

# NAE-CHYUN CHEN

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## EDUCATION

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<b>Johns Hopkins University (JHU)</b> , <i>Ph.D. Student in Computer Science</i>	08/2018 – present
<i>Advisor: Dr. Ben Langmead</i>	
<b>National Taiwan University (NTU)</b> , <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”	
<b>NTU</b> , <i>B.S. in Electrical Engineering and B.A. in Economics (double degree)</i>	09/2010 – 06/2015

## RESEARCH EXPERIENCE

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<b>Langmead Lab, JHU</b>	08/2018 – present
<i>Reduce alignment bias using pan-genome-based methods</i>	
• Designed population-specific genomes and alignment strategies to reduce alignment bias [1, 5].	
• Analyzed HLA genotyping accuracy using different variant-inclusion strategies for a graph aligner [2].	
<b>Lab for Data Processing Systems, NTU</b>	09/2013 – 07/2017
<i>Design algorithms, software and hardware that process genomic data</i>	
• Developed a sequence aligner for Nanopore reads in C/C++ (MS thesis).	
• Proposed a memory efficient algorithm to build FM-index and implemented it on an FPGA [3].	
• Implemented accelerators for genomic sequence processing software on ASICs [4].	

## SELECTED PUBLICATIONS & PRESENTATIONS

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### 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
3. [Nae-Chyun Chen](#), et al., “**A memory-efficient FM-Index constructor for next-generation sequencing applications on FPGAs**,” in *Proceedings of IEEE ISCAS*, 2018
4. [Nae-Chyun Chen](#), et al., “**Power efficient special processor design for Burrows-Wheeler-transform-based short read sequence alignment**,” in *Proceedings of the IEEE BioCAS*, 2015

### PRESENTATION

5. [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

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- Programming Languages: Python, C/C++, R, Verilog
  - Toolkit: ~~TeX~~TeX, git, ggplot2, gdb, Bash, Snakemake