

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: Bioinformatics & Biostatistics

2015.9 - present

Rank: **1/27** GPA: 3.81/4.0

Minor: Computer Science

2017.3 - present

UCLA, Los Angeles, California, USA

Cross-disciplinary Scholars in Science and Technology research

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 Computational Genomics, specifically in developing biological sequence analysis methods, as well as their downstream applications in biology and medicine.

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 on 3381 mouse cells and compared with previous method Kallisto, ANT showed a capacity of saving useful information like raw reads and umis, while remained competitive in terms of speed at cell level. 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 in 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 82% and AUC 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 College Students' Innovative Practice Plan in Shanghai Jiao Tong University and I received an A+ (highest).

PUBLICATIONS

Shichao Pang, **Junchen Yang**, Yilei Zhao, Yixue Li, Jingfang Wang. Computational Prediction and Functional Analysis of Arsenic Binding Proteins in Human Cells, *Quantitative Biology* (submitted)

TECHNICAL STRENGTHS

Computer Languages Python, C++, R, HTML, CSS, JavaScript
Additional Skills BASH, Django, L^AT_EX

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