

YUE SHI PH.D.

I am a highly accomplished bioinformatician with extensive academic experience in developing and executing complex DNA/RNA research projects. My expertise in bioinformatics and data science is demonstrated through a strong publication record in genomics with lead authorship, presentations at prestigious conferences, and my role as a peer reviewer for several respected academic journals. As a bioinformatics scientist, I am interested in all aspects of genomics and bioinformatics, with a particular focus on evolution, liquid biopsies, interpretable machine learning, and the development of automated, reproducible NGS workflows.

EDUCATION

- | | | |
|------|---|------------------|
| 2019 | ● Ph.D., Biology University of Washington | 📍 Seattle, WA |
| 2013 | ● M.S., Ecology Ocean University of China | 📍 Qingdao, China |
| 2010 | ● B.S., Biological Sciences Ocean University of China | 📍 Qingdao, China |

RESEARCH EXPERIENCE

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| Current 2022 | ● Scientist I Department of Human Oncology, University of Wisconsin - Madison 📍 Remote |
|----------------------|---|
- Optimized a pan-cancer targeted DNA sequencing panel.
 - Developed bioinformatics pipelines to call somatic mutations and copy number alterations using circulating cell-free DNA.
 - Characterized the features of tumor-derived fragments in cell-free DNA.
 - Identified novel targets for cancer treatment development by utilizing machine learning and big data mining.
 - Conducted survival analyses and estimated circulating tumor DNA fractions for clinical trials.
 - Automated routine tasks for NGS data preprocessing and analysis, specifically for RNA-seq and targeted DNA-seq.
 - Mentored MD/PhD students on data science projects.



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CONTACT

📍 Omak, WA
✉ [Gmail](#)
🐦 [Twitter](#)
📄 [GitHub](#)
in [LinkedIn](#)

SKILLS

R/RStudio

Quarto/R Markdown

Bash

Git/GitHub

GitHub Actions

Snakemake

ChatGPT/Code Interpreter

NGS Analyses

Made with the R package
[pagedown](#).

The source code is available on
github.com/melodysyue/CV_YS.

Last updated on 2023-12-11.

2022
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2020



Postdoctoral Fellow

College of Fisheries and Ocean Sciences, University of Alaska
Fairbanks

📍 Remote

- Developed a bioinformatics pipeline to detect structural variants.
- Conducted genome scan analyses within a comparative genomics framework.
- Developed SNP panels to improve the resolution of population structure for fisheries management.
- Developed a bioinformatics pipeline to estimate the number of contributing individuals in DNA mixture samples.

2020
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2019



Postdoctoral Research Scientist

College of Natural Resources, University of Wisconsin - Stevens Point

📍 Remote

- Conducted reduced-representation sequencing library preparation for approximately 2,900 samples.
- Developed normalization protocols using the OT-2 liquid handling robot.
- Trained master's students in DNA metabarcoding bioinformatics pipelines.

2019
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2012



Graduate Research Assistant

Department of Biology, University of Washington

📍 Seattle, WA

- Enhanced the laboratory's high-throughput sequencing capacity by establishing experimental design guidelines, optimizing library preparation protocols, managing reference databases, and setting up bioinformatics pipelines for amplicon sequencing data.

2017
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2016



Project Consultant

BIOFAB, University of Washington

📍 Seattle, WA

- Conducted presentations to promote BIOFAB's automated workflows and attract new clients.
- Designed and oversaw molecular cloning projects for clients.
- Gathered feedback from clients and collaborated with team members to incorporate new features into the Aquarium software.



SELECTED PUBLICATIONS

2023



Fragmentomic analysis of circulating tumor DNA targeted cancer panels

Annals of Oncology. [10.1016/j.annonc.2023.06.001](https://doi.org/10.1016/j.annonc.2023.06.001)

- Kyle T. Helzer, Marina Sharifi, Jamie M. Sperger, Yue Shi, et al.

2023



Conserved islands of divergence associated with adaptive variation in sockeye salmon are maintained by multiple mechanisms

Molecular Ecology. 00, 1–21. [10.1111/mec.1712600](https://doi.org/10.1111/mec.1712600)

- Peter T. Euclide, Wesley A. Larson, Yue Shi, et al.

For a comprehensive list of publications, please visit [my ORCID profile](#)

- 2023 ● **Towards absolute abundance for conservation applications: estimating the number of contributors via microhaplotype genotyping of mixed-DNA samples**
Molecular Ecology Resources. 00: 1-13. [10.1111/1755-0998.13816](https://doi.org/10.1111/1755-0998.13816)
· Yue Shi, Cory M. Dick, Kirby Karpan, et al.
- 2023 ● **Gene flow influences the genomic architecture of local adaptation in six riverine fish species**
Molecular Ecology (FROM THE COVER). 32: 1549-1566. [10.1111/mec.16317](https://doi.org/10.1111/mec.16317)
· Yue Shi, Kristen L. Bouska, Garrett J. McKinney, et al.
- 2022 ● **High-density genomic data reveal fine-scale population structure and pronounced islands of adaptive divergence in lake whitefish (*Coregonus clupeaformis*) from Lake Michigan**
Evolutionary Applications. 15: 1776-1797. [10.1111/eva.13475](https://doi.org/10.1111/eva.13475)
· Yue Shi, Jared J. Homola, Peter T. Euclide, et al.
- 2022 ● **A chromosomal inversion may facilitate adaptation despite periodic gene flow in a freshwater fish**
Ecology and Evolution. 12: e8898. [10.1002/ece3.8898](https://doi.org/10.1002/ece3.8898)
· Matt J. Thorstensen, Peter T. Euclide, Jennifer D. Jeffrey, Yue Shi, et al.
- 2021 ● **Prey partitioning between sympatric wild carnivores revealed by DNA metabarcoding: a case study on wolf (*Canis lupus*) and coyote (*Canis latrans*) in northeastern Washington**
Conservation Genetics. 22: 293-305. [10.1007/s10592-021-01337-2](https://doi.org/10.1007/s10592-021-01337-2)
· Yue Shi, Yves Hoareau, Ellen M. Reese, et al.
- 2021 ● **Shift of maternal gut microbiota of Tibetan Antelope (*Pantholops hodgsonii*) during the periparturition period**
Current Microbiology. 78: 727-738. [10.1007/s00284-020-02339-y](https://doi.org/10.1007/s00284-020-02339-y)
· Yue Shi, Zi-Yan Miao, Jian-Ping Su, et al.
- 2021 ● **eDNA metabarcoding outperforms traditional fisheries sampling and reveals fine-scale heterogeneity in a temperate freshwater lake**
Environmental DNA. 3: 912-929. [10.1002/edn3.197](https://doi.org/10.1002/edn3.197)
· Rebecca R. Gehri, Wesley A. Larson, Kristen Gruenthal, Nicholas M. Sard, Yue Shi



ACADEMIC SERVICES



Peer Reviewer

- Philosophical Transactions of the Royal Society B
- Molecular Ecology
- JCI Insight
- PeerJ
- Journal of Mammalogy
- Frontiers in Marine Science
- Current Microbiology



CONFERENCE PARTICIPATION



Oral Presentation

- 151th American Fisheries Society (AFS) Annual Meeting
- 150th AFS Annual Meeting
- 47th Annual Alaska Chapter AFS Meeting
- 2018 North American Congress for Conservation Biology (NACCB)
- 2018 University of Washington (UW) Scholar's Studio
- 2016 3rd Conservation Biology Forum



Poster Presentation

- 2018 Sigma Xi Annual Meeting - Big Data Symposium



Attendee

- 2023 Hormone-Dependent Cancers Conference, Gorden Research Conference
- 2023 NCI Cancer Diagnosis Program Workshop: ctDNA in Cancer Treatment and Clinical Care

FELLOWSHIPS AND AWARDS



Fellows and Awards

- 2018 Washington Research Foundation - Benjamin Hall Fellowship
- 2018 UW Biostatistics Summer Institute Scholarship
- 2017 Riddiford-Truman Award
- 2016 Chester Fritz and Boeing International Fellowship for Research/Study
- 2015 Wingfield-Ramenofsky Award
- 2012 Hall International Fellowship



Travel Awards

- 2021 AFS Genetics Section Postdoc Travel Award
- 2018 UW Biology Graduate Student Travel Grant
- 2018 Graduate and Professional Student Senate Travel Grant
- 2018 NACCB Student Travel Award