

# Junchen Yang

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EDUCATION	Shanghai Jiao Tong University, Shanghai, China	
	Major: Bioinformatics & Biostatistics	2015.9 - present
	Rank: <b>1/27</b> GPA: 3.81/4.0 (3.68/3.93/3.93 for each year)	
	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 INTERESTS	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
	<i>Research Intern</i> , Scalable Analytics Institute, Advisor: <b>Prof. Wei Wang</b> <b>ANT: Alignment-Narrowed TCC Matrix in Single-cell RNA-seq Quantification</b> <ul style="list-style-type: none"><li>• Developed an algorithm called ANT that transforms the genome alignment results to build TCC matrix (Transcript Compatibility Counts matrix).</li><li>• ANT is comprised of 3 components, genome alignment of reads using STAR, alignment narrowing with an intersection idea, and matrix construction.</li><li>• 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 <a href="#">here</a>.</li></ul>	
	Shanghai Jiao Tong University, Shanghai, China	2018.3 - 2018.7
	<i>UG Researcher</i> , Dept.Bioinformatics&Biostatistics, Advisor: <b>Prof. Jingfang Wang</b> <b>Computational Prediction and Functional Analysis of Arsenic Binding Proteins in Human Cells</b> <ul style="list-style-type: none"><li>• Developed a web-based predicting tool for arsenic-binding proteins based on the position-specific score matrix and the single mutation free energy profile.</li><li>• The tool is freely <a href="#">available</a>. The tool is based on Django (a python web framework), deployed together with Nginx and uWSGI.</li><li>• This work has been invited as an oral presentation in ISB 2018, and the full manuscript has been submitted to <i>Quantitative Biology</i> for publication.</li></ul>	
	Shanghai Jiao Tong University, Shanghai, China	2017.4 - 2018.3
	<i>UG Researcher</i> , Dept.Bioinformatics&Biostatistics, Advisor: <b>Prof. Yi Xiong</b> <b>Drug Combination Database and Predictive Model Construction Based on Drug and Target Information</b> <ul style="list-style-type: none"><li>• Developed the front-end of the database (Django framework).</li><li>• Developed the ensemble prediction model of drug combinations with teammates. The first layer consists of Naive Bayes, SVM, Random Forest, AdaBoost</li></ul>	

and Gradient Boost, the second layer is XGBoost. The model can predict potential drug combinations with an accuracy 82% and AUC 88%.

- 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,  $\text{\LaTeX}$

**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