

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

Honored Outstanding Student Leader (3 times)	09/2013 -09/2015
Honored Second-class Scholarship	09/2015

CURRENT RESEARCH INTERESTS

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- Developing computational tools for spatial transcriptomics data analysis, including cell-cell communication, 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 implement 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. 	

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

PUBLICATION

1. **Yuzhou Chang**, Fei He, Juexin Wang, Shuo Chen, Jingyi Li, Jixin Liu, Yang Yu, Li Su, Anjun Ma, Carter Allen, Yu Lin, Shaoli Sun, Bingqiang Liu, Jose Otero, Dongjun Chung, Hongjun Fu, Zihai Li, Dong Xu, Qin Ma. "RESEPT: tissue architecture inference and visualization from spatially resolved transcriptomics." *BioRxiv* (2021).
2. Shuo Chen, **Yuzhou Chang**, Liangping Li, Diana Acosta, Cody Morrison, Cankun Wang, Dominic Julian, Mark E. Hester, Geidy E. Serrano, Thomas G. Beach, Qin Ma, Hongjun Fu. "Spatially resolved transcriptomics reveals unique gene signatures associated with human temporal cortical architecture and Alzheimer's pathology." *BioRxiv* (2021).
3. Carter Allen, **Yuzhou Chang**, Brian Neelon, Won Chang, Hang J. Kim, Zihai Li, Qin Ma, Dongjun Chung. "A Bayesian Multivariate Mixture Model for Spatial Transcriptomics Data." *BioRxiv* (2021).
4. **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).
5. 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). (**IF = 13.78**)
6. 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). (**IF = 14.3**)
7. 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. (**IF = 11.5**)
8. 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).
9. 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. (**IF = 13.6**)
10. 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. (**IF = 11.7**)
11. 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

- 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**, 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

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| • Poster presentation at ISMB/ECCB 2021 as part of the Special Session Single Cell and Spatial Data Analysis | 06/30/2021 |
| • PIIO Second Annual Immuno-Oncology Symposium, Columbus, Ohio, USA | 11/2020 |
| • Forum on Advancements in <i>Immunology</i> 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 (<i>Microbiota, Metagenomics & Health</i>), auditor, Suzhou, China. | 09/2017 |

PROFESSIONAL MEMBERSHIP AND HONORS

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| • Member of International Society for Computational Biology (ISCB) | 06/2021-
06/2021 |
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