



# 生物信息学研究中心

Center of Bioinformatics

## 学术报告

**题目:** Needles in Haystacks: Thinking about fast evolutionary processes by genome analysis of tumors and RNA viruses

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**时间:** 8月16日(星期四) 上午 10:00

**地点:** 思源楼 1013 室

**Abstract:** Cancer is the result of an accumulation of genomic alterations that synergistically cooperate to cause uncontrolled cell growth. The development of high throughput technologies is allowing to map the landscape of genomic alterations and to disentangle the combinatorial nature of these alterations. We will show some examples of these alterations in tumors of Hematopoietic and Lymphoid Tissues, including Hairy Cell Leukemia (HCL), Acute Lymphoblastic Leukemias, Diffuse Large B-cell Lymphoma and Chronic Lymphocytic Leukemia. For instance, we were able to identify a heterozygous mutation in BRAF (V600E) present in 100% of HCLs, presenting a new therapeutic opportunity through BRAF inhibitors. We will also show a novel fusion protein in Glioblastoma Multiforme. The fusion protein localizes to mitotic spindle poles, has constitutive kinase activity and induces mitotic and chromosomal segregation defects and triggers aneuploidy. Inhibition of FGFR kinase corrects the aneuploidy and oral administration of an FGFR inhibitor prolongs survival of mice harboring intracranial FGFR3-TACC3-initiated glioma. These examples show how the development of computational tools in genomic data leads to the identification of novel therapeutic targets in cancer.