

Chathurani Ranathunge Ph.D.

Houston, TX 77077 • <https://caranathunge.github.io/>

SUMMARY

- Computational Biologist with 13+ years of experience, specializing in biomarker discovery, and immuno-oncology.
- Experienced in analyzing multiple types of Next Generation Sequencing (NGS) data (RNA-seq, ChIP-seq, proteomics).
- Proficient in R and Python. Developed and published the R package **promor** (12,000+ downloads) for mass spectrometry-based proteomics data analysis and ML-based predictive modeling.
- Experienced in leading interdisciplinary collaborations in both clinical and research settings.

PROFESSIONAL EXPERIENCE

FYR Bio

Senior Computational Biologist

Missoula, MT

05/2025-Present

- Partnered with internal teams and external stakeholders to define analytical requirements, interpret results, and deliver data-driven insights across multiple disease programs.
- Led the development of FYR's production-scale proteomics data analysis pipeline and established internal quality control standards for omics data processing and interpretation.
- Presented analytical findings and recommendations to internal project teams and external stakeholders.
- Led integrative multi-omics analyses to support biomarker discovery and pharmacodynamic studies across oncology and neurodegenerative disease programs.
- Built an automated system for visualization and report generation.

UH SEQUENCING AND GENE EDITING CORE, UNIVERSITY OF HOUSTON

Lead Bioinformatics Scientist

Houston, TX

03/2024-05/2025

- Collaborated with multidisciplinary teams of molecular biologists, immunologists, and clinicians to design mRNA-based preventive vaccines for breast cancer.
- Developed automated pipelines (**R**, **Python**) for identification and in-silico validation of gene fusion candidates for vaccines, reducing the processing time by 90%
- Developed a bioinformatics workflow to analyze epigenetic data from **ChIP-Seq** experiments.
- Delivered reports and presentations to external collaborators translating complex bioinformatics findings into actionable insights for clinical research.

EASTERN VIRGINIA MEDICAL SCHOOL

Senior Research Associate, Computational Biology

Norfolk, VA

09/2021-03/2024

- Collaborated with cross-functional teams of mass spectrometrists, computer scientists, and clinicians to analyze and interpret proteomics and clinical data to identify early detection biomarkers for prostate cancer.
- Developed the **R** package, **promor**, to streamline **proteomics** data analysis and ML-based predictive modeling, resulting in 2 peer reviewed publications and 3 presentations.

UNIVERSITY OF FLORIDA
Postdoctoral Research Associate

Gainesville, FL
07/2018-07/2021

- Constructed NGS libraries from Arctic moss samples for sequencing.
- Developed and maintained NGS data pipelines for automated processing of genomics data (**RAD-seq and target capture sequencing**), facilitating downstream population genetic, phylogenetic, analysis.
- Provided training and guidance to 3 junior researchers/analysts, promoting their professional growth.
- Presented scientific reports and presentations to internal and external collaborators translating research findings into actionable insights for ecological studies.

MISSISSIPPI STATE UNIVERSITY
Graduate Research/Teaching Assistant

Starkville, MS
08/2013-05/2018

- Developed **qPCR assays** for short tandem repeat (STR) containing genes and performed molecular analysis to investigate the role of STRs in gene expression regulation.
- Conducted statistical, differential expression, and enrichment analysis on bulk **RNA-seq, qPCR, and PCR** data identifying over 400 STRs involved in gene expression regulation in sunflowers.
- Trained and mentored 7 junior researchers promoting their professional development.
- Published 5 research articles (first author) and presented 12 research talks and 3 posters.

WAYAMBA UNIVERSITY OF SRI LANKA
Assistant Lecturer

Makandura, Sri Lanka
11/2011-07/2013

- Supervised 2 undergraduate research projects resulting in 2 peer-reviewed publications.
- Taught 2 lower level and 4 upper-level laboratory courses, including Genetic Engineering.

EDUCATION

MISSISSIPPI STATE UNIVERSITY
Doctor of Philosophy (Ph.D.) in Biological Sciences

Starkville, MS
2018

WAYAMBA UNIVERSITY OF SRI LANKA
Bachelor of Science (B.Sc.) in Agriculture, Major in Biotechnology

Makandura, Sri Lanka
2011

SKILLS

- Programming Languages: Python, R, Perl, Bash
- Data Analysis: High Performance Computing Clusters (HPC), SLURM, conda, Bioconductor, R package development
- Version Control: Git, GitHub
- Data Visualization: ggplot2, matplotlib
- Analysis & Reporting: RMarkdown, Quarto, Jupyter, LaTeX
- Omics Disciplines: Genomics (RAD-seq, Target capture sequencing), Proteomics (DIA), Transcriptomics (bulk RNA-seq), ChIP-seq
- NGS Data Analysis: Genome/Transcriptome Assembly (Bowtie, BWA, Trinity, samools), Differential Expression (DESeq2, edgeR), Enrichment Analysis (blast2GO), Databases (NCBI, GTEx, TCGA,

COSMIC), ChIP-seq Analysis (MACS2, deepTools), Variant analysis (IGV, UCSC genome browser), Tandem Repeats (RepeatSeq, Tandem Repeat Finder)

- Molecular Techniques: PCR, qPCR, DNA and RNA isolation, NGS library preparation

HONORS & AWARDS (SELECTED)

- Best Poster (Computational Mass Spectrometry) (2022), International Society for Computational Biology
- Emerging Scholar (2019), East Carolina University
- Young Scientist Excellence Award (2018), Mid-South Computational Biology and Bioinformatics Society
- Outstanding Graduate Research Assistant of the Year (2018), Dept. of Biological Sciences, MSU
- Finalist - Graduate Research Assistant of the Year (2018), MSU
- W. D. Hamilton Award - Honorable Mention (2017), Society for the Study of Evolution
- Outstanding Oral Presentation- Botany (2017), Botanical Society of America (Southeastern section)
- Outstanding Oral Presentation - Cell and Mol. Biology (2017), Association of Southeastern Biologists
- Outstanding Graduate Teaching Assistant of the Year (2017), Dept. of Biological Sciences, MSU
- Finalist – Donald Zacharias Graduate Teaching Assistant of the Year (2017), MSU
- Oral Presentation - Second Place (2016), Mid-South Computational Biology and Bioinformatics Society
- Graduate Student Research Award (2016), Botanical Society of America
- Dr. Dharmawansa Senadhira Award for Best Performance in Biotechnology (2012), Wayamba University

PUBLICATIONS (SELECTED)

Google scholar profile: <https://scholar.google.com/citations?user=52NfTAUAAAAJ&hl=en>

- **Chathurani Ranathunge** and Mark E. Welch. Clinal variation in short tandem repeats linked to gene expression in sunflower (*Helianthus annuus* L.). *Biomolecules* 14.8 (2024). 944.
- **Chathurani Ranathunge**, Sagar S Patel, Lubna Pinky, Vanessa L Correll, Shimin Chen, O John Semmes, Robert K Armstrong, C Donald Combs, Julius O Nyalwidhe. promor: a comprehensive R package for label-free proteomics data analysis and predictive modeling. *Bioinformatics Advances* 3.1 (2023).
- **Chathurani Ranathunge**, Gregory L Wheeler, Melody E Chimahusky, Andy D Perkins, Sreepriya Pramod, Mark E Welch. Transcribed microsatellite allele lengths are often correlated with gene expression in natural sunflower populations. *Molecular Ecology* 29.9 (2020) pp. 1704–1716.

LICENSES & CERTIFICATIONS

- Computational Biology Certificate (2018), Institute for Genomics, Biocomputing, and Biotechnology, Mississippi State University