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Integrative Medicine: Incorporating Complementary Therapies into Clinical Practice

Artificial intelligence based microorganism image analysis for infectious disease diagnostics

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Abstract Microorganism image analysis is a critical tool in infectious disease diagnostics, permitting accurate identification and classification of pathogens in clinical samples. By incorporating Artificial Intelligence (AI), this process becomes crucially more efficient and precise, with AI algorithms trained to classify features such as morphology, size, and color. Despite, challenges like background noise, staining inconsistencies, and image distortions can hinder analysis, entailing advanced preprocessing and feature extraction techniques. This research presents the Sunflower Optimized Naive Bayes Classifier (SONBC), a novel approach aimed at addressing these challenges and improving diagnostic performance. The process begins with the collection of a comprehensive dataset of microorganism images, followed by preprocessing using the Gaussian Filter to reduce noise and enhance image quality. Feature extraction is conducted utilizing Independent Component Analysis (ICA), which isolates and refines critical attributes for accurate classification. The SONBC classifier then accomplishes exceptional performance metrics, exhibiting recall of 98.45%, precision of 95.79%, accuracy of 97.48%, and an F1 score of 97.7%, demonstrating its capacity to minimize diagnostic errors and certify reliable results. These metrics highlight its ability in reducing false negatives and positives, which are critical for timely and accurate diagnoses. By providing rapid and precise identification of microorganisms, SONBC has the possibility to revolutionize infectious disease diagnostics, empowering medical professionals to make informed treatment decisions quickly. This approach not only enhances patient results by assisting targeted therapies but also reduces diagnostic delays, which are critical in controlling the spread of infectious diseases. For its successful incorporation into clinical workflows, it needs to certify the technology's safety, effectuality, and accessibility. SONBC represents a transformative advancement in the use of AI for infectious disease diagnostics, presenting a scalable solution to global healthcare challenges and paving the way for more dependable and efficient diagnostic methods.

Keywords: pathogen classification, diagnostics, sunflower optimized naive bayes classifier (SONBC), gaussian filter, independent component analysis (ICA)

1. Introduction

The pathogenic microorganisms that produce contagious diseases include bacteria, viruses, parasites, and fungi. The illnesses may or may not present with symptoms. When left untreated, some viral infections, like the human immunodeficiency virus (HIV), might be largely asymptomatic yet have disastrous effects after a short period. From microbes to microorganisms, infectious diseases can spread differently. For example, viruses like HIV can only be transmitted via close physical contact. Influenza virus bacteria are disseminated by droplets expelled after a sneeze, cough, or chatting to one another within a few meters of one another. Zoonotic diseases are contagious conditions that can spread to humans when transferred from animals to humans (Agrebi & Larbi, 2020). The scientific community has long been concerned about infectious diseases, but recently it has become more so as pandemics have caused crises in world health. The spreading of the human monkeypox virus and the severe acute respiratory syndrome coronavirus two has resulted in significant morbidity and mortality. As is typical of most newly developing infections, there are typically few readily accessible diagnostic tests and inadequate therapeutic and preventative choices. Due to the absence of laboratory researchers and healthcare personnel, as well as the difficulty in treating these infections, AI has considerably benefited clinicians in this regard (Marletta et al., 2023). The prevention of infectious diseases, the creation of anti-infected drugs, and management-related policy decisions shall also act as potential uses of AI in infectious diseases. It focuses on possible future developments of AI in infectious diseases and some limitations for utilizing such methods more generally (Shen et al., 2018). Disinfecting clinical samples, culturing, analyzing, and completing the process of genome sequencing are all part of the microscopic identification process. The pathogenic bacteria can be rather difficult to characterize and take a long time to cultivate, hence there exists a poor way of assessing the accuracy of the diagnosis. After learning the genetic characteristics of the pathogenic microbe, the microscopic inspection, the Polymerase Chain Reaction (PCR), and immunological tests can be used to determine the infectious disorders (Zhu et al., 2021). Medical testing facilities typically employ standard diagnostic procedures that include microbe detection based on distinct cultural features, nucleic acid testing (NAT), and enzyme-linked immunosorbent assay (ELISA). Nonetheless, their applicability is restricted because of the general limitations of the aforementioned procedures, which are laborious, time-consuming, costly, machine-dependent, and unable to perform quick onsite identification. Several techniques, Photothermal nanomaterials-based PCR, refractory NAD, and biosensors were developed to increase the detection rate and accuracy of NAT (Wang et al., 2021). The study aims to evaluate how well infectious disease diagnostics can be carried out using microorganism image analysis methods. Here, the study proposed the SONBC approach to provide better efficiency in evaluating infectious diseases.

The further part of the study includes Phase II, which indicates the related works; Phase III, the proposed methodology; Phase IV, the result and discussion; and Phase V, the conclusion.

2. Related Works

Kaushal and Gupta (2022) outlined the development and improvement of the sensitivity and specificity of the IDDAP decision support system, which is dependent on ontologies for diagnosing infectious diseases and prescribing antibiotics. Rawson et al. (2020) presented the use of AI in clinical microbiology for whole genome sequencing of microbial pathogens, automatic cultural plate reading, image analysis of gram stains, and identifying bacterial isolates utilizing MALDI-TOF information. They have also investigated the use of AI in disease surveillance, epidemiology, and infection prevention and control, particularly concerning hospital-acquired infections. li et al. (2019) presented an overview of the efficiency and methods of TPs in inhibiting bacteria to offer a fresh perspective on the diagnosis, prevention, and treatment of oral disorders and improve dental public health worldwide. Xu (2019) suggested the subject of study known as reverse microbial etiology. Unexpected microorganisms are isolated, and categorized, and their potential to spread infection, outbreaks, or an outbreak is evaluated. To safeguard world health and economy and maintain global security, they advise a list of probable infections and a plan for protection, management, and preparations. Kong and Shen (2023) examined how digital image analysis was used to develop methods for counting microorganisms. The first division of the microorganisms is into bacteria and other microbes. The relevant articles are condensed using techniques for image segmentation. Study Casapu and Moldovanu (2024) examined the evolution of CBMIA techniques with two crossed pipelines for microbe classification. All connected studies are categorized in the initial pipeline according to the respective microorganism application areas. This pipeline makes it simple for microbiologists to gain insight into all application domains and discover CBMIA approaches they are interested in applying. Study Hu et al. (2024) outlined a group of infectious disorders caused by intracellular bacteria for which FISH testing has demonstrated its efficacy. Infections with respiratory viruses, gastrointestinal disorders, mycobacterial diseases, extremely harmful pathogens as well and fastidious organisms, such as spirochete have been handled using FISH techniques has been widely applied in infectious illness recognition, with the promise for prompt identification and control. However, study Siddique et al. (2024) examined issues such as data heterogeneity, accessibility, excellence, and ethical implications. Balancing intricacy and comprehension, and also addressing privacy issues, is critical to effective deployment.

3. Proposed Methodology

Artificial intelligence is frequently used for image classification, in which an algorithm is trained to identify and sort images into various groups or labels. A well-curated and diversified dataset, a strong system design, and efficient training methods are necessary for achieving high accuracy in image categorization. AI-based microorganism image analysis has the potential to be a potent tool for the early diagnosis of diseases brought on by these microbes. Figure 1 denotes the flow of this research.

3.1. Dataset

This dataset, obtained from Kaggle (https://www.kaggle.com/datasets/mdwaquarazam/microorganism-image-classification), is a collection of images of eight different types of micro-organisms in individual folders. They are Euglena, Paramecium, Rod bacteria, Hydra, Amoeba, Spherical bacteria, Yeastand Spiral bacteria. There are many images in each folder that represent the distinctive traits of these micro-organisms, making them an ideal training data set for classification in machine learning and image recognition. This collection of varied images is conducive to investigating microbial diversity and classification techniques.

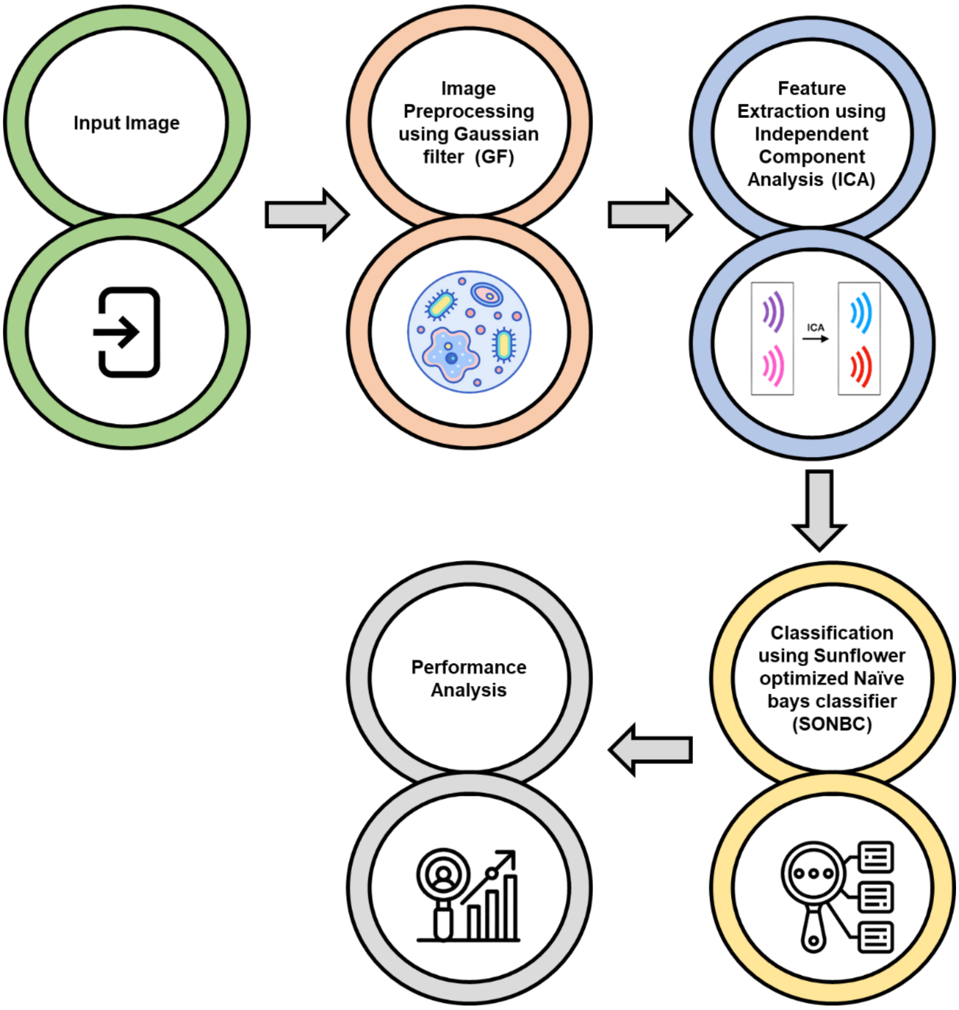

Figure 1 Flow of this research

3.2. Preprocessing using Gaussian filter (GF)

Original data have to be made ready for study or modeling by a process called preprocessing. Gaussian filtering is a common preprocessing technique in computer vision and image processing to filter out noise and improve images. A Gaussian kernel, which assigns weights to every pixel in the image based on how far away from the center of the kernel, is convolved with the image to produce the effect. Gaussian filter is applied to filter the images prior to the classification process. This method, selected by the shape of the Gaussian function, is a linear filter with weighted values for each member. This method was adopted because it can filter images by improving since this filter has a centered kernel. For the removal of noise that is commonly distributed, this filter is very effective. The values of each member in the resulting Gaussian smoothing filter may be estimated or calculated using the following equation (1).

$$g(v,z) = \frac{1}{d} d^{\frac{v^2+z^2}{2\sigma^2}} \quad (1)$$

Here, σ denotes the standard deviation, and d is the constant of normalization.

3.3. Feature extraction using independent component analysis (ICA)

The ICA divides a multivariate random signal into several unique passwords. All indicators are meant to be independent, and it is thought that the number of observed signals is proportionate to the number of distinct motions. Consider that have n linear mixes of$y_1 \dots y_m$. Every blending is a linear fusion of n different components.

$$y_i = b_{i1}s_1 + b_{i2}s_2 + \cdots + b_{im}T_m \quad (2)$$

Here, $(k = 1\,ton)$ denotes the independent variables. It can safely be assumed that the average of the distinct components and the mixing factors is 0. For convenience, we'll utilize vector terminology and refer to these mixes $y_{1.}y_2y_m$. "s" represents the empty variables. If they use A as a mixing matrix, then the mixing paradigm is expressed as$y = B_t$. This type of analysis is known as independent component analysis.

3.4. Classification using Sunflower Optimized Naïve Bayes Classifier (SONBC)

Sunflowers follow an identical routine daily, waking up and moving with the sun, such as the hands of a clock. The inverse law emission is a significant environment optimization in this context. According to the law, the radiation intensity is inversely related to the square of distances, meaning that as distance increases, radiation intensity (quantity) decreases proportionately. In this situation, the plants will acquire more UV rays if it is closer to the sun, and the radiation level will tend to remain relatively constant in this range. Yet, since a plant's solar radiation impacts when distance towards the rising sun increases, the research will employ similarly significant Steps for getting as near to the global optimal as feasible. The amount of heat R that every plant receives is determined by equation (3):

$$R_j = \frac{o}{4\pi q_j^2}, \tag{3}$$

Here, o is the power source, and measures how far a plant is from the finest at the moment, j. The sunflower faces the sun in the following directions:

$$\vec{T}_j = \frac{V^* - V_j}{\|V^* - V_j\|}, j = 1,2, \dots, m_o \tag{4}$$

The sunflowers' procedure in the position t is computed using equation (5):

$$c_j => \lambda \times O_j(\|V_j + V_{j-1}\|) \times \|V_j + V_{j-1}\| \tag{5}$$

Here,λdenotes the constant rate that describes an "inertial" dislocation of the flowers, $and O_j(\|V_j + V_{j-1}\|)$indicates the probability of pollination. Thus, the highest phase is described in equation (6):

$$c_{max} = \frac{\|V_{max} + V_{min}\|}{2 \times M_{pop}} \tag{6}$$

Here, V_{max} and $V_{min}$are the upper and the lower bound values, $and M_{pop}$ is the number of flowers in the total population. Real plantations to be established in equation (7):

$$\vec{V}_{j+!} = \vec{V}_j + c_j + \vec{t}_j. \tag{7}$$

The formation of an individual population is the first step in the method. This population could be even or random. The assessment of every person enables the determination of which one will become the sun, i.e., the individual with the highest estimation. However, it may be modified in the future to allow for the use of sunlight. Then, every other person will position themselves towards the sun as sunflowers and walk randomly by taking random steps in a particular direction. Algorithm 1 defines the sunflower optimization algorithm.

Algorithm 1: Sunflower Optimization (SFO)
Initiate the random collection of n flowers
Locate the sun (best option $s*$) in the initial group
Every flower should face the sun
while ($k < MaxDays$)
Calculate the direction of rotation for each develop
Eliminate (%) flowers further away from the sun
Measure the stages for every flower
Best b Flowers will nourish near the sun
Assess the innovative entities
Updating the sun if an innovative type beats the record
End while
The best solution discovered.

The NB classifier employs strong independence constraints and is a probabilistic classifier A search image is described as a set$R = \{r\}$A search image is described as a distribution$o\left(\frac{r}{d}\right)$. Given equal priors $o(d)$, the category is described as equation (8).

$$\hat{d} = arg\ arg\ max_{d\epsilon D} O(d/R) \ \ = arg\ arg\ max_{d\epsilon D} O \left\{ \prod_{r\epsilon R} o(e/d) \right\}$$

$$\hat{d} = arg\ arg\ max_{d\epsilon D} O(d/R) \ \ = arg\ arg\ max_{d\epsilon D} O\{\prod_{r\epsilon R} \ o(e/d)\} \quad (8)$$

The most common methods for creating a (sparsity) representative for an inquiry on a list of models are discussed in the following sections, and it validates how the Naive Bayes model could be modified to use these depictions. Every flower patch releases billions of pollen gametes in the actual world frequently. To keep things simple, it also presumptively believes that each sunflower only generates one pollen gamete, so every reproduction occurs independently.

4. Results

The model is implemented in Python 3.6. Every component defined was created with Pytorch and sped on a single Tesla V100 GPU. Microorganisms in both the healthy and pathological states should be included in this dataset. Here, the study has compared with some of the traditional methods like Machine learning deep learning (ML+DL) (Rani et al., 2022), deep learning (DL) (Treebupachatsakul and Poomrittigul, 2020), and Binarized-Greyscale-Hybrid algorithm with Multi-Region Binarization (Bigham) (Luo et al., 2021), and the suggested technique is Sunflower optimization using naïve Bayes classifier (SONBC).

The degree to which an image classification algorithm can precisely assign labels to images is known as its accuracy. Accuracy in image classification refers to measuring how well a machine learning model correctly identifies the class or label of a given image. It is typically estimated as the proportion of correct forecasts to the overall amount of forecasts generated through the simulation on a given set of images. To calculate accuracy, the study compares the predicted label of each image to its true label and counts the amount of instances the predicted label corresponds to the actual labeling. Finally, it divides the result by the total amount of images in the collection. The algorithm's accuracy can be determined by applying the equation as follows:

Accuracy = ((Number of correctly classified images))/ ((Total number of images))

If a model predicts the labels of 1000 images and correctly identifies 900 of them, its accuracy would be 90%.

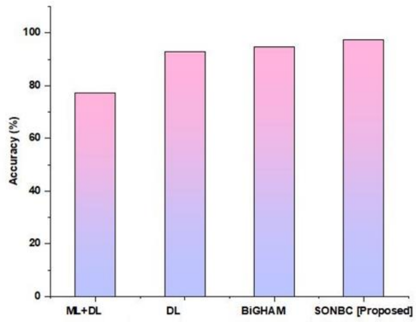

Figure 2. Graphical representation of accuracy.

Table 1. Numerical representation of accuracy.

Methods	Accuracy (%)
ML+DL (Rani et al., 2022)	77.32
DL (Treebupachatsakul and Poomrittigul, 2020)	92.88
Bigham (Luo et al., 2021)	94.68
SONBC [Proposed]	97.48

Denotes the accuracy compared with traditional and suggested techniques, and Table 1 represents the numerical outcomes of accuracy. Compared to other conventional methods, the suggested SONBC provides a high level of performance. Precision is an indicator utilized for image categorization to measure the method's accuracy in identifying true positives (correctly classified images) among all images classified as positive. In terms of image categorization, precision is defined as equation (9):

$$Precision = TP/((TP + FP)\ ) \quad (9)$$

Specifically, Precision is defined as the proportion of true positives (TP) to the total number of true and false positives (FP) The true positives represent the ratio of accurately classified images, whereas the false positives represent the number of inaccurately classified images. The precision metric indicates the percentage of correctly classified positive images by dividing the TP by the total number of positive classifications.

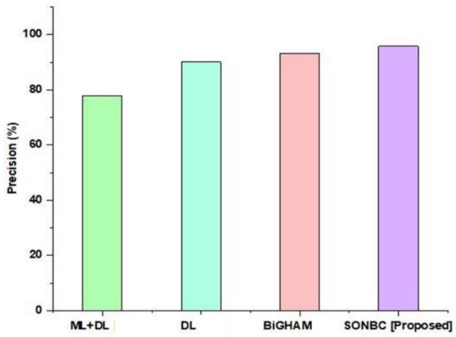

Figure 3. Graphical representation of precision.

Table 2. Numerical representation of precision.

Methods	Precision (%)
ML+DL (Rani et al., 2022)	77.88
DL (Treebupachatsakul and Poomrittigul, 2020)	90.07
Bigham (Luo et al., 2021)	93.23
SONBC [Proposed]	95.79

Denotes the precision comparison with traditional and suggested techniques, and Table 2 represents the numerical outcomes of precision. Compared to other conventional methods, the suggested SONBC provides a high level of performance. A recall is generally an indicator of success that assesses the efficacy of a categorization algorithm. Particularly, it proportion of TP to the total TP and false negatives (FN):

$$Recall = \frac{TP}{(TP+FN)} \tag{10}$$

In image classification recall gauges, the fraction of real positive events. (i.e., images belonging to a specific class) that the model correctly identifies as positive. In other words, when it's more important to precisely determine every example of a certain class, even if it means classifying some negative instances as positive.

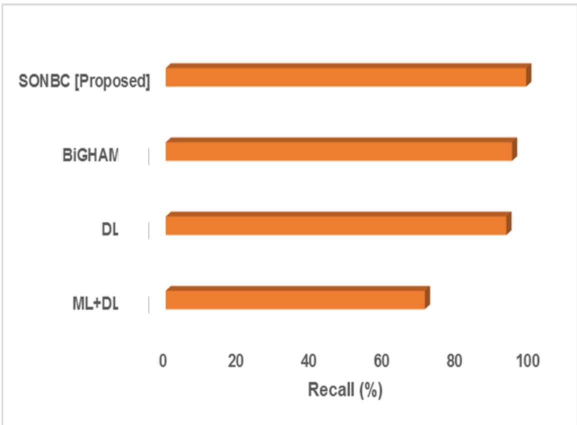

Figure 4. Graphical representation of recall.

Table 3. Numerical representation of recall.

Methods	Recall (%)
ML+DL (Rani et al., 2022)	70.78
DL (Treebupachatsakul and Poomrittigul, 2020)	93.02
Bigham (Luo et al., 2021)	94.58
SONBC [Proposed]	98.45

Refers to the comparison of recall using conventional and proposed methods, and Table 3 is the quantitative results of recall. In comparison with other traditional methods, the proposed SONBC achieves a high performance level. In image classification, F1 scores are a widely used measure for assessing the performance of a classifier. The f1 score can be quantified by equation (12):

$$F1\ score = 2 * \frac{(precision * recall)}{(precision + recall)}$$

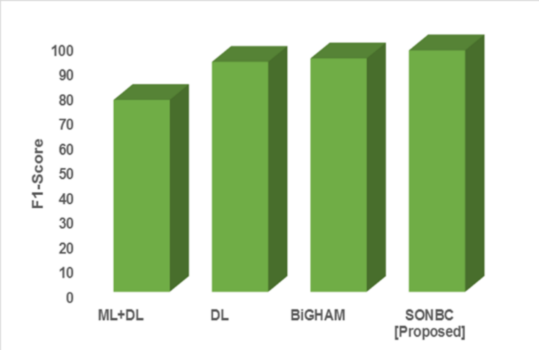

Figure 5. Graphical representation of F1 score.

Table 4. Numerical representation of F1 score.

Methods	F1-Score
ML+DL (Rani et al., 2022)	77.62
DL (Treebupachatsakul and Poomrittigul, 2020)	93.04
Bigham (Luo et al., 2021)	94.42
SONBC [Proposed]	97.7

Denotes the comparison of the f1 score with traditional and suggested techniques, and Table 4 represents the numerical outcomes of f1 score. Compared to other conventional methods, the suggested SONBC provides a high level of performance. Overall, the F1 score is a valuable metric in image categorizing as it allows for a comprehensive the effectiveness of the classification is evaluated using recall and precision as criteria.

5. Discussion

The use of artificial intelligence (AI) in the diagnosis of infectious diseases was studied by (Agrebi & Larbi, 2020), who commented that AI can enhance pathogen detection efficiency and accuracy. They point out how AI can be applied to analyze complex patterns of data, for example, imaging, to support precise and timely diagnosis. The research recognizes difficulties including inconsistent data and the requirement for strong validation in clinical settings. Nevertheless, its application in contexts with limited resources is restricted by its reliance on high-quality datasets and computing resources.

The use of AI in the diagnosis of infectious illnesses was covered by (Kaushal & Gupta, 2022), who concentrated on machine learning and deep learning methods. It emphasizes how these techniques increase diagnostic precision, particularly when detecting complicated and uncommon infections. The research additionally explores at issues like how effective AI model training requires big datasets and a lot of processing power. It encourages the creation of classifiers like SONBC to improve the diagnosis of diseases. But the generalizability of AI-based diagnostic models is constrained by the absence of defined methodologies and possible biases in training data.

The DL methodology (Treebupachatsakul & Poomrittigul, 2020) is restricted to techniques for microorganism image classification that rely on neural networks. It proved that it could produce accurate forecasts and accomplish balanced categorization performance. The method consistently maintains a strong classification model and detects beneficial instances. Its reliance on neural network-based techniques, however, limits its capacity to adapt to a wider range of classification problems and more complicated datasets.

The BiGHAM approach (Luo et al., 2021) uses multi-region Binarization in conjunction with the Binarized-Greyscale-Hybrid algorithm to classify microorganisms. Its 94.68% accuracy rate demonstrated how successful it is in exact categorization. The technique demonstrated dependable detection of true positives with a precision of 93.23%. The recall score of 94.58% demonstrated how well it detected almost all positive cases. Bigham, with an F1 score of 94.42%, is a strong technique for image classification, however SONBC outperforms it across the board.

The recommended SONBC technique uses ICA for reliable feature extraction and advanced preprocessing with Gaussian Filters to reduce noise and inconsistencies, therefore addressing the shortcomings of earlier approaches. In comparison with previous approaches that utilized large datasets and neural networks, SONBC is more adaptive to challenging classification tasks. It overcomes biases and validation issues in AI-based diagnostics by minimizing diagnostic mistakes with its high accuracy and recall rates. It is also appropriate for environments with limited resources due to its simplified design, which lowers computing needs. By improving diagnostic reliability, this development provides up the possibilities to more effective and scalable infectious disease diagnostics.

6. Conclusion

Infectious disease detection by microorganism image analysis can provide useful information for diagnosis, treatment, and prevention. Infectious disease prevalence and spread among different populations and geographic locations can be obtained by microorganism image analysis and can be applied to inform public health programs. This study suggested a SONBC methodology that provides fast and reliable results, which can help healthcare practitioners make more informed treatment choices and provides an opportunity to alter the treatment of infectious diseases. Comparing conventional approaches with the proposed SONBC technique provides 98.45% of recall, 95.79% of precision, 97.48% of accuracy, and 97.7% of f1 score which is better than other conventional methods. Future strategies include a regular stage in which the filamentous morphotype is measured by image analysis as defined above and an analysis procedure that utilizes molecular techniques to recognize the filamentous organisms if filament growth has been identified. This would detect an increase in filaments before visible sludge bulking occurs. Such a strategy would be an excellent addition to the expanding body of knowledge regarding the biology of uncultivated filamentous bacteria.

Ethical considerations

All datasets used in this study, including those sourced from Kaggle (https://www.kaggle.com/datasets/mdwaquaraza m/microorganism-image-classification), are publicly available and come with licenses that grant permission for research use.

Conflict of Interest

The authors declare no conflicts of interest

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