Yangyang Li

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Self-introduction

I am intensely interested in classic machine learning and deep learning. I like applying the knowledge on Genomics, Transcriptomics, and I am passionate about exploring the secrets in the process of life.

Education

University of Minnesota — Minnesota, US
Ph.D. in Bioinformatics and Computational Biology — *Sep. 2020 – Present*

China Agricultural University (985) — Beijing, CN
Master in bioinformatics — *Sep. 2018 – June 2020*

Northeast Agricultural University (211) — Harbin, CN
Bachelor of Arts in Agronomy — *Sep. 2014 – June 2018*

Research Experience

Ph.D. in Bioinformatics and Computational Biology — Sep. 2020 – Present
University of Minnesota — *Minnesota, US*

- Develop a tool to detect cryptic exons and apply deep learning to mine the relationship between alternative splicing and cancer.
- Compare the performance of current tools used to detect alternative splicing variants

Master — Sep. 2018 – June 2020
China Agricultural University — *Beijing, CN*

- Dissection of 1,400 genomic 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.

Technical Skills

Languages: Python, C/C++, HTML/CSS, R
Deep Learning Frameworks: Pytorch
Developer Tools: Git, Docker, TravisCI, Google Cloud Platform, VS Code, PyCharm, Vim, Linux
Libraries: Pandas, NumPy, Matplotlib, Seaborn, Jupyter, Biopython, ...

Certifications and MOOCs

- Machine Learning
- Deep Learning

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