Shiwani Limbu

Github, Linkedin
Portfolio: https://www.shiwanilimbu.com/

SUMMARY

Self-motivated and highly enthusiastic computational biologist with experience in **both computational and wet lab techniques,** and **demonstrates collaborative behavior** with a high degree of integrity, accuracy, and attention to detail.

PUBLICATIONS

- **Limbu S**, Kumar A. Targeting the SPP1-CD44 Axis in Pediatric High-Grade Glioma through Integrated Single-Cell and Structural Bioinformatics Approaches. Manuscript under review.
- **Limbu S, McCloskey KE.** An Endothelial Cell Is Not Simply an Endothelial Cell. Stem Cells Dev. 2024 Aug 9. https://doi.org/10.1089/scd.2024.0088
- **Limbu S, McCloskey KE.** Stemness genes and miR-1247 expression is associated with clinicopathological parameters and prognosis in lung adenocarcinoma. Plos One. PLoS ONE 18(11): e0294171. https://doi.org/10.1371/journal.pone.0294171
- **Limbu S.** Impact of evolutionary selection on dynamic behavior of MCAK protein. https://doi.org/10.1101/2020.12.04.412650

EXPERIENCE

University of Kansas Medical Center, Bioinformatics Research Assistant June 2024 - Current

- **Project:** Identification of genetic and molecular changes associated with aberration of Extravillous trophoblast cells in pregnancy failure. – Github link private as per organizational requirements.
- Collected and analyzed over ~300k single cell RNA-seq data obtained from in-house sequencing and public database.
- Used Python and R programming and applied tools such Cellranger, Seurat, Scanpy, DoubletFinder, Harmony, Tradeseq, Slingshot, Cellchat to integrate samples and identify cell types, markers, cell differentiation pathways, cell-cell communication, and pseudotime calculations.
- Regularly updated code and documentation on GitHub, maintaining version control best practices to ensure project integrity and traceability in a fast-paced work environment.
- Led project weekly presentation and meeting discussions with manager and colleagues.

University of California Merced, Graduate Student OPT June 2024 - Current

- **Project:** Targeting the SPP1-CD44 Axis in Pediatric High-grade glioma through Integrated Single-Cell and Structural Bioinformatics Approaches. – Project Github link, Manuscript draft link
- Reviewed and collected markers for diverse range to differentiate as well as transitioning tumor and immune cell types in pediatric high-grade glioma.
- Collected pediatric high grade glioma single cell RNA-seq data from public databases.
- Applied Seurat, DoubletFinder, Harmony, Tradeseq, Slingshot, Cellchat to integrate samples and identify cell types and trace signals associated with T cell exhaustion.
- Collaborated with a researcher to explore antibody design to target a cytokine involved in T cell exhaustion.
- Applied tangram to map single cell RNAseq on to spatial RNA-seq data, and Signac to integrate single cell RNA-seq with single cell ATAC-seq data.

University of California Merced, Graduate Student Aug 2021 - May 2024

- Used Python and R programming languages, and methods such as DeSeq2, Limma, gene set enrichment analysis (GSEA), Cox-proportional hazard model and Kaplan-Meier curve based survival analysis, Immune infiltration test, and miRNA target prediction to identify key miRNA molecules regulating immune infiltration rate in Lung adenocarcinoma. – Manuscript link

- Applied next-generation sequencing data analysis pipelines to preprocess and analyze quality metrics, and hypothesis inference using tools such as Bowtie2, Hisat2, MACS2, CUT&TAG, samtools, fastqc, picard, featureCounts, IGV, SRAToolkit, and UCSC Genome browser.
- Applied multiomics data analysis (RNAseq, copy number variant, methylation, and Chipseq) to identify genomic changes affecting immune cell infiltration in Cancer. – My workflow blog page link
- Created a variant annotation workflow to predict deleterious mutations from vcf file. – Github link
- Experienced in differentiating **human embryonic stem cells (hESCs)** into **mature endothelial cells** to advance research in vascularization within the **Tumor Microenvironment**.
- **Generated Tumor spheroids** and implemented protocols for **testing cell migration.**
- Used **Flow cytometry** for cell sorting, as well as antibody titration.
- Skilled in using **Ultracentrifuge** for organelle isolation and protein separation.
- Proficient in using **Spectrophotometers** for quantification of bacterial growth and enzyme activity.
- Proficiently utilized **Thermal Cycler and Gel Electrophoresis** in **PCR experiments** for DNA amplification and analyzing gene repeat size variations through electrophoretic DNA separation.
- **Plasmid Isolation** and **DNA Purification and Quantification**, successfully isolated pGlo plasmid from overnight cultures of transformed cells and determined plasmid DNA concentrations in E. coli samples.
- Applied **Affinity Chromatography** for purification of GFP from E. coli cells transformed with pGLO™.
- One year of experience working as a lab safety manager.

EDUCATION

- **Master's in Quantitative and Systems Biology**,
  University of California, Merced 2021-May 2024
- **Bachelor's in biotechnology**,
  Graphic Era University, India 2012-2016

AWARDS

- **Graduate Student Researcher Award**, University of California, Merced May 2023
- **Quantitative and Systems Biology Summer Research Fellowship**,
  University of California, Merced April 2023
- **Teaching Assistant Topoff award**, University of California, Merced May 2022

COURSERA CERTIFICATIONS

- Diabetic Retinopathy Detection with Artificial Intelligence
- Breast Cancer Prediction Using Machine Learning
- Cervical Cancer Risk Prediction Using Machine Learning

TEACHING EXPERIENCE

- Contemporary Biology Lab, UC Merced Aug 2021-Dec 2021
- Introduction to Molecular Biology Lab, UC Merced Jan 2022-May 2022
- Mathematical Modelling for Biology, UC Merced June 2022-Dec 2022
- Statistics for Scientific Data Analysis, UC Merced Jan 2023-May 2023
- Introduction to Molecular Biology Lab, UC Merced Aug 2023-Dec 2023