中央研究院 ACADEMIA SINICA 1928

統計科學研究所
INSTITUTE OF STATISTICAL SCIENCE

學　術　演　講

講　題：Whole genome and transcriptome sequencing using long-read sequencing technology

講　者：Prof. Akihiro Fujimoto
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時　間：2024年3月12日(星期二)，10:30-12:00

地　點：統計所B1演講廳

Abstract

Next-generation sequencers (NGS) have enabled whole-genome sequencing and greatly advanced genetic research. However, due to the short read lengths and limitations of information analysis methods, it is believed that the current analysis of the genome and transcriptome is not perfect. Our research aims to reveal a comprehensive picture of the genome and transcriptome that is challenging to detect using conventional analysis methods and to elucidate their functional significance. We have been conducting research on the detection of intermediate-sized insertions and deletions, the detection of microsatellite polymorphisms/mutations, analysis of somatic mutations in cancer using a long-read sequencer, development of haplotype reconstruction methods through local assembly, and analysis of cancer transcripts using a long-read sequencer. In this presentation, I will introduce a summary of our previous studies and discuss two recent studies: comprehensive analysis of genetic variations in Mycobacterium tuberculosis genomes and identification of isoform-specific expression quantitative loci (eQTLs) using long-read transcriptome data.

※ 茶　會：10：10開始。

※ 實體與線上視訊同步進行。