

JAMES RENNIE BEQUEST

REPORT ON EXPEDITION / PROJECT / CONFERENCE

Expedition/Project/ Biomedical and Bioinformatic Research Internship

Conference Title:

June 4th 2026

Travel Dates:

Location:

Liang Laboratory, Department of Physiology, University of Arizona,
Tucson, Arizona, USA

Group member(s):

Yanchen Zhao

Aims:

The aim of this internship was to gain practical experience in biomedical research by working in both wet-lab and dry-lab settings. Specifically, I aimed to learn how human tissue and cell samples are prepared for downstream molecular analysis, including vessel dissection, cell culture, PCR, gel electrophoresis, and endothelial-cell enrichment. I also aimed to develop bioinformatics skills for analysing single-cell and spatial transcriptomic data, with a focus on quality control, dimensionality reduction, clustering, marker-gene identification, and cell-type annotation using Scanpy.

Photography consent form attached:

(please refer to your award letter)

☒ Yes

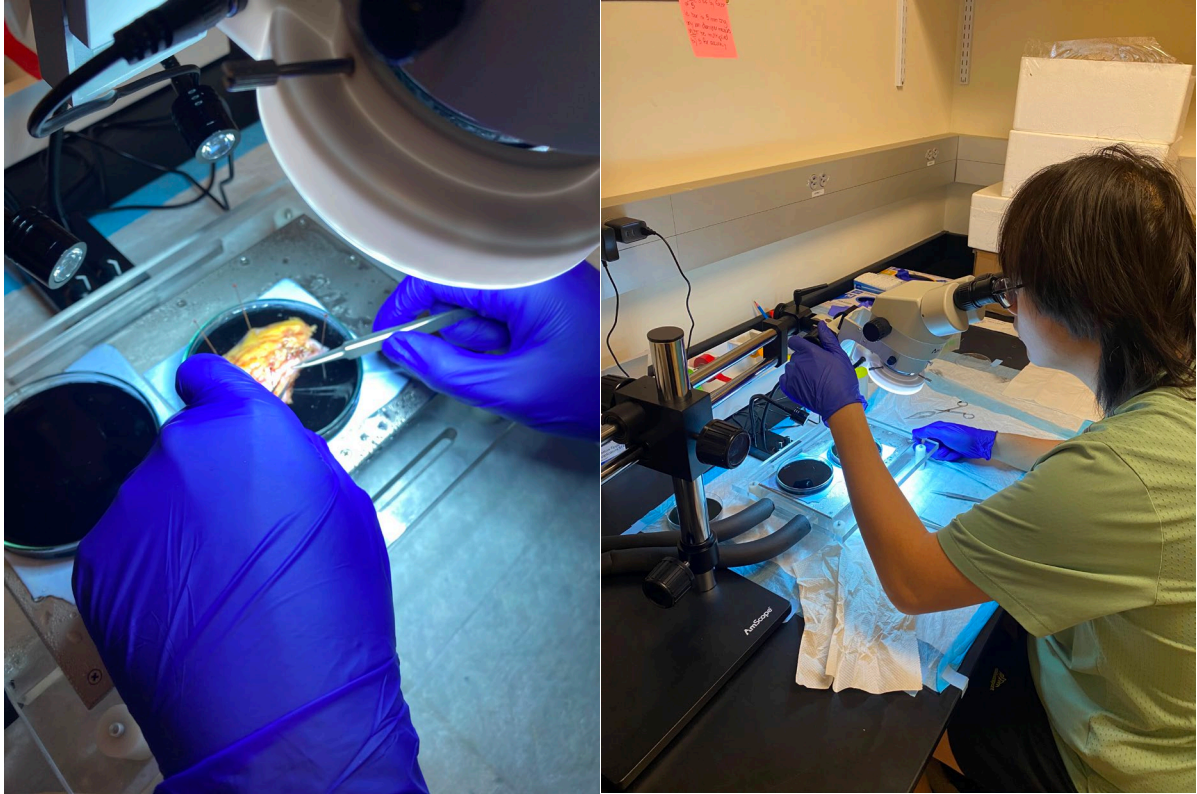
☐ No

OUTCOME (a minimum of 500 words):-

During my internship in the Liang Laboratory at the University of Arizona, I gained a broad introduction to biomedical research by participating in both laboratory-based and computational work. This experience helped me understand how biological samples are collected, prepared, analysed, and interpreted as part of a research workflow.

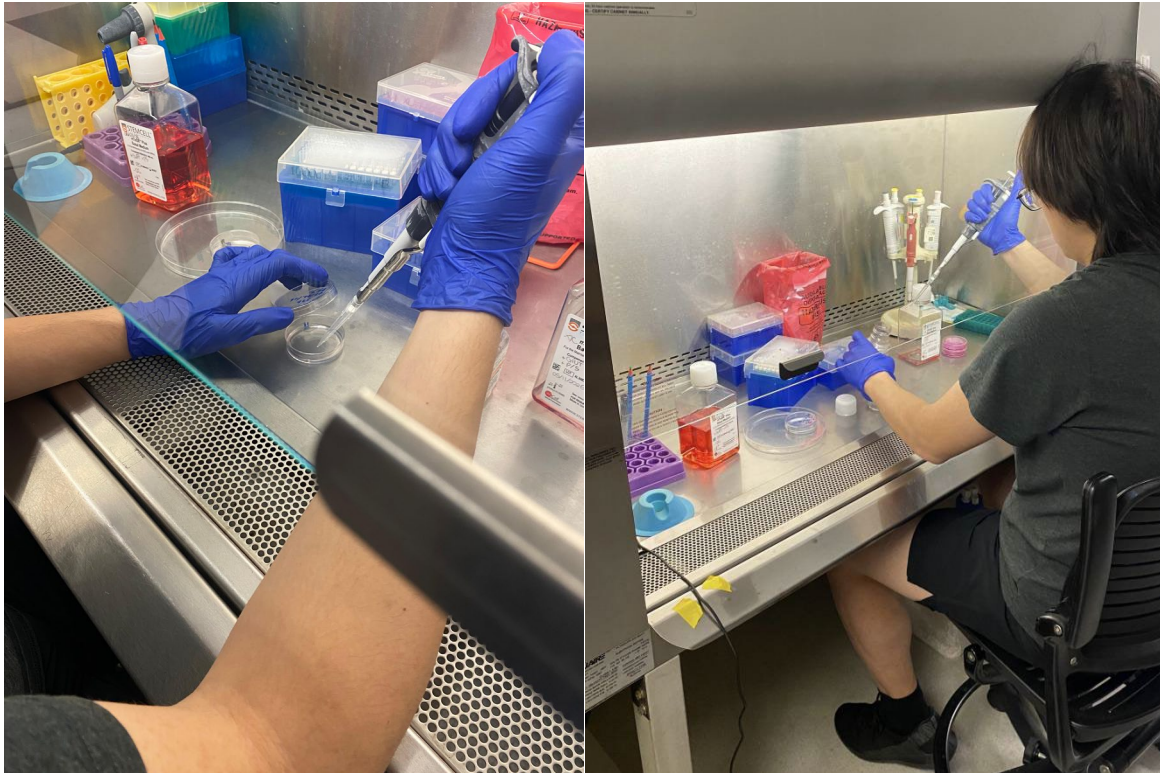
A major part of the wet-lab training involved tissue dissection and sample preparation. I observed and practised the identification of blood vessels within adipose tissue, learning how arteries and veins can be distinguished by their structure, elasticity, lumen appearance, and surrounding tissue. I learned that careful dissection is essential because unwanted fibres or surrounding tissue can affect sample purity and downstream analysis. I also became more familiar with how samples may be divided for different experimental purposes, such as RNA sequencing, protein measurement, smart sequencing, and whole-genome DNA sequencing.

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I also gained experience in cell culture and stem-cell-related laboratory techniques. I learned how to prepare media, change media, assess cell confluency under the microscope, detach cells using accutase, centrifuge and resuspend cells, count cells using trypan blue, and replate cells onto Matrigel-coated dishes. Later in the internship, I practised media changing and sub-culturing more independently under supervision. This improved my confidence in sterile technique, careful pipetting, timing, and routine cell-culture maintenance.

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In addition, I learned molecular biology techniques including PCR, agarose gel preparation, gel electrophoresis, and gel cutting. I developed a clearer understanding of the PCR cycle, including DNA denaturation, primer annealing, and polymerase extension. I also learned practical details such as preparing agarose gels, adding DNA dye, loading or handling small volumes carefully, locating bands under UV light, and cutting gel bands for downstream use. These tasks helped me appreciate the importance of precision, contamination control, and consistency in molecular experiments.

Another important wet-lab experience was endothelial-cell enrichment and shipping preparation. I learned that mixed differentiated cell populations may contain only a fraction of endothelial cells, so enrichment can be performed using endothelial-cell-specific antibodies linked to magnetic materials. I observed how magnetic separation can be used to isolate the desired cell population, and how cells are then prepared in flasks for shipping. This gave me a better understanding of how cell identity, sample handling, and logistics are connected in collaborative biomedical research.

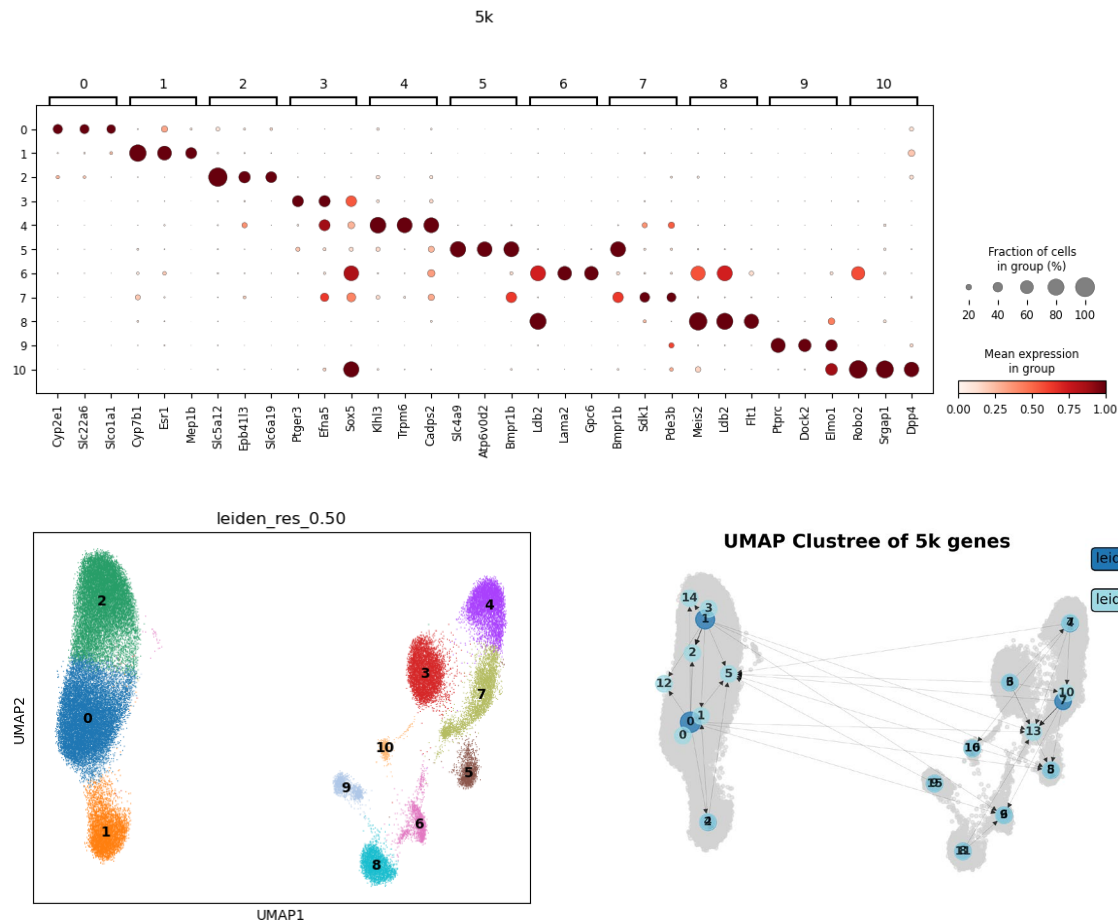
Alongside the wet-lab training, I worked on dry-lab analysis of single-cell and spatial transcriptomic data using Scanpy. I first learned how to set up the computational environment on the University of Arizona HPC system using micromamba, Jupyter Notebook, and required Python packages. I then studied the main steps of a single-cell RNA-seq workflow, including quality control, normalization, logarithm transformation, feature selection, PCA, nearest-neighbour graph construction, UMAP visualisation, Leiden clustering, and marker-gene analysis.

A key part of my work was learning how to interpret UMAP plots and clustering results. I compared datasets with different gene panels, including a smaller 379-gene dataset and a larger 5k-gene dataset. I found that the smaller dataset provided less information for cell-type annotation, whereas the larger dataset gave clearer and more representative marker-gene patterns. I also learned how parameter choices, such as the number of principal components, number of neighbours, UMAP minimum distance, and Leiden resolution, can

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strongly influence clustering results. For example, reducing the number of PCs and adjusting neighbour settings improved the UMAP structure for the smaller gene panel.

I also learned how to identify marker genes for clusters using statistical filtering, including adjusted p-values and expression-percentage thresholds. I used marker-gene dotplots and UMAP marker-expression plots to assess whether clusters corresponded to expected cell types. This helped me understand that marker genes are not only useful for annotation, but can also reveal possible data-quality issues, such as mitochondrial-gene enrichment or co-expression of markers from different major cell types, which may suggest low-quality cells or doublets. Later, I used broader cell-type marker sets first before attempting more specific annotation, which reduced the risk of assigning incorrect identities too early.



Overall, this internship gave me practical insight into the connection between experimental biology and computational data analysis. I improved my wet-lab skills in dissection, cell culture, PCR, gel work, and endothelial-cell preparation, while also developing my ability to analyse and interpret single-cell transcriptomic data. Most importantly, I learned that biomedical research requires both technical accuracy and biological judgement: high-quality data depend on careful sample handling, and meaningful interpretation depends on appropriate computational choices and critical evaluation of results. This experience strengthened my interest in molecular genetics and biomedical research, and it has given me a stronger foundation for future research projects at university.