



KUAN-HAO CHAO

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






RESEARCH INTERESTS AND SKILLS

- **Research Interests:** Computational Genomics, Machine Learning, Genomic Variant, Genome Assembly, Transcriptome Assembly, Transcriptomics (RNA-Seq), Genome Annotation, Sequence Indexing, Lift-over
- **Skills:** C/C++, Python, R, Java, Bash | \LaTeX , Git, make, cmake, Snakemake, Docker, Web, Unity, Android

EDUCATION




Johns Hopkins University (JHU) <i>Ph.D. in Computer Science, Advisor: Steven Salzberg Ph.D. and Mihaela Pertea Ph.D.</i>	Baltimore, MD 08/2021 – Present
The Australian National University (ANU) <i>Exchange Student in Engineering & Computer Science</i>	Canberra, Australia 07/2019 - 07/2020
National Taiwan University (NTU) <i>Bachelor of Science in Electrical Engineering</i>	Taipei, Taiwan 09/2016 - 01/2021

EXPERIENCE

Salzberg & Pertea Lab, Center for Computational Biology, JHU <i>Advisors: Steven Salzberg Ph.D. & Mihaela Pertea Ph.D.</i> <i>Position: Ph.D. Student, Software: multiStringTie  C++  Assembly: Han1  </i>	Baltimore, MD 08/2021 – Present Publication [2]
Langmead Lab, Department of Computer Science, JHU <i>Advisors: Ben Langmead Ph.D. & Sanjit A. Seshia Ph.D. (University of California, Berkeley)</i> <i>Position: Research Student, Software: WGT (Wheeler-Graph-Toolkit)  C++, Preprint [1]</i>	Baltimore, MD 11/2021 – Present
HK Tsai Lab, Institute of Information Science, Academia Sinica <i>Advisor: Huai-Kuang Tsai Ph.D.</i> <i>Position: Research Assistant, Software: SPIFFED   </i>	Taipei, Taiwan 08/2020 - 02/2021
Lanfear Lab, Division of Ecology and Evolution, ANU <i>Advisor: Robert Lanfear Ph.D.</i> <i>Position: Research Assistant, Software: sangeranalyseR  (83 ★)  5000+   Bioconductor, Publication [3]</i>	Canberra, Australia 07/2019 - 07/2020
Bioinformatics Core Lab, Centers of Genomic and Precision Medicine, NTU <i>Advisors: Eric Y. Chuang Ph.D. & Tzu-Pin Lu Ph.D.</i> <i>Position: Research Assistant, Software: RNASeqR  (11 ★)  4500+   Bioconductor, Publication [4]</i>	Taipei, Taiwan 01/2018 - 07/2019

PUBLICATIONS

* CO-FIRST AUTHOR, † CORRESPONDING AUTHOR

1. **Kuan-Hao Chao**^{†*}, Pei-Wei Chen*, S.A. Seshia, and B. Langmead[†], “WGT: Tools and algorithms for recognizing, visualizing and generating Wheeler graphs” in *bioRxiv*, 2022 
2. **Kuan-Hao Chao**[†], A.V. Zimin, M. Pertea, and S.L. Salzberg[†], “The first gapless, reference-quality, fully annotated genome from a Southern Han Chinese individual” in *bioRxiv (G3: Genes, Genomes, Genetics in press)*, 2022 
3. **Kuan-Hao Chao**[†], K. Barton, S. Palmer, and R. Lanfear[†], “sangeranalyseR: simple and interactive analysis of Sanger sequencing data in R” in *Genome biology and evolution*, 2020 
4. **Kuan-Hao Chao**, Y.-W. Hsiao, Y.-F. Lee, C.-Y. Lee, L.-C. Lai, M.-H. Tsai, T.-P. Lu, E.Y. Chuang[†], “RNASeqR: an R package for automated two-group RNA-Seq analysis workflow” in *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2019 