

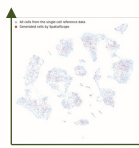
# scRNA-seq reference



Deep Generative model



Learned distribution



# Input

## Input

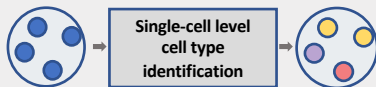
### Spatial data

(Visium, Slide-seq, MERFISH, etc.)

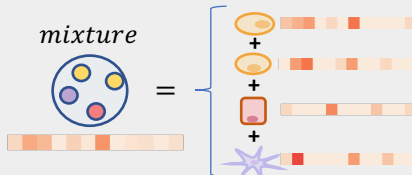
## i. Nuclei segmentation



## ii. Cell type identification

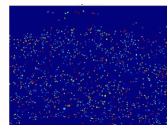


## iii. Gene expression decomposition

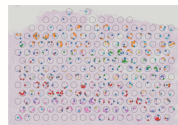


## SpatialScope

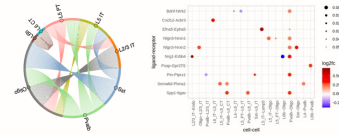
# Results



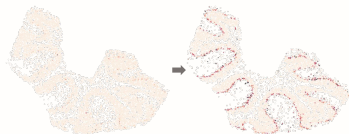
Nuclei segmentation



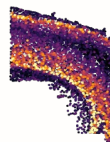
Cell type identification



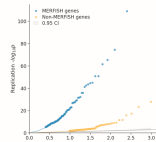
Cell-cell interactions



Correct dropouts



Imputation

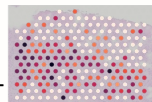


Spatially DE genes

expression

location

image



Spot	x	y
$S_1$	$x_1$	$y_1$
$S_2$	$x_2$	$y_2$
$S_3$	$x_3$	$y_3$
$S_4$	$x_4$	$y_4$
$\vdots$	$\vdots$	$\vdots$
$S_{n-2}$	$x_{n-2}$	$y_{n-2}$
$S_{n-1}$	$x_{n-1}$	$y_{n-1}$
$S_n$	$x_n$	$y_n$

