HONGLIN WANG

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OVERVIEW

- 5+ years of experience in Data Mining, Machine Learning, Deep Learning, Computer Vision and Bioinformatics.
- Proficient in analysis massive bio-related datasets using various Machine Leaning and Statistical models.

EDUCATION

UNIVERSITY OF CONNECTICUT, **School of Engineering**   Storrs, CT
Ph. D. in Computer Science and Engineering   *Jan 2019 - Present*
Research interests: Applying Machine Learning in bio-related datasets (e.g., Single cell clustering and cell identification from images), Bioinformatics (e.g., gene pathway analysis & extension, cell-cell communication, and spatial genomics analysis).

UNIVERSITY OF CONNECTICUT, **School of Engineering**   Storrs, CT
M. Sc. in Computer Science and Engineering   *Jan 2019*
Master Thesis: A Method to Score Pathways Using Heuristic Rules.

UNIVERSITY OF ELECTRONIC SCIENCE AND TECHNOLOGY OF CHINA,   Chengdu, China
School of Information and Software Engineering   *May 2017*
B. Eng. in Software Engineering (Mainframe Computers)
Awards: First class of people fellowships in 2014 and 2015.

WORK AND RESEARCH EXPERIENCE

UConn Information Technology Services   Storrs, CT
Web developer / Software Engineer   *May 2019 − Present*

- Collaborate with developers to build interactive web user interfaces to query and visualize various scientific databases. (PHP, Python, JavaScript, MySQL, JSON)

UConn Computer Science and Engineering Department   Storrs, CT
Research Assistant   *Jan 2019 − Present*

- Develop and deploy pipelines for analysis single-cell data using multiple Machine Learning methods. (T-SNE, UMAP, PCA, K-NN)
- Design Machine Learning models to classify cell types with single-cell data. (Neural Network, SVM, Regression)
- Apply methods to identify cells from single-cell images. (OpenCV, Scikit-image)
- Study of route-based pathway analysis methods for bulk and single-cell omics data. (Data Mining, Machine Learning, Visualization, Python, R)
- Analyze cell-cell communication for spatial genomic data with self-developed program. (Machine Learning, Visualization, Python, MATLAB)
- Design and publish automated workflows for next generation sequencing data analysis and visualization. (Python, JavaScript, Bash, Java)

RECENT PUBLICATION

Conference

- [**22' ACM-BCB**]. **Wang, Honglin**, Pujan Joshi, Chenyu Zhang, Peter F. Maye, David W. Rowe, and Dong-Guk Shin, [rCom: a route-based framework inferring cell type communication and regulatory network using single cell data](#), 13th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics, 2022.

- [**22' BIBM**]. C. Zhang, P. Joshi, **Wang, Honglin**, S. -H. Hong, R. Yan and D. -G. Shin, [Pola Viz Reveals Microglia Polarization at Single Cell Level in Alzheimer's Disease](#), 2022 IEEE International Conference on Bioinformatics and Biomedicine (BIBM), 2022.

- [**21' BIBM**]. **Wang, Honglin**, Pujan Joshi, Seung-Hyun Hong, Dong-Ju Shin, and Dong-Guk Shin, [ctBuilder: A framework for building pathway crosstalks by combining single cell data with bulk cell data](#), IEEE International Conference on Bioinformatics and Biomedicine (BIBM), 2021.

- [**21' BIBM**]. Joshi, Pujan, **Wang, Honglin**, Salvatore Jaramillo, Seung-Hyun Hong, Charles Giardina, and Dong-Guk Shin, [Identification of Crosstalk between Biological Pathway Routes in Cancer Cohorts](#), IEEE International Conference on Bioinformatics and Biomedicine (BIBM), 2021.

- [**20' BIBM**]. **Wang, Honglin**, Pujan Joshi, Seung-Hyun Hong, Peter F. Maye, David W. Rowe, and Dong-Guk Shin, [cTAP: A Machine Learning Framework for Predicting Target Genes of a Transcription Factor using a Cohort of Gene Expression Data Sets](#), IEEE International Conference on Bioinformatics and Biomedicine (BIBM), 2020.

- [**20' BIBM**]. Joshi, Pujan, Brent Basso, **Wang, Honglin**, Seung-Hyun Hong, Charles Giardina, and Dong-Guk Shin, [Identification of Key Biological Pathway Routes in Cancer Cohorts](#), IEEE International Conference on Bioinformatics and Biomedicine (BIBM), 2020.

- [**20' ICCBB**]. Joshi, Pujan, **Wang, Honglin**, Brent Basso, Seung-Hyun Hong, Charles Giardina, and Dong-Guk Shin, [A Framework for Route Based Pathway Analysis of Gene Expression Data](#), International Conference on Computational Biology and Bioinformatics, 2020.

Journals

- [**22' BMC Genomics**]. **Wang, Honglin**, Pujan Joshi, Seung-Hyun Hong, Peter F. Maye, David W. Rowe, and Dong-Guk Shin. [Predicting the targets of IRF8 and NFATc1 during osteoclast differentiation using the machine learning method framework cTAP](#), BMC genomics 23, no. 1 (2022): 1-18.

- [**22' Methods**]. Joshi, Pujan, Brent Basso, **Wang, Honglin**, Seung-Hyun Hong, Charles Giardina, and Dong-Guk Shin. [rPAC: Route based pathway analysis for cohorts of gene expression data sets](#). Methods 198 (2022): 76-87.

TECHNICAL CAPABILITIES

• Machine Learning	Feature Selection, Dimensionality Reduction, Prediction, Classification, Clustering. (e.g., Random Forest, SVM, Bayesian Networks, Regression, Neural Network)
• Bioinformatics packages	GOstat, GSEA, SPIA, KEGG, Seurat, Scanpy, BLAST, Tophat, Cufflinks, SALMON, STAR, SAMTools, DAVID, UCSC Genome Browser.
• Data Visualization	PowerBI, Matplotlib, Plotly, Python Dash, Cytoscape, Tableau.
• Programming Languages	Python, PHP, JavaScript, Java, R, C/C++, MATLAB.
• DBMS	MySQL, MongoDB.
• Miscellaneous Tools	Jupyter Lab, GitHub, Apache, Scikit-learn, Pandas, NumPy, PyTorch, OpenCV, Scikit-image.