ANALYSIS OF MICROBIOLOGICAL SAMPLES USING THE SEGMENT ANYTHING MODEL

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Abstract: *This paper describes the application of the Segment Anything Model (SAM) to the analysis and image processing of microbiological samples containing common types of bacteria and yeast that can be found in various environments. The SAM model was tested on images from the AGAR dataset, which contains 18,000 images of microbiological samples containing five microorganisms such as Staphylococcus aureus, Bacillus subtilis, Pseudomonas aeruginosa, Escherichia coli, and Candida albicans.*

Key words: *image segmentation, instance segmentation, semantic segmentation, computer vision, microbiology*

1. INTRODUCTION

Microbiological contaminants such as bacteria, fungi, viruses, yeast, and protozoa are of great interest, and concern to food manufacturers due to the potential risk of food poisoning or food spoilage (Maruthamuthu et al., 2020) (Talo, 2019). The increasing demand for digital microbiological data presents an opportunity for microbiologists and laboratory professionals to easily detect microorganisms (Egli et al., 2020). This change can personalize diagnostics and treatments, improve digital data quality, and reduce healthcare costs. Conventional culture-based methods for microbial detection are time-consuming, while digital imaging has attracted attention for its rapid approach. Digital microbiology also has the potential to significantly impact public health and pathogen surveillance. To embrace digitalization, microbiology laboratories must develop expertise in digital medicine and food analysis, including data handling, perception, and infrastructure (Soni et al., 2022).

In recent years, methods such as computer vision, artificial intelligence (AI), and machine learning (ML) trained on large amounts of labeled data, have been increasingly used for automated analysis of medical images and microbiological samples (Goodswen et al., 2021). These methods could be used for the recognition of four different types of microorganisms: bacteria, algae, protozoa, and fungi (Rani et al., 2022). Convolutional neural networks and models such as ResNet-50 can be used to determine the category of microbiological samples (Majchrowska et al., 2021) (Rani et al., 2022) (Talo, 2019). Semantic segmentation is a computer vision method used to analyze images of microbial samples when it is necessary to precisely determine different regions of the image based on their semantic meaning, assigning a class label to each pixel in an image (Zawadzki et al., 2021). Models such as Faster R-CNN and Cascade R-CNN can be used to count colonies of bacteria in images of microbiological samples that can detect individual objects and determine their class. The instance segmentation method aims to provide a detailed understanding of the image by distinguishing between different instances of individual bacterial colonies within an image and assigning each pixel belonging to unique colonies (Zawadzki et al., 2021).

The Segment Anything Model (SAM) developed and trained by Meta company, is used for image segmentation (instance segmentation) (Kirillov et al., 2023). This model was trained using over one billion masks on 11 million images. The SAM model has the possibility of zero-shot generalization, so it can be used for the segmentation of objects in images without additional training. The SAM model can analyze images from a wide range of areas, including biomedical, agricultural, autonomous driving, etc.

2. METHODS

In this study we used the AGAR dataset (Majchrowska et al., 2021) (Annotated Germs for Automated Recognition) that contains 18,000 images, 12,750 higher-resolution (4000×6000px) and 5250 lower-resolution (2048×2048px) images of microbiological samples in Petri dishes. This dataset contains five microorganisms: Staphylococcus aureus, Bacillus subtilis, Pseudomonas aeruginosa, Escherichia coli, and Candida albicans. The microbial cultures were incubated on Trypticase Soy Agar (TSA) plates at 37°C for 18-24 hours. The images from this dataset were taken under diverse lighting conditions with two different cameras.

Staphylococcus aureus, Bacillus subtilis, Pseudomonas aeruginosa, Escherichia coli, and Candida albicans are common types of bacteria and yeast that can be found in various environments, including food microbiology or clinical environment. These microorganisms are commonly studied in microbiology and often used as model organisms for various research purposes, including drug discovery, understanding pathogenicity, and studying host-microbe interactions.

The data flow diagram of the process for the detection and identification of individual bacterial colonies based on the SAM model is presented in Figure 1. The procedure starts with recording a microbial sample using a camera (P1) that generates a digital image that is processed using the SAM model (P2). After the image (D1) is processed using the SAM model, a new image (D2) is obtained in which the bacterial colonies are marked with different colors. As a result of this processing, a CSV (D3) file is also generated that contains the coordinates of the bounding boxes as well as a large number of image files with segmentation masks of each of the identified microbial colonies (D4). The disadvantage of the current version of the SAM model is that it cannot determine the classes of detected objects. An additional convolutional neural network (CNN) should be used to determine the classes of identified items. To identify the classes of individual colonies, it is necessary to crop (P5) smaller images of individual microbiological cultures (D5) from the image of the microbiological sample (D1) using the coordinates of the bounding boxes from the CSV file (D3). Images of individual microbial colonies are then sent to the CNN network (P4), which tries to determine what type of bacteria or yeast is present in that image. In the next step (P5), each of the images from the segmentation mask set (D4) is assigned microbial classes determined by the CNN network (P4).
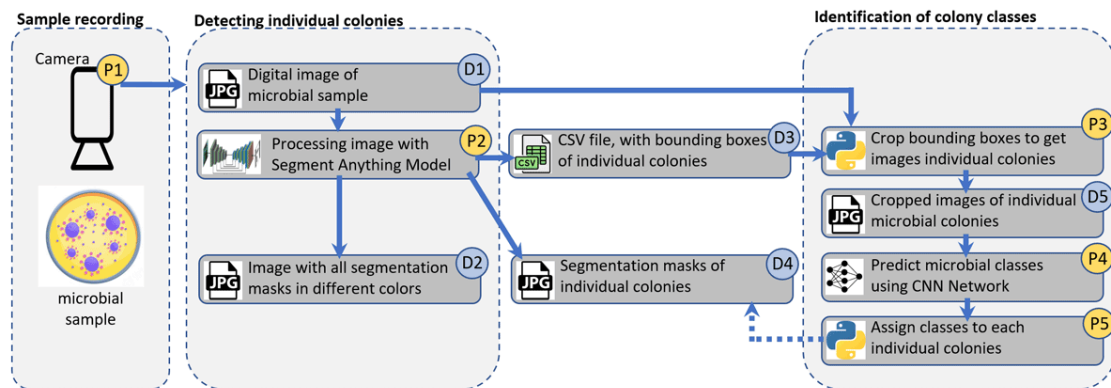

Figure 1: Data flow for detection and identification of individual bacterial colonies

3. RESULTS

After processing the microbiological sample image, the SAM model generates a series of segmentation masks that are saved as separate files for each detected object. Along with the segmentation masks, the model produces a CSV file containing the bounding box coordinates, area, and several other parameters for each detected object, Fig.2. Figure 3 shows a) an image of a microbiological sample, b) an image where the bounding boxes from the SCV file are drawn over the same image sample at the positions where microbiological colonies were detected.

id	area	bbox_x0	bbox_y0	bbox_w	bbox_h	point_input_x	point_input_y	predicted_iou	stability_score	crop_box	crop_box	crop_box_w	crop_box_h
0	6275	879	783	97	83	928	800	1.01563251	0.976960719	0	0	2048	2048
1	5426	797	837	85	79	864	864	1.012376785	0.987010598	0	0	2048	2048
2	7662	841	323	101	96	864	352	1.011579633	0.989614427	0	0	2048	2048
3	6675	1502	592	88	93	1568	672	1.011025429	0.990754545	0	0	2048	2048
4	8226	1238	747	103	99	1312	800	1.011019468	0.986357629	0	0	2048	2048
5	10555	721	386	110	121	800	416	1.010838509	0.990380108	0	0	2048	2048
6	6990	1437	993	101	86	1504	1056	1.009401202	0.98650378	0	0	2048	2048
7	9878	250	836	108	108	288	928	1.009243488	0.985229075	0	0	2048	2048
8	7668	1205	924	101	99	1248	928	1.005910873	0.986789286	0	0	2048	2048
9	7275	1595	533	101	95	1632	544	1.005382538	0.984997272	0	0	2048	2048
10	10983	1378	588	107	125	1440	608	1.004524469	0.98830992	0	0	2048	2048
11	8511	1129	1021	108	98	1184	1056	1.004201531	0.989136755	0	0	2048	2048
12	5916	1638	1094	88	82	1696	1120	1.004196286	0.989404619	0	0	2048	2048
13	6455	1349	464	87	91	1376	544	1.002831221	0.986910999	0	0	2048	2048
14	5113	871	724	92	72	928	736	1.002191186	0.974146247	0	0	2048	2048

Figure 2: CSV file with CSV file with the bounding box of detected objects
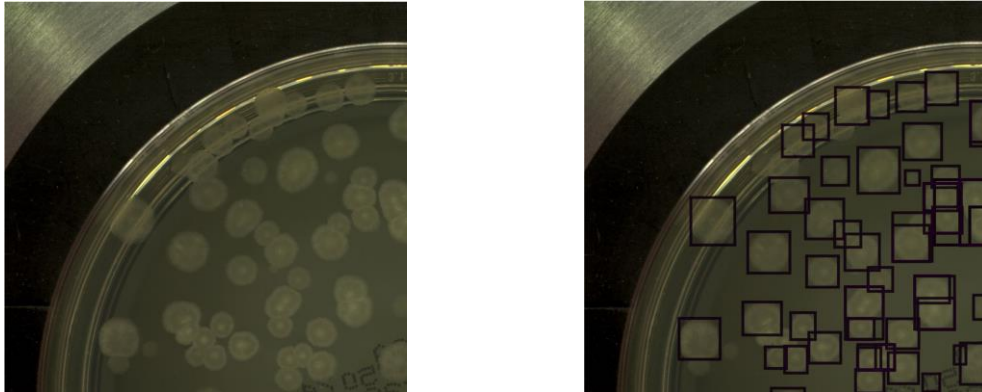

Figure 3: a) Original image of microbiological samples, b) bounding box drawn over the original image

Figure 4 shows a) an image of a microbiological sample and b) an image generated by the SAM model where all detected segmentation masks of individual microbial colonies are shown in different colors.
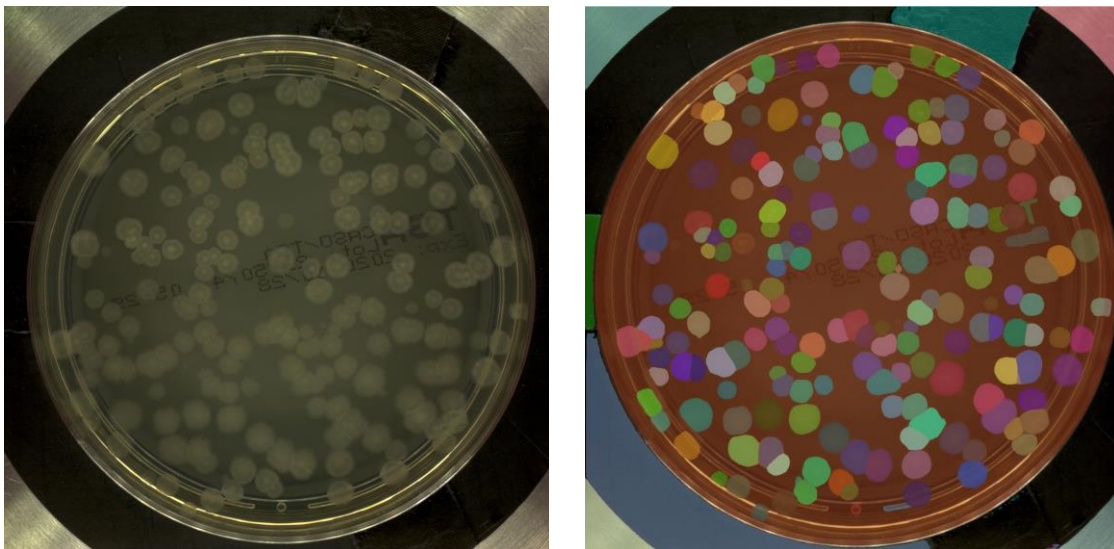

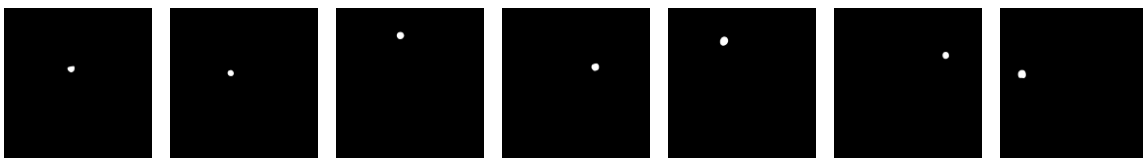*Figure 4: a) Original image of microbiological samples, b) Image processed with the SAM model*

Figure 5. Segmentation masks generated by the SAM model

Figure 5 shows some of the 190 segmentation masks that are the result of processing image 2 using the SAM model.

The precision of SAM model predictions can be determined using Intersection over Union (IoU) metrics (1), which allows comparing predicted bounding boxes with bounding boxes from the dataset.

$$UiO = \frac{Area\ of\ Overlap}{Area\ of\ Union} \tag{1}$$

Since the AGAR dataset does not contain mask files for example segmentation, if we want to determine the accuracy of the predicted masks, we would need to manually label the images from this dataset before calculating the accuracy.

4. DISCUSSION

Models such as Faster R-CNN and Cascade R-CNN (Majchrowska et al., 2021) were previously employed for microbe detection, in this study is used the novel Segment Anything model, which, in addition to object detection, also provides precise instance segmentation. Another significant difference between the R-CNN model and the approach based on the SAM model is that before the R-CNN model is used for image processing, it is necessary to collect images for a dataset, perform labeling, and training of the model. If we want to use SAM models to detect microbial cultures, we can simply download pre-trained models that are trained on datasets containing images from a large number of different domains.

5. CONCLUSIONS

Digitalization, computer vision, and artificial intelligence will have a significant impact on the methods of testing microbiological samples in laboratories. Rapid detection of microorganisms on analyzed articles using automated methods will prevent contaminated products from entering the market and withdrawing them from the market. The Segment Anything model showed excellent results in the processing of images of microbiological samples without additional training. Since the SAM model generates a CSV file with the coordinates of the identified objects, this model can be easily integrated into software that counts microbial colonies on Petri dish images.

6. REFERENCES

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