Developing An AI-based Particle-tracking Algorithm For Cardiac Muscle Cell Growth and Contractility

Rickerson Geneus, Matthew Hutchins, Hannah Maken, Dr. Christopher Solis

College of Education, Health, and Human Sciences, Florida State University

Introduction

Our goal is to evaluate images showing the assembly and disassembly processes, which will be important examples for constructing an algorithm to estimate sarcomere growth within cardiac muscle cells. Reaching this objective will make a substantial contribution to our knowledge of the dynamics of the heart muscle and may also yield new perspectives on exercise physiology and heart health. The study of sarcomere growth in real time may yield important insights into the heart's response to different stimuli, which could guide the creation of effective treatments for cardiovascular disorders. Furthermore, this approach might be used more broadly to investigate the cellular dynamics of other muscle tissues, which would promote tissue engineering and regenerative medicine. This multidisciplinary approach has the potential to spur innovation and advancement in the field of biomedical research and lead to groundbreaking discoveries. The expansion of each individual cardiac muscle cell propels the heart's growth in response to exercise. Sarcomere construction, the cytoskeletal framework seen in muscle cells, facilitates this expansion. Our team has the ability to stimulate cells to work harder in a lab setting, which causes the cells to spontaneously boost the creation of sarcomeres.

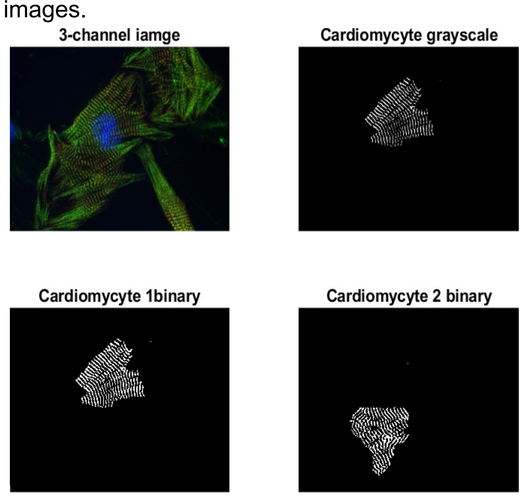
Methods

The mechanical loading and unloading of heart cells (cardiomyocytes) that is performed externally was elicited by drugs via an intrinsic stimulus. These drugs modify the sarcomere by changing the myosin tension within it. Myosin activator OM (6 h, 0.5 micromolar) or Myosin Inhibitor Mava (6 h, 1 micromolar) were added to neonatal rat ventricular myocytes (NRVMs). Prior reports dictated which concentrations were chosen [2]. Cultures of cells that were treated with Mava and OM in glass dishes were blocked, fixed, and stained with primary and secondary antibodies [1] known for immunofluorescence and were captured in an epifluorescence microscope (Zeiss Axio Observer.Z1). Images were analyzed and refined using the MATLAB compiler and its various features.

Results

So far in the research we have found a large amount of valuable info from a literature analysis and have created various image samples that will be used to test the AI we develop to scan sarcomeres, In the literature review it was found that using the coding language and compiler MATLAB to program and design the algorithm for the AI would be the most efficient way to create the AI [3, REFS]. In the process of seeking the best way to code, we also discovered that tools within MATLAB like the Image Segmenter, the auto cluster, and the image viewer may be used to create the pictures that the AI will use to learn how to process images. In the literature analysis we also discovered how accurate other AI algorithms have been at analyzing other medical images.

Figure 1: Classification of Sarcomeres for the Ground Truth Data Set –- UT_01



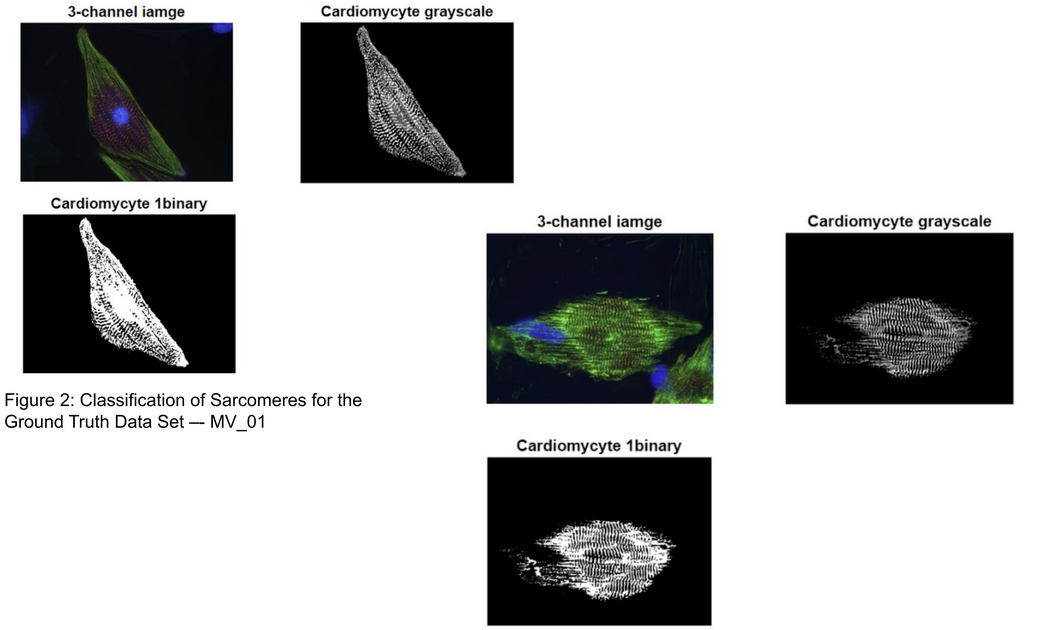


Figure 2: Classification of Sarcomeres for the Ground Truth Data Set — MV_01

Figure 3: Classification of Sarcomeres for the Ground Truth Data Set –- OM_01

Discussion

We identified the cell segmenter that was the most suitable and efficient to generate ground truths from the WT, OM, and MV cardiomyosite images. Alongside with generated images, we had two outputs: the binary and the grayscale. The binary and the grayscale files will serve as inputs to train the neural network. A total of 8 repetitions per treatment will be needed for the full ground truth data set. Subsequently, the neural network will be trained using 30% of the ground truth data set as the training data set while the other 70% will be used as the test data set.

Acknowledgements

- Dr. Christopher Solis
- Brooke Gilbert
- Katherine Martinez

References

- Boateng SY, Belin RJ, Geenen DL, Margulies KB, Martin JL, Hoshijima M, de Tombe PP & Russell B (2007). Am J Physiol Heart Circ Physiol 292, H259–H269.
- Toepfer CN, Sharma A, Cicconet M, Garfinkel AC, Mu€cke M, Neyazi M, Willcox JAL, Agarwal R, Schmid M, Rao J et al. (2019). Circ Res 124, 1172– 1183.
- Karabağ, C., & Reyes-Aldasoro, C. C. (2022). bioRxiv, 2022-06.
- Dima, A. A., Elliott, J. T., Filliben, J. J., Halter, M., Peskin, A., Bernal, J., ... & Plant, A. L. (2011). Cytometry Part A, 79(7), 545-559.
- Saha, M., & Chakraborty, C. (2018). IEEE Transactions on Image Processing, 27(5), 2189-2200.
- Vicar, T., Balvan, J., Jaros, J., Jug, F., Kolar, R., Masarik, M., & Gumulec, J. (2019). BMC bioinformatics, 20(1), 1-25.