

Junchen Yang

4-221, Biology Building, Shanghai Jiao Tong University, Shanghai, China, 200240

• (+86)131-6208-0289 • 2015yang@sjtu.edu.cn • jcyang.net

EDUCATION

Shanghai Jiao Tong University, Shanghai, China

Major 1: Biotechnology (Bioinformatics Pioneering Class)

2015.9 - present

Major 2: Computer Science

2017.3 - present

Rank: **1/27** GPA: 3.81/4.0 in Department of Bioinformatics and Biostatistics

UCLA, Los Angeles, California, USA

Cross-disciplinary Scholars in Science and Technology (CSST) research program 2018.7 - 2018.9

GPA: 4.0/4.0

RESEARCH INTEREST

I have a broad interest in Bioinformatics and Computational Biology. Current major interest is in developing biological sequence analysis methods and processing next-generation sequencing data.

RESEARCH EXPERIENCE

UCLA, Los Angeles, California, USA

2018.7 - 2018.9

Research Intern, Scalable Analytics Institute, Advisor: **Prof. Wei Wang**

ANT: Alignment-Narrowed TCC Matrix in Single-cell RNA-seq Quantification

- Developed an algorithm called ANT that transforms the genome alignment results to build Transcript Compatibility Counts (TCC) matrix. ANT is comprised of 3 components, genome alignment of reads using STAR, alignment narrowing with an intersection idea, and matrix construction.
- Tested ANT on 3381 mouse cells and compared it with previous method Kallisto, in which ANT showed a capacity of saving useful information like raw reads and umis while remained competitive regarding speed. More details of the implementation and visualization are [here](#).

Shanghai Jiao Tong University, Shanghai, China

2018.3 - 2018.7

Undergraduate Researcher, Dept. Bioinformatics & Biostatistics, Advisor: **Prof. Jingfang Wang**
Computational Prediction and Functional Analysis of Arsenic Binding Proteins in Human Cells

- Developed a web-based predicting tool called Arsenic Finder for arsenic-binding proteins based on the position-specific score matrix and the single-mutation free energy profile. Arsenic Finder is based on Django (a python web framework), deployed together with Nginx and uWSGI. It is freely [available](#).
- This work has been invited as an oral presentation at the *2018 International Conference on Computational Systems Biology* and the full manuscript has been submitted to *Quantitative Biology* for publication.

Shanghai Jiao Tong University, Shanghai, China

2017.4 - 2018.3

Undergraduate Researcher, Dept. Bioinformatics & Biostatistics, Advisor: **Prof. Yi Xiong**

Drug Combination Database and Predictive Model Construction Based on Drug and Target Information

- Developed the front-end of the database (Django framework).
- Developed the ensemble prediction model of drug combinations with teammates, which can predict potential drug combinations with an accuracy of 82% and AUC of 0.88. The base classifiers are Naive Bayes, SVM, Random Forest, AdaBoost, and Gradient Boost. The meta classifier is XGBoost.

- The project received an A (highest) in the 15th Undergraduate Innovation Research Program in Shanghai Jiao Tong University, and I received an A+ (highest).

PUBLICATIONS

1. Shichao Pang, **Junchen Yang**, Yilei Zhao, Yixue Li, Jingfang Wang. Computational Prediction and Functional Analysis of Arsenic Binding Proteins in Human Cells. *Quantitative Biology*. (under review)
2. Yi Xiong, Qiankun Wang, **Junchen Yang**, Xiaolei Zhu, Dong-Qing Wei. PredT4SE-Stack: Prediction of Bacterial Type IV Secreted Effectors From Protein Sequences Using a Stacked Ensemble Method. *Frontiers in Microbiology*.

TECHNICAL STRENGTHS

Computer Languages Python, C++, R, HTML, CSS, JavaScript
Additional Skills BASH, Django, \LaTeX

SELECTED AWARDS

National Scholarship (highest honor for undergraduates in China, top 0.2% nationwide)	2017,2018
Lixin Tang Scholarship (top 1%)	2017
Merit Student Award of Shanghai Jiao Tong University	2016,2017
UCLA-CSST Scholarship	2018