Shixiang Wang
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ORCID

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: Rui-Hua Xu[5]

Education

2016 — 2021 **PhD in Cancer Biology**, ShanghaiTech University & Shanghai Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences
Supervisor: Xue-Song Liu[6]

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

Major grants and funding

2022 — 2023 **General Project, China Postdoctoral Science Foundation**[7] (¥ 80k), Developing new method for ecDNA identification and exploring its biomarker potential

Awards & honours

2021 **2021 Outstanding Graduate Award of Shanghai**, 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)

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 **(representative work)**

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

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

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 **(representative work)**

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

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 **(representative work)**

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

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

2020 J08 **Sigflow: an automated and comprehensive pipeline for cancer genome mutational signature analysis**
S. Wang, Z. Tao, T. Wu, X. Liu
Bioinformatics **(representative work)**

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

J06 **Antigen presentation and tumor immunogenicity in cancer immunotherapy response prediction**
S. Wang, Z. He, X. Wang, H. Li, X. Liu
eLife **(representative work)**

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 **(representative work)**

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

J03 **Sex Differences in Cancer Immunotherapy Efficacy, Biomarkers, and Therapeutic Strategy**
S. Wang†, L. An Cowley†, X. Liu
Molecules

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 **(representative work)**

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

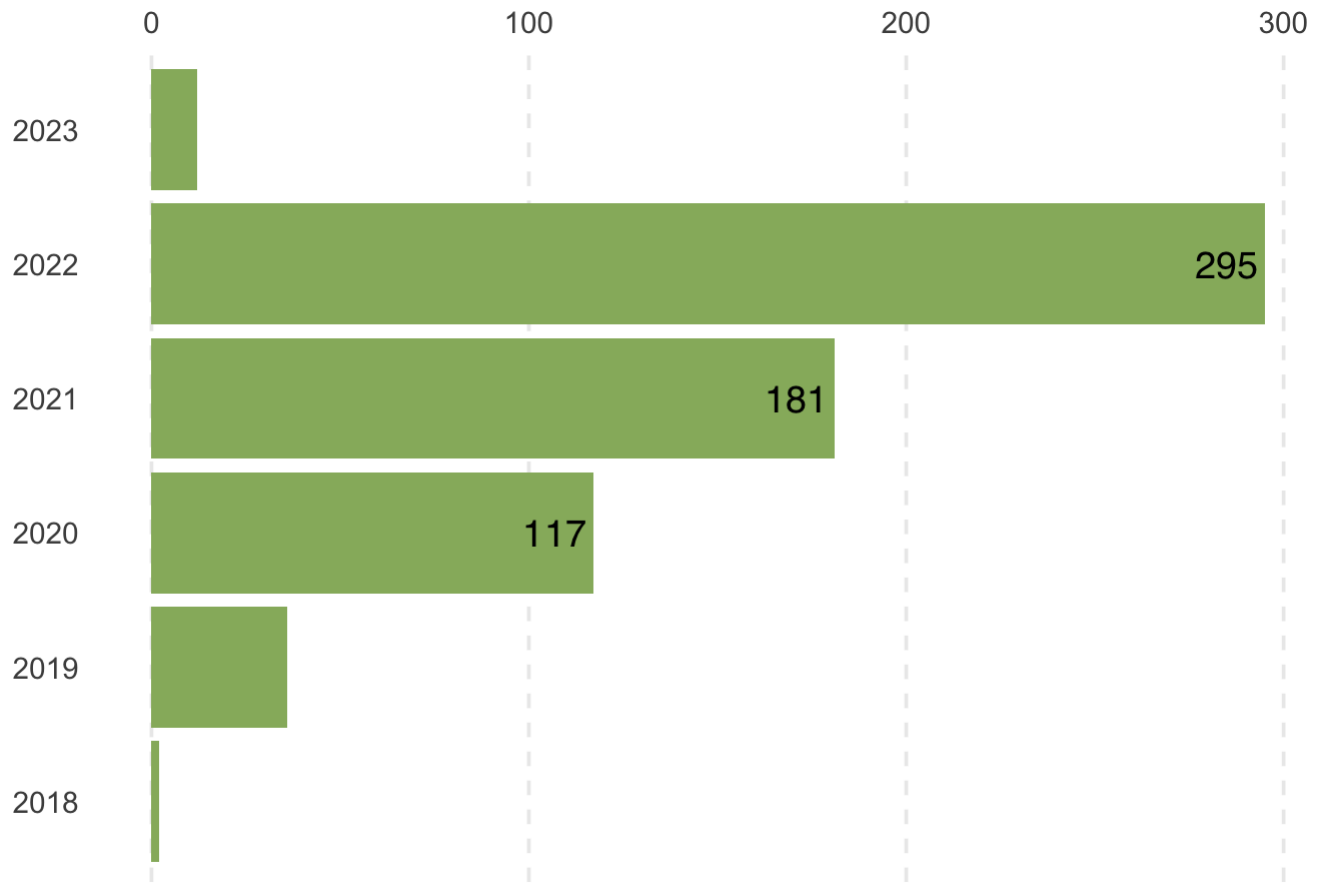
2022 P3 **Onlinemeta: A Web Server For Meta-Analysis Based On R-shiny**
Y. Yi, A. Lin, C. Zhou, J. Zhang#, S. Wang#, P. Luo#
bioRxiv

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

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



data from Google Scholar (https://scholar.google.com/citations?user=FvNp0NkAAAAJ)

Talks

2020 T1 **BioC Asia 2020**[8], Online
Sigflow: an automated and comprehensive pipeline for cancer genome mutational signature analysis[9]

Poster presentations

2020 P1 **BioC Asia 2020**[10]
Sigflow: an automated and comprehensive pipeline for cancer genome mutational signature analysis[11]

2019 P2 **ShanghaiTech University, BioForum 2019**, Shanghai, China
Antigen presentation and tumor immunogenicity in cancer immunotherapy response prediction

Teaching experience

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

Service

2019 — present **Reviewer** Briefings in Bioinformatics[12], Frontiers in Immunology[13], Frontiers in Oncology[14], Frontiers in Cell and Developmental Biology[15]

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://slst.shanghaitech.edu.cn/lxs_en/main.htm↩
7. https://jj.chinapostdoctor.org.cn/website/index.html↩
8. https://biocasia2020.bioconductor.org/↩
9. https://www.youtube.com/watch?v=nzAxPDTznm4↩
10. https://biocasia2020.bioconductor.org/↩
11. https://f1000research.com/posters/9_1217_
12. https://academic.oup.com/bib↩
13. https://www.frontiersin.org/journals/immunology↩
14. https://www.frontiersin.org/journals/oncology↩
15. https://www.frontiersin.org/journals/cell_and_developmental_biology_