

Using a Single-Shot Multi box Detector to Find Microorganisms

¹ G. Sudheer Kumar, ² R. Bhavya,

¹Assistant Professor, Megha Institute of Engineering & Technology for Women, Ghatkesar.

² MCA Student, Megha Institute of Engineering & Technology for Women, Ghatkesar.

Article Info

Received: 30-04-2025

Revised: 16-06-2025

Accepted: 28-06-2025

Abstract

Given the prevalence of previous pandemics throughout human history, the development of methods to identify microorganisms has unquestionably benefited the scientific community. The necessity for novel and rapid detection approaches has grown in recent years due to the increasing frequency of pandemics throughout the globe. The present research suggests an as-yet-untested method for microbe detection: the Single-Shot Multibox Detector (SSD). The 840 photos from 21 different microbial groups (40 photographs each) are part of the EMDS-6 Dataset, which is used by the suggested model. In terms of performance, accuracy, and precision, the selected model, SD-MobileNetV2FPN-Lite320x320, from the TensorFlow 2 model zoo, has shown to be more than satisfactory when it comes to identifying microorganisms. The findings demonstrate how versatile and resilient this SSD-based method is. In addition to outlining the present project's future scope, we also talk about the outcomes.

Index Terms— Topics covered include microbes, EMDS-6, Tensorflow, single shot detectors, and object detection.

I. INTRODUCTION

The impact of microorganisms, which make up a large portion of Earth's biodiversity, is substantial in many fields, such as agriculture, medicine, and industry. Their influence on the delicate equilibrium of our ecosystem is two-sided. One good aspect is the immense value they provide due to their metabolic capacities and ubiquitous nature. The intricate carbon, nitrogen, sulfur, and phosphorus cycles are especially dependent on microbes for their delicate balance maintenance. The continual flow of compounds that support life is guaranteed by their capacity to recycle fundamental components. They are the building blocks of food webs and chains, and they help ecosystems be more productive. Soil fertility and agricultural yields are both improved by the actions of certain microorganisms known as Plant Growth-Promoting Rhizobacteria (PGPRs). This microbial adaptability, however, is not without its glaring negative aspect. When some microorganisms invade

their hosts and steal nutrition, it may lead to infectious illnesses [1] [2]. There have been many infectious disease outbreaks in the 21st century, such as SARS in 2003, swine flu in 2009, MERS in 2012, Ebola from 2013 to 2016, Zika in 2015, and most recently, the COVID-19 pandemic in 2019 [3]. Long detection cycles and poor accuracy are two major drawbacks of traditional methods of microbe identification, such as manual microscopic detection techniques. As a result, computer image analysis techniques should be used to the problem of microorganism identification. [4]. This research presents a new method for microbe detection utilizing the Single Shot Multi-box detector (SSD) that is quicker, more efficient, and more accurate. One of SSD's main selling points is how well it can distinguish things in photos using only one deep neural network. Unlike previous methods that rely on object proposals, SSD simplifies the process by combining all calculations into one network, doing away with the

need to generate proposals and then resample. A more precise detection method is essential for developing vaccines and other effective treatments to combat the global healthcare consequences of antimicrobial resistance (AMR), as well as for gaining a better understanding of how microbes behave. Research into methods to enhance the innate immune system or reduce the infections' virulence mechanisms might lead to better treatment outcomes [6]. What follows is the structure of the rest of the paper. Section II presents the literature review. Section III provides an overview of the methodologies used, Section IV presents the findings along with commentary, and Sections V and VI analyze the paper's conclusion and potential future endeavors, correspondingly.

II. LITERATURE REVIEW

Detecting microorganisms is crucial in many different areas, including environmental monitoring and medical diagnosis. Because microbes are so little and come in such a variety of forms, detecting them is no easy task. Here are just a few of the most common ways that microbes might be detected: Type A. Microscopy When it comes to microbiology, microscopy is a must-have instrument for microbial identification, observation, and investigation. Microscopes, which are instruments for magnifying objects too tiny for the human eye, are used in this process. The use of microscopy allows scientists and researchers to study the structure, behavior, and microscopic morphology of microbes. The most basic characteristics used to identify microorganisms are their size and form, however there are other criteria as well. Nevertheless, a great deal of specialized knowledge is required for microscopy-based detection [7]. Culturing (B) Louis Pasteur, a famous French microbiologist and scientist, created microbial culture in the 1860s [8], making it one of the earliest techniques used to identify the presence of bacteria. This technique, which is sometimes called the gold-standard test, relies on a bacterial growth medium. As part of the culturing process, samples are prepared, then they are multiplied, diluted, placed on plates, counted, and finally, isolated into single-species colonies. [9]. Despite its widespread usage, this method of microbe identification has the serious downside of taking an inordinate amount of time to

complete all of its processes [10]. The Polymerase Chain Reaction (PCR) was developed by Kary Mullis in 1985 and is a cornerstone method in molecular biology for detecting microorganisms [11]. By using DNA polymerase and certain primers, PCR is able to amplify target genes. After going through the denaturation, annealing, and extension phases of PCR, DNA bands may be seen by gel electrophoresis. One example of PCR's versatility is real-time PCR, which uses fluorescence signals produced by labeled primers. [12] Biosensors (D) These are analytical instruments that can identify the existence of germs. Several bio-recognition traits and biological components are included into this apparatus to facilitate detection. To replace time-consuming and error-prone traditional detection methods, these technologies convert physiological reactions into measurable signals. The bio-processing, medicinal, agricultural, and food safety sectors all make use of them because of their exceptional sensitivity and specificity. The term "biosensor" can refer to a wide variety of devices, some of which are electrochemical, others are optical, still others use fluorescence-based optical sensors to detect microbes, chemiluminescence biosensors use the light emitted when chemicals are in motion, colorimetric biosensors use changes in color to identify microbes, and so on. [13] [10] [14]. E. Assays using antibodies Reactions between antigens and antibodies are the basis of immunoassay procedures such as the Enzyme-Linked Immunosorbent Assay (ELISA). Using the color that is generated during this reaction, it is possible to determine the amount of analytes in a sample. To perform an immunoassay, a sample containing the analyte of interest is applied to a surface that has been immobilized with a specific antibody. When the analyte binds to the immobilized antibodies, an antigen-antibody complex is formed. The next step is to inject a different set of antibodies that will bind to the formed complex. These antibodies are often tagged with enzymes or fluorescent tags. An enzyme or fluorescence assay may establish the analyte's existence and quantity, laying the groundwork for a diagnosis. [15] Research into microbe identification has changed dramatically, moving away from antiquated approaches and toward cutting-edge computer vision algorithms. since it comes to microbes, the complexities and forms are difficult for traditional methods to capture, especially since they depend so much on human feature extraction. However, formidable substitutes have arisen in the form of state-of-the-art machine learning and deep learning approaches. Machine learning (ML) has completely changed the way microorganisms are detected by using unstructured data from many different historical periods. In the middle of the twentieth century, supervised learning methods such

as Bayes classifiers and linear discriminant analysis laid the groundwork for training models using known categories. A sea change occurred in the 1980s due to the fast development of supervised learning tools including decision trees, support vector machines, AdaBoost, and random forests. Unsupervised learning methods, which aim to discover patterns in the absence of labeled data, gave rise to techniques like hierarchical clustering, K-means, and spectral clustering [16]. The deep learning paradigm change that introduced higher dimensional methods to microbedetection relied heavily on convolutional neural networks and long short-term memory networks in particular. New developments in microbial identification, such as LeNet-5 and AlexNet, have been brought about by the advent of deep learning since 2012. This revolutionary shift from classical machine learning to deep learning has made automated, highly accurate, and efficient microbe identification methods a reality. The timeline highlights the different techniques from each era that contributed to the present state of highly advanced microbial detection capabilities [16].

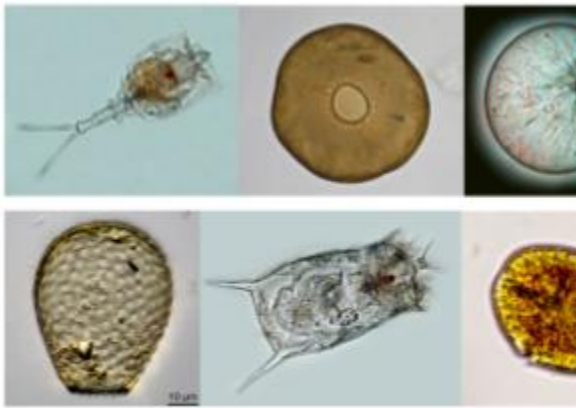


Fig. 1. Sample Images from dataset

III. METHODOLOGY

A. Database For this model's implementation, we consulted the Environmental Microorganism Image Dataset, Sixth Version (EMDS-6). Peng Zhao et al. [17] created a dataset with 21 microbial classifications and 40 pictures per class. Each picture has its own unique set of annotation boxes, and none of them were pre-made. Some examples of the dataset's photos are shown in Fig. 1.

A. Algorithm Section C: Model Structure This study makes use of the SSD MobileNet V2 FPNLite 320x320 model from the TensorFlow 2 Model Zoo. This model is an update to the classic

SSD, a well-liked object detection framework that can identify several objects in a single frame. Object identification and regional proposal networks (RPN)-based methods need two steps each; SSD streamlines the process by combining them into one. It does object categorization and segmentation simultaneously [18]. SSD In order to do classification or detection jobs, MobileNetV2 employs a convolutional neural network (CNN) design that supplies high-level features. To make object detection easier, detection networks like SSD are used instead of the fully linked and softmax layers that are normally included in classification networks. This model has become a prominent option because it provides a fair compromise between the two competing objectives of fast processing in real time and accurate identification. It undergoes pretraining using the COCO dataset's weights. The architecture is described in Section III-B, which focuses on its application to the dataset indicated before. The model is made up of three main parts: the feature extractor (FPN-Lite), the detection network (Single-Shot Multibox Detector, or SSD), and the base network (MobileNetV2), which is necessary for feature extraction. The research elucidates the functions of these parts in object identification in great detail. It also delves into the costs and benefits of real-time processing speed vs accuracy,

Algorithm 1 SSD MobileNetV2 FPNLite Object (320x320)**Input:** 320x320 RGB Image**Output:** List of detected objects with their bound and class scores**Pre-processing:**

- Resize the input image to 320x320 pixels
- Normalize pixel values

Base Network (MobileNetV2):

- Forward pass through the MobileNetV2 back

Feature Pyramid Network (FPN):

- Compute feature maps at different scales

Anchor Box Generation:

- Generate anchor boxes of various sizes and as

Prediction Head:**for** i **in** number of feature maps **do**

- Apply convolutional layers to each feature
- Predict class scores and bounding box offset anchor box

end for**Decode Predictions:**

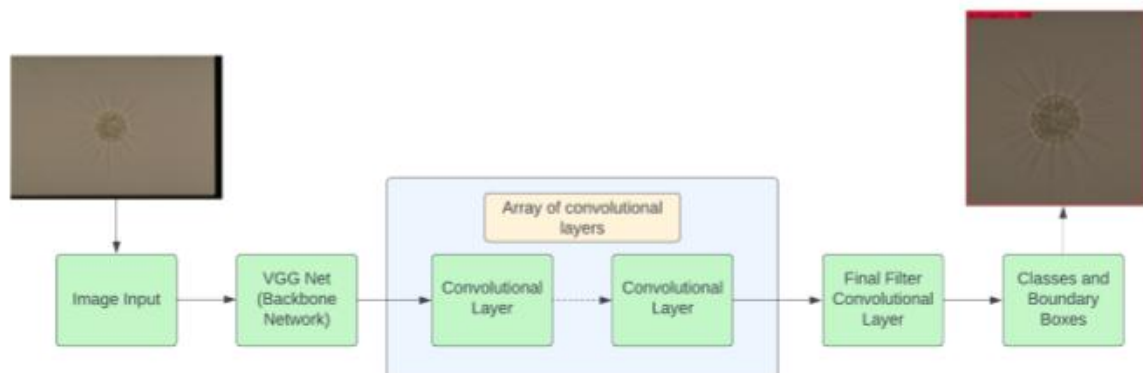
- Transform predicted offsets to bounding box c
- Apply non-maximum suppression to filter out ping boxes

Post-processing:

- Filter and keep the top N bounding boxes confidence scores

Output: List of detected objects with their bound and class scores

when dealing with difficulties associated with recognizing things of different sizes, particularly tiny items. MobileNetV2 is designed to perform computer vision tasks efficiently, particularly on devices with limited resources, such as embedded systems and mobile devices. The utilization of inverted residuals with linear bottlenecks—which helps reduce computational overhead while preserving the network’s capacity to represent complex features in the data—is one of the key improvements for enhanced performance and efficiency introduced in this version of MobileNet, which builds upon the original. Additionally, MobileNetV2 relies on depthwise separable convolutions. Deep convolution and pointwise convolution are the two parts of the normal convolution process that these convolutions separate. This decoupling makes the model more simpler and quicker by cutting down on the amount of parameters and computing needs. When it comes to devices that have limited processing capabilities, this improvement is invaluable. The width and resolution multipliers in MobileNetV2 provide a great deal of versatility. By adjusting the model's width using the width multiplier, one may change the number of channels in each layer. A dataflow for the same is shown in Figure 2. You may change the input picture size using the resolution multiplier as well. With its versatility, users may discover the perfect combination of speed and accuracy, making MobileNetV2 a versatile tool that optimizes resources for a wide range of applications.

**Fig. 2. Model Dataflow Diagram**

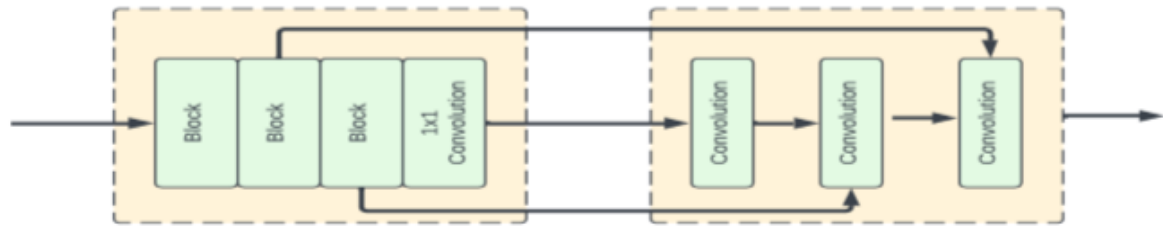


Fig. 3. Mobilenet V2 integration in SSD

usage. Real-time, resource-constrained activities, such as edge computing and mobile image identification, are well-suited to the adaptable neural network architecture known as MobileNetV2. Applications with limited computing resources are ideal for its efficiency and versatility, which enable it to achieve competitive accuracy with fewer parameters [19]. The design incorporates the Feature Pyramid Network (FPN) component to tackle the problem of object detection at various sizes, with a focus on tiny objects. The feature pyramid idea is the basis of FPN-Lite's design, which improves object identification speed and accuracy. In this part, we'll look at how FPN-Lite facilitates multi-scale object identification and how it builds feature pyramids. Dataflow (D) Diagram The suggested model's dataflow is shown in Fig. 2. The overarching goal of this solution is to use convolutional neural networks to make quicker predictions. Annotated photos provide input to our model, as is the case with all convolutional models. In this study, the conventional VGG Net serves as the backbone neural network that receives these inputs. The model then moves ahead by way of a series of convolutional neural networks. The absence of weight update and backward propagation is the distinguishing feature of this design, which is why it is called the "Single Shot Detector." There is a little performance hit since this design decision puts speed ahead of accuracy. After the forward pass is finished, the predictions are consolidated and the output is provided by a final filter convolutional layer. This simplified method is ideal for situations requiring real-time prediction since it enables quick object recognition.

metrics used to evaluate the model: 1) The mAP, or mean average precision, is an all-encompassing metric for evaluating the model's microbial recognition accuracy. The high mAP score of 87.1% that our model achieved indicates its versatility in detecting and classifying microbes. 2) The proportion of correctly predicted microbial occurrences relative to all positive cases expected is called precision. We have By successfully reducing the number of false positives, the model was able to achieve an impressive accuracy score of 75.6%. 3) Remember: A model's recall—also called sensitivity or true positive rate—measures how well it can detect all instances of relevant microbes in the dataset. The high number of true positives collected by our model (87.6% recall score) indicates its efficacy. One general measure of the model's ability to correctly identify microbes across all classes is the mean average precision, or mAP. With an impressive mAP score of 87.1%, our model proved to be capable of detecting and classifying microorganisms in various environments.



Fig. 4. Detection of an Actinophrys Microorganism

IV. RESULTS AND DISCUSSIONS

A. Measurements and Results of the Model Evaluation Tests on the EMDS-6 dataset revealed that the microbe identification model, which used the SSD MobileNet V2 FPNLite 320x320 architecture, performed quite well. The sample outputs obtained are shown in Figures 4, 5, 6, 7, and 8. Here are the main



Fig. 5. Detection of a Colpoda Microorganism

B. Conference Calls The attained mAP of 87.1% shows that the model is strong at identifying microbes, and the 75.6% accuracy and 87.6% recall show that we managed to get a good mix of real and false positives. These findings show that our SSD MobileNet Lite 320x320 V2-based microorganism identification model is dependable and very successful for many different kinds of applications. The model's potential use in areas including microbiology, healthcare, and environmental monitoring is shown by its capacity to correctly detect and characterize microorganisms in various settings (Fig. 4, Fig. 5).

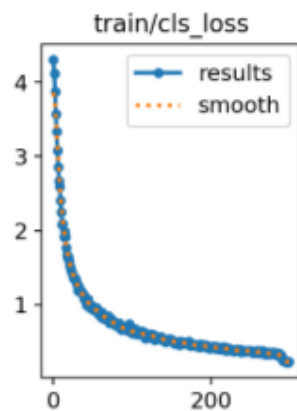


Fig. 6. Training Graphs on microorganism class loss

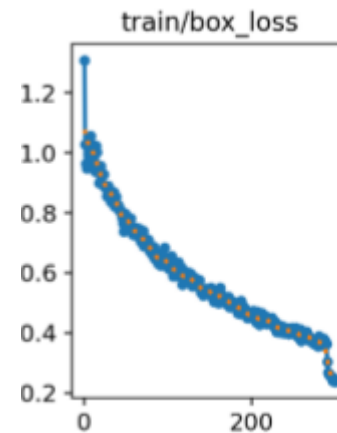


Fig. 7. Training Graphs on box loss

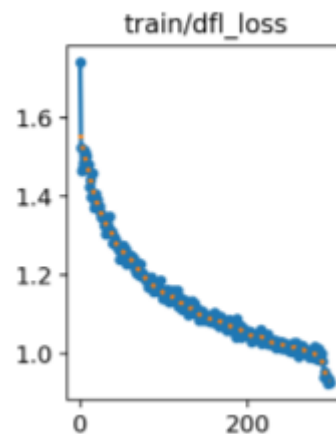


Fig. 8. Training Graphs on distribution focal loss

Taken together, the quantitative measurements and qualitative visual assessments show that the proposed microbe identification approach performs very well. The strong mAP, accuracy, and recall ratings indicate that it might significantly impact microorganism-related applications and research.

V. CONCLUSION

The study presents a compelling argument for the efficacy of Single-Shot Multibox Detectors (SSD) in the domain of microbe detection using the large and diverse EMDS-6 dataset as a testbed. We have shown, by extensive testing and analysis, that our SSD-based model has outstanding recall and accuracy rates when properly categorizing microorganisms from various classes. The generated model's performance exceeded expectations and it is quite stable, despite the fact that speed detection was the primary goal. Equipped with 87.1% mAP, 75.6% accuracy, and 87.6% recall, the

metrics reach extreme levels. Because of their scalability and adaptability, solid-state drives (SSDs) have the ability to change the microbe detection sector, according to this research. SSDs have several uses in environmental monitoring, healthcare, and microbiology. As we further expand and improve SSD, it will become a vital tool for automated microbial identification and analysis in a range of academic and commercial settings. However, its potential in microbe detection remains untapped. The effective use of SSDs in this case signifies a pivotal turning point in the pursuit of more precise and efficient methods for microbe identification.

VI. FUTURE WORK

Object tracking, face identification, pedestrian detection, and, more specifically, microbe detection are just a few of the many uses for SSD and its variants. The current state of SSD research is centered toward enhancing accuracy while maintaining speed, addressing problems like occlusions and crowded scenes, and tailoring the model for specific needs like medical imaging and remote sensing. In conclusion, solid-state drives (SSDs) constitute a major step forward in object recognition, opening up a plethora of practical uses for their efficiency and effectiveness. It is possible to build on this work to create a model that can recognize these microbes in a video stream; then, by refining this model, we can create one that can dependably detect the bacteria while keeping its speed advantage. SSD and its variations are versatile tools that have many uses, one of which is detecting microbes. Methods such as improved post-processing, integration with real-time systems, model compression, transfer learning, and dataset augmentation might be helpful in this regard.

REFERENCES

- [1] A. Gupta, R. Gupta, and R. L. Singh, "Microbes and environment," Principles and applications of environmental biotechnology for a sustainable future, pp. 43–84, 2017.
- [2] A. Pathak, P. Navaneeth, M. Gupta, A. Pradeep, B. G. Nair, P. V. Suneesh, R. Elangovan, L.-R. Sundberg, V. Marjom"aki, and T. S. Babu, "Revolutionizing gram-negative bacteria detection: Flim and multicolor imaging based selective interaction study using colistin passivated carbon dots," Sensors and Actuators B: Chemical, vol. 395, p. 134433, 2023.
- [3] R. E. Baker, A. S. Mahmud, I. F. Miller, M. Rajeev, F. Rasambainarivo, B. L. Rice, S. Takahashi, A. J. Tatem, C. E. Wagner, L.-F. Wang et al., "Infectious disease in an era of global change," Nature Reviews Microbiology, vol. 20, no. 4, pp. 193–205, 2022.
- [4] P. Ma, C. Li, M. M. Rahaman, Y. Yao, J. Zhang, S. Zou, X. Zhao, and M. Grzegorzec, "A state-of-the-art survey of object detection techniques in microorganism image analysis: from classical methods to deep learning approaches," Artificial Intelligence Review, vol. 56, no. 2, pp. 1627–1698, 2023.
- [5] W. Liu, D. Anguelov, D. Erhan, C. Szegedy, S. Reed, C.-Y. Fu, and A. C. Berg, "Ssd: Single shot multibox detector," in Computer Vision–ECCV 2016: 14th European Conference, Amsterdam, The Netherlands, October 11–14, 2016, Proceedings, Part I 14. Springer, 2016, pp. 21–37.
- [6] E. Anderson, B. Nair, V. Nizet, and G. Kumar, "Man vs microbes—the race of the century," Journal of Medical Microbiology, vol. 72, no. 1, p. 001646, 2023.
- [7] G. Haddad, S. Bellali, T. Takakura, A. Fontanini, Y. Ominami, J. Bou Khalil, and D. Raoult, "Scanning electron microscope: a new potential tool to replace gram staining for microbe identification in blood cultures," Microorganisms, vol. 9, no. 6, p. 1170, 2021.
- [8] M. Bonnet, J. C. Lagier, D. Raoult, and S. Khelaifia, "Bacterial culture through selective and non-selective conditions: the evolution of culture media in clinical microbiology," New microbes and new infections, vol. 34, p. 100622, 2020.
- [9] M. Ferone, A. Gowen, S. Fanning, and A. G. Scannell, "Microbial detection and identification methods: Bench top assays to omics approaches," Comprehensive Reviews in Food Science and Food Safety, vol. 19, no. 6, pp. 3106–3129, 2020.
- [10] A. Pathak, "Fluorimetric and impedimetric sensors for the detection of pathogenic bacteria using carbon dots."
- [11] J. D. Kaunitz, "The discovery of pcr: Procurement of divine power," Digestive diseases and sciences, vol. 60, no. 8, pp. 2230–2231, 2015.

[12] V. Sankarapandian, K. Nitharsan, K. Parangusados, P. Gangadaran, P. Ramani, B. A. Venmathi Maran, and M. P. Jogalekar, "Prebiotic potential and value-added products derived from spirulina laxissima sv001—a step towards healthy living," BioTech, vol. 11, no. 2, p. 13, 2022.

[13] S. Remya and T. Anjali, "An intelligent and optimal deep learning approach in sensor based networks for detecting microbes," IEEE Sensors Journal, 2023.

[14] S. Sadanandan, K. Ramkumar, N. P. Pillai, P. Anuvinda, V. Devika, K. Ramanunni, M. Sreejaya et al., "Biorecognition elements appended gold nanoparticle biosensors for the detection of food-borne pathogens-a review," Food Control, p. 109510, 2022.

[15] L. Xu, X. Bai, S. Tenguria, Y. Liu, R. Drolia, and A. K. Bhunia, "Mammalian cell-based immunoassay for detection of viable bacterial pathogens," Frontiers in Microbiology, vol. 11, p. 575615, 2020.