

國立清華大學數學系訪問學者學術演講

NTHU Department of Mathematics

Visiting Scholar Colloquium

Title Cross-species transcriptome analysis using Gromov-Wasserstein optimal transport

Speaker Dr. Yuya Tokuta (Kyoto University)

Time 2025.03.20 (Thu.) 16:30-17:30

Venue <https://ntucc.webex.com/ntucc->

(online) [en/j.php?MTID=m11c24df284ce00ad16b5521fe5ad168d](https://ntucc.webex.com/j.php?MTID=m11c24df284ce00ad16b5521fe5ad168d)



Abstract

While mammalian genomes remain highly conserved throughout evolution, transcriptional and epigenetic regulation is crucial in driving species-specific differences at the cellular level. Even within a single organism, cells sharing the same genome differentiate into diverse cell types through variations in gene regulation and epigenetic modifications, which establish distinct gene expression patterns. Advances in biological big data, collectively known as omics data, have made genomic and epigenomic information increasingly accessible, with transcriptomics emerging as a particularly active area of research. In this talk, we will introduce a data-driven cross-species analysis method based on Gromov-Wasserstein optimal transport, which we developed based on an observation in systems biology, reformulated as a mathematical problem dealing with transcriptome data. Our method calculates gene-to-gene correspondences between RNA-seq data across species and quantifies their differences regarding the gene-to-gene correspondences. We validated it using real data, obtaining gene-to-gene correspondences between mice and humans primordial germ cell-like cell induction processes and a phylogenetic tree-like dendrogram of six mammalian pluripotent stem cells. This is joint work with T. Nakamura, K. Fujiwara, M. Nagano, M. Saitou, Y. Imoto, and Y. Hiraoka.