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Deep Neural Network-Based Approach for Small-Size Colony Counting in the Textile Industry

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ABSTRACT
This study proposes a multi-scale feature map fusion method based on deep neural networks (DNNs) to achieve accurate Small-size colony counting under complex backgrounds and microscopic conditions, with a specific focus on textile-related microbial detection. By constructing a DNN model, the method performs feature extraction and analysis on small-sized colony images derived from textile samples, employing a convolutional feature fusion algorithm to enhance the recognition capability for small-target colonies— a critical need in textile antibacterial performance assessment. Experimental results, validated using a large number of textile microbial samples, indicate that, compared with the traditional manual visual counting method, the proposed approach shows no statistical significance in counting differences, while achieving higher precision and meeting reproducibility requirements. The method offers high efficiency, traceability, and repeatability, enabling rapid colony counting with simultaneous saving of results and images for subsequent verification, thus greatly optimising the textile quality control process. This approach can substantially improve counting accuracy, reproducibility, and automation, fully meeting standard detection requirements for antibacterial textiles and providing strong technical support for textile microbial analysis. Moreover, while initially developed for textile applications, it also holds potential for other industrial microbial detection scenarios.

KEYWORDS
colony counting, image recognition, deep neural network(DNN), multi-scale feature map fusion, antibacterial textiles

INTRODUCTION

Microbial detection plays a critical role in product quality control and biomedical research, providing essential evidence for product quality evaluation [1,2]. In the textile industry, microbial detection is particularly vital for ensuring the safety and efficacy of functional textiles. Antibacterial textiles (ATs) inhibit microbial growth to reduce odours and improve hygiene, while medical and healthcare textiles (MHTs) require strict microbial load monitoring to ensure safe use [3,4]. The antibacterial performance of ATs is primarily achieved by incorporating chemical antibacterial agents or natural antimicrobial components, which disrupt microbial cell walls or interfere with metabolic processes to inhibit growth [5,6]. These textiles are widely applied in

medical protection, home furnishings, and sportswear. MHTs are also applied in wound care and personal hygiene products.

As a key step in microbial detection, colony counting quantitatively analyses microorganisms by enumerating colonies on a solid agar medium in terms of colony-forming units (CFUs). Its accuracy directly influences antibacterial efficacy evaluation and product quality determination [7]. The traditional manual visual counting method — where operators observe colony morphology on Petri dishes with the naked eye and count manually-remains prevalent [8,9]. However, this method is inherently limited by its time-consuming nature, low efficiency, and susceptibility to operator fatigue and subjective judgment, leading to poor inter-operator reproducibility [10,11]. These drawbacks severely hinder the efficiency of microbial detection and the standardisation of quality control in ATs and MHTs.

Computer vision has emerged as a powerful, non-invasive tool for automated detection, classification, and quantification of microorganisms in diverse imaging environments, offering scalable and reproducible solutions to the traditionally labour-intensive task of microbial surveillance[12]. In the past, segmentation methods were categorised into classical and machine learning methods. Furthermore, these methods are subcategorised into threshold-based, region-based, and edge-based, which belong to classical methods, supervised and unsupervised machine learning based methods, which belong to the machine learning category [13].In recent years, alternative techniques such as image analysis [14,15], microfluidic dipsticks [16], and bioluminescence [17] have been developed. Among these, the rapid advancement of artificial intelligence (AI) has enabled intelligent colony counting. Studies demonstrate that AI-powered counters automatically identify and enumerate colonies using advanced image processing and machine learning algorithms, thereby reducing human error, significantly improving counting efficiency and accuracy, and ensuring strong repeatability [18,19].

To address the limitations of manual counting, this study proposes a deep neural network (DNN)-based small-size colony counting approach, aiming to further enhance accuracy and efficiency. The method constructs a DNN model for feature extraction and analysis of small colony images, employing a multi-scale convolutional feature fusion strategy to improve small-target recognition. This research seeks to achieve a technological breakthrough in microbial detection, promote applications in ATs and related fields, and contribute to improved public health safety and healthcare quality.

TECHNICAL PRINCIPLES AND SYSTEM ARCHITECTURE

System Components

The artificial intelligence (AI)-powered automatic colony counter is composed of three primary parts: the image acquisition and input system, the image processing software system, and the data storage system. The image acquisition and input system includes an industrial camera, an industrial lens, an LED panel light source,

and the corresponding electronic circuitry. The image processing software system is a desktop program specifically created for performing digital image processing on the input images. The data storage system is a computer host system that is responsible for storing and displaying the processed series of data. During its operation, the software system utilises the image input device to capture digital images of the well-cultured colonies. These images are then transmitted to the computer terminal technology platform through USB data communication. Subsequently, the input digital images are subjected to a series of image processing steps. After this processing, the system outputs the colony counting results. If the situation requires, these results can undergo artificial correction. Once the counting process is finished, the relevant files can be saved, and all the output data is stored in the computer.

The system was developed on the Windows 10 platform with CUDA 9.0, and the software was implemented in Python. The operational workflow comprises four stages: image acquisition and input, image processing, colony counting and analysis, and result output with data storage.

The basic workflow is illustrated in Figure 1. The workflow initiates with capturing images of petri dishes containing microbial colonies via specialised equipment. These images then undergo extraction to isolate valid petri dish regions, removing background interferences. Next, preprocessing refines images through noise reduction, contrast enhancement, and parameter standardisation for stable analysis. Automated colony counting follows, leveraging algorithms to identify and tally colonies by morphological features. Result verification checks accuracy: correct counts proceed to the final output, while errors trigger manual correction via visual interfaces. Parallelly, count data is organised, stored in a database, and exportable on demand, integrating counting precision with systematic data management.

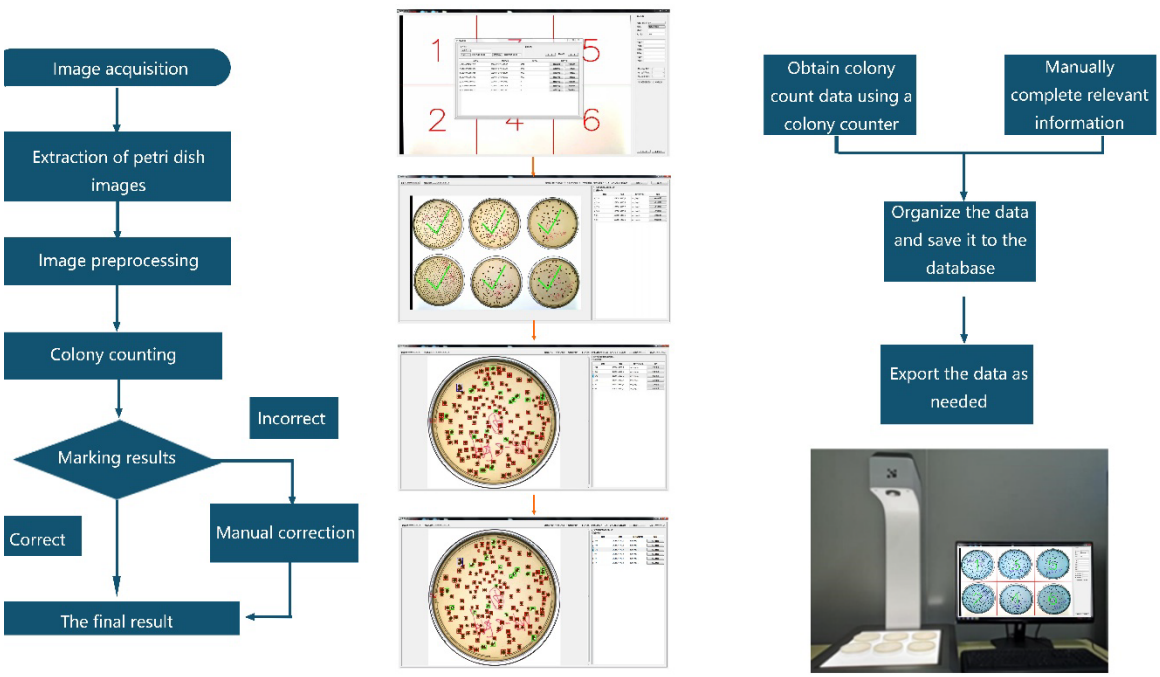

Figure 1. Basic workflow of the system operation

Image Preprocessing and Acquisition Strategy

The quality of the image is of utmost importance for the precise image recognition of small colonies. High-quality images can guarantee that the contours, morphological characteristics, and unique features of the colonies are accurately captured. This, in turn, makes it easier to distinguish them from background noise. If the image resolution is insufficient (<0.1 mm per pixel at 90 mm petri-dish scale), fine details of the colonies may be lost. On the other hand, if the lighting conditions are not ideal, shadows or glare may appear in the image. Both of these situations can make it difficult to detect small colonies and increase the probability of false positive detection or false negative detection. The quality of the image directly determines the accuracy and reliability of the image recognition of small colonies. Therefore, high-quality images can substantially enhance the detection efficiency, reduce errors, and improve the performance and credibility of the entire microbial detection process.

During the image acquisition and input stage, the software interface of the industrial camera is employed to precisely regulate the lens aperture, the zoom focal length, and the focus distance. Additionally, the illumination system is controlled to ensure the capture of clear and well-lit images that are appropriate for subsequent processing. In the image processing stage, an edge detection operator is utilised to accurately extract the contours of the Petri dish. This helps in correctly positioning the dish and effectively eliminating background interference outside the dish. As a result, it allows for precise segmentation of the target area and sets up favourable conditions for colony counting.

After the initial automated colony counting is completed, the results are displayed on the desktop program interface, where operators have the option to make manual corrections if needed. In cases where the model produces errors such as false positive detections or false negative detections — for instance, when the colony colour closely resembles that of the solid culture medium or when adjacent colonies are not properly distinguished — the operator can utilise the interface to click the left mouse button to increase the count or the right mouse button to decrease it. This allows for precise adjustment of the counting results. The corrected data is then automatically stored in the database, ensuring the accuracy and reliability of the final data to meet the industry's stringent precision requirements.

DESIGN OF THE MULTI-SCALE CONVOLUTIONAL FEATURE MAP FUSION ALGORITHM

Core Structure and Working Principle

In this study, a multi-scale feature map fusion strategy combined with image data augmentation is employed to enhance the features of small-sized colonies and improve detection performance. Specifically, after the deep neural network (DNN) performs convolution and pooling operations on the original image, multiple feature maps of different resolutions are obtained. To fully utilise the information embedded in these feature maps, the last five layers — denoted from largest to smallest as C1, C2, C3, C4, and C5 — are selected. First,

a 1×1 convolution is applied to C5 to produce M5, which is then Upsampled to match the spatial resolution of C4. This upsampled M5 is added element-wise to the output of C4 after its own 1×1 convolution, producing the fused feature map M4. The same operation is applied sequentially to C3 and C2 to generate M3 and M2. Finally, M5, M4, M3, and M2 are each passed through a convolution layer to produce feature maps with an equal output channel dimension of If the image resolution 256. By fusing feature maps from different network depths — via deconvolution-based upsampling to a unified scale — this architecture preserves both low-level and high-level features acquired during each convolution and downsampling stage, thereby minimising information loss and enabling more accurate detection of small-sized colony targets. The architecture of the multi‑scale feature map aggregation algorithm is illustrated in Figure 2.

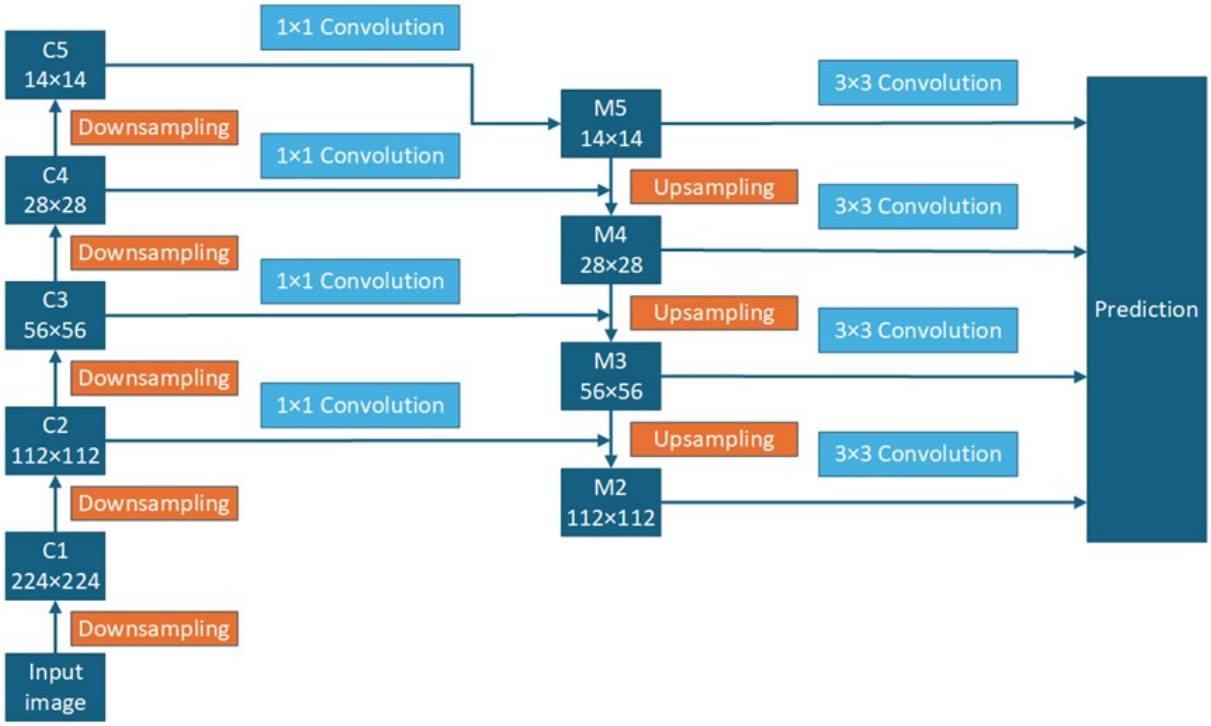

Figure 2. Architecture of the multi-scale feature map aggregation algorithm

Small-Target Enhancement Mechanism

In small-size colony recognition, combining low-level contour features with high-level semantic features is essential. The former, extracted via an edge detection operator, delineates Petri dish contours and removes background noise, providing clear boundaries for colony identification. The latter, obtained from the deep neural network (DNN) feature maps, are enhanced through multi-scale feature map fusion and deconvolution-based upsampling to strengthen small-target features and improve detection performance. To mitigate strong background noise, air bubble or droplet interference, the system applies binarisation processing (adaptive thresholding method) and threshold filtering, retaining only results that meet the set

criteria to reduce false positive detection. Additionally, a manual correction function allows operators to adjust misclassified or undetected colonies, further improving robustness and accuracy.

EXPERIMENTAL DESIGN AND VALIDATION

Accuracy Test

The accuracy test was performed using the pour plate method with disposable Petri dishes to measure both the total bacterial colony count and the total fungal colony count. Twenty batches of non-sterile disposable face masks were randomly selected for colony counting. The results were obtained using both the traditional manual visual counting method and the instrument-based method, and the two sets of results were compared to determine whether there was any statistical significance between them. The detailed data are shown in Table 1.

Table 1. Accuracy test data

Sample ID	Total bacterial colony count /(CFU/dish)			Total fungal colony count/(CFU/dish)		
	Manual	Instrument	RSD (relative standard deviation)/%	Manual	Instrument	RSD (relative standard deviation)/%
1#	150	152	0.94	54	56	2.57
2#	95	92	2.27	76	76	0.00
3#	128	129	2.89	90	94	3.07
4#	81	83	1.72	38	35	5.81
5#	42	44	6.43	124	128	2.24
6#	21	23	18.00	68	65	3.19
7#	50	47	4.37	44	42	20.20
8#	246	244	0.58	115	114	0.62
9#	76	77	2.74	84	84	0.00
10#	176	179	1.20	63	60	3.45
11#	22	30	21.76	24	31	18.00
12#	45	50	7.44	35	42	12.86
13#	79	89	8.42	57	61	4.79
14#	158	156	0.90	178	167	4.51
15#	182	186	1.54	140	143	1.50
16#	143	139	2.01	126	120	3.45
17#	110	118	4.96	110	119	5.56
18#	90	86	3.21	90	85	4.04
19#	70	79	8.54	70	76	5.81
20#	89	91	1.57	68	63	5.40

Precision Test

To verify Precision, ten batches of sterile medical masks were randomly selected. A suitable concentration of bacterial suspension was added to each sample, and the instrument-based method was used for detection. Each sample was tested in seven parallel trials, and the relative standard deviation (RSD) was calculated. The results are shown in Table 2.

Table 2. Precision test data

Sample ID	Counting method	Colony count/(CFU/dish)							RSD (relative standard deviation)/%
		Trial 1	Trial 2	Trial 3	Trial 4	Trial 5	Trial 6	Trial 7	
21#	Manual	249	245	239	246	247	251	249	1.59
	Instrument	260	259	257	261	255	253	262	1.27
22#	Manual	112	114	120	116	119	117	121	2.79
	Instrument	115	119	113	120	121	118	119	2.42
23#	Manual	89	91	87	86	85	90	91	2.76
	Instrument	90	92	93	94	92	91	90	1.63
24#	Manual	310	319	315	309	312	314	318	1.21
	Instrument	320	324	325	321	326	322	323	0.67
25#	Manual	156	154	153	158	159	156	157	1.35
	Instrument	160	162	164	159	160	162	163	1.12
26#	Manual	103	104	109	104	106	107	105	1.96
	Instrument	110	109	107	108	109	107	110	1.17
27#	Manual	210	215	217	215	210	216	214	1.31
	Instrument	220	219	218	220	219	217	221	0.61
28#	Manual	99	98	100	97	101	98	99	1.36
	Instrument	100	101	101	102	100	102	103	1.10
29#	Manual	78	80	84	79	77	80	78	2.89
	Instrument	80	83	80	82	79	82	83	1.97
30#	Manual	198	200	199	203	201	198	201	0.91
	Instrument	200	203	201	199	200	201	202	0.67

Reproducibility Test

Different operators independently counted colonies on the same Petri dish using both the traditional manual visual counting method and the instrument-based counting method. The relative standard deviation (RSD) was calculated for each method to evaluate its reproducibility. The results are shown in Table 3.

Table 3. Reproducibility test data

Operator	Colony Count/(CFU/dish)	
	Manual	Instrument
1	235	240
2	240	239
3	238	241
4	241	237
5	235	242
RSD (relative standard deviation)/%	1.17	0.80

RESULTS ANALYSIS AND VISUALIZATION

As shown in Table 1 and Figure 3, the percentage of cases where the relative standard deviation (RSD) between the traditional manual visual counting method and the instrument-based counting method for total bacterial colony count was less than 10% reached 90%. For the total fungal colony count, this compliance rate was 85%. The deviation in plate colony counting between the two methods was generally small. A paired t-test was performed using SPSS software under the assumption that there was no difference in the overall mean of the count results between the two methods. The results showed that within the 95% confidence interval, all P-values exceeded 0.05. Therefore, the null hypothesis was not rejected, indicating that there was no statistically significant difference in the count results between the visual method and the instrumental method. This study also considered colony counts across different ranges. When the colony count fell below 50 colony-forming units (CFU) per dish, the accuracy of the instrument-based method decreased, with some samples showing an RSD greater than 10%. This may be due to the colour of the colonies being similar to that of the solid culture medium, the presence of air bubbles whose colour was close to that of the colonies, or water mist and droplets inside the Petri dish affecting the image recognition capability of the counting device. Consequently, under low-colony-count conditions, the fully automatic colony counter — constrained by the image recognition algorithm, optical system, and culture medium characteristics — may exhibit false negative detections of very small colonies and false positive detections caused by bubbles, resulting in reduced accuracy. Although no statistically significant differences were observed compared with manual counting, practical applications require either manual correction or the selection of a more suitable detection method to ensure result reliability.

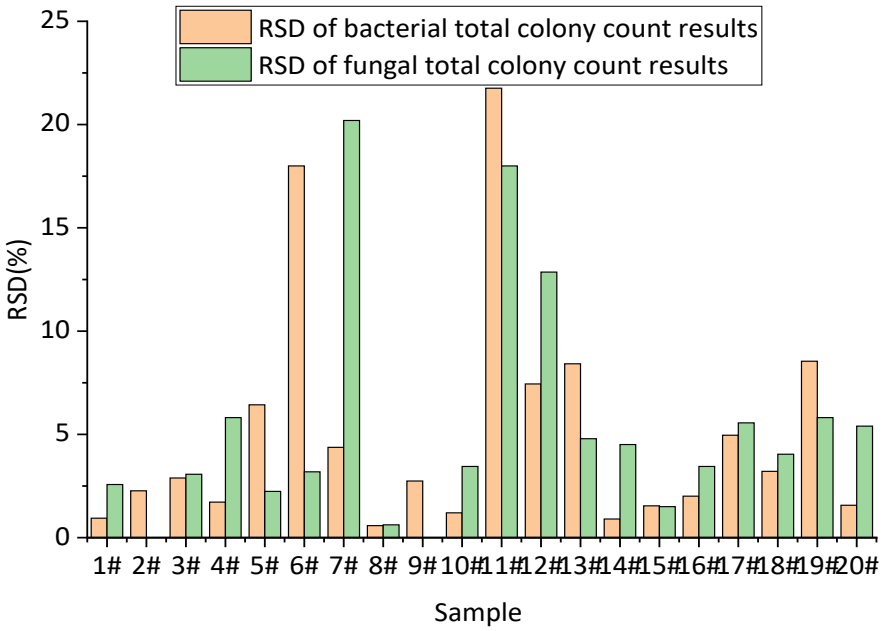

Figure 3. RSD for the accuracy test

As shown in Table 2 and Figures 4 and 5, the relative standard deviation (RSD) values obtained by both the traditional manual visual counting method and the instrument-based counting method were below 10%. The instrument-based method achieved an average RSD of 1.26%, compared with 1.81% for the manual method, indicating that the instrument-based method exhibited overall higher precision. In addition, for most samples, the instrument-based counts were higher than those obtained manually. This is likely because extremely small colonies on the plate, which are invisible to the naked eye and thus omitted in manual counting, can be detected by the fully automated colony counter through multi-scale feature map fusion, image preprocessing, and other techniques that enhance small-target recognition.

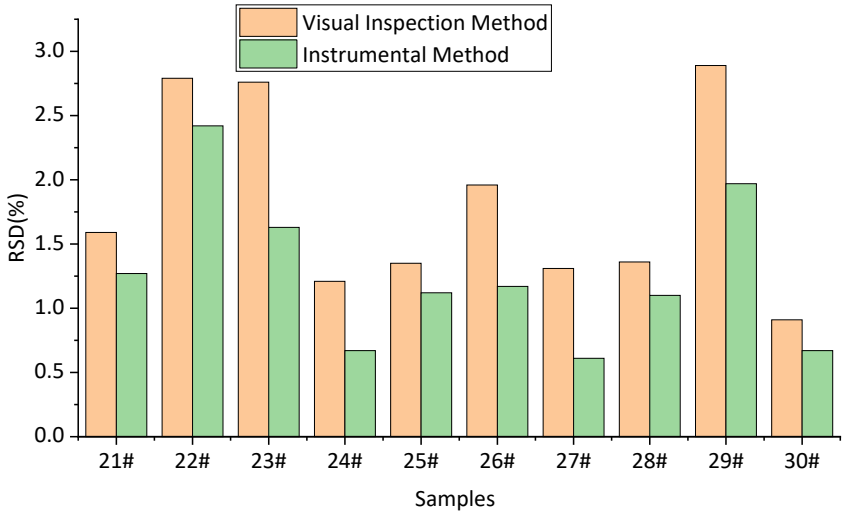

Figure 4. RSD for the precision test

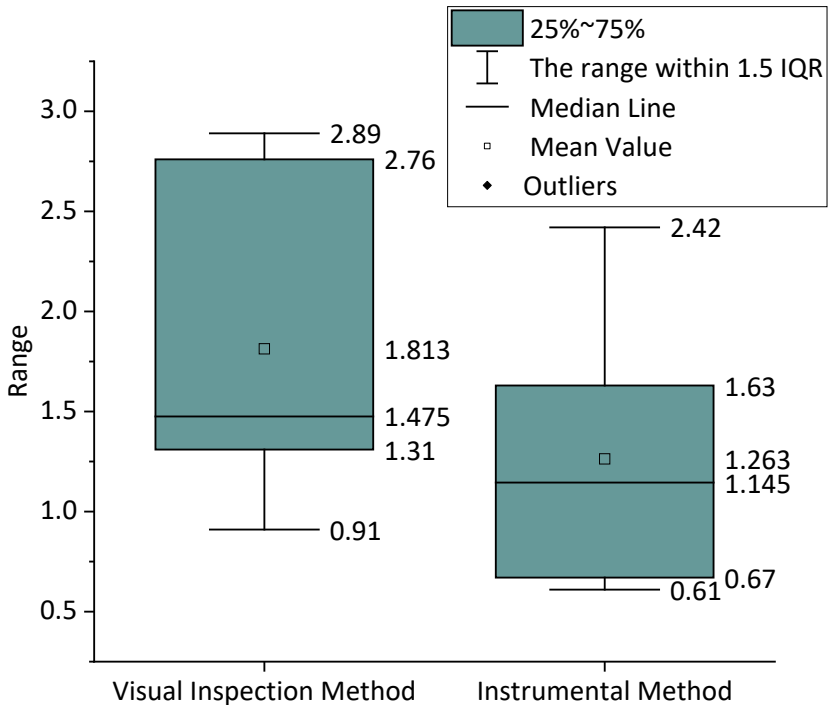

Figure 5. Boxplot for the precision test

As shown in Table 3, when different operators performed colony counting using both the traditional manual visual counting method and the instrument-based counting method, the relative standard deviation (RSD) values were 1.17% and 0.80%, respectively. Both values were well below the 10% threshold, meeting the reproducibility requirement.

Operational assessments involving multiple users confirmed that the fully automated colony counter is straightforward to operate. During image acquisition and input, no manual adjustment of illumination is required, as the system automatically optimises lighting to achieve the best imaging conditions. Depending on testing requirements, the system allows one-click counting for either four or six Petri dishes and enables the selection of the appropriate sample group before measurement. During the counting process, operators can manually add or remove colonies to correct false positive detections or false negative detections. Additional functions include input of sample dilution factors, automated report generation, and other user-friendly features.

DISCUSSION

The multi-scale feature map fusion method significantly enhances small-target detection performance by integrating feature maps of different resolutions— a capability of critical importance for microbial analysis in textile applications. This approach is particularly effective under complex backgrounds and microscopic imaging conditions commonly encountered in textile testing, where it can substantially improve the accuracy

and robustness of colony counting for evaluating antibacterial textiles. By fully leveraging the multi-level feature representations extracted by a deep neural network (DNN), the method minimises information loss, resulting in more precise recognition of small-sized colonies. However, certain limitations remain in textile-specific scenarios. When the background colour of the medium is similar to that of the target colonies, or when strong background noise caused by water mist, air bubbles, or droplets is present in the petri dish during textile microbial testing, the rate of false positive detection may increase. Under such circumstances, incorporating manual correction is necessary to maintain counting accuracy.

Continuous training of the artificial intelligence (AI) model using textile-specific datasets and the integration of a misclassification correction mechanism are critical for performance improvement in textile applications. Iterative training across diverse textile scenarios enables the model to learn fabric-specific interference features, effectively reducing false detections and enhancing its generalisation ability in textile microbial testing. The misclassification correction mechanism allows textile lab operators to directly amend model errors related to fabric background interference, further refining detection outcomes for antibacterial textile assessment.

Future work could focus on incorporating an attention mechanism or adaptive threshold to further optimise the method for textile applications. The attention mechanism could enable the model to more efficiently focus on the target colony region, dynamically suppressing the interference caused by the similarity between the background colour of the medium and the colour of the colonies, directly addressing the issue of target misrecognition caused by background interference. The adaptive threshold has been proven effective in dealing with interference problems in existing research — for example, to mitigate strong background noise caused by water mist, air bubbles, and droplets, the system has previously employed binarisation processing (adaptive thresholding method) and threshold filtering, retaining only the detection results that meet the set criteria to reduce the false positive detection rate. These enhancements would strengthen the applicability of the multi-scale feature map fusion approach for complex textile samples, expanding its potential impact in the field of microbial detection for antibacterial textiles and supporting more efficient quality control in textile production.

CONCLUSION

The multi-scale feature map fusion method based on a deep neural network (DNN) demonstrates outstanding performance in the recognition of very small colonies, offering distinct advantages in the detection of antibacterial textiles and medical and healthcare textiles.

By integrating feature maps from multiple scales, the method significantly enhances the detection capability for small-sized colonies in textile-derived samples, effectively improving both the accuracy and reproducibility of colony counting.

Experimental results, validated using textile microbial samples, indicate that, compared with the traditional manual visual counting method, this approach shows no statistically significant difference in counting results while achieving higher precision and meeting reproducibility requirements.

In addition, it offers high efficiency, traceability, and repeatability, enabling rapid colony counting for textiles while saving both the results and Petri dish images for subsequent data review and verification, thus optimising textile quality control.

Looking ahead, this method holds strong potential for extension to other industrial microbial detection scenarios, such as fermented beverage microbial quality monitoring and aquaculture water microbial analysis. Within the textile industry, its impact is direct and transformative: by enabling high-precision, automated counting of small-sized colonies in textile microbial samples, it strengthens the reliability of antibacterial performance evaluations—a cornerstone of quality control for antibacterial textiles and medical healthcare textiles. This advancement streamlines textile testing workflows, reduces reliance on manual labour, and ensures consistent adherence to industry standards, thereby accelerating product development cycles and enhancing the credibility of textile safety claims. Furthermore, the method is envisioned to be seamlessly integrated with cloud computing, edge AI, and real-time monitoring systems, thereby unlocking scalable, low-latency deployments that significantly enhance its industrial relevance. Cloud-based data synchronisation will enable multi-point data sharing for centralised management and large-scale analysis, while edge AI ensures on-site, real-time inference and remote interpretation, allowing experts to review complex samples online, collectively driving transformative advances in microbial detection and related industries.

Author Contributions

Conceptualisation – Yang C, Li Y, Luo X; methodology – Li Y, Zhang Y; formal analysis – Zhang Y, Zhang Z; investigation – Li Y, Chen G; resources – Li Z, Chen G; writing–original draft – Li Y, Zhang Y, Zhang Z; writing–review and editing – Yang C, Luo X; visualisation – Zhang Y; supervision – Yang C, Luo X. All authors have read and agreed to the published version of the manuscript.

Conflicts of Interest

The authors declare no conflict of interest.

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