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METABOLIC NETWORK ANALYSIS AND ITS APPLICATION IN UNDERSTANDING THE BIOLOGY OF AGING

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Project Summary: An overarching theme of systems biology is the investigation of complex biological processes as an integrated interaction of its many components. Such integrated connections are often represented as a dense and an enmeshed web of biochemical conversions. Among the significant types of biochemical networks, cellular metabolism provides a direct description of the phenotype of the organism and one of the best indicators of the physiological state and the behavior of a cell. Here, we explore computational tools and algorithms in generating relevant predictions of metabolic flux profiles in model organisms. Additionally, we developed an algorithm, FBA, to infer changes in the metabolic state of an organism by incorporating differential transcriptomic data with a genome-scale reconstruction of its metabolic model. Aging and metabolism are closely connected. Like metabolism, the complexity in the onset and progression of aging process has warranted a systems-oriented approach in an effort to understand the biological processes that contribute to an increasing vulnerability in an organism. Lastly, in this work, we shed light on the transcriptional roadmap of events in the aging process using bioinformatic and metabolic analysis.

CV. Sudharshan received his B.Tech in Industrial Biotechnology from SASTRA University in 2012. He worked in Dr. Sengupta's lab for Nanomedicine at the Harvard – MIT Health Science and Technology for his Bachelors thesis. He received his MSc in Chemical and Bioengineering from Department of Chemistry and Applied Biosciences from ETH, Zurich in 2015 after completing his Masters thesis in Prof. Dr. Konrad Hungenbeuhler's group. He joined Prof. Dr. Gunawan's lab in 2016 as a doctoral candidate and transitioned to the deMello group in 2018.

