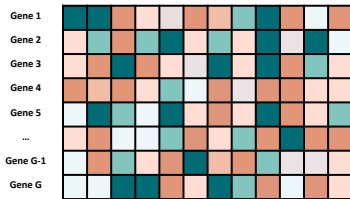




S₁ S₂ S₃ S₄ S₅ S₆ S₇ S₈ ... S_{N-2} S_{N-1} S_N



Spatial transcriptomics expression

Spot	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 _{N-1}	x _{N-1}	y _{N-1}
S _N	x _N	y _N

Location information

Input

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 Location information



Target U : Gene Co-expression Covariance

Output

Gene Expression Correlation Matrix

