Indian Institute of Science
Centre for BioSystems Science and Engineering
BSSE Seminar

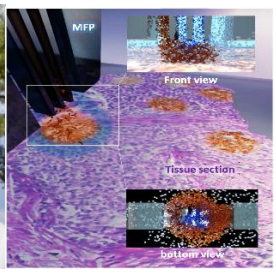
16th April 2019, 4:00PM, Tuesday, MRDG Seminar Hall, 1st floor, Biological Sciences Building

Microscale biochemical assays for multiomic profiling of tumor sections

Dr. Aditya Kashyap
IBM Research - Zurich

ABOUT THE SPEAKER:

Dr. Aditya Kashyap joined IBM Research - Zurich in January 2014 in the Science and Technology department where he currently is a post-doctoral researcher. While working on biophysical and bioanalytical methods at IBM, he obtained a multidisciplinary doctorate in 2018 at ETH Zurich from Dept. Biosystems science and engineering. He develops biological assays using a liquid scanning probe technology to obtain spatially resolved multiomic profiles of tumors, with a broader interest in applications within personalized medicine. He has authored and co-authored 9 journal publications, 4 patents and given talks at several conferences, and also received IBM Research Division Awards for his work. Prior to working at IBM, he obtained his masters' in biomedical engineering at ETH Zurich, with a focus in tissue engineering for cartilage regeneration and his bachelors' in biotechnology at SASTRA university, India. He also worked at Wyss institute at Harvard medical school on soft lithography for building tumor models using his experience in tissue engineering.



ABSTRACT

Every organism is an expression of the fine balance between order and chaos. Tumor biology, not being exempt from this complexity, expresses 'chaos' in the form of heterogeneity, and overlooking it by averaging data across whole tumors often makes profiles inaccurate and their treatment ineffective. To address this particular challenge and to bridge the divide between research and clinics, our group introduced an open-space microfluidic technology called the microfluidic probe (MFP). The MFP enables microscale biochemical assays that can both deposit biomarker specific ligands and extract cells from tissue sections using hydrodynamic flows. By implementing the critical steps in current pathology workflows, we can accelerate the protocol implementation and obtain quantifiable genomic, transcriptomic and proteomic information from the same tissue sample. This also provides interactive control over the 'scale/spatial resolution' of analysis. In this talk, I will focus on the assay implementations for spatial genomics (Spatialyse) and *in situ* proteomics (qμIC). It is my hope that this work will provide an incentive to different communities to integrate translatable multi-scale solutions that are useful for clinics, thereby enabling their transition into the next-generation of pathology.