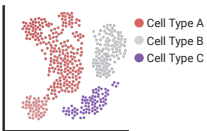
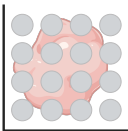


## Input

scRNA-seq  
transcriptomics

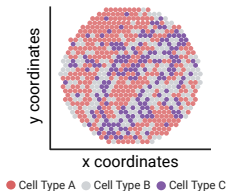


spatial transcriptomics  
(ST)



## Pre-processing

Aligned scRNA-seq to ST  
using CytoSPACE



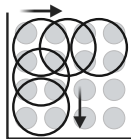
**SPECIAL**

**SP**atial Transcriptomics

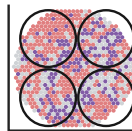
**CE**ll-Cell Interaction **AL**gorithm

1) Divide spatial slides into regions

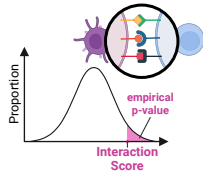
for bulk ST: sliding windows



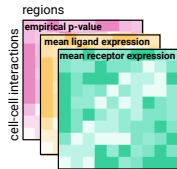
for SlideSeqV2: k-means clustering



2) Run SOCIAL steps 1  
through 3 on each region



3) Accommodate for  
variations across regions



## Output

cell-type-specific ligand-  
receptor interaction activity

