

Chathurani Ranathunge Ph.D.

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

SUMMARY

- Computational Biologist with 13+ years of experience, specializing in transcriptomics, proteomics and NGS-based biomarker discovery for oncology.
- Experienced in converting transcriptomics and proteomics pipelines into production software.
- Designed and implemented LLM-assisted workflows to streamline omics data analysis, quality assessment, and biological interpretation.
- Developed and published the R package promor (13,000+ downloads) for mass spectrometry-based proteomics data analysis and ML-based predictive modeling.

PROFESSIONAL EXPERIENCE

FYR Bio

Senior Computational Biologist

Missoula, MT

05/2025-Present

- Led analytical strategy across multiple disease programs to address complex scientific questions and generate insights for decision-making.
- Led the development of FYR's production-scale transcriptomics and proteomics pipelines using AWS infrastructure, including LLM-assisted automated workflows for data interpretation, quality assessment, and reporting.
- Performed integrative multi-omics analyses supporting biomarker discovery, drug development, and pharmacodynamic studies across oncology and neurodegenerative disease programs.

UH SEQUENCING AND GENE EDITING CORE, UNIVERSITY OF HOUSTON

Lead Bioinformatics Scientist

Houston, TX

03/2024-05/2025

- Designed mRNA-based preventive vaccines for breast cancer in collaboration with clinicians and immunologists.
- Developed automated pipelines (R, Python) for identification and in-silico validation of gene fusion candidates for vaccines, reducing the processing time by 90%
- Developed an automated workflow to analyze epigenetic data from ChIP-Seq experiments.

EASTERN VIRGINIA MEDICAL SCHOOL

Senior Research Associate, Computational Biology

Norfolk, VA

09/2021-03/2024

- Collaborated with cross-functional teams to identify early detection biomarkers for prostate cancer using proteomics and clinical data.
- 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

- Developed and maintained genomics data analysis pipelines for population genetic and phylogenetic analysis of Arctic ecosystems.
- Trained 3 junior researchers/analysts in bioinformatics analysis and NGS library preparation.

MISSISSIPPI STATE UNIVERSITY
Graduate Research/Teaching Assistant

Starkville, MS
08/2013-05/2018

- Conducted statistical, differential expression, and population genetic analyses on transcriptomics data to identify over 400 short tandem repeats (STRs) involved in gene expression regulation in sunflowers, leading to 5 publications (first author), 12 research talks, and 3 poster presentations.
- Trained and mentored 7 junior researchers promoting their professional development.

WAYAMBA UNIVERSITY OF SRI LANKA
Assistant Lecturer

Makandura, Sri Lanka
11/2011-07/2013

- Supervised undergraduate research projects and taught laboratory courses in molecular biology

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; Version Control: Git, GitHub
- Data Analysis & Infrastructure: High Performance Computing Clusters, AWS, SLURM, conda, Bioconductor, R package development,; Data Visualization: ggplot2, matplotlib
- Omics Disciplines: Genomics (RAD-seq, Target capture sequencing), Proteomics (DIA), Transcriptomics (bulk RNA-seq), Epigenetics (ChIP-seq), Multiomics analysis

HONORS & AWARDS (SELECTED)

- Best Poster (Computational Mass Spectrometry) (2022), International Society for Computational Biology
- Young Scientist Excellence Award (2018), Mid-South Computational Biology and Bioinformatics Society
- W. D. Hamilton Award - Honorable Mention (2017), Society for the Study of Evolution
- Oral Presentation - Second Place (2016), Mid-South Computational Biology and Bioinformatics Society

PUBLICATIONS (SELECTED)

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

- **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).