

Step2: Spatial Pattern Analysis

This module employs the Spatiotopos algorithm to identify spatially co-varying molecular modules and discover cross-modal pattern correlations.

- Step 1: Construct k-nearest neighbor spatial networks for each omics layer
- Step 2: Identify spatially variable features by comparing actual Earth mover's distance (EMD) against a null distribution from 500 random permutations
- Step 3: Cluster significant features into spatial modules
- Step 4: Quantify cross-omics pattern correlations using Moran's I (spdep)
- Step 5: Screen pattern-specific features

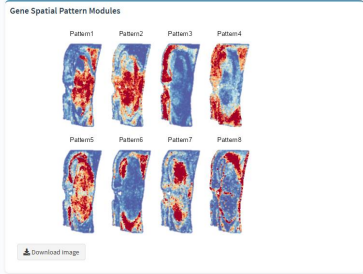
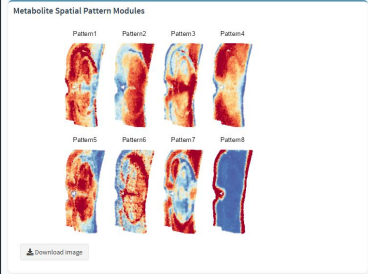
Click 'Start spatial pattern analysis' to initiate the workflow.

Note: Computational time varies with feature count. Please avoid duplicate submissions.

Start spatial pattern analysis

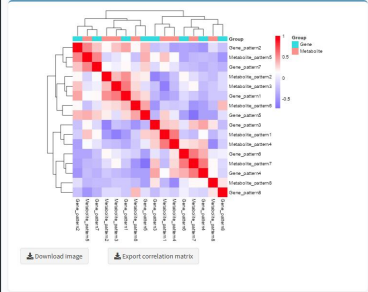
Spatial Pattern Modules

Identified spatial pattern modules for metabolites (left) and genes (right).



Cross-Omics Pattern Correlation

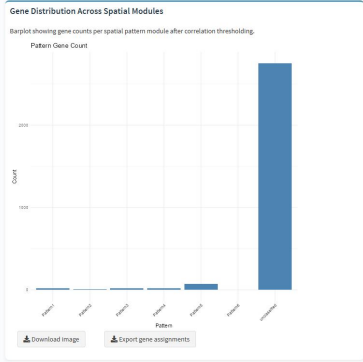
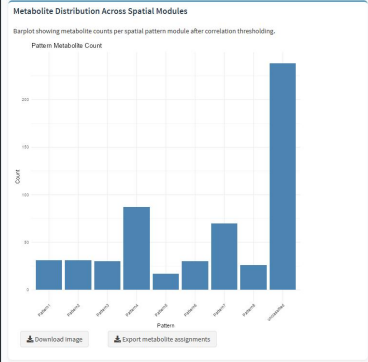
Moran's I correlation matrix quantifying spatial co-variation between metabolite and gene pattern modules. Significance levels: *p<0.05, **p<0.01, ***p<0.001.



Pattern-Specific Feature Classification

Features are assigned to spatial modules based on spatial correlation:

- Correlation >0.5: Assigned to best-matching module
- Correlation <0.5: Categorized as 'unclassified'



Spatial Distribution of Pattern-Specific Features

Visualize spatial expression patterns of top module-associated features. Select modules and features below:

The top 300 features per module (ranked by correlation) are designated as 'pattern-specific features' for functional analysis.

