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Computational model for proliferation-able muscle stem cells

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By understanding the ability for stem cells to proliferate and differentiate will improve the capability to treat debilitating diseases like cancer, cachexia or muscular dystrophy. However, characterization of these processes in stem cells is very challenging due to the diverse nature of triggering signals and cellular interactions. Therefore, it is very important to administer and track the complex factors responsible for stem cell proliferation and differentiation in order to design an appropriate treatment. In this proposed system, a computational model for proliferation-able muscle stem cell populations, also known as satellite cells, has been presented. Although muscle regeneration is fundamentally dependent on its resident satellite cell, few studies have characterized the regulatory mechanisms of this heterogeneous cell population. Based on the clinical study, it has been found that, these time variant mechanisms are random in nature, and can be conceptualized by stochastic model. The objective of this paper is to formulate a novel multi-branching stochastic theory for uniquely characterizing the proliferative muscle stem cells as well as quantifying these cell populations. In this approach, heterogeneous cell populations as a whole and homogeneous for a particular period of time termed cells transition time has been considered. These research efforts would enhance the understanding of the characteristics of muscle stem cells and their implementation in therapeutic strategies.

Keywords: Myogenic markers; therapeutic process; detection; muscle stem (satellite) cell; proliferation- able; heterogeneity; stochastic process