

COVID-19 detection from medical images using hummingbird-optimized VGG16 framework

Roshima Biju¹, Warish Patel¹, Kesavan Suresh Manic²

¹Department of Computer Science Engineering, Parul University, Vadodara, India

²AI Research Centre, College of Engineering, National University of Science and Technology, Muscat, Oman

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ABSTRACT

The rapid spread of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) created a major diagnostic challenge worldwide, highlighting the need for reliable automated approaches to assist clinicians in detecting coronavirus disease 2019 (COVID-19) from medical images. This study introduces a unified detection framework designed to deliver robust and accurate classification performance across different imaging modalities. The proposed model was developed and evaluated on computed tomography (CT) and chest X-ray datasets. The workflow comprises five key stages: image acquisition and resizing, deep-feature extraction, handcrafted feature extraction, feature optimization, and binary classification. The proposed system achieved high diagnostic performance, yielding approximately 99.33% accuracy for CT images and about 99.40% accuracy for X-ray images. The results demonstrate the framework's robustness and its potential as effective tool for computer-aided COVID-19 diagnosis.

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Corresponding Author:

Roshima Biju

Department of Computer Science Engineering, Parul University

Vadodara, Gujarat 391760, India

Email: roshima2010@gmail.com

1. INTRODUCTION

Artificial intelligence (AI) has emerged as a transformative tool in medical imaging, offering significant support for disease diagnosis and clinical decision-making. During the coronavirus disease 2019 (COVID-19) pandemic, chest computed tomography (CT) and X-ray scans became key modalities for rapid patient screening, and numerous AI-based models were introduced to assist radiologists [1]–[3]. While these systems demonstrated encouraging results, their clinical adoption remains limited due to issues such as dependency on a single imaging modality, lack of generalization, and limited interpretability. Recent studies [4], [5] highlight the continuing need to improve diagnostic accuracy for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), particularly as new viral variants continue to emerge.

The increasing demand for accurate and efficient diagnostic support has driven extensive research on AI-based COVID-19 detection frameworks. Various deep learning, machine learning, and hybrid models have been proposed to enhance accuracy and speed while reducing manual interpretation time. Table 1 summarizes a review of recent literature on COVID-19 detection using medical imaging. The review outlined indicates that hybrid frameworks, which combine deep and handcrafted features, often outperform individual model approaches by capturing complementary characteristics of medical images [6].

This research paper intends to propose a new AI-driven COVID-19 detection framework that combines the strengths of deep learning and handcrafted feature extraction. A convolutional pretrained neural

network, VGG16, is utilized to extract hierarchical global features, while local binary pattern (LBP) captures fine-grained texture information. Together, these features provide a richer representation of lung images. To enhance efficiency, the hummingbird algorithm (HBA), a bio-inspired optimization technique modeled on hummingbird foraging behavior, is used to identify the most relevant features while reducing redundancy.

The optimized findings are subsequently classified using random forest (RF) and k-nearest neighbor (KNN), evaluated via a rigorous five-fold cross-validation process. Experiments conducted on balanced datasets—3,000 CT images and 4,800 chest X-rays, evenly split between positive and negative cases—demonstrated excellent performance. The framework achieved 99.33% accuracy on CT scans with RF and 99.38% on X-rays with KNN, underscoring its robustness across modalities.

Unlike prior studies limited to one imaging type as shown in Table 1, the proposed system performs consistently on both CT and X-ray data, enhancing its applicability in diverse clinical settings, including resource-constrained regions. Its modular design allows seamless integration into radiological workflows and potential extension to other respiratory diseases. By combining accuracy, interpretability, and flexibility, this framework represents a significant step forward in AI-assisted diagnostics, supporting faster, more reliable decision-making in healthcare. The novelty and strength of this research are: i) implementation of a multimodality imaging framework combining deep learning-based feature extraction with handcrafted descriptors, further optimised HBA; ii) introduction of hybrid feature-driven approach for detecting COVID-19 in CT and X-ray images, validated through five-fold cross-validation to enhance detection accuracy.

The remainder of this paper is structured as follows: section 2 examines the proposed methodology in detail, including various stages of image processing, feature extraction, optimization, and classification. Section 3 presents the experimental protocols and outcomes, along with comparative performance evaluation. Section 4 is the conclusion of the paper with insights, limitations, and further research possibilities.

Table 1. Overview of methods for COVID-19 detection using medical image modalities

Existing model	Methodology	Image modality	Classifier	Results (accuracy %)
Nettur <i>et al.</i> [7]	Hybrid deep learning model using VGG16, DenseNet121, and MobileNetV2 features reduced via principal component analysis (PCA).	CT images	Support vector machine (SVM)	98.93
Liu <i>et al.</i> [8]	Convolutional neural network (CNN) model optimized with particle swarm optimization (PSO) algorithm.	X-rays, CT	Inbuilt CNN layer	97 (X-ray), 83 (CT)
Ren <i>et al.</i> [9]	Hybrid model of deep learning architecture CNN (ResNet50 + transformer)	X-rays, CT	Inbuilt CNN layer	97.65 (X-ray), 99.12 (CT)
Muhyeddin <i>et al.</i> [10]	Ensemble model combining various CNNs'	X-rays	Inbuilt CNN layer	90
Kabir <i>et al.</i> [11]	Knowledge distillation (teacher–student CNN).	X-rays	Inbuilt CNN layer	96.08
Kannan <i>et al.</i> [12]	Hybrid feature extraction (CNN + LBP) model optimized with the firefly algorithm (FA).	X-rays	KNN	96.48
Biju <i>et al.</i> [6]	Hybrid VGG16 + LBP + pyramid histogram of oriented gradients (PHOG) + Bayesian model averaging (BMA).	X-rays	KNN	99.17
Apostolopoulos and Mpesiana [13]	CNN model (MobileNet v2).	X-rays	Inbuilt CNN layer	96.78
Zhang <i>et al.</i> [14]	COVID-DenseNet (a CNN-based model).	X-rays	Inbuilt CNN layer	97
Mao <i>et al.</i> [15]	Transfer learning with SVM.	X-rays	SVM	95
Hariri and Avcı [16]	Lightweight CNN.	X-rays	Inbuilt CNN layer	89.89
Randieri <i>et al.</i> [17]	Lightweight 19-layer CNN.	X-rays	Inbuilt CNN layer	97.48
Oltu <i>et al.</i> [18]	A hybrid model (DenseNet201 + transformer).	X-rays	Softmax	97.87
Salama <i>et al.</i> [19]	CNN-based COVID-19 classification.	X-rays	Inbuilt CNN layer	91.5
Monday [20]	Transfer learning + CNN model.	X-rays	Inbuilt CNN layer	90

2. METHOD

This section presents the designed framework used to analyze the chosen dataset consisting of X-rays and CT slices of the chest. It also explains the various steps applied to differentiate between normal cases and COVID-19 cases in both imaging modalities. The methodology was developed to provide a systematic analysis of the two imaging modalities for COVID-19 detection. The following subsection introduces the overall framework adopted in this study and provides an overview of the proposed approach.

2.1. Framework

The overall taxonomy of the proposed framework is shown in Figure 1, summarizing the sequential stages of image preprocessing, feature extraction (deep and handcrafted), feature optimization through the HBA, and binary classification with five-fold cross-validation. As shown in Figure 1, the process begins with the systematic collection of lung images, comprising data from both healthy individuals and patients diagnosed with COVID-19. To maintain consistency, the size of all images was changed to $224 \times 224 \times 1$ pixels before feature extraction. From these processed images, both deep and handcrafted features were derived.

Deep features were obtained using the pretrained model VGG16, which produced a one-dimensional feature vector suitable for further analysis. In parallel, complementary structural details were captured by using the LBP technique, extracting texture-based handcrafted features. Each feature set was then refined through the HBA, which helped in selecting the most relevant attributes. Finally, the optimized deep and handcrafted features were serially fused, where the two feature vectors were sequentially merged to form a single hybrid feature vector before feature selection and classification.

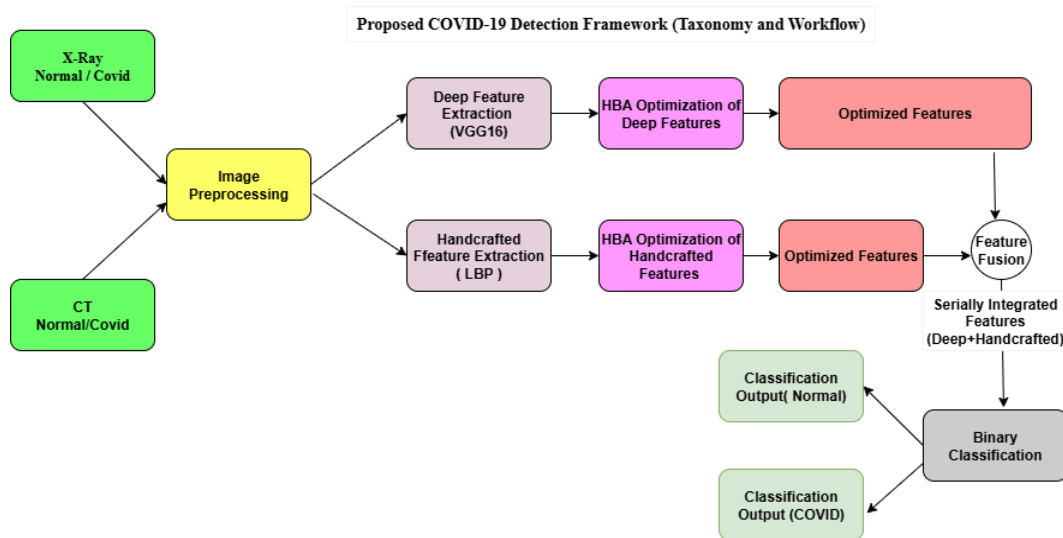


Figure 1. Taxonomy and workflow of the proposed multimodal COVID-19 detection framework

2.2. Image modal database

The dataset employed in this study was obtained from IEEE DataPort and corresponds to the dataset titled COVID-19 and normal chest X-ray uploaded by Monday [20]. The repository entry was created in 2021 and last updated in Dec. 2025. The dataset is publicly available under an open-access license, which permits usage for research and non-commercial purposes with proper citation. All images were resized to $224 \times 224 \times 1$ pixels prior to feature extraction, and data augmentation techniques were applied to improve model generalization. During this study, 4,800 X-ray (2,400 healthy and 2,400 COVID-19) and 3,000 CT (1,500 healthy and 1,500 COVID-19) images are reviewed for the assessment. The distribution of the images across the training, testing, and total sets is summarized in Tables 2 and 3. To provide a clearer understanding of the data used in this work, sample images from the dataset are displayed in Figures 2 and 3. Finally, all the considered pretrained deep learning models (PDLMs) are examined against the considered database, and the results are evaluated.

Table 2. Summary of the X-ray dataset employed in the experimental evaluation

Class	Image resolution	Total images	Training samples	Testing samples
Normal	$224 \times 224 \times 3$	2,400	2,160	240
COVID19	$224 \times 224 \times 3$	2,400	2,160	240

Table 3. Summary of the CT dataset employed in the experimental evaluation

Class	Image resolution	Total images	Training samples	Testing samples
Normal	$224 \times 224 \times 3$	1,500	1,350	150
COVID19	$224 \times 224 \times 3$	1,500	1,350	150

2.3. Deep feature mining

The effectiveness of the proposed framework largely depends on the deep features extracted from the selected PDLMs [21], [22]. For this study, widely used architectures including AlexNet, ResNet18, ResNet34, ResNet50, ResNet101, VGG16, and VGG19 were employed for evaluation. To ensure consistency across models, the following parameter settings were adopted: initial weights were initialized with ImageNet features, the total number of training episodes was set to 100, the Adam optimizer was applied, pooling was performed using either max or average operations, ReLU was used as the activation function for hidden layers, and sigmoid was chosen for the classifier output. The dataset comprised 2,160 X-ray training images, 1,350 CT images, and 240 validation images of X-ray and 150 images of chest CT, with classification performance validated using a 5-fold cross-validation strategy.

Before model training, image augmentation was applied to expand the dataset and improve generalization. Augmentation techniques included horizontal and vertical flips, rotations, zooming (0.4), width and height shifts (0.4 each), and shear transformations (0.3). These operations enhanced the diversity of the training data and helped the models learn more discriminative features. Through this process, each PDLM was able to extract robust deep features that contributed significantly to the overall framework.

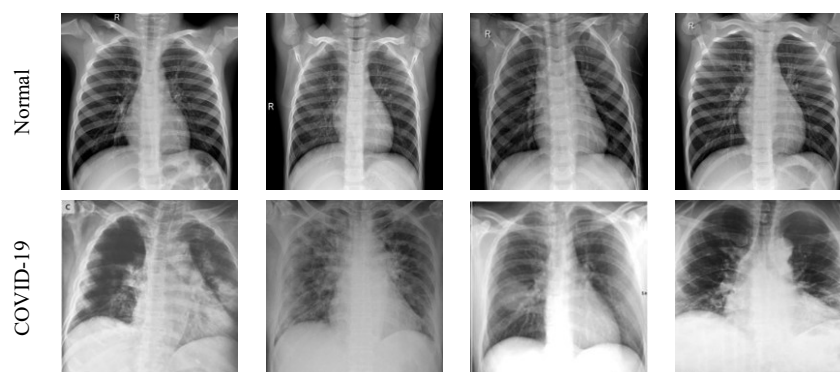


Figure 2. Samples of normal and COVID-19 X-ray images selected for experimental evaluation

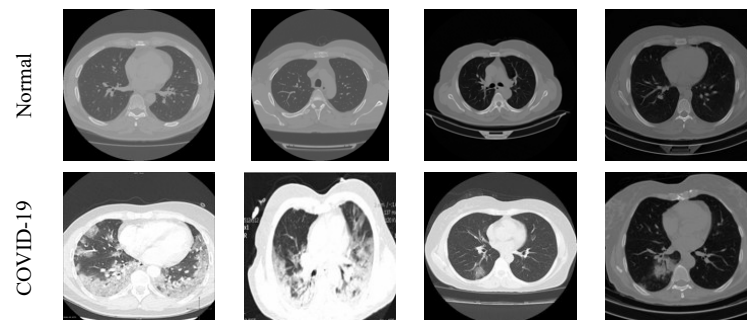


Figure 3. Samples of normal and COVID-19 CT images selected for experimental evaluation

2.4. Handcrafted-feature mining

In addition to deep features extracted through pretrained models, handcrafted texture features were incorporated using the LBP technique, which is a powerful descriptor that captures local spatial patterns within an image by comparing each pixel with its surrounding neighbors [23]. In this work, handcrafted features were retrieved with the help of the LBP technique [24], [25] with varying weights, as previously discussed in related research. To capture essential texture information, LBP was applied with weights ranging from $W = 1$ to 4.

2.5. Feature selection using the hummingbird algorithm

Selection of the features plays a crucial role in this study. In the proposed framework, the HBA algorithm is employed to refine the features extracted from both chest X-rays and CT scans. HBA replaces

PSO velocity, genetic algorithm (GA) genetic operators, and FA distance parameters with a memory-guided foraging mechanism that improves convergence speed and feature selection stability.

Here, each food source in the hummingbird search analogy represents a possible feature subset, while the nectar replenishment rate corresponds to the fitness value that measures the quality of the subset for classification. The algorithm simulates how hummingbirds prioritize flowers based on nectar quality and availability, thereby guiding the search toward the most informative features. By iteratively updating the “visit table,” which records how frequently features are selected, the algorithm ensures that highly discriminative deep and handcrafted features receive greater emphasis. Initial steps of the process are shown in (1) and (2).

2.5.1. Initialization

The algorithm starts by assigning initial values for HB and the visit table as shown in (1) and (2).

- Initialisation of humming birds, where R is a random number generated in the range $[0, 1]$, L is lower limit of search space, U is upper limit of search space, i is flower quantity, and X_i is position of i^{th} flower.

$$X_i = L + R(U - L) \quad \text{for } i = j = 1, 2, \dots, n \quad (1)$$

- Initialisation of visit table, here $[VT](i, j)$ shows the bird's visit to a specific flower for collecting the nectar. The visit table in HBA is a memory structure that records how many times an HB has visited a particular food source.

$$[(VT)](i, j) = \{\text{null}; \text{if } i = j\}, (0; \text{if } i \neq j)\} \quad (2)$$

2.5.2. Foraging patterns

In HBA, the HB is categorized into three foraging patterns based on territorial, guided, and migration. HBs perform three-dimensional searches on selected regions, utilizing axial flight, diagonal flight, and omnidirectional flight. Their ultimate goal is to find the ideal solution for a given problem by performing 3-dimensional searches, and the process is shown in (3) to (11).

- Guided foraging: in the guided foraging phase, the hummingbird is directed toward a flower with a favorable nectar source. The variable $[VT](i, j)$ denotes the selected target flower. Once the target has been determined, the hummingbird moves toward it according to the search mechanism described in (3) to (5).
 - Axial flight: the axial flight mechanism can be expressed using (3). Where $D^{(i)}$ denotes the direction vector associated with i^{th} dimension, d represents the dimensionality of the search space and $\text{randi}([1, d])$ is the random integer generator that selects a value within the range of 1 to d . In this foraging pattern, the hummingbird moves along a single randomly selected axis of the search space. The direction vector $D(i)$ in (3) activates one dimension while others remain zero, allowing local exploitation without disturbing all variables.

$$\text{Axial flight} = D^{(i)} = \begin{cases} 1 & \text{if } i = \text{randi}([1, d]) \\ 0 & \text{else} \end{cases} \quad \text{for } i = 1, 2, \dots, d \quad (3)$$

- Diagonal flight: where $\text{randperm}(k) = \text{random permutation of integers from 1 to } k$. In diagonal flight, the hummingbird moves simultaneously along multiple randomly chosen axes within the search space, as defined in (4). The $\text{randperm}(k)$ function generates a random permutation of dimensions, allowing the bird to explore in more than one direction at once. This behavior increases search diversity and helps the algorithm escape local optima during optimization.

$$\text{Diagonal flight} = D^{(i)} = \begin{cases} 1 & \text{if } i = P(j), j \in [1, k], P = \text{randperm}(k), k \in [2, [R \cdot (d-2)] + 1] \\ 0 & \text{else} \end{cases} \quad (4)$$

- Omnidirectional flight: in the omnidirectional flight phase, $D^{(i)} = 1$ in (5) indicates that all components of the directional vector are activated, enabling simultaneous updates across all dimensions for global exploration. The guided foraging is mathematically as (6) and (7).

$$\text{Omnidirectional flight} = D^{(i)} = 1 \quad (5)$$

$$V_i(t+1) = X_{i, \text{tar}}(t) + (a * D * (X_i(t) - X_{i, \text{tar}}(t))) \quad (6)$$

$$a \sim N(0,1) \quad (7)$$

Here $X_i(t)$ corresponds to the position of the i^{th} flower at iteration t , whereas $X_{i,tar}(t)$ refers to the target flower selected for the current search step. The parameter a is randomly sampled from a standard normal distribution with mean 0 and variance 1. The position update for HB towards i^{th} flower is modeled in (8), where f , the fitness specifies the flower with a better nectar-refilling rate.

$$X_i(t+1) = \begin{cases} X_i(t) & f(X_i(t)) \leq f(V_i(t+1)) \\ V_i(t+1) & f(X_i(t)) > f(V_i(t+1)) \end{cases} \quad (8)$$

- ii) Territorial foraging: the territorial foraging behavior is modeled using (9) and (10).

$$V_i(t+1) = X_i(t) + (b * D * X_i(t)) \quad (9)$$

$$b \sim N(0,1) \quad (10)$$

In these equations, the parameter b controls the extent of local exploration and is generated from a normal distribution with a mean of 0 and a standard deviation of 1. After obtaining nectar from a target flower, the honey badger may continue searching for additional food sources within its immediate surroundings rather than moving directly toward other flowers. This local search mechanism enables the algorithm to investigate nearby regions of search space and exploit promising solutions more effectively.

- iii) Migration foraging, where $X_{worst}(t+1)$ = new position of the HB when the food source becomes worse (lack of nectar). When a territory's food source is depleted, the HB migrates to far-away locations to identify an appropriate new food source. While doing so, the HB will travel to longer distances to locate this food source.

$$X_{worst}(t+1) = L + R(U - L) \quad (11)$$

Over multiple iterations, HBA converges toward subsets with higher classification accuracy. Less informative or redundant features are dropped, while the most discriminative DF + HF remain. The final output will be an optimized feature vector→used for classification (normal vs COVID-19).

2.6. Model classification and performance validation

In the proposed work, initial evaluation was carried out using the SoftMax classifier to assess the effectiveness of the chosen PDLMS. Once these results were obtained, additional experiments were conducted with a range of binary classifiers, including naïve Bayes (NB), logistic regression (LR), KNN, decision tree (DT), RF, and SVM. The effectiveness of the approach was then quantified using standard performance metrics derived from the confusion matrix, namely correct positives (PC), correct negatives (NC), incorrect positives (Pi), and incorrect negatives (Ni). These values were used for the calculation of several measures such as accuracy, precision, sensitivity, specificity, and F1-score to deliver a detailed assessment of the classification performance. The mathematical expression for these measures is presented in (12) to (16) [26]–[28].

$$Accuracy = (Pc + Nc)/(Pc + Nc + Pi + Ni) \quad (12)$$

$$Precision = (Pc)/(Pc + Pi) \quad (13)$$

$$Sensitivity = (Pc)/(Pc + Ni) \quad (14)$$

$$Specificity = (Nc)/(Nc + Pi) \quad (15)$$

$$F1 - score = (2Pc)/(2Pc + Pi + Ni) \quad (16)$$

3. RESULT AND DISCUSSIONS

The experimental evaluation was carried out on a computing platform equipped with an Intel i5 processor operating at 2.6 GHz, 18 GB of RAM, and 4 GB of VRAM, using Python® as the development environment. The current study extends earlier standalone X-ray-based feature extraction approaches by introducing a multimodal framework involving both X-ray and CT datasets together with HBA-based

optimized hybrid feature fusion [6]. For evaluation, a total of 4,800 chest images, comprising 2,400 normal cases and 2,400 COVID-19 positive cases, and 3,000 CT chest images, which comprises of 1500 normal and 1500 COVID-19 positive cases, were utilized for measuring the performance of the PDLMs on the designated classification task.

Model performance was evaluated using multiple metrics including accuracy, precision, sensitivity, specificity, and F1-score to ensure comprehensive assessment of diagnostic performance. The comparative analysis presented in Table 4 shows that overall, VGG16 shows higher accuracy (89.7%), sensitivity (99.3%), and recall (90.4%) for CT images, outperforming the other tested models. For X-ray images, VGG16 again demonstrated strong performance, while ResNet18 and ResNet101 also achieved notable accuracies of 91.87%. These results indicate that multiple architectures are effective for X-ray classification, whereas VGG16 provides a distinct advantage for CT scans. Considering its superior performance in CT and competitive results for X-rays, VGG16 was selected for subsequent stages of the study, including feature extraction and classification. This choice ensures that the framework is built on a stable and reliable model, thereby enhancing its diagnostic capability across different imaging modalities and providing a robust foundation for further optimization and validation.

Table 4. Comparative analysis of various PDLM

Image	Scheme	TP	FN	TN	FP	Accuracy	Precision	Sensitivity	Specificity	F1-score
CT	AlexNet	131	20	134	15	88.3333	89.7260	86.7550	89.9329	88.2155
	ResNet18	128	19	135	18	87.6667	87.6712	87.0748	88.2353	87.3720
	ResNet34	132	19	132	17	88.0000	88.5906	87.4172	88.5906	88.0000
	ResNet50	135	12	128	25	87.6667	84.3750	91.8367	83.6601	87.9479
	ResNet101	133	16	130	21	87.6667	86.3636	89.2617	86.0927	87.7888
	VGG16	146	1	123	30	89.6667	82.9545	99.3197	80.3922	90.4025
	VGG19	134	17	130	19	88.0000	87.5817	88.7417	87.2483	88.1579
X-ray	AlexNet	212	29	218	21	89.5833	90.9871	87.9668	91.2134	89.4515
	ResNet18	224	18	217	21	91.8750	91.4286	92.5620	91.1765	91.9918
	ResNet34	218	23	220	19	91.2500	91.9831	90.4564	92.0502	91.2134
	ResNet50	219	22	217	22	90.8333	90.8714	90.8714	90.7950	90.8714
	ResNet101	220	19	221	20	91.8750	91.6667	92.0502	91.7012	91.8580
	VGG16	219	22	222	17	91.8750	92.7966	90.8714	92.8870	91.8239
	VGG19	218	21	218	23	90.8333	90.4564	91.2134	90.4564	90.8333

The outputs generated by the convolutional layers of VGG16 for a representative test image are illustrated in Figure 4, with the feature maps for CT shown in Figure 4(a) and those for X-ray shown in Figure 4(b). In the radar plots shown in Figure 5, each polygon illustrates how effectively a model balances five evaluation metrics: accuracy, precision, sensitivity, specificity, and F1-score. For the CT dataset in Figure 5(a), most models produce relatively compact shapes, while VGG16 shows a broader spread, reflecting stronger overall performance. In the case of the X-ray dataset given in Figure 5(b), VGG16, ResNet18, and ResNet101 generate wider and more evenly distributed polygons, indicating superior classification ability when compared to AlexNet and VGG19, which yield smaller and less stable patterns.

After identifying VGG16 as the most suitable pretrained model, both deep and handcrafted features were extracted from the medical images, and these feature sets were subsequently optimized using the HBA. This feature selection step enabled the retrieval of the most informative attributes from both feature sets, resulting in a hybrid representation that combined the strengths of DF and HF. The resulting feature subset was evaluated using several machine learning classifiers under a five-fold cross-validation framework, and the corresponding results are reported in Table 5. The analysis highlights that, for CT image classification, the RF classifier delivered the strongest performance, achieving an accuracy of 99.33% in distinguishing COVID-19 cases from normal cases. In contrast, the KNN classifier produced the best results for X-ray images, demonstrating superior classification capability for this imaging modality. These findings suggest that the proposed framework maintains strong predictive performance across different types of medical images and effectively adapts to varying classification scenarios.

During the experimental analysis, a limited number of samples were incorrectly classified, mainly as false positive cases. This may occur because certain normal chest images contain visual patterns that resemble COVID-19 infection characteristics. Factors such as image noise, low image contrast, and variations in scanning conditions can also influence the extracted features and affect classification performance. Despite these challenges, the proposed hybrid feature-based framework achieved high sensitivity, specificity, and F1-score values, demonstrating its effectiveness in accurately distinguishing between the target classes.

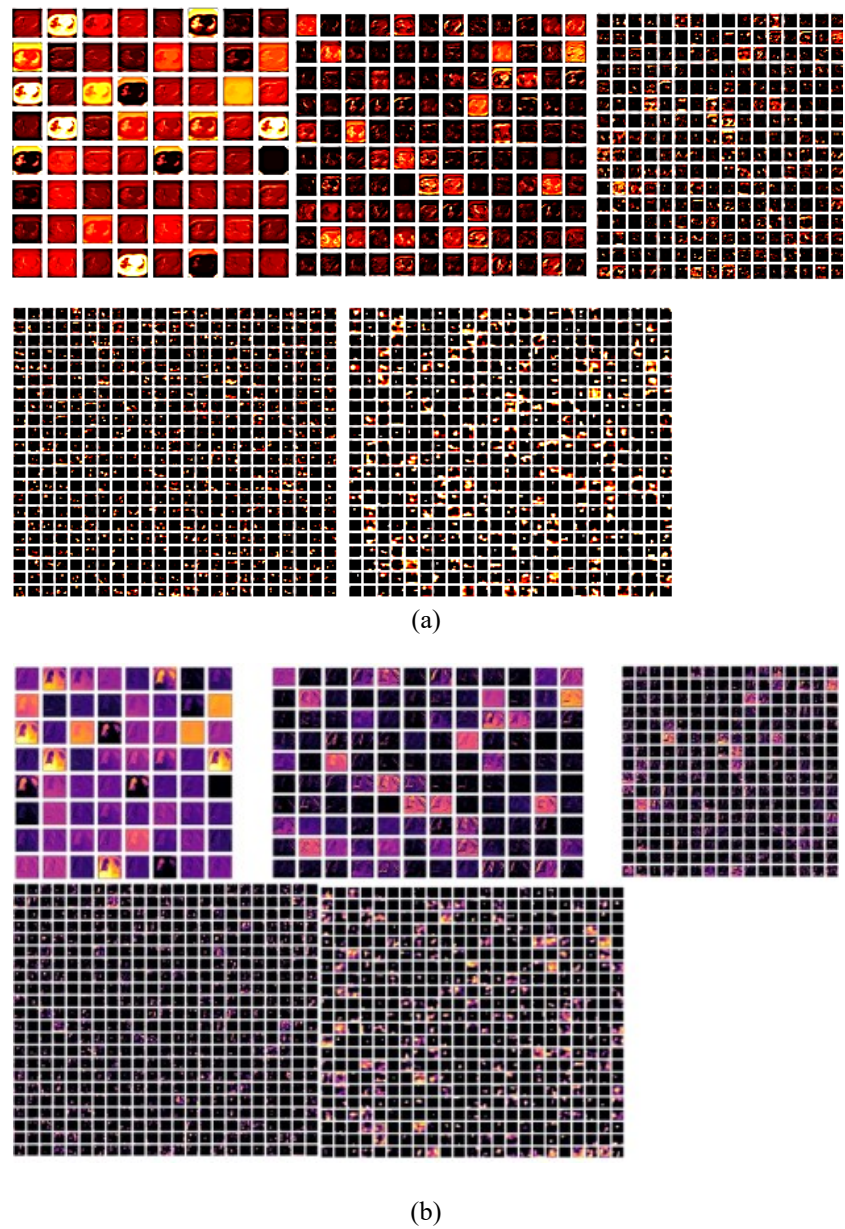


Figure 4. Output feature maps generated by different convolutional layers of the VGG16 network for (a) CT and (b) X-ray

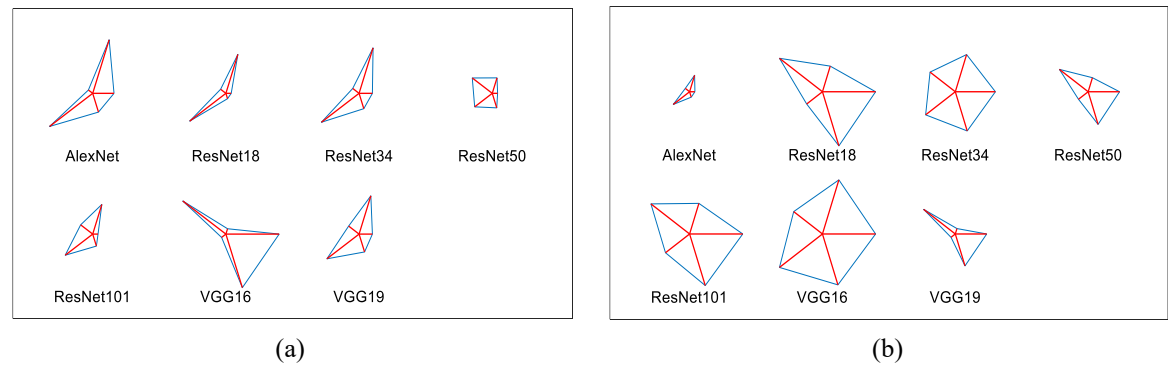


Figure 5. Radar plot for (a) CT and (b) X-ray dataset

Table 5. Outcomes of the proposed model using different classifiers

Image	Scheme	TP	FN	TN	FP	Accuracy	Precision	Sensitivity	Specificity	F1-score
CT	SoftMax	144	5	146	5	96.6667	96.6443	96.6443	96.6887	96.6443
	NB	143	6	148	3	97.0000	97.9452	95.9732	98.0132	96.9492
	LR	148	3	146	3	98.0000	98.0132	98.0132	97.9866	98.0132
	KNN	149	2	148	1	99.0000	99.3333	98.6755	99.3289	99.0033
	DT	145	5	148	2	97.6667	98.6395	96.6667	98.6667	97.6431
	RF	149	0	149	2	99.3333	98.6755	100	98.6755	99.3333
X-ray	SVM	147	2	145	6	97.3333	96.0784	98.6577	96.0265	97.3510
	SoftMax	236	5	233	6	97.7083	97.5207	97.9253	97.4895	97.7226
	NB	237	2	238	3	98.9583	98.7500	99.1632	98.7552	98.9562
	LR	237	5	231	7	97.5000	97.1311	97.9339	97.0588	97.5309
	KNN	239	0	238	3	99.3750	98.7603	100	98.7552	99.3763
	DT	234	8	233	5	97.2917	97.9079	96.6942	97.8992	97.2973
	RF	237	1	238	4	98.9583	98.3402	99.5798	98.3471	98.9562
	SVM	238	1	238	3	99.1667	98.7552	99.5816	98.7552	99.1667

The performance of different classification algorithms is illustrated in Figure 6, with the results for the CT image ia presented in Figure 6(a) and those for the X-ray presented in Figure 6(b). The spider charts offer an intuitive way to compare the classifiers, with broader coverage indicating stronger overall results. Analysis of the CT dataset shows that RF consistently produced the most competitive outcomes. However, for the X-ray dataset, KNN emerged as the strongest performer, achieving better results than the other evaluated classifiers.

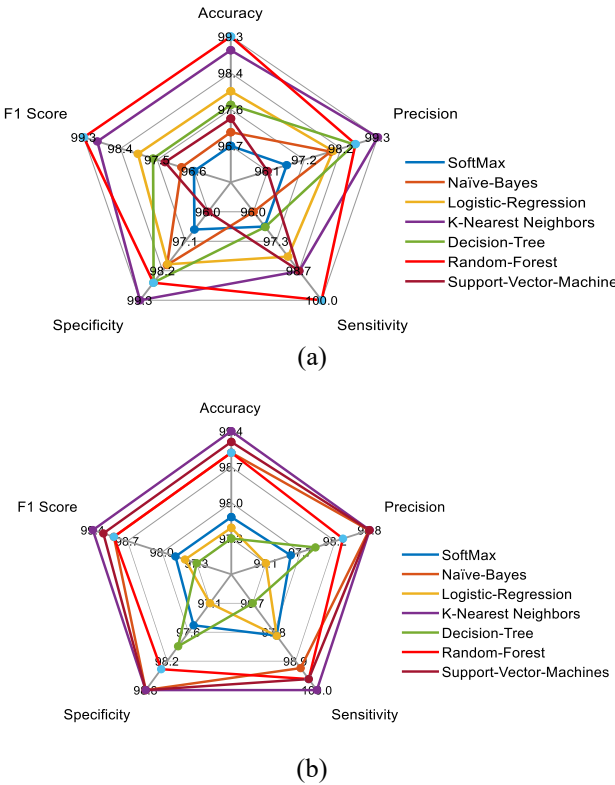


Figure 6. Spider plot for (a) CT and (b) X-ray

The performance trends observed in Figure 7, with accuracy presented in Figure 7(a) and loss in Figure 7(b), provide insight into the learning process of the network. Both training and validation results exhibit a stable pattern, with accuracy remaining above 99% while the loss decreases steadily as training progresses, indicating effective model convergence. Figure 8 depicts the ROC analysis of the proposed hybrid feature-based classifier. The observed curves confirm the strong class-separation capability of the model, highlighting its effectiveness in classification tasks.

To further validate the effectiveness of the developed framework, its performance was compared with that of previously reported approaches. As illustrated in Figure 9, the proposed multimodal strategy achieved higher classification accuracy than several methods documented in the literature. The improvement

observed suggests that combining information from multiple imaging modalities can enhance diagnostic performance and support more reliable disease detection.

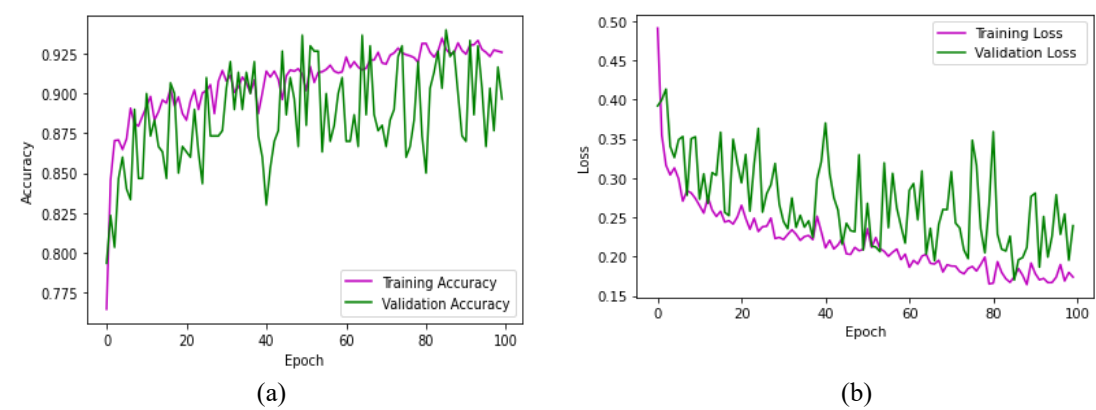


Figure 7. Graph for (a) accuracy and (b) loss

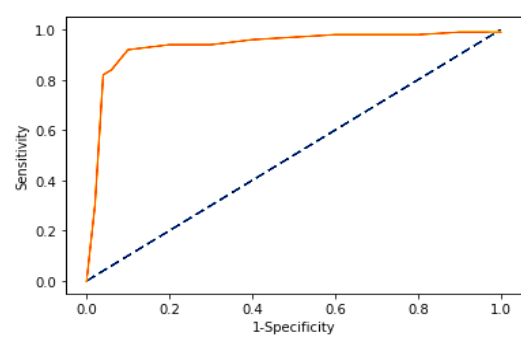


Figure 8. ROC curve of the proposed method

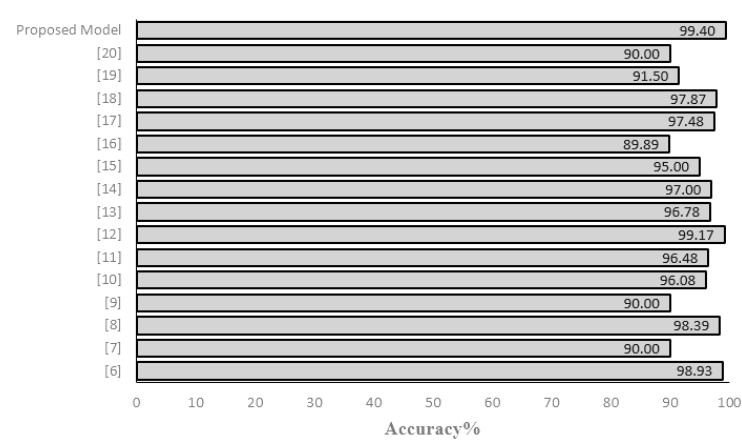


Figure 9. Comparative analysis of the classification accuracy achieved by the proposed framework and previously reported approaches

3.1. Ablation study and component contribution analysis

To better understand the impact of the individual components within the proposed framework, an ablation-based discussion was carried out. The framework is composed of three major stages: deep feature extraction using VGG16, extraction of handcrafted features, and feature optimization using the HBA. This analysis aims to investigate how each stage contributes to the overall effectiveness of COVID-19 classification.

The results summarized in Table 4 reveal that VGG16 was the most effective deep learning architecture among the models evaluated. For CT image analysis, it consistently obtained the highest values

across the considered performance measures, demonstrating its ability to capture informative and discriminative image characteristics. A similar pattern was observed for X-ray datasets, where VGG16 maintained strong performance relative to the other pretrained networks. Based on these observations, VGG16 was selected as the deep feature extraction backbone for the proposed system.

Earlier studies listed in Table 1 have reported that combining heterogeneous feature representations with feature-selection mechanisms can improve classification performance by reducing redundancy and increasing class discrimination [6]–[20]. Building upon these findings, the present framework integrates deep and handcrafted descriptors to exploit complementary information embedded within medical images. The resulting feature space is subsequently refined using HBA, which identifies the most informative attributes while discarding features that contribute little to the classification process.

The effectiveness of the optimized feature representation is evident from the results presented in Table 5. Across both imaging modalities, the hybrid feature set delivered consistently strong performance when evaluated using different machine learning classifiers. For CT images, the RF classifier achieved the highest classification accuracy of 99.33%, whereas the KNN classifier produced the best result for X-ray images with an accuracy of 99.38%. These findings demonstrate that feature optimization, when combined with deep and handcrafted representations, substantially enhances the discriminative capability of framework.

The ablation study further indicates that the overall success of the proposed approach arises from the interaction of all three components. VGG16 extracts high-level semantic information, handcrafted descriptors capture additional texture characteristics, and HBA improves feature quality through the selection of relevant attributes. Together, these stages produce a compact and informative feature representation that supports highly accurate and reliable COVID-19 classification for both CT and X-ray datasets.

4. CONCLUSION

This study developed a reliable framework model for automated detection of COVID-19 with the help of CT and X-ray images of the chest. By combining VGG16-based deep features, handcrafted descriptors, and HBA optimization, the model achieved high accuracies of 99.33% for CT and 99.40% for X-ray images, demonstrating strong cross-modality performance. These results confirm the framework's potential as a practical diagnostic aid in medical imaging. However, the study is limited by the size of the dataset and the requirement for improved model explainability through techniques such as gradient-weighted class activation mapping (Grad-CAM). The current study does not include a comparative analysis of HBA with alternative metaheuristic optimization methods such as PSO, GA, and the FA. As this investigation was outside the scope of the present work, it has been identified as a direction for future research. Subsequent studies will perform a detailed comparison to better evaluate the relative strengths of these optimization techniques. While the present study focuses on COVID-19 detection, future work will examine whether the proposed framework can be effectively adapted to identify other lung-related diseases. Additional research will also aim to streamline the computational process, making the system more suitable for real-world deployment in portable devices and low-resource clinical settings.

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AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

Name of Author	C	M	So	Va	Fo	I	R	D	O	E	Vi	Su	P	Fu
Roshima Biju	✓	✓	✓	✓	✓	✓		✓	✓	✓			✓	
Warish Patel		✓				✓		✓	✓	✓	✓	✓		
Kesavan Suresh Manic	✓		✓	✓			✓			✓	✓		✓	

C : Conceptualization

M : Methodology

So : Software

Va : Validation

Fo : Formal analysis

I : Investigation

R : Resources

D : Data Curation

O : Writing - Original Draft

E : Writing - Review & Editing

Vi : Visualization

Su : Supervision

P : Project administration

Fu : Funding acquisition

CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest.

DATA AVAILABILITY

The data that support the findings of this study are available in <https://iee-dataport.org/open-access/covid-19-and-normal-chest-x-ray>.

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BIOGRAPHIES OF AUTHORS



Roshima Biju    is research scholar in Department of Computer Science Engineering, Parul University, Vadodara, Gujarat 391760, pursuing Ph.D. in the area of heuristic algorithm applications. She has published six articles in the area of the medical image classification. She has been granted an Australian patent in COVID-19 disease detection using chest radiograph on September 2021. Her research interests include heuristic algorithm supported optimization, machine learning framework development for medical data assessment, and deep-learning assisted scheme development for medical data examination. She can be contacted at email: roshima2010@gmail.com.



Dr. Warish Patel    has conducted extensive research in the domains of artificial intelligence (AI), machine learning (ML), and the internet of things (IoT), with a particular focus on healthcare applications. He is currently serving as an associate professor in the Department of Computer Engineering, Faculty of Engineering and Technology, and as director and researcher at Parul Institute of Engineering and Technology, Parul University. He is also a senior IEEE member. His work emphasizes the internet of medical things (IoMT) for advanced disease diagnosis and real-time patient monitoring, integrating secure, intelligent, and scalable frameworks for smart healthcare systems. He has further contributed to next-generation healthcare analytics, including explainable AI, predictive modeling, and federated learning approaches, to enhance both accuracy and trust in medical decision-making. Building on his doctoral and postdoctoral research under the guidance of eminent scholars, he has gained international exposure through collaborations, publications, and conference presentations across Europe, strengthening his expertise in AI-driven healthcare solutions, medical imaging, cybersecurity, and data-driven clinical decision support systems. His academic and professional contributions bridge cutting-edge technologies with real-world applications, creating a meaningful impact on both research and industry. He can be contacted at email: warishkumar.patel@paruluniversity.ac.in.



Assoc. Prof. Dr. Kesavan Suresh Manic    is head of the Artificial Intelligence Research Centre at the National University, Oman, and adjunct professor at Torrens University, Australia. With a Ph.D. in Electrical Engineering and 24 years of experience, his research focuses on AI, machine learning, healthcare, education, and agriculture. He has 130+ publications, four patents, and has developed impactful AI models including A2M, BIMANIC, and Manic Tree Trekker. He has led research projects worth over half a million USD, collaborating with MOE, MOHERI, MTCIT, and MAFWR. He has supervised 12 Ph.D. scholars to completion and secured four patents. His leadership has earned him national and international awards, with his innovations recognized in reputed forums and the media. His consultancy and funded initiatives continue to deliver impactful AI solutions for education, healthcare, agriculture, and sustainability. He can be contacted at email: sureshmanic@nu.edu.om.