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Chang, Kai-Li

Education

06/2023-present	Baylor college of medicine, Houston, USA PhD student at Genetic and Genomics program
06/2020	National Cheng Kung University, Tainan, Taiwan **M.S.** in Department of Physiology, College of Medicine
06/2018	National Cheng Kung University, Tainan, Taiwan **B.S.** in Department of Life Sciences, College of Life Sciences

Research interests

- Apply machine learning techniques to uncover novel insights from genomics data
- Decipher molecular mechanism underlying tumor progression

Publications († Equal Contribution)

- Tzu-Chieh Lin†, Yen-Ling Liu†, Yu-Ting Liu†, Wan-Hsin Liu, Zong-Yan Liu, **Kai-Li Chang**, Chin-Yao Chang, Hung Chih Ni, Jia-Hsin Huang, and Huai-Kuang Tsai. TRIPBASE: a database for identifying the human genomic DNA and lncRNA triplexes. *NAR Genomics and Bioinformatics*. 2023 June ;5; lqad043.
- **Kai-Li Chang†**, Jia-Hong Chen†, Tzu-Chieh Lin, Jun-Yi Leu, Chen-Fu Kao, Jin Yung Wong, and Huai-Kuang Tsai. Short human eccDNAs are predictable through sequences. Briefings in Bioinformatics. 2023 April; bbad147.
- Ya-Chi Lin, Yun-Chin Wang, Yueh-Chun Lee, Hui-Hsuan Lin, **Kai-Li Chang**, Yu-Chieh Tai, and Kuei-Yang Hsiao. CircVIS: a platform for circRNA visual presentation. *BMC Genomics*. 2022 June; 22, 921.
- Ya-Chi Lin, Yueh-Chun Lee, **Kai-Li Chang,** and Kuei-Yang Hsiao. Analysis of common targets for circular RNAs. *BMC Bioinformatics*. 2019 July; 20, 372.

Research experiences

07/2021-present	**Research assistant**, Institute of Information Science, Academia Sinica - Advisor: Prof. Huai-Kuang Tsai - Project: Predict extrachromosomal circular DNAs (eccDNAs) using deep learning models - Implemented convolutional neural networks to predict extrachromosomal circular DNAs based on DNA sequences. The model achieved 80 % precision, recall, and accuracy. - Developed DeepCircle, a bioinformatics pipeline that includes data preprocessing, model training, inference, and data visualization using Python and shell script (https://github.com/bio-it-station/DeepCircle). - Project: Application of object detection algorithms for predicting genomic elements with variable lengths - Built a Faster R-CNN model that incorporates a feature pyramid network as a backbone model using PyTorch.

- o Applied multiprocessing in pipelines to reduce processing time by >10 fold.
  - o Applied noisy student and data augmentation techniques for training models using genomics data.
  - o Implemented a pipeline that optimizes memory usage to allow model training with 10 million DNA sequences.
- Maintain and upgrade a Linux computing cluster composed of 7 individual computers.

09/2020- 01/2021 **Research intern**, German Cancer Research Center (DKFZ)
- Advisor: Prof. Pavlo Lutsik
- Developed an R package that facilitates exploratory analysis and hypothesis generation using genomics and epigenomics data from The Cancer Genome Atlas
- Implemented a user-friendly graphical interface with R Shiny.
- Visualized high-dimensional data with t-SNE and UMAP

09/2018- 09/2020 **Master Student**, National Cheng Kung University, Department of Physiology
- Advisor: Prof. Shaw-Jenq Tsai
- Thesis: Functional study of protein arginine methyltransferase 4 (PRMT4) in colorectal cancer
- Performed overexpression and knockdown experiments in colorectal cancer cell lines to elucidate the roles of PRMT4 in tumor progression and drug resistance.
- Analyzed RNA-seq and ChIP-seq data to identify genes that PRMT4 transcriptionally regulates via histone modifications.
- Performed immunofluorescence to investigate the subcellular localization of PRMT4
- Received three awards due to excellent work on my master's thesis and academic excellence.

09/2016- 06/2018 **Undergraduate Researcher**, National Cheng Kung University, Department of Physiology
- Advisor: Prof. Shaw-Jenq Tsai
- Supervisor: Prof. Kuei-Yang Hsiao
- Streamlined bioinformatics pipelines for identification of circular RNAs from next-generation sequencing data
- Developed a tool for predicting functional impact of circular RNAs based on circular RNA-miRNA-mRNA association (see Publications).
- Identified circRNAs with coding potential (see Publications).
- Generated overexpression vectors for circular RNAs.

Extracurricular activity

06/2019 **Teaching assistant** of Physiology at the Department of Physiology, National Cheng Kung University
- Organized and taught human physiology experiments to medical students

02/2019 **Student representative** of Department of Physiology, National Cheng Kung University

06/2016 **Director** of training department of Life Sciences Student Association

- Coordinated workshops and lectures to improve the understanding of future career options for students in the department

01/2016 **Coordinator** of Life Sciences Camp, National Cheng Kung University
- Organized lectures and molecular biology experiments for teaching the high school students

Docent at the Bike Festival at National Cheng Kung University

03/2015   ●   Introduced the Department of Life Sciences to the general public

Honors and awards

6/2020 **Valedictorian** of the Department of Physiology, National Cheng Kung University

6/2020 **Honorary member**, awarded by the Phi Tau Phi scholastic honor society due to academic excellence (top 1%)

5/2020 **MOST-DAAD summer institute programme**, scholarship awarded by DAAD (the German Academic Exchange Service) and MOST (Ministry of Science and Technology, Taiwan) for a three-month internship in DKFZ

12/2019 **Outstanding poster award**, 2019 Multiomics and Precision Medicine Joint conference, TBSB (Taiwan Bioinformatics and Systems Biology Society)

11/2019 **Award of Excellence in poster presentation of thesis work**, Department of Physiology, National Cheng Kung University

03/2017 **College Student Research Scholarship**, award to undergraduate students with excellent research potential by MOST

12/2015 **Scholarship of Academic Excellence**, Department of Life Sciences, National Cheng Kung University

Skills and techniques

Programming languages: Python, R, Bash
Data analysis: NumPy, SciPy, Scikit-learn
Deep learning: PyTorch, Keras, TensorFlow
Machine learning: PCA, t-SNE, UMAP, hierarchical clustering, k-means clustering
Data visualization: seaborn, matplotlib, ggplot, R Shiny
Others: Linux, pip, Conda, Slurm, PostgreSQL
Laboratory techniques: PCR, molecular cloning, cell culture, western blot, immunofluorescence
Languages: Mandarin (native), English (advanced, TOEFL 107/120)

Conference Proceedings

- **Kai-Li Chang** and Kuei-Yang Hsiao (2019) "Analysis of common targets for circular RNAs." 2019 Multiomics and Precision Medicine Joint conference, TBSB (Taiwan Bioinformatics and Systems Biology Society), Tainan, Taiwan.
- **Kai-Li Chang**, Kuei-Yang Hsiao, Sunny Sun, and Shaw-Jenq Tsai (2017) "The development of a bioinformatics platform for identification of coding circRNAs in colorectal cancer." 2017 Conference on bioinformatics and bioindustrial experience sharing, Tainan, Taiwan.