

# Woo Seok **Jung**

St. Louis, MO, 63108 | (562) 760-8825 | [wooseok.j.jung@gmail.com](mailto:wooseok.j.jung@gmail.com) | [www.jungwooseok.com](http://www.jungwooseok.com) | [wsjung](https://wsjung.com) | [woosjung](https://woosjung.com)

## EDUCATION

---

### Washington University in St. Louis

PH.D. IN COMPUTER SCIENCE

St. Louis, MO

2020 - Expected Aug. 2026

### University of Puget Sound

B.S. IN MATHEMATICS AND COMPUTER SCIENCE

Tacoma, WA

2016-2020

*Senior Thesis:* ChirpGAN: Generative adversarial networks to synthesize bird vocalizations.

*Study Abroad:* Danish Institute for Study Abroad (Focus: Artificial Neural Networks and Deep Learning), 2019.

## PROFESSIONAL SUMMARY

---

Computational biologist with six years of experience applying statistical, machine learning, and AI models to analyze large-scale multi-omics datasets to study transcriptional gene regulation. Doctoral researcher specializing in transcriptional gene regulatory networks. Proven track record of developing reproducible HPC pipelines (Nextflow/Docker) and novel ensemble learning frameworks (METANet) to solve complex multi-omics challenges.

## SKILLS

---

**Languages:** Python, R, SQL, Bash/Shell

**Tools:** Docker, Singularity, Nextflow, AWS, Linux (SLURM, SGE), Git

**Methods:**

- **Bioinformatics:** Multi-omics Integration, Network Inference, Differential Expression
- **Statistical Modeling:** GLMs, Mixed-Effect Models, Hypothesis Testing, Bayesian Hyperparameter Optimization
- **ML/Deep Learning:** Ensemble Learning, Neural Networks, Transformers

**Libraries:**

- **Python:** Scikit-learn, Pandas, NumPy, statsmodels, PyTorch, TensorFlow/Keras
- **R:** Tidyverse, Bioconductor, mgcv, glmnet, seurat, xgboost, caret, ggplot2

## PUBLICATIONS

---

**Wooseok J Jung**, et al., METANet: A supervised ensemble learning framework for reconstructing direct and functional tissue-specific transcription factor networks, *bioRxiv*, 2025.10.10.681634.

Mengze Li, Zeyuan Song, Eric Reed, Tanya T. Karagiannis, Stacy Andersen, Michael Brent, Chase Mateusiak, Sandeep Acharya, **Wooseok J Jung**, et al., Whole blood transcriptional signatures of age and survival identified in Long Life Family and Integrative Longevity Omics Studies, *bioRxiv*, 2025.07.15.664976.

Vaha Akbary Moghaddam, Sandeep Acharya, Michaela Schwaiger-Haber, and Shu Liao, **Wooseok J Jung**, et al., Gene-Embedded Multi-Modal Networks for Population-Scale Multi-Omics Discovery, *bioRxiv*, 2025.01.22.634403.

Sandeep Acharya, Vaha Akbary Moghaddam, **Wooseok J Jung**, et. al., FISHNET: A Network-based Tool for Analyzing Gene-level P-values to Identify Significant Genes Missed by Standard Methods, *bioRxiv*, 2025.01.29.635546.

Sandeep Acharya, Shu Liao, **Wooseok J Jung**, et. al., A methodology for gene level omics-WAS integration identifies genes influencing traits associated with cardiovascular risks: the Long Life Family Study, *Human Genetics*, 143, 1241–1252 (2024).

Yiming Kang, **Wooseok J Jung**, Michael R Brent, Predicting which genes will respond to transcription factor perturbations, *G3 Genes|Genomes|Genetics*, Volume 12, Issue 8, August 2022, jkac144.

*Full publication list available on Google Scholar*

## OPEN SOURCE SOFTWARE

---

**FISHNET** Implements the FISHNET method for HPC systems using Singularity/Docker containers available on GitHub.  
**nf-core/omicsgenetraitassociation** Nextflow pipeline which performs multi-omics meta analysis available on nf-core.  
**corrmeta** R implementation of correlated meta-analysis available on CRAN.

## TEACHING AND MENTORING EXPERIENCE

---

### Washington University in St. Louis

St. Louis, MO

Fall 2022

#### GRADUATE TEACHING ASSISTANT - ALGORITHMS IN COMPUTATIONAL BIOLOGY

- Delivered lectures on differential expression analysis and transcription factor (TF) activity inference.
- Aided in scientific understanding of material via weekly office hours, grading, and Piazza responses.

### University of Puget Sound, Math/CS Department

Tacoma, WA

#### DEPARTMENT ASSISTANT, STUDENT INSTRUCTOR

Jan. 2017 - May 2020

- Co-instructed lab sessions for Data Structures and Operating Systems courses. Graded coursework and held office hours for several Computer Science and Math courses.

### Mentored Trainees:

#### WASHINGTON UNIVERSITY IN ST. LOUIS

2025-2026

Mingyue Ding, Undergraduate Assistant

2023-2025

Daniel Ruskin, Undergraduate Assistant (now PhD candidate at UMD)

2021-2025

Thomas Westbrook, Undergraduate Assistant (now PhD candidate at UPenn)

## ADDITIONAL EXPERIENCE

---

### CJ OliveNetworks

Seoul, South Korea

#### DIGITAL TRANSFORMATION (DT) INTERN

May 2020 - Aug. 2020

- Conducted feasibility review of SOTA time-series forecasting literature, identifying and pitching the Temporal Fusion Transformer (TFT) architecture.
- Developed and evaluated MVP implementations for retail sales forecasting and video summarization.
- Presented results to the Board of Directors: demonstrated a 12% increase in 14-day and 21-day accuracy, leading to the successful adoption of the TFT model.

## HONORS & AWARDS

---

### Genome Analysis Training Program (GATP)

NHGRI grant T32 HG000045

2022-2025

### Goman Book Award

May 2020

### Thomas and Hilda Jack Department Scholarship

Dec. 2019

### McCormick Scholar Award

May 2019

### McGill Family Department Scholarship

2018-2019

### Dean's List Award

2017-2020

## EXTRACURRICULAR ACTIVITY

---

### Association for Computing Machinery (ACM) Student Chapter

University of Puget Sound

#### CHAPTER CHAIR

2017-2020

- Organized annual distinguished speakers lectures, high school student shadowing experiences, and computing workshops.