

YANGYANG LI

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SELF-INTRODUCTION

I am a third-year Ph.D. candidate with a focus on deep learning and algorithm development for complex biological problems. My area of expertise is machine learning-based, data-driven domains. Armed with a passion for applying this knowledge to scientific issues, I am eager to contribute and further my knowledge in a fast-paced professional environment.

RESEARCH EXPERIENCE AND PROJECT

|   |   |
|---|---|
| <b>Northwestern University</b><br><i>Ph.D. in Bioinformatics</i>  | Chicago, US<br><i>June 2022 – June 2025</i>     |
| <ul style="list-style-type: none"><li>Formulated a deep generative model tailored for sequencing data simulation</li><li>Introduced a graph algorithm to identify non-linear transcripts in long-read data, achieving a 20x speedup</li><li>Crafted a web application for graph algorithm visualization</li><li>Designed a Python interface for a C-based command-line tool, gaining 20% performance boosts</li></ul> |   |
| <b>University of Minnesota</b><br><i>Ph.D. in Bioinformatics and Computational Biology</i>  | Minneapolis, US<br><i>Sep. 2020 – June 2022</i> |
| <ul style="list-style-type: none"><li>Developed a transformer-based deep learning model to predict causality between gene fusion and structural variation</li><li>Pioneered an algorithm to discern non-linear structure variations in transcriptomes</li><li>Conducted a comprehensive assessment of the effectiveness of leading tools for the detection of alternative splicing variants</li></ul>                 |   |
| <b>China Agricultural University</b><br><i>Master in Crop Bioinformatics</i>  | Beijing, CN<br><i>Sep. 2018 – June 2020</i>     |
| <ul style="list-style-type: none"><li>Identified pivotal features in 1,400 maize genomics datasets to enhance agronomic traits</li><li>Undertook a study to map the relationship between genetic variations and maize ear attributes in 450 natural populations</li></ul>   |   |

EDUCATION

|   |   |
|---|---|
| <b>Northwestern University</b><br><i>Ph.D in Bioinformatics</i>                                 | Chicago, US<br><i>June 2022 – June 2025</i>     |
| <b>University of Minnesota</b><br><i>Ph.D. in Bioinformatics and Computational Biology</i>      | Minneapolis, US<br><i>Sep. 2020 – June 2022</i> |
| <b>China Agricultural University</b><br><i>Master in Crop Bioinformatics</i>                    | Beijing, CN<br><i>Sep. 2018 – June 2020</i>     |
| <b>Northeast Agricultural University</b><br><i>Bachelor of Arts in Agricultural Engineering</i> | Harbin, CN<br><i>Sep. 2014 – June 2018</i>      |

TECHNICAL SKILLS

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| <b>Languages and Frameworks:</b> C/C++, Python, Rust, Pytorch, Jax, Candle, GGML   |
| <b>Developer Tools:</b> Neovim, Git, Docker, GitHub Action, CMake, HTML, Gcc, Clang, Linux, L <sup>A</sup> T <sub>E</sub> X          |
| <b>Specializations:</b> Algorithm Development, Concurrency Programming, Data Analysis and Visualization, Natural Language Processing |

PUBLICATIONS

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

Li, Yangyang, & Yang, R. (2023). Pxblat: An ergonomic and efficient python binding library for blat. *bioRxiv*. doi: 10.1101/2023.08.02.551686