**Cell Segmentation and Tracking using Deep Learning Techniques**

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**Abstract**

Cell movement tracking is an important task in many biological and biomedical applications, since it helps us understand cellular activity, disease processes, and therapeutic development. Traditional cell tracking approaches frequently rely on manual annotation or simple algorithms, which can be time-consuming, error-prone, and limited in scalability. In recent years, deep learning models have emerged as useful tools for automating cell tracking processes, bringing the possibility of better accuracy and efficiency. This thesis aims to bridge this gap by developing a user-friendly platform for cell tracking, catering to users with limited coding knowledge. The platform leverages deep learning models and the trackpy module for seamless tracking of cells in diverse datasets. For cell segmentation, we use the U-Net architecture, which is a convolutional neural network (CNN) intended for semantic segmentation. The U-Net model is trained on a dataset part of the 2018 Data Science Bowl which contains cellular pictures that includes several cell types and imaging modalities. The dataset has been established in a way to test the knowledge of an algorithm that can go through several variations. Each mask has its own independent nuclei as masks are not allowed to overlap with each other. Experimental results show that the U-Net model is highly effective at accurately segmenting individual cells from complex backgrounds, outperforming existing segmentation approaches. For tracking, we integrate the YOLOv8 object detection framework and the trackpy module into the platform. YOLOv8 excels in object detection across frames and thus we will take advantage of its superior performance in the microscopic world, while trackpy offers robust trajectory analysis capabilities. By providing both these tools, our platform enables users to effortlessly track cells in their datasets, visualize trajectories, and extract quantitative metrics without the need for extensive programming expertise. We validate the platform's performance using benchmark datasets and demonstrate its effectiveness in diverse real-world applications. Furthermore, we emphasize the platform's potential to democratize cell tracking research, enabling researchers from diverse backgrounds to leverage advanced tracking techniques and accelerate scientific discoveries. In conclusion, this thesis presents a novel platform for user-friendly cell movement tracking, bridging the gap between advanced tracking methodologies and researchers with limited coding experience. The platform makes it possible for different people to use it for their research thus promoting health understanding as well as coming up with solutions on how diseases can be controlled.

1. **Introduction**

Cell movement tracking is an essential aspect that contributes greatly in various scientific fields including biology, medicine, and bioengineering. Understanding how cells move, proliferate, and interact provides insights into fundamental biological processes, particularly during disease onset, medication discovery, and development. Traditionally, cell tracking was done manually by tagging them or using basic computer systems that involved manual work, needing too much time, and often bringing mistakes due to human factors. However, the rise of research done within deep learning algorithms has resulted in a paradigm shift in how cell monitoring is conducted, with the promise of automation and accurately scalable outcomes. The development of deep learning technology has resulted in a paradigm shift in cell tracking, with the promise of automation, accuracy, and scalability.

This introduction sets the stage for the exploration of cell motion tracking through deep learning models and aims to segment and track individual cells within complex biological environments. We provide a background to the significance of cell tracking in various scientific contexts, highlighting its applications in cell biology, cancer research, immunology, and tissue engineering. We then discuss the limitations of traditional tracking methods and the potential benefits of integrating deep learning techniques into the cell tracking workflow.

* 1. **Importance of cell tracking**

Cell movement is a basic process in biology which covers areas like cell differentiation, division, division, and cell interaction with other cells surrounding them or constituents of the matrix around them. In multi-cellular living organisms, movements of cells are important during embryo growth, tissue repair processes as well as immune response or wound recovery. Dysregulation of cell migration can bring about diseases when it becomes abnormal especially during pathological cases such as cancer spread away from original locations where they started growing up into other distant parts like the lungs invading other organs like the liver or bones, autoimmune disorders, and developmental abnormalities. Therefore, precise, and comprehensive tracking of cell movement is critical for understanding both normal physiological processes and disease states.

Taking cancer research as an example, tracking cancer cell migration within the tumor microenvironment offers insights about tumor development, invasion, and response to therapy. Similarly, in immunology, tracking the mobility of immune cells within tissues aids in understanding immune surveillance, inflammation, and host-pathogen interactions. Furthermore, in tissue engineering and regenerative medicine, monitoring the migration and integration of implanted cells is critical for improving tissue repair and organ transplantation procedures. In general, cell movement monitoring can be thought of as a foundation for better understanding complicated biological processes and directing treatment decisions.

* 1. **Challenges of Traditional Tracking Methods**

Despite its importance, cell movement tracking has historically been a labor-intensive and error-prone process. Manual tracking methods, which involve visually annotating cell trajectories in microscopy images, are time-consuming and subject to observer bias. Automated tracking algorithms, while offering increased efficiency, often struggle with complex biological environments, where cells exhibit heterogeneous morphology, density, and motility patterns. Additionally, traditional algorithms may lack robustness in handling occlusions, cell divisions, and other dynamic events commonly encountered in live-cell imaging experiments.

Furthermore, traditional tracking methods often rely on human-designed characteristics or rules which might fail to capture the full complexity of cellular behavior. Huge amounts of parameter tuning are necessary in order to use these techniques, which in turn may not work under various experiments or types of cells. As a result, there is an increasing demand for more complex tracking approaches that can adapt to the diverse and dynamic nature of biological systems.

* 1. **Promise of Deep Learning in Cell Tracking**

Deep learning, which is a subfield of artificial intelligence that has been inspired by the structure and function of the human brain, is now being used in cell tracking where it has proved to be very beneficial. Harnessing lots of labelled information and computer processing power enables deep learning algorithms to capture complex relationships within raw datasets without requiring manual feature extraction. Neural-network architectures like convolutional nets (CNNs) or recurrent neural nets (RNNs) have proved to be beneficial computer vision related tasks such as object detection, segmentation, and classification.

When it comes to cell tracking, deep learning has a number of advantages over traditional techniques. Deep learning models can automatically learn key features from microscopy images, by capturing spatial and temporal data in cell behavior. It has the ability to accurately segment individual cells and track them across different frames, all under varying conditions (e.g., dense populations or noisy images). Moreover, deep learning models can adapt to different experimental conditions and cell types, offering a broad range of applications with flexibility and scalability.

* 1. **Structure of Thesis**

This thesis explores the application of deep learning models for cell movement tracking, with a focus on segmentation and tracking methodologies. In the following chapters, we delve into the technical details of our approach, including the architecture of deep learning models, the preprocessing of microscopy data, and the evaluation of tracking performance. We present experimental results on benchmark datasets and discuss the implications of our findings for biological research and medical applications. Furthermore, we highlight the potential challenges and future directions in the field of deep learning-based cell tracking.

This thesis explores the application of deep learning models in cell movement tracking, more specifically on segmentation and tracking techniques. This paper will give an account of our methodology in technical details like deep learning model architecture, microscopy data preprocessing, and evaluation of tracking quality. Moreover, experimental results from benchmark datasets are included while discussing the impacts of this research for biological studies and medical applications. Additionally, we will be examining some of the possible challenges and future works that could come up in the field to tracking cells using deep learning technology.

1. **Literature Survey**

Paper (1) presents ZeroCostDL4Mic, a platform democratizing DL for microscopy by lever- aging Google Colab’s free resources, allowing researchers without coding expertise to perform various DL tasks. The platform ensures reproducibility through detailed training reports and supports tasks, for example, segmentation, object detection, and denoising. ZeroCostDL4Mic is user-friendly, covering end-to-end workflow, and adaptable to other Jupyter Notebook platforms.

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| Ref No. | Objectives | Problem Statement | Methodology | Advantages | Disadvantages | Performance Measure |
| (1) | Democratize microscopy DL via ZeroCostDL4Mic by offering free access to high-performance computing resources and simplifying DL for noncoders.  | | Addresses the challenge of democratizing access to deep learning (DL) for microscopy, overcoming the barrier of requiring powerful computational resources and coding expertise for training DL networks in image analysis tasks |  |  |  |  |
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**Problems Statement & Objectives**

**Methodology**

**Dataset**

**References**

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