# scRNA-seq reference data

## Cell-level molecular profile ($X$)

| | Gene 1 | Gene 2 | ... | Gene $P$ |
|---|---|---|---|---|
| Cell 1 | 23 | 19 | ... | 0 |
| Cell 2 | 0 | 139 | ... | 18 |
| ⋮ | ⋮ | ⋮ | ⋱ | ⋮ |
| Cell $M$ | 0 | 0 | ... | 56 |

## Cell types ($c$)

| | cellType |
|---|---|
| Cell 1 | Cell type 1 |
| Cell 2 | Cell type 2 |
| ⋮ | ⋮ |
| Cell $M$ | Cell type 4 |

# Spatially resolved transcriptomics data

## Spot-level molecular profile ($Y$)

| | Gene 1 | Gene 2 | ... | Gene $P$ |
|---|---|---|---|---|
| Spot 1 | 23 | 19 | ... | 0 |
| Spot 2 | 0 | 139 | ... | 18 |
| ⋮ | ⋮ | ⋮ | ⋱ | ⋮ |
| Spot $N$ | 0 | 0 | ... | 56 |

## Geospatial profile ($T$)

| | Coord. $x$ | Coord. $y$ |
|---|---|---|
| Spot 1 | 16.9 | 9.0 |
| Spot 2 | 16.9 | 11.1 |
| ⋮ | ⋮ | ⋮ |
| Spot $N$ | 18.0 | 10.1 |

## A robust Bayesian deconvolution model

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

$+$
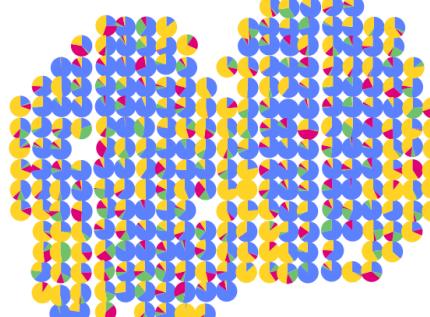
$$\boldsymbol{\pi}_{i\cdot}|z_i = d, \boldsymbol{\alpha}_{d\cdot} \sim \mathrm{Dir}(\boldsymbol{\pi}_{i\cdot}; \boldsymbol{\alpha}_{d\cdot}), \pi_{ik} = \omega_{ik}/\sum_{k'=1}^{K}\omega_{ik'}$$

$$\omega_{ik}|\delta_{ik}, \alpha_{dk} \sim \delta_{ik}\mathrm{I}(\omega_{ik}=0) + (1-\delta_{ik})\mathrm{Ga}(\alpha_{dk}, 1)$$

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

## Cell type deconvolution

### Estimated cell type proportion ($\boldsymbol{\Pi}$)

| | Cell type 1 | Cell type 2 | Cell type 3 | Cell type 4 |
|---|---|---|---|---|
| Spot 1 | 0.5 | 0.1 | 0.1 | 0.3 |
| Spot 2 | 0.4 | 0.0 | 0.2 | 0.4 |
| ⋮ | ⋮ | ⋮ | ⋱ | ⋮ |
| Spot $N$ | 0.75 | 0.0 | 0.0 | 0.25 |

## Spatial domain detection

### Estimated spatial domain ($\boldsymbol{z}$)