# Leveraging network representations for cancer histopathology and spatial-omics

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# Projects and contributions

Association with spatial transcriptomics


Clustering for interactive segmentation

Revisiting benign biopsies

Studying lipomatosis through ISS

Rethinking morpho-omics integration

TissUUmaps 3.0

Multiplex analysis tools

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# Projects and contributions

| Project | Imaging type | Spatial-omics | Outcome |
|---|---|---|---|
| Association with spatial transcriptomics (P1) | Prostatectomy H&E | 10X Visium | Published in *Cancers*[1] |
| Clustering for interactive segmentation (P2) | Cancer H&E | — | Technical presented at *NeurIPS LMRL* workshop[2]; Tool evaluation ongoing |
| Revisiting benign biopsies (P3) | Prostate needle H&E | — | Testing ongoing |
| Study of lipomatosis ISS (P4) | Lymph node DAPI | *In-situ* sequencing | Data collection ongoing |
| Rethinking spatial-omics morphological integration (P5) | H&E and DAPI | 10X Xenium | Design ongoing |
| TissUUmaps 3.0 | Various | Various | Publication process[3] |
| Multiplex analysis tools | Various | Various | Publication process[4] |


1. Chelebian, Eduard, et al. "*Morphological Features Extracted by AI Associated with Spatial Transcriptomics in Prostate Cancer*" Cancers 13.19 (2021): 4837.
2. Chelebian, Eduard, et al. "*Seeded iterative clustering for histology region identification*" NeurIPS LMRL workshop arXiv:2211.07425 (2022).
3. Pielawski, Nicolas, et al. "*TissUUmaps 3: Interactive visualization and quality assessment of large-scale spatial omics data*" bioRxiv (2022).
4. Behanova, Andrea, et al. "*TissUUmaps 3 Tools for Visualization & Quality Control in Large-scale Multiplex Tissue Analysis*" bioRxiv (2022).

# Thank you for listening

 https://eduardchelebian.github.io/

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