



統計科學研究所

INSTITUTE OF  
STATISTICAL SCIENCE



## Seminar

Title : Whole genome and transcriptome sequencing using long-read sequencing technology

Speaker : Prof. Akihiro Fujimoto

( Department of Human Genetics, Graduate School of Medicine, The University of Tokyo )

Time : 10:30 ~ 12:00, Tuesday, March 12, 2024

Place : Auditorium, B1F, Institute of Statistical Science

## 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.

※ Tea reception starts at 10 : 10.

※ Online live streaming through Cisco Webex will be available.