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

Reduce alignment bias using pan-genome-based methods

- Designed population-specific genomes and alignment strategies to reduce alignment bias [1, 3].
- Analyzed HLA genotyping accuracy using different variant-inclusion strategies for a graph aligner [2].

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

Design algorithms, software and hardware to process genomic data efficiently

- 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 – present

- Developed a population-aware DeepVariant model that outperformed the baseline by 5%.
- Submitted an abstract to Biological Data Science (2020, virtual).

Technical Intern, *IC Compiler II Team, Synopsys* 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, Brad Solomon, and Ben Langmead, **"Improving linear alignment accuracy and reducing bias using reference flow,"** *Genome Informatics*, CSHL, USA, 2019 (poster)

SKILLS

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