Nae-Chyun Chen

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RESEARCH INTERESTS AND SKILLS

- **Research Interests:** Computational Genomics, Pangenomics, Sequence Alignment, Variant Calling, Lift-over, Computational Immunogenomics, Domain Specific Computing Architecture
- **Programming Languages:** Python, C/C++, R, Rust, Verilog
- **Toolkits:** LaTeX, git, Bash, Snakemake, unittest, Docker, make, cmake

EDUCATION

Johns Hopkins University (JHU), *Ph.D. Student in Computer Science*	08/2018 – 08/2022 (estimated)
Advisor: Dr. Ben Langmead	
National Taiwan University (NTU), *M.S. in Electronics Engineering*	09/2015 – 07/2017
Advisor: Dr. Yi-Chang Lu (Lab for Data Processing Systems)	

- Thesis: "A Novel Long Read Aligner Using Fast Seeding and Linking Strategies"

NTU, *B.S. in Electrical Engineering and B.A. in Economics (double degrees)*	09/2010 – 06/2015

RESEARCH EXPERIENCE

Langmead Lab, *JHU*	08/2018 – present

- Reducing reference bias using a complete human reference and population genetic information [1,3,4].

Genome Informatics Section, *NHGRI, NIH*	04/2021 – present

- Generated lift-over and browser resources for the first complete human genome [2].

Lab for Data Processing Systems, *NTU*	09/2013 – 07/2017

WORKING EXPERIENCE

Research Intern, *DeepVariant Team, Google Health*	05/2020 – 12/2020

- Developed a population-aware DeepVariant model that reduced SNP errors by 5% [5].

Technical Intern, *IC Compiler II Team, Synopsys*	06/2016 – 08/2016

SELECTED PUBLICATIONS

1. Nae-Chyun Chen, L. Paulin, F. Sedlazeck, S. Koren, A. Phillippy, B. Langmead, **"Improved sequence mapping using a complete reference genome and lift-over,"** in *bioRxiv*, 2022
2. S. Nurk*, S. Koren*, A. Rhie*, M. Rautiainen*, ... Nae-Chyun Chen, ... A. Phillippy, **"The complete sequence of a human genome,"** in *Science*, 2022
3. Nae-Chyun Chen, B. Solomon, T. Mun, S. Iyer, B. Langmead, **"Reference flow: reducing reference bias using multiple population genomes,"** in *Genome biology, 2021*
4. T. Mun*, Nae-Chyun Chen*, B. Langmead, **"LevioSAM: fast lift-over of variant-aware reference alignments,"** in *Bioinformatics, 2021*
5. Nae-Chyun Chen, A. Kolesnikov, S. Goel, T. Yun, P.-C. Chang*, A. Carroll*, **"Improving variant calling using population data and deep learning,"** in *bioRxiv, 2021*
6. M.-J. Lin*, Y.-C. Lin*, Nae-Chyun Chen*, ... P.-L. Chen, **"Profiling Germline Adaptive Immune Receptor Repertoire with gAIRR Suite,"** in *bioRxiv*, 2020