



Single Cell Analyst: A user-friendly platform for multi-omics data analysis



Lu Pan^{1#}, Bufu Tang^{2#}, Xuan Zhang^{3#}, Paolo Parini¹, Roman Tremme⁴,
Joseph Loscalzo⁵, Volker M. Lauschke¹, Bradley A. Maron⁵, Paola Paci⁶, Ingemar Ernberg¹, Nguan Soon Tan⁷,
Ákos Végvári¹, Zehuan Liao^{1,7}, Sundararaman Rengarajan⁸, Roman Zubarev¹,
Yuxuan Fan⁹, Xu Zheng⁹, Xinyue Jian⁹, Ren Sheng^{10*}, Zhenning Wang^{9*}, Xuexin Li^{9*}

¹Karolinska Institutet, ²Fudan University, ³Kunming Medical University,

⁴University of Tuebingen, ⁵Harvard Medical School, ⁶Sapienza University of Rome, ⁷Nanyang Technological University,

⁸Northeastern University(Boston), ⁹China Medical University, ¹⁰Northeastern University

Lu Pan, Bufu Tang, Xuan Zhang, Paolo Parini, Roman Tremme, Joseph Loscalzo, Volker M. Lauschke, Bradley A. Maron, Paola Paci, Ingemar Ernberg, Nguan Soon Tan, Ákos Végvári, Zehuan Liao, Sundararaman Rengarajan, Roman Zubarev, Yuxuan Fan, Xu Zheng, Xinyue Jian, Ren Sheng, Zhenning Wang, Xuexin Li, 2025, Comprehensive analysis of multi-omics single-cell data using the singlecellsingle-cell analyst. *iMeta* 4: e70038. <https://doi.org/10.1002/imt2.70038>



Introduction

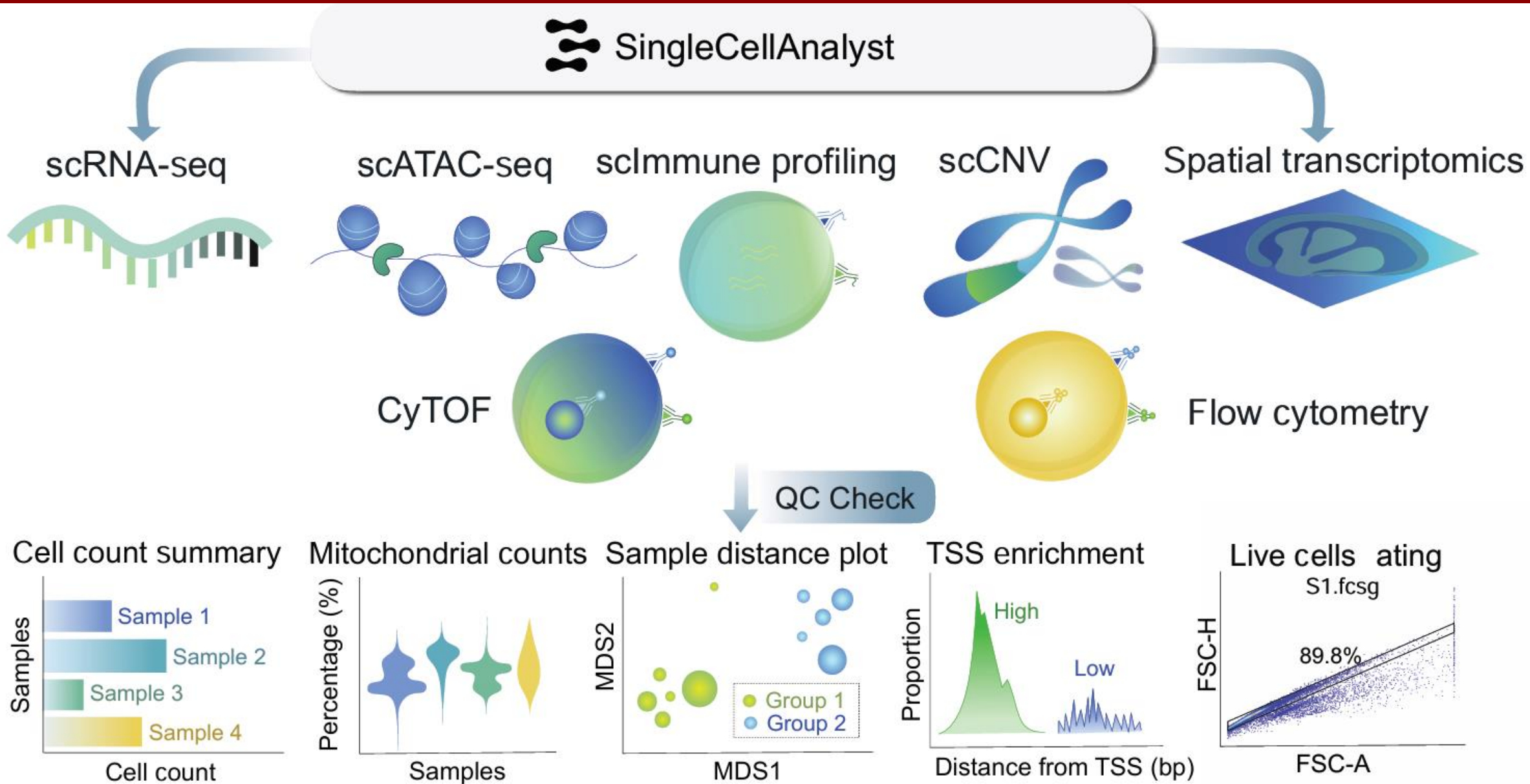


Figure 1.a



Highlights

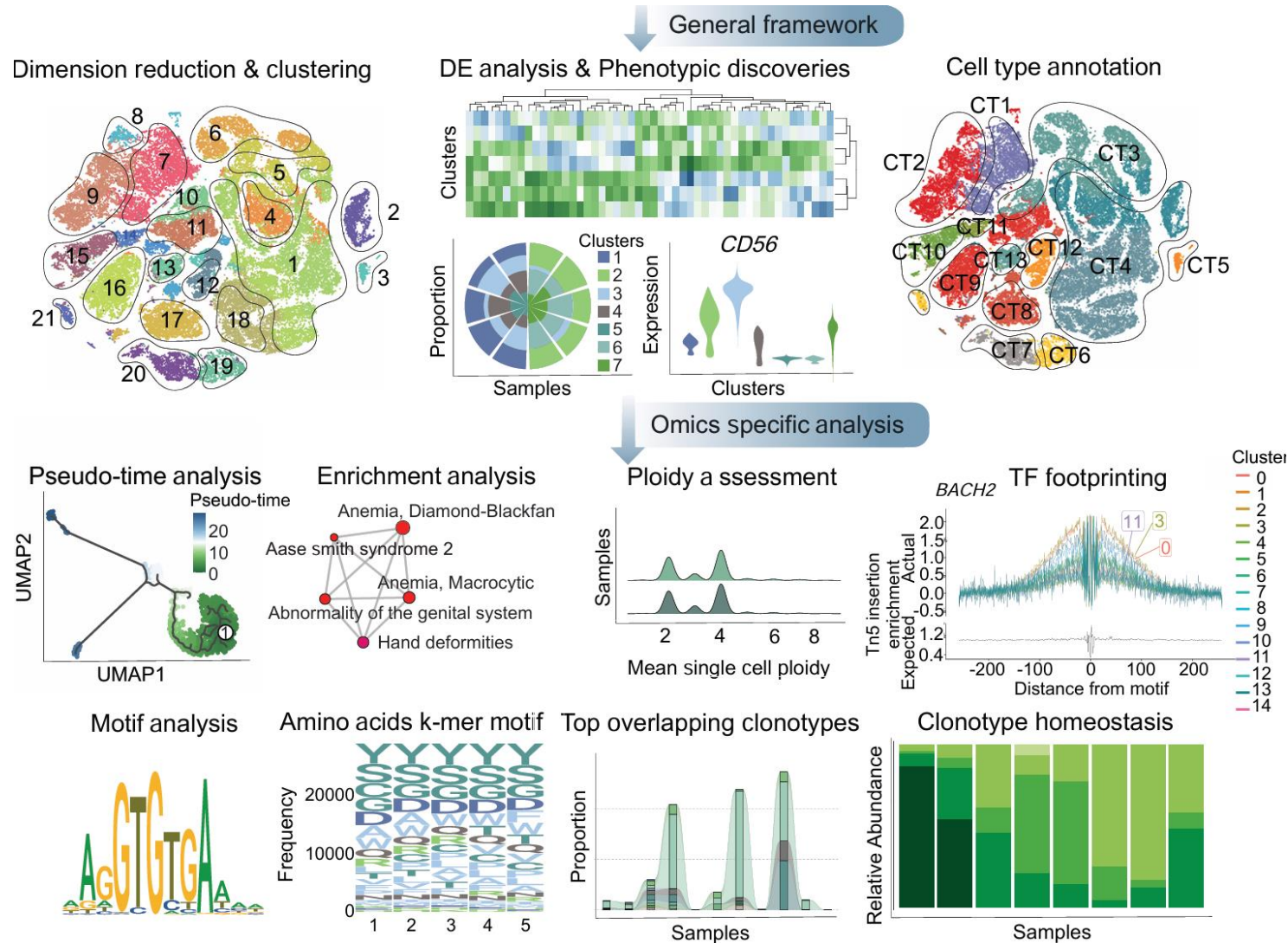
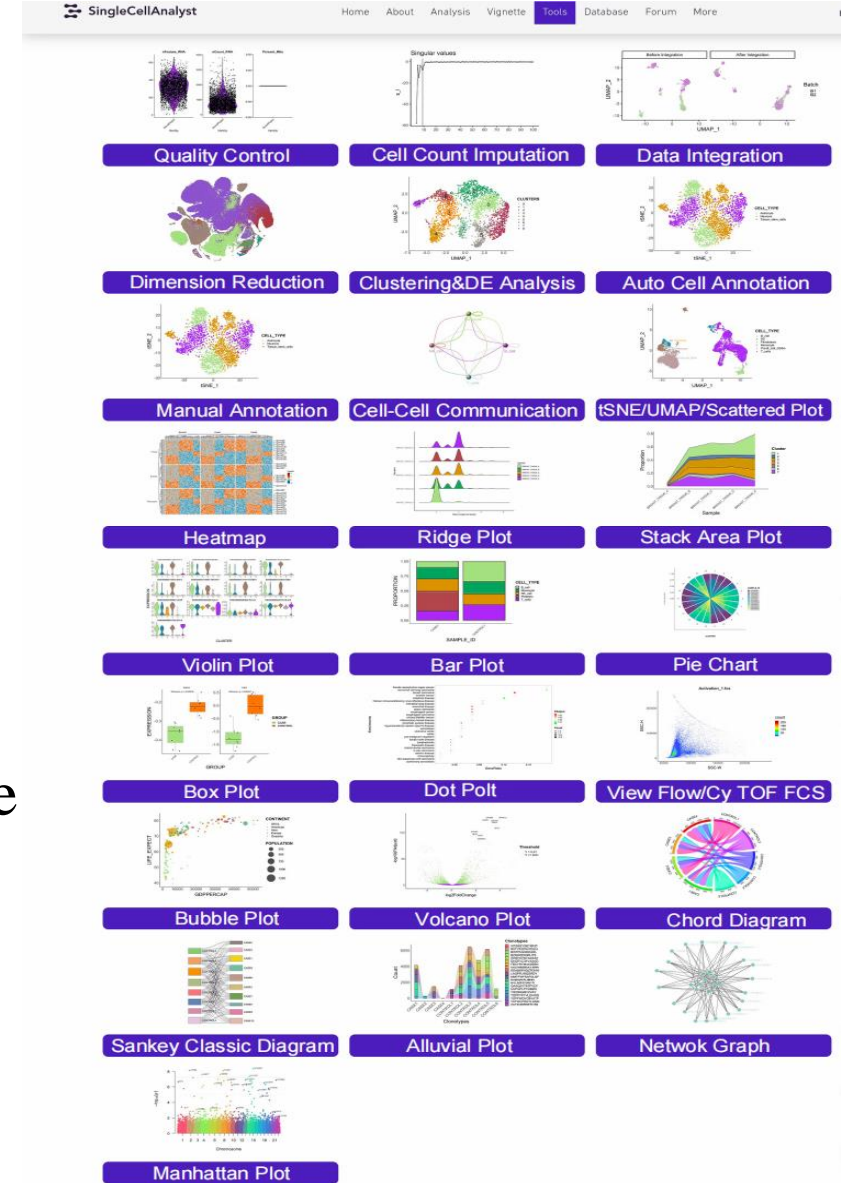
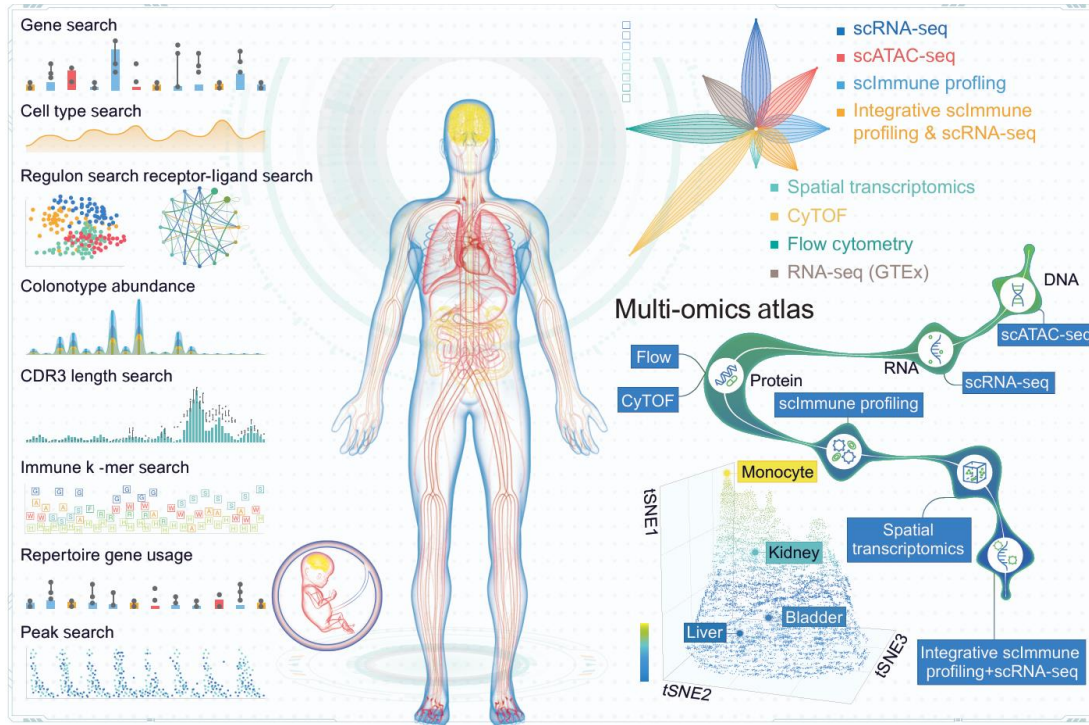


Figure 1.b

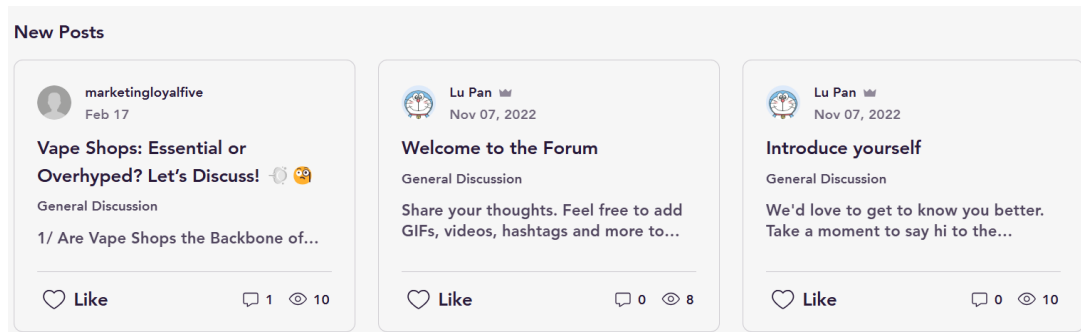
1. Single cell analyst is a web-based platform for comprehensive multi-omics single-cell data analysis, supporting six single-cell omics types and spatial transcriptomics.
2. It eliminates the need for coding, offering an intuitive, user-friendly interface accessible to researchers at all levels.
3. The platform automates key analysis steps, including quality control, data processing, and phenotypic analysis, delivering interactive, publication-ready visualizations.
4. Single cell analyst streamlines workflows, making complex multi-omics analyses accessible without requiring extensive computational expertise.



Overview of Single cell analyst



(Figure 2) Overview of the single cell analyst database

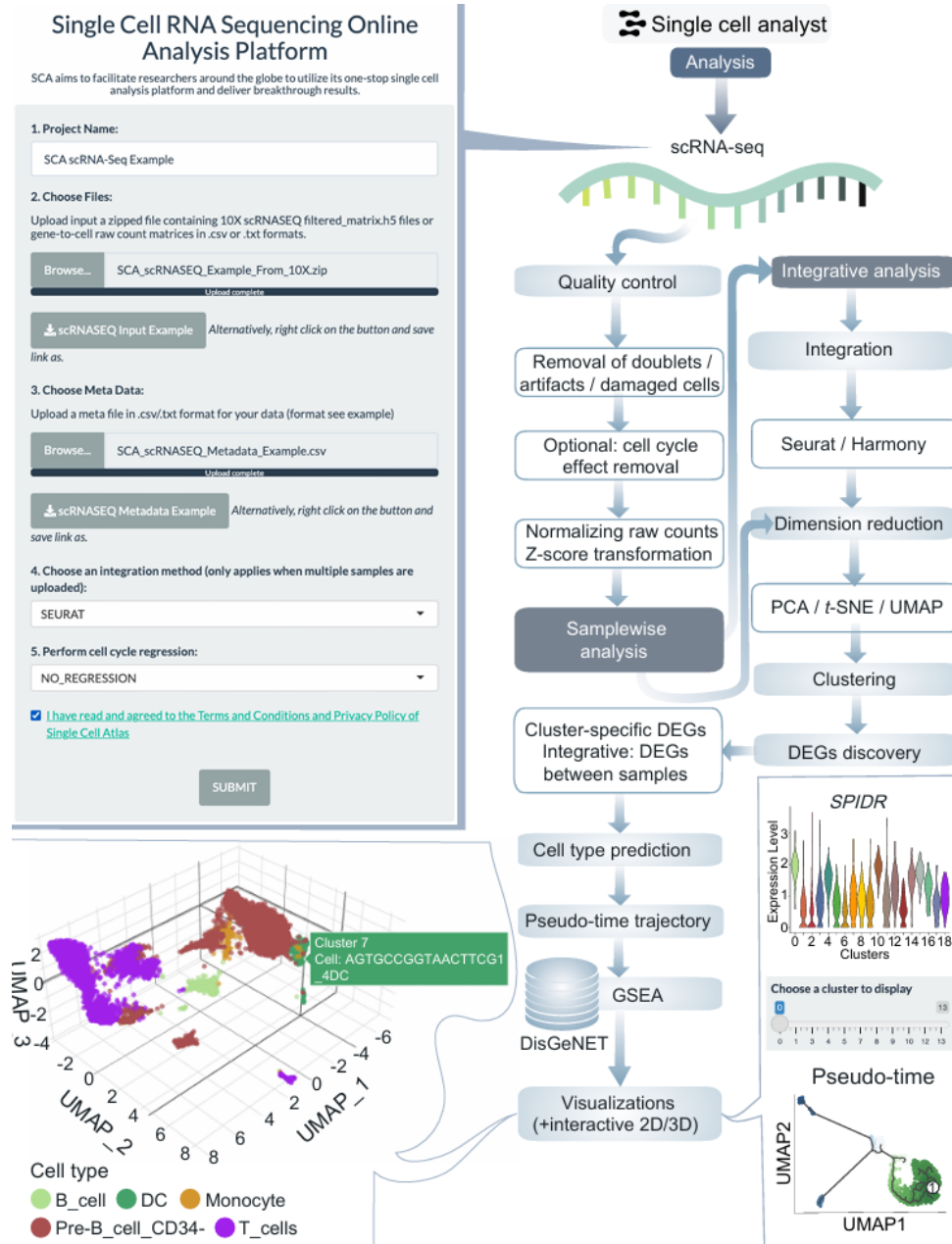


Platform Forum

Platform Tool



Case 1: ScRNA-seq analysis



Within the scRNA-seq workflow, beyond the standard QC and data processing steps, single cell analyst enables users to evaluate cell type predictions, perform differential expression analysis, conduct pathway and enrichment analyses, and infer pseudotime trajectories for clusters or cell types. Users can specify starting points for pseudotime analysis based on their biological questions. For multi-sample datasets, the platform conducts integrated analysis, allowing users to compare phenotypic differences between healthy and diseased samples or other experimental conditions. This workflow is ideal for investigating gene expression dynamics and cell state transitions in various biological contexts.

Figure 3. ScRNA-seq Analysis Framework



Case 2: ScATAC-seq analysis

Single Cell ATAC Online Analysis Platform

SCA aims to facilitate researchers around the globe to utilize its one-stop single cell analysis platform and deliver breakthrough results.

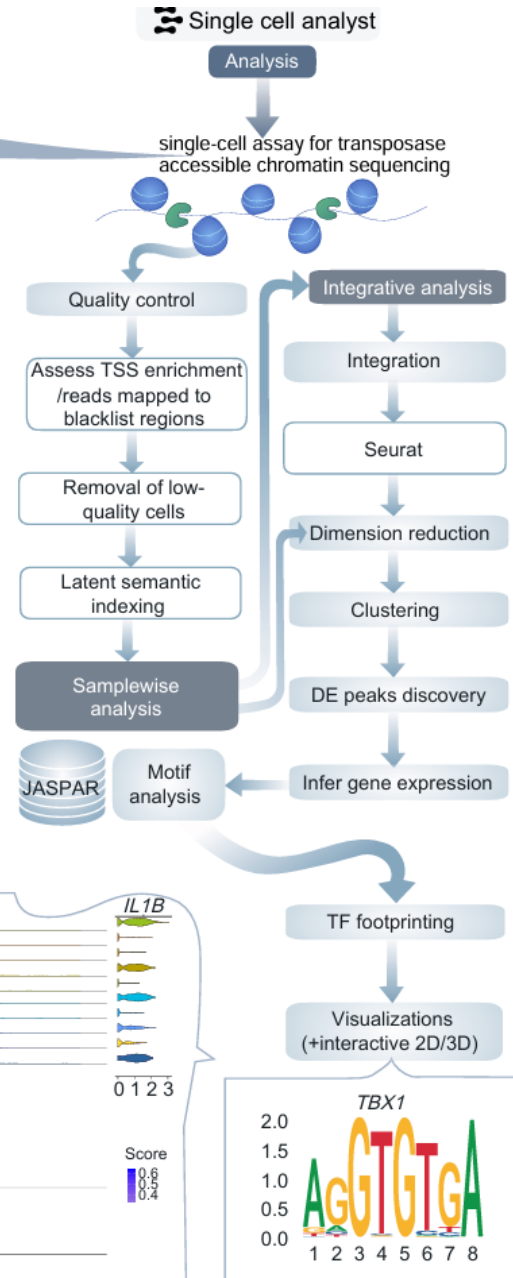
1. Project Name:
SCA scATAC Example

2. Choose Files:
Upload input a zipped file containing 10X scATAC 1) peak_bc_matrix.h5, 2) fragments.tsv.gz and 3) its index.tbi file, 4) per_barcode_metrics.csv or singlecell.csv files. (Please submit after the upload is completed)
Browse... SCA_scATAC_Example_From_10X.zip
SCA_scATAC_Example_From_10X_Large.zip

3. Choose Meta Data:
Upload a meta file in .csv/.txt format for your data (format see example, please submit after the upload is completed)
Browse... SCA_scATAC_Metadata_Example.csv
Upload complete

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In the scATAC-seq workflow, QC steps such as transcription start site (TSS) enrichment and nucleosome banding pattern assessment are complemented by downstream analyses, including the identification of accessible chromatin regions and motif footprinting. The workflow also calculates gene activity scores, enabling researchers to link chromatin accessibility to gene expression. Users can explore cis-co-accessible networks and enriched motifs, providing insights into regulatory elements driving cellular functions. For multi-sample datasets, integrated analyses reveal shared and unique chromatin features across conditions.

Figure 4. ScATAC-seq Analysis Framework



Case 3: ScImmune Profiling

scImmune Online Analysis Platform

SCA aims to facilitate researchers around the globe to utilize its one-stop single cell analysis platform and deliver breakthrough results.

1. Project Name:

SCA_scImmune_Example

2. Choose Files:

Upload input a zipped file containing 10X Immune Profiling 1) filtered contig, 2) filtered consensus, 3) filtered gene matrix .h5 files (please click submit only after all your files have been uploaded):

Browse... SCA_scImmune_Example_From_10X.zip

Upload complete

scImmune Input Example Alternatively, right click on the button and save link as.

3. Choose Meta Data:

Upload a meta file in .csv/.txt format for your data (format see example)

Browse... SCA_scImmune_Metadata_Example.csv

Upload complete

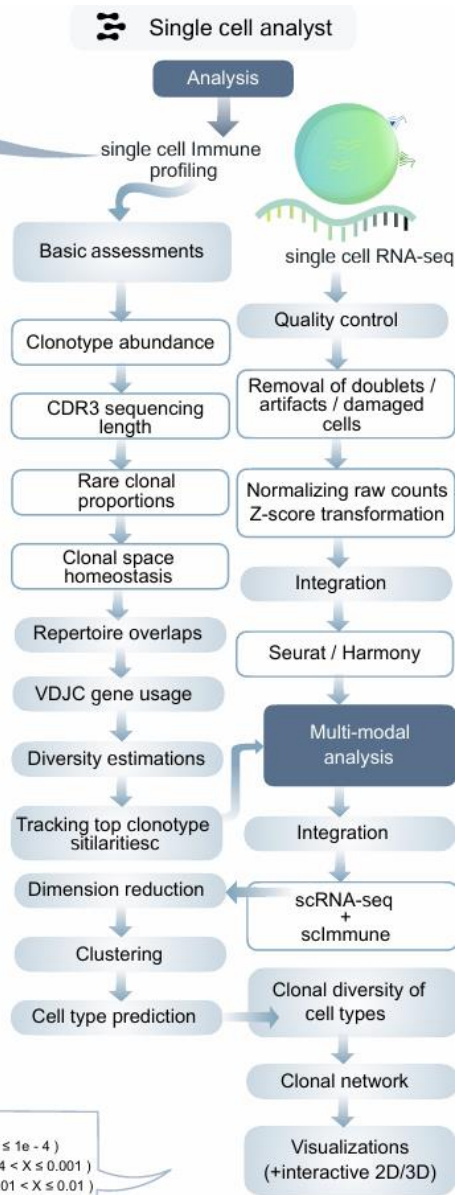
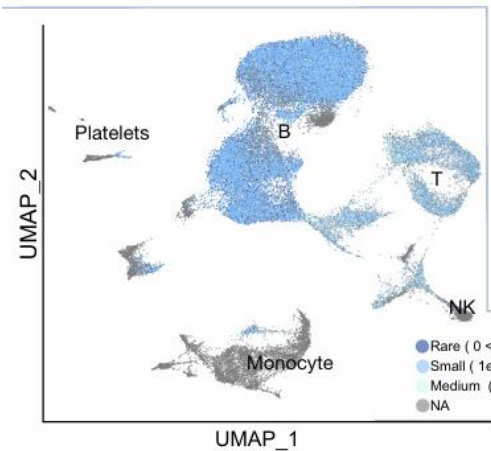
scImmune Metadata Example Alternatively, right click on the button and save link as.

4. Choose an Integration method (only applies when multiple samples are uploaded):

Harmony

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The scImmune Profiling workflow is tailored for immune repertoire analyses, offering detailed insights into clonotype abundance, CDR3 sequence length distributions, and VDJC gene usage. The platform facilitates repertoire overlap analyses, spectratyping, and clonal diversity estimations. For multimodal datasets, the integration of scRNA-seq and immune profiling data allows the mapping of clonotype expansions onto predicted cell types. This approach enables researchers to study immune responses in health and disease, such as clonal expansions in cancer immunotherapy or autoimmunity.

Figure 5.ScImmune Profiling Analysis Framework



Case 4: ScCNV analysis

Single Cell CNV Online Analysis Platform

SCA aims to facilitate researchers around the globe to utilize its one-stop single cell analysis platform and deliver breakthrough results.

1. Project Name:

SCA scCNV Example

2. Choose Files:

Upload a zip file containing 10X format CNV mappable regions .bed file, cnv calls .bed file and summary metrics .csv file for all your samples (please click submit only after all your files have been uploaded):

Browse... SCA_scCNV_Example_From_10X.zip
Upload complete

scCNV Input Example *Alternatively, right click on the button and save link as.*

3. Choose Meta Data:

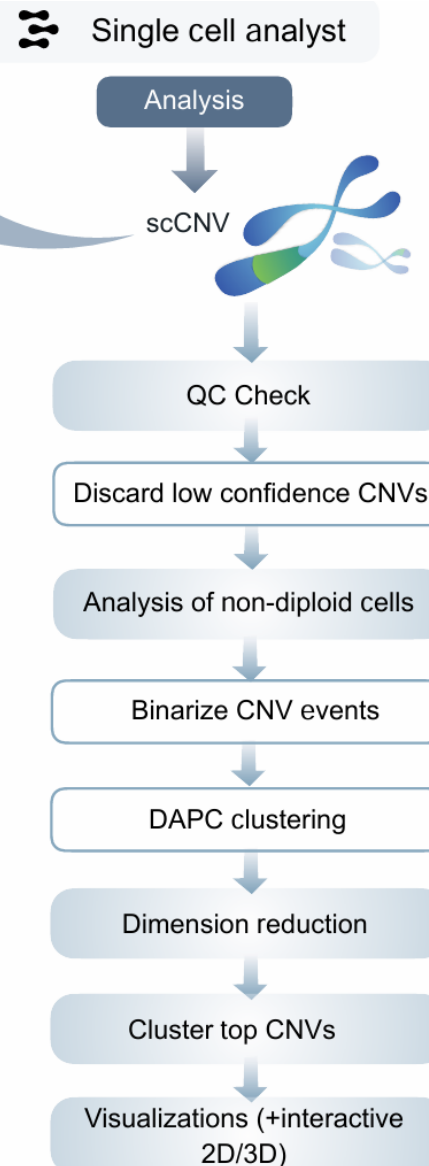
Upload a meta file in .csv/.txt format for your data (format see example)

Browse... SCA_scCNV_Metadata_Example.csv
Upload complete

scCNV Metadata Example *Alternatively, right click on the button and save link as.*

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The scCNV workflow provides a detailed view of CNVs at the single-cell level. It identifies ploidy levels and clusters cells based on CNV profiles, facilitating the detection of subpopulations with specific genomic aberrations. For multi-sample datasets, phylogenetic analyses and hierarchical clustering enable the identification of shared and unique CNV patterns across samples. This workflow is particularly suited for studies of cancer, where CNVs play a critical role in tumor progression and heterogeneity.

Figure 6.ScCNV Analysis Framework

Summary




- ❑ Single Cell Analyst(<https://www.singlecellanalyst.org/>) is a user-friendly platform for multi-omics analysis, supporting six single-cell omics types and spatial transcriptomics with standardized workflows and 20+ tools.
- ❑ Regular updates ensure flexibility, and a built-in forum fosters user collaboration.
- ❑ Platform URL: <https://www.singlecellanalyst.org/>

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 office@imeta.science
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