

Nae-Chyun Chen

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Research Interests

Computational Genomics, Sequence Alignment, Variant Calling, Pangenomics, Computational Immunogenomics, Domain Specific Computing Architecture, High Performance Computing

Education

- **Ph.D. in Computer Science**, 08/2018 - present
Johns Hopkins University, Baltimore, Maryland, USA
Advisor: Ben Langmead
- **M.S. in Electronics Engineering**, 08/2015 - 06/2017
National Taiwan University, Taipei, Taiwan
Advisor: Yi-Chang Lu
Thesis: *A Novel Long Read Aligner Using Fast Seeding and Linking Strategies*
- **B.S. in Electrical Engineering and B.A. in Economics (double degree)**, 09/2010 - 06/2015
National Taiwan University, Taipei, Taiwan
- **Exchange student**, 08/2014 - 12/2014
University of Illinois at Urbana-Champaign, Champaign, Illinois, USA

Professional Experience

- **Google, virtual, USA**
DeepVariant Team
Research Intern (full-time), 05/2020 - 08/2020
Student Researcher (part-time), 08/2020 - 12/2020
- **Synopsys, Sunnyvale, California, USA**
IC Compiler II Team
Technical Intern (full-time), 06/2016 - 08/2016

Peer-Reviewed Journal Papers

- [J2] **Nae-Chyun Chen**, Brad Solomon, Taher Mun, Sheila Iyer, Ben Langmead. 2021. Reference flow: reducing reference bias using multiple population genomes. *Genome biology*. <https://doi.org/10.1186/s13059-020-02229-3>
- [J1] Jacob Pritt, **Nae-Chyun Chen**, Ben Langmead. 2018. FORGe: prioritizing variants for graph genomes. *Genome biology*. <https://doi.org/10.1186/s13059-018-1595-x>

Pre-prints

- [P3] Taher Mun*, **Nae-Chyun Chen***, Ben Langmead. 2021. LevioSAM: Fast lift-over of alternate reference alignments. *bioRxiv*. <https://doi.org/10.1101/2021.02.05.429867>
- [P2] **Nae-Chyun Chen**, Alexey Kolesnikov, Sidharth Goel, Taedong Yun, Pi-Chuan Chang*, Andrew Carroll*. 2021. Improving variant calling using population data and deep learning. *bioRxiv*. <https://doi.org/10.1101/2021.01.06.425550>
- [P1] 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. 2020. Profiling Germline Adaptive Immune Receptor Repertoire with gAIRR Suite. *bioRxiv*. <https://doi.org/10.1101/2020.11.27.399857>

* Equal contribution.

Peer-Reviewed Conference Papers

- [C8] Yi-Lun Liao, Yu-Cheng Li, **Nae-Chyun Chen**, Yi-Chang Lu. 2018. Adaptively Banded Smith-Waterman Algorithm for Long Reads and Its Hardware Accelerator. In *2018 IEEE 29th International Conference on Application-specific Systems, Architectures and Processors (ASAP)*. IEEE. <https://doi.org/10.1109/ASAP.2018.8445105>
- [C7] **Nae-Chyun Chen**, Yu-Cheng Li, Yi-Chang Lu. 2018. A Memory-Efficient FM-Index Constructor for Next-Generation Sequencing Applications on FPGAs. Accepted by *2018 IEEE International Symposium on Circuits and Systems (ISCAS)*. IEEE. <https://arxiv.org/abs/2102.03045>¹
- [C6] Mao-Jan Lin, Chih-Yu Chang, Yu-Cheng Li, **Nae-Chyun Chen**, Yi-Chang Lu. 2018. A Hybrid Flow for Multiple Sequence Alignment with a BLASTn Based Pairwise Alignment Processor. In *2018 IEEE International Symposium on Circuits and Systems (ISCAS)*. IEEE. <https://doi.org/10.1109/ISCAS.2018.8351254>
- [C5] Chih-Yu Chang, Yu-Cheng Li, **Nae-Chyun Chen**, Xiao-Xuan Huang, Yi-Chang Lu. A special processor design for nucleotide basic local alignment search tool with a new banded two-hit method. In *2016 IEEE Nordic Circuits and Systems Conference (NORCAS)*. IEEE. <https://doi.org/10.1109/NORCHIP.2016.7792921>

¹This paper was accepted by 2018 IEEE ISCAS, but later removed because the co-author presented on-behalf of us hadn't fulfilled the presentation requirement. We posted the manuscript to arXiv with the agreement from IEEE.

- [C4] Chun-Shen Liu, **Nae-Chyun Chen**, Yu-Cheng Li, Yi-Chang Lu. An FPGA-based quality filter for de novo sequence assembly pipeline. In *2016 IEEE Asia Pacific Conference on Circuits and Systems (APCCAS)*. IEEE. <https://doi.org/10.1109/APCCAS.2016.7803916>
- [C3] Xiao-Xuan Huang, Chun-Hsien Ho, Yu-Cheng Li, **Nae-Chyun Chen**, Yi-Chang Lu. Step shift: A fast image segmentation algorithm and its hardware implementation for next-generation sequencing fluorescence data. In *2016 IEEE Asia Pacific Conference on Circuits and Systems (APCCAS)*. IEEE. <https://doi.org/10.1109/APCCAS.2016.7803933>
- [C2] Yi-Hsiang Chen, **Nae-Chyun Chen**, Yu-Hsiang Kao, Yu-Cheng Li, Yi-Chang Lu. Queue-based segmentation algorithm for refining depth maps in light field camera applications. In *2016 IEEE 5th Global Conference on Consumer Electronics*. IEEE. <https://doi.org/10.1109/GCCE.2016.7800346>
- [C1] **Nae-Chyun Chen**, Tai-Yin Chiu, Yu-Cheng Li, Yu-Chun Chien, Yi-Chang Lu. Power efficient special processor design for burrows-wheeler-transform-based short read sequence alignment. In *2015 IEEE Biomedical Circuits and Systems Conference (BioCAS)*. IEEE. <https://doi.org/10.1109/BioCAS.2015.7348380>

Awards and Honors

- [A4] Novatek Fellowship. 2016. Novatek Microelectronics Corp, Hsinchu, Taiwan.
- [A3] People's Choice Award, Three-Minute Thesis Competition at NTU. 2016. National Taiwan University, Taipei, Taiwan.
- [A2] Best Tourism App Award, Chunghwa Telecom Hami Apps Competition. 2014. Chunghwa Telecom Co., Taipei, Taiwan.
- [A1] Bronze Medal and Outstanding Paper Award, Altera Innovate Asia FPGA Design Competition. 2013. Terasic Inc., Hsinchu, Taiwan.

Contributed Open Source Tools

- [T3] Bowtie-majref (2021): major-allele reference indexes for Bowtie and Bowtie 2 (primary author). <https://github.com/BenLangmead/bowtie-majref>
- [T2] LevioSAM (2021): fast lift-over of alternate reference alignments (primary author; joint with Taher Mun). <https://github.com/alshai/levioSAM>
- [T1] Reference flow (2021): reducing reference bias using multiple population genomes (primary author). https://github.com/langmead-lab/reference_flow

Invited Talks and Lectures

- Using population data to aid genomic data processing. School of Medicine, National Taiwan University. *Taipei, Taiwan*. 2021.
- Using population data to aid genomic data processing. Institute of Biomedical Sciences, Academia Sinica. *Taipei, Taiwan*. 2021.
- Aligning to multiple linear population genomes. ACT Genomics Co.. *Taipei, Taiwan*. 2021.
- Variant-aware reference genome and sequence alignment. School of Medicine, National Taiwan University. *Taipei, Taiwan*. 2020.
- An FPGA-based quality filter for de novo sequence assembly pipeline. 2016 IEEE Asia Pacific Conference on Circuits and Systems (APCCAS). *Jeju, South Korea*. 2016.

Poster Presentations

- Improving variant calling using population data and deep learning. Cold Spring Harbor Laboratory Meeting on Biological Data Science. *Virtual*. 2020.
- Improving linear alignment accuracy and reducing bias using reference flow. Cold Spring Harbor Laboratory Meeting on Genome Informatics. *Cold Spring Harbor, New York, USA*. 2019.
- Improved linear alignments through selective re-alignment of diverse references. Research in Computational Molecular Biology (RECOMB). *Washington D.C., USA*. 2019.
- Predicting open chromatin using transcription factor binding motifs and expression levels (co-presented with Xinyu A. Feng and Arun Das). JHU Chromatin and Chromosome workshop. *Baltimore, Maryland, USA*. 2019.
- Power efficient special processor design for burrows-wheeler-transform-based short read sequence alignment. 2015 IEEE Biomedical Circuits and Systems Conference (BioCAS). *Atlanta, Georgia, USA*. 2015.

Teaching

- **Department of Computer Science, Johns Hopkins University, Baltimore, Maryland, USA**
Teaching Assistant
EN 601.446/646 Sketching and Indexing for Sequences, Spring 2021
- **Department of Electrical Engineering, National Taiwan University, Taipei, Taiwan**
Teaching Assistant
EE 4039 Computer Architecture, Fall 2016
EE 4039 Computer Architecture, Spring 2016
CommE 5018 Data Compression, Fall 2015

Mentoring

- **Department of Computer Science, Johns Hopkins University, Baltimore, Maryland, USA**
High school internship mentor (Sheila Iyer, 2019)
Undergraduate researcher mentor (Sheila Iyer, 2020-present)
- **Department of Electrical Engineering, National Taiwan University, Taipei, Taiwan**
Undergraduate researcher mentor (Yi-Lun Liao, 2017-2018)
Undergraduate researcher mentor (Chih-Yu Chang, 2015-2016)

Professional Activities

- **Sub-reviewer**
Intelligent Systems for Molecular Biology (ISMB), 2021
Genome Biology, 2021
Intelligent Systems for Molecular Biology (ISMB), 2020
Bioinformatic, 2020
Scientific Reports, 2019

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