

NAE-CHYUN CHEN

+1-443-467-5174 | naechyun@jhu.edu | <https://naechyun.github.io>

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, JHU	08/2018 – present
<i>Reduce alignment bias using pan-genome-based methods</i>	
• Designed population-specific references and alignment strategies to reduce alignment bias [1].	
• Analyzed HLA genotyping accuracy using different variant-inclusion strategies for a graph aligner [2].	
Lab for Data Processing Systems, NTU	09/2013 – 07/2017
<i>Design algorithms, software and hardware to process genomic data efficiently</i>	
• 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 – 08/2020
Student Researcher , <i>DeepVariant Team, Google Health</i>	08/2020 – present
• 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
• Evaluated the correlation of two routing methods in IC Compiler II.	

SELECTED PUBLICATIONS & PRESENTATIONS

PUBLICATIONS

1. [Nae-Chyun Chen](#), Brad Solomon, Taher Mun, Sheila Iyer, and Ben Langmead, “**Reducing reference bias using multiple population reference genomes**,” in *BioRxiv*, 2020
2. Jacob Pritt, [Nae-Chyun Chen](#), and Ben Langmead, “**FORGE: prioritizing variants for graph genomes**,” in *Genome biology*, 2018

PRESENTATION

3. [Nae-Chyun Chen](#), Alexey Kolesnikov, Sidharth Goel, Taedong Yun, Pi-Chuan Chang, Andrew Walker Carroll, “**Improving variant calling using population data and deep learning**,” *Biological Data Science*, virtual, 2020 (poster)

SKILLS

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