

YANGYANG LI

yangyang.li@northwestern.edu | [personal blog](#) | github.com/cauliyang

SELF-INTRODUCTION

I am intensely interested in the data-driven domains including classic machine learning and deep learning. I am also an engineer and I am mainly working on developing algorithms and software to handle problems on Genomics, Transcriptomics.

EDUCATION

Northwestern University <i>Ph.D in Bioinformatics</i>	Chicago, US <i>June. 2022 – present</i>
University of Minnesota <i>Ph.D. in Bioinformatics and Computational Biology</i>	Minnesota, US <i>Sep. 2020 – June. 2022</i>
China Agricultural University <i>Master in Crop Bioinformatics</i>	Beijing, CN <i>Sep. 2018 – June 2020</i>
Northeast Agricultural University <i>Bachelor of Arts in Agronomy</i>	Harbin, CN <i>Sep. 2014 – June 2018</i>

RESEARCH EXPERIENCE AND PROJECT

Northwestern University <i>Ph.D. in Bioinformatics domain</i> <ul style="list-style-type: none">Develop algorithm and deep learning model to emulate long-read sequencerDevelop algorithm and tools to map gene fusion to structure variations of genomics	Chicago, US <i>Sep. 2022 – Present</i>
University of Minnesota <i>Ph.D. in Bioinformatics and Computational Biology</i> <ul style="list-style-type: none">Develop algorithm to detect non-linear structure variations in transcriptomeCompare the performance of current tools used to detect alternative splicing variants	Minnesota, US <i>Sep. 2020 – Present</i>
China Agricultural University <i>Master in Crop Bioinformatics</i> <ul style="list-style-type: none">Dissection of 1,400 genomics data, extracted from eight maize populations. I adapt the bin map method to construct high-density genetic maps suitable for QTL mapping and detection, which regulate multiple, important agronomical traits.Conducting Genome-Wide Association Analysis (GWAS) to determine the association between SNPs and maize ear traits in 450 natural populations.	Beijing, CN <i>Sep. 2018 – June 2020</i>

TECHNICAL SKILLS

Languages and Frameworks: C/C++, Python, R, Pytorch
Developer Tools: Git, Docker, TravisCI, PyCharm, Clion, VS Code, Vim, Linux, Gcc, Clang
Specializations: Software and Algorithm Development, Concurrency, Data Analysis and Visualization, Natural Language Processing

GRANTS AND HONORS

- Second Prize of Academic Scholarship (2019)
- Agricultural Scholarship (2016)
- Encouragement Scholarship (2014)

CONFERENCE TALK

- The 7th Mathematical, Computer and Life Sciences Interdisciplinary Young Scholars Forum

PUBLICATIONS

Fry, J., **Li, Yangyang**, & Yang, R. (2022, 09). ScanExitronLR: characterization and quantification of exitron splicing events in long-read RNA-seq data. *Bioinformatics*. Retrieved from <https://doi.org/10.1093/bioinformatics/btac626>