MAO-JAN LIN

mj.maojanlin@gmail.com ◇ maojanlin.github.io

3400 N Charles St. Baltimore, MD 21218

(667) · 444 · 9532 ◇ last updated: Nov 5, 2025

RESEARCH INTERESTS

Computational Genomics, Immunogenomics, Pangenomics, Reference Bias, Sequence Alignment, Variant Calling

EDUCATION

Johns Hopkins University   *08/2021 – present*
PhD Candidate in Computer Science (expected graduation: 2026)
Advisor: Dr. Ben Langmead
Qualifying project advisor: Dr. Yana Safonova

National Taiwan University   *09/2016 – 06/2019*
Master of Science in Electronics Engineering
Advisor: Dr. Yi-Chang Lu
Thesis: "A Parallel Design of Dynamic Programming Sequence Aligner with Affine Gap Traceback"

National Taiwan University   *09/2012 – 06/2016*
Bachelor of Science in Electrical Engineering

PROFESSIONAL EXPERIENCE

Roche   06/2024–08/2024
Summer Intern, Computational Biology Molecular Lap Applications   *Remote*

· Developed a structural variant calling pipeline to enhance recall and precision for the Sequencing by expansion (SBX) platform.

Apple   01/2018–07/2018
Product Design Intern, Input Device Team   *Taipei/Shanghai*

· Built software analysis tools on the production line for Apple's upstream manufacturer.
· Developed circuit solutions and prototype software to a new MacBook keyboard design.
· Built an embedded system with serial communication interfaces in Python for the keyboard prototype.
· Planned experimental designs for product life test and failure analysis.

Himax   07/2017 – 08/2017
Summer Intern, Video Image Processing Team   *Taipei*

· Developed compression algorithms for 3D depth sensing solutions.
· Built a camera noise model based on experimental data and probability theory.

PEER-REVIEWED JOURNAL PAPERS

See Google Scholar for more information.

* Equal contribution

3. **Mao-Jan Lin**, Ben Langmead, Yana Safonova. (2025). IGLoo enables comprehensive analysis and assembly of immunoglobulin heavy-chain loci in lymphoblastoid cell lines using PacBio high-fidelity reads. *Cell Reports Methods*. https://doi.org//10.1016/j.crmeth.2025.101033

2. **Mao-Jan Lin**, Sheila Iyer, Nae-Chyun Chen, Ben Langmead. (2024). Measuring, visualizing and diagnosing reference bias with biastools. *Genome Biology*. https://doi.org/10.1186/s13059-024-03240-8

1. ***Mao-Jan Lin**, *Yu-Chun Lin, *Nae-Chyun Chen, Allen Chilun Luo, Sheng-Kai Lai, Chia-Lang Hsu, Jacob Shujui Hsu, Chien-Yu Chen, Wei-Shiung Yang, Pei-Lung Chen. (2022). Profiling Genes Encoding the Adaptive Immune Receptor Repertoire with gAIRR Suite. *Frontiers in Immunology*. https://doi.org/10.3389/fimmu.2022.922513

PRE-PRINTS

2. Kuan-Ta Huang, Yu-Hsuan Yang, **Mao-Jan Lin**, Sheng-Kai Lai, Ting-Hsuan Chou, Chieh-Yu Lee, Tsung-Kai Hung, Chia-Lang Hsu, Ya-Chien Yang, Chien-Yu Chen, Pei-Lung Chen, Jacob Shu-Jui Hsu. (2025). gAIRR-wgs: An Algorithm to Genotype T Cell Receptor Alleles Using Whole Genome Sequencing Data. *bioRxiv*. https://www.biorxiv.org/content/10.1101/2025.10.11.681280v2.abstract

1. Yu-Hsuan Yang, Chi-Yuan Yao, **Mao-Jan Lin**, Kuan-Ta Huang, Yu-Hui Lin, I-Hsuan Chiu, Sheng-Kai Lai, Chih-Yeh Chen, Ya-Chien Yang, Chia-Lang Hsu, Jacob Shujui Hsu, Chien-Yu Chen, Pei-Lung Chen. (2025). Unmasking Human T Cell Receptor Germline Diversity: 335 Novel Alleles Identified in 47 Pangenome Reference Individuals Using the gAIRR Suite. *bioRxiv*. https://www.biorxiv.org/content/10.1101/2025.05.24.655452v1.abstract

PEER-REVIEWED CONFERENCE PAPERS

5. Ruei–Ting Chien, **Mao–Jan Lin**, Yang–Ming Yeh, Yi–Chang Lu. (2022). Traceback Memory Reduction for Three-Sequence Alignment Algorithm with Affine Gap Models. *IEEE Asia-Pacific Signal and Information Processing Association Annual Summit and Conference (APSIPA)*. https://doi.org/10.23919/APSIPAASC55919.2022.9980113

4. Yu-Cheng Li, **Mao-Jan Lin**, Xiao-Xuan Huang, Chien-Yu Chen, and Yi-Chang Lu. (2019). Comprehensive Study of Keywords for Sequence-Based Automatic Annotation of Protein Functions. *IEEE Bioinformatics and BioEngineering (BIBE)*. https://doi.org/10.1109/BIBE50027.2020.00012

3. Ming-Hung Chen, **Mao-Jan Lin**, Yu-Cheng Li, and Yi-Chang Lu. (2019). Banded Pair-HMM Algorithm for DNA Variant Calling and Its Hardware Accelerator Design. *IEEE Bioinformatics and BioEngineering (BIBE)*. https://doi.org/10.1109/BIBE.2019.00107

2. **Mao-Jan Lin**, Yu-Cheng Li, and Yi-Chang Lu. (2018). Hardware Accelerator Design for Dynamic-Programming-Based Protein Sequence Alignment with Affine Gap Tracebacks. *IEEE Bio-medical Circuits and Systems Conference (BioCAS)*. https://doi.org/10.1109/BIOCAS.2019.8919080

1. **Mao-Jan Lin**, Chih-Yu Chang, Yu-Cheng Li, Nae-Chyun Chen, and Yi-Chang Lu. (2018). A Hybrid Flow for Multiple Sequence Alignment with a BLASTn Based Pairwise Alignment Processor. *IEEE International Symposium on Circuits and Systems (ISCAS)*. https://doi.org/10.1109/ISCAS.2018.8351254

POSTER PRESENTATION

6. Extending IGLoo to light chains: High-resolution analysis and assembly of IGK and IGL loci in lymphoblastoid cell lines with PacBio HiFi reads. Workshop on Algorithms in Bioinformatics (WABI). *College Park, Maryland, USA*. 2025.

5. IGLoo—Profiling the immunoglobulin heavy chain locus in lymphoblastoid cell lines with PacBio high-fidelity sequencing reads. Cold Spring Harbor Laboratory Meeting on Biological Data Science. *Cold Spring Harbor, New York, USA*. 2024.

4. Measuring, visualizing and diagnosing reference bias with biastools. Cold Spring Harbor Laboratory on Genome Informatics. *Cold Spring Harbor, New York, USA*. 2023.

3. Biastools provides detailed measurements and diagnoses for reference bias. Workshop on emerging methods in sequence analysis (WEMSA). *University park, Pennsylvania, USA*. 2023.

2. Profiling germline adaptive immune receptor repertoire with gAIRR Suite. Cold Spring Harbor Laboratory on Genome Informatics. *Virtual*. 2021.

1. A Hybrid Flow for Multiple Sequence Alignment with a BLASTn Based Pairwise Alignment Processor. IEEE International Symposium on Circuits and Systems (ISCAS). *Florence, Italy*. 2018.

TEACHING AND MENTORSHIP

TEACHING EXPERIENCE

- **Department of Computer Science, Johns Hopkins University**
  Teaching Assistant
  EN.601.446/646 Sketching and Indexing, Spring 2025
  EN.601.451 Introduction to Computational Immunogenomics, Fall 2022
  Guest Lecturer
  EN.601.451 Introduction to Computational Immunogenomics, Fall 2022

- **Department of Biomechanical Engineering, National Taiwan University**
  Teaching Assistant and Guest Lecturer
  BME5938 Bioinformatics Algorithms, Summer 2020

MENTORSHIP

- **Department of Computer Science, Johns Hopkins University**
  Ethan Chang, undergraduate researcher (2025)
  - Developed and benchmarked an experimental setup to assess how alignment accuracy changes with increasing pangenome size, identifying the point of diminishing returns in genome inclusion.

- **Department of Electrical Engineering, National Taiwan University**
  Ming-Hung Chen, undergraduate researcher (2019)
  - Designed and implemented an hardware accelerator for GATK HaplotypeCaller.

SOFTWARE

- **impute-first alignment framework:** create personalized references with imputation to reduce reference bias and enhance variant calling accuracy.
  collaborated with Kavya Vaddadi and Sina Majidian
  https://github.com/kvaddad1/impute-first

- **IGLoo:** measure V(D)J recombination in human Immunoglobulin(IG) loci in lyphoblastoid cell lines.
  https://github.com/maojanlin/IGLoo

- **Biastools:** measuring reference bias in sequence alignment in different setup.
  https://github.com/maojanlin/biastools

- **gAIRR-suite:** profiling human T-cell Receptor (TR) and IG in sequence data.
  https://github.com/maojanlin/gAIRRsuite