NAE-CHYUN CHEN

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EDUCATION

Johns Hopkins University (JHU), *Ph.D. Student in Computer Science*　　08/2018 – present
　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-degree)*　　09/2010 – 06/2015

RESEARCH EXPERIENCE

Langmead Lab, *JHU*　　08/2018 – present
- Developed methods using one [2] or multiple variant-aware references [3] to reduce reference bias.
- Analyzed HLA genotyping accuracy using different variant-inclusion strategies for graph genome [4].

Lab for Data Processing Systems, *NTU*　　09/2013 – 07/2017
- Developed a sequence aligner for Nanopore reads in C/C++ (MS thesis).
- Designed algorithms and accelerators for genomic sequence processing on ASICs and FPGAs.

WORKING EXPERIENCE

Research Intern, *DeepVariant Team, Google Health*　　05/2020 – 12/2020
- Developed a population-aware DeepVariant model that reduced SNP errors by 5% [1].

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

SELECTED PUBLICATIONS

1. 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*
2. T. Mun*, Nae-Chyun Chen*, and B. Langmead, **"LevioSAM: Fast lift-over of alternate reference alignments,"** in *bioRxiv, 2021* (co-first author)
3. Nae-Chyun Chen, B. Solomon, T. Mun, S. Iyer, and B. Langmead, **"Reference flow: reducing reference bias using multiple population genomes,"** in *Genome biology, 2021*
4. J. Pritt, Nae-Chyun Chen, and B. Langmead, **"FORGe: prioritizing variants for graph genomes,"** in *Genome biology, 2018*

SKILLS

- Programming Languages: Python, C/C++, R, Verilog
- Toolkit: LaTeX, git, gdb, Bash, Snakemake, unittest