👤 CAREER PROFILE

Highly analytical and skilled bioinformatics analyst dealing with biology problems including translational control and tumor immunotherapy. Now, I'm a postdoctoral researcher in Wuhan University, and a bioinformatics with 9 years of experience in computational biology, intergration algorithms, and genomic datasets. Currently I am exploring statin resistance mechanisms in song lab 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 fininshed 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 bioinfomatic 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

POST-DOC   September 2024 - Now
WHU, college of life sciences

Using bioinformatics and AI tech to investigate lipid metabolism in song lab.

- Building multi-omics and deep learning model in lipid and cholesterol metabolism.
- Statins resistance mechanism

📋 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 - The Chromosome-Based Rubber Tree Genome Provides New Insights into Spurge Genome Evolution and Rubber Biosynthesis.

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

Genomic feature extraction - Genomic feature extraction in bioinformatics

Human lipid metabolism - Human multi-omics analysis

📄 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, Lin Zhang, Zhonghua Li, Qinghua Zhang, Daojun Yuan, 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

Sitao Zhu
Ph.D

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📞 130 7277 4610

🕐 China/Wuhan

🌐 https://sitaoz.github.io/

💼 zhusitao

💻 SitaoZ

🛒 zhusitao

🐦 @zhusitao

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📄 Resume PDF

EDUCATION

Ph.D in Biology
Wuhan University
September 2020 - July 2024

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 THEME

How to use?

Star

- The Chromosome-Based Rubber Tree Genome Provides New Insights into Spurge Genome Evolution and Rubber Biosynthesis

  Liu, Jin et al.

  Mol Plant. 2019

- Identification of 12 cancer types through genome deep learning

  Yingshuai Sun, Sitao Zhu, Kailong Ma, Weiqing Liu, Yao Yue, Gang Hu, Huifang Lu & Wenbin Chen.

  Sci Rep. 2019

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

  Weipeng Hu et al.

  biorxiv. 2020

- Plant HEM1 specifies a condensation domain to control immune gene translation

  Yulu Zhou, Ruixia Niu, Zhijuan Tang, Rui Mou, Zhao Wang, Sitao Zhu, Hongchun Yang, Pingtao Ding & Guoyong Xu.

  Nat. Plants. 2023

- RNAirport: a deep neural network-based database characterizing representative gene models in plants

  Sitao Zhu, Shu Yuan, Ruixia Niu, Yulu Zhou, Zhao Wang, Guoyong Xu.

  J. Genet. Genomics. 2024

- Genetically-encoded targeted protein degradation technology to remove endogenous condensation-prone proteins and improve crop performance

  Ming Luo, Sitao Zhu, Hua Dang, Qing Wen, Ruixia Niu, Jiawei Long, Zhao Wang, Yongjia Tong, Yuese Ning, Meng Yuan & Guoyong Xu.

  Nat Commun, 2025.

🔧 SKILLS & PROFICIENCY

Biology & Bioinformatics

Python & Django

Linux

HTML5 & CSS

Adobe Illustrator

R & RStudio