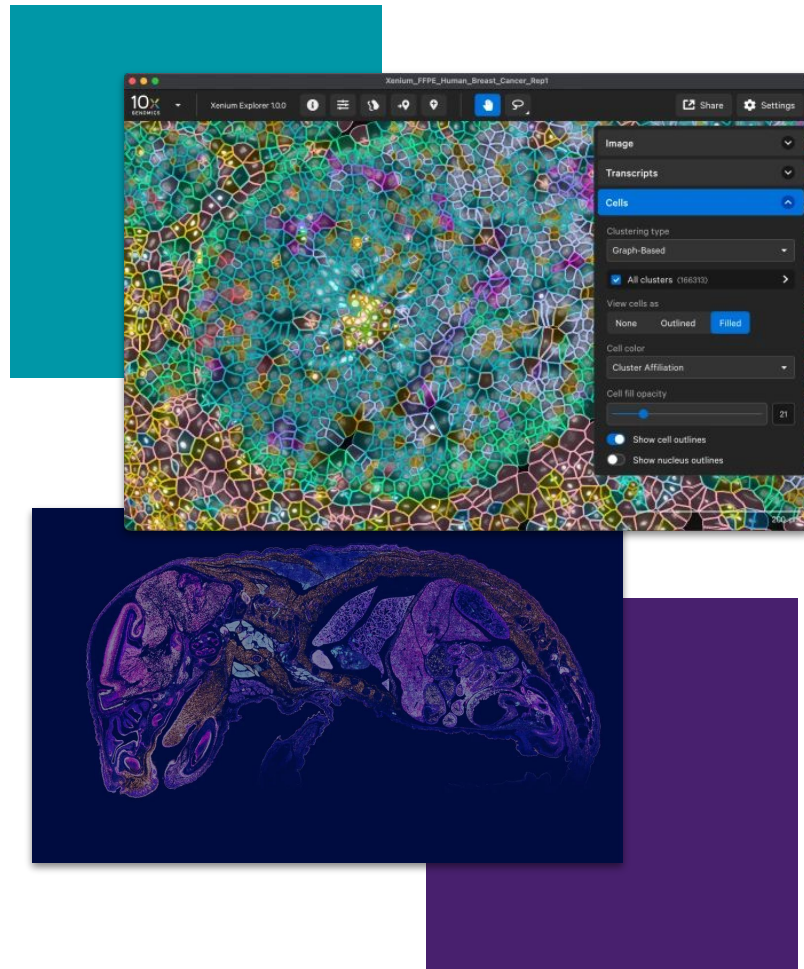


Using spatial transcriptomics to elucidate human liver structure

Nikita Sajai

Data Scientist in Bruce Wang Lab and UCSF Liver Center

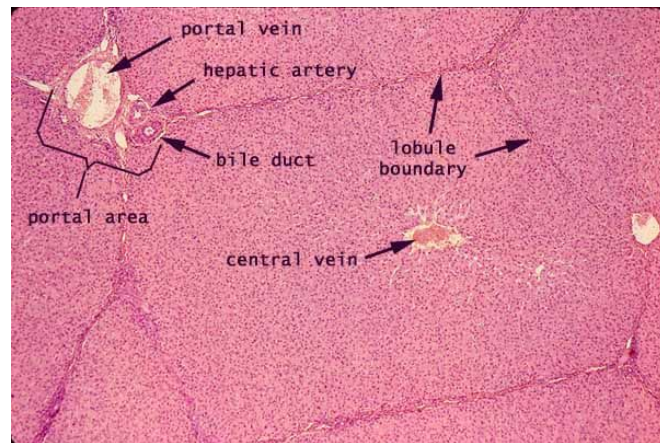
4/19/24



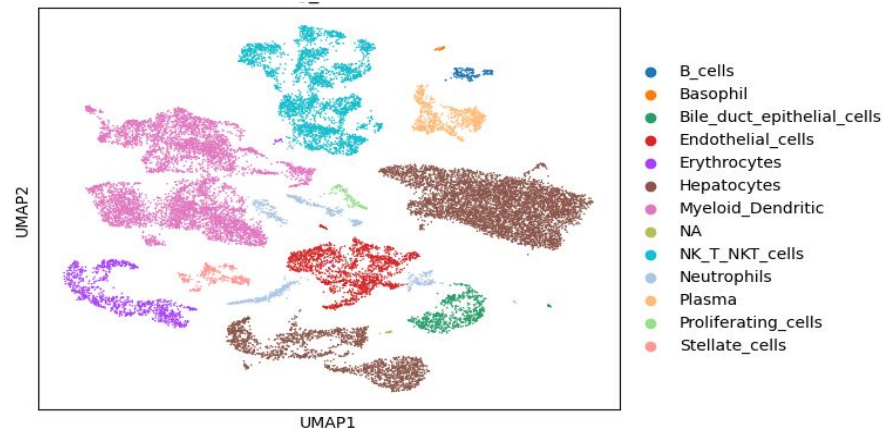
Why use Spatial Transcriptomics?

Orients cells in the liver landscape

Less damaging



Human Liver Single Cell Data (*Tabula Sapiens*)



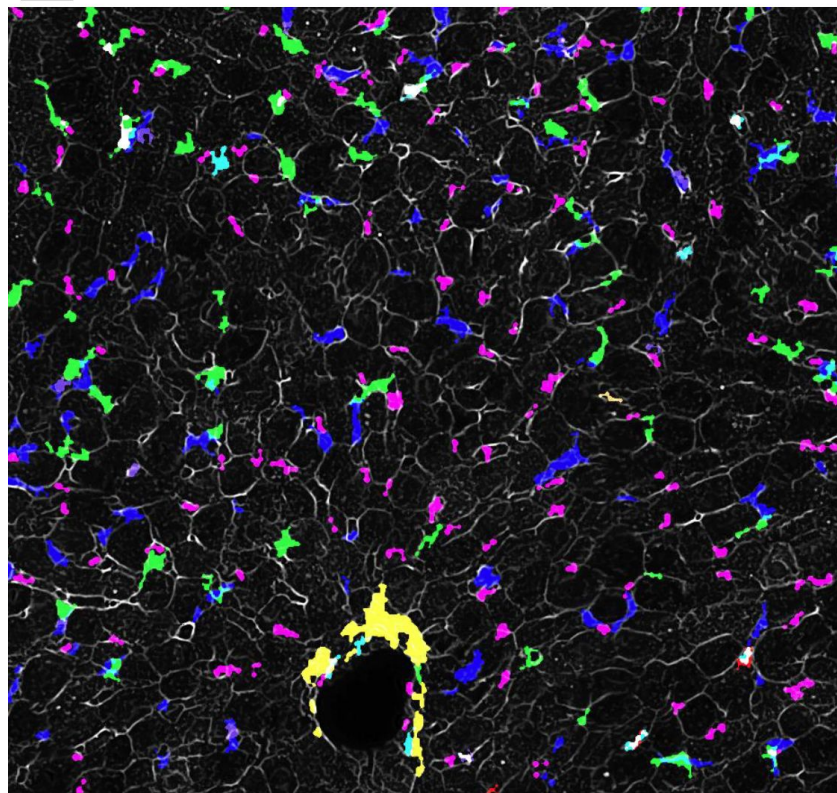
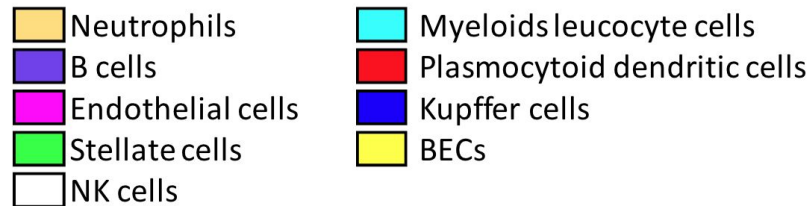
smFISH-based spatial transcriptomics

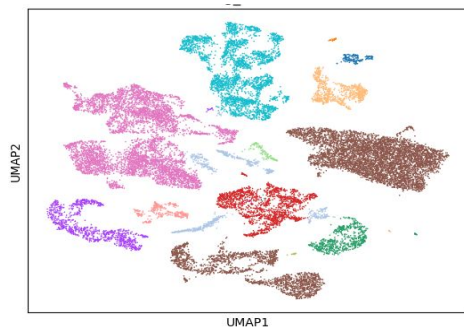
Expands upon older smFISH techniques

Up to 500 gene panel

Visualize most liver cell types in situ at a single-cell resolution

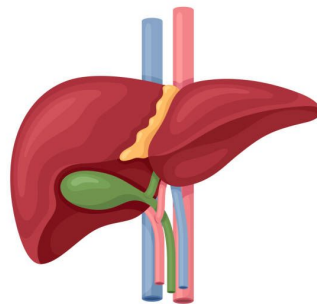
Orients cells in the liver landscape





Tabula Sapiens Consortium (2022)

- B_cells
- Basophil
- Bile_duct_epithelial_cells
- Endothelial_cells
- Erythrocytes
- Hepatocytes
- Myeloid_Dendritic
- NA
- NK_T_NKT_cells
- Neutrophils
- Plasma
- Proliferating_cells
- Stellate_cells



Top Level

Current panel:	
Healthy liver gene panel size	300
Number of cell types:	81

Hepatocytes

26 markers
6 subtypes

Endothelial Cells

28 markers
9 subtypes

BECs

15 markers
4 subtypes

Mesenchymal cells

16 markers
4 subtypes

Myeloid Dendritic

27 markers
10 subtypes

NK/T/NKT cells (Lymphocytes)

72 markers
26 subtypes

Neutrophils

2 markers

Erythrocytes

2 markers

Proliferating cells

2 markers

Basophils

2 markers

B cells

17 markers
4 subtypes

Thank you!

Abhishek Murti

Aris Taychameekiachi

Charles Lim

Cindy Ament

Elise Lelou

Matthew Choi

Saphia Nguyen

Bruce Wang



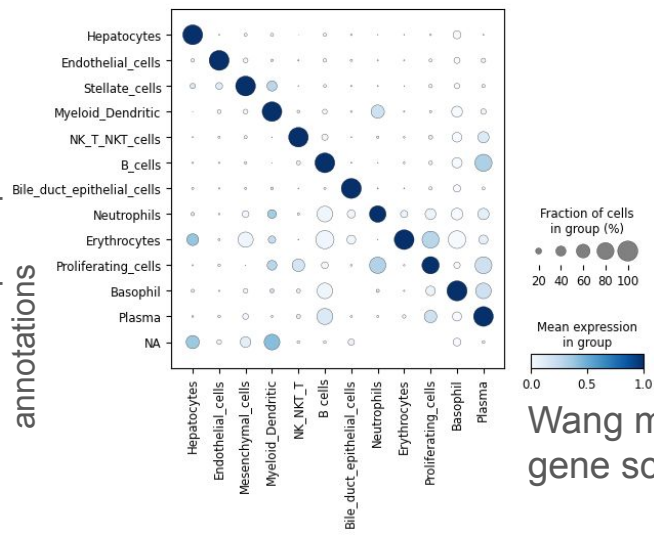
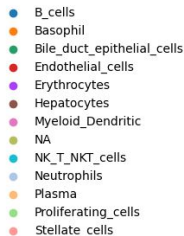
University of California
San Francisco

Amar Nijagal


Ari Molofsky




Tabula Sapiens published
Bile_ annotations



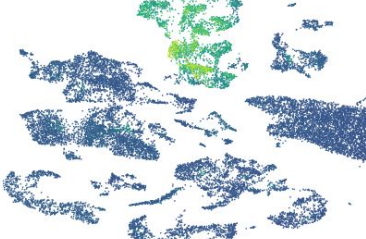
Wang marker gene scores



A UMAP plot showing cell clusters. The x-axis is labeled 'UMAP1' and the y-axis is labeled 'UMAP2'. The plot displays several distinct clusters of points. A color bar on the right indicates density, ranging from -1.5 (dark purple) to 2.0 (yellow). The clusters are colored according to this density scale, with some clusters showing higher density (yellow/green) and others lower density (purple/blue).



A UMAP plot showing cell clusters. The x-axis is labeled 'UMAP1' and the y-axis is labeled 'UMAP2'. The plot displays several distinct clusters of cells. A color scale on the right indicates the cell cycle phase, ranging from -1 (dark purple) to 5 (yellow). The clusters are primarily dark blue/purple, indicating they are in the G1 phase, with a central cluster showing a mix of green and yellow, indicating S and G2 phases.



A UMAP plot showing the distribution of cells. The x-axis is labeled 'UMAP1' and the y-axis is labeled 'UMAP2'. The plot displays several distinct clusters of cells. A color bar on the right indicates a density scale from -2 (dark purple) to 4 (yellow). The clusters are colored according to this scale, with some clusters showing higher density (yellow/green) and others showing lower density (dark blue/purple).

Developing the panel

Author	Publication	N cells	scRNA-seq method
Tabula Sapiens Consortium (2022)	The Tabula Sapiens: A multiple-organ, single-cell transcriptomic atlas of humans Science	22539	Seqwell
Andrews (2022)	Single-Cell, Single-Nucleus, and Spatial RNA Sequencing of the Human Liver Identifies Cholangiocyte and Mesenchymal Heterogeneity	73295	10X
Guilliams (2022)	Spatial proteogenomics reveals distinct and evolutionarily conserved hepatic macrophage niches	167598	10X
Dominguez Conde (2022)	Cross-tissue immune cell analysis reveals tissue-specific features in humans	51552	10X
MacParland (2018)	Single cell RNA sequencing of human liver reveals distinct intrahepatic macrophage populations	8444	10X