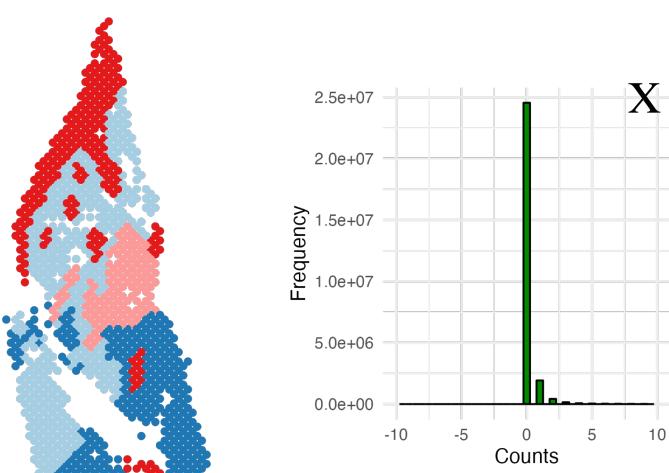


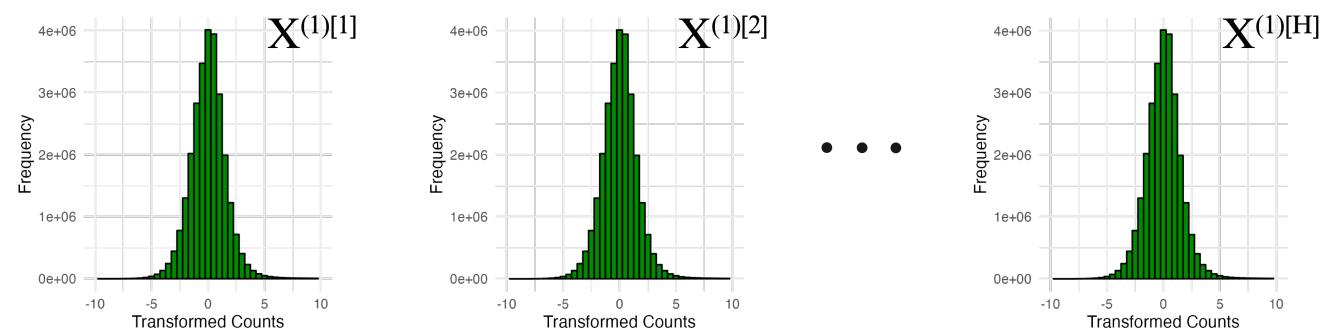
Spatial Transcriptomics Spatially-Resolved Gene Expression



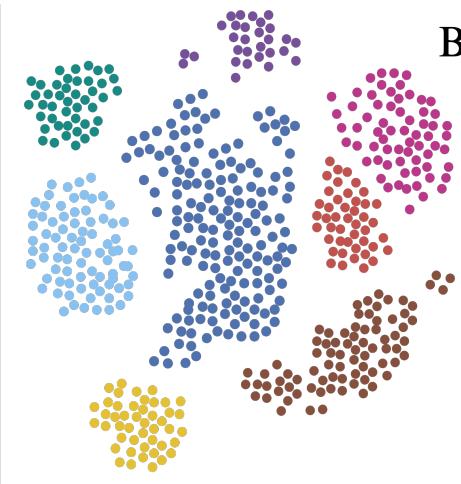
ZI-HGT Zero-Inflated Hierarchical Generalized Transformation Model

$$h = 1, \dots, H: \quad \frac{\exp(X_{i,j}^{(1)[h]})}{1 + \exp(X_{i,j}^{(1)[h]})} \left| \begin{array}{l} X_{i,j}^{[0]} = 0, X_{i,j} \sim \text{Beta}(\alpha_0 - \kappa_0, \kappa_0) \\ X_{i,j}^{(1)[h]} \mid X_{i,j}^{[0]} = 1, X_{i,j} \sim \text{Gamma}(\alpha_1 + X_{i,j}, \alpha_1 + 1) \end{array} \right.$$

$$X_{i,j}^{(1)[h]} \mid X_{i,j}^{[0]} = 1, X_{i,j} \sim \text{Gamma}(\alpha_1 + X_{i,j}, \alpha_1 + 1)$$



Single-Cell RNA-Sequencing



CARD Conditional AutoRegressive Deconvolution

$$h = 1, \dots, H:$$

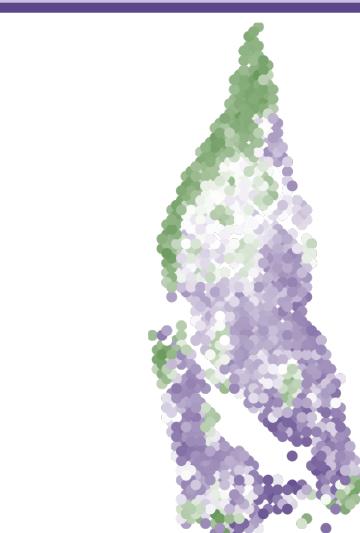
$$X^{(1)[h]} = BV^{[h]'} + E, \quad E_{i,j} \sim N(0, \sigma_e^2)$$

$\hat{V}^{[1]}$	Cancer Cells	ecm-myCAFs	...	Tregs
Location 1	0.71	0.12	...	0.01
Location 2	0.76	0.09	...	0.03
:				
Location N	0.12	0.32	...	0.17

$\hat{V}^{[2]}$	Cancer Cells	ecm-myCAFs	...	Tregs
Location 1	0.71	0.12	...	0.01
Location 2	0.76	0.09	...	0.03
:				
Location N	0.12	0.32	...	0.17

$\hat{V}^{[H]}$	Cancer Cells	ecm-myCAFs	...	Tregs
Location 1	0.71	0.12	...	0.01
Location 2	0.76	0.09	...	0.03
:				
Location N	0.12	0.32	...	0.17

Estimated Cell-Type Proportions



Pointwise 95% Credible Intervals

