Xue Zeng

The Rockefeller University

Laboratory of Human Genetics and Genomics

1230 York Avenue, New York, NY

Email: xue.zeng@yale.edu

Phone: (203) 909-7802

Website: xue-zeng.com

EXECUTIVE SUMMARY

- Computational biologist with 5 years of experience in human genomics studying the genetic mechanism of diseases using statistical approaches and NGS technologies (WES, WGS, long-read sequencing, targeted deep sequencing, RNAseq, proteomics, and others)
- Led multiple large-scale genomic studies of complex disorders in collaboration with clinicians and statisticians worldwide, resulting in 2 first-authored and 8 co-authored publications in high-impact scientific journals (200+ citations) and inclusion as personnel on 2 R01 research grants
- Led a biomarker study of immuno-oncology (IO) pre-clinical and clinical trial data which involves integrative analyses and visualization of WES, RNAseq, IHC, and clinical data
- Built bioinformatics pipelines for data processing and statistical tests of genomics datasets
- Fluent in Python, R, R Markdown, Unix/Bash, and AWS; proficient in C++ and MATLAB

EDUCATION

2018-Present	Visiting student, The Rockefeller University, New York, NY
2015-Present	Ph.D. candidate, Yale University, New Haven, CT
2011-2015	B.S., Bioscience, Huazhong University of Sci & Tech (HUST), China (1st/48)

WORK EXPERIENCE

Jun 2019 - Aug 2019   **Translational Bioinformatics Intern**
Early Stage Immuno-Oncology, Bristol-Myers Squibb

- Curated and analyzed clinical trial data of over 400 patients with advanced NSCLC enrolled in the FRACTION program which examined the efficacy of multiple IO treatment combinations.
- Interrogated the mutational and gene expression signatures, genes, pathways, and biomarkers associated with different outcomes in IO-Naïve and IO-Experienced patients using internal NGS data and the TCGA database.
- Developed and curated bioinformatics pipelines using R on AWS platform for parsing clinical data, pathogenic variant filtering, statistical tests for association analyses, and data visualization.

RESEARCH EXPERIENCE

Mar 2016 - Present   **Graduate Research Assistant**
Yale University & The Rockefeller University (Dr. Richard P. Lifton)

- Led a multi-national genomic study on the genetic mechanism of Vein of Galen malformation (VOGM), coordinating multiple research groups across 4 nations, resulting in 2 first-authored publications in *Neuron* and *Trends in Molecular Medicine* (cover story).
- Collaborated with clinical fellows on investigation of genetic mechanism of congenital hydrocephalus, resulting in a second-authored cover story in *Neuron*.
- Led the *de novo* analysis on the world's largest cohort of congenital heart disease (CHD) with over 4,000 patients, resulting in a co-authored publication in *Nature Genetics*.
- Worked extensively with clinicians and statisticians worldwide on genomic studies of various congenital disorders and development of genomic tools, resulting in 6 co-authored publications.
- Built in-house bioinformatics pipelines for data processing and visualization, variant calling, and statistical association analyses of germline, somatic, mosaic, and structural variants.

Jun 2012 - May 2015   **Undergraduate Research Assistant**
Center for Human Genome Research (Dr. Qing Wang), HUST
▪ Mutation screen on > 1,000 CHD patients using High Resolution Melting Analysis.
▪ Conducted *in vitro* glutathione S-transferase (GST) pull down and Western blot to identify the interaction site between MOG1 and $Na_v1.5$.

Key laboratory of Molecular Physics (Dr. Yunjun Yan), HUST
▪ Performed molecular cloning, targeted mutagenesis, vector transformation, enzyme assays and characterized the expression of 4 cellulases in bioengineering projects in *E. coli* and yeast.
▪ Worked with 18 undergraduate researchers as a leader of an experimental team of 4 members to design two synthetic biology projects winning Silver Medals in both the iGEM (International Genetically Engineered Machine Competition) Asian (2013) and Global (2014) Jamborees

SELECTED PUBLICATIONS (*Co-First Author, [#]Co-Second Author)
▪ **Zeng X**, et al. (2019). EphrinB2-EphB4-RASA1 signaling in human cerebrovascular development and disease. ***Trends in Molecular Medicine***.
▪ Duran D*, **Zeng X***, et al. (2018). Mutations in chromatin modifiers and Ephrin signaling components in Vein of Galen malformation. ***Neuron***.
▪ Furey CG*, Choi J*, Jin SC[#], **Zeng X**[#], et al. (2018). *De Novo* Mutation in Genes Regulating Neural Stem Cell Fate in Human Congenital Hydrocephalus. ***Neuron***.
▪ Jin SC*, Homsy J*, Zaidi S*, Lu Q, Morton S, DePalma S, **Zeng X**, et al. (2017). Contribution of rare transmitted and *de novo* variants among 2,871 congenital heart disease probands. ***Nature Genetics***.

SELECTED TALKS
Oct 2019   **Selected talk**, American Society of Human Genetics 2019 Annual Meeting
"Mutations in ephrinB2-EphB4-RASA1 signaling underlie VOGM"
Oct 2018   **Selected talk**, Bench to Bassinet Face-to-Face, NHLBI
"New significant genes identified through WES and MIPS using 8,196 CHD cases"
May 2018   **Invited talk**, Rare Disease Seminar, Department of Genetics, Yale University
"Mutation in epigenetic and signaling regulators of neurovascular development in VOGM"

RELEVANT COURSES
❖Quantitative Genomics and Genetics (Weill Cornell Medical School) ❖Genomic Methods for Genetic Analysis (Yale) ❖Computational Statistics (Yale) ❖Machine Learning (Coursera)

HONORS AND AWARDS
2019   Conference Travel Fellowship, Yale University
2012- 2014   National Scholarship, the Ministry of Education, China (top 1% of students)
2014   1st Prize, Experimental Skills Competition, Ministry of Education, Hubei, China
2013   Top 20 Outstanding Undergraduate Award, HUST (top 20/35,000 students)

LEADERSHIP AND TEACHING
2018-Present   Board member, WISeR (Women In Science at Rockefeller)
2013, 2014   Leader of Experimental Group, HUST iGEM Team
2016, 2017   Teaching Fellow (BIOL103 and GENE625), Yale University