

# SHIXIANG WANG

PhD student of Bioinformatics at [Xue-Song Liu lab, ShanghaiTech University](#), currently working on cancer genomics and immunotherapy biomarker by biostatistic skills. I am a fan of R (particularly), Python and Golang. I love open source and open science. I have developed many R package and shared much experience about coding and data analysis on many platforms.

For some details,

- I have advanced experience in using R and Shell for data preprocessing, data cleaning and data interpretation.
- I have moderate experience in using R for statistical modeling and data visualization.
- I master developing pure R packages and have a little experience in Python package, R Shiny and Rcpp development.
- I can combine multiple programming languages/tools to create analysis pipeline. I know how to use Docker to package analysis environment and enhance reproducible research.
- I can process raw genomic data and analyze them. I have moderate experience in somatic variant calling (including SNV, INDEL and CNV), differential expression analysis and enrichment analysis.
- I know how to do machine learning (including deep learning) and have applied some technologies to my projects.
- I like to write with R Markdown (including Markdown) and share my knowledge to others in many ways.
- I love to contribute open-source scientific tool development (e.g. [maftools](#), [forestmodel](#)).
- Last not but least, I enjoy learning and researching.



## CONTACT

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- 📄 [github.com/ShixiangWang](https://github.com/ShixiangWang)
- 🔗 [ShixiangWang.github.io](https://ShixiangWang.github.io)
- 🎧 [elegant-r](#)

## 🎓 EDUCATION

2021  
|  
2016

### PhD., Biology

ShanghaiTech University

📍 Shanghai, CN

### PhD., Biology

University of Chinese Academy of Sciences

📍 Beijing, CN

### PhD., Biology

Shanghai Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences

📍 Shanghai, CN

2016  
|  
2012

### B.E., Biomedical Engineering

University of Electronic Science and Technology of China

📍 Chengdu, CN

## SELECTED TOOLS

### Bioinformatics

- [sigminer](#)
- [sigflow](#)
- [ezcox](#)
- [metawho](#)
- [UCSCXenaTools](#)
- [UCSCXenaShiny](#)
- [DoAbsolute](#)
- [IDConverter](#)
- [neopeptides](#)
- [install\\_GISTIC](#)

### Fun

- [tinyscholar](#)
- [contribution](#)
- [loon](#)
- [R search extension](#)
- [flymaps](#)

*Last updated on 2020-11-22.*



## PUBLICATIONS

2020

### **Sigflow: an automated and comprehensive pipeline for cancer genome mutational signature analysis**

*Bioinformatics* (2020)

• Wang, S., Tao, Z., Wu, T., & Liu, X. S. \*

### **Can tumor mutational burden determine the most effective treatment for lung cancer patients?**

*LUNG CANCER MANAGEMENT* (2020)

• Wang, S., He, Z., Wang, X., Li, H., Wu, T., Sun, X., ... & Liu, X. S. \*

2019

### **Antigen presentation and tumor immunogenicity in cancer immunotherapy response prediction**

*Elife* (2019)

• Wang, S., He, Z., Wang, X., Li, H., & Liu, X. S. \*

### **The predictive power of tumor mutational burden in lung cancer immunotherapy response is influenced by patients' sex**

*International journal of cancer* (2019)

• Wang, S., Zhang, J., He, Z., Wu, K., & Liu, X. S. \*

### **Ras Downstream Effector GGCT Alleviates Oncogenic Stress**

*iScience* (2019)

• He, Z. #, Wang, S. #, Shao, Y. #, Zhang, J. #, Wu, X., Chen, Y., ... & Liu, X. S. \*

### **Sex Differences in Cancer Immunotherapy Efficacy, Biomarkers, and Therapeutic Strategy**

*Molecules* (2019)

• Wang, S. #, Cowley, L. A. #, & Liu, X. S. \*

### **The UCSCXenaTools R package: a toolkit for accessing genomics data from UCSC Xena platform, from cancer multi-omics to single-cell RNA-seq**

*Journal of Open Source Software* (2019)

• Wang, S., & Liu, X. S. \*

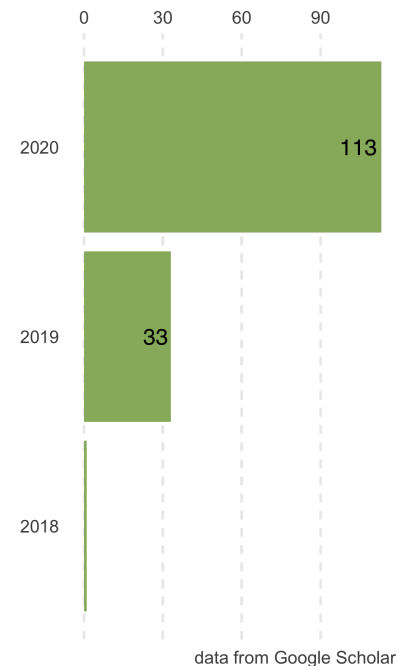
2018

### **APOBEC3B and APOBEC mutational signature as potential predictive markers for immunotherapy response in non-small cell lung cancer**

*Oncogene* (2018)

• Wang, S. #, Jia, M. #, He, Z., & Liu, X. S. \*

- Citation = 150
- H-index = 4
- I10-index = 4





## CONFERENCE PROCEEDINGS

2020

**Sigflow: an automated and comprehensive pipeline for cancer genome mutational signature analysis**

BioC Asia 2020

📍 Shanghai, CN

• Wang, S., Tao, Z., Li, H. M., Wu, T., & Liu, X. S. \*

2019

**Antigen presentation and tumor immunogenicity in cancer immunotherapy response prediction**

BioForum 2019 at ShanghaiTech University

📍 Shanghai, CN

• Wang, S., He, Z., Wang, X., Li, H., & Liu, X. S. \*