# HE JIAXIN

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## Education

**City University of Hong Kong (CityU)** **Jul 2022 – Aug 2023**

*Master of Science in Biomedical Engineering.* *Hong Kong, China*

**Shanghai Jiao Tong University (SJTU)** **Sep 2017 – Jun 2021**

*Bachelor of Agronomy in Plant Science and Technology* *Shanghai, China*

## Publication

- SARS-CoV-2 immune recall response immunodominance and autoreactivity signature in autoimmune SLE patients and healthy people. (Under preparation)
- Zhenzhen Hao, **Jiaxin HE**, Junyong MA. MaxEnt modeling for predicting suitable habitats for wild ungulates: a case study of typical canyons in the Sanjiangyuan Nature Reserve of China. (Under Review)

## Experience

**School of Life Science, Peking University (PKU)** **Aug 2023 – Now**

*Research Assistant* *Beijing, China*

*Supervisor: Prof. CHEN Yuezhou*

- Constructed a pipeline to process raw high-throughput sequencing (NGS) data of bulk B cell receptor (BCR) repertoire by using R and Shell scripts and immunoinformatics database.
- Integrated and developed a R toolkit for downstream analysis of antibody and BCR repertoire, and applied to comparison of antibody repertoires between healthy and diseased cohort.
- Preprocessed single cell sequence (sc-seq) from 10X Single Cell Immune Profiling pipeline to obtain multimodal information like transcriptome, surface proteins, antigen specificity and BCR sequence of human lymphocytes.
- Analyzed single cell multimodal data of lymphocytes from both human and mouse with different immunological background, which ran from 10X & BD platform to explore the immune memory longevity.

**China Geological Survey** **Dec 2023 – Jun 2024**

*Research Assistant (Part time)* *Beijing, China*

*Supervisor: Dr. MA Junyong*

- Trained machine learning models, specificlly Maximum entropy (Maxent) and random forest (RF) model to predict optimal species distribution district by input of climatic environmental factors and species occurrences data.

## Research

3D Genomics Single Cell Hi-C Data Analysis with Multi-layer Networks

*Master Dissertation* Feb 2023 – Aug 2023

*Advisor: Prof. LI Shuaicheng, Department of Biomedical Engineering, CityU*

- Identified the basic 3D structure unit TAD of chromosomes by utilizing mature graph clustering algorithm to the simulated single cell high-throughput Chromosome conformation capture (Hi-C) data.
- Calculated the multilayer-graph mathematics properties of aggregating multi single cell Hi-C data to find potential biological significance.

Salt Tolerance Research on Transgenic Plants with Expression of Bacterial *Why* Genes

*Bachelor Thesis* Sep 2020 – Jun 2021

*Advisor: Prof. ZUO Kaijin, School of Agriculture and Biology, SJTU*

- Constructed the phylogenetic tree of bacterial *why* genes. Expressed the bacterial *why* gene in model plant Arabidopsis successfully and studied the salt tolerance of transgenic plants under different salt concentrations.

## Skills

Language: English (Fluent), Chinese (Native)

Coding Projects:

- R (Proficient): VDJ seq downstream analysis toolkit, Single cell analysis pipeline of BD platform.
- Python (Proficient): Lymphocytes information integration system, Multi-layer network analysis.
- Linux shell scripts (Proficient): quick Stand-alone IgBlast installation.
- Web Development (familiar): E-commerce backend development with Java, Lab Website design.