IGB Spatial Omics Initiative

Slides and recording will be available at
https://www.igb.illinois.edu/facilities-services/spatial-omics-initiative

Mission

Bioengineering
Chemical and Biomolecular Engineering
Chemistry
Computer Science
Ecology, Evolution, and Behavior
Electrical and Computer Engineering
Geography and Geographic Information Systems
Mechanical Science and Engineering
Molecular and Integrative Physiology
National Center for Supercomputing Applications
Physics
Plant Biology
Psychology
Roy J. Carver Biotechnology Center
Statistics

To bring together researchers from **different disciplines** across the University of Illinois

to make new breakthroughs in **genomic biology**

by developing new ways to measure, analyze, and interpret **spatial omics data**.

Background

1. Spatial omics data are spectacular.
   - Subcellular gene expression data from mouse brain
   - Joint spatial chromatin and expression data from mouse brain

2. Spatial structure reveals organization and function.

Vision

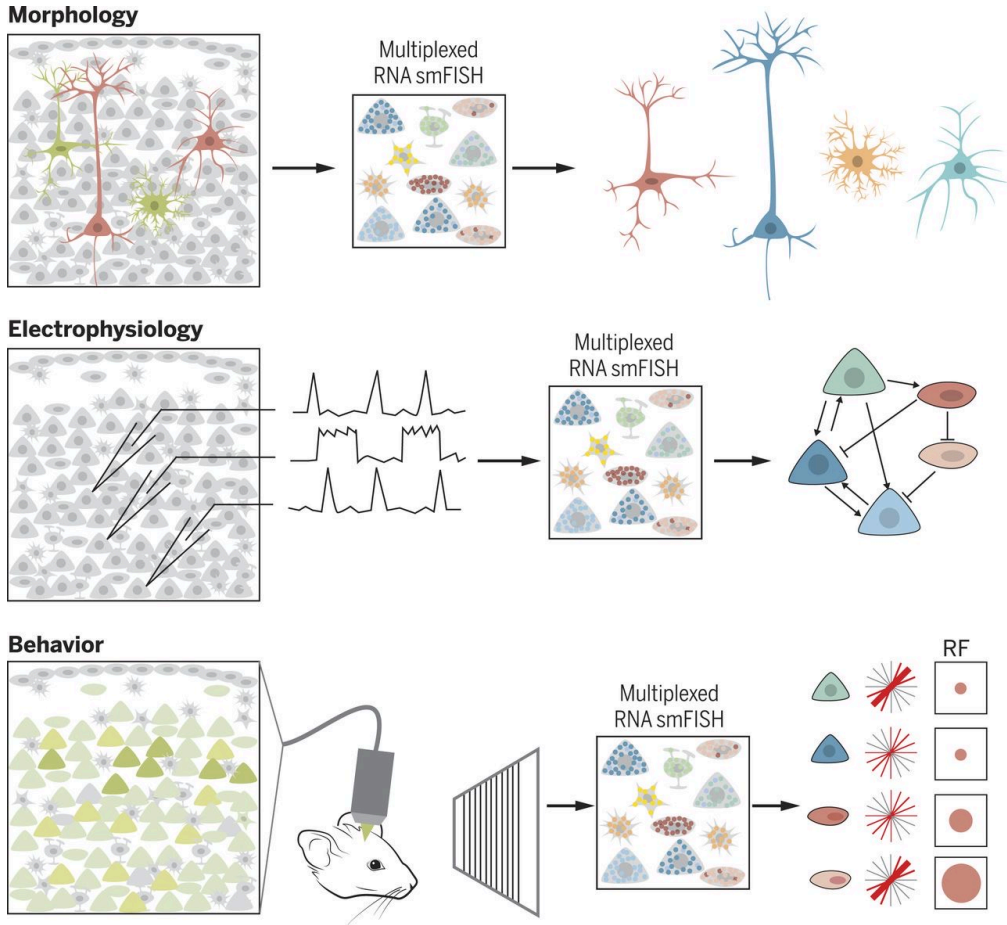
Integrated spatial neuroscience

Neuroscientists

Theorists

Engineers

Analysts



https://vizgen.com/mapping-the-whole-mouse-brain/

https://www.science.org/doi/10.1126/science.aan6827

Rationale 1: cutting-edge

Review Article | Published: 17 May 2023

Single-cell and spatial transcriptomics: deciphering brain complexity in health and disease

Monika Piwecka, Nikolaus Rajewsky & Agnieszka Rybak-Wolf

Nature Reviews Neurology **19**, 346–362 (2023) | Cite this article

Abstract

In the past decade, single-cell technologies have proliferated and improved from their technically challenging beginnings to become common laboratory methods capable of determining the expression of thousands of genes in thousands of cells simultaneously. The field has progressed by taking the CNS as a primary research subject – the cellular complexity and multiplicity of neuronal cell types provide fertile ground for the increasing power of single-cell methods. Current single-cell RNA sequencing methods can quantify gene

A molecularly defined and spatially resolved cell atlas of the whole mouse brain

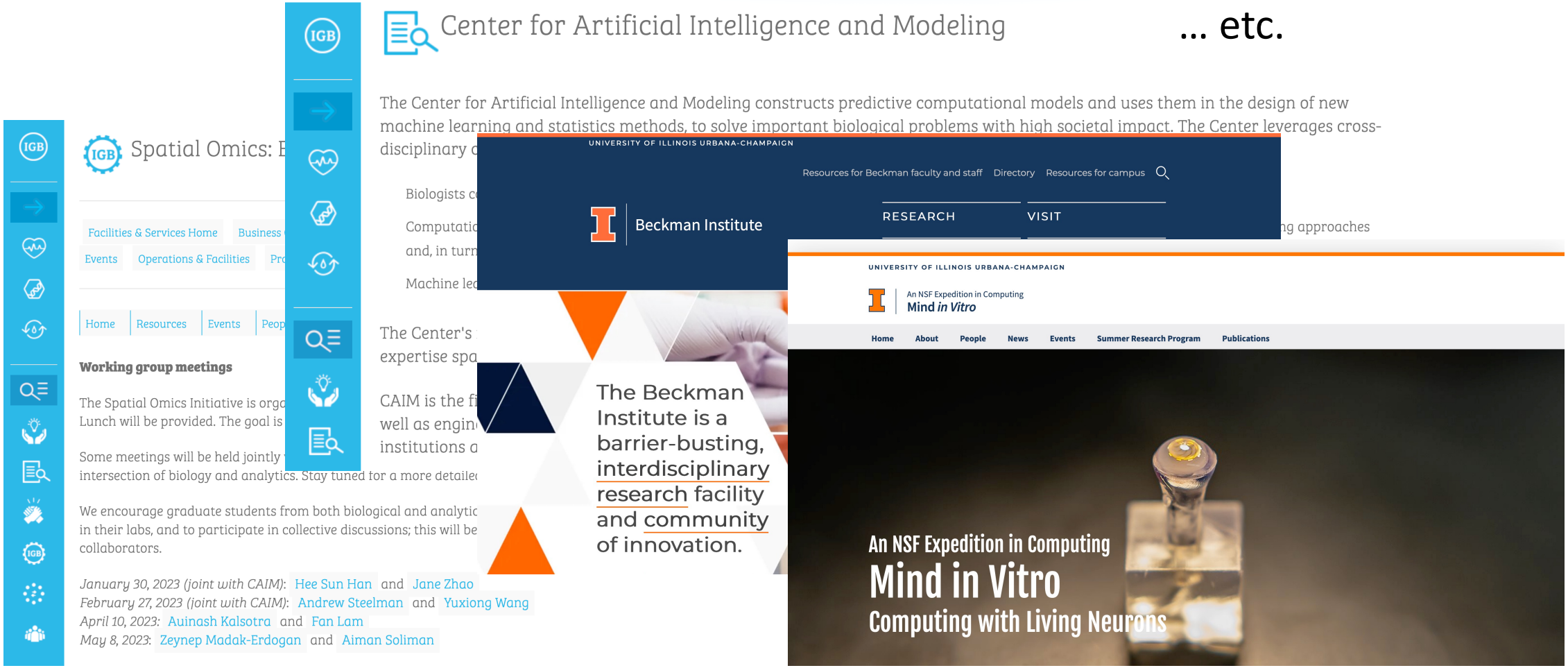
Meng Zhang, Xingjie Pan, Won Jung, Aaron Halpern, Stephen W. Eichhorn, Zhiyun Lei, Limor Cohen, Kimberly A. Smith, Bosiljka Tasic, Zizhen Yao, Hongkui Zeng, Xiaowei Zhuang

doi: https://doi.org/10.1101/2023.03.06.531348

Abstract

In mammalian brains, tens of millions to billions of cells form complex interaction networks to enable a wide range of functions. The enormous diversity and intricate organization of cells in the brain have so far hindered our understanding of the molecular and cellular basis of its functions. Recent advances in spatially resolved single-cell transcriptomics have allowed systematic mapping of the spatial organization of molecularly defined cell types in complex tissues[1–3]. However, these approaches have only been applied to a few brain regions[1–11] and a comprehensive cell atlas of the whole brain is still missing. Here, we imaged a panel of >1,100

Rationale 2: active campus



... etc.

Rationale 3: heavily funded

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Sharing Opportunities & Successes

Comprised of federal and non-federal members and affiliates, the BRAIN Initiative Alliance mission is to coordinate and facilitate communications from its members related to The BRAIN Initiative®.

Chan Zuckerberg Initiative

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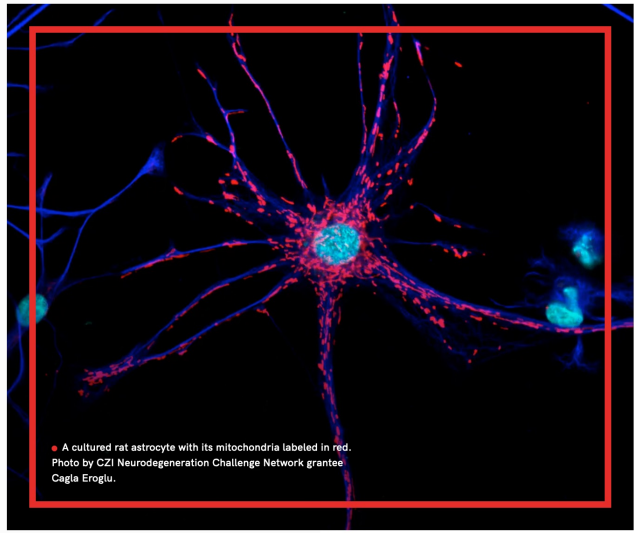
Neurodegeneration Challenge Network (NDCN)

The CZI Neurodegeneration Challenge Network (NCDN) was launched in 2018 with the vision that progress in solving neurodegenerative diseases will come from bringing new people into the neurodegeneration field from diverse disciplines and expertise; supporting interdisciplinary collaborations; empowering the broader scientific community with robust tools and platforms, and creating a culture of open science.

We're excited by the scientific advances achieved through this collaborative, interdisciplinary research model and look forward to



A cultured rat astrocyte with its mitochondria labeled in red. Photo by CZI Neurodegeneration Challenge Network grantee Cagla Eroglu.

Proposed plan for the Spatial Omics Initiative

1. Collaborative proposals
2. Campus funding
3. Center grants

Example target collaborative proposals

Title	Mechanism	Deadline	Budget
NIH Blueprint for Neuroscience Research: Tools and Technologies to Explore Nervous System Biomolecular Condensates https://grants.nih.gov/grants/guide/rfa-files/RFA-DA-24-039.html	R21	Nov 14, 2023	Up to $275K
BRAIN Initiative: Theories, Models and Methods for Analysis of Complex Data from the Brain https://grants.nih.gov/grants/guide/rfa-files/RFA-DA-23-039.html	R01	Sep 12, 2024	$150K - $250K per year
BRAIN Initiative: Team-Research BRAIN Circuit Programs - TeamBCP (U19 Basic Experimental Studies with Humans Required) https://grants.nih.gov/grants/guide/rfa-files/RFA-NS-22-039.html	U19	Sep 13, 2024 (will be renewed?)	Not limited
NSF Computational and Data-Enabled Science and Engineering (CDS&E) https://new.nsf.gov/funding/opportunities/computational-data-enabled-science-engineering-3	Meta-program	Varies	

Example: biomolecular condensates

Article | Open Access | Published: 29 May 2023

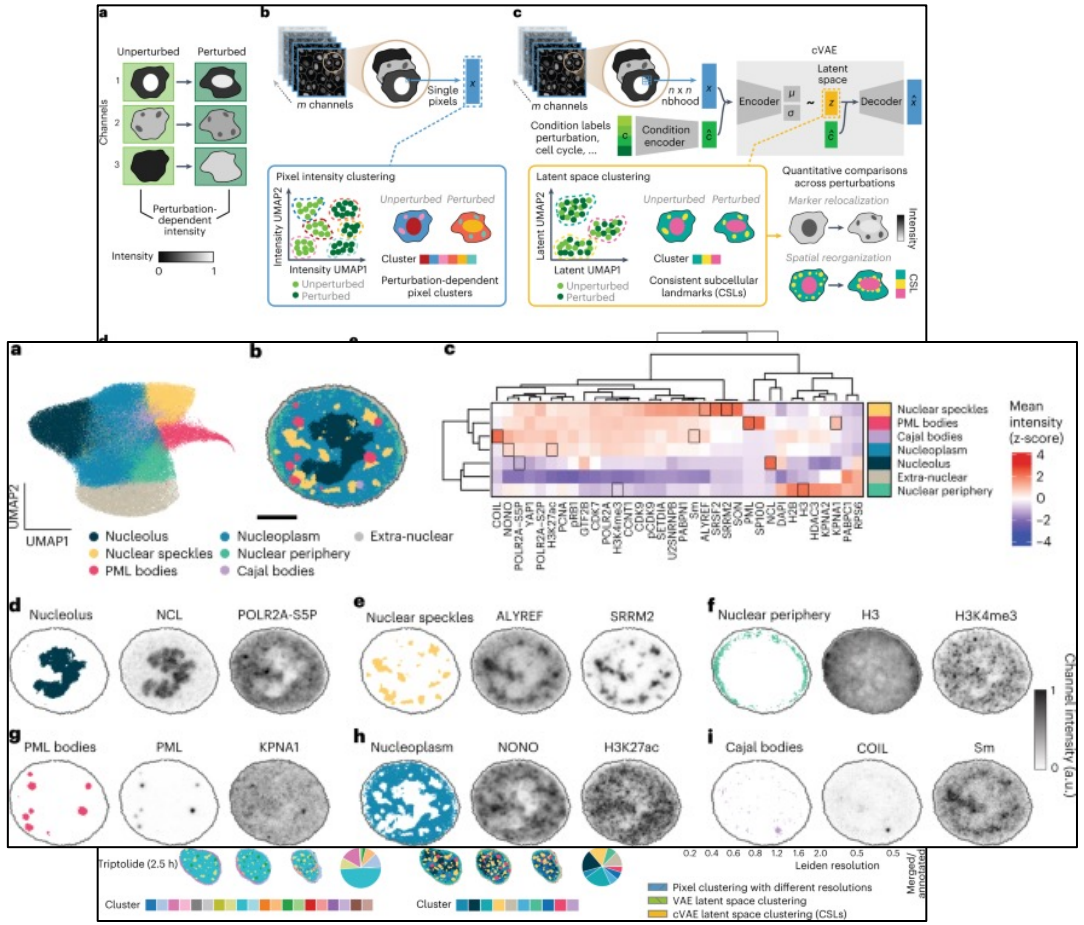
Learning consistent subcellular landmarks to quantify changes in multiplexed protein maps

Hannah Spitzer orcid.org/0000-0002-7858-0936[1 na1], Scott Berry orcid.org/0000-0002-1838-4976[2,3 na1], Mark Donoghoe orcid.org/0000-0003-0212-6443[4], Lucas Pelkmans ✉[2] & Fabian J. Theis ✉ orcid.org/0000-0002-2419-1943[1,5,6]

Nature Methods **20**, 1058–1069 (2023) | Cite this article

Subjects

Machine learning | Nuclear organization | Organelles | Transcription



Abstract

Highly multiplexed imaging holds enormous promise for understanding how spatial context shapes the activity of the genome and its products at multiple length scales. Here, we introduce a deep learning framework called CAMPA (Conditional Autoencoder for Multiplexed Pixel Analysis), which uses a conditional variational autoencoder to learn representations of molecular pixel profiles that are consistent across heterogeneous cell populations and experimental perturbations. Clustering these pixel-level representations identifies consistent subcellular landmarks, which can be quantitatively compared in terms of

Example: theories of the brain

COMMENTARY | APPLIED MATHEMATICS |

Neuronal network complexity strengthens activity robustness

Jorge Golowasch Authors Info & Affiliations

July 24, 2023 | 120 (31) e2309988120 | https://doi.org/10.1073/pnas.2309988120

THIS ARTICLE HAS BEEN UPDATED

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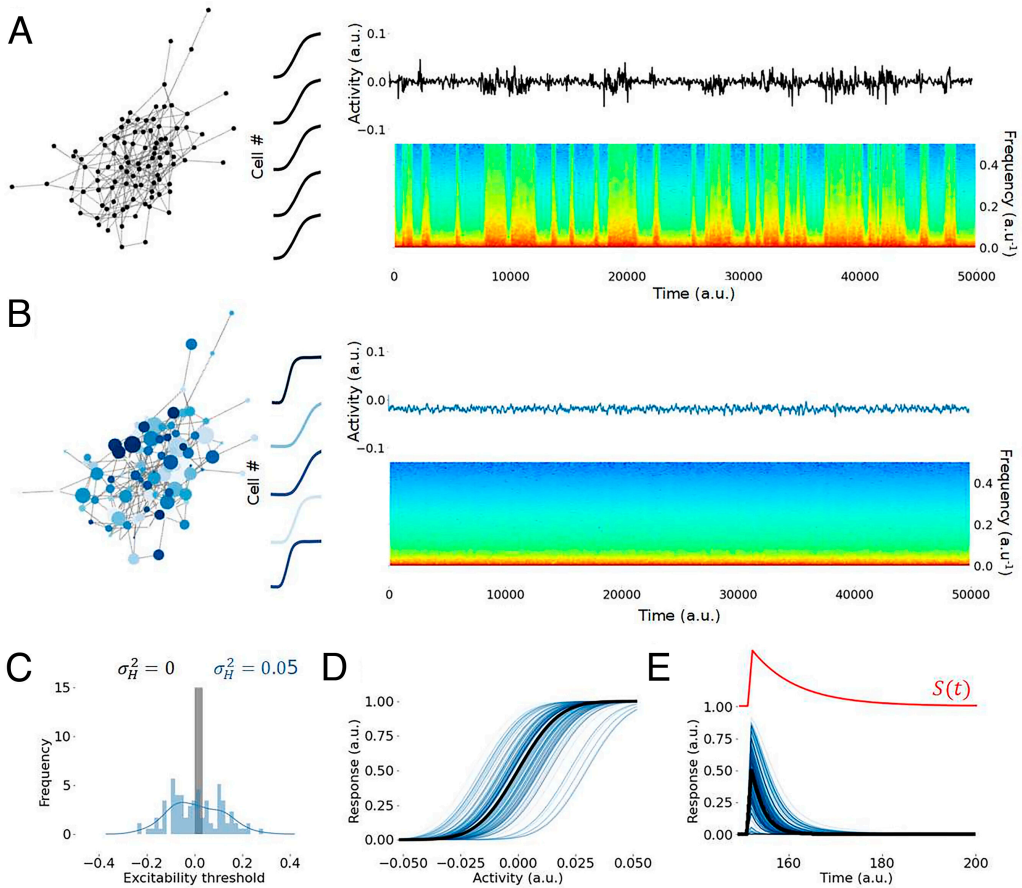
A debate about whether complexity in systems such as ecological or neuronal networks makes them more or less stable has been going on for several decades, starting perhaps with May's original claim that complex systems are inherently unstable (1). However, it is everyone's personal experience that, as individuals, we appear to remain qualitatively the same over time and during our responses to a large range of perturbations. Disease and catastrophic events may change this temporarily or permanently, but neuronal networks and their activities appear to be remarkably stable over time and robust to perturbations. Most of us would also probably readily agree that neuronal and ecological networks are quite complex. What factors contribute



https://www.pnas.org/doi/full/10.1073/pnas.2218841120

Example: brain circuits

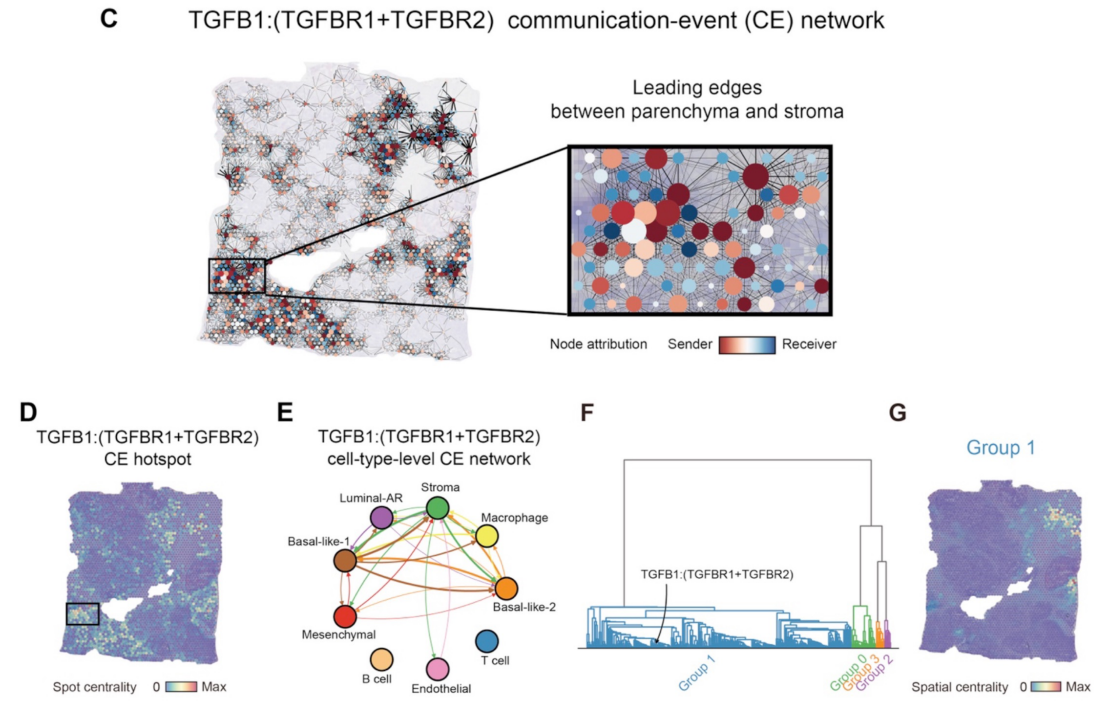
Decoding functional cell–cell communication events by multi-view graph learning on spatial transcriptomics

Haochen Li, Tianxing Ma, Minsheng Hao, Wenbo Guo, Jin Gu, Lei Wei, Xuegong Zhang

doi: https://doi.org/10.1101/2022.06.22.496105

Abstract

Cell–cell communication events (CEs) are mediated by multiple ligand–receptor pairs. Usually only a particular subset of CEs directly works for a specific downstream response in a particular microenvironment. We name them as functional communication events (FCEs) of the target responses. Decoding the FCE-target gene relations is important for understanding the machanisms of many biological processes, but has been intractable due to the mixing of multiple factors and the lack of direct observations. We developed a method HoloNet for decoding FCEs using spatial transcriptomic data by integrating ligand–receptor pairs, cell-type spatial distribution and downstream gene expression into a deep learning model. We modeled CEs as a multiview network, developed an attention-based graph learning method to train the model for generating target gene expression with the CE networks, and decoded the FCEs for specific downstream genes by interpreting the trained model. We applied HoloNet on three



Spatial Omics Initiative infrastructure

- Please email spatial@igb.Illinois.edu with a few sentences about how your research interests might intersect with spatial neuroscience. We (organizers) will identify emerging themes and create subgroups.

- Slack channel to connect with others
- Monthly meetings for parallel discussions on collaborative proposals:
  - *October 2, 2023*
  - *November 6, 2023*
  - *December 4, 2023*

Discussion

- Ideas?
- How else can IGB support you?
- Please spread the word!