Abstract: Cancer is a complex disease and one of the leading causes of death in adults. Recent advances in genomics technologies have enabled generating multiple types of high throughput data on all major cancer types, paving way for data-driven discoveries that have considerably advanced diagnosis, stratification, and treatment of cancer patients. I will discuss recent efforts from my group to develop computational methods for detecting cancer-associated mutations from genomics data, and then apply multivariate analysis approaches on these mutations to uncover aspects of cancer evolution. Our results are relevant for diagnosis and stratification of cancer patients.

Bio: Dr. Subhajyoti De completed his BS in engineering from the Indian Institute of Technology, Kharagpur, India before pursuing a PhD from the University of Cambridge, UK in the laboratory of Prof. Sarah Teichmann. There he developed computational biology approaches to study genetic variations and mutational signatures associated with human genome evolution. As a Human Frontier Science Program Fellow in the group of Prof. Franziska Michor at Harvard University, Dr. De investigated cancer as a somatic evolutionary process. He was able to demonstrate that genetic and epigenetic abnormalities in cancer genomes show non-random, context-dependent patterns.

In his independent laboratory, first at Univ. Colorado and currently at the Rutgers Cancer Institute of New Jersey, Dr. De is investigating cancer as a complex, adaptive system using genomic, computational, and systems-level approaches. He is a recipient of NIH/NCI PSOC Trans-network Young Investigator award, and Webb-Waring Scholar award. His work has been supported by the NIH, United Against Lung Cancer Foundation and Boettcher Foundation.