



Canadian Journal of Undergraduate Research: Abstract Template

It All Stems from Them: The First Step in the Framework of Understanding Hematopoietic Stem Cells in a Dynamic System

Theme – Biomedical Sciences

Type of project: Research

Kyle Palacios, BSc Student [1], Janet L. He, Bsc Student [2], Hanson Sun, BSc Student [3], Qais Alsharif, BSc Student [4]

[1] School of Biomedical Engineering, University of British Columbia, Vancouver, British Columbia, Canada V6T 1Z3

[2] School of Biomedical Engineering, University of British Columbia, Vancouver, British Columbia, Canada V6T 1Z3

[3] Department of Science, University of British Columbia, Vancouver, British Columbia, Canada V6T 1Z3

[4] School of Biomedical Engineering, University of British Columbia, Vancouver, British Columbia, Canada V6T 1Z4

Undergraduate Author Email: kpalacios02@gmail.com

Hematopoietic stem cells (HSCs) are a type of stem cell that can develop into any type of blood cell. The ability to regulate HSC function can be pivotal to sustaining proper blood production and homeostasis in an organism over its lifetime. This study aims to develop a framework whereby information about HSCs, or any differentiating cell can be collected and analyzed. To do so, the study utilized single-cell RNA sequencing (scRNA-seq), Cell-cell communication inference (CCC inference), Ordinary differential equations (ODE), and a Cellular Potts model (CPM). ScRNA-seq was used to determine the gene expression profile of individual hematopoietic stem cells. Specifically, scRNA-seq was performed on Peripheral Blood Mononuclear Cells. Results from scRNA-seq determined the genes most commonly expressed in mature blood cells. CCC was performed using the CellChat package in R to investigate the particular interactions of these genes involved in hematopoietic stem cell differentiation. The interactions between the genes were then modeled using a system of ordinary differential equations and visualized using Python. In order to validate our findings, a CPM was then created with Morpheus to model the cellular system in real-time. The use of a multiscale CPM can analyze the emergent and qualitative behavior of a group of cells through different cell-cell interaction pathways. Specifically in this project, a CPM model was created to analyze the proliferative behavior of Myeloid Progenitor Cells, while building a framework to study Notch, CD99, diffusive signaling, and other cell interaction pathways in the future.