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SÉMINAIRE

Analyzing the genomic landscape of liquid tumors

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When a patient contract cancer, the diagnosis and the treatment options are decided based on phenotypic factor such as the primary organ and the pathology of the tumors. However, recent discoveries have shown than the molecular pathogenesis of the tumor may be a better indicator of the prognosis and the adequate therapeutical targets, underlining the need for a better understanding of the genomic characteristics of the disease. In order to solve this issue, initiatives such as TCGA have sequenced large groups of disease samples and used the size of the cohort to distinguish between driver and passenger events. We propose to adopt the same approach to analyze liquid tumors, where widespread heterogeneity within the tumor as well as between patients adds even more noise to the measurements. We will show the software infrastructure we built in order to track and analyze the samples as well as two examples of such studies. The first cohort we will discuss is a cohort of 53 patients with acute myeloid leukemia (AML). AML is the most common type of leukemia in adult, and the is still poorly understood. All these patients achieved complete remissions after standard chemotherapy and later suffered from relapse. We performed whole exome sequencing of germline tissue, primary sample as well as relapsed sample for each of these patients and will show analysis of this data compared to the knowledge that we have of the disease. The second cohort we will discuss is a cohort of 189 adult patients with B-cell acute lymphoblastic leukemia (B-ALL). B-ALL is the most common leukemic malignancy in the pediatric population but most of the knowledge that we have from the adult form of the disease is actually deduced from the childhood form. We will present here a integrated and targeted DNA/RNA sequencing solution that allowed us to extract short events (point substitutions and short insertions and deletions) as well as copy number aberrations, rearrangements and fusion events. We will use these two cases to discuss common problems that arise when analyzing genomic data as well as potential solutions."