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Automated Detection of Bacterial Colonies in Petri Dishes Using YOLOv5 and Computer Vision

Sergio Arturo Meza Miguel Huerta, Rafael Guzmán Cabrera, Teodoro Córdova Fraga,
Jose Marco Balleza Ordaz, Svetlana Kashina*

***Abstract*—Automation of microbiological analysis is a growing need in both academia and industry due to the repetitive and error-prone nature of manual bacterial colony counting. This work proposes an automated approach based on computer vision and deep learning for the segmentation and detection of bacterial colonies in Petri dish cultures. YOLOv5 convolutional neural network was used, trained on a public dataset composed of images of Escherichia coli, Pseudomonas aeruginosa, and Staphylococcus aureus colonies. The dataset was manually annotated and augmented using data augmentation techniques. Subsequently, preprocessing strategies were applied to enhance image quality, improving edge detection. The results show a significant improvement in evaluation metrics after preprocessing: mean average precision (mAP) increased from 72.1% to 94.6%, accuracy from 70.1% to 92.7%, and recall from 67.1% to 89.3%. These figures significantly exceed results reported in previous work on the same domain and validate the use of models such as YOLOv5 in colony detection tasks without classification by type. This approach offers an effective, rapid and low-cost solution for automating bacterial colony counting, constituting a viable alternative to existing semi-automated methods..**

***Index Terms*—Bacterial colonies, Petri dishes, YOLOv5, computer vision.**

I. INTRODUCTION

The automatization of frequently repeated processes is fundamental for both academic and industrial areas, due to time, cost and labor optimization. In microbiology, many procedures follow standardized protocols. The most common one is the development of bacterial cultures, which can be performed by two methods: liquid culture and Petri dish surface culture. The Petri dish culture analysis is a laborious process and requires manual count of colony forming units (CFU) and constant supervision to impede external contamination. This procedure is repetitive and may be subjected to human errors, for these reasons it is important to automate CFU counting.

In previous works, the semi-automated system was introduced by Rodrigues et al. [1], in which the authors used image processing techniques for the segmentation and detection of bacterial colonies, obtaining results with an accuracy between 84% and 95% depending on the colony type.

In most of the research that seek to segment and detect bacterial colonies in Petri dishes with solid medium, it is usually done through image processing. Particularly, Majchrowska et al. in 2021 reported Deep Learning use, where an error of less than 5% is reported for the bacteria count, and a Mean Average Precision (mAP) between 52% and 59%.

In addition to developments in colony detection, there is clear interest from the scientific community in automating colony classification and detection using machine learning techniques due to their non-invasive nature. In the field, where are some works, which exhaustively describe advances in classification [3], including classic models such as the k nearest neighbors method (K-NN) and Support Vector Regression (SVR) [4–8], with reported accuracy rates between 90% and 99%. Also, some methodologies that use deep learning for classification [9–13] presented accuracy rates between 52% and 78.47%.

Subsequently, Rodrigues et al. proposed a novel approach [14], in which they used pre-trained convolutional neural network (CNN) models such as residual neural network (RESNET) for bacterial colonies classification, achieving accuracies between 83% and 92%, depending on the colony type. These results are comparable to those previously obtained with a semi-automatic system.

Several studies have proposed automating bacterial colony segmentation and counting using image processing techniques, obtaining significant results. However, current technological advances present new opportunities to improve these processes. This work presents a hybrid approach that combines image processing with deep learning techniques, specifically convolutional neural networks (CNNs), with the aim of optimizing bacterial colony segmentation and counting in culture images.

II. METHODOLOGY

A. *Dataset*

For this study, a database of images of bacterial cultures in Petri dishes from Rodrigues et al. was used. These images correspond to colonies of Escherichia coli, Pseudomonas aeruginosa, and Staphylococcus aureus, obtained under controlled conditions.[1]

B. *Procedure*

For development, the images were uploaded to the Roboflow labeling platform, where a manual annotation process was performed to identify and delimit all bacterial colonies present in each image. After obtaining the labeled images, data augmentation was performed. Data normalization and

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Sergio Arturo Meza Miguel Huerta, Teodoro Córdova Fraga, Jose Marco Balleza Ordaz, Svetlana Kashina1 are with the Division of Science and Engineering, University of Guanajuato, Mexico.

Rafael Guzmán Cabrera is wirh the Engineering Division, University of Guanajuato, Mexico.

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augmentation techniques were applied through rotations, color scaling, brightness and contrast adjustments, and "salt and pepper" noise induction. With the results of the labeled and augmented dataset, it was randomly divided into three partitions: training, validation, and testing. The partitions were divided into the following proportions:

- 80% for training,
- 10% for validation,
- 10% for testing.

The labeled and partitioned data were used to train a pre-trained network with CNN architecture. For this case, a YOLOv5 network (You Only Look Once version 5) was used.

The 80/10/10 partition is a standard partition when working with CNN models. However, this can vary considerably within models. 50/50 partitions have been reported in [3], which specifically mentions a 50/50 partition for bacterial colony classification. This allows for robust adjustment of the model's hyperparameters. However, after obtaining the first results, retraining was sought by performing preprocessing techniques such as edge reinforcement.

C. *Performance statistics*

For performance statistics, since this is a pre-trained CNN model, the following metrics were used for object detection to determine the performance of our model: mAP (Mean Average Precision), Recall, and Accuracy.

Precision measures the proportion of true positives among all positive predictions made by the model:

$$Precision = \frac{True\ positive}{True\ positive + False\ Positive}. \qquad (1)$$

Recall indicates the proportion of true positives correctly identified by the model among all elements that belong to the positive class:

$$Recall = \frac{True\ positive}{True\ positive + False\ negative}. \qquad (2)$$

Mean Average Precision (mAP) is the average of the Average Precisions (AP) calculated for each class. Average Precision is obtained from the area under the Precision-Recall curve.

$$mAP = \frac{1}{N} \times \sum_{i=1}^{N} AP_i. \qquad (3)$$

Here N is the total number of classes and AP_i is the average precision for class i

III. RESULTS AND DISCUSSION

First, detection was performed without preprocessing the images, which led to the metrics presented below in Figure 1. The result, while not satisfactory, is significantly positive considering the lack of preprocessing.

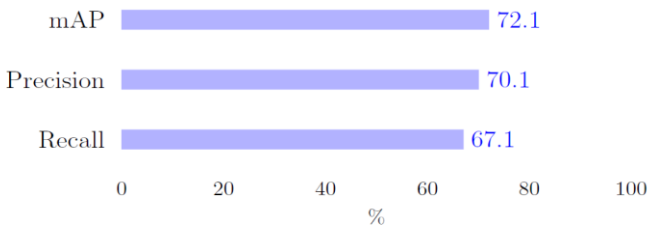

Fig. 1. Evaluation results of the model without preprocessing.

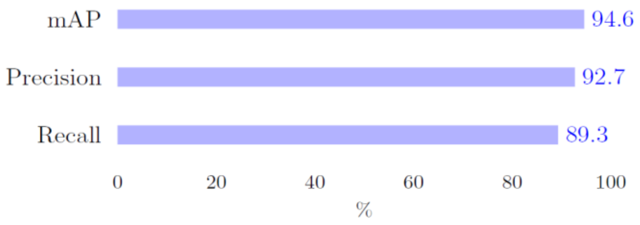

Fig. 2. Model evaluation results.

Despite these metrics exceeding 50% for a detection methodology without classifying the type of bacteria, these results are considerably low to automate the process of segmenting and counting bacterial colonies within the Petri dish. Therefore, image preprocessing was performed to enhance the edges, and to be more selective with the data augmentation ratios.

For these statistics, the following results were obtained, as shown in Figure 2.

It can be seen that mAP was of 94.6%, a Precision of 92.7%, and a Recall of 89.3%. These results are expressed generally for all bacterial colonies, since classification is not sought within the model; the main interest was its performance in detecting bacterial colonies.

The mAP of 94.6% is a satisfactory result, as the model exhibits high accuracy in detecting bacteria. A Precision of 92.7% indicates a low rate of false positives. On the other hand, the 89.3% Recall reflects its lower detection rate, with a 10.7% chance of missing objects. This is a particular problem for images with a large number of bacteria, given that the more colonies there are within the image, the more likely it is to miss objects present within the image. These results are significantly better than the first results obtained for colony detection.

The mAP augmented from 72.1% to 94.6%, and accuracy increased from 70.1% to 92.7%. Finally, Recall increased from 67.1% to 89.3%. As it can be seen, the original mAP showed a significant result, since [2] reported an mAP of 52% to 59% for the worst and best models, while in this work the result was 72.1% without using preprocessing, and after using preprocessing for the images it resulted in a detection rate of 94.6%.

Unlike most articles that work with ResNet versions for colony classification and detection, Yolov5 was used in this paper. Since Yolov5 is a CNN model that has been used in recent years [15], researchers used the Yolov5 model to detect microorganisms in different environments as a lower-cost and time-consuming alternative, demonstrating the model's versatility and technical capabilities.

The results obtained in this work were highly positive. As explained in the introduction, semi-automated models such as that of Rodrigues et al. [1] report accuracies between 84% and 95%. Our fully automated model, without preprocessing, achieves an accuracy of 70.1%, and after applying preprocessing, it improves to 92.7%, placing it within the range of semi-automated models.

Furthermore, when compared with works such as those of Majchrowska et al. [2], which report mAP between 52% and 78.47% with a 5% error margin, our model presents a minimum mAP of 72.1% and a maximum of 94.6%, significantly surpassing these results.

IV. CONCLUSIONS

The implementation of YOLOv5 proved to be an effective and efficient alternative for bacterial colony detection, with a reasonable computational cost and high accuracy. This validates its applicability in environments where colony counting and segmentation automation is required without the need to classify the bacteria type.

Future work could explore colony classification by type, integrating segmentation and classification methods into a joint model, and applying these techniques to other types of microorganisms or culture conditions.

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