Nae-Chyun Chen

Ph.D. student
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Research Interests

Computational Genomics, Pangenomics, Sequence Alignment, Variant Calling, Lift-over, Computational Immunogenomics, Domain Specific Computing Architecture

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

* Equal contribution

[J4] Nurk, Sergey*, Sergey Koren*, Arang Rhie*, Mikko Rautiainen*, ... **Nae-Chyun Chen**, ... Adam Phillippy. 2022. The complete sequence of a human genome. *Science.* https://doi.org/10.1126/science.abj6987

[J3] Taher Mun*, **Nae-Chyun Chen***, Ben Langmead. 2021. LevioSAM: Fast lift-over of alternate reference alignments. *Bioinformatics.* https://doi.org/10.1093/bioinformatics/btab396

[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

* Equal contribution

[P3] **Nae-Chyun Chen**, Luis Paulin, Fritz Sedlazeck, Sergey Koren, Adam Phillippy, Ben Langmead. 2022. Improved sequence mapping using a complete reference genome and lift-over. *bioRxiv,* https://www.biorxiv.org/content/10.1101/2022.04.27.489683

[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

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] [1] **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

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[1]This 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.

[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

[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

[T6] Chaintools (2022): utilities for the genomic chain format (primary author; joint with Nancy F. Hansen). https://github.com/milkschen/chaintools

[T5] LevioSAM2 (2022): fast and accurate coordinate conversion between assemblies (primary author). https://github.com/milkschen/leviosam2

[T4] Matchall (2021): accurate matching of variant alleles using local haplotypes (primary author). https://github.com/milkschen/matchall

[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 (2020): reducing reference bias using multiple population genomes (primary author). https://github.com/langmead-lab/reference_flow

Invited Talks and Lectures

- Reducing reference bias in genomic sequence data processing. Academic Seminar, Boston Taiwanese Biotechnology Association (BTBA). *Virtual.* 2022.

- Using population data to improve genomic data processing. Department of Computer Science, National Yang Ming Chiao Tung University. *Hsinchu, Taiwan.* 2022.

- Fast and accurate coordinate conversion between assemblies. PacBio Workshop at Cold Spring Harbor Laboratory Meeting on Genome Informatics. *Virtual.* 2021.

- Fast and accurate coordinate conversion between assemblies. The Telomere-to-Telomere (T2T) consortium and Human Pangenome Reference (HPRC) Consortium meeting. *Virtual.* 2021.

- 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.

- Sequence processing in the human MHC region. School of Medicine, National Taiwan University. *Virtual.* 2020.

- 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

- Fast and accurate coordinate conversion between assemblies. Cold Spring Harbor Laboratory Meeting on Genome Informatics. *Virtual.* 2021.

- 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**
  Teaching Assistant
  EN 601.446/646 Sketching and Indexing for Sequences, Spring 2021

- **Department of Electrical Engineering, National Taiwan University**
  Teaching Assistant
  EE 4039 Computer Architecture, Fall 2016
  EE 4039 Computer Architecture, Spring 2016
  CommE 5018 Data Compression, Fall 2015

Mentorship

- **Department of Computer Science, Johns Hopkins University**
  Steven Solar: undergraduate researcher (2022)
  - Design data-driven methods to characterize alignments that could benefit from pangenome-based alignment methods

- **Department of Computer Science, Johns Hopkins University**
  Sheila Iyer: high school internship (2019), undergraduate researcher (2020-2021)
  - Measured and analyzed reference bias in DNA sequence alignment ([J2])
  - The work won the 1st place at the Fairfax County Regional Science Fair and was presented at the 2020 Sigma Xi Student Research Showcase

- **Department of Electrical Engineering, National Taiwan University**
  Yi-Lun Liao: undergraduate researcher (2017-2018)
  - Designed and implemented an accelerator for the Smith-Waterman algorithm ([C8])

  Chih-Yu Chang: undergraduate researcher (2015-2016)
  - Developed a processor for the BLAST tool ([C5])

Professional Activities

Reviewer

- BMC Genomics: 2021

Sub-reviewer

- IEEE International Workshop on High Performance Computational Biology (HiCOMB): 2022

- Research in Computational Molecular Biology (RECOMB): 2021

- Genome Biology: 2021, 2021

- ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB): 2021

- Intelligent Systems for Molecular Biology (ISMB): 2021, 2020

- Bioinformatic: 2020

- Scientific Reports: 2019

(Last updated: April 29, 2022)