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Optimization of cell annotation process: combining manual and automatic labeling in biomedical data analysis optoelectronic systems

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ABSTRACT

Modern biomedical research requires highly accurate and scalable image annotation, especially when working with cryomicroscopic data. One of the key stages in analyzing such images is the annotation of cellular structures, which is essential for training machine learning models. This paper explores an approach to optimizing the process of cell annotation by combining manual and automatic labeling within the CVAT (Computer Vision Annotation Tool) environment. The proposed method integrates the precision of manual annotation with the efficiency of automated segmentation algorithms, significantly reducing labor costs and improving reproducibility. During the study, the capabilities of CVAT were analyzed, built-in automated tools were tested, and scenarios for their combined use with manual corrections were described. The advantages of the hybrid approach, common errors, and ways to minimize them are discussed. The results demonstrate that combined annotation enables faster preparation of training datasets without significant loss of quality, especially when working with large volumes of images. This approach may be beneficial for automated biomedical data analysis systems where rapid scaling is required without compromising accuracy.

Keywords: cell annotation, cryomicroscopy, CVAT, image segmentation, manual labeling, automatic labeling, machine learning, biomedical imaging, data annotation tools

1. INTRODUCTION

Image annotation is one of the key stages in data preparation for training computer vision models, especially in biomedical analysis tasks. In recent years, there has been a growing interest in cryomicroscopic imaging, as it enables the study of cellular ultrastructure and biological tissues in their native (undisturbed) state thanks to imaging at ultra-low temperatures. However, the high resolution and large volume of such images present significant challenges for manual processing, particularly when scaling up research efforts.

The classical approach based on manual annotation is time-consuming, labor-intensive, and requires highly qualified experts, making it inefficient when thousands of images need to be labeled. Moreover, manual work is prone to subjective errors that may vary between annotators. These limitations drive the need for hybrid solutions that combine the precision of manual annotation with the speed and scalability of automated algorithms^{1,2,3}.

Modern annotation tools such as CVAT (Computer Vision Annotation Tool) offer researchers powerful features to implement such hybrid approaches. CVAT supports manual object labeling as well as semi-automatic and automatic methods through integration with machine learning models. This makes it particularly well-suited for medical imaging tasks, where accuracy, flexibility, and scalability are crucial^{3,4,5}.

This study explores a methodology that combines manual and automatic annotation in CVAT to optimize the cell labeling process on cryomicroscopic images. The approach examines how using preliminary automated annotations followed by manual refinement can significantly reduce labor costs and accelerate training dataset preparation, while maintaining the high accuracy required for model development^{7,8,9}.

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Additionally, this work discusses CVAT setup, selection of annotation tools, evaluation of annotation quality, as well as common errors and strategies to minimize them. The result is a reproducible and efficient methodology that can be applied in biomedical and scientific projects working with large volumes of complex imaging data^{10,11,12,13}.

2. MATERIALS AND METHODS

This study utilized modern tools and technologies to optimize the process of annotating cryo-microscopic cell images and automate the data processing stages. The primary material for the research consisted of cryo-microscopic cell images (Fig. 1) obtained through high-resolution microscopes at low temperatures. These images provide detailed information on cellular structures such as membranes, nuclei, mitochondria, and other organelles, allowing for the examination of cellular anomalies and pathologies. The images were divided into training, validation, and test sets to ensure comprehensive model testing.

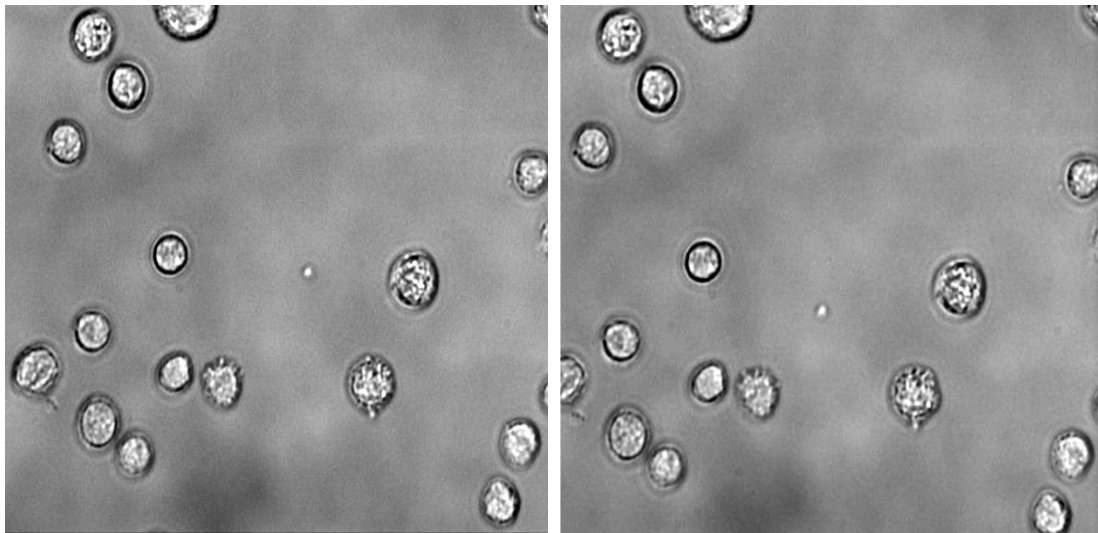


Figure 1. Examples of Cryo-microscopic cell images: after 10 min from start freezing protocol (left); after 15 min from start freezing protocol (right)

The system used for data annotation was CVAT (Computer Vision Annotation Tool), designed specifically for annotating images. This system provides a user-friendly interface for creating annotations using both manual and semi-automatic methods. Manual annotation involved drawing bounding boxes or masks around the cells, while automatic annotation was based on image segmentation algorithms. A critical component for storing and managing large volumes of data was MinIO, which provided a high-performance solution for storing images and annotations, significantly speeding up the process of data upload and access. For image processing and data preparation, Python libraries such as NumPy and OpenCV were used, along with deep learning frameworks like TensorFlow and Keras^{14,15,16}. Before being uploaded into the CVAT system, the images underwent preprocessing, which included normalization, conversion into standard formats (e.g., TIFF or PNG), and brightness adjustment to ensure data uniformity for subsequent annotation. A Convolutional Neural Network (CNN) method was chosen for building the machine learning model, as it demonstrated high efficiency in segmentation and object detection tasks. The model was trained using the prepared annotated data, with data augmentation techniques such as rotation and scaling applied to increase the model's overall accuracy^{17,18,21,22}.

Model performance was evaluated using standard metrics such as IoU (Intersection over Union), Precision, Recall, and F1-score, which allowed for an objective assessment of annotation quality and cell detection accuracy. These metrics not only measured prediction accuracy but also evaluated completeness, which is crucial in biomedical applications where each cell is significant. Notably, all stages of the work were integrated into a single pipeline using Docker and Jupyter technologies, ensuring standardization, reproducibility of experiments, and flexibility in working with various datasets and models. Thus, the chosen approach effectively and accurately annotated large volumes of data while ensuring the reproducibility of results and scalability of the process. The combination of automatic and manual annotation methods, along with the use of high-performance tools for data storage and processing, significantly improved the quality and speed of cell image annotation, which is critical for further research in the field of biomedical analysis^{3,19,20}.

3. RESEARCH RESULTS AND DISCUSSION

During this study, a hybrid methodology for annotating cryomicroscopic cell images was implemented and tested, based on sequential application of automatic annotation followed by manual correction in the CVAT (Computer Vision Annotation Tool) environment. The goal was to achieve an optimal balance between annotation speed and the quality of the created annotations, which are necessary for training machine learning models.

The experimental dataset consisted of high-resolution cryomicroscopic images (TIFF and PNG formats) containing various cellular structures. The images were preprocessed for normalization and conversion to a format supported by CVAT. A total of 150 images were used for the experiment, of which 100 were used for annotation and 50 for model testing. Three annotation scenarios were implemented and compared: Manual annotation only: Annotating cells manually from scratch; Automatic annotation only: Using a pre-trained segmentation model without manual adjustments; Hybrid approach: Automatic annotation followed by manual review and refinement. The analysis of time spent annotating a single image showed the following results: Manual annotation: On average, 9–12 minutes/image. Automatic annotation: Less than 1 minute/image, but without validation. Hybrid approach: 4–6 minutes/image. This means that the hybrid approach allows saving 50–60% of the time compared to fully manual annotation, while significantly improving the scalability of the process. To assess the quality of annotations, standard metrics were used: IoU (Intersection over Union); Precision; Recall; F1-score (Table1).

Table 1. Structural diagram of the block of preliminary prototyping of splints (1 - patient; 2 - CT of the upper respiratory tract; 3 - downloading the Dicom file; 4 - image preprocessing and filtering; 5 - localization of curvature of the nasal septum; 6- medical image segmentation unit; 7- calculation of the length of the nasal septum)

Method	IoU	Precision	Recall	F1-score
Manual Annotation	0.86	0.91	0.88	0.89
Automatic Annotation	0.72	0.78	0.69	0.73
Hybrid Approach	0.83	0.88	0.85	0.86

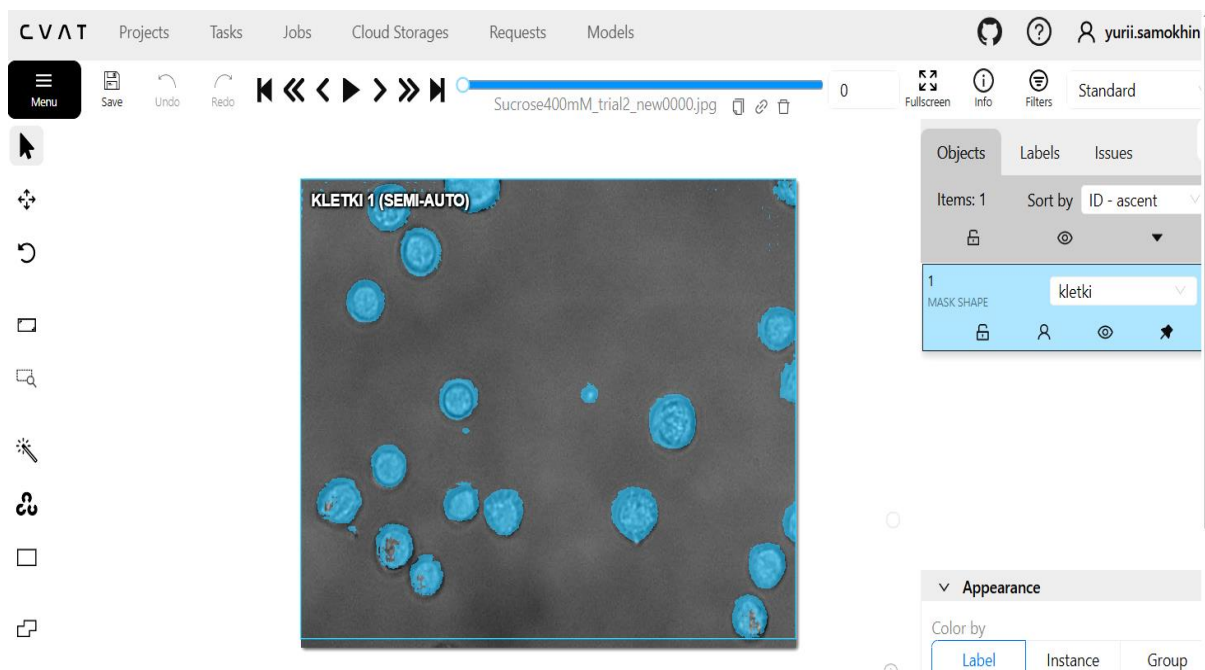


Figure 2. Structural diagram of the block of preliminary prototyping of splints (1 - patient; 2 - CT of the upper respiratory tract; 3 - downloading the Dicom file; 4 - image preprocessing and filtering; 5 - localization of curvature of the nasal septum; 6- medical image segmentation unit; 7- calculation of the length of the nasal septum.)

The hybrid approach demonstrated almost the same quality as manual annotation, but with significantly lower time costs. It was especially effective for images with repetitive structures and distinct boundaries.

During the analysis, typical errors of automatic annotations were identified: Merging of closely located cells into one area; Incomplete recognition of cells with blurred boundaries; Missing annotations for small or partially occluded objects; The hybrid approach proved highly effective in correcting these issues through manual adjustment

The use of combined annotation offers the following advantages: Time savings without significant loss of quality; Reduction of human error due to automatic pre-annotation; Versatility — the method can be scaled to other image types and objects; Integration into the model training pipeline, making the annotation process reproducible and modular.

Thus, the results of the experiment confirm that combining manual and automatic annotation in CVAT is a practical, efficient, and accurate solution for preparing biomedical datasets, particularly for cell detection in cryomicroscopic images (Fig. 2).

4. CONCLUSIONS

The study proposed and tested a combined approach to annotating cryo-microscopic cell images using CVAT (Computer Vision Annotation Tool). This method, which combines automatic annotation with subsequent manual verification and correction, significantly improved the efficiency of preparing annotated data while maintaining high annotation quality, which is crucial for creating training datasets for machine learning.

One of the main advantages of the proposed method is the reduction in annotation time. Manual annotation typically took 9–12 minutes per image, while automatic annotation reduced this process to under 1 minute but required additional verification. Using the combined approach allowed annotation time to be reduced to 4–6 minutes per image, which is 50–60% faster than the fully manual method. This is especially important when dealing with large datasets, which is often the case in biomedical research.

Despite the time savings, the quality of annotations in the combined approach was almost identical to manual annotation. Evaluation using standard quality metrics such as IoU, Precision, Recall, and F1-score showed that the proposed method could achieve high accuracy comparable to manual annotation while significantly reducing time costs. This confirms that the combined approach is optimal in terms of balancing speed and accuracy.

The use of automatic methods for preliminary annotation effectively addresses common issues such as object merging and missing small or partially obscured cells. These errors can be successfully corrected during manual review, making the method flexible and suitable for various types of images. This approach significantly reduces error rates, as confirmed by the successful correction of object merging and the detection of blurred cells.

Moreover, the combined approach allows for the scalability of the annotation process to large datasets, making it a universal tool for working with biomedical images. The possibility of integrating this method into reproducible pipelines using technologies such as Docker and Jupyter enhances the standardization and reproducibility of scientific research.

Ultimately, the combined annotation method using CVAT represents a highly effective strategy for preparing high-quality training datasets in the field of biomedical image analysis. It significantly improves the quality of scientific research, accelerates data preparation for machine learning, and aids in the creation of more accurate analysis models. This approach has broad potential for application in medical diagnostics and scientific research, accelerating the process of detecting anomalies in cellular structures and diseases.

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