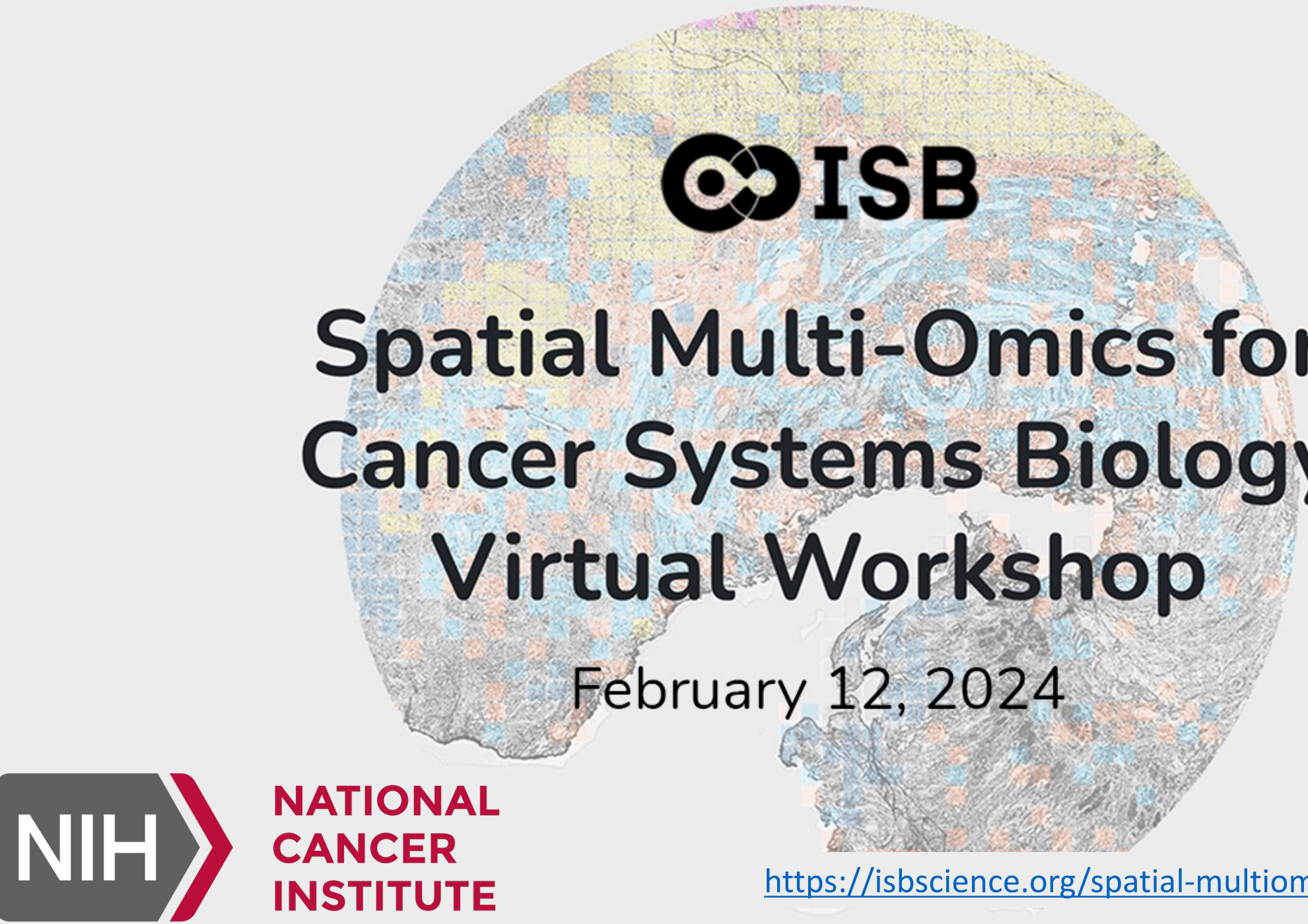

Spatial Multi-Omics for Cancer Systems Biology Virtual Workshop

February 12, 2024

NIH NATIONAL CANCER INSTITUTE

https://isbscience.org/spatial-multiomics-workshop/#agenda

Jim Heath
President Institute for Systems Biology
Professor Univ of Washington

Conflicts: Scientific Advisory Board: AtlasXomics and Nanostring

Paid Consultant: Regeneron

Research Funding in past 5 years from Merck, Gilead

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Put your questions in the chat!

Dominic Lewis

Allison Kudla

Thanks to our sponsors

AtlasXomics

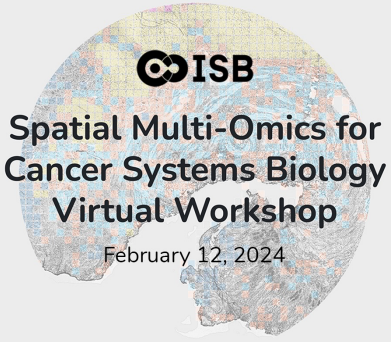
Session One: 8:30 PT
Experimental and Computational Methods I

Speaker: Rong Fan, PhD
Sequencing-based spatial multi-omics mapping

Speaker: Ruben Dries, PhD
The GIOTTO software tools

Speaker: Lu Wei, PhD
Spatial metabolic imaging

15 min Q&A roundtable



Session Two 10:00 PT
Experimental and Computational Methods II

Chair: Vésteinn Thorsson, PhD
Introduction and relating spatial features across assay Platforms

Speaker: Robert Krueger, PhD
Visual analytics for imaging-based spatial biology profiling

Speaker: Joseph Beechem, PhD
Spatial molecular imaging of FFPE cancer samples at any spatial-plex allows true systems biology understanding

Speaker: Lyla Atta
Evaluating normalization approaches for imaging-based spatial profiling technologies

15 min Q&A roundtable

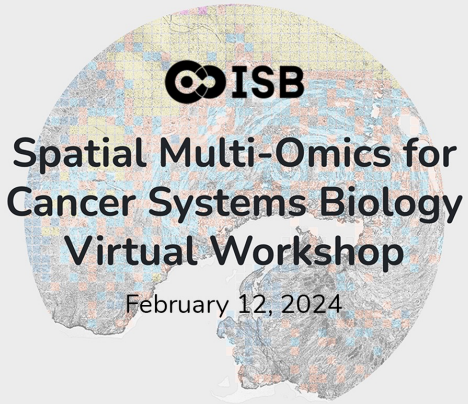
Session Three (12:00 PT):
Applications of Spatial Multi-Omics

Chair: Wei Wei, PhD
Introduction to applications of spatial multiomics

Speaker: Katie Campbell, PhD
Applications of spatial multiomics tools

Speaker: Sandro Santagata, MD, PhD
Applications of spatial multiomics tools

15 min Q&A roundtable

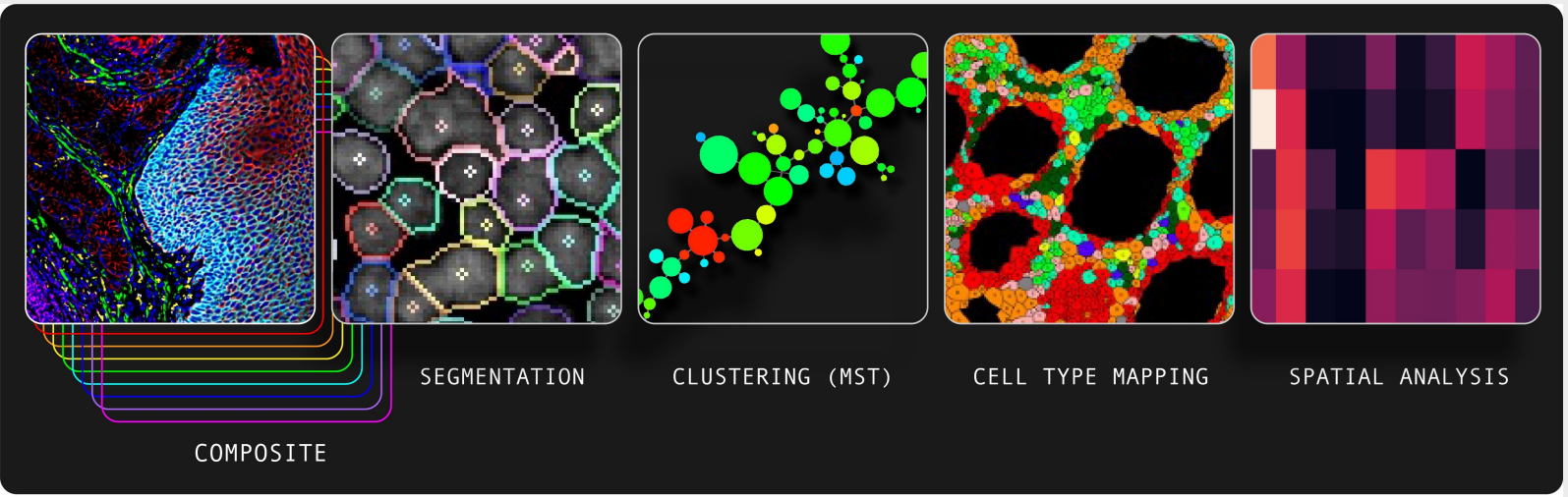


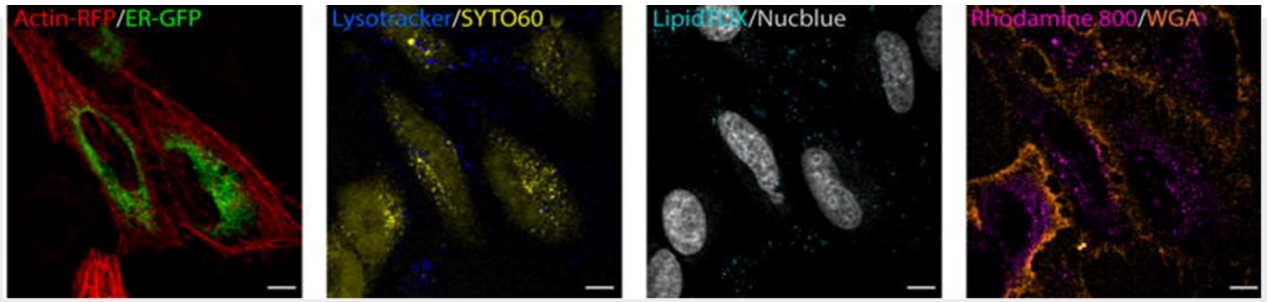
Session Four (13:15 PT):
Practical Methods in Spatial Omics

Rong Fan his group members from Yale University
Shuozhen Bao
Alev Baysoy
Zhiliang Bai
lead a practical tutorial with Jupyter notebooks and GitHub software, etc., to teach ‘hands-on’ experimental methods and computational tools for spatial omics and data analysis

Multiplex antibody Immunofluorescence (example here is CODEX)

Black, et al. (Nolan group) Nat Protocols (2021), Gotsev,… Nolan, Cell (2018)





Super Multiplex vibrational imaging in in single cells—L. Wei,… W. Min Nature 2017

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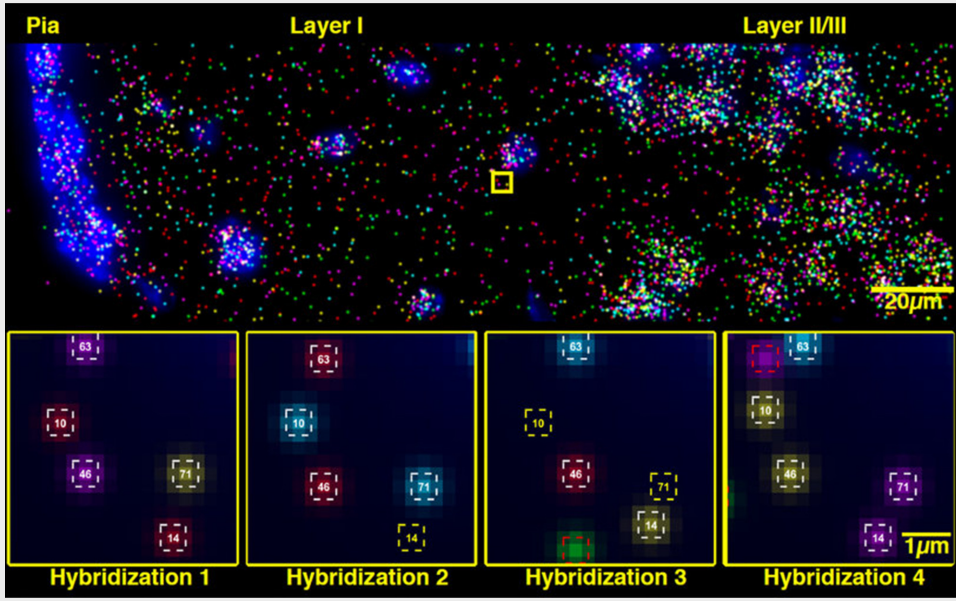
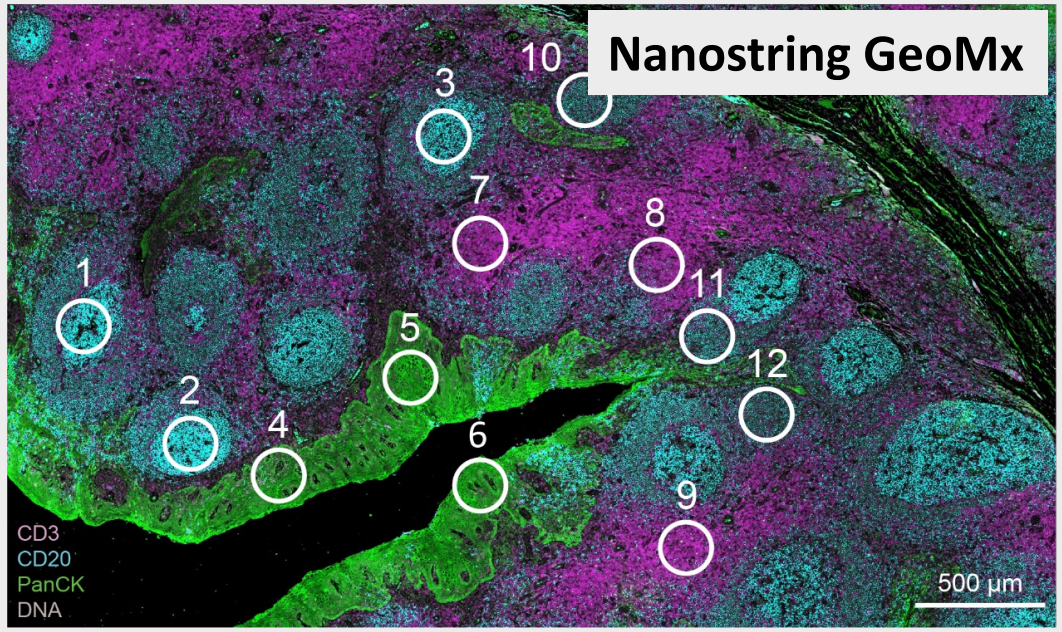
Spatial Transcriptomics –
Nature Method of the Year 2020

Single cell in situ highly multiplex proteomics and transcriptomics and metabolomics and epigenomics tools are 5-10 years old.



seqFISH+ images 10^4 mRNAs in single cells—with high accuracy and sub-diffraction-limit resolution

Long Cai group, Neuron 2016, Nature 2019



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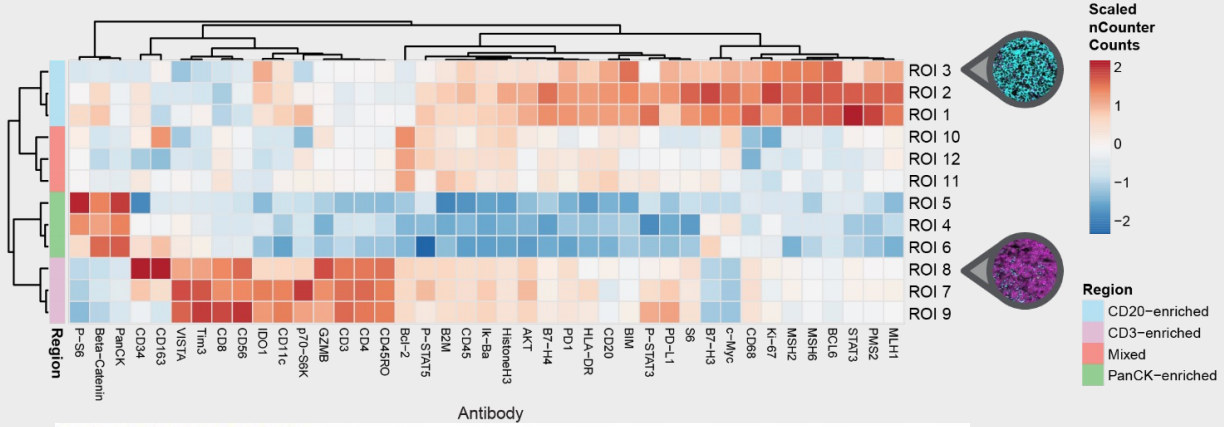
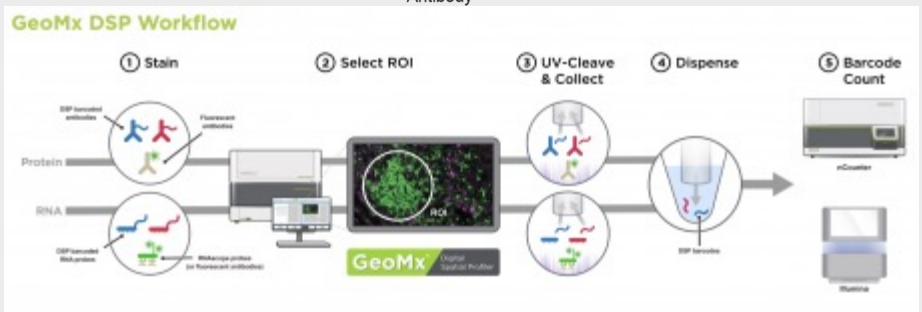
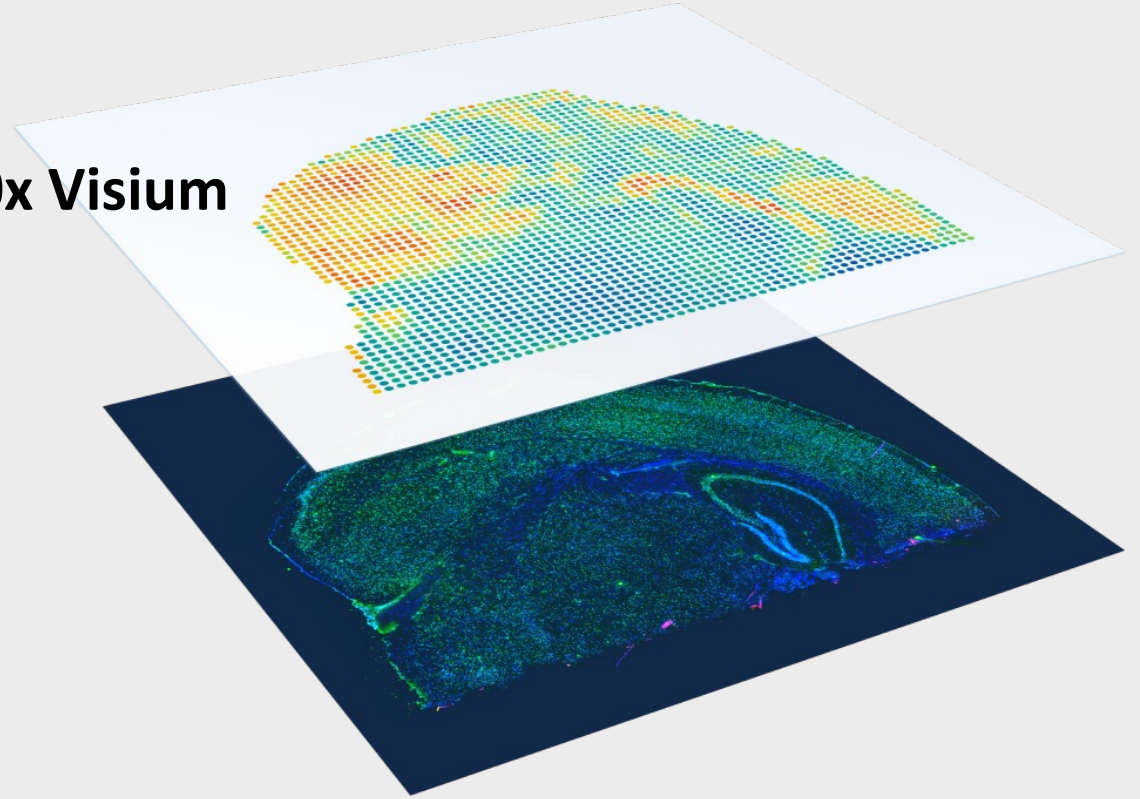
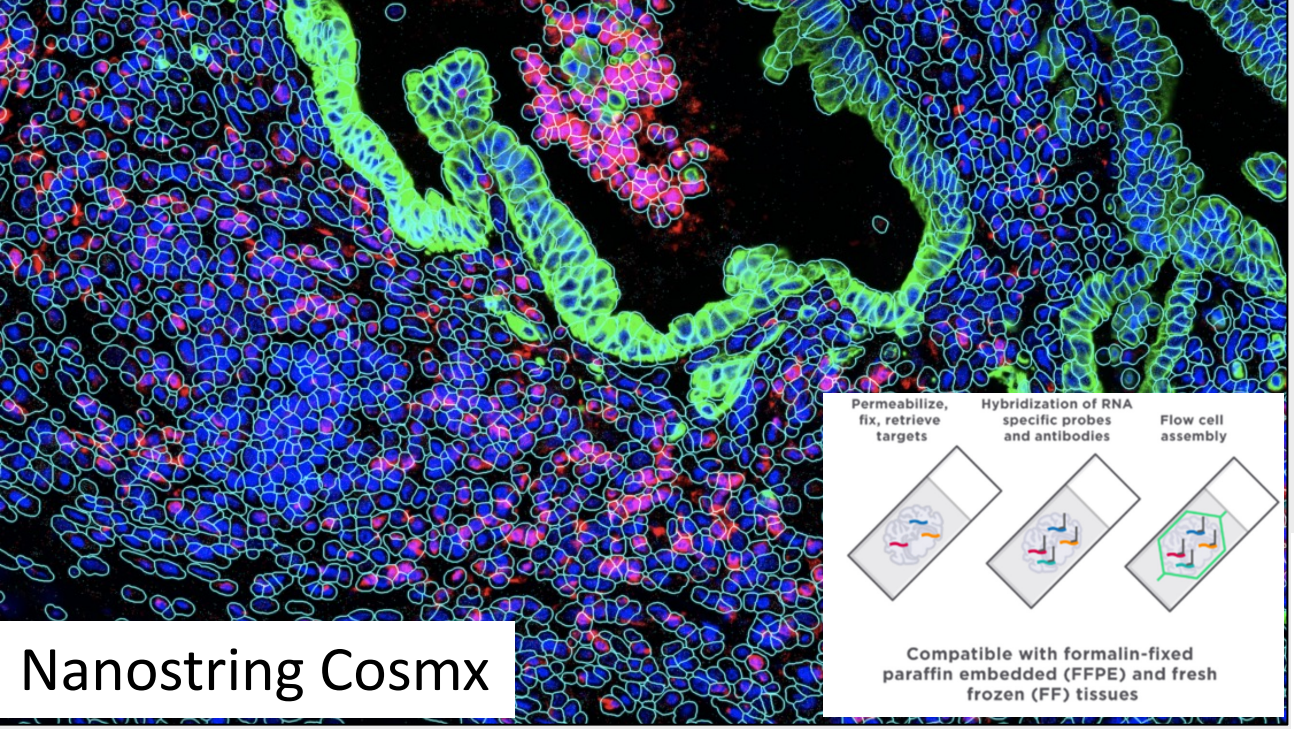
Proteins and Transcripts at high (multi-cellular) resolution
With targeted probes and next gen sequencing





10x Visium





Nanostring Cosmx

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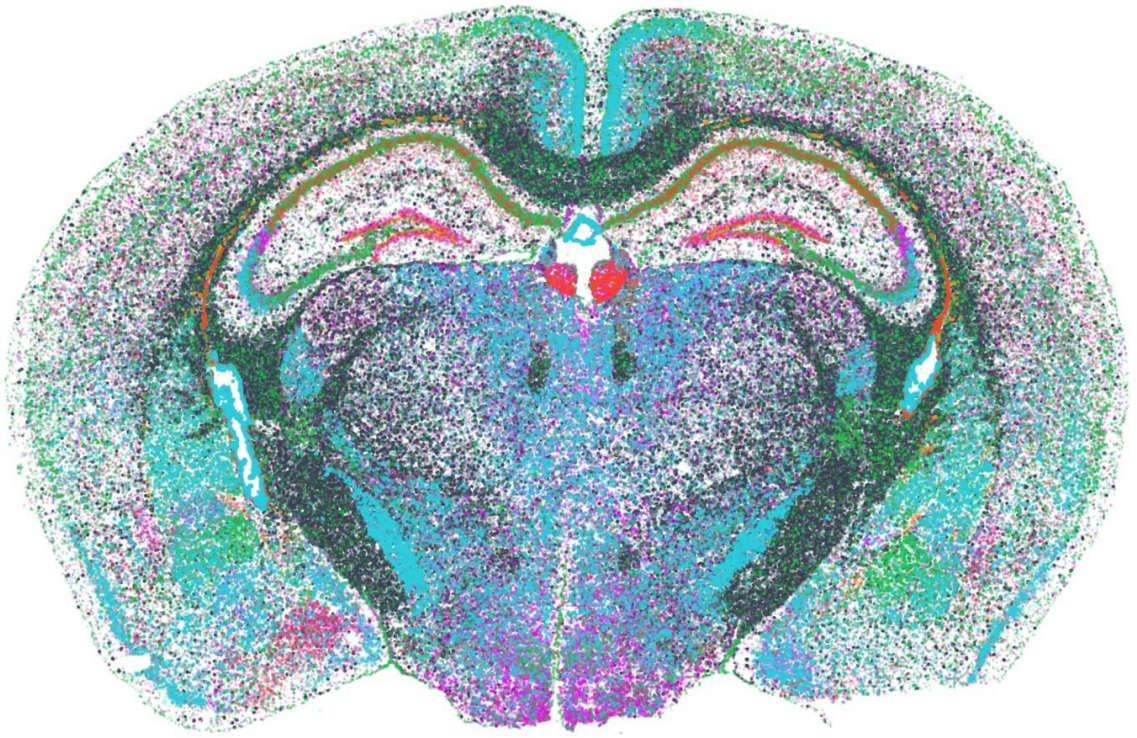
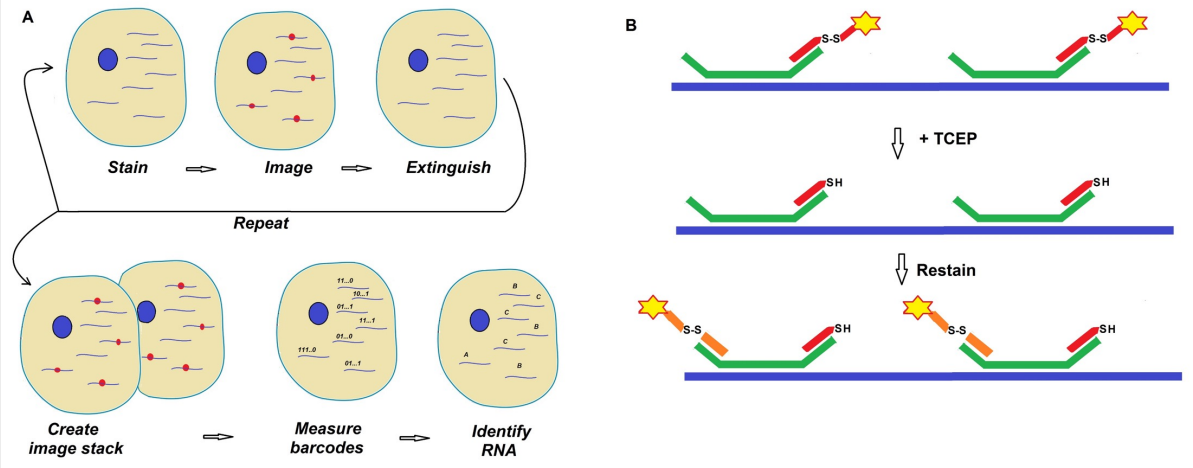
Subcellular resolution from multiple toolsets



Vizgen MerFISH probes

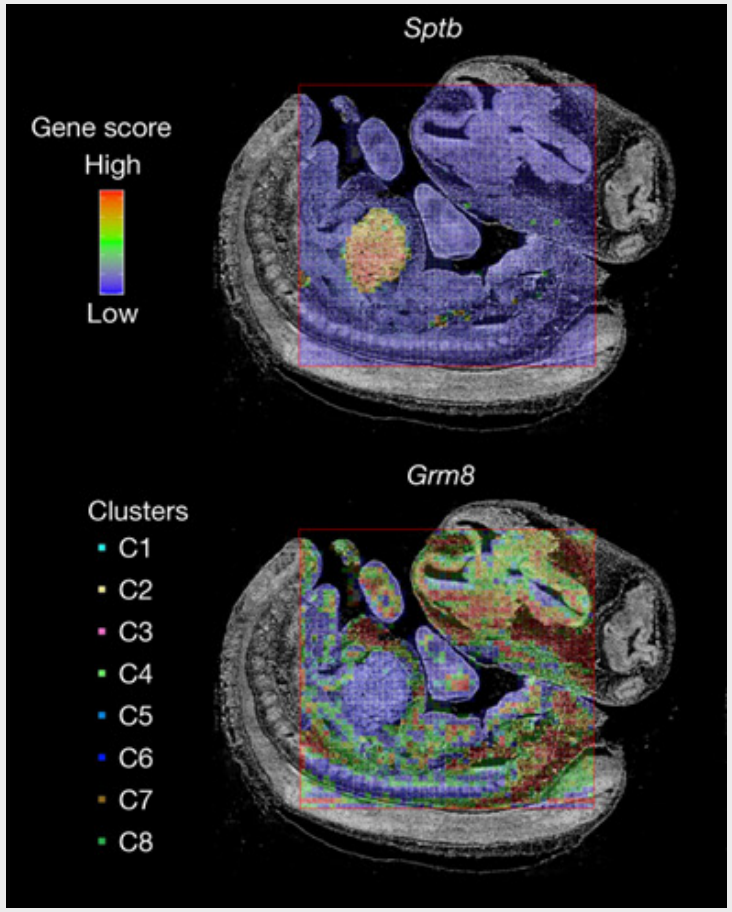


Epigenetics

Metabolomics

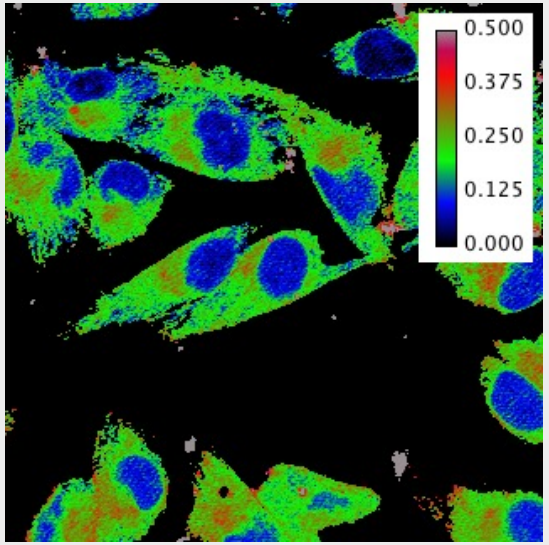
Spatial ATAC-seq & other Multiomics
(Dbit-seq methods) R. Fan Group, Yale
AtlasXomics, Inc.

Y. Deng, … R. Fan. *Nature* 2022

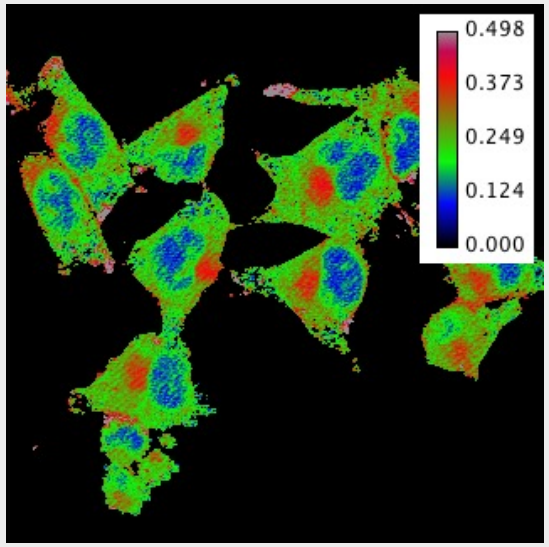


Raman (metabolic) Imaging: No labels, live cells, near video rate

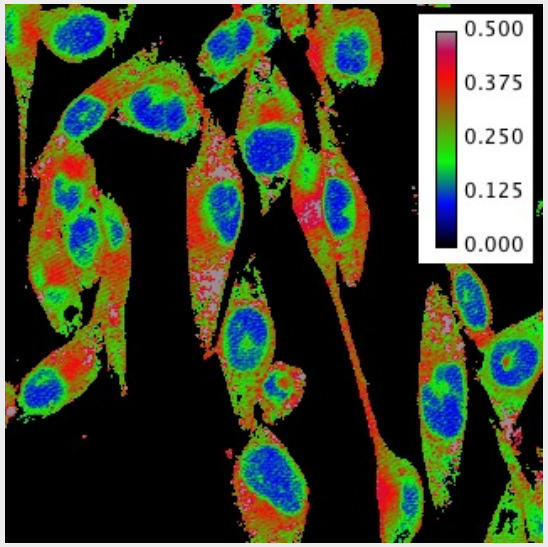
M409 Neural crest



M229 plastic



M262 Melanocytic



J. Du, .. L Wei *Nat. Comm* 2019

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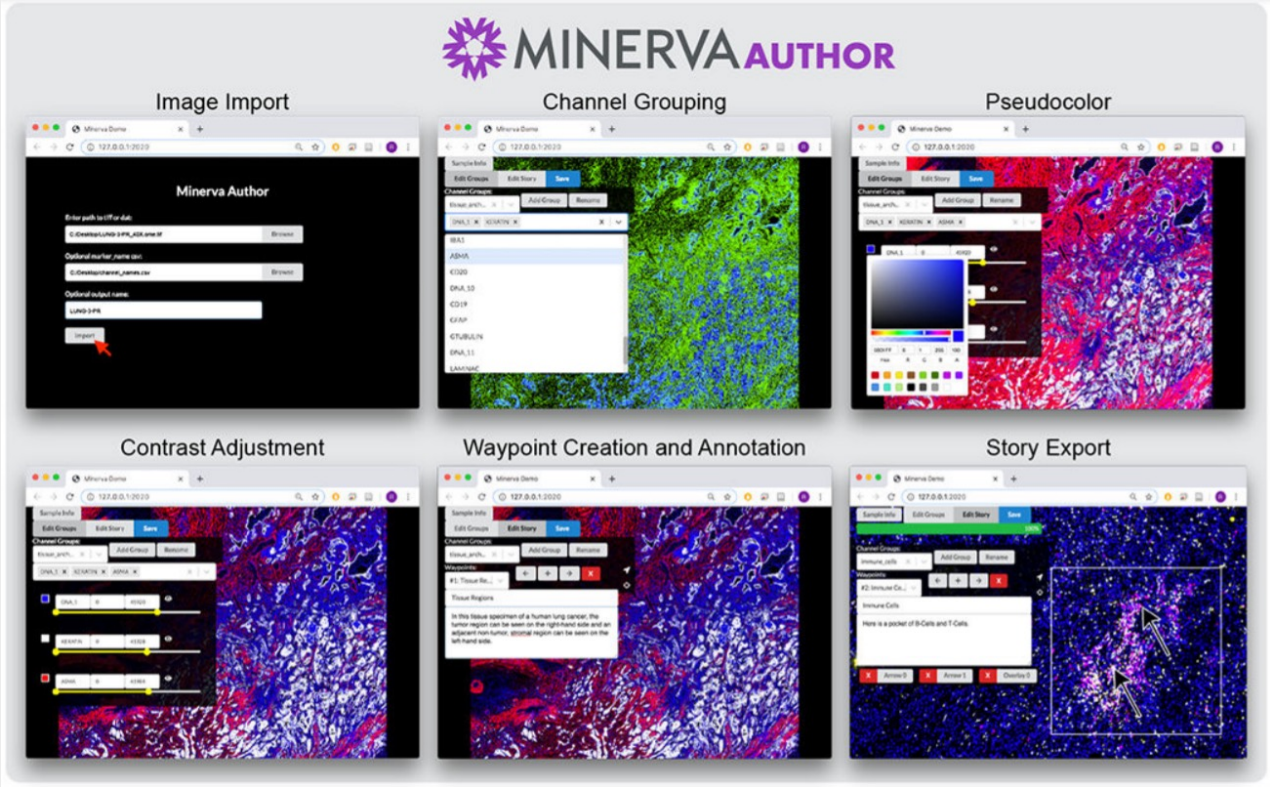
R. Dries Group, Gen. Bio (2021)

Sorger Group, J. Open Source Software (2020).



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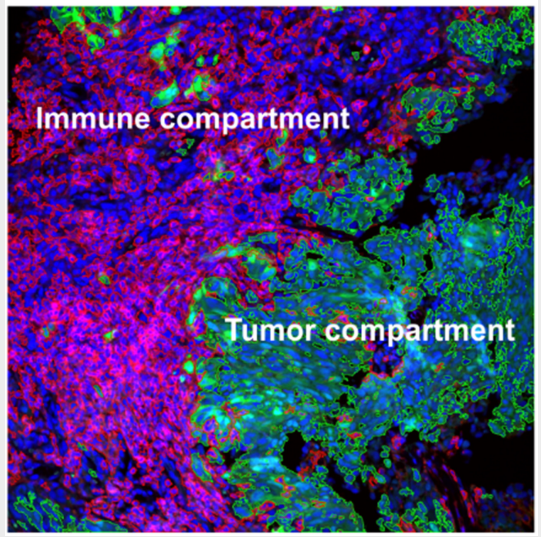
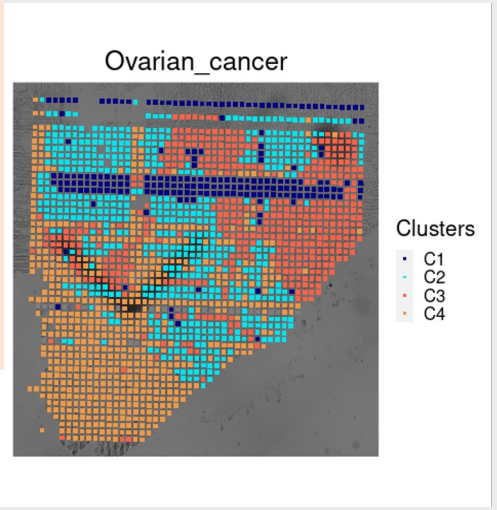
Why it's worth making computational methods easy to use. **J. Fan Nat 2022**

In any new field, confounding factors can limit the transportability of results from one platform to another, or across labs

Tissue Types
- live cells
- FFPE
- fresh frozen
- size
- prep details



Data Quality
- spatial variations
- # of transcripts/pixel
- # fragments/pixel
- alignment with ground truth



Ground Truth References
- nuclear staining?
- H&E images?
- Immunofluorescence?
- Algorithms?

Data Integration
- tissue specific cell atlases
- integration across omics
- lab-to-lab variations and standards
- benchmarking algorithms

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