

Kuan-Hao Chao

BIOINFORMATICS · COMPUTATIONAL BIOLOGY · SOFTWARE ENGINEERING · BIOENGINEERING

✉ kuanhao.chao@gmail.com | 🏠 kuanhao-chao.github.io/ | 📧 Kuanhao-Chao | 📺 kuan-hao-chao | 🐦 @KuanHaoChao

TOEFL iBT Total: 103 (R:27, L:27, S:25, W:24)

EDUCATION

Australian National University (ANU)

Exchange (Non-Degree) at ANU College of Engineering and Computer Science

Canberra, Australia

Jul. 2019 - Exp. Jun. 2020

National Taiwan University (NTU)

B.S. in Electrical Engineering, College of Electrical Engineering & Computer Science

Taipei, Taiwan

Jun. 2016 - Exp. Jan. 2021

SKILLS

Programming Language Python, R, C/C++, Java, \LaTeX

Programming Skills Keras, Pandas, Scikit-learn, Django/Flask, Git, R package, Android App, Web Development, Unity Game

PUBLICATION

KH Chao, K Barton, S Palmer, and R Lanfear (2020). "sangeranalyseR: simple and interactive analysis of Sanger sequencing data in R", in *bioRxiv*. doi: [10.1101/2020.05.18.102459](https://doi.org/10.1101/2020.05.18.102459) [Accepted at *Genome Biology and Evolution* with Minor Revisions]

KH Chao, YW Hsiao, YF Lee, CY Lee, LC Lai, MH Tsai, TP Lu, and EY Chuang (2019). "RNASeqR: an R package for automated two-group RNA-Seq analysis workflow", in *IEEE/ACM Transactions on Computational Biology and Bioinformatics*. doi: [10.1109/TCBB.2019.2956708](https://doi.org/10.1109/TCBB.2019.2956708)

RESEARCH POSITION & EXPERIENCE

Jul. 2020 - Present **Research Assistant** @ Institute of Information Science, Academia Sinica

Taipei, Taiwan

Jul. 2020 - Present **Research Assistant** @ Institute of Epidemiology and Preventive Medicine, NTU

Taipei, Taiwan

Sep. 2019 - Jun. 2020 **Research Assistant** @ Division of Ecology and Evolution, ANU

Canberra, Australia

Jan. 2018 - Jun. 2019 **Research Student** @ Centers of Genomic and Precision Medicine, NTU

Taipei, Taiwan

sangeranalyseR: simple and interactive processing of Sanger sequencing data in R

Canberra, Australia

✔ **ACCEPTED WITH MINOR REVISIONS** | [PAPER_{LINK}](#), [BIOCONDUCTOR_{LINK}](#), [GITHUB_{LINK}](#), [DOCUMENTATION_{LINK}](#)

Sep. 2019 - Jun. 2020

- **ADVISOR** : Prof. Robert Lanfear_{LINK}
- **POSITION** : Research Assistant @ *Molecular Evolution and Phylogenetics Lab, ANU*
- **SKILLS** : Sanger sequencing data analysis, R package development, R S4 object-oriented programming, Shiny application
- Developed sangeranalyseR with features including read trimming, detecting secondary peaks, chromatogram plotting, contigs alignment, and phylogenetic tree prediction to provide a flexible and reproducible way of analyzing Sanger sequencing data in R.
- Designed to construct contigs from multiple reads with three well-designed S4 classes and two user-friendly R Shiny apps.
- Accepted at *Genome Biology and Evolution* (GBE) with minor revisions as a first-authored paper.
- Available on Bioconductor 3.12 Release with me as the main developer and package maintainer.

RNASeqR: an R package for automated two-group RNA-Seq analysis workflow

Taipei, Taiwan

✔ **PUBLISHED** | [PAPER_{LINK}](#), [BIOCONDUCTOR_{LINK}](#), [GITHUB_{LINK}](#), [ICIBM SLIDES_{LINK}](#)

Apr. 2018 - Dec. 2018

- **ADVISOR** : Prof. Eric Y. Chung_{LINK}, Prof. Tzu-Pin Lu_{LINK}
- **POSITION** : Research Student @ *Bioinformatics and Biostatistics Core Lab, Center of Genomic and Precision Medicine, NTU*
- **SKILLS** : RNA-seq data analysis, R package development, Linux shell programming
- Developed a two-group RNA-Seq R package with a six-step automated workflow including quality assessment, HISAT2 reads alignment, StringTie quantification, gene-level differential analyses, GO functional analysis, and KEGG pathway analysis.
- Gave a talk on RNASeqR in *International Conference on Intelligent Biology and Medicine (ICIBM 2019)* at Columbus, Ohio.
- Published in *IEEE/ACM Transactions on Computational Biology and Bioinformatics* (TCBB) as a first-authored regular paper.
- Available on Bioconductor 3.12 Release with me as the main developer and package maintainer.

Elution profile-based protein complexes inference algorithm

Taipei, Taiwan

✔ **IN PREPARATION** | [GITHUB_{LINK}](#)

Jul. 2020 - Present

- **ADVISOR** : Prof. Tsai, Huai-Kuang_{LINK}
- **POSITION** : Research Assistant @ *Institute of Information Science, Academia Sinica*
- **SKILLS** : Machine Learning, Convolutional neural network, Protein elution profile (cofractionation) data analysis
- Developed new software to improve EPIC, the current best elution profiles-based complexes prediction tool published in *Nature Methods*, which detects complexes from elution profiles (EPs) through clustering predicted protein-protein interactions (PPIs)
- Predicted PPIs by constructing a CNN model learning on raw protein EPs using 5-fold cross-validation. My model outperformed EPIC that applies random forests and support vector machine classifiers on self-selected scoring features by increasing AUC and AUPRC by approximately 10%. The work is in preparation with me as the **co-first author** and **lead developer**.

Vaccine cost-effectiveness evaluation simulation website

Taipei, Taiwan

✔ **IN PREPARATION** | [GITHUB_LINK](#) WEBSITE: [HTTP://140.112.136.49:8005](http://140.112.136.49:8005)

Jul. 2020 - Present

- **ADVISOR** : Prof. Tzu-Pin Lu [Link](#)
- **POSITION** : Research Assistant @ *Institute of Epidemiology and Preventive Medicine, NTU*
- **SKILLS** : Model Simulation, Markov chain model, Django web development, Django-Q task scheduler
- Built a mathematical Markov chain model to simulate numbers of people infected after being vaccinated by trivalent or quadrivalent inactivated influenza vaccines (TIV/QIV) and the cost-effectiveness with different vaccine coverage to help assess public health policies.

Electronic Health Record (EHR) phenotypes & genotypes extraction

Taipei, Taiwan

✔ **IN PREPARATION** | WEBSITE: [HTTP://140.112.30.198:8000/METAMAP/](http://140.112.30.198:8000/METAMAP/)

Jan. 2019 - Jun. 2019

- **ADVISOR** : Prof. Yun-Cheng Tsai [Link](#)
- **POSITION** : Research Assistant @ *College of Medicine AI team, NTU*
- **SKILLS** : Text-mining, Django web development, Online tool: MetaMap; Clinphen; Phenolyzer
- Developed a text-mining website to get the phenotype and genotype information from free text in electronic health records (EHR).

TB-NGS: *Mycobacterium tuberculosis* DNA sequencing analysis web server

Taipei, Taiwan

✔ **IN PREPARATION** | [GITHUB_LINK](#)

Jan. 2019 - Present

- **ADVISOR** : Prof. Eric Y. Chung [Link](#), Prof. Tzu-Pin Lu [Link](#)
- **POSITION** : Research Student @ *Bioinformatics and Biostatistics Core Lab, Center of Genomic and Precision Medicine, NTU*
- **SKILLS** : NGS pipeline development, Django web deployment, snakemake pipeline, Celery task distributor
- Built a *M. tuberculosis* reference-based genomes assembly website to compare their variant calling and drug-resistant results.

HONORS, AWARDS & CONFERENCE EXPERIENCE

- 2019 **Oral Presentation**, International Conference on Intelligent Biology and Medicine (ICIBM 2019) *Columbus, U.S.A.*
- 2019 **College Student Research Fellowship**, Fellowship from Taiwan Ministry of Science and Technology *Taipei, Taiwan*
- 2018 **Outstanding Research Prize (1st prize)**, NTU Centers of Genomics and Precision Medicine Contest *Taipei, Taiwan*
- 2017 **Elite Prize (1st prize)**, 2017 HackNTU, one of the biggest Hackathon in Taiwan (451 people) *Taipei, Taiwan*
- 2017 **Exhibition with Taipei City Government**, World Congress on Information Technology 2017 (WCIT 2017) *Taipei, Taiwan*

AWARDED PROJECT

Smart Bus Bell: 2017 HackNTU transportation 1st prize project

Taipei, Taiwan

[GITHUB_LINK](#), [VIDEO_LINK](#) (NATIONWIDE HACKATHON; 451 PEOPLE)

Aug. 2017

- Designed and Developed an user-end Android app in the three-person team to provide real-time bus information in Taipei.
- Presented with Taipei City Government on the topic of "Smart City" in the World Congress on Information Technology 2017 (WCIT).

TEACHING ASSISTANT EXPERIENCE

Department of Electrical Engineering, National Taiwan University

Taipei, Taiwan

EECS DESIGN AND IMPLEMENTATION COURSE TA (*cornerstone, self-tracking car*) [GITHUB_LINK](#), [VIDEO_LINK](#)

Feb. 2019 - Jun. 2019

- Designed lecture materials, developed final project program and scoring server for the final project contest. (lead developer)

Center for General Education, National Taiwan University

Taipei, Taiwan

DATA SCIENCE PROGRAMMING COURSE TA (*Data Science, R*) [GITHUB_LINK](#), [PHOTO_LINK](#)

Sep. 2018 - Jan. 2019

- Designed and taught interactive workshops explaining basics of Git, R Shiny application, and R package development.
- Designed programming assignment, prepared additional materials, graded assignments, and solved problems for students.

INTERNSHIP

Institute of Information Science, Academia Sinica

Taipei, Taiwan

SUMMER RESEARCH INTERN (*lncRNA, bioinformatics*) [CERTIFICATE_LINK](#), [PHOTO_LINK](#)

Jul. 2018 - Aug. 2018

- **ADVISOR** : Huai-Kuang Tsai [Link](#)
- Uncovered tandem repeat lncRNA and double-stranded DNA binding sites by comparing real experiment data to software predictions.

Institute for Information Industry

Taipei, Taiwan

SOFTWARE ENGINEER INTERN (*Apache Spark, cluster-computing, data preprocessing, visualization*)

Jan. 2018

- **ADVISOR** : Ching-Hao Mao [Link](#)
- Preprocessed and visualized data by writing Apache Spark code to help the team build a system to find insiders in the company.

LEADERSHIP

Student Association of Electrical Engineering, NTU

Taipei Taiwan

DIRECTOR OF NTUEE+ DEPARTMENT

Aug. 2018 - Jun. 2019

- Held workshops and interviewed outstanding alumni to connect them with Electrical Engineering undergraduates.