1. <https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1007673>

(not imp)

The paper presents DeLTA (Deep Learning for Time-lapse Analysis), an innovative tool for automating the analysis of single-cell microscopy data. DeLTA employs two consecutive U-Net deep learning models for cell segmentation, tracking, and lineage reconstruction, aiming to eliminate the need for manual intervention while ensuring high accuracy and enabling high-throughput analysis.

To ensure robust performance, the research team trained the DeLTA models on a diverse set of samples, including data from their own experiments and literature. This approach minimizes the need for further training on new mother machine data.

In addition to the deep learning algorithm, the paper introduces a set of scripts and graphical user interfaces to facilitate interaction between the Python-based U-Net implementation and Matlab for creating and curating training sets.

By automating image processing, DeLTA provides rapid access to quantitative, dynamic measurements of single cells. This capability opens up possibilities for real-time cell tracking in various experimental settings, potentially enabling applications such as feedback control of gene expression in single cells.

1. <https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0243219>

(Very imp)

The paper introduces a novel method for segmenting touching cells in microscopy images, utilizing a unique representation of cell borders inspired by distance maps. This approach can effectively handle touching and close cells during training, making it robust to annotation errors and suitable for underrepresented cell types.

Central to this method is the utilization of a convolutional neural network (CNN), specifically an adapted U-Net architecture with two decoder paths, to predict neighbor distances for cell segmentation. By leveraging CNN-based techniques, the proposed method significantly enhances the accuracy and efficiency of cell segmentation in microscopy images.

Moreover, the paper adapts a graph-based cell tracking algorithm to evaluate the segmentation method for cell tracking. This algorithm incorporates movement estimation in the cost function, allowing for the re-linking of tracks with missing segmentation masks over a short sequence of frames, thereby improving overall tracking performance.

The effectiveness of the combined tracking by detection method, based on the proposed segmentation approach, was demonstrated through multiple top-three rankings in the IEEE ISBI 2020 Cell Tracking Challenge. This success underscores the method's efficacy and competitiveness across diverse datasets, highlighting its potential for real-world applications in cell tracking and analysis.

1. <https://web.archive.org/web/20210717223201id_/https://www.biorxiv.org/content/biorxiv/early/2021/03/10/2021.03.10.434806.full.pdf>

imp

The paper introduces DeepSea, a deep-learning model specifically designed for the segmentation and tracking of single cells in time-lapse microscopy images. DeepSea stands out for its versatility and trainability, offering precise segmentation and tracking capabilities even in challenging imaging modalities like phase-contrast live microscopy sequences.

One of the key advancements of DeepSea lies in its ability to achieve higher precision compared to existing models in segmenting and tracking single cells. This is particularly valuable for imaging modalities such as phase-contrast, which are widely accessible and non-toxic but present challenges for accurate analysis.

The practical application of DeepSea is showcased in the paper through its use in studying cell size regulation in embryonic stem cells. This demonstration highlights the model's effectiveness in analyzing fundamental cellular processes at the single-cell level with high temporal resolution. Such capabilities are crucial for understanding dynamic cellular behaviors and advancing our knowledge of complex biological systems.

1. <https://ieeexplore.ieee.org/abstract/document/9834915>

veryimp

The paper introduces EmbedTrack, a novel convolutional neural network (CNN) that revolutionizes cell analysis by simultaneously performing cell segmentation and tracking within a single framework. This unified approach addresses a longstanding challenge in the field, offering automation for both segmentation and tracking processes.

A distinctive feature of EmbedTrack is its ability to predict interpretable embeddings, specifically offsets of cell pixels to their respective cell centers and bandwidths. These embeddings enable the model to effectively segment and track cells in images, providing valuable insights into cell dynamics.

To validate its efficacy, the proposed method is rigorously evaluated on nine 2D datasets from the Cell Tracking Challenge. The results underscore the effectiveness of EmbedTrack, with the model delivering competitive performance on seven out of nine datasets, including achieving top rankings in three instances.

Further promoting transparency and collaboration, the authors have made the source code of EmbedTrack publicly available. This open-source implementation enhances reproducibility and facilitates the advancement of research in the field. Interested researchers can access the code at https://git.scc.kit.edu/kit-loe-ge/embedtrack [^1].

1. <https://elifesciences.org/articles/59187>

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The paper introduces 3DeeCellTracker, a newly developed program by Wen et al., which harnesses the power of deep learning to segment and track cells in 3D time-lapse images. This innovative tool offers versatility in image analysis, capable of handling various types of images acquired from cutting-edge microscope systems. As a result, it serves as a valuable resource for researchers in biology, medical research, and drug development.

A notable feature of 3DeeCellTracker is its user-friendly interface, distinguishing it from existing algorithms. By prioritizing ease of use and delivering consistent results, it streamlines the process for scientists analyzing cell activities over time in 3D images. This accessibility enhances the adoption of the program among researchers, regardless of their expertise level in computational biology or image analysis.

The algorithm's broad applicability is showcased through successful applications in diverse research areas. From tracking the activity of nerve cells in microscopic worms to monitoring beating heart cells in small fish and studying cancer cells in laboratory settings, 3DeeCellTracker demonstrates its effectiveness across different domains of research. This versatility underscores its potential to contribute significantly to various fields of study and advance our understanding of complex biological processes.

1. <https://academic.oup.com/bioinformatics/article/37/2/285/6070098>

The paper introduces CellTracker, a user-friendly software designed for automated cell segmentation and tracking in time-lapse microscopy images. It encompasses essential steps in image analysis, including project management, image pre-processing, cell segmentation, tracking, manual correction, and statistical analysis such as quantifying cell size and fluorescence intensity.

One of CellTracker's key features is its flexibility and scalability. It provides an annotation tool and supports model training from scratch, offering a customizable solution for dataset analysis tailored to specific research needs.

Furthermore, CellTracker is open-source software released under the GPL-3.0 license, ensuring accessibility and allowing researchers to modify and adapt the tool as needed. This open-source nature promotes collaboration and facilitates innovation in the field of cell image analysis.

Resources related to CellTracker, including the source code, instruction manual, and demos, are readily available on GitHub. This availability promotes transparency and simplifies the adoption of the software by the scientific community, enabling researchers to leverage its capabilities for their own studies.

1. <https://www.nature.com/articles/s41592-019-0403-1>

The paper offers a comprehensive survey of three crucial tasks in cell image analysis: segmentation, tracking, and classification, underscoring their significance in biomedical research and drug discovery. It highlights the advancements achieved in these areas through the application of deep learning technologies.

In addition to outlining the progress made, the paper addresses the challenges encountered when applying machine-learning algorithms to cell image analysis. It emphasizes the existing gap between academic research and practical implementation while reviewing advanced machine learning technologies like active learning, transfer learning, and noisy learning. These approaches aim to mitigate challenges such as data scarcity and annotation workload associated with deep learning methods.

Unlike previous surveys, this paper provides a more technical perspective on deep learning in cell image analysis. It explores the promising outcomes of deep learning-based approaches in cell segmentation and tracking, showcasing their potential to uncover intricate biological phenomena underlying cellular phenotypes. This technical insight contributes to a deeper understanding of the capabilities and implications of deep learning in advancing cell image analysis methodologies.

1. <https://www.mdpi.com/1999-4893/15/9/313>

The paper delves into AI methods tailored for traditional label-free microscopy techniques such as Phase Contrast (PhC), Differential Interference Contrast (DIC), and Brightfield (BF), with the aim of capturing dynamic cell behavior over time.

A thorough review of recent advancements in cell segmentation, event detection, and tracking specific to label-free microscopy imaging is provided, offering valuable insights for biological and biomedical studies.

The study presents an efficient image segmentation pipeline comprising image reconstruction, foreground-background segmentation, seed-point extraction, and cell segmentation tailored to various label-free microscopy techniques.

Furthermore, it conducts a comprehensive comparison of cell image segmentation methods designed for common label-free microscopy techniques, contributing to a deeper understanding of fundamental biological events observable through these methods.

In addition to the methodological discussion, the paper also compiles lists of publicly available software, datasets, and evaluation metrics commonly used for assessing the effectiveness of the discussed methods. This effort enhances accessibility and reproducibility in the field of label-free microscopy imaging, facilitating further research and development in this area.

1. <https://www.sciencedirect.com/science/article/pii/S2352711018301882>

The paper introduces Usiigaci, an all-in-one, semi-automated pipeline designed for stain-free, instance-aware segmentation, tracking, and visualization of cell movement and morphological changes in phase contrast microscopy (PCM).

Usiigaci achieves stain-free, instance-aware segmentation through the utilization of a mask regional convolutional neural network (Mask R-CNN). This method is particularly crucial for accurately segmenting cells in PCM images with high cell density.

In addition to segmentation, the paper presents a Trackpy-based cell tracker equipped with a graphical user interface. This feature enhances the tracking process and facilitates data verification, ensuring the accuracy of cell tracking results.

The performance of Usiigaci is validated using electrotaxis of NIH/3T3 fibroblasts, showcasing its capability to provide highly accurate cell movement and morphological information for quantitative cell migration analysis.

Usiigaci significantly contributes to advancing the field by offering a reliable tool for researchers to analyze cell migration quantitatively. This capability is essential for various biological and biomedical studies, enabling deeper insights into cellular behaviors and facilitating the development of novel therapeutic strategies.

**Conclusion:**

Using deep learning, you can tackle a wide range of complex tasks across various domains, including computer vision, natural language processing, and biomedical research. In computer vision, deep learning models excel at tasks like image classification, object detection, and image segmentation, enabling applications such as autonomous driving, facial recognition, and medical imaging analysis. In natural language processing, deep learning models can understand and generate human-like text, leading to advancements in machine translation, sentiment analysis, and chatbots. In biomedical research, deep learning is revolutionizing fields like genomics, drug discovery, and medical image analysis by extracting meaningful patterns from large datasets, aiding in disease diagnosis, drug development, and personalized medicine. Overall, deep learning empowers researchers and practitioners to solve complex problems, extract valuable insights from data, and drive innovation across a wide range of disciplines.