

# HE Jiaxin

Email: jaxonhe1021@outlook.com | Tel.: (86) 18621810890

## EDUCATION

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**City University of Hong Kong (CityU), Hong Kong, China** 08/2022 – 08/2023  
Master of Science in Biomedical Engineering  
**Shanghai Jiao Tong University (SJTU), Shanghai, China** 09/2017 – 06/2021  
Bachelor of Agriculture in Plant Science & Technology

## EXPERIENCE

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**Research Assistant** 08/2023 – now  
*School of Life Science, Peking University (PKU), Beijing, China.*  
*Advisor: Dr. CHEN Yuezhou*

- Engaged in immunology bioinformatics analysis, especially in B lymphocytes (B cell) of SARS-CoV-2 patients and vaccinators.
- Constructed high-quality B cell receptor (BCR) repertoire from raw Next Generation Sequencing platform illumine sequencing files. Analyzed the BCR repertoire by clonal relationship, somatic hypermutations, gene usage frequency etc. to study the antibody differences from different populations in response to SARS-CoV-2.
- Analyzed single cell multimodal data of cellular transcriptome (scRNA-seq), cell-surface proteins (CITE-seq and cell Hashtag) and antibody sequence (BCR repertoire) from 10X and BD single cell sequencing platform. Analyzed differences in antibody repertoire composition and gene expression across populations.

**Research Assistant (part-time)** 10/2023 – now  
*Institute of Geo-Environment Monitoring, China Geological Survey (CGS), Beijing, China*  
*Advisor: Dr. MA Junyong*

- Trained Maximum entropy model, random forest model and logistic regression model with data from 19 climatic environmental factors and species occurrences, to predict *Ungulate* species distribution (SDMs) in Tibet region.

## RESEARCH

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**3D Genomics Single Cell Hi-C Data Analysis with Multi-layer Networks**  
*Master Dissertation* 02/2023 – 08/2023  
*Advisor: Prof. LI Shuaicheng (Department of Biomedical Engineering, CityU)*

- Applied Spectral clustering algorithm on multilayer graphs to successfully identify the topological associated domain (TAD) region, the basic 3D structure unit of chromosomes, on simulated Hi-C data.
- Calculated the network properties of Hi-C data by constructing Hi-C data into the form of multilayer network to find potential biological significance.

**Salt Tolerance Research on Transgenic Plants with Expression of Bacterial *Why* Genes**  
*Bachelor Thesis* 09/2020 – 06/2021  
*Advisor: Prof. ZUO Kaijin (School of Agriculture and Biology, SJTU)*

- Expressed the bacterial *why* gene in model plant *Arabidopsis* successfully. Studied the salt tolerance of transgenic plants under different salt concentrations.

## ABILITIES

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Language: English (IELTS 6), Mandarin (Native)

Computer Skills: Python, R, Linux (Proficient in data analysis & bioinformatics), Java, html, css, sql (Familiar with web development), Adobe PS, AI, MS office (intermediate)