Chathurani Ranathunge Ph.D.

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SUMMARY

- Bioinformatics Scientist with 10+ years of experience, specializing in cancer biomarker discovery, immuno-oncology, and evolutionary biology.
- Experienced in analyzing multiple types of Next Generation Sequencing (NGS) data (RNA-seq, ChIP-seq, genomics, proteomics).
- Proficient in R and Python. Developed and published the R package promor (7000+ downloads) for mass spectrometry-based proteomics data analysis.
- Experienced in leading interdisciplinary collaborations in both clinical and research settings.

PROFESSIONAL EXPERIENCE

UH SEQUENCING AND GENE EDITING CORE, UNIVERSITY OF HOUSTON **Houston, TX**
Lead Bioinformatics Scientist **03/2024-Present**

- Collaborated with multidisciplinary teams of molecular biologists, immunologists, and clinicians to design mRNA-based preventive vaccines for breast cancer.
- Developed an automated pipeline (**R, Python**) that reduced processing time for identifying gene fusion candidates for vaccines from hours to seconds, achieving over a 99% improvement in efficiency.
- Built a pipeline for in-silico validation of gene fusions from **RNA-seq** data, reducing analysis time by 80%
- 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 **Norfolk, VA**
Senior Research Associate, Computational Biology **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 machine learning based predictive modeling, resulting in 2 peer reviewed publications and 3 presentations.
- Created reports using **RMarkdown** and **Quarto** to effectively communicate results from statistical data analysis to both technical and non-technical stakeholders.
- Utilized **git/GitHub** for version control to ensure collaboration and code integrity within the teams

UNIVERSITY OF FLORIDA **Gainesville, FL**
Postdoctoral Research Associate **07/2018-07/2021**

- Collaborated with multi-disciplinary research teams from 2 universities on field expeditions in the Arctic, to study rapidly changing ecosystems.
- Constructed NGS libraries from Arctic moss samples for Illumina 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 **Starkville, MS**
Graduate Research/Teaching Assistant **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 in common sunflower.
- 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.
- Taught 4 lower level and 3 upper-level biology laboratory courses.

WAYAMBA UNIVERSITY OF SRI LANKA **Makandura, Sri Lanka**
Assistant Lecturer **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 **Starkville, MS**
Doctor of Philosophy (Ph.D.) in Biological Sciences 2018

WAYAMBA UNIVERSITY OF SRI LANKA **Makandura, Sri Lanka**
Bachelor of Science (B.Sc.) in Agriculture, Major in Biotechnology 2011

SKILLS

- Programming Languages: Python, R, Perl, Bash
- Data Analysis: High Performance Computing Clusters (HPC), SLURM, conda, Bioconductor, R package development (testthat, roxygen, pkgdown)
- 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