

Yuzhou Chang

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

EDUCATION

Ph.D. student	08/2018 – present	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

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

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- 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 - present
<ul style="list-style-type: none"> • 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
<ul style="list-style-type: none"> • RNA-seq library preparation. 	

- Sequencing & Quality control.
- BaseCalling to FASTQ transform.

Chu's Lab, Research assistant, CPU, Nanjing, Jiangsu. China.

09/2016-
12/2016

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

PUBLICATION

1. Wang, J., Li, J., Kramer, S. T., Su, L., **Chang, Y.**, Xu, C., ... & Xu, D. (2023). Dimension-agnostic and granularity-based spatially variable gene identification. *bioRxiv*, 2023-03.
2. Ma, A., Wang, X., Li, J., Wang, C., Xiao, T., Liu, Y., ... & Ma, Q. (2023). Single-cell biological network inference using a heterogeneous graph transformer. *Nature Communications*, *14*(1), 964.
3. **Chang, Y.**, Liu, J., Ma, A., Jiang, S., Krull, J., Yeo, Y. Y., ... & Ma, Q. (2022). Spatial omics representation and functional tissue module inference using graph Fourier transform. *bioRxiv*, 2022-12.
4. Song, N. J., Allen, C., Vilgelm, A. E., Riesenber, B. P., Weller, K. P., Reynolds, K., ... & Li, Z. (2022). Treatment with soluble CD24 attenuates COVID-19-associated systemic immunopathology. *Journal of Hematology & Oncology*, *15*, 1-18.
5. 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.
6. **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.
7. **Yuzhou Chang**, Jixin Liu, Zihai Li, Bingqiang Liu, Qin Ma. SpaGFT is a graph Fourier transform for tissue module identification from spatially resolved transcriptomics. (Nature Biotechnology in the second revision)
8. 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.
9. 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)
10. 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.
11. 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.
12. 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).
13. 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.
 14. 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.
 15. 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).
 16. 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).
 17. **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).
 18. 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.
 19. 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).
 20. 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.
 21. Yu, Xiaoyan, Xiao-Lu Teng, Feixiang Wang, Yuhan 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.
 22. 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://bmb1.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