Shixiang Wang
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Research summary

I am a computational biologist working on cancer genomics. I use bioinformatics skills to decode the unfound patterns in cancer, and explore biomarkers for explaining the cancer heterogeneity and predicting the efficacy of cancer treatments, mainly in immunotherapy.

I am passionate about open science and developing open-source analysis toolkits. Because of this, currently I am a community member of Openbiox[1], rOpenSci[2] and Bioconductor[3]. My long-term goal in academic field is being a master in a subfield of cancer bioinformatics and trying my best to continually boost the open-source bioinformatics ecosystem in China.

Research positions

2021 — present **Postdoctoral Researcher**, Experiment Research Department, Sun Yat-sen University Cancer Center[4]
Supervisor: Prof. Rui-Hua Xu[5]; Cooperate with Prof. Qi Zhao[6]

Education

2016 — 2021 **PhD in Cancer Biology**, ShanghaiTech University[7] & Shanghai Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences[8]
Supervisor: Prof. Xue-Song Liu[9]

2012 — 2016 **B.E. in Biomedical Engineering**, University of Electronic Science and Technology of China
Supervisor: Prof. Yang Xia

Major grants and funding

2022 — 2023 **China Postdoctoral Science Foundation**[10] (¥ 80k), General Project

2024 — 2026 **National Natural Science Foundation of China**[11] (¥ 300k), Young Scientists Fund

Awards & honours

2021 **2021 Outstanding Graduate Award**, ShanghaiTech University

2020 **National Scholarship for Doctoral Students**, ShanghaiTech University

ShanghaiTech University Class A Postgraduate Academic Scholarship, ShanghaiTech University

Publications

Journal articles (fully reviewed, † for co-first, * for corresponding)

2023 J19 **Unveiling the interplay between mutational signatures and tumor microenvironment: a pan-cancer analysis**
L. Luo, S. Li, C. Wei, J. Ma, L. Qian, Y. Chen, S. Wang*, Q. Zhao*
Frontiers in Immunology **(JCR Q1, CAS Q2, IF: 8.8)**

J18 **Accurate prediction of pan-cancer types using machine learning with minimal number of DNA methylation sites**
W. Ning, T. Wu, C. Wu, S. Wang, Z. Tao, G. Wang, X. Zhao, K. Diao, J. Wang, J. Chen, F. Chen, X. Liu
Journal of Molecular Cell Biology **(JCR Q1, CAS Q2, IF: 8.4)**

J17 **The repertoire of copy number alteration signatures in human cancer**
Z. Tao†, S. Wang†, C. Wu†, T. Wu, X. Zhao, W. Ning, G. Wang, J. Wang, J. Chen, K. Diao, F. Chen, X. Liu
Briefings in Bioinformatics **(JCR Q1, CAS Q2, IF: 14.0)**

2022 J16 **Hiplot: a comprehensive and easy-to-use web service for boosting publication-ready biomedical data visualization**
J. Li†, B. Miao†, S. Wang†, W. Dong†, H. Xu†, C. Si†, W. Wang, S. Duan, J. Lou, Z. Bao, H. Zeng, Z. Yang, W. Cheng, F. Zhao, J. Zeng, X. Liu, R. Wu, Y. Shen, Z. Chen, S. Chen, M. Wang, H. Consortium
Briefings in Bioinformatics **(JCR Q1, CAS Q2, IF: 14.0)**

J15 **Deciphering clonal dynamics and metastatic routines in a rare patient of synchronous triple-primary tumors and multiple metastases with MPTevol**
Q. Chen, Q. Wu, Y. Rong, S. Wang, Z. Zuo, L. Bai, B. Zhang, S. Yuan, Q. Zhao
Briefings in Bioinformatics **(JCR Q1, CAS Q2, IF: 14.0)**

J14 **Quantification of neoantigen-mediated immunoediting in cancer evolution**
T. Wu, G. Wang, X. Wang, S. Wang, X. Zhao, C. Wu, W. Ning, Z. Tao, F. Chen, X. Liu
Cancer Research **(JCR Q1, CAS Q1, IF: 13.3)**

J13 **UCSCXenaShiny: an R/CRAN package for interactive analysis of UCSC Xena data**
S. Wang†, Y. Xiong†, L. Zhao†, K. Gu†, Y. Li, F. Zhao, J. Li, M. Wang, H. Wang, Z. Tao, T. Wu, Y. Zheng, X. Li, X. Liu
Bioinformatics **(JCR Q1, CAS Q3,, IF: 7.3)**

2021 J12 **Ggct (γ-glutamyl cyclotransferase) plays an important role in erythrocyte antioxidant defense and red blood cell survival**
Z. He, X. Sun, S. Wang, D. Bai, X. Zhao, Y. Han, P. Hao, X. Liu
British Journal of Haematology **(JCR Q1, CAS Q2, IF: 8.6)**

J11 **Copy number signature analysis tool and its application in prostate cancer reveals distinct mutational processes and clinical outcomes**
S. Wang, H. Li, M. Song, Z. Tao, T. Wu, Z. He, X. Zhao, K. Wu, X. Liu
PLoS Genetics **(JCR Q1, CAS Q2, IF: 8.2)**

J10 **Pan-cancer noncoding genomic analysis identifies functional CDC20 promoter mutation hotspots**
Z. He†, T. Wu†, S. Wang†, J. Zhang†, X. Sun, Z. Tao, X. Zhao, H. Li, K. Wu, X. Liu
iScience **(JCR Q1, CAS Q2, IF: 6.1)**

J09 **Association of CSMD1 with Tumor Mutation Burden and Other Clinical Outcomes in Gastric Cancer**

X. Wang†, S. Wang†, Y. Han, M. Xu, P. Li, M. Ke, Z. Teng, P. Huang, Z. Diao, Y. Yan, Q. Meng, Y. Kuang, W. Zheng, H. Liu, X. Liu, B. Jia

International Journal of General Medicine **(JCR Q2, CAS Q4, IF: 2.5)**

2020 J08 **Sigflow: an automated and comprehensive pipeline for cancer genome mutational signature analysis**

S. Wang, Z. Tao, T. Wu, X. Liu

Bioinformatics **(JCR Q1, CAS Q3, IF: 7.3)**

2019 J07 **Can tumor mutational burden determine the most effective treatment for lung cancer patients?**

S. Wang, Z. He, X. Wang, H. Li, T. Wu, X. Sun, K. Wu, X. Liu

Lung Cancer Management **(IF: 2.8)**

J06 **Antigen presentation and tumor immunogenicity in cancer immunotherapy response prediction**

S. Wang, Z. He, X. Wang, H. Li, X. Liu

eLife **(JCR Q1, CAS Q1, IF: 9.3)**

J05 **The predictive power of tumor mutational burden in lung cancer immunotherapy response is influenced by patients' sex**

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

International Journal of Cancer **(JCR Q1, CAS Q1, IF: 7.4)**

J04 **Ras downstream effector GGCT alleviates oncogenic stress**

Z. He†, S. Wang†, Y. Shao†, J. Zhang†, X. Wu, Y. Chen, J. Hu, F. Zhang, X. Liu

iScience **(JCR Q1, CAS Q2 IF: 6.1)**

J03 **Sex Differences in Cancer Immunotherapy Efficacy, Biomarkers, and Therapeutic Strategy**

S. Wang†, L. An Cowley†, X. Liu

Molecules **(JCR Q2, CAS Q2 IF: 4.9)**

J02 **The UCSCXenaTools R package: a toolkit for accessing genomics data from UCSC Xena platform, from cancer multi-omics to single-cell RNA-seq**

S. Wang, X. Liu

Journal of Open Source Software

2018 J01 **APOBEC3B and APOBEC mutational signature as potential predictive markers for immunotherapy response in non-small cell lung cancer**

S. Wang†, M. Jia†, Z. He, X. Liu

Oncogene **(JCR Q1, CAS Q1, IF: 9.9)**

The journal impact factors mentioned above are derived from the maximum values in the history of journal impact factors. Journal impact factors, Chinese Academy of Sciences (CAS) categorization, and JCR categorization were all uniformly updated on 2023.11.02. For future publications that are included, I will update them selectively and will no longer perform uniform updates on all publications.

Preprints (not reviewed, † for co-first, * for corresponding)

2023 P5 **TCCIA: A Comprehensive Resource for Exploring CircRNA in Cancer Immunotherapy**
S. Wang†, Y. Xiong†, Y. Zhang†, H. Wang, M. Chen, J. Li, P. Luo, Y. Luo, M. Hecht, B. Frey, U. S Gaipl, X. Li, Q. Zhao, H. Ma, J. Zhou
bioRxiv

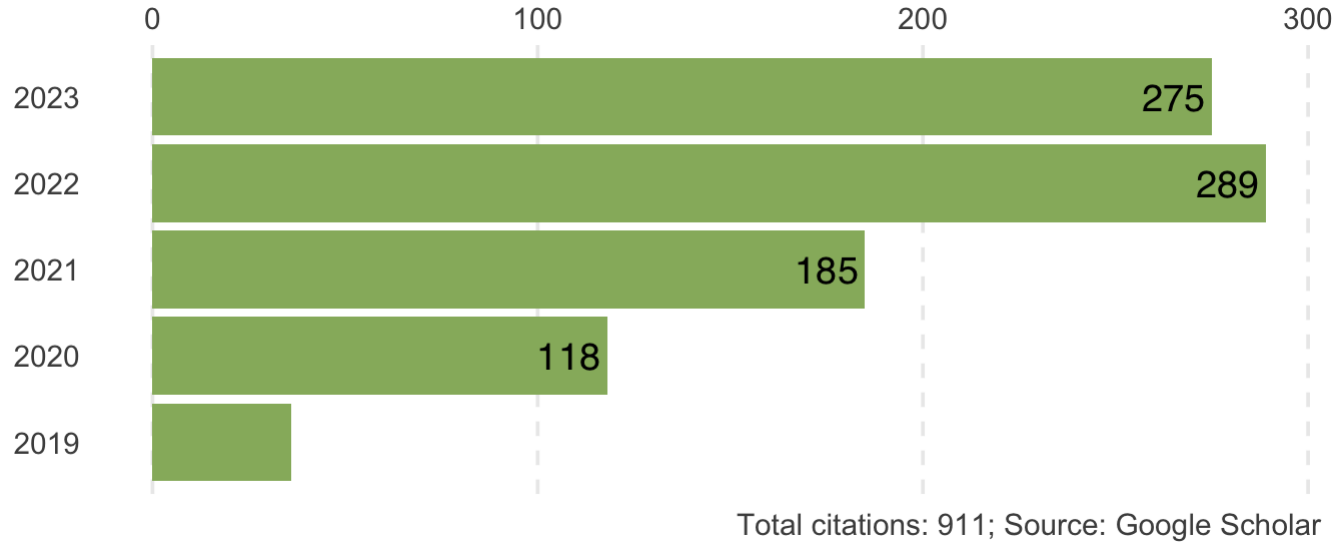
2022 P4 **The repertoire of copy number alteration signatures in human cancer**
Z. Tao†, S. Wang†, C. Wu†, T. Wu, X. Zhao, W. Ning, G. Wang, J. Wang, J. Chen, K. Diao, F. Chen, X. Liu
bioRxiv

P3 **Onlinemeta: A Web Server For Meta-Analysis Based On R-shiny**
Y. Yi, A. Lin, C. Zhou, J. Zhang*, S. Wang*, P. Luo*
bioRxiv

2021 P2 **ezcox: An R/CRAN Package for Cox Model Batch Processing and Visualization**
S. Wang, X. Liu, J. Li, Q. Zhao
arXiv

2020 P1 **Revisiting neoantigen depletion signal in the untreated cancer genome**
S. Wang†, X. Wang†, T. Wu†, Z. He, H. Li, X. Sun, X. Liu
bioRxiv

Cited by



Total citations: 911; Source: Google Scholar

Talks

2020 T1 **BioC Asia 2020**[12], Online
Sigflow: an automated and comprehensive pipeline for cancer genome mutational signature analysis[13]

Poster presentations

2019 P1 **ShanghaiTech University, BioForum 2019**, Shanghai, China
Antigen presentation and tumor immunogenicity in cancer immunotherapy response prediction

2020 P2 **BioC Asia 2020**[14]
Sigflow: an automated and comprehensive pipeline for cancer genome mutational signature analysis[15]

Teaching experience

2019 **Teaching assistant, Cancer Biology**, ShanghaiTech University
Teacher: Xue-Song Liu

2023 **Supervisor**, Open Source Promotion Plan 2023[16]
Student: Shensuo Li

Service

2021 — present **Review Editor in in Cancer Immunity and Immunotherapy** Frontiers[17]

2021 — present **Director of Bioinformatics Weekly Project**[18] Openbiox, for curation and sharing of bioinformatics knowledge and news

2019 — present **Reviewer** Briefings in Bioinformatics[19], Journal of Translational Medicine[20], STAR Protocols[21], Frontiers in Immunology[22], Frontiers in Oncology[23], Frontiers in Cell and Developmental Biology[24]

Links

1. https://github.com/openbiox↩
2. https://ropensci.org/↩
3. https://www.bioconductor.org/↩
4. http://english.sysucc.org.cn/↩
5. http://english.sysucc.org.cn/info_19.aspx?itemid=154↩
6. https://seqworld.com/↩
7. https://www.shanghaitech.edu.cn/↩
8. http://cemcs.cas.cn/↩
9. https://slst.shanghaitech.edu.cn/lxs_en/main.htm↩
10. https://jj.chinapostdoctor.org.cn/website/index.html↩
11. https://www.nsfc.gov.cn/↩
12. https://biocasia2020.bioconductor.org/↩
13. https://www.youtube.com/watch?v=nzAxPDTznm4↩

14. https://biocasia2020.bioconductor.org/↩
15. https://f1000research.com/posters/9-1217↩
16. https://summer-ospp.ac.cn/org/prodetail/2351d0245?lang=zh&list=pro↩
17. https://www.frontiersin.org/↩
18. https://openbiox.github.io/weekly/↩
19. https://academic.oup.com/bib↩
20. https://translational-medicine.biomedcentral.com/↩
21. https://www.cell.com/star-protocols/home↩
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24. https://www.frontiersin.org/journals/cell-and-developmental-biology↩