Research Assessment #7

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Bian, Qin, and Patrick Cahan. "Computational Tools for Stem Cell Biology." *Trends in biotechnology* vol. 34,12 (2016): 993-1009. doi:10.1016/j.tibtech.2016.05.010

Assessment: Research Assessment #7

For my research assessment, I chose to do my assignment on "Computational Tools for Stem Cell Biology" by researchers Qin and Cahan. While reading this paper, I was impressed by the amount of information that the researchers could add to the paper. The paper essentially covers the entire field of computational stem cell biology. They specifically talk about single-cell OMIC analysis, they use evidence to show how it changes our understanding of stem cells. I learned much about specific techniques and data tools researchers have used to model stem cells computationally. The authors use over twenty research papers and experiments that provide various examples of approaches to stem cell modeling. It also discusses how these tools are used to find stem cell lineages and cell differential potential and determine what factors guide cell identity.

This paper and the many studies it references are crucial to my ISM journey. Although I conceptually understand the topics and different ideas that relate to my original work, I have struggled to find methods and techniques to implement the plan. This paper references many techniques and tools I plan to use in my project. For example, I specifically liked Mogrify, which helps predict transcription factors, and Wanderlust, which remakes stem cell lineage trajectories to see how the cell differentiates. Understanding these techniques and tools helps me know how machine learning and gene profiling can

be applied in my field of research. They will significantly help me improve in incorporating computational methods in regenerative and tissue engineering.

The paper covers many different topics but can be broken down into three main ideas/challenges: improvement problem, assessment, and lineage bias problem. The improvement problem focuses on optimizing differentiation conditions, the assessment problem focuses on evaluating engineered cells, and the lineage bias problem focuses on variability in stem cell differential potential. Each study they talk about is analyzed by how well it addresses these issues and how it uses single-cell OMICs and machine learning. This study was well organized, and each study discussed was easy to understand. This information builds on my knowledge of stem cell differential potential and processes. I just discovered so many problems associated with the variability of differential potential. The new information showed me that these processes are much more complex than I previously thought. I now need to consider these problems when creating my project.

Based on what I learned from this research paper, I have many ideas and plans. My main project is to create a computational model of stem and ocular cells and see how they interact with each other. With the knowledge from this paper, I could use tools like FISSEQ and TIVA Tag to model how stem cells might adapt to the existing structure of the eye. I could also use tools like RaceID to detect rare or unique responses in the ocular cells when the stem cells are transplanted. Moreover, when creating the stem cells digitally, I could use tools like ScoreCard or Pluritest to see how the genes are expressed and the cells' lineages. Other tools like CellNet or Mogrify could also be used in my project to determine what transcription factors I need to use to ensure the cells differentiate into stem cells. I have new questions about how to create tools like these myself that are geared to a specific purpose. To answer this question, I plan to look into more of the studies the researchers mentioned to see what they did and what methods they used.

This paper was very encouraging and exciting to read. The information was helpful and organized so readers could understand what was happening. It was useful as it brought me closer to reaching my goals for ISM this year. What was helpful for me was finding out about all the different tools researchers used before I started building. It was comforting to find out there were tools I could use; I was worried that I might need to do everything from scratch. The paper also highlights the challenges and problems in stem cell biology. It shows how far the field has advanced along with specific tools researchers have used, but it also points out the challenges and problems that remain today.