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Integrating Motorized Microscopy and YOLO-Based Deep Learning for Automated Cell Detection*

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Abstract

Microscopic imaging is a fundamental tool in biological research for numerous types of studies, including cellular behavior and dynamics analysis. However, the automated processing of microscopy samples remains a challenging task. On the image formation and sensing side, illumination, positioning and other acquisition conditions, such as marginally varying object distances over time can heavily affect data quality. On the analysis side, small cell size, clustered populations, and class imbalances between dominant cellular states and transient but critical events such as mitosis or apoptosis limit the effectiveness of automated detection approaches. Addressing these challenges requires a unified approach that considers both acquisition and intelligent analysis strategies.

In this work we present an integrated microscopy framework that combines a custom-built, high-throughput, motorized imaging platform with a deep learning-based cell detection and tracking pipeline. The platform is designed around a linear three-axis stage, precise motor control with high reduction ratio, and an infinity-corrected objective system mounted on a near-infrared camera. This configuration performs controlled, repeatable and scalable microscopic data acquisition, and

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therefore enables us to build consistent datasets suitable for automated analysis.

The collected microscopy data are analyzed by a YOLO-based object detection model [3], which is optimized for cellular imaging and integrated with an enhanced DeepSORT tracking algorithm [1] to maintain cell identity throughout a sequence of samples. The pipeline is able to accurately localize and classify individual cells while ensuring correct association frame by frame.

A key challenge addressed in this study is the skewed distribution between common cellular patterns and transient biological events well documented in microscopy imaging datasets [2, 4]. To mitigate this, targeted augmentation methods and training strategies are implemented to enhance sensitivity to underrepresented cellular classes while retaining robust detection and tracking behavior.

The proposed framework integrates controlled microscopy acquisition with class-imbalance-aware deep learning approaches and tracking methods that preserve object identity to achieve stable detection and tracking outcomes across both frequent and minority cell categories. Controlled and consistent imaging conditions enable the acquisition of microscopy datasets compatible with deep learning-based modeling. The unified detection-tracking pipeline supports scalable and automated processing of large-scale microscopy image datasets while preventing identity loss across temporal sequences. Collectively, this integrated approach demonstrates the importance of jointly considering hardware and artificial intelligence components when designing reliable and biologically interpretable automated microscopy analysis systems.

Beyond the scope of the current findings, the integrated approach serves as a foundational step towards more intelligent microscopy platforms. By coupling motorized acquisition mechanisms with automated detection and tracking, the system could dynamically adapt control parameters, such as sampling frequency, region of interest, and illumination intensity, to detected cellular events or trajectories. Overall, this work highlights the necessity of integrated hardware and deep learning pipeline design to deliver robust, scalable, and biologically meaningful automated cell analysis.

References

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