

# YANGYANG LI

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## SELF-INTRODUCTION

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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

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

## RESEARCH EXPERIENCE AND PROJECT

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<b>Northwestern University</b> <i>Ph.D. in Bioinformatics domain</i> <ul style="list-style-type: none"><li>Develop algorithm and deep learning model to emulate long-read sequencer</li><li>Develop algorithm and tools to map gene fusion to structure variations of genomics</li></ul>	Chicago, US <i>Sep. 2022 – Present</i>
<b>University of Minnesota</b> <i>Ph.D. in Bioinformatics and Computational Biology</i> <ul style="list-style-type: none"><li>Develop algorithm to detect non-linear structure variations in transcriptome</li><li>Compare the performance of current tools used to detect alternative splicing variants</li></ul>	Minnesota, US <i>Sep. 2020 – Present</i>
<b>China Agricultural University</b> <i>Master in Crop Bioinformatics</i> <ul style="list-style-type: none"><li>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.</li><li>Conducting Genome-Wide Association Analysis (GWAS) to determine the association between SNPs and maize ear traits in 450 natural populations.</li></ul>	Beijing, CN <i>Sep. 2018 – June 2020</i>

## TECHNICAL SKILLS

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**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

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

## CONFERENCE TALK

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

## PUBLICATIONS

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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>