scRNA-seq reference data

Cell-level molecular profile

	Gene 1	Gene 2	⋯	Gene P
Cell 1	23	19	⋯	0
Cell 2	0	139	⋯	18
⋮	⋮	⋮	⋱	⋮
Cell M	0	0	⋯	56

Cell type information

	cellType
Cell 1	Cell type 1
Cell 2	Cell type 2
⋮	⋮
Cell M	Cell type 4

Spatial transcriptomics data

Spot-level molecular profile

	Gene 1	Gene 2	⋯	Gene P
Spot 1	23	19	⋯	0
Spot 2	0	139	⋯	18
⋮	⋮	⋮	⋱	⋮
Spot N	0	0	⋯	56

geospatial profile

	x	y
Spot 1	16.9	9.0
Spot 2	16.9	11.1
⋮	⋮	⋮
Spot N	18.0	10.1

A zero-inflated negative binomial mixture model with Markov random field prior

$$x_{mj}|c_m = k, \gamma_j, \mu_{kj}, \mu_{0j}, \psi_j, \zeta_{mj} = 0 \sim \gamma_j \mathrm{NB}\left(x_{mj};\ v_m\mu_{kj}, \psi_j\right) + (1-\gamma_j)\mathrm{NB}(x_{mj};\ v_m\mu_{0j}, \psi_j)$$

$$y_{ij}|\pi_{ik}, \gamma_j, \mu_{kj}, \mu_{0j}, \emptyset_j, \eta_{ij} = 0 \sim \gamma_j \mathrm{NB}\left(y_{ij};\ s_i \textstyle\sum_{k=1}^{K} \pi_{ik}\,\mu_{kj}, \emptyset_j\right) + (1-\gamma_j)\mathrm{NB}\left(y_{ij};\ s_i\mu_{0j}, \emptyset_j\right)$$

$$+$$

$$\boldsymbol{\pi}_{i\cdot}|z_i = d, \boldsymbol{\alpha}_{d\cdot} \sim \mathrm{Dir}(\boldsymbol{\pi}_{i\cdot};\ \boldsymbol{\alpha}_{d\cdot})$$

$$\pi(z_i = d|\boldsymbol{z}_{-i}) \propto \exp\left(e_d + f \textstyle\sum_{i'=1}^{N} g_{ii'}\, \mathrm{I}(z_{i'} = d)\right)$$

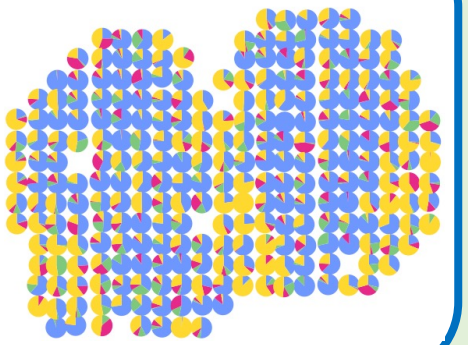
Cell type deconvolution

Spatial domain identification

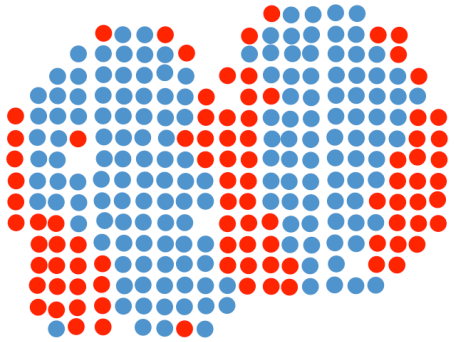
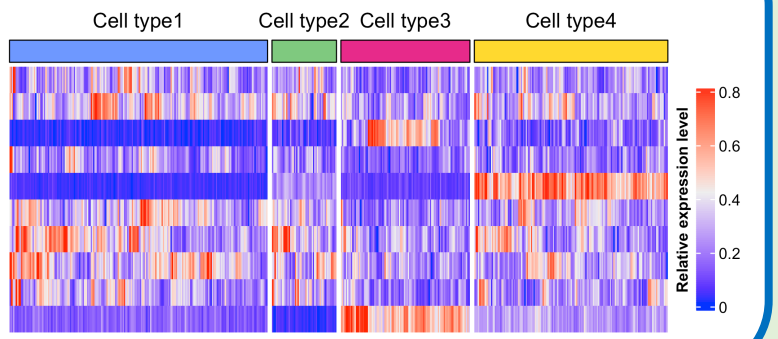
Discriminating gene detection

Estimated cell type proportion

	Cell type 1	Cell type 2	Cell type 3	Cell type 4
Spot 1	0.51	0.06	0.09	0.34
Spot 2	0.29	0.01	0.17	0.53
⋮	⋮	⋮	⋱	⋮
Spot N	0.75	0.10	0.11	0.04



Estimated spatial domain



Heatmap of detected discriminating genes