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Ph.D. DISSERTATION DEFENSE

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Degree:	Doctor of Philosophy
School/Department:	Biomedical Engineering
Date:	Thursday, August 13th, 2026
Time/Location:	11:30 a.m./ McLean Hall, Room 104
Title:	Development of Artificial Intelligence Tools for Cell Characterization in Biomedical Imaging
Chairperson:	Dr. Xiaojun Yu, Department of Biomedical Engineering, School of Engineering & Sciences
Committee Members:	Dr. Yu Gan, Department of Biomedical Engineering, School of Engineering & Sciences Dr. Antonia Zaferiou, Department of Biomedical Engineering, School of Engineering & Sciences Dr. Sang Won Bae, Department of Systems Engineering, School of Engineering & Sciences

ABSTRACT

Automated cell characterization is increasingly important in biomedical imaging because modern experiments generate large and complex image datasets that are difficult to analyze manually with consistency and throughput. This dissertation develops artificial-intelligence-based tools for converting biomedical images into biologically meaningful measurements across multiple applications.

First, an optical coherence tomography-based deep learning workflow was developed for automated cell characterization in three-dimensional bioprinted hydrogel scaffolds, supporting segmentation, viability-related intensity analysis, three-dimensional reconstruction, and morphology-related feature extraction. Second, TeCoDi-Refiner was developed to improve noisy cell masks in dynamic microscopy sequences by using temporal context, self-supervised image features, and diffusion-based restoration. Third, a tracking-aware framework was designed to preserve cell identity across time using memory-bank association, bi-directional consistency, motion gating, missing-object recovery, and morphology-aware biological constraints. Finally, an image-aware sparse Mixture-of-Experts framework was developed for automated ovarian follicle rupture detection in ex vivo ovulation assays.

Together, these studies demonstrate how artificial intelligence can support cell characterization across static, dynamic, volumetric, and assay-level biomedical imaging tasks while emphasizing the importance of matching model design to the biological question and imaging context.