

Multimodal and real-time profiling of spatial cellular ecosystems

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1:30PM-2:50PM

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Abstract:

Multicellular ecosystems are fundamental units of tissue biology but are challenging to profile across modalities, over time, and in clinical settings. In this talk, I will introduce two complementary machine learning frameworks to address these challenges. The first, called Spatial EcoTyper, was designed to identify multicellular ecosystems called spatial ecotypes (SEs) from single-cell spatial transcriptomics data and recover them from single-cell, spatial, and bulk transcriptomic data. The second, called Liquid EcoTyper, is an interpretable AI framework for quantifying SEs from both tissue and non-invasively from cell-free DNA methylation data. The utility of this approach will be demonstrated using results from our recent work on noninvasive profiling of spatial ecotypes in the tumor microenvironment. Together, these methods provide a unified basis for deciphering and tracking tissue biogeography in cancer, autoimmune disease, fibrosis, and other pathological conditions.

Reading List:

1. Zhang W, Brown EL, Usmani A, Earland N, Kang M, Olelewe C, Viswanathan A, Chauhan PS, Steen CB, Jeon HS, Avagyan S, Alahi I, Semenkovich NP, Schwab JC, Sachs CM, Qaium F, Harris PK, Cai Q, Gentles AJ, Knight J, Graham RP, Bacchiocchi A, Lucas PC, Fields RC, Szol M, Halaban R, Chen DY, Chaudhuri AA, Newman AM. Non-invasive profiling of the tumour microenvironment with spatial ecotypes. *Nature*, 2026. 654:1076-1087.

2. Gulati GS, D'Silva JP, Liu Y, Wang L, Newman AM. Profiling cell identity and tissue architecture with single-cell and spatial transcriptomics. *Nat Rev Mol Cell Biol*, 2025. 26:11-31.