis parameters in real time according to their needs. Meanwhile, the project management and collaborative analysis functions facilitate the communication and sharing of results between teams and promote collaborative research through multi-user collaboration and permission management.

In summary, SeekSoul Online, as a cloud platform focusing on single-cell multi-omics analysis, provides researchers with a convenient, efficient and comprehensive data analysis solution. It has significantly lowered the threshold for single-cell multi-omics data analysis, and improved research efficiency and quality through its user-friendly interface, complete analysis process, precise cell annotation, interactive analysis and reporting functions,

as well as efficient project management and collaboration capabilities. While the current platform has certain limitations, we will implement ongoing updates to reference datasets, enhance artificial intelligence technology, and incorporate single-cell ATAC-seq analysis, etc. With the continuous iteration and improvement of the platform, it is expected to become an important tool for researchers to mine single-cell multi-omics data, providing strong support for revealing cellular mysteries and overcoming disease challenges.

REFERENCES

1. Rebuffet L., Melsen J.E., Escaliere B., et al. (2024). High-dimensional single-cell analysis of human natural killer cell heterogeneity. *Nat. Immunol.* **25**:1474-1488. DOI:10.1038/s41590-024-01883-0
2. Chen X., Huang Y., Huang L., et al. (2024). A brain cell atlas integrating single-cell transcriptomes across human brain regions. *Nat. Med.* **30**:2679-2691. DOI:10.1038/s41591-024-03150-z
3. Thomas T., Friedrich M., Rich-Griffin C., et al. (2024). A longitudinal single-cell atlas of anti-tumour necrosis factor treatment in inflammatory bowel disease. *Nat. Immunol.* **25**:2152-2165. DOI:10.1038/s41590-024-01994-8
4. Zhang H., Wang T., Gong H., et al. (2023). A novel molecular classification method for osteosarcoma based on tumor cell differentiation trajectories. *Bone Res.* **11**:1. DOI:10.1038/s41413-022-00233-w
5. Zhang P., Wang X., Cen X., et al. (2025). A deep learning framework for in silico screening of anticancer drugs at the single-cell level. *Natl. Sci. Rev.* **12**:nwae451. DOI:10.1093/nsr/nwae451
6. Peng L., Hu Y., Mankowski M.C., et al. (2022). Monospecific and bispecific monoclonal SARS-CoV-2 neutralizing antibodies that maintain potency against B.1.617. *Nat. Commun.* **13**:1638. DOI:10.1038/s41467-022-29288-3
7. Erfanian N., Heydari A.A., Feriz A.M., et al. (2023). Deep learning applications in single-cell genomics and transcriptomics data analysis. *Biomed. Pharmacother.* **165**:115077. DOI:10.1016/j.biopha.2023.115077
8. Huang S. (2023). Efficient analysis of toxicity and mechanisms of environmental pollutants with network toxicology and molecular docking strategy: Acetyl tributyl citrate as an example. *Sci. Total Environ.* **905**:167904. DOI:10.1016/j.scitotenv.2023.167904
9. Mu H., Chen J., Huang W., et al. (2024). OmicShare tools: A zero-code interactive online platform for biological data analysis and visualization. *iMeta* **3**:e228. DOI:10.1002/imt2.228
10. Wang X., Pei Z., Hao T., et al. (2022). Prognostic analysis and validation of diagnostic marker genes in patients with osteoporosis. *Front. Immunol.* **13**:987937. DOI:10.3389/fimmu.2022.987937
11. Sherman B.T., Hao M., Qiu J., et al. (2022). DAVID: A web server for functional enrichment analysis and functional annotation of gene lists (2021 update). *Nucleic Acids Res.* **50**:W216-W221. DOI:10.1093/nar/gkac194
12. Tang Z., Kang B., Li C., et al. (2019). GEPIA2: An enhanced web server for large-scale expression profiling and interactive analysis. *Nucleic Acids Res.* **47**:W556-W560. DOI:10.1093/nar/gkz430
13. Xie C., Mao X., Huang J., et al. (2011). KOBAS 2.0: A web server for annotation and identification of enriched pathways and diseases. *Nucleic Acids Res.* **39**:W316-322. DOI:10.1093/nar/gkr483
14. Efremova M., Vento-Tormo M., Teichmann, et al. (2020). CellPhoneDB: Inferring cell-cell communication from combined expression of multi-subunit ligand-receptor complexes. *Nat. Protoc.* **15**:1484-1506. DOI:10.1038/s41596-020-0292-x
15. Jin S., Guerrero-Juarez C.F., Zhang L., et al. (2021). Inference and analysis of cell-cell communication using CellChat. *Nat. Commun.* **12**:1088. DOI:10.1038/s41467-021-21246-9
16. Browaeys R., Saelens W., and Saey Y. (2020). NicheNet: Modeling intercellular communication by linking ligands to target genes. *Nat. Methods* **17**:159-162. DOI:10.1038/s41592-019-0667-5
17. Kumar N., Mishra B., Athar M., et al. (2021). Inference of Gene Regulatory Network from Single-Cell Transcriptomic Data Using pySCENIC. *Methods Mol. Biol.* **2328**:171-182. DOI:10.1007/978-1-0716-1534-8_10
18. Gao R., Bai S., Henderson Y.C., et al. (2021). Delineating copy number and clonal substructure in human tumors from single-cell transcriptomes. *Nat. Biotechnol.* **39**:599-608. DOI:10.1038/s41587-020-00795-2
19. Patel A.P., Tirosch I., Trombetta J.J., et al. (2014). Single-cell RNA-seq highlights intratumoral heterogeneity in primary glioblastoma. *Science* **344**:1396-1401. DOI:10.1126/science.1254257
20. Bergen V., Lange M., Peidli S., et al. (2020). Generalizing RNA velocity to transient cell states through dynamical modeling. *Nat. Biotechnol.* **38**:1408-1414. DOI:10.1038/s41587-020-0591-3
21. Qiu X., Mao Q., Tang Y., et al. (2017). Reversed graph embedding resolves complex single-cell trajectories. *Nat. Methods* **14**:979-982. DOI:10.1038/nmeth.4402
22. Kapil G., Agrawal A., Attallaah A., et al. (2020). Attribute based honey encryption algorithm for securing big data: Hadoop distributed file system perspective. *PeerJ Comput. Sci.* **6**:e259. DOI:10.7717/peerj-cs.259

23. Saurabh S., Young-Sik J., and Jonghyuk P. (2016). A survey on cloud computing security: Issues, threats, and solutions. *J Netw Comput Appl* **75**:200–222. DOI:10.1016/j.jnca.2016.09.002
24. Wu T., Hu E., Xu S., et al. (2021). clusterProfiler 4.0: A universal enrichment tool for interpreting omics data. *Innovation (Camb)* **2**:100141. DOI: 10.1016/j.xinn.2021.100141
25. Chen G., Ning B., and Shi T. (2019). Single-Cell RNA-Seq Technologies and Related Computational Data Analysis. *Front. Genet.* **10**:317. DOI:10.3389/fgene.2019.00317
26. Stuart T., Butler A., Hoffman P., et al. (2019). Comprehensive Integration of Single-Cell Data. *Cell* **177**:1888–1902 e1821. DOI: 10.1016/j.cell.2019.05.031
27. Korsunsky I., Millard N., Fan J., et al. (2019). Fast, sensitive and accurate integration of single-cell data with Harmony. *Nat. Methods* **16**:1289–1296. DOI:10.1038/s41592-019-0619-0
28. Aran D., Looney A.P., Liu L., et al. (2019). Reference-based analysis of lung single-cell sequencing reveals a transitional profibrotic macrophage. *Nat. Immunol.* **20**:163–172. DOI:10.1038/s41590-018-0276-y
29. Jiang S., Qian Q., Zhu T., et al. (2023). Cell Taxonomy: A curated repository of cell types with multifaceted characterization. *Nucleic Acids Res.* **51**:D853–D860. DOI:10.1093/nar/gkac816

FUNDING AND ACKNOWLEDGMENTS

This work was supported by a grant from the National Key Research and Development Program of China (2023YFC3402700). The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

AUTHOR CONTRIBUTIONS

Zongwen Li and Guangxin Zhang conceived the platform and idea. Xin Liu planned the project, and drafted the manuscript. Chenhua Wu performed validation of the English version and coordinated outreach activities. Jiaxin Wang designed the graphical user interface. Lili Pan, Wanhai Chen, Teng Gao, Haifeng Guo, and Qun Ma implemented the main code. All authors have given final approval for the manuscript to be published and have agreed to be responsible for all aspects of the manuscript. Shaozhao Jiao proposed modification suggestions. All authors contributed to the manuscript and approved the final version.

DECLARATION OF INTERESTS

The authors declare no competing interests.

ETHICAL STATEMENT AND PATIENT CONSENT

Not applicable.

DATA AND CODE AVAILABILITY

Example datasets for single-cell transcriptome and SeekSpace single-cell spatial transcriptome data were downloaded as list in [Table1](#).

SUPPLEMENTAL INFORMATION

It can be found online at <https://doi.org/10.59717/j.xinn-life.2025.100156>