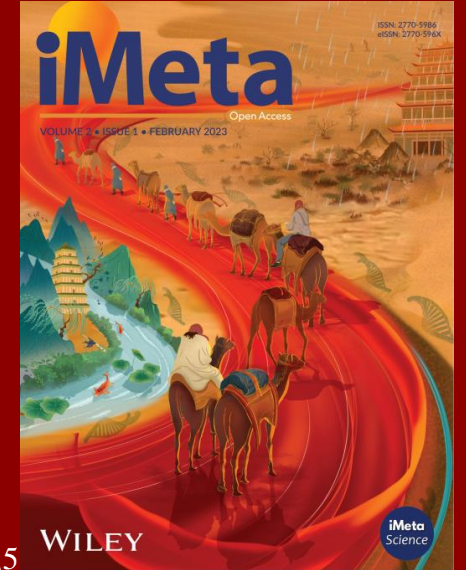




Single Cell Analyst: 一个专注于多组学分析的 用户友好型在线分析平台



潘璐^{1#}, 汤步富^{2#}, 张旋^{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,
范雨煊⁹, 郑旭⁹, 简新月⁹, 盛韧^{10*}, 王振宁^{9*}, 李薛鑫^{9*}

¹卡罗林斯卡医学院、²复旦大学、³昆明医科大学、⁴德国蒂宾根大学、⁵哈佛医学院、⁶罗马第一大学、⁷南洋理工大学、
⁸美国东北大学、⁹中国医科大学、¹⁰东北大学

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>



简介

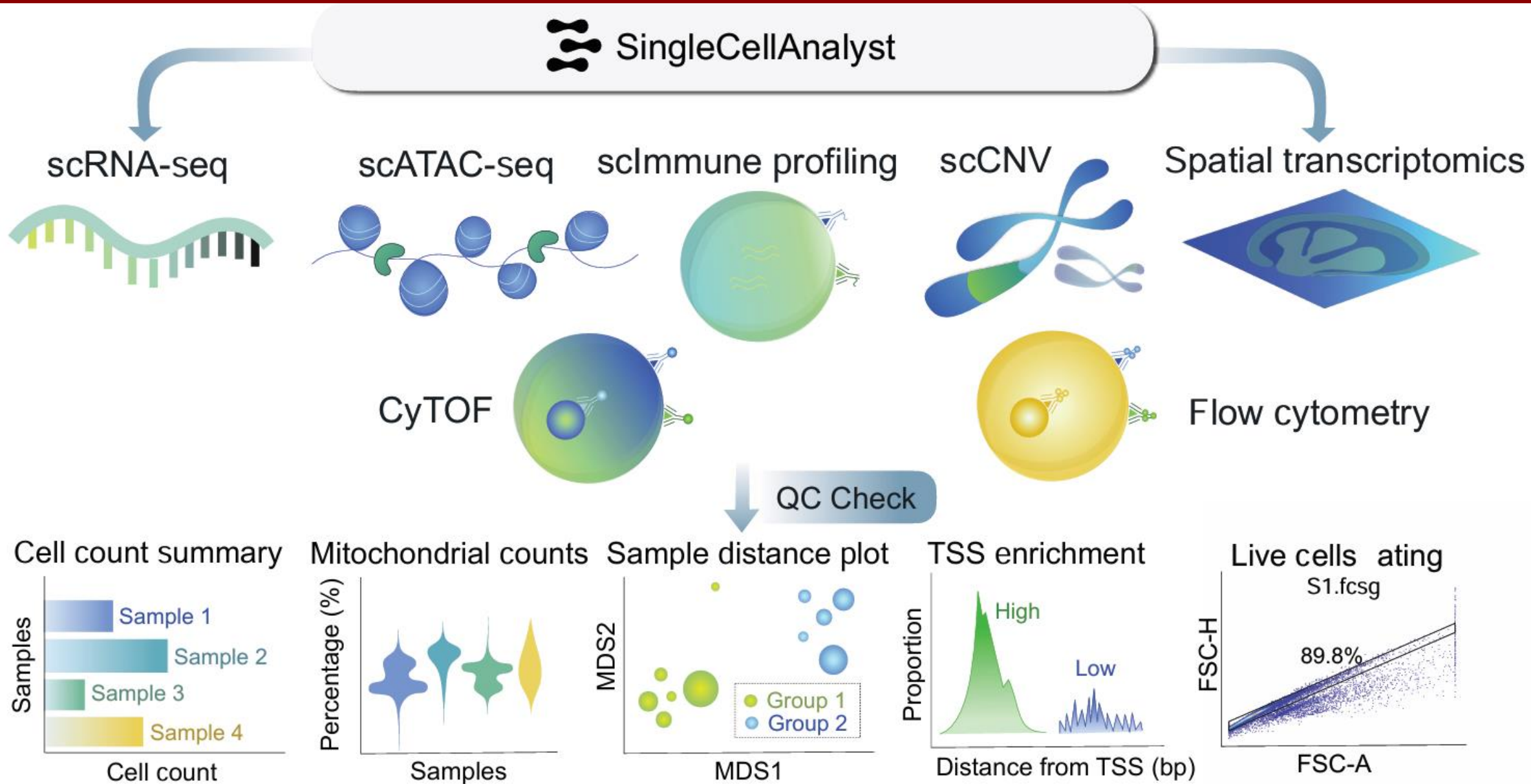
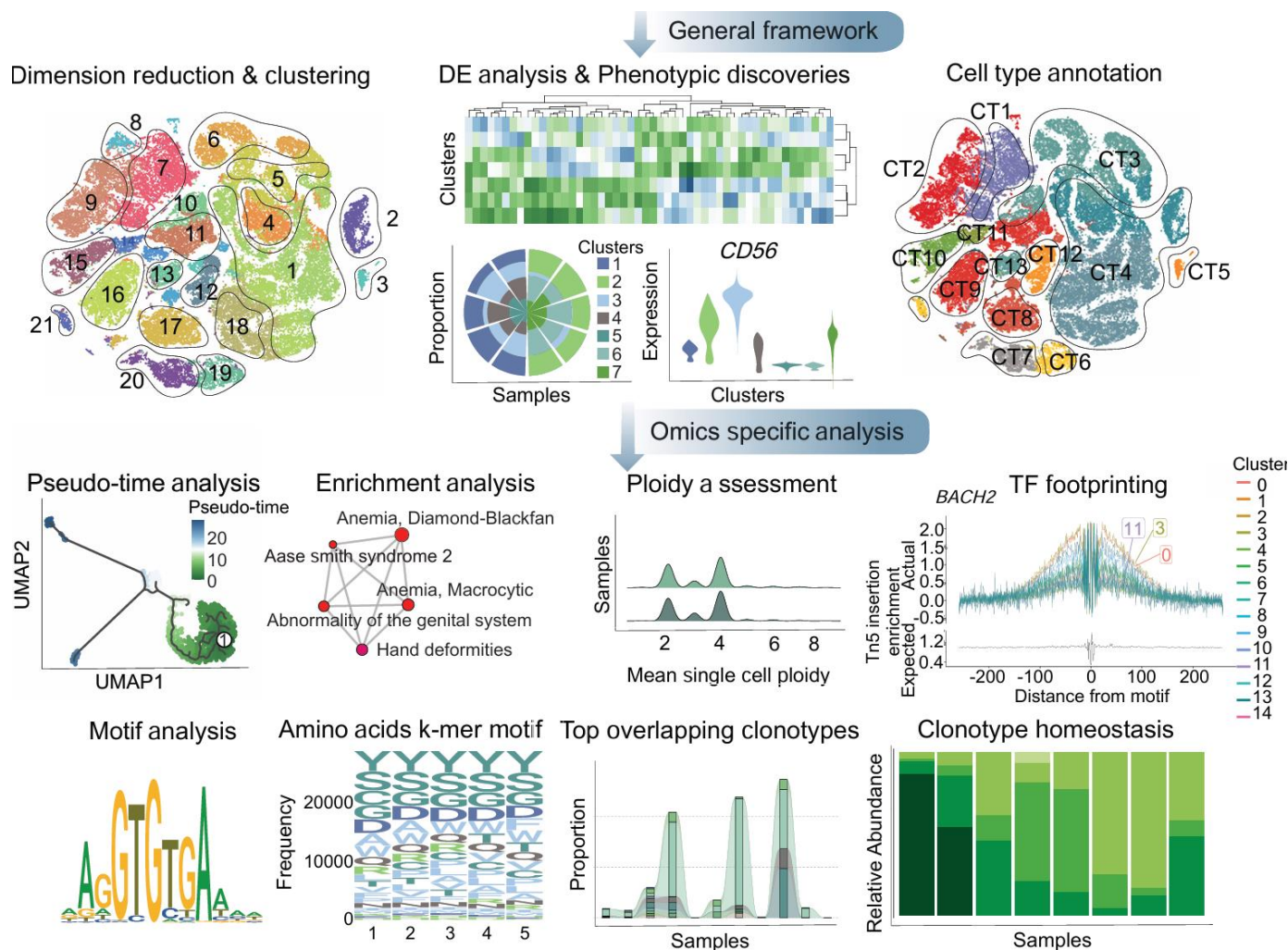


图1.a平台简介



亮点



1. 本平台是全能分析平台：支持6大单细胞组学技术及空间转录组学分析。

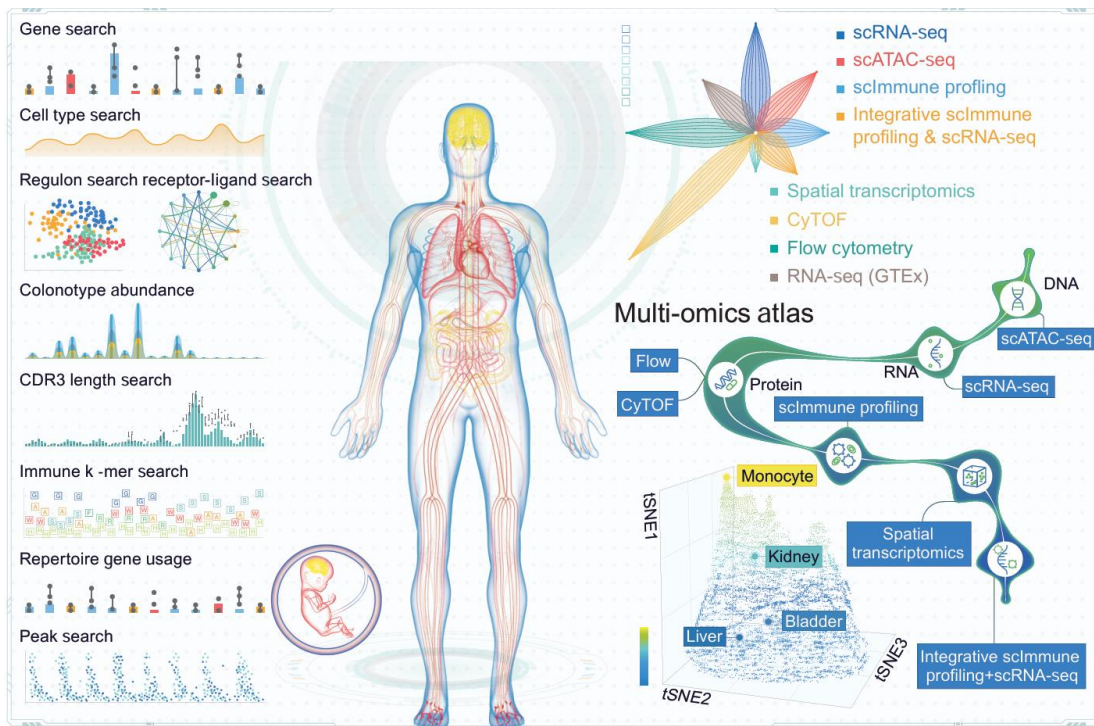
2 零门槛操作：无需编程基础，直观友好的交互界面满足各层级研究者需求。

3. 智能分析流水线：自动化完成质控、数据预处理、表型分析等关键步骤，一键生成可直接投稿的交互式图表。

4. 极简工作流程：无需复杂生信背景，即可轻松完成高阶多组学整合分析。

图1.b 分析流程

Single cell analyst平台概述



(图2) 单细胞分析数据库概述

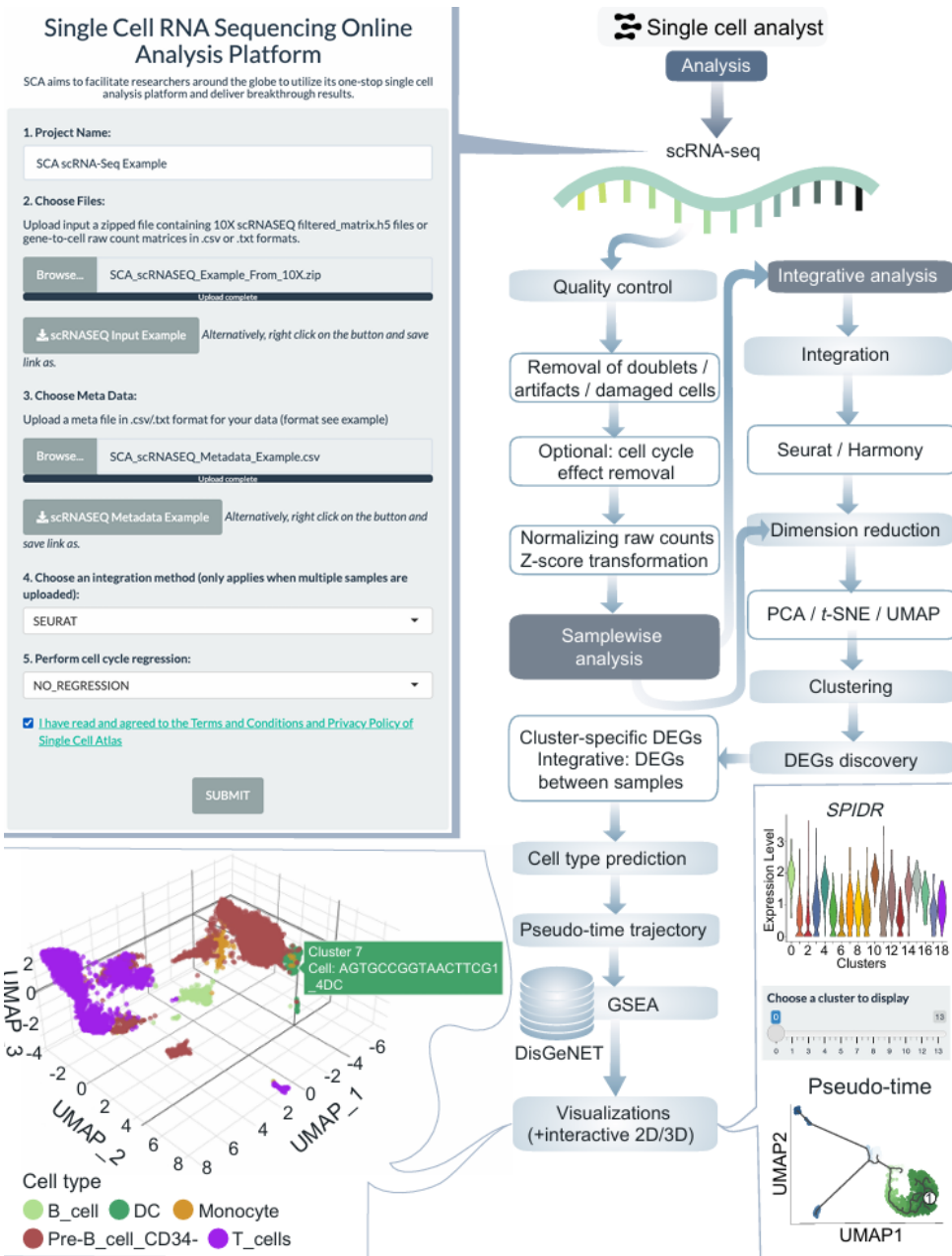
The screenshot shows the 'New Posts' section of the forum. It features three posts by user 'Lu Pan' dated Nov 07, 2022. The first post is 'Welcome to the Forum' with 8 likes. The second is 'Introduce yourself' with 10 likes. The third is partially visible, 'Vape Shops: Essential or Overhyped? Let's Discuss!'. The forum interface includes user avatars, post titles, categories, and engagement metrics like likes and replies.

平台论坛

The screenshot displays the 'SingleCellAnalyst' web application interface. The top navigation bar includes 'Home', 'About', 'Analysis', 'Vignette', 'Tools', 'Database', 'Forum', and 'More'. The main area is a grid of 30 tool buttons, each accompanied by a small preview image of the tool's output. The tools include: Quality Control, Cell Count Imputation, Data Integration, Dimension Reduction, Clustering&DE Analysis, Auto Cell Annotation, Manual Annotation, Cell-Cell Communication, tSNE/UMAP/Scattered Plot, Heatmap, Ridge Plot, Stack Area Plot, Violin Plot, Bar Plot, Pie Chart, Box Plot, Dot Plot, View Flow/Cy TOF FCS, Bubble Plot, Volcano Plot, Chord Diagram, Sankey Classic Diagram, Alluvial Plot, Network Graph, and Manhattan Plot.

平台工具

案例一：ScRNA-seq分析



除标准QC与数据处理步骤外，该平台支持评估细胞类型预测、执行差异表达分析、开展通路与富集分析，并推断细胞簇或类型的拟时序轨迹。用户可根据生物学问题自定义拟时序分析的起始点。针对多样本数据集，平台执行整合分析以比较健康与患病样本或其他实验条件的表型差异。该流程特别适用于研究不同生物学背景下的基因表达动态与细胞状态转换。

图3. ScRNA-seq分析流程框架图



案例二：ScATAC-seq分析

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.

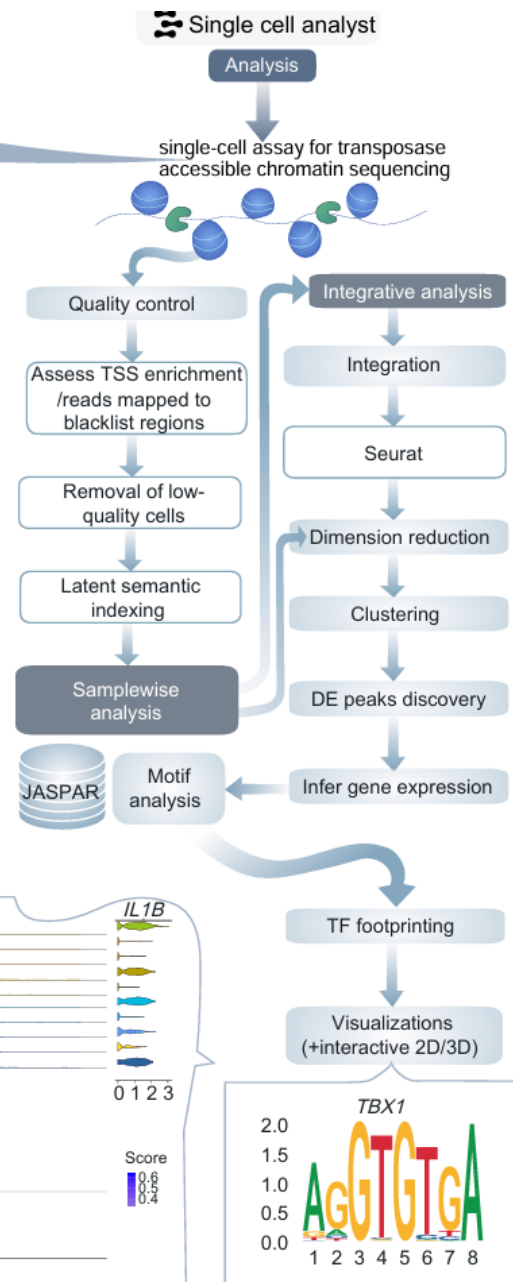
1. Project Name:
SCA scATAC Example

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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在scATAC-seq流程中，TSS富集度与核小体条带模式评估等QC步骤，与可及染色质区域识别、motif足迹分析等下游分析相结合。通过计算基因活性分数，研究人员能将染色质可及性与基因表达关联。用户可探索顺式共可及网络与富集motif，解析驱动细胞功能的调控元件。多样本整合分析能揭示不同条件间共有的和特异的染色质特征。

图4. ScATAC-seq分析流程框架图



案例三：单细胞免疫谱分析

sclImmune 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_sclImmune_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_sclImmune_Example_From_10X.zip

Upload complete

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_sclImmune_Metadata_Example.csv

Upload complete

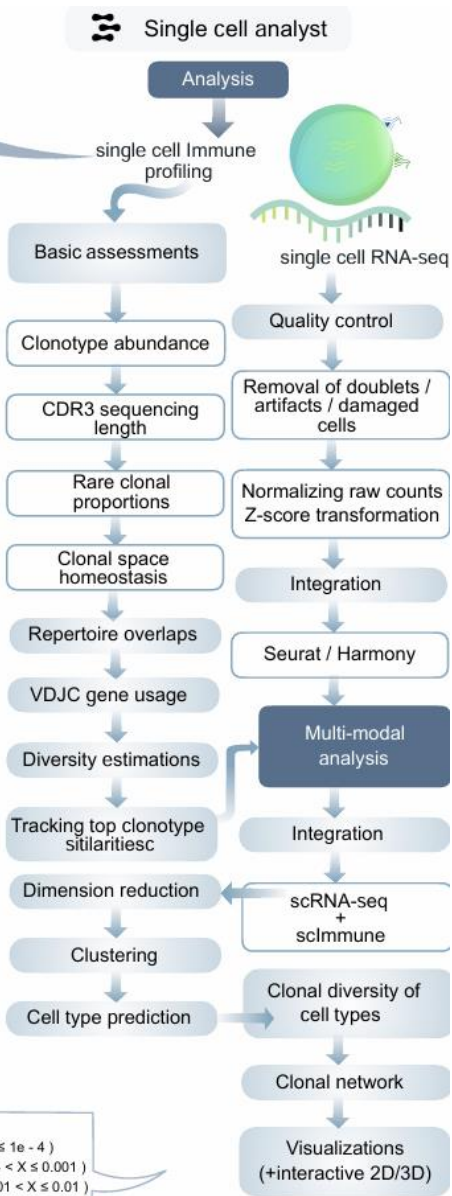
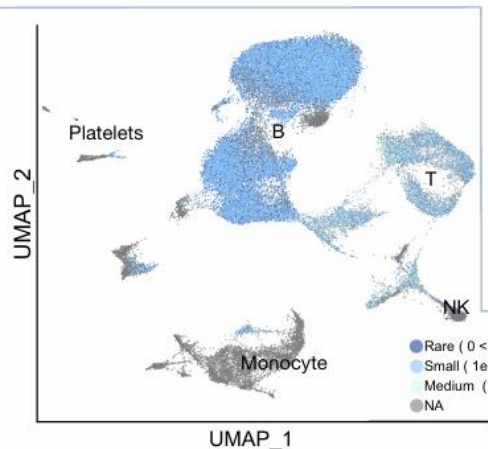
Alternatively, right click on the button and save link as.

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

Harmony

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sclImmune Profiling流程专为免疫受体库分析设计，提供克隆型丰度、CDR3序列长度分布及VDJC基因使用频率等深度解析。平台支持受体库重叠分析、谱型分型与克隆多样性评估。对于多组学数据，整合scRNA-seq与免疫谱数据可将克隆型扩增映射至预测细胞类型，助力研究癌症免疫治疗或自身免疫疾病中的克隆扩增等免疫应答机制。

图5.单细胞免疫谱分析流程框架图

案例四：ScCNV分析

该流程在单细胞层面解析拷贝数变异（CNV），通过识别ploidy水平并基于CNV谱聚类细胞，可检测具有特定基因组异常的子群。多样本分析中的系统发育树与层次聚类能鉴定样本间共有的和独特的CNV模式，尤其适用于CNV在肿瘤进展与异质性中起关键作用的癌症研究。

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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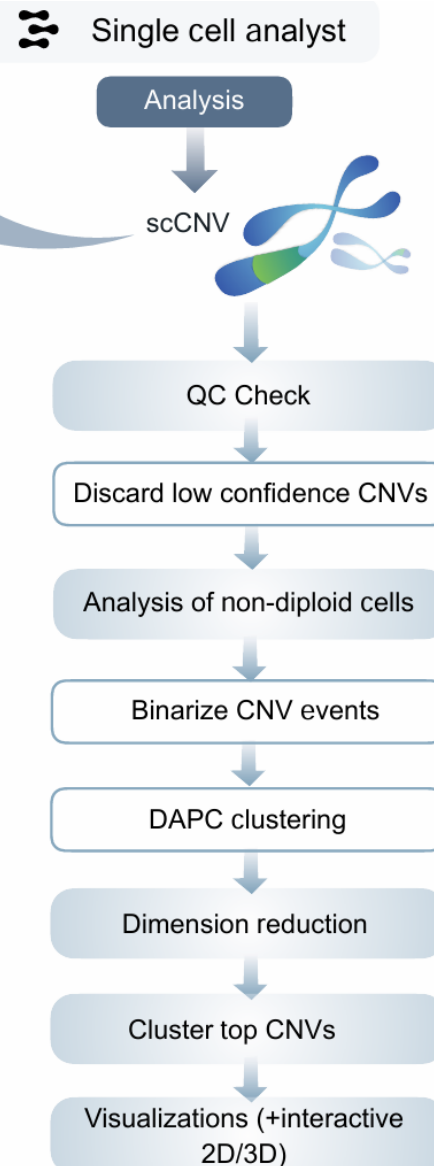


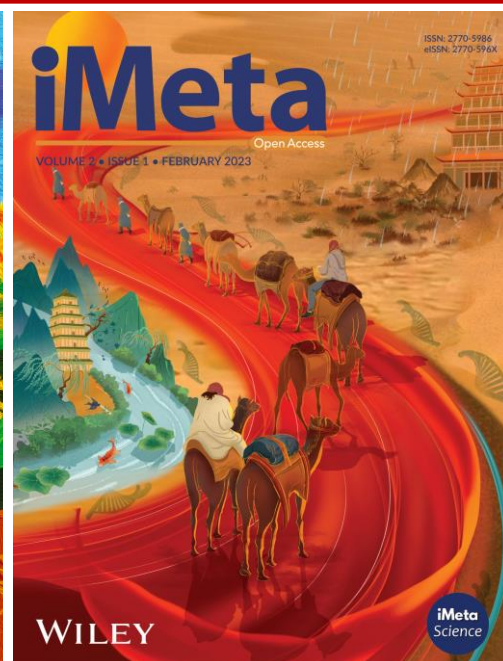
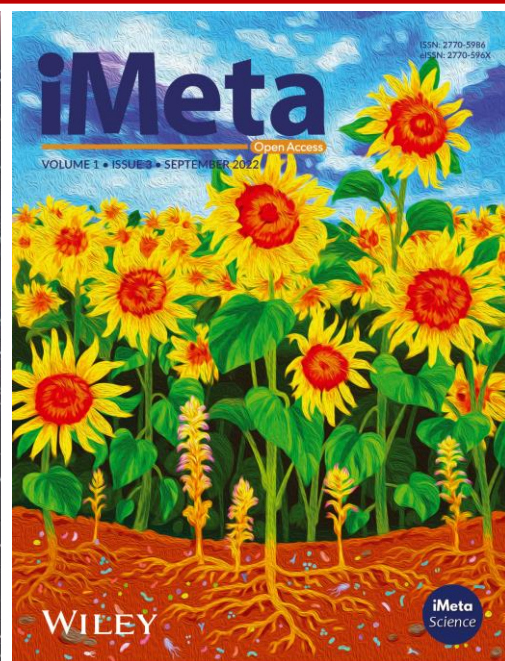
图6.ScCNV分析流程框架图



总结

- 在这项研究中，我们介绍了一个专注于多组学分析的用户友好型在线分析平台Single Cell Analyst;
- 目前平台已配备了6种单细胞组学和空间转录组技术在线分析和20多种独立工具，平台将持续更新，满足用户开展标准化和个性化的分析;
- 平台还提供论坛版块，旨在方便用户进行学术交流和反馈咨询;
- 平台网址：<https://www.singlecellanalyst.org/>

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