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Artificial Intelligence (AI) for accelerated detection of pathogenic and spoilage microbes in food systems

ABSTRACT

The rapid and accurate detection of microbial contamination is critical for ensuring food safety, preventing foodborne illness outbreaks, reducing economic losses, and minimizing food waste caused by spoilage. Traditional methods, such as culture-based assays and molecular techniques, are often labor-intensive and require days to detect trace-level microbial contamination. Recent advancements in artificial intelligence (AI) offer promising alternatives, providing faster, more accurate and potentially sensitive microbial detection solutions. This bulletin explores the challenges of current microbial detection techniques, the potential of AI technologies to improve microbial detection, and future directions for the integration of AI-based approaches into food systems.

1. INTRODUCTION

Microbial contamination in food systems is a global concern, contributing to foodborne illness outbreaks, food spoilage, and significant economic losses. The World Health Organization (WHO) estimates that contaminated food causes 600 million illnesses and 420,000 deaths annually worldwide (WHO, 2024). In addition to these health risks, global estimates suggest that around 40% of the food is not consumed due to pre-harvest loss or postharvest food waste, which amounts to approximately 931 million tons annually (Snyder & Worobo, 2018; UNEP, 2021). Among these losses, microbial food spoilage is a major factor, with around 25% of marketable yields lost during postharvest across a wide range of food products (Alegbeleye et al., 2022; Palumbo et al., 2022; Snyder & Worobo, 2018; Zhao et al.,

2022). As millions of people worldwide suffer from inadequate nutrition, the loss of edible food due to microbial contamination further limits access to safe and nutritious food, especially in regions with high levels of food insecurity (Quintieri et al., 2023). Moreover, food production requires significant natural resources, including water, land, and energy. This food waste associated with microbial contamination also contributes to unnecessary environmental strain and resource depletion (Kohli et al., 2024). Thus, the detection of bacterial and yeast contamination in food systems requires effective and timely detection methods to mitigate these risks. However, traditional detection methods, such as culture-based techniques and nucleic acid assays, are often slow and labor-intensive, taking several days to yield results, especially when target microorganisms are present at low contamination levels. Rapid and accurate microbial detection is essential to prevent contamination and safeguard public health and food quality.

In this bulletin, we explore the potential of AI technologies to enhance microbial detection in terms of speed, cost, and accuracy. By reviewing recent studies, we highlight the challenges and limitations of traditional microbial detection methods. Furthermore, we discuss how AI can bridge these gaps through advancements in deep learning and image analysis, offering faster, more precise, and cost-effective detection methods to improve food safety and reduce food spoilage.

2. THE CHALLENGES OF BACTERIAL AND YEAST DETECTION IN FOOD SYSTEMS

2.1. Bacterial detection

Bacterial contamination is a leading cause of foodborne illness globally. Pathogens such as *Salmonella*, Shiga-like toxin-producing *Escherichia coli*, and *Listeria monocytogenes* are frequently associated with contaminated food products, leading to major outbreaks that affect public health and food industries (Qiu et al., 2021). Contaminated food products often reach consumers before pathogens can be detected, resulting in costly recalls and liability issues for manufacturers (Aladhadh, 2023). Culture-based methods have been the “gold standard” approach for detecting bacterial pathogens in food systems (Ferone et al., 2020). The culture-based approach includes multiple steps of sample preparation, incubation times, and analyses. These steps typically include pre-enrichment, selective enrichment, selective and differential

plating, serological confirmation, and biochemical screening (Ferone et al., 2020). The culture-based detection approaches are time-consuming and labor-intensive and can require more than 3 days to obtain a result. These assays include multiple steps, including the preparation of culture media, inoculation into plates, and colony screening. In addition, low sensitivity due to the diversity of microorganisms in the specimens is another limitation of this method.

Complementary to culture-based detection, nucleic acid amplification such as real-time polymerase chain reaction (RT-PCR), loop-mediated isothermal amplification (LAMP), and sequencing technologies such as whole genome sequencing (WGS) have emerged as leading alternative approaches for detecting bacterial pathogens in diverse food systems (Ferone et al., 2020; Gieron et al., 2023; Panwar et al., 2023). For these methods, bacterial nucleic acids are recovered after initial enrichment or from colonies formed on culture plates, both of which require time for microbial growth and preparation before detection can proceed (Ferone et al., 2020). Though highly sensitive, these methods are susceptible to interference from food residues in enrichment cultures and external nucleic acid contamination from the experimental environment, such as airborne contaminants (Rajapaksha et al., 2019). In addition, most of these solutions are generally more costly and labor-intensive than culture-based methods, as these approaches require molecular-grade environment and reagents to isolate nucleic acids from bacteria followed by non-isothermal or isothermal amplification of nucleic acids using specific primers, enzymes, and fluorescence/colorimetric probes (Ferone et al., 2020). Furthermore, the positive results from nucleic acids-based approaches are not necessarily related to the presence of live bacterial cells because the positive signals could also be from the dead bacterial cells or viable but not culturable cells (Rajapaksha et al., 2019). Thus, a combination of nucleic acid-based and culture-based tests are commonly used in food industries to confirm the presence of live and culturable bacterial pathogens. Overall, there is a significant unmet need to reduce detection time and improve specificity to detect these target bacteria in food systems, potentially at the point of detection in processing facilities and QA/QC labs with limited molecular capabilities.

2.2. Yeast detection

Yeast contamination of food products, while less harmful than bacterial pathogens, can lead to significant spoilage issues. Common spoilage yeasts, such as *Rhodotorula*, *Candida*, and *Geotrichum*, thrive in diverse food matrices, from dairy products to fruit juices and

fermented foods (Fleet, 2011). Certain yeast species, such as *Candida*, can also serve as opportunistic pathogens in humans, causing infections (Fleet, 2011). Spoilage yeasts reduce the shelf life of food and beverage products by causing off-flavors, texture degradation, and gas production. Traditional plating assays have been used to enumerate the total yeast and mold count. This culture-based detection method takes 2-3 days (Green & Moehle, 1999) and only provides total yeast and mold counts without detailed classification of the yeast species. This lack of classification fails to provide information on the degree of spoilage risk, as different yeasts exhibit varying characteristics, resistance to environmental factors, and metabolic activities. To further classify yeast species, cultivation and biochemical methods are required. This process takes 5-7 days as it involves the enrichment and isolation of yeasts on various types of growth media to inhibit interference from background microflora (Ferone et al., 2020; Tubia et al., 2018).

To address the above-mentioned limitations of currently used detection methods, nucleic acid-based methods such as PCR and DNA sequencing have similar challenges as discussed above for the detection of bacteria (Aboutalebian et al., 2022; Hutzler et al., 2012; Lai et al., 2022). Additionally, matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) has been used to detect yeast species in various sectors, including the wine industry, where it has been used to identify yeast strains for different wine varieties (Usbeck et al., 2014; Zhang et al., 2020). Nevertheless, these methods still require specialized personnel and sophisticated equipment and generally need 2-3 days for the enrichment and/or isolation of yeast colonies. During this time, the contaminated products may already be on the market. This delay, combined with the high costs and resource demands, makes these techniques less practical for routine use in the food industry. Therefore, there is a need for fast, cost-effective, and accurate detection of yeast for routine spoilage yeast monitoring and spoilage control.

3. AI IN MICROBIAL DETECTION: TECHNOLOGIES AND OPPORTUNITIES

Recent advancements in AI have shown significant potential in improving detection and classification processes across various industries, including healthcare and agriculture (Esteva et al., 2019; Patrício & Rieder, 2018). Deep learning models, particularly those applied to image analysis, have evolved to process large datasets and detect objects with increasing precision. These models automatically extract features from images and thus reduce the need for manual

intervention. This technology is now being translated and further developed to improve microbial detection in food systems.

Traditional image analysis methods, such as thresholding, edge detection, and classical machine vision techniques, have been widely used for microbial detection by identifying objects such as microbial colonies based on shape, color, or size (Bär et al., 2020; Chiang et al., 2015; Choudhry, 2016). However, these methods rely on predefined rules and manually selected features, which are effective for detecting the presence of microbial colonies but lack the capability to classify different microbial species. When relatively complex optical properties such as optical scattering properties of colonies were used, this approach could enable the detection of *Listeria monocytogenes* and other species of *Listeria* (Banada et al., 2007). However, this approach could not be generalized for diverse bacterial species because the basic morphological characteristics calculated by traditional image analysis methods could not distinguish between microbial colonies with similar appearances. In contrast, AI-based microbial detection leverages deep learning models, particularly convolutional neural networks, to computationally analyze microbial images and automatically extract complex patterns beyond simple morphology (i.e., shape, color, or size). Unlike traditional methods that depend on manually set parameters, AI models learn directly from raw image data, enabling them to recognize species-specific features such as subtle variations in individual cell size and shape or microcolony growth patterns (Park et al., 2025). This data-driven approach allows AI models to classify microbial species with high accuracy, even when visual differences are minimal. Additionally, AI-based methods can process and integrate multimodal data, such as combining microscopy images with hyperspectral or fluorescence signals, enhancing the species classification of AI models.

AI-based microbial detection also offers several key advantages over conventional microbial detection methods. First, AI models can process large datasets rapidly, enabling near real-time microbial analysis compared to traditional culture-based methods, which require days for microbial identification. Second, AI techniques can be integrated with multiple imaging and spectral methods to enhance sensitivity and specificity while eliminating the need for extensive sample preparation. Additionally, some of the AI-based microbial detection methods are cost-effective because they do not require sophisticated instruments for microbial identification. These approaches can reduce the dependency on specialized expertise and lowers the overall cost of implementation, making AI-based microbial detection a scalable and

accessible solution for food safety monitoring. Thus, AI can serve as an early screening tool, identifying potential microbial contamination at an initial stage, which can then be combined with molecular methods for further discrimination of species and serotypes and validation of the results. The general architecture of several AI-based microbial detection approaches follows these key steps:

- 1) Data acquisition: Images or spectroscopy data of microbial samples are captured using techniques such as brightfield microscopy, fluorescence microscopy, hyperspectral imaging, and spectroscopy methods to collect detailed microbial data.
- 2) Feature extraction and model training: Various AI algorithms, primarily convolutional neural networks, are employed to extract important features such as cell shape, size, and spectral patterns from raw data (Table 1). During training, a validation dataset is used for fine-tuning the hyperparameters of the AI model to improve the prediction accuracy.
- 3) Model validation: Once training is complete, the model is validated on unseen datasets to evaluate its accuracy and generalizability. This step ensures that the model performs well in real-world microbial detection scenarios before being deployed.

Based on this framework, some recent studies have explored the potential of AI and imaging techniques to improve microbial detection in food systems (Chen et al., 2024; Huang et al., 2023; Kang et al., 2024; Kim et al., 2021; Ma et al., 2023; Shankarnarayan & Charlebois, 2024; Yi et al., 2023). By integrating AI with spectral and optical-based images, these studies demonstrate how AI can be leveraged to address the current challenges in microbial detection (Table 1). For instance, Kang et al. (2024) developed a 3D convolutional neural network model to classify different pathogenic bacteria using hyperspectral microscopic imaging (Fig. 1). Similarly, Chen et al. (2024) used deep convolutional neural networks to classify six common foodborne pathogens, including *E. coli* and *Salmonella*, from microscopic images of bacteria on slides stained with a Gram stain. Their model achieves 90-100% accuracy, offering an automated alternative to traditional manual microscopy, reducing misjudgment, and improving detection speed and accuracy (Fig. 2). In another study, Kim et al. (2021) used a support vector machine to classify bacterial species by analyzing bacterial aggregation patterns on paper microfluidic chips, with a smartphone capturing the data. The machine learning model was able

to classify five bacterial species, including *Salmonella* and *Pseudomonas aeruginosa*, with over 93% accuracy in less than 10 minutes. Ma et al. (2023) employed a You Only Look Once version 4 (YOLOv4) model to detect bacterial microcolonies after just 3 hours of cultivation. The model achieved an average precision of 94%, demonstrating the potential to accelerate bacterial detection without a sophisticated instrument (Fig. 3). Especially, this study used non-selective nutritious media to support the cultivation and detection of multiple bacterial genus and species. The use of non-selective culture media combined with AI can overcome the limitations of selective culture media in two ways. First, non-selective culture media offer a more universal method for detecting multiple bacterial species in a single analysis, eliminating the need for multiple selective culture assays. Second, traditional culture-based methods rely on observing colony characteristics (e.g., color and shape) on selective agar, but closely related microbial strains may grow on the same media, reducing the ability to differentiate between target pathogens and non-target microorganisms (Nigro & Steward, 2015). In contrast, this AI-based method can differentiate closely related microbial species with high accuracy. Yi et al. (2023) recently developed an AI-biosensing framework that utilizes phage-induced lysis to precisely detect *E. coli* in the presence of non-target bacteria from field-collected water samples within 5.5 h (Fig. 4). While many AI-based models have been developed for bacterial detection and classification, fewer studies have leveraged AI techniques to detect yeasts (Park et al., 2025). Huang et al., (2023) applied fuzzy automatic contrast enhancement and the YOLOv5 framework to detect *Saccharomyces cerevisiae* cells from microscopic images. Additionally, Shankarnarayan & Charlebois (2024) developed a model based on Inception V3 to discriminate between four *Candida* species using cells prepared on glass slides. These studies demonstrated the potential of AI technologies in enhancing microbial detection accuracy (70-100%) and speed (< 5.5 h). However, the sensitivity of AI-based microbial detection in food products remains an ongoing challenge, as only a few studies have reported detailed sensitivity data for their deep learning models (Table 1). By integrating deep learning models and innovative frameworks, AI approaches can significantly reduce detection times and offer reliable and automated alternatives to traditional methods.

4. CHALLENGES AND FUTURE DIRECTION IN AI-BASED MICROBIAL DETECTION

Despite the significant potential of AI in microbial detection, several challenges must be addressed for widespread adoption for real-world deployment. One of the main challenges is

data quality and availability, as AI models rely on large, high-quality datasets for effective training (Liang et al., 2022; Savadjiev et al., 2019). Acquiring such datasets remains a critical limitation because it requires consistent data collection methods and extensive wet lab results. To address these limitations, generative adversarial networks and diffusion models offer potential by generating synthetic datasets to supplement training on microbes with limited available data (Karras et al., 2020; Liu et al., 2020). Additionally, using pre-trained models developed from microbial image datasets rather than general datasets like COCO, can improve detection efficiency. These pre-trained models may improve the training efficiency to detect unique morphological or spectral characteristics of target microbes with significantly reduced labeled datasets. Secondly, training machine learning models requires substantial computational resources to process large datasets and optimize algorithms. While end-users or consumers typically do not need high computing power, developers face significant challenges in training deep learning models. To address this challenge, cloud-based and edge computing solutions can help developers overcome the heavy computational demands (Deng et al., 2020). In addition, cybersecurity is an important future consideration as AI-enabled systems expand in food safety monitoring. As these technologies continue to develop, ensuring secure data transmission and protecting AI models from potential tampering will be crucial to maintaining trust in their deployment (Nair et al., 2024). Though not a current widespread concern, it is essential to address these challenges proactively as AI becomes more integrated into food safety practices.

One of the key areas for future development is the standardization of AI-enabled detection systems. Standardization will help minimize biological, physical, and personnel variations, which can affect detection accuracy. For example, biological variations in microbial conditions such as different microbial strains or environmental stressors, or physical variations in data collection like lighting conditions, microscopy techniques, and agar mediums, as well as personnel variations stemming from operator expertise and detection sites, must be accounted for to improve consistency and reliability in microbial detection. However, balancing the standardization with customization is essential to ensure that methods are both broadly applicable and adaptable to specific needs. Similar to the FDA Bacteriological Analytical Manual, standardization could involve selecting strains, defining data collection protocols, and setting uniform training and prediction standards for wide deployment. At the same time, customization should enable users to adapt models to specific food products and microbial

challenges, which provides flexibility in handling different environments and contamination scenarios.

Another important future direction is the development of portable AI-based microbial detection devices. These devices could be employed directly in the food manufacturing facilities, enabling rapid on-site microbial detection. Advances in edge computing will improve the portability and deployability of AI models. For spoilage detection, AI models for microbial detection can be integrated with product characteristics, such as pH, water activity, and packaging conditions, to create a more comprehensive prediction of spoilage risks.

Further challenges involve data sharing and result explainability. Data sharing across industries and research institutions is often limited due to proprietary restrictions, privacy concerns, and regulatory barriers, which hinder model development and validation. Encouraging open-access microbial image datasets and fostering collaborations among academia, regulatory agencies, and industry stakeholders could help accelerate AI adoption. Additionally, AI models must provide interpretable results to facilitate regulatory approval and user confidence. Current deep learning models often operate as "black boxes", making it difficult to understand their decision-making processes. Developing explainable AI approaches, such as visualization techniques or feature attribution methods, will be key to increasing transparency and acceptance among food safety professionals. Involving scientists, policymakers, and other stakeholders in the AI adoption process will be crucial for ensuring public acceptance and regulatory alignment. Stakeholder engagement can guide policy frameworks for AI-driven microbial detection, addressing ethical concerns, liability issues, and best practices for validation and standardization. Collaboration among food safety agencies, microbiologists, and AI researchers can also help shape regulatory guidelines that balance innovation with safety and reliability. By addressing these challenges, AI-based microbial detection can achieve greater acceptance and integration into real-world food safety practices.

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Table 1. Current AI-based approaches for microbial detection and classification.

Target microbes	Sample preparation	Imaging approach	Algorithm	Detection time	Accuracy	Sensitivity	Reference
<i>E. coli</i>	Staining with SYBR Green after phage-induced lysis	Fluorescence microscopy at 100× magnification	Faster R-CNN	< 5.5h	80-100%	10 ² CFU/ml	Yi et al. (2023)
<i>E. coli</i>	Microcolony formation on agar media	Phase-contrast microscopy at 60× magnification	YOLOv4	3h	R ² of 0.995	10 CFU/g	Ma et al. (2023)
Bacterial pathogens	Cells on glass slides with Gram staining	Brightfield microscopy at 63× magnification	CNN	-	90-100%	-	Chen et al. (2024)
Bacterial pathogens	Cells on glass slides	Hyperspectral microscopy	3D-GhostNet	-	90-100%	-	Kang et al. (2024)
Bacterial pathogens	Peptide-conjugated particles mixed with bacterial cells on microfluidic chip	Smartphone-based imaging	SVM	< 10 min	93.30%	10 CFU/ml	Kim et al. (2021)
<i>Candida</i> species	Wet mount of cells using saline on glass slides	Brightfield microscopy at 100× magnification	Inception V3	-	69.0-97.0%	-	Shankarnarayan & Charlebois (2024)
<i>S. cerevisiae</i>	Cells on petri dish	Achromatic microscopy at 90× magnification with fuzzy automation contrast enhancement	YOLOv5	-	94.20%	-	Huang et al. (2023)

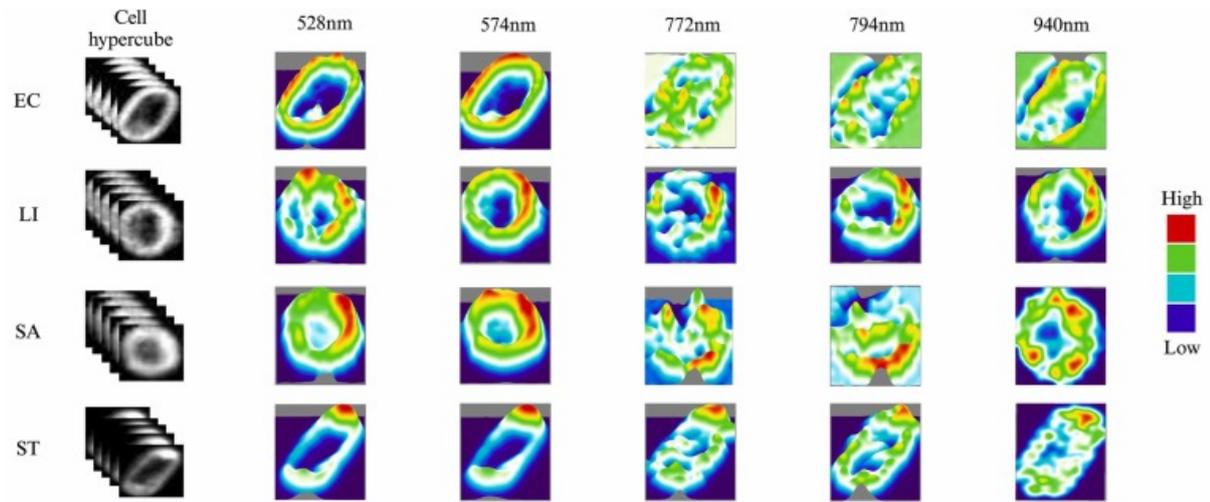
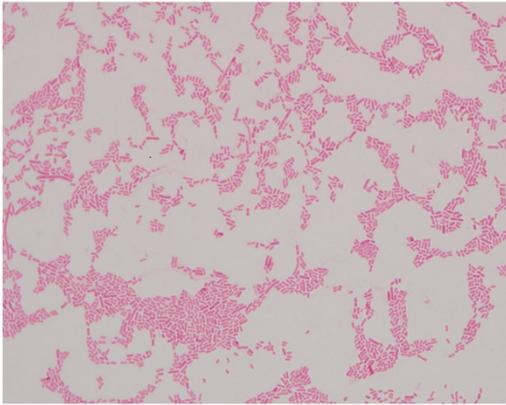
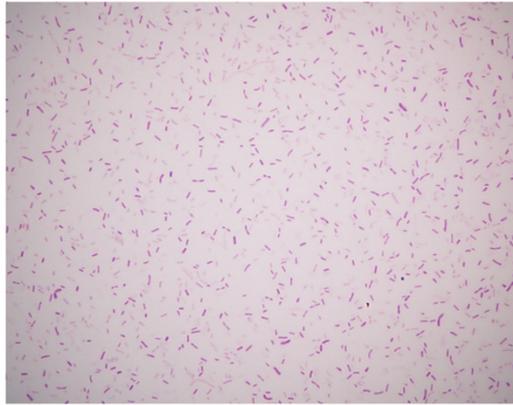


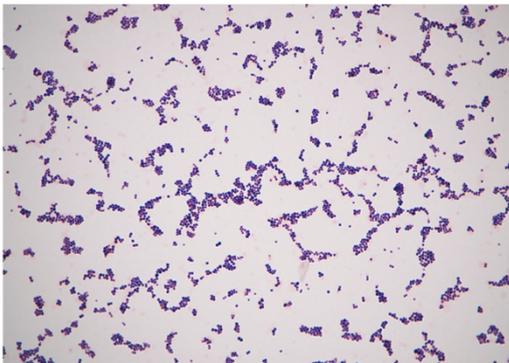
Fig. 1. Spectral images of various foodborne pathogens. EC: *Escherichia coli*, LI: *Listeria monocytogenes*, SA: *Staphylococcus aureus*, and ST: *Salmonella Typhimurium*. (Kang et al., 2024)



Escherichia coli (O157:H7)



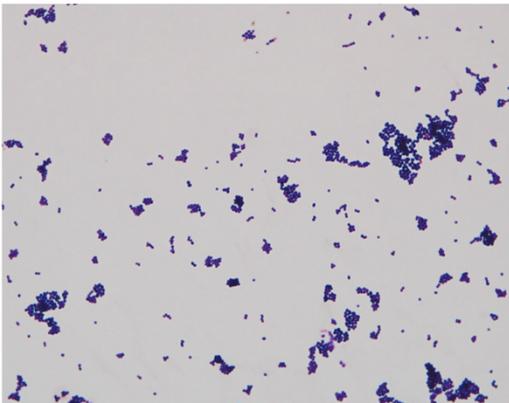
Vibrio parahaemolyticus



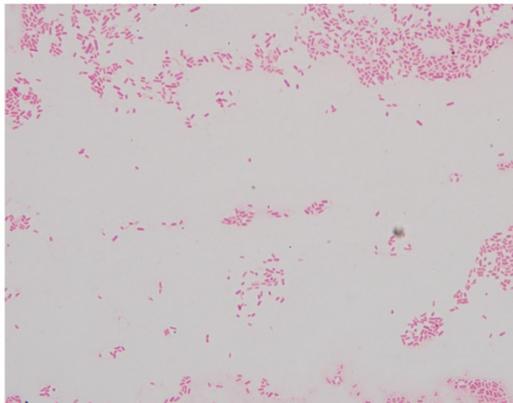
Staphylococcus aureus



Bacillus cereus



Streptococcus hemolyticus



Salmonella typhi

Fig. 2. Typical microscopic pictures of *Escherichia coli* O157:H7, *Vibrio parahaemolyticus*, *Staphylococcus aureus*, *Bacillus cereus*, *Salmonella typhi*, and *Streptococcus hemolyticus*. (Chen et al., 2024)

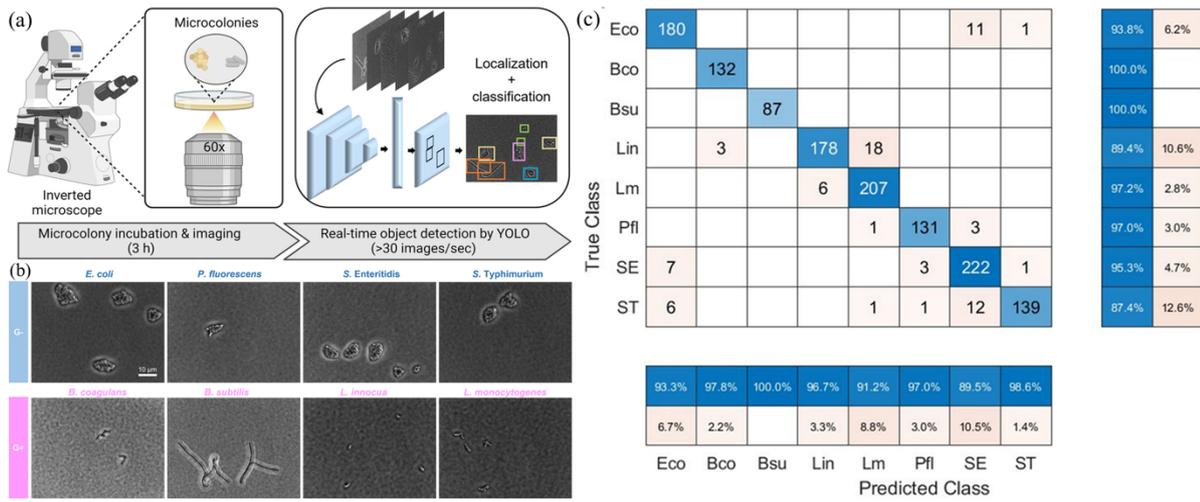


Fig. 3. (a) Workflow of YOLO-based bacterial microcolony classification. (b) Representative bacterial microcolonies of eight different species. (c) Confusion matrix for microcolony classification of *Escherichia coli* and other common spoilage and pathogenic bacterial species. (Ma et al., 2023)

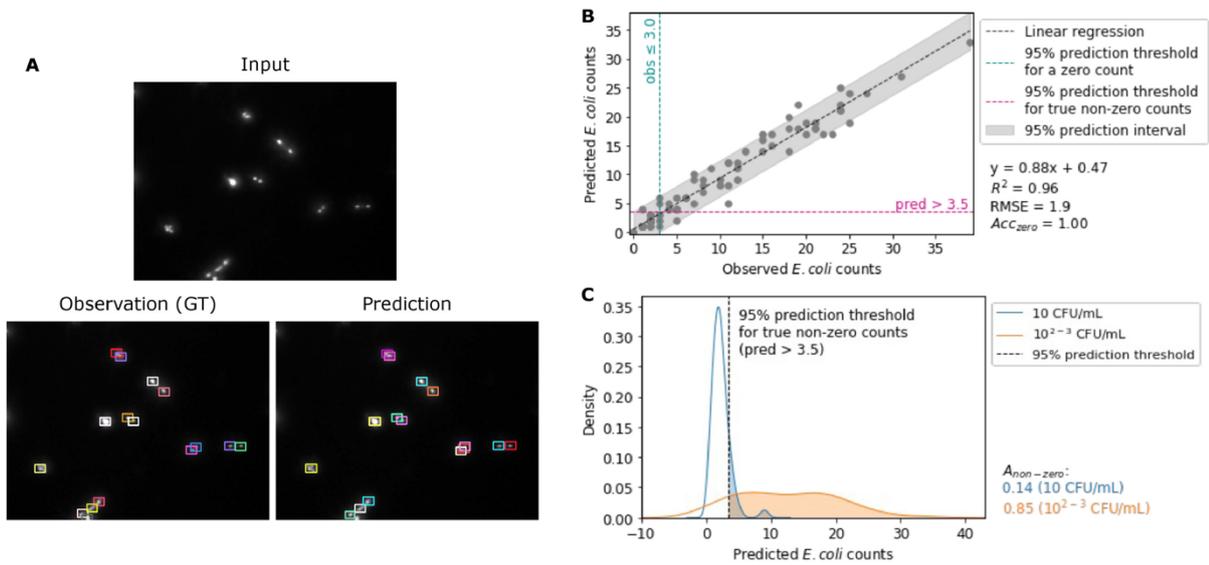


Fig. 4. AI model for the detection of *Escherichia coli* exposed to T7 phages. (A) Example test images with their respective observed and predicted bounding boxes; (B) Observed-predicted plots for evaluating *Escherichia coli* quantification performance; (C) 95% prediction thresholds for true non-zero counts. (Yi et al., 2023)

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