WENJING MA

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Education

Ph.D. student in Computer Science (Biomedical Informatics Track)

expected 2024

Department of Computer Science, Emory University, Atlanta, GA, U.S.

GPA: 4.0/4.0

Advisor: Dr. Hao Wu

Visiting Scholar in Bioinformatics

08/2018 -- 06/2019

Center for Public Health Genomics, University of Virginia, Charlottesville, VA, U.S.

Advisor: Dr. Chongzhi Zang

M.S. and B.S. in Computer Science and Technology

09/2010 -- 06/2017

Beijing University of Posts and Telecommunications (BUPT), Beijing, China

Rank: 20/297

Professional Experience

IT Support Engineer

08/2017 -- 06/2018

Investment Center, State Administration of Foreign Exchange, Beijing, China

Research Interests

- Develop machine learning and deep learning methods with application in single-cell genomics data
- Integrate single-cell multi-comics data to reveal gene regulatory network and explore epigenetic diseases such as neurodegenerative disease, obesity, cancer, etc.

Publications and posters

(*: equal contribution)

- 1. **Wenjing Ma**, Zhenjia Wang, Yifan Zhang, Neal E. Magee, Yayi Feng, Ruoyao Shi, Yang Chen, Chongzhi Zang. BARTweb: a web server for transcriptional regulator association analysis. *NAR Genomics and Bioinformatics*, (2021). DOI [website] [RECOMB 2019 poster]
- 2. **Wenjing Ma**, Kenong Su, Hao Wu. Evaluation of some aspects in supervised cell type identification for single-cell RNA-seq: classifier, feature selection, and reference construction. *Under second-round review in Genome Biology*, (2021). [project link]
- 3. **Wenjing Ma**, Sumeet Sharma, Peng Jin, Shannon L. Gourley, Zhaohui Qin. LRcell: A R Bioconductor package for Differential CELL type change analysis using Linear/logistic Regression. *Under review*, (2021). [R package]
- 4. Sumeet Sharma*, **Wenjing Ma***, Kerry J. Ressler, Thea Anderson, Dan. C. Li, Peng Jin, Shannon L. Gourley, Zhaohui Qin. Dysregulation of prefrontal oligodendrocyte linage cells across mouse models of adversity and human major depressive disorder. *Under review*, (2021).

Honors

Women in Natural Sciences Fellowship Innovative Mention, Google Girls' Hackathon 2016 (5/40) Honorable Mention, Interdisciplinary Contest in Modeling (ICM) Emory University, U.S., 2019 -- Present Google, China, 2016 COMAP, U.S., 2013

Research Experience

Evaluation in supervised cell type identification for single-cell RNA-seq

01/2020 -- Present

- Evaluate 9 classifiers and 6 feature selection strategies along with levels of discrepancies between reference and target datasets.
- Explore pooling and purification strategies when constructing reference dataset.

Cell-type specific transcriptional activity identification

08/2019 -- Present

- Identify Cell-type marker genes by applying non-parametric tests to an unbiased mouse brain single-cell RNA-seq dataset.
- Detect key cell type involved in other bulk RNA-seq experiments without using deconvolution methods.
- Collaborate with School of Medicine at Emory University and apply *LRcell* to psychiatry disorders.
- Collaborate with Neuroscience Institute at Georgia State University and apply *LRcell* to Alzheimer's and obesity.

Transcription factor association analysis

08/2018 -- 06/2019

- Develop a web server named <u>BARTweb</u> for the identification of TFs that regulate a given gene set or genomic binding profile by leveraging publicly available TF ChIP-seq datasets, H3K27ac ChIP-seq profiles and DNase I Hypersensitive Sites.
- Optimize data structure and algorithm to improve performance and shorten workflow execution time.