# 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.





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 variants 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/RStudic

Quarto/R Markdowr

Bash

Git/GitHub

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 2023-09-17.

2022 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 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 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 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

· 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

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

For a comprehensive list of publications, please visit my **ORCID** profile

Towards absolute abundance for conservation applications: estimating 2023 the number of contributors via microhaplotype genotyping of mixed-DNA samples Molecular Ecology Resources. 00: 1-13. 10.1111/1755-0998.13816 · Yue Shi, Cory M. Dick, Kirby Karpan, et al. Gene flow influences the genomic architecture of local adaptation in six 2023 riverine fish species Molecular Ecology (FROM THE COVER). 32: 1549-1566. 10.1111/mec.16317 · Yue Shi, Kristen L. Bouska, Garrett J. McKinney, et al. High-density genomic data reveal fine-scale population structure and 2022 pronounced islands of adaptive divergence in lake whitefish (Coregonus clupeaformis) from Lake Michigan Evolutionary Applications. 15: 1776-1797. 10.1111/eva.13475 · Yue Shi, Jared J. Homola, Peter T. Euclide, et al. A chromosomal inversion may facilitate adaptation despite periodic 2022 gene flow in a freshwater fish Ecology and Evolution. 12: e8898. 10.1002/ece3.8898 · Matt J. Thorstensen, Peter T. Euclide, Jennifer D. Jeffrey, Yue Shi, et al. Prey partitioning between sympatric wild carnivores revealed by DNA 2021 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 · Yue Shi, Yves Hoareau, Ellen M. Reese, et al. Shift of maternal gut microbiota of Tibetan Antelope (Pantholops 2021 hodgsonii) during the periparturition period Current Microbiology. 78: 727-738. 10.1007/s00284-020-02339-y · Yue Shi, Zi-Yan Miao, Jian-Ping Su, et al.

eDNA metabarcoding outperforms traditional fisheries sampling and

· Rebecca R. Gehri, Wesley A. Larson, Kristen Gruenthal, Nicholas M. Sard,

reveals fine-scale heterogeneity in a temperate freshwater lake

Environmental DNA. 3:912-929. 10.1002/edn3.197

2021

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**

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

### Poster Presentation

· 2018 Sigma Xi Annual Meeting - Big Data Symposium

## Attendee

- $\cdot$  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