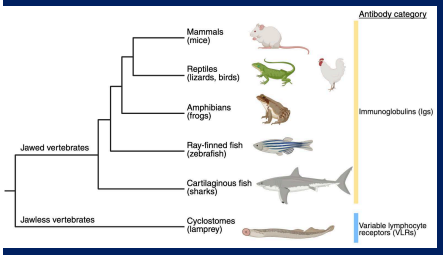
Quantitative & Systems Biology Student Presentations

Date: 9/25/2025
Time: 10:30 AM - 11:45 AM
Location: SSB 130

Anthony Wang



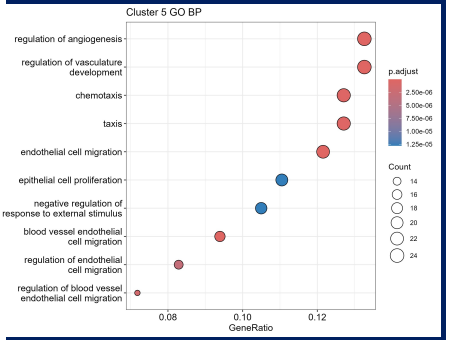
Abstract:

Monoclonal antibodies (mAbs) are invaluable reagents and are used extensively in both basic biological research and medicine. An expedient and inexpensive platform to produce robust and stable monoclonal antibodies that can be distributed using an open-source model is highly desirable. To this end, we submit that we can exploit the lamprey immune system and synthetic biology to rapidly and inexpensively generate robust lamprey-based antibodies ("lampribodies") to protein and glycan targets. Lampreys have evolved a convergent adaptive immune system and are able to produce diverse immune repertoires comparable to that of the jawed vertebrates (e.g., mouse, human). This platform would be much more expedient than the current methods for generating monoclonal antibodies and would provide a useful and affordable tool for various areas of research and medicine.

About the Student:

I am a fifth-year graduate student in Dr. Chris Amemiya's lab. I joined the lab as a rotation student in 2021 and have since been working on this "lampribody" project. Through my training so far, I have been able to learn many techniques in molecular biology and very interesting things about lamprey and E. coli. I have also had the honor to work with undergraduate researchers and learn from each other. I hope that together we can develop this robust antibody platform that may benefit many others.

Maria Mendoza



Abstract:

Human Umbilical Vein Endothelial Cells (HUVECs) are a common human primary cell type that is used in many labs around the world because it is relatively affordable and easy to access. Scientists use this endothelial cell to study many physiological processes and pathologies including angiogenesis. Here, 11 publicly available single cell HUVEC datasets were downloaded, and low-quality cells were removed. Datasets were then harmonized and prepared for integration. The Seurat pipeline was used to integrate the 11 datasets for joint analysis using R as a coding platform. For the first analysis, all cells were clustered and differential gene expression analysis was performed to identify the identity of each cluster. For the second analysis, we explored the effects of cell culturing conditions on gene expression patterns. Our data showed gene expression pattern differences between different culturing conditions.

About the Student:

My name is Maria Mendoza and I am in my last year of PhD here at UC Merced. During my time here, I participated in two computational internships at the Joint Genome Institute and at Roche, Genentech, respectively. Here, I learned how to perform single cell analysis studies to discover new cell-type and disease-associated markers. My current studies focus on elucidating the diversity that exists in endothelial cells from different tissues.

For more information, contact: Bercem Dutagaci
bdutagaci@ucmerced.edu