

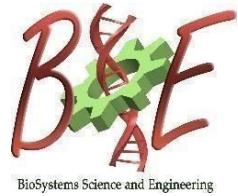


Indian Institute of Science

Centre for BioSystems Science and Engineering

BSSE Seminar

21st January 2020 (Tuesday), 2:30 PM, MRDG Seminar Hall, 1st floor,
Biological Sciences Building



BioSystems Science and Engineering

Big Omics Data-Driven Computational Approaches for Stem Cell Systems Biology

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ABOUT THE SPEAKER



Dr. Srikanth Ravichandran obtained a B.Sc. degree in Physics and M.Sc. degree in Biophysics and Crystallography from the University of Madras in 2003 and 2005, respectively. He obtained his doctorate in Physics (Theoretical Systems Biology) from the University of Delhi and ICGEB in New Delhi. Currently, he is working as a Research Associate in the Luxembourg Centre for Systems Biomedicine, at the University of Luxembourg. His expertise lies in mathematical modelling, bioinformatics tool development, omics data integration and analysis. He had received the CSIR Senior Research Fellowship (2008) and University of Luxembourg's Internal Research Grant - ASTROSYS, in 2017. He is interested in Theoretical Systems Biology for stem cell research, Big (omics) data driven modelling, Structure and dynamics of complex biochemical networks and bio-inspired systems design.

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ABSTRACT

A key objective of regenerative medicine and bioengineering is achieving quantitative and robust control over the fate and behavior of individual cells and their populations. Central to this endeavor are stem cells, with the capacity for sustained self-renewal and potential to differentiate into specialized cell types. For a systematic exploitation of these abilities of stem cells for therapeutic applications, especially in the context of ageing related disorders, a basic understanding of the complex cellular processes such as development, reprogramming, tissue repair, differentiation, and loss/maintenance of pluripotency is essential. Due to the inherent complexity of these cellular processes, computational systems approaches that harness the wealth of big omics data can aid in this endeavor. In this talk, I will present the computational approaches that we have recently developed to distill useful insights from single-cell RNA-seq data. These approaches are general and are applicable to any stem cell system, and I will present their application to neural, and muscle stem cells, for the identification of key targets for stem cell rejuvenation in order to counteract ageing related degeneration of stem cell functionality. Further, I will briefly present an ongoing work that aims to delineate functional cellular heterogeneity from single-cell RNA-seq data. Finally, I will conclude by discussing some of my ideas for future work.