IGB Spatial Omics Initiative

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

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
Rationale 1: cutting-edge

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
Rationale 2: active campus

Center for Artificial Intelligence and Modeling

The Center for Artificial Intelligence and Modeling constructs predictive computational models and uses them in the design of new machine learning and statistics methods, to solve important biological problems with high societal impact. The Center leverages cross-disciplinary expertise across domains of Machine learning, Data mining, and Network science. The Center's expertise spans various domains of medicine, including Precision medicine, personalized medicine, and in tumor biology.

The Beckman Institute is a barrier-busting, interdisciplinary research facility and community of innovation.

An NSF Expedition in Computing Mind in Vitro
Computing with Living Neurons
Rationale 3: heavily funded

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®.

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
Proposed plan for the Spatial Omics Initiative

1. Collaborative proposals
2. Campus funding
3. Center grants
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<thead>
<tr>
<th>Title</th>
<th>Mechanism</th>
<th>Deadline</th>
<th>Budget</th>
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<tbody>
<tr>
<td>NIH Blueprint for Neuroscience Research: Tools and Technologies to</td>
<td>R21</td>
<td>Nov 14, 2023</td>
<td>Up to $275K</td>
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<td>Explore Nervous System Biomolecular Condensates</td>
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<td>BRAIN Initiative: Theories, Models and Methods for Analysis of</td>
<td>R01</td>
<td>Sep 12, 2024</td>
<td>$150K - $250K per year</td>
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<td>Complex Data from the Brain</td>
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<tr>
<td>BRAIN Initiative: Team-Research BRAIN Circuit Programs - TeamBCP</td>
<td>U19</td>
<td>Sep 13, 2024</td>
<td>Not limited</td>
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<td>(U19 Basic Experimental Studies with Humans Required)</td>
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<tr>
<td>NSF Computational and Data-Enabled Science and Engineering (CDS&amp;E)</td>
<td>Meta-program</td>
<td>Varies</td>
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Example: biomolecular condensates

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...
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
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

This article is a preprint and has not been certified by peer review ([what does this mean?]).

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 mechanisms 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!