Xin Xiong

Email: onlybelter@outlook.com Website: https://onlybelter.github.io/

EDUCATION

Shanghai Jiao Tong University

Feb. 2016 – Mar. 2020 (expect)

Master of Engineering in Computer Science, Advisor: Professor Hai Zhao.

Research interests: Machine Learning for Natural Language Processing. In particular, word embedding and its application in the representation of small molecules.

Classes: Algorithm Analysis and Design, Database System Concepts, Introduction to Artificial Intelligence, Cloud Computing, Natural Language Processing.

Xi'an Polytechnic University

Sep. 2006 - Jul. 2010

BE in Bioengineering

WORK EXPERIENCE

Shenzhen Institutes of Advanced Technology (SIAT), CAS

Jun 2020 - present, department of biology, Research Assistant

Southern University of Science and Technology

March 2019 - March 2020, department of biology, Research Assistant

Interdisciplinary Research Center of Biology and Chemistry (IRCBC), CAS

May 2016 - March 2019, Research Assistant

Genminix Informatics Ltd.,Co.

May 2011 - April 2016, Department of R&D

I applied a patent during this period of time: Xin Xiong, Qi Li. The method of quick search and visualization of feed-forward loop. C.N. Patent 201410112193X filed on June 18, 2014 and issued on July 6, 2016.

Sangon Biotech (Shanghai) Co., Ltd.

October 2010 - April 2011, Department of Sequencing

RESEARCH PROJECTS

Relation between EMT and CD8+ T cells in tumor

Jun. 2020 - present

Mainly focus on deconvolution of bulk cell RNA-Seq data of tumors and try to find out the

relation between EMT and CD8+ T cells in immune infiltrated tumors.

Allele-specific sgRNA designing in mouse-rat fusion cell Aug. 2019 – Jan. 2020 Designing a sgRNA library which contains 3 kind of sgRNAs for targeting mouse genome only, rat genome only and both genomes.

CCS prediction and web server development

Feb. 2018 - Mar. 2019

Comparing the similarity of small molecules in high dimension and selecting features (molecular descriptors) to improve performance of the machine-learning-based CCS (Collision Cross-Section) prediction algorithm. I also development 3 user-friendly web server about CCS prediction and database search.

PUBLICATIONS

- ➤ Zhou, Z., Luo, M., Chen, X., Yin, Y., **Xiong, X.**, Wang, R., & Zhu, Z. J. (2020). Ion mobility collision cross-section atlas for known and unknown metabolite annotation in untargeted metabolomics. Nature communications, 11(1), 1-13.
- Shen, X., Wang, R., **Xiong, X.**, Yin, Y., Cai, Y., Ma, Z., ... & Zhu, Z. J. (2019). Metabolic reaction network-based recursive metabolite annotation for untargeted metabolomics. Nature communications, 10(1), 1-14.
- Zhou, Z., Shen, X., Chen, X., Tu, J., Xiong, X., Zhu, Z. J., & Wren, J. (2018). LipidIMMS Analyzer: Integrating multi-dimensional information to support lipid identification in ion mobility—mass spectrometry based lipidomics. Bioinformatics, 1, 3.
- Zhou, Z., Tu, J., Xiong, X., Shen, X., & Zhu, Z. J. (2017). LipidCCS: Prediction of Collision Cross-Section Values for Lipids with High Precision to Support Ion Mobility–Mass Spectrometry-Based Lipidomics. Analytical Chemistry, 89(17), 9559-9566.
- Zhou, Z., Xiong, X., & Zhu, Z. J. (2017). MetCCS predictor: a web server for predicting collision cross-section values of metabolites in ion mobility-mass spectrometry based metabolomics. Bioinformatics, 33(14), 2235-2237.

SKILLS

Software Python, R, TensorFlow, MySQL, Docker Languages Chinese (native), English (fluent)

I created sever user-friendly web servers to support the data analysis workflow using HTML/CSS/Angular on the frontend and Python/R/DjangoMySQL/Docker in the backend. I am familiar with common machine learning models (or statistics models) from linear regression to deep learning and I use these models on my daily work to analyze RNA-Seq data (bulk and single cell) or LC-MS data (identify and quantify natural small molecules). I also develop tools and algorithms by Python or R and package workflow together.

Hai Zhao, Professor, Shanghai Jiao Tong University, zhaohai@cs.sjtu.edu.cn					