Guest Lecture

@ St. John's Research Institute

St. John's National Academy of Health Sciences

Deciphering the somatic mutational processes and driver mutations in cancer genomes

Venue: Ground Floor Conference Hall, SJRI Admin Block

Date: 27th November, 2018 (Tuesday)
2:00 PM to 3:00 PM

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Tata Institute of Fundamental Research,

Bangalore , India

About the Speaker :

Sabarinathan Radhakrishnan is a faculty at NCBS, Bangalore; and his lab is focused on the study of cancer driver mutations using computational and functional genomics approaches. He did his post-doctoral work in the area of computational cancer genomics in Prof. Nuria Lopez-Bigas' group at the Institute for Research in Biomedicine (IRB), Barcelona, Spain. Prior to that, he obtained his PhD in Bioinformatics from the University of Copenhagen (Denmark).

About the Lecture:

Cancer is caused by genetic mutations, often referred to as "drivers", that confer selective growth advantage to malignant cells. However, the identification of driver mutations in sequenced cancer genomes is challenging and requires a detailed understanding of the underlying mutational processes (that is, how somatic mutations are accumulated and distributed in the genome of cancer cells during their development), especially in functionally crucial regions such as in genes and regulatory regions. In this talk, I will present our recent findings on how DNA-binding regulatory proteins (like transcription factors) influence the local somatic mutation rate in the cancer genomes. These findings have important implications for the understanding of mutational and DNA repair processes, as well as for the identification of cancer driver mutations. Furthermore, in the last part of the talk, I will present our current work on the analysis of whole genomes of 2,500 tumors from 37 types of cancer to identify the landscape of coding and non-coding driver mutations in each patient's tumor. In this study, we found that the genomic events are at the root of virtually all tumors, with each carrying on average 4.6 driver mutations.