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SENCA-st: Integrating Spatial Transcriptomics and Histopathology with Cross Attention Shared Encoder for Region Identification in Cancer Pathology

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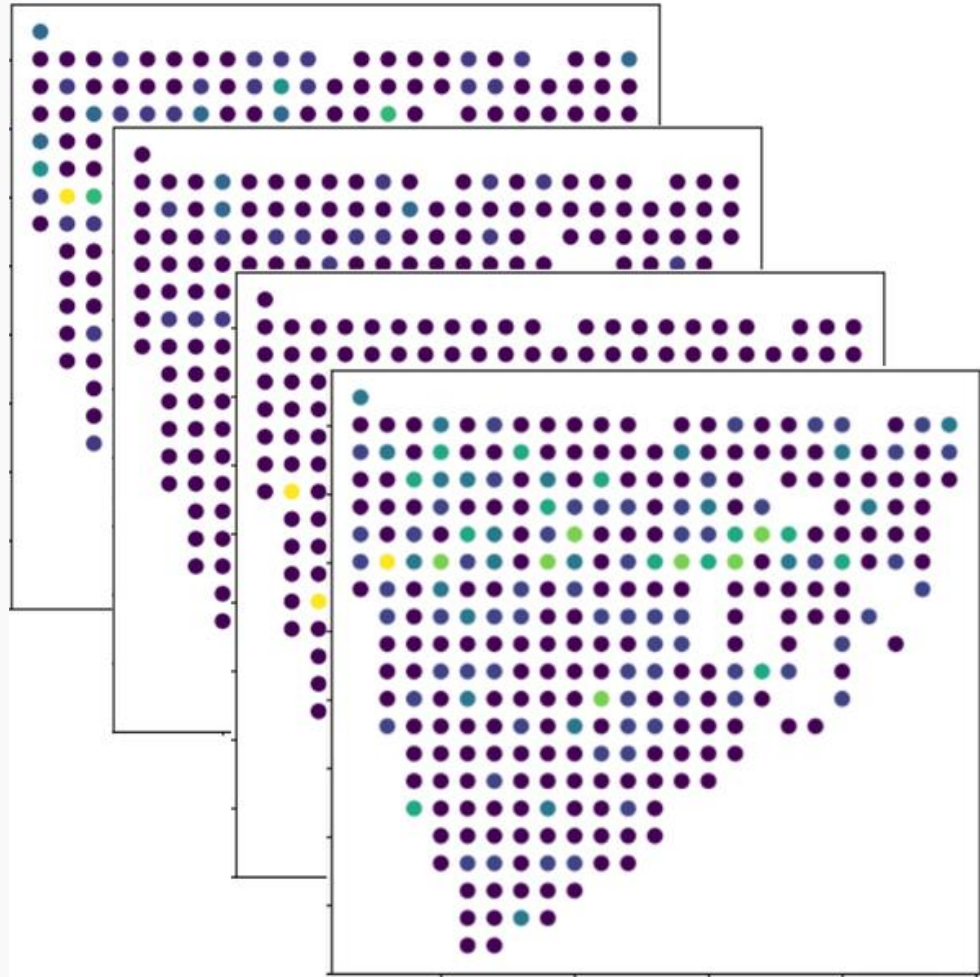


Introduction

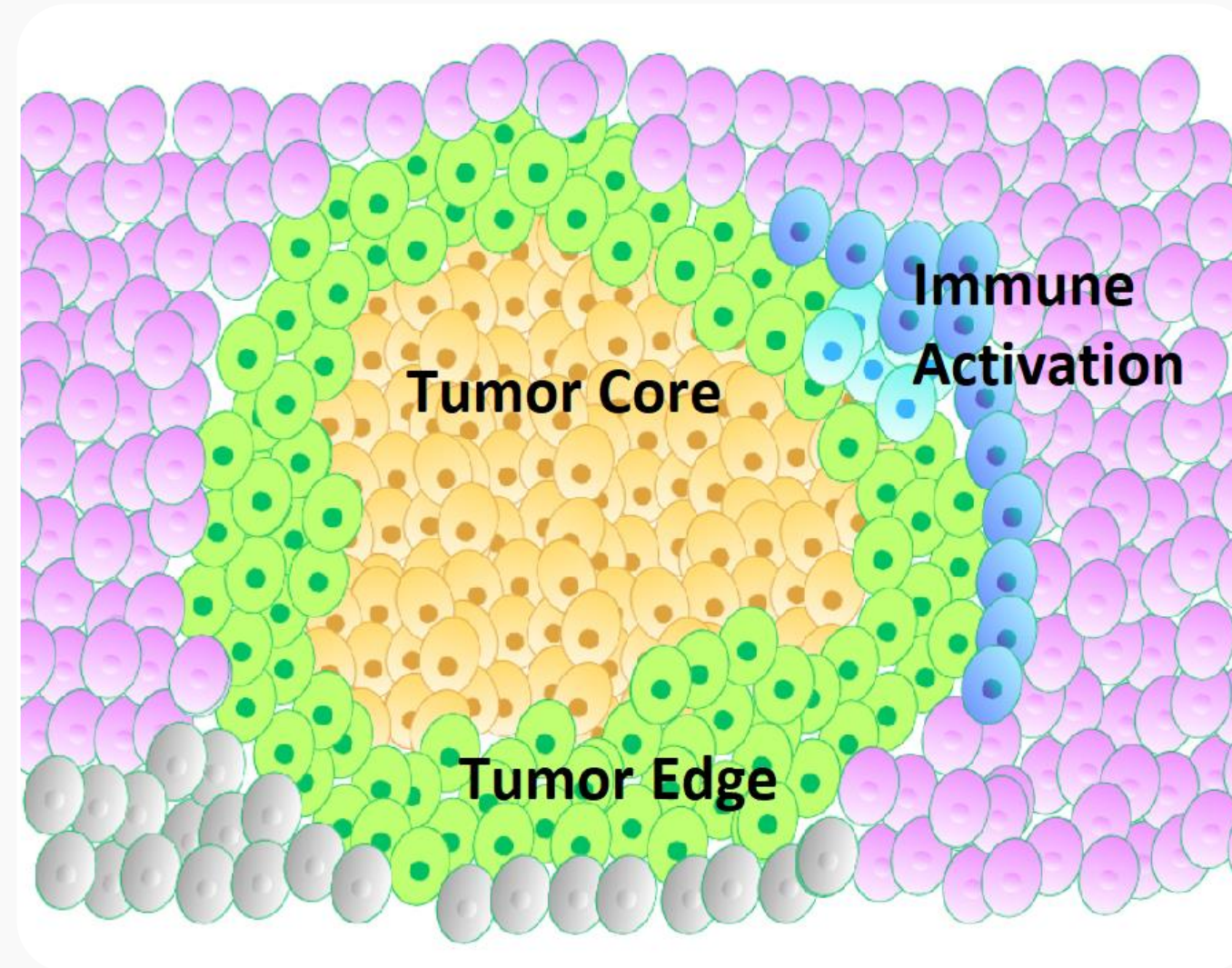
What is Spatial Transcriptomics?

Tumor Heterogeneity and Tumor Micro-Environment?

Where existing methods fail? (balancing both modalities)



Spatial Transcriptomics



Tumor Heterogeneity and Tumor Micro-Environment

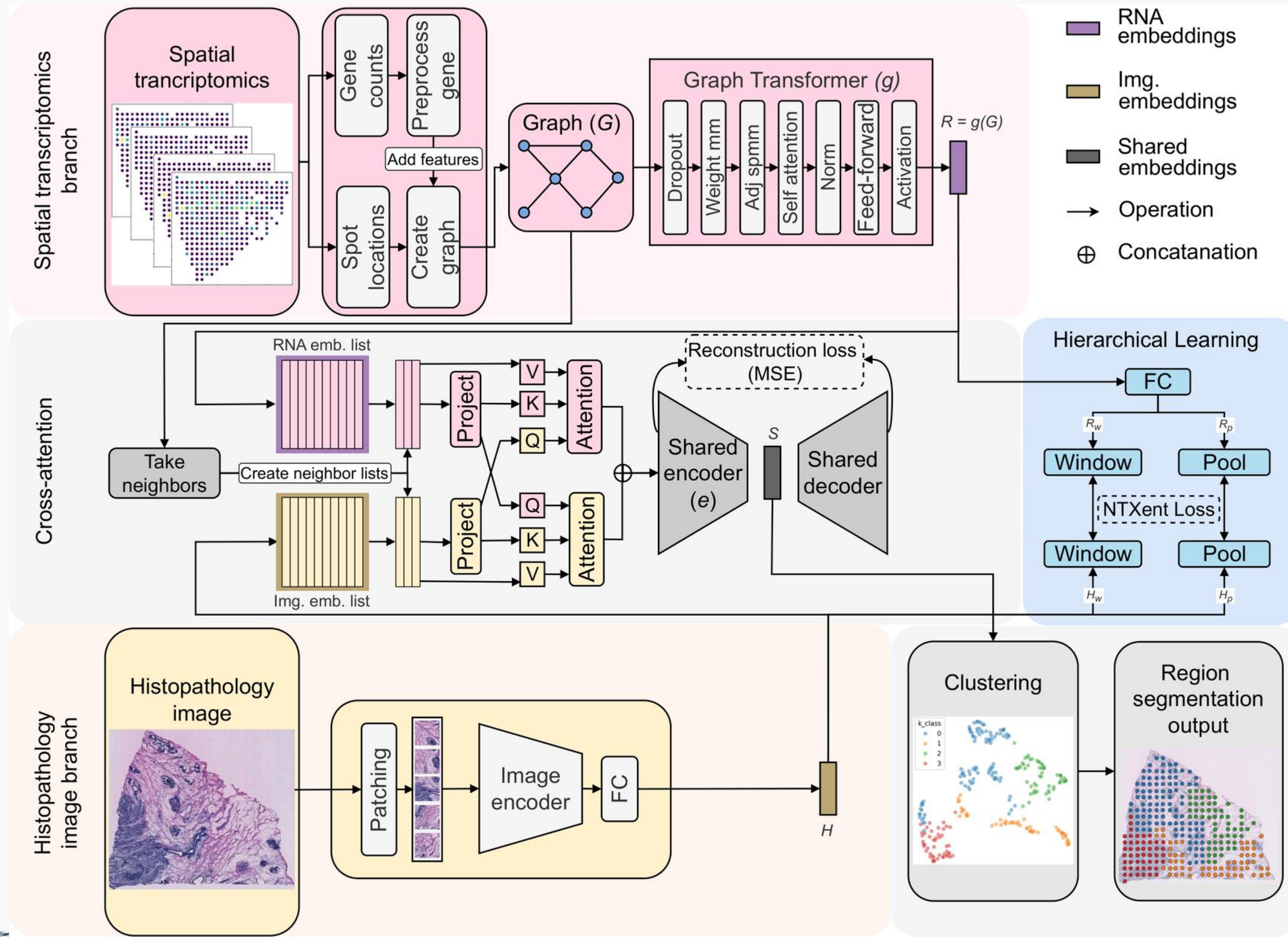
SENCA-st

(Shared Encoder with Neighborhood Cross Attention)

- Emphasizes regions that are structurally similar but functionally different using neighborhood cross-attention.
- As well as hierarchical learning in which feature flow is controlled at according to resolution.
- Ultimately leading our model achieving SOTA results.



Architecture



Results

Ground Truth



SpaGCN (ARI: 0.305)



DeepST (ARI: 0.307)



conST (ARI: 0.186)



ConGcR (ARI: 0.361)



SENCA-st (ARI: 0.518)



Fig: Comparison on H1 sample of HER2ST Dataset

Table 1: HER2ST Full Dataset Results

Model	ARI (Mean)	ARI (Median)
BayesSpace [1]	0.100	0.071
SpaGCN [2]	0.195	0.230
DeepST [3]	0.237	0.257
conST [4]	0.149	0.111
ConGcR [5]	0.268	0.258
ConGaR [5]	0.187	0.184
SENCA-st (Ours)	0.304	0.320

Table 2: Extended Experiments on other types

Sample Name	(Type)	ARI
CID44971	(TNBC)	0.326
CID4535	(ER+)	0.272
1160920F	(TNBC)	0.300

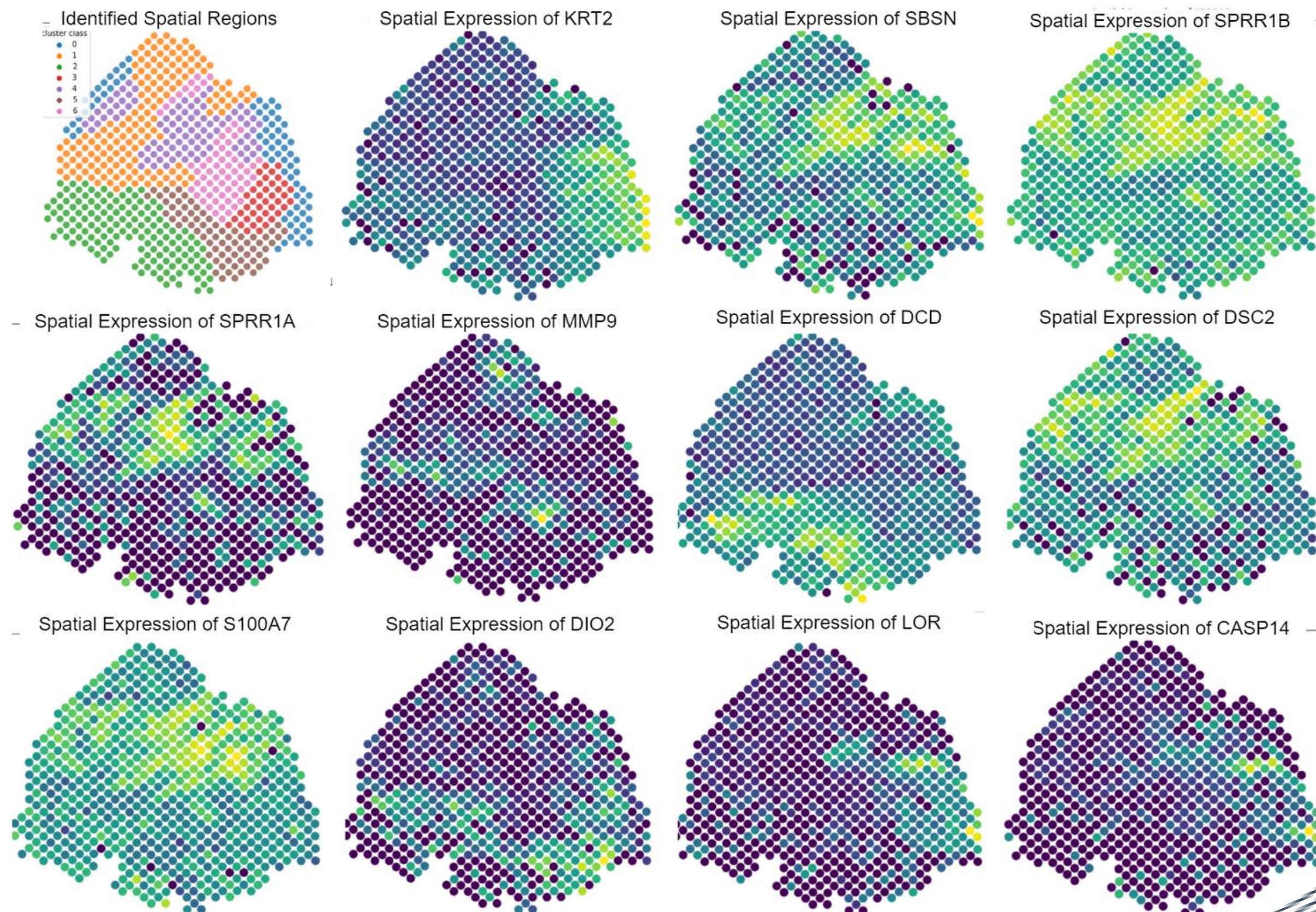
Datasets: Andersson et al. Nature Communications 2021, Wu et al. Nature genetics 2021

- 1) Zhao et al. Nature Biotechnology 2021
- 2) Hu et al. Nature Methods 2021
- 3) Zu et al. Nucleic Acid Research 2022
- 4) Zong et al. BioRxiv 2022
- 5) Lin et al. CSBJ 2024

Results

Marker genes of patient 2 sample of Squamous Cell Carcinoma detected with Wilcoxon test

Gene Name	Cluster	P-value
KRT2	0	4.771447×10^{-11}
FLG	0	2.019676×10^{-07}
KLK7	0	1.831156×10^{-03}
DSC1	0	8.774093×10^{-03}
MMP9	1	1.095943×10^{-10}
MMP1	1	1.095943×10^{-10}
CCL21	1	2.575223×10^{-08}
MMP3	1	1.880689×10^{-07}
DCD	2	5.048839×10^{-38}
IGFBP5	2	5.310009×10^{-31}
DCN	2	1.315863×10^{-18}
KRT2	3	5.668670×10^{-14}
COL1A1	3	1.488934×10^{-08}
COMP	3	1.488934×10^{-08}
LOR	3	1.542446×10^{-07}
SPRR1B	4	2.752813×10^{-35}
S100A7	4	1.199169×10^{-31}
SPRR1A	4	1.281949×10^{-30}
SBSN	4	1.844224×10^{-29}
DSC2	4	4.377951×10^{-27}
IGFBP4	5	4.068289×10^{-18}
CCDC80	5	8.295423×10^{-17}
DIO2	5	8.428684×10^{-11}
FAAP20	6	6.318033×10^{-05}
CASP14	6	3.996734×10^{-03}



Ablations

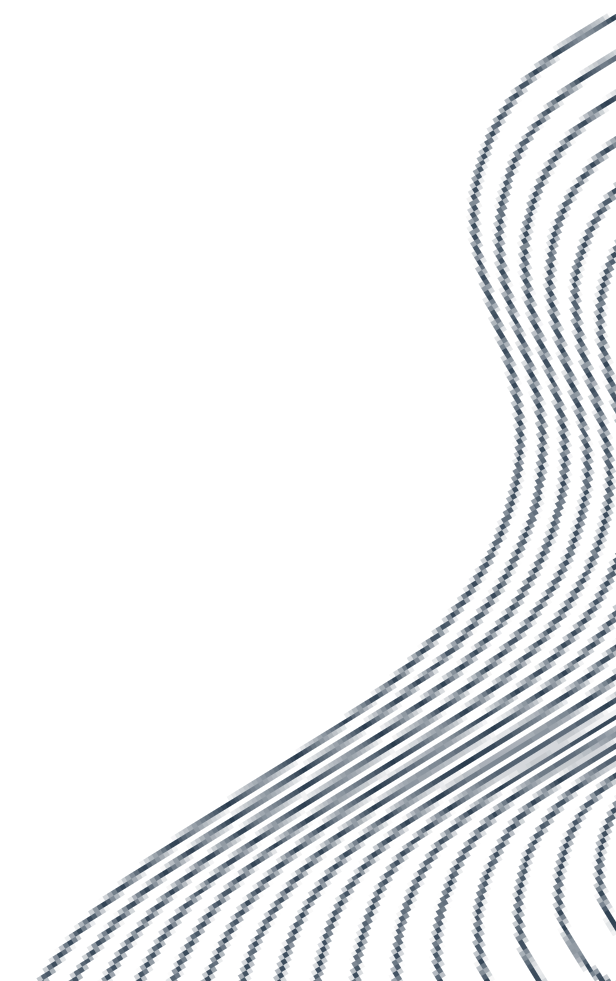


Table 4. Ablation Studies - Quantitative Results. We conducted ablation experiments isolating key components of the system by removing them and benchmarking with the HER2ST dataset to study their effect.

Ablation Experiment	ARI (Mean)
Normal	0.3039
Without Cross-Attention Weights	0.2218
Without Hierarchical Learning	0.2495

Discussions

- Balancing information from spatial transcriptomics and histopathology for useful discoveries
- We leverage neighborhood cross-attention as well as hierarchical learning.
- Implications
- Impact
- Future works



Conclusion

Acknowledgments - This project was partially supported by Accelerating Higher Education Expansion and Development (AHEAD) Operation funded by the World Bank

Code - <https://github.com/shanaka-liyanaarachchi/SENCA-st>



The image features a minimalist design with the text "Thank You" centered on a white background. The text is rendered in a dark blue, classic serif font. Two decorative elements, consisting of multiple thin, parallel lines that create a wavy, tunnel-like effect, are positioned in the top-left and bottom-right corners, framing the central text.

Thank You