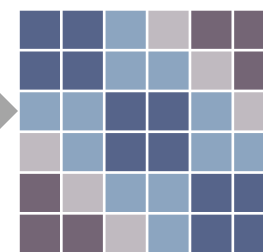**spMGM**

Matrix Normal Graphical Model

$$Y = G + S + I_{GS} + \epsilon$$
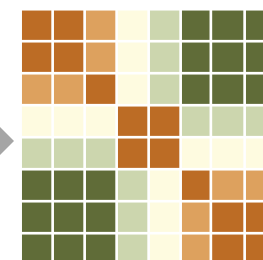
G, S: Gene and spatial fixed effect

I_{GS}: Gene and spatial interaction effect

$$\text{Vec}(I_{GS}) \sim N(0, U \otimes V)$$
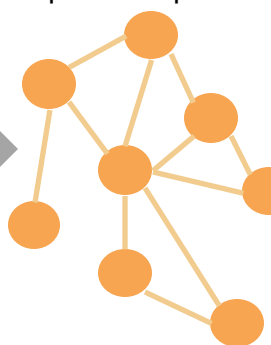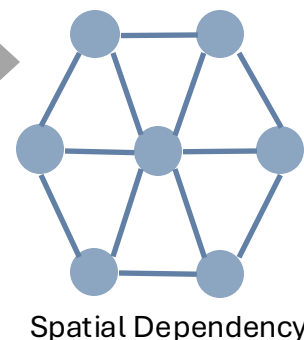
V: Gaussian Kernel of Spatial Distance

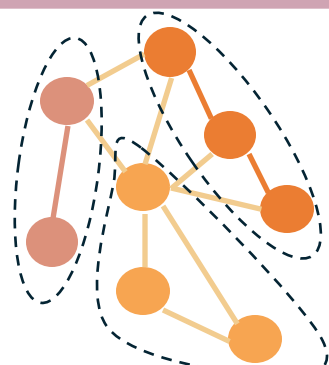**Target Parameter U:** Gene Expression Covariance

Location	x	y
S_1	x_1	y_1
S_2	x_2	y_2
S_3	x_3	y_3
S_4	x_4	y_4
S_5	x_5	y_5
S_6	x_6	y_6
...	...	...
S_N	x_N	y_N

Location Coordinate

Spatially Resolved Gene Expression

Spatial Dependency
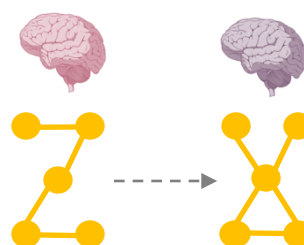
Gene Dependency

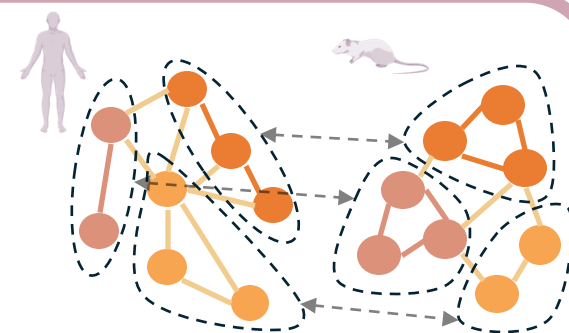Module Detection

Gene Set Analysis

- Gene ontology
- Reactome
- KEGG
- WIKIPATH

Change of Network

Cross-species Module Alignment