中央大學物理學系

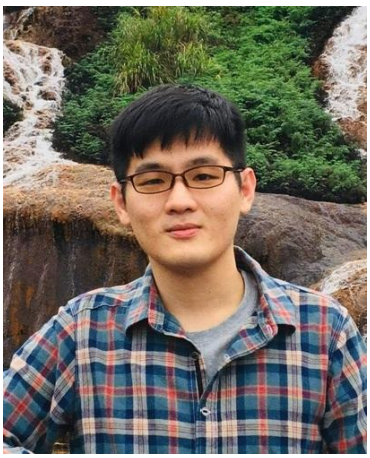
Department of Physics, National Central University

# Colloquium

## Network Analysis of the Transcriptional State Space: Correlation Geometry, Multiscale Structure, and Perturbation-induced Rewiring


**Prof. Te-Lun Mai (麥德倫)**

**Department of Life Science,NTU**

**Date: 2026/09/22 (Tue)**

**Venue: S4-625**

**Time: 14:00**


Abstract :

Gene expression data can be viewed as observations in a high-dimensional transcriptional state space, with gene-gene correlations defining a relational geometry among its coordinates and biological perturbations deforming that geometry. This talk examines two complementary operations on this space: edge-level rewiring under perturbation and recursive coarse-graining of correlation structure.

In a study of GL24-mediated growth suppression of metastatic triple-negative breast cancer cells, differential co-expression analysis identified gene pairs whose correlations appeared or disappeared in responsive cell lines while showing no differential co-expression in a non-responsive cell line. The resulting phenotype-filtered networks captured perturbation-associated changes in topology and highlighted processes related to metabolic alterations, proliferation, and migration or invasion, while complementing differential expression findings that converged on apoptosis.

To resolve organization beyond individual edges, I will then introduce Minimum Span Clustering Network (MSCN). MSCN recursively merges clusters according to their nearest-neighbor relationships in a correlation-derived distance space, producing a deterministic multilevel hierarchy with explicit parent-child structure. Applied to two autism brain transcriptome cohorts, this hierarchy resolved signals ranging from fine-grained neuronal and synaptic processes to broader developmental and immune-related programs. Long noncoding RNAs were subsequently mapped onto the mRNA architecture, and statistical mediation analysis prioritized candidate TF-lncRNA-mRNA mediation axes for further validation.

These examples support a relational view of the transcriptome: expression amplitudes capture only part of the system, whereas local topology, multiscale organization, and perturbation-induced deformation reveal distinct aspects of biological structure. I will also discuss what such correlation geometry can and cannot establish under finite-sample constraints and without direct causal validation.