

## Chang, Kai-Li

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### Education

- 08/2023- Baylor college of medicine, Houston, USA  
present 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
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### Research interests

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

- 07/2021- **Research assistant**, Institute of Information Science, Academia Sinica  
present
- Advisor: Prof. Huai-Kuang Tsai
  - Project: Predict extrachromosomal circular DNAs (eccDNAs) using deep learning models
    - o Implemented convolutional neural networks to predict extrachromosomal circular DNAs based on DNA sequences. The model achieved 80 % precision, recall, and accuracy.
    - o 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
    - o 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.

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### 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
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- 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
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## 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
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## 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)

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## 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.
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