SPEECH INFORMATION (For Conference Program Book)	
Topic	Contamination-Aware and Clinical-Contextualized AI for Infectious Disease Diagnosis by Metagenomic Sequencing
Abstract	Rapid, accurate pathogen identification is essential for timely therapy in the critically ill patients. Metagenomic next-generation sequencing (mNGS) is a culture-independent, hypothesis-free diagnosis, yet its utility is hindered by site-specific contamination, tissue-specific colonization, host immune status, prior antibiotic exposure, and pathogen-specific biases. In this talk, we first characterize the complexities of sequencing profiles across various specimen types and pathogens, demonstrating their time-, pathogen-, hospital-, and host-dependencies. This complexity makes traditional negative-control filtration unreliable and limits the applicability of machine learning due to training data sparsity. To address these constraints, we introduce a continuously refreshed, stratified knowledgebase that models background microbial distributions by specimen types, host factors, and pathogen-specific biases. We couple large language models (LLMs) with a statistical calibration layer to distinguish true etiologic pathogens from background microbes, constraining LLM nondeterminism that yielding interpretable classification. We further orchestrate a set of AI agents that integrate conventional microbiology tests, radiology, patient history, and mNGS profiles to generate diagnosis reports aware of clinical contexts. Finally, we show how agentic AI can guide the design of targeted next-generation sequencing (tNGS) panels by leveraging mNGS-derived priors and literature-grounded evidences. Together, these methods provide a high-fidelity, contamination-aware infection diagnosis in clinical metagenomics across diverse specimens, host factors, and hospitals, improving diagnostic accuracy and aligning with clinical context.