

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
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- 🗣️ [elegant-r](#)

EDUCATION

2021
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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
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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 2020-10-02.



PUBLICATIONS

2020

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

LUNG CANCER MANAGEMENT 8.4 (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 8 (2019): e49020

• 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 145.10 (2019): 2840-2849.

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

Ras Downstream Effector GGCT Alleviates Oncogenic Stress

iScience 19 (2019): 256-266

• 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 24.18 (2019): 3214

• 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 4.40 (2019): 1627.

• Wang, S., & Liu, X. S. *

2018

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

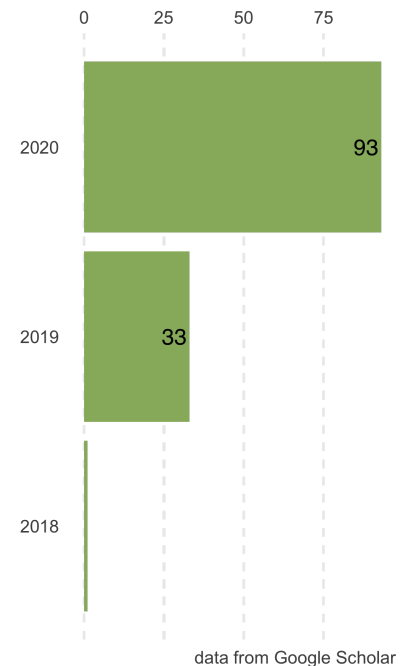
Oncogene 37.29 (2018): 3924-3936

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

• Citation = 130

• H-index = 4

• I10-index = 4



CONFERENCE PROCEEDINGS

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. *