

Deep Learning for Cellular Image Analysis

With the recent advances in computer vision and machine learning, investigation and interpretation of imaging data has been extensively explored. This paper presents an intersection between deep learning and cellular image analysis with the applications of image classification, image segmentation, object tracking, and augmented microscopy. Image processing has expanded the scope of deriving information in the field of medical sciences by rendering the information in temporal and spatial domains.

The paper speaks of the advancement in the techniques for solving computer vision challenges. While the conventional machine learning techniques work feature engineering, deep learning renders the supervised and unsupervised methods with built in feature engineering. With a focus on bioscience applications, the main concern is the development of a combination of data and software. Deep learning requires enormous computational resources when compared to other frameworks. It requires an annotated training dataset, effective training models and implementation of the trained models over unused dates.

Diversity, high quality and error free annotations, are prominent aspects of model training for high accuracy. Data processing methods such as data augmentation and transfer learning methods are useful in overcoming the barriers. With access to GPUs, inbuilt computations and derivatives, deep learning frameworks perform the implementations of their own.

The major tradeoff between overfitting and underfitting, often reduces the performance of the architecture. Overfitting depicts the poor performance on the validation dataset, while undercutting explains the failure in learning from the training dataset. Transfer learning serves as a robust technique to overcome the overfitting challenges when it comes to smaller datasets. The pre-trained weights with larger datasets can be used on the smaller datasets, which computes the overfit and minimizes it.

Image classification:

The major advantage of image classification is the transfer learning to use the pre-trained model/weights trained with larger dataset, to modify the final layer and apply it for the smaller dataset of annotated data. To implement image classification on cell morphology, instead of evaluating the labels of the images, a feature extraction approach has been employed. In a recent study, researchers used a fluorescent differentiation marker to construct a ground truth before training a classifier to directly identify differentiated cells. Researchers combined microfluidics and microfluidics to separate protein localisation and cell-to-cell interactions are used to classify cells.

These results show that deep learning is a useful tool for biologists who want to better interpret their imaging data.

Image segmentation:

Image segmentation refers to the partitioning of images for insights and features from the image data. Semantic segmentation provides a pixel-level annotation by partitioning the image into semantically meaningful parts as classes.

Instance segmentation are deep learning schemas for segmentation. Improved segmentation accuracy boosts object tracking in live-cell imaging and diffraction-limited object tracking. Deep learning approaches based on object detection have also been modified for instance segmentation. Faster R-CNN and Retinanet are two approaches that predict bounding boxes for all objects in an image and employ non-maximum suppression to eliminate redundant bounding-box predictions. R-CNN, one of the most accurate methods for instance segmentation on general-purpose datasets, to anticipate each bounding box. These methods have been used for cellular data for successful implementation.

Object tracking:

Object tracking is the technique of following an object in a series of images. It consists of two parts: object detection and object linkage. Nearest-neighbor, state-space models, and linear programming are examples of traditional techniques. Multiple indicators like item centroids, intensity, and morphology are merged into a similarity score in linear-programming techniques to link objects between frames. Complex behaviors like disappearance, splitting, and merging may be treated with linear programming. Deep learning has been used to track diffraction-limited particles, animals, and cells in recent years. Deep learning, on the other hand, enhances segmentation accuracy, which is important because tracking success is strongly dependent on precise identification of the objects to be tracked in each frame. By tracking a single object, attempting to acquire a similarity score directly from data for use in a linear-programming framework, or treating tracking as a reinforcement learning problem, deep learning techniques to object linking perform well on general-purpose datasets.

Augmented microscopy:

The extraction of latent information from biological images, such as the identification of the positions of cellular nuclei in bright-field images, is known as augmented microscopy.

Deep learning works well with augmented microscopy. To date, each method has compared spatially synchronized transmitted light images with images from other modalities in order to find significant correlations between the images. A conditional generative model featured two unique networks: one to learn variations in nucleus and cell shape, and another to learn the relationships among subcellular structures. On a per-pixel basis, Google researchers used a modular method to anticipate the placement and strength of distinct fluorescent markers. Multi-task and transfer learning were used extensively in their research to create networks that were resistant to a variety of imaging conditions, modalities, labels, sample kinds, and acquisition conditions. Other applications of augmented microscopy employ deep learning in real time to give content-aware picture denoising, increase image resolution, and alleviate axial undersampling (to reduce phototoxicity).

All of these advancements would benefit researchers who conduct live-cell imaging investigations and those working in spatial genomics by replacing existing analysis pipelines with more accurate deep learning alternatives, resulting in a significant reduction in curation time. The article suggests combining tool development with biological discoveries.