

## Shiwani Limbu

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### SUMMARY

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

### SKILLS

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- **NGS data analysis:** GATK, Bowtie2, Hisat2, samtools, fastqc, picard, featureCounts, IGV, DESeq2, limma, MuTect2, SRAToolkit, Seurat, Scanpy, UCSC Genome browser, Ingenuity Pathway Analysis, CLC Genomics
- **Machine learning:** scikit-learn (decision tree, random forest, gradient boost).
- **Programming:** Python, R, Git
- **Statistical Modelling:** Hypothesis testing, Linear regression, and Dimensionality reduction (Principal Component analysis), ROC analysis, Hierarchical and K-means clustering, Anova test, Welch Test, Fisher's exact test, Students T-test, Cox-proportional Hazard model, Kaplan Meier plots.
- **Wet Lab:** Flow cytometry, Stem cell differentiation, Cell culture (Stem cells, HUVECS, Embryonic stem cells, Fibroblast, Smooth muscle cell, A549 LUAD cell line, and Pericytes) maintenance and freezing, Tumor spheroid generation, Transwell migration assay, 3D cells culture, Cell staining, Western blot, PCR, Gel electrophoresis, Plasmid purification, cell culture imaging, Fiji image analysis and image processing.

### BIOINFORMATICS SOFTWARES DEVELOPED

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- **VariantAnnotator:** <https://github.com/Sashoss/VariantAnnotator>  
Python package for annotating variants obtained from whole genome sequencing.
- **TMAP:** <https://github.com/Sashoss/TMAP/tree/main>  
Python package for downloading, pre-processing, normalization, concatenation, differential expression analysis, and unsupervised machine learning application on GEO data.

### BIOINFORMATICS EXPERIENCE (3 years of experience)

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- Applied NGS RNASeq data analysis using Bowtie2, Hisat2, samtools, and featurecounts ([https://github.com/Sashoss/MyNGSWorkflows/blob/main/RNASeq\\_readAlign\\_workflow.sh](https://github.com/Sashoss/MyNGSWorkflows/blob/main/RNASeq_readAlign_workflow.sh)), and **MuTect2 for somatic variant call**.
- Led **multiomics data analysis** (RNAseq, copy number variant, methylation, and Chipseq) to identify genomic changes associated with immune cell infiltration in Cancer ([https://github.com/Sashoss/MyNGSWorkflows/blob/main/TCGA\\_workflow.R](https://github.com/Sashoss/MyNGSWorkflows/blob/main/TCGA_workflow.R)).
- Applied **Scanpy** and **Seurat** to **analyze Single-cell RNAseq data**.
- Applied **MACS2** and **SEACR** for **CUT&TAG peak calling**.
- Developed a python package (**VariantAnnotator** and **TMAP**).
- Applied **differential expression, immune cell infiltration, gene set enrichment analysis (GSEA), and survival analysis** to identify Lung Adenocarcinoma biomarker (<https://doi.org/10.1371/journal.pone.0294171>).
- Developed **machine learning** model to differentiate between endothelial and non-endothelial cells using **Transcriptomic data**.

## **WETLAB EXPERIENCE (2 years of experience)**

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- 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 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.

## **TEACHING EXPERIENCE**

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| • 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  |

## **PUBLICATIONS**

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- **Limbu S, McCloskey KE.** Endothelial cell microenvironments, subphenotypes, and fate. (manuscript in preparation).
- **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. doi: <https://doi.org/10.1101/2020.12.04.412650>

## **EDUCATION**

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| • <b>Master's in Quantitative and Systems Biology,</b><br>University of California, Merced | 2021-May 2024 |
| • <b>Bachelor's in biotechnology,</b><br>Graphic Era University, India                     | 2012-2016     |

## **AWARDS**

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| • <b>Graduate Student Researcher Award,</b> University of California, Merced                              | May 2023   |
| • <b>Quantitative and Systems Biology Summer Research Fellowship,</b><br>University of California, Merced | April 2023 |
| • <b>Teaching Assistant Topoff award,</b> University of California, Merced                                | May 2022   |

## **COURSERA CERTIFICATIONS**

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- [Diabetic Retinopathy Detection with Artificial Intelligence](#)
- [Breast Cancer Prediction Using Machine Learning](#)
- [Cervical Cancer Risk Prediction Using Machine Learning](#)