Shixiang Wang

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Education

- 2016.09 ~ Present, Ph.D Student, Cancer Biology (focusing on cancer informatics), ShanghaiTech. University, Shanghai, China
- 2012.09 ~ 2016.07, B.E. Biomedical Engineering,
  University of Electronic Science and Technology of China, Chengdu, China

Professional skills

- Programming levels:
  - R ⋆ ⋆ ⋆ ⋆ ⋆
  - Shell ⋆ ⋆ ⋆
  - Python ⋆ ⋆ ⋆
  - Golang ⋆⋆
- Data analysis. I have advanced experience in using R and Shell for data preprocessing, data cleaning and data interpretation.
- Statistics. I have moderate experience in using R for statistical modeling and data visualization.
- Package/pipeline development. I master developing pure R packages and have a little experience in Python package and R Shiny development. I can combine multiple languages to create analysis pipeline.
- Genomic analysis. 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.

- Clinical analysis. I know how to construct survival models and interpret results.
- Machine learning. I know how to do machine learning (including deep learning) and have applied some technologies to my projects.
- Writing. I like to write with R Markdown (including Markdown) and share my knowledge to others in many ways (e.g. GitHub Issue, Jianshu, Wechat, and etc.).

Developments

- **sigminer** (https://cran.r-project.org/package=sigminer): mutational signature analysis and visualization in R.
- **ezcox** (https://cran.r-project.org/package=ezcox): operate a batch of univariate or multivariate Cox models and return tidy result.
- **DoAbsolute** (https://github.com/ShixiangWang/DoAbsolute): automate ABSOLUTE calling for multiple samples in parallel way.
- **metawho** (https://cran.r-project.org/package=metawho): simple R implementation of "Meta-analytical method to Identify Who Benefits Most from Treatments".
- **UCSCXenaTools** (https://cran.r-project.org/package=UCSCXenaTools): an R package for downloading and exploring data from UCSC Xena data hubs.
- **UCSCXenaShiny** (https://cran.r-project.org/package=UCSCXenaShiny): a Shiny based on UCSCXenaTools.
- **contribution** (https://cran.r-project.org/package=contribution): generate contribution table for credit assignment in a project.
- **loon** (https://pypi.org/project/loon/): a Python toolkit for operating remote host based on SSH.
- **sync-deploy** (https://github.com/ShixiangWang/sync-deploy): a Shell toolkit for deploying script/command task on a remote host, including up/download files, run script and more.

More activities about my development and contribution can be viewed at github.com/ShixiangWang.

Publications

Total citations: 73. (Data source: Google Scholar. Update time: 2020-05-28)

- **Wang, S.**, He, Z., Wang, X., Li, H., & Liu, X. S. (2019). Antigen presentation and tumor immunogenicity in cancer immunotherapy response prediction. *eLife*, 8, e49020. https://doi.org/10.7554/eLife.49020 (PDF)
- **Wang, S.**, He, Z., Wang, X., Li, H., Wu, T., Sun, X., … & Liu, X. S. (2019). Can tumor mutational burden determine the most effective treatment for lung cancer patients?. *Lung Cancer Management*. https://doi.org/10.2217/lmt-2019-0013 (PDF)
- **Wang, S.**, Cowley, L. A., & Liu, X. S. (2019). Sex differences in Cancer immunotherapy efficacy, biomarkers, and therapeutic strategy. *Molecules*, 24(18), 3214. (PDF)
- **Wang, S.** & Liu, X. S. (2019). 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), 1627, https://doi.org/10.21105/joss.01627 (PDF)
- He, Z., **Wang, S.**, Shao, Y., Zhang, J., Wu, X., Chen, Y., … & Liu, X. S. (2019). Ras downstream effector GGCT alleviates oncogenic stress. *iScience*. (PDF)
- **Wang, S.**, Zhang, J., He, Z., Wu, K., & Liu, X. S. (2019). The predictive power of tumor mutational burden in lung cancer immunotherapy response is influenced by patients' sex. *International journal of cancer*, 145(10), 2840-2849. (PDF)
- **Wang, S.**, Jia, M., He, Z., & 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), 3924-3936. (PDF)