

# Unsupervised discovery of tissue architecture in multiplexed imaging

---

In the format provided by the authors and unedited

**Extended Data Table 1:** Summary of features of existing methods for detection of higher-order tissue patterns. UTAG requires less input compared to similar methods as it does not require cell type annotation, and allows joint inference of microanatomical domains across slides. This also reduces the burden of result interpretation required from the user (domain interpretation only once for the entire dataset instead of for each slide).

Method	Underlying model	Resolution	Cell type annotation	Application unit	Programming language
UTAG	Graph (Message Passing) + Clustering	Single cell	Not required	<b>Across slides &amp; Per slide</b>	Python
SpatialLDA	Graph (Niche distribution) + Latent Dirichlet Allocation	Single cell	Required	<b>Across slides &amp; Per slide</b>	Python
SpaGene	Graph Permutation + Non-negative Matrix Factorization	Single cell	Not required	Per slide	R
HMRF (Giotto)	Hidden Markov Random Field	Single cell & Spot Based	Not required	Per slide	R
BayesSpace	Bayesian Hidden Markov Random Field	Spot Based	Not Applicable	Per slide	R
SpaGCN	Graph Convolutional Neural Network	Single cell & Spot Based	Not required	Per slide	Python