

Tutorial

1st Overall Distribution Analysis

Spatial Pattern Analysis

Clustering Analysis and Cell Annotation

Differential Analysis

Functional Association Analysis

Data Visualization

SMIntegration: Spatial Multi-omics Integration Platform

SMIntegration is an innovative open-source platform for integrated analysis of spatial transcriptomics and metabolomics data. It addresses critical challenges in spatial multi-omics by providing:

- Comprehensive integrated spatial analysis:** Joint analysis pipeline from initial visualization to biological interpretation
- Multimodal pattern discovery:** Multiple algorithms for identifying spatially co-varying regions and gene-metabolite modules
- Flexible differential analysis:** Comparative analysis supporting multiple region definition strategies
- Inter-group network comparisons:** Construction and comparison of condition-specific correlation networks for differential molecules (DEGs/DAMs)
- Interactive visualization:** Dynamic exploration of spatial distributions and co-localization patterns

Core Analytical Modules

1st Overall Distribution Analysis

Initial data visualization of spatial distributions

Clustering Analysis and Cell Annotation

Spatial domain detection with multiple algorithms and automated cell type mapping

Functional Association Analysis

Pathway annotation and cross-omics functional integration

Spatial Pattern Analysis

Identification of spatially co-varying gene-metabolite modules

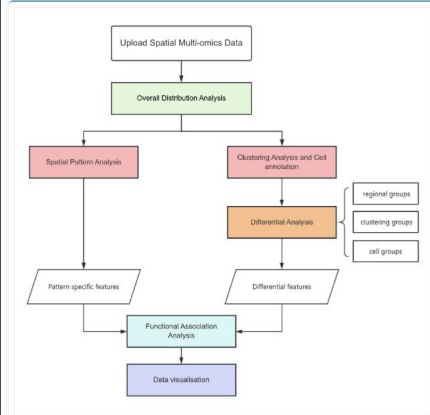
Differential Analysis

DEGs/DAMs discovery and region-specific network construction

Data Visualization

Advanced spatial imaging including co-localization and multi-feature views

Analysis Workflow



Data Preparation Requirements

Critical Preprocessing Steps:

- Resolution Harmonization:** Aggregate higher-resolution data (e.g., 10x100 for 500m²-50µm conversion)
- Spatial Registration:** Two options available:
 - Option A (Built-in Tool): Check "Perform Registration" in the Upload tab. Supports manual orientation adjustment (Rotate/Flip) followed by automatic alignment, powered by [RStitching](#). [Download Interactive Tutorial PDF](#)
 - Option B (External Tools): Align coordinates using SpatialData (scripts provided on GitHub)
- Metabolite Identification:** Requires annotated metabolite names (not m/z values)

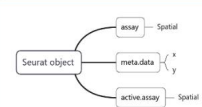
Input File Specifications

Option 1: Seurat Object Format (Recommended)

You need to upload two separate Seurat objects (.rds file):

Spatial Metabolomics Object			Spatial Transcriptomics Object		
Component	Content	Slot Name	Component	Content	Slot Name
Assay	Metabolite intensity matrix	Spatial	Assay	Gene expression matrix	Spatial
Meta Data	Spatial coordinates	x, y in meta.data	Meta Data	Spatial coordinates	x, y in meta.data
Active Assay	Must be named "Spatial"	active.assay	Active Assay	Must be named "Spatial"	active.assay

[Download metab Seurat demo](#) [Download trans Seurat demo](#)



Important Note:

For both formats, the assay name must be "Spatial" in each Seurat object. The platform expects this naming convention to correctly identify the data modality.

Option 2: Text Matrix Format

You need to upload two separate files:

Spatial Metabolomics File			Spatial Transcriptomics File		
Column	Description	Example	Column	Description	Example
1	Metabolite Name	metabolite 1	1	Gene ID	gene 1
2	X Coordinate	123	2	X Coordinate	123
3	Y Coordinate	134	3	Y Coordinate	134
4	Intensity	2.0	4	HtCount	2

[Download demo spatial metabolomics data](#) [Download demo spatial transcriptomics data](#)

spatial metabolomics				
metabolite name	x	y	intensity	
metabolite 1	123	134	2	
metabolite 2	144	165	1	
metabolite 3	165	144	1	
metabolite 4	234	245	1	
spatial transcriptomics				
gene id	x	y	htcount	
gene 1	123	134	2	
gene 2	144	165	1	
gene 3	165	144	1	
gene 4	234	245	1	

Additional Resources

[Source Code & Local Installation Guide](#)

Technical Support

For immediate assistance:

- Documentation:** Comprehensive guides available in Help section
- Email:** danghaizhe@genomics.cn