Webinar Information	Information
Webinar Description	A hands-on, interactive tutorial to harness the power of kidney single cell and spatial transcriptomics data
Abstract	Emerging single-cell omics and spatial transcriptomics technologies provide unprecedented opportunities and challenges for molecular biology studies, especially in kidney research. How to model these vast sequencing data in different modalities, perform computational analyses, and interpret mechanisms by identifying biological and pathological meaningful cell types, regulatory relations, and key markers are central questions in this area.
Objectives	• To understand the basic principles of deep learning, graph representation learning, and model interpretation. • To understand the specifics of computational tools such as scGNN, DeepMAPS, and BSP, and become aware of the appropriate tools to use in different applications in single-cell multi-omics and spatial transcriptomics studies of kidney research. • To gain hands-on experience in applying tools and interpreting results using standalone python-based software scGNN, R-based BSP, webserver-based DeepMAPS, and integrated AI-ready platform.
Date(s) & Time	Monday Dec 2 11:00am-3:00pm EST Tuesday Dec 3 11:00am-3:00pm EST
Zoom meeting link	https://iu.zoom.us/w/86968508902
GitHub Links	OKRA Tutorial 2024- https://github.com/juexinwang/OKRA_Tutorial2024 scGNN- https://github.com/juexinwang/scGNN DeepMAPS- https://bmblx.bmi.osumc.edu/ BSP- https://github.com/juexinwang/BSP Niche- https://github.com/rimelof/intro_spatial_localization_workshop/

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Speakers-	• Mauminah Raina PhD **Indiana University- Indianapolis** Student in Department of Biomedical Engineering and Informatics • Mr. Yi Jiang PhD **The Ohio State University** PhD student at The Ohio State University • Ricardo Melo Ferreria PhD **Indiana University-Indianapolis** Assistant Research Professor of Medicine • Mahla Asghari, MS. **Indiana University-Indianapolis School of Medicine** Department of Medicine • Michael Eadon MD **Indiana University-Indianapolis** Associate Professor of Medicine • Juexin Wang PhD **Indiana University- Indianapolis** Department of Biomedical Engineering and Informatics Luddy School of Informatics Computing and Engineering & Center for Computational Biology and Bioinformatics • Qin Ma PhD **The Ohio State University** Professor • Dong Xu PhD **University of Missouri** Curators' Distinguished Professor • Mingyao Li PhD **University of Pennsylvania** Professor of Biostatistics and Digital Pathology Department of Biostatistics Epidemiology and Informatics Department of Pathology and Laboratory Medicine Perelman School of Medicine-
Special Guests-	Deepak Nihalani- NIH/NIDDK Amanda Anderson- UAB

From Basic Informatics to Machine Learning Program Schedule

Day 1	Time	Organization	Speaker	Email
Special Guest	11a-11:15a	NIH/NIDDK	Deepak Nihalani	Deepak.nihalani@nih.gov
Around the Block: Neighborhoods in Kidney Health and Disease	11:15a-12:00p	Indiana University	Michael Eadon	meadon@iu.edu
Use ChatGPT and Machine learning in single cell multi-omics studies and in kidney research	12p-12:30p	University of Missouri	Dong Xu	xudong@missouri.edu
Break	12:30p-12:45p	Break	Break	Break
Applications 1: Introduction to biological analyzing methods	12:45p-1:45p	Indiana University	Mauminah Raina	mraina@iu.edu
Introduction to 10X Visium and Xenium spatial transcriptomics technologies and applications to kidney disease	1:45p-2:30p	Indiana University	Ricardo Melo Ferreira	rimelof@iu.edu
Applications 2: Spatial localization of cell types and functional tissue units across conditions. Implementation in 10X Visium and Xenium kidney samples	2:30p-3:00p	Indiana University	Mahla Asghari	masghari@iu.edu

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Day 2	Time	Organization	Contact Name	Email
Special Guest	11a-11:05a	UAB/OKRA	Amanda Anderson	ahanderson@uab.edu
Unlocking the power of Spatial Omics with AI	11:05a-11:50a	University of Pennsylvania	Mingyao Li	mingyao@pennmedicine.upenn.edu
Overview: Introduction to single-cell multi-omics and spatial transcriptomics and corresponding challenges	11:50a-12:20p	Ohio State University	Qin Ma	Qin.Ma@osumc.edu
Break	12:20p-12:40p	Break	Break	Break
Applications 2: Single-cell RNA-seq dataset acquisition, model training, and analysis using scGNN plus integrate ChatGPT	12:40p-1:25p	Indiana University	Juexin Wang	wangjuex@iu.edu
Applications 3: Spatial transcriptomics dataset acquisition, model fitting, and analysis	1:25p- 2:20p	Indiana University	Mauminah Raina	mraina@iu.edu
Applications 4: Single-cell multi-omics dataset acquisition, model training and analysis	2:20p- 3:00p	Ohio State University	Yi Jiang	Yi.Jiang@osumc.edu