

Yuzhou Chang

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Github: <https://github.com/BMEngineerR>

EDUCATION

Postdoc	1/2024 – present	Joint post doc, Immuno-Oncology Informatics Group, Pelotonia Institute for Immuno-Oncology, OSU, OH, 43210, USA Beth Israel Deaconess Medical Center, Harvard Medical School, Boston, MA, 02215, USA
Ph.D.	08/2018 – 12/2023	Biomedical Sciences Graduate Program The Ohio State University, Columbus, OH, 43210, USA Advisor: Prof. Qin Ma, Prof. Zihai Li Training: <i>statistic modeling, Bioinformatics, and Computational System Biology.</i>
B.E.	09/2012-06/2016	Biopharmaceutical China Pharmaceutical University, Nanjing, Jiangsu, China Advisor: Weihua Chu

HONORS

ICIBM 2023 Student & Trainee Travel Award	07/2023
Award for Excellence in Research (Grad Student)	Dec/2021
Honored Outstanding Student Leader (3 times)	09/2013 -09/2015
Honored Second-class Scholarship	09/2015

CURRENT RESEARCH INTERESTS

- Graph signal processing for spatial transcriptomics
- Developing computational tools for spatial transcriptomics data analysis, including cell-cell communication and tissue architecture identification based on deep learning framework/ other machine learning.
- Applying spatial transcriptomics on immuno-oncology.
- Gene regulatory network inference.

RESEARCH & WORK EXPERIENCE

Qin Ma Lab, Graduate Research Assistant, The Ohio State University, Columbus, OH.	04/2019 – 12/2023
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- Spatial transcriptomics analysis
- Gene regulatory network Inference
- scRNA-Seq data analysis
- Methylation data analysis

Trained in Illumina Company for True-seq kit implementation in RNA-Seq process, student, Illumina, Shanghai, China. 01/2017 - 06/2018

- RNA-seq library preparation.
- Sequencing & Quality control.
- BaseCalling to FASTQ transform.

Chu's Lab, Research assistant, CPU, Nanjing, Jiangsu. China. 09/2016-

- Perform experiment (microbial culture, drug-sensitive test, extract DNA)

12/2016

PUBLICATION

1. Hany A.Abdel-Hafiz, Saravana Kumar Kailasam Mani, Wesley Huang, Kenneth H. Gouin, **Yuzhou Chang**, Tong Xiao, Qin Ma, Zihai Li, Simon RV Knott, and Dan Theodorescu. "Single-cell profiling of murine bladder cancer identifies sex-specific transcriptional signatures with prognostic relevance." *Iscience* 26, no. 9 (2023).
2. Wang, Juexin, Jinpu Li, Skyler T. Kramer, Li Su, **Yuzhou Chang**, Chunhui Xu, Michael T. Eadon, Krzysztof Kiryluk, Qin Ma, and Dong Xu. "Dimension-agnostic and granularity-based spatially variable gene identification using BSP." *Nature Communications* 14, no. 1 (2023): 7367.
3. Anjun Ma, Xiaoying Wang, Jingxian Li, Cankun Wang, Tong Xiao, Yuntao Liu, Hao Cheng et al. "Single-cell biological network inference using a heterogeneous graph transformer." *Nature Communications* 14, no. 1 (2023): 964.
4. **Yuzhou Chang**, Jixin Liu, Anjun Ma, Sizun Jiang, Jordan Krull, Yao Yu Yeo, Yang Liu et al. "Spatial omics representation and functional tissue module inference using graph Fourier transform." *bioRxiv* (2022): 2022-12.
5. No-Joon Song, Carter Allen, Anna E. Vilgelm, Brian P. Riesenberger, Kevin P. Weller, Kelsi Reynolds, Karthik B. Chakravarthy et al. "Treatment with soluble CD24 attenuates COVID-19-associated systemic immunopathology." *Journal of Hematology & Oncology* 15 (2022): 1-18.
6. Shuo Chen, **Yuzhou Chang**, Liangping Li, Diana Acosta, Yang Li, Qi Guo, Cankun Wang et al. "Spatially resolved transcriptomics reveals genes associated with the vulnerability of middle temporal gyrus in Alzheimer's disease." *Acta Neuropathologica Communications* 10, no. 1 (2022): 1-24.
7. **Yuzhou Chang**, Fei He, Juexin Wang, Shuo Chen, Jingyi Li, Jixin Liu, Yang Yu et al. "Define and visualize pathological architectures of human tissues from spatially resolved transcriptomics using deep learning." *Computational and structural biotechnology journal* 20 (2022): 4600-4617.
8. **Yuzhou Chang**, Jixin Liu, Zihai Li, Bingqiang Liu, Qin Ma. SpaGFT is a graph Fourier transform for tissue module identification from spatially resolved transcriptomics. (BioRxiv,2023)
9. Mor Kenigsbuch, Pierre Bost, Shahar Halevi, **Yuzhou Chang**, Shuo Chen, Qin Ma, Renana

- Hajbi et al. "A shared disease-associated oligodendrocyte signature among multiple CNS pathologies." *Nature neuroscience* (2022): 1-11.
10. Hyunwoo Kwon, Johanna M. Schafer, No-Joon Song, Satoshi Kaneko, Anqi Li, Tong Xiao, Anjun Ma, **Yuzhou Chang**, et al. "Androgen conspires with the CD8+ T cell exhaustion program and contributes to sex bias in cancer." *Science Immunology* (2022)
 11. Johanna M. Schafer, Tong Xiao, Hyunwoo Kwon, Katharine Collier, **Yuzhou Chang**, Hany Abdel-Hafiz, Chelsea Bolyard et al. "Sex-biased adaptive immune regulation in cancer development and therapy." *Iscience* (2022): 104717.
 12. Anqi Li, **Yuzhou Chang**, No-Joon Song, Xingjun Wu, Dongjun Chung, Brian P. Riesenber, Maria Velegraki et al. "Selective targeting of GARP-LTGF β axis in the tumor microenvironment augments PD-1 blockade via enhancing CD8+ T cell antitumor immunity." *Journal for immunotherapy of cancer* 10, no. 9 (2022): e005433.
 13. Carter Allen, **Yuzhou Chang**, Brian Neelon, Won Chang, Hang J. Kim, Zihai Li, Qin Ma, and Dongjun Chung. "A Bayesian multivariate mixture model for high throughput spatial transcriptomics." *Biometrics* (2022).
 14. Shuo Chen, Diana Acosta, Liangping Li, Jiawen Liang, **Yuzhou Chang**, Cankun Wang, Julie Fitzgerald et al. "Wolframin is a novel regulator of tau pathology and neurodegeneration." *Acta Neuropathologica* 143, no. 5 (2022): 547-569.
 15. Shuo Chen, **Yuzhou Chang**, Liangping Li, Geidy E. Serrano, Thomas G. Beach, Karen E. Duff, Qin Ma, and Hongjun Fu. "Spatial transcriptomics of human middle temporal gyrus reveals layer-specific gene expression in early Alzheimer's disease." *Alzheimer's & Dementia* 17 (2021): e050540.
 16. Juexin Wang, Anjun Ma, **Yuzhou Chang**, Jianting Gong, Yuexu Jiang, Hongjun Fu, Cankun Wang, Ren Qi, Qin Ma, Dong Xu. "scGNN: a novel graph neural network framework for single-cell RNA-Seq analyses." *Nature Communications* (2021).
 17. Ma, Anjun, Adam McDermaid, Jennifer Xu, **Yuzhou Chang**, and Qin Ma. "Integrative methods and practical challenges for single-cell multi-omics." *Trends in Biotechnology* (2020).
 18. **Yuzhou Chang**, Carter Allen, Changlin Wan, Dongjun Chung, Chi Zhang, Zihai Li, and Qin Ma. "IRIS-FGM: an integrative single-cell RNA-Seq interpretation system for functional gene module analysis." *Bioinformatics* (2020).
 19. Ma, Anjun, Cankun Wang, **Yuzhou Chang**, Faith H. Brennan, Adam McDermaid, Bingqiang Liu, Chi Zhang, Phillip G. Popovich, and Qin Ma. "IRIS3: integrated cell-type-specific regulon inference server from single-cell RNA-Seq." *Nucleic Acids Research* 48, no. W1 (2020): W275-W286.
 20. Li, Qi-Zhang, **Yu-Zhou Chang**, Kai-Qi Su, Xiao-Lei Wang, Xiao-Hui Bai, and Xuan-Wei Zhou. "Cloning and Characterization of Promoters of the Fungal Immunomodulatory Protein Genes from *Ganoderma* spp.(Agaricomycetes) and Their Response to Methyl Jasmonate and Salicylic Acid." *International journal of medicinal mushrooms* 20, no. 2 (2018).
 21. Yu, Xiaoyan, Yimin Lao, Xiao-Lu Teng, Song Li, Yan Zhou, Feixiang Wang, Xinwei Guo, Siyu Deng, **Yuzhou Chang**, Xuefeng Wu, Zhiduo Liu, Lei Chen, Li-Ming Lu, Bin Li, Bing Su, Jing Jiang, Hua-Bing Li, Chuanxin Huang, Jing Yi, Qiang Zou. "SEN3 maintains the stability and function of regulatory T cells via BACH2 deSUMOylation." *Nature Communications* 9, no. 1 (2018): 1-11.
 22. Yu, Xiaoyan, Xiao-Lu Teng, Feixiang Wang, Yuhang Zheng, Guojun Qu, Yan Zhou, Zhilin Hu, Zhongqiu Wu, **Yuzhou Chang**, Lei Chen, Hua-Bing Li, Bing Su, Liming Lu, Zhiduo Liu, Shao-

- Cong Sun, Qiang Zou. "Metabolic control of regulatory T cell stability and function by TRAF3IP3 at the lysosome." *Journal of Experimental Medicine* 215, no. 9 (2018): 2463-2476.
23. Li, Qi-Zhang, **Yu-Zhou Chang**, Kai-Qi Su, Xiao-Lei Wang, Xiao-Hui Bai, and Xuan-Wei Zhou. "Cloning and Characterization of Promoters of the Fungal Immunomodulatory Protein Genes from *Ganoderma* spp.(Agaricomycetes) and Their Response to Methyl Jasmonate and Salicylic Acid." *International Journal of Medicinal Mushrooms* 20, no. 2 (2018).

TOOL DEVELOPMENT

- SpaGFT: spatial omics features representation based on Graph Fourier Transform
- RESEPT: a deep learning framework for tissue architecture identification based on spatial transcriptomics data. (<https://github.com/OSU-BMBL/RESEPT>)
- SPRUCE: A Bayesian Multivariate Mixture Model for Spatial Transcriptomics Data. (in development)
- IRIS-FGM: an integrative single-cell RNA-Seq interpretation system for functional module analysis (<https://bioconductor.org/packages/release/bioc/html/IRISFGM.html>)
- scGNN: single-cell Graph Neural Network (<https://github.com/juexinwang/scGNN>)
- IRIS3: Integrated cell-type-specific Regulon Inference Server from Single-cell RNA-Seq (<https://bmbi.bmi.osumc.edu/iris3/>)

TEACHING EXPERIENCES

- **Guest lecturer**, Analysis and Applications of Genome-Scale Data (BMI 8130), Autumn 2023, Department of Biomedical Informatics, The Ohio State University.
- **Guest lecturer**, Applications of Machine Learning and Artificial Intelligence in Biomedical Informatics (BMI 8050), Autumn 2020, Department of Biomedical Informatics, The Ohio State University.
- **Guest lecturer**, Single Cell RNAseq Analysis, Public Packages, and In-house Web Server, Clustering (BD4ISU, ISU/OSU meetings), July 2020, Department of Biomedical Informatics, The Ohio State University.

POSTER & PRESENTATION

- Poster presentation in “Spatial Biology 2023 US” at Boston. The poster title is “Spatial omics feature representation using graph Fourier transform.” 06/2023
- An invited talk “Spatial transcriptomics algorithms and the trend of spatial omics” at MWACD 2022 annual meeting. 11/2021
- Poster and flash talk at PIIO Second Annual Immuno-Oncology Symposium, Columbus, Ohio, USA
- Flash talk at The ISCB Rocky Mountain Bioinformatics Conference 12/2021
- Poster presentation at ISMB/ECCB 2021 as part of the Special Session Single Cell and Spatial Data Analysis 06/30/2021
- Poster at PIIO Second Annual Immuno-Oncology Symposium, Columbus, Ohio, USA 11/2020
- Forum on Advancements in *Immunology* Research (FAIR) Immunology forum, Shanghai Institute Immunology, Shanghai, China 3/2018
- Shanghai Institute Immunology-the Walter & Eliza Hall Institute (SII-WEHI) Shanghai, China 11/2017
- Cold Spring Harbor Asia (*Microbiota, Metagenomics & Health*), auditor, Suzhou, China. 09/2017

PROFESSIONAL MEMBERSHIP AND HONORS

- Member of Association of Biomolecular Resource Facilities (ABRF) 10/2022
- Member of International Society for Computational Biology (ISCB) 06/2021