

NAE-CHYUN CHEN

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EDUCATION

Johns Hopkins University (JHU) , <i>Ph.D. Student in Computer Science</i>	08/2018 – present
<i>Advisor: Dr. Ben Langmead</i>	
National Taiwan University (NTU) , <i>M.S. in Electronics Engineering</i>	09/2015 – 07/2017
<i>Advisor: Dr. Yi-Chang Lu (Lab for Data Processing Systems)</i>	
• Thesis: “A Novel Long Read Aligner Using Fast Seeding and Linking Strategies”	
NTU , <i>B.S. in Electrical Engineering and B.A. in Economics (double-degree)</i>	09/2010 – 06/2015

RESEARCH EXPERIENCE

Langmead Lab , <i>JHU</i>	08/2018 – present
• Developed methods using one [2] or multiple variant-aware references [1] to reduce reference bias.	
• Analyzed HLA genotyping accuracy using different variant-inclusion strategies for graph genome [4].	
Lab for Data Processing Systems , <i>NTU</i>	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 , <i>DeepVariant Team, Google Health</i>	05/2020 – 12/2020
• Developed a population-aware DeepVariant model that reduced SNP errors by 5% [3].	
Technical Intern , <i>IC Compiler II Team, Synopsys</i>	06/2016 – 08/2016

SELECTED PUBLICATIONS

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1. [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
 2. T. Mun*, [Nae-Chyun Chen](#)*, and B. Langmead, “**LevioSAM: fast lift-over of variant-aware reference alignments**,” in *Bioinformatics*, 2021
 3. [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
 4. J. Pritt, [Nae-Chyun Chen](#), and B. Langmead, “**FORGe: prioritizing variants for graph genomes**,” in *Genome biology*, 2018

SKILLS

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