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External Seminar Series

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zoom

"Characterizing the Interplay of Multi-Omics Mechanisms in Cancers"

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Abstract: Multi-omics analysis has emerged as a powerful tool for uncovering the molecular mechanisms underlying complex diseases, such as cancer and aging-related disorders. This approach involves integrating data from multiple layers of biological information, including genomics, epigenomics, transcriptomics, and microbiomics, to gain a more comprehensive understanding of the physiological mechanisms and the events that contribute to the genesis and progression of diseases. By combining these different datasets, we can identify key molecular pathways, potential biomarkers, and therapeutic targets that may not be apparent when analyzing each dataset in isolation.

Our hybrid (wet and dry) laboratory develops computational methods and an integrative database for sequencing analyses and omics interplay mining. In particular, we have designed a toolkit to study the interplay between DNA methylation and transcription factor binding activities, which includes the MethMotif database and its API, TFregulomeR. This allows us to understand the effect of DNA methylation changes in regulatory pathways. Interestingly, integrative analyses performed by our toolkit have brought to light a novel chromatin state (transiting state), which is associated with methylated ZBTB33 binding sites, a transcription factor which has been reported to play a critical role in TGFβ signaling regulation of metastasis in breast cancer.

Because DNA methylation aberrations are also linked to genome instability, we have created NanoVar, an efficient, fast, and low-depth (8X) third generation sequencing structural variant (SV) caller for long-read sequencing datasets generated by Oxford Nanopore Technologies. NanoVar employs an AI neural network model trained on simulated datasets. In patient samples, it detects not only genomic aberrations but also uncovers non-pathological alternative sequences or alleles found in healthy individuals. The low sequencing depth requirements of NanoVar make it possible to use Nanopore sequencing for accurate SV characterization at a lower cost, making it suitable for clinical studies and population genetics research.

Finally, it has been reported that oncomicrobes are responsible for about 20% of all cancers and directly impact DNA methylation changes. I will also be presenting our preliminary results on the mapping of the microbiome in tumors and its potential association with the immune response.

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