

CAREER PROFILE

Highly analytical and skilled Bioinformatics Analyst dealing with biology problems including translational control and tumor immunotherapy. Now, I'm a Ph.D candidate in Wuhan Univ, and a bioinformatics with 8 years of experience in computational biology, integration algorithms, and genomic datasets. Currently looking for a suitable position to contribute my knowledge of molecular biology and computer science in research for analyzing DNA and developing human diseases cures.

EXPERIENCES

Bioinformatic researcher

July 2016 - 2019 July

BGI research

Being a bioinformatics analyst, I collaborated with my colleagues to research in rubber project. I finished the re-sequencing section independently. I also used WDL and python to construct automatic pipeline in WGS and WES for cancer treatment. I was also involved in the pre-development work of the spatial transcriptome. As a lecturer of BGI College, I am also responsible for the training of college interns from WHU, HUST and HZAU in Wuhan.

- Analysis of cooperative projects
- Automatic bioinformatic pipelines
- Training of college interns

Bioinformatics and AI

July 2019 - September 2020

Genoimmune, BGI

In the department of bioinformatic in Genoimmune, my work mainly includes deep learning model building for neoantigen affinity prediction. Meanwhile, I also update the EPIP (epitope presentation integrated prediction) software.

- Building deep learning model in neoantigen affinity prediction
- Update EPIP, a machine learning software for MHC affinity prediction

PROJECTS

The following are some of the projects I have participated in, the details are as follows:

Multi-omics - Multi-omics maps of cotton fibre reveal epigenetic basis for staged single-cell differentiation.

Rubber Tree - A responsive website template designed to help web developers/designers market their services.

EPIP - EPIP: MHC-I epitope prediction integrating mass spectrometry derived motifs and tissue-specific expression profiles

Multi-Pan - A comprehensive deep learning model for MHC epitope prediction.

Automatic pipeline construction - Automatic pipeline construction in spatial transcriptome

PUBLICATIONS

I list some publications in this section. Described below.

- Multi-omics maps of cotton fibre reveal epigenetic basis for staged single-cell differentiation
Maojun Wang, Pengcheng Wang, Lili Tu, Sitao Zhu, ..., Xianlong Zhang
Nucleic Acids Res. 2016
- GhJAZ2 negatively regulates cotton fiber initiation by interacting with the R2R3-myb transcription factor GhMYB25-like
Haiyan Hu, Xin He, Lili Tu, Longfu Zhu, Sitao Zhu, Zonghe Ge, Xianlong Zhang
Plant J. 2016
- The Chromosome-Based Rubber Tree Genome Provides New Insights into Spurge Genome Evolution and Rubber Biosynthesis
Liu, Jin et al.
Molecular Plant. 2019
- Identification of 12 cancer types through genome deep learning
Sun, Y., Zhu, S., Ma, K. et al.
Sci Rep. 2019
- EPIP: MHC-I epitope prediction integrating mass spectrometry derived motifs and tissue-specific expression profiles
Weipeng Hu et al.



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📄 Resume PDF

EDUCATION

Ph.D candidate in biology

Wuhan University

September 2020 - Present

MSc in Crop genetics and breeding

Huazhong Agricultural University

September 2013 - June 2016

BSc in Agriculture

Yangtze University

September 2009 - June 2013

LANGUAGES

Chinese (Native)

English (Professional)

INTERESTS

Climbing

Basketball

Music

ABOUT THEMES

How to use?

Star

SKILLS & PROFICIENCY

