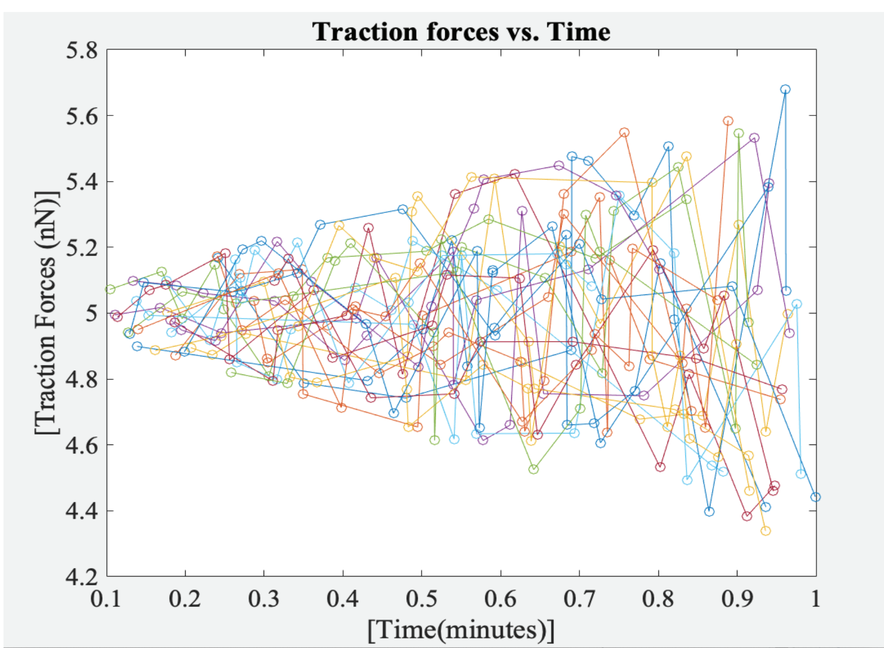
Computational Model of Tensional Homeostasis of Focal Adhesions at Subcellular Level

Team 40: **Selina Qin, Jiaming Zhang**
Technical Advisors: **Dimitrije Stamenovic, Michael L. Smith**

Homeostasis is a core concept in understanding body behaviour in biology and physiology; it refers to the self-regulating process by which an organism can maintain internal stability while adjusting to changing external conditions. Though, there is a lack of research on homeostasis on a smaller scale, where this project will explore tensional homeostasis at the focal adhesion (FA) points of the cell on the subcellular level. When a cell reaches a homeostatic state, the morphology of the cell will fluctuate to external stimulus. Specifically, this research will analyze how the displacement and fluctuation at the FA level will affect tensional homeostasis when the mechanical force is applied to the cell. FA are dense molecular assemblies and actin stress fibres connect together. This computation modelling is proposed to simulate cellular fluctuations that mimic in vivo laboratory cell fluctuations when the cell is responding to a stimulus such as traction force. This study introduces the Monte Carlo algorithm into the simulation process, so as to maximize the use of mathematical models to analyze the relationship between various transformations in the tensional homeostasis process to reduce physical laboratory experiments. As shown in Graph 1, the horizontal axis represents the full duration of an in vivo experiment and the vertical axis represents random traction forces generated by the Monte-Carlo function. The different coloured lines represent one simulation of cellular fluctuation. These data can be used to predict the threshold when the cell reaches the homeostatic balance. Our long term goal is for these data to be used in further research to perform analysis on cellular behaviours relating to reaching the success of homeostasis and hence be a critical need in preventing diseases caused by the disruption of homeostasis such as cancer and artherocolosis.



Graph 1: Traction forces for FA points within experiment time simulated in Matlab