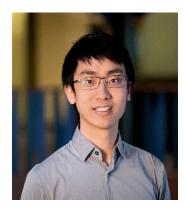# Inferring super-resolution tissue architecture by integrating spatial transcriptomics with histology

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Spatial transcriptomics (STs) has demonstrated enormous potential for generating intricate molecular maps of cells within tissues. Despite the availability of many ST platforms, none of them provides a comprehensive solution. An ideal ST platform should achieve single-cell resolution, cover the whole transcriptome, and be cost-effective. While such ST data are difficult to collect physically using existing platforms, they can be constructed in silico using innovative machine learning algorithms. Here we present iStar, a generative computer vision model that integrates low-resolution ST measurements with high-resolution histology images to construct spatial gene expression data at near-single-cell-resolution. The resulting model not only enhances gene expression resolution but also enables gene expression prediction in tissue sections where only histology images are available. The application of iStar to healthy and diseased samples across diverse datasets demonstrates its efficacy in facilitating scientific inquiries and performing clinical tasks, including tissue segmentation, cell type inference, cancer detection, and tumor microenvironment analysis, all with state-of-the-art accuracy and efficiency.

**Thursday, January 11, 2024, 3:30-4:30PM Eastern**

**133 Rosenau Hall**

Zoom Link:
**https://unc.zoom.us/j/98423779288?pwd=b0tqYThCQTAxeDdTQ0FRY3RnazdwQT09**

**Meeting ID: 984 2377 9288**

**Passcode: 631794**

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