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
  Lab for Data Processing Systems. Advisor: Dr. Yi-Chang Lu
  - 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 and allelic biases using pan-genome-based methods

  - Analyzed HLA genotyping accuracy using different variant-inclusion strategies for a graph aligner [2].
  - Designed population-specific genomes and alignment strategies to reduce alignment bias [1, 4].

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

Design software, hardware and algorithms for genomic data processing

  - 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 ASIC [4].

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,* 975219 (2020)

2. Jacob Pritt, Nae-Chyun Chen, and Ben Langmead, **"FORGe: prioritizing variants for graph genomes,"** in *Genome biology* 19.1 (2018): 220

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

PRESENTATIONS

4. Nae-Chyun Chen, Brad Solomon, and Ben Langmead, **"Improving linear alignment accuracy and reducing bias using reference flow,"** *Genome Informatics*, CSHL, USA, 2019 (poster)

5. Xinyu A. Feng, Nae-Chyun Chen, and Arun Das, **"Predicting open chromatin using transcription factor binding motifs and expression levels,"** *JHU Chromatin and Chromosome workshop*, 2019 (poster)

SKILLS

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