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Full Length Research Article

A HYBRID TRANSFER LEARNING MODEL WITH OPTIMIZED SVM USING HONEY BADGER OPTIMIZATION ALGORITHM FOR MULTI-CLASS LUNG CANCER CLASSIFICATION

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ABSTRACT
Lung cancer is a fatal disease with a high mortality rate in patience. Early and accurate detection of this disease plays a crucial role in improving a patient's chances of survival. Traditional methods, such as Computed Tomography (CT) scans, have historically been employed for tumor localization and assessing cancer severity. However, these methods are time-consuming and may pose risks, including patient mortality before tumor identification. Given the challenges associated with lung cancer classification and the limitations of existing practices, there is a pressing need for innovative clinical data assessment tools to complement biopsies and offer a more precise characterization of the disease. Recent literature suggests the application of deep learning techniques for lung cancer detection. However, efficient training of deep learning models requires a substantial amount of data, and the availability of annotated data for lung cancer detection is often constrained, potentially resulting in overfitting or under-fitting issues and inaccurate predictions. To address these challenges, this dissertation proposes a novel deep learning architecture based on the hybridization of three pre-trained models with a support vector machine (SVM) optimized using the honey badger optimization algorithm (HBA). The process involves pre-processing the input images to ensure compatibility with pre-trained models, implementing augmentation techniques to expand the dataset and prevent overfitting, and employing a hybrid model consisting of AlexNet, VGG16, and GoogleNet for feature extraction. The extracted features are combined to generate hybrid features, which are then fed into a multi-class SVM optimized with HBA for classification. The proposed model was trained and tested using a lung cancer dataset from Iraq-Oncology Teaching Hospital and the National Centre for Cancer Diseases (IQ-OTH/NCCD), comprising 1190 images across three categories: normal, benign, and malignant. The model underwent validation and was compared with existing literature works. The results demonstrated superior performance, achieving an overall accuracy of 98% in accurately detecting different categories of lung cancer. This result demonstrates the capability of the proposed model compared to other existing models from the literature.

Keywords: Lung cancer; transfer learning; CT-scans; AlexNet; VGG16; GoogleNet; SVM; honey badger algorithm.

INTRODUCTION

Lung cancer is the most common kind of cancer to end in mortality, and this is mostly attributable as the disease is diagnosed at a very later stage (Asuntha & Srinivasan, 2020). There is presently no possibility that a therapy will be discovered that will be effective. Lung cancer is commonly acknowledged to have one of the highest mortality rates among all types of cancer, regardless of whether a country is classified as developed or developing (Travis, 2020). An increase in the rate of urbanization, an increase in the average life expectancy, and the adoption of western lifestyles are some of the reasons that are contributing to the rise in the prevalence of lung cancer in emerging countries (Nigudgi & Bhyri, 2023). Both the early diagnosis of cancer and the continued health of those who already have the illness are crucial to the prevention and treatment of lung disease.

Worldwide, lung cancer is among the most prevalent forms of the disease and ranks among the leading causes of mortality due to the disease. It is responsible for 13% of all newly diagnosed instances of cancer and 19% of all deaths caused by cancer globally. It is anticipated that 1.8 million new cases of lung cancer were diagnosed in the year 2021. In India, 6.9% of all new instances of cancer and 9.3% of all fatalities linked to cancer are attributable to lung cancer. This percentage applies to people of both sexes. In terms of new cancer cases, lung cancer accounts for 6.9% percent (Malik & Raina, 2015) (Maharjan *et al.*, 2020).

The field of computer vision has seen significant advancement in recent years, and its applications are expanding across a wide range of business sectors. The use of computer vision technologies to medical diagnosis has also emerged as a prevalent trend. In this case, the particular application to the diagnosis of lung cancer is equally beneficial for study. Image processing is widely used in several commercial spheres. X-ray imaging of the lungs makes use of it in order to locate areas of the organ that may be harbouring malignant growths. Several procedures like image quality enhancement, segmentation, extraction of region of interest are often performed to extract meaningful information from the input scan. The majority of the time, digital image processing will make use of a wide variety of techniques in order to combine a number of separate features of a picture into a single unified whole. This is done in order to improve the overall quality of the image (Marentakis et al., 2021). This investigation makes use of a novel approach in order to concentrate on one specific facet of the overarching picture of the lungs. The divided area may be observed in a number of various ways, including when lighted in a variety of different ways and from a variety of different positions.

Given the challenges associated with lung cancer classification and the limitations of existing practices, there is an urgent requirement for innovative clinical data assessment tools that can complement traditional biopsies, thereby enhancing the precision of disease characterization. In light of recent advancements in deep learning, numerous researchers have endeavoured to develop lung cancer classification models aimed at aiding in the early detection of this

life-threatening disease.

For instance, a study by Almas et al., (2019) conducted a comparative analysis of GoogleNet and AlexNet for lung cancer detection. The evaluation utilized the LIDC-IDRI image dataset, assessing the models based on accuracy and processing time. The findings of the study reveal that both models yield comparable results in terms of their efficacy for lung cancer detection. This underscores the potential of deep learning techniques in contributing to the improvement of diagnostic tools for lung cancer assessment.

In a study conducted by Kalaivani et al., (2020), a deep neural network is devised and assessed for the purpose of detecting lung cancer from CT images. The classification of lung images into normal or malignant categories is achieved through the utilization of a densely connected convolutional neural network (DenseNet) in conjunction with an adaptive boosting algorithm. The dataset employed for experimentation consists of 201 lung images, with 85% allocated for training and the remaining 15% utilized for testing and classification. The experimental outcomes revealed that the proposed method attained a notable accuracy of 90.85%, showcasing the efficacy of the developed deep neural network in the accurate classification of lung images for the detection of potential malignancies.

Agarwal et al., (2021) describes a method for classifying lung tumors as malignant or benign that combines a Convolutional Neural Network (CNN) with the AlexNet. This method was compared with the traditional neural network system and their approach achieves a high degree of accuracy than the compared technique. However, this method can only handle binary classification.

In a study conducted by Nanglia et al., (2021), a hybrid algorithm is introduced, incorporating a Support Vector Machine (SVM) classifier integrated with a feed-forward backpropagation neural network (FFBPNN). The aim is to alleviate the computational complexity associated with the classification of lung cancer. The dataset utilized for this research comprises 500 images, with 75% of the data allocated for training purposes and the remaining 25% employed for classification. The proposed hybrid algorithm operates through a three-block mechanism. The first block focuses on dataset pre-processing, the second block is dedicated to feature extraction, incorporating optimization via Genetic Algorithm, and the terminal block handles classification through FFBPNN. Notably, the overall classification accuracy achieved by the proposed algorithm is reported as 98%. It is essential to highlight that while the proposed method demonstrates high accuracy, the application is tailored for binary classification.

Recently, (Nigudgi & Bhyri, 2023) presneted a lung cancer CT image classification using hybrid-SVM transfer learning approach. This work combine three pre-trained models for feature extraction and then applied SVM for the classification process. They evaluated their work using IQ-OTH/NCCD dataset which is a multi-classification dataset and compared with other approaches using accuracy. The results obtained indicates that their work achieved a superior performance in comparison with other works in the literature. Although, their work achieved a reasonable accuracy for the classification, the sensitivity of the minority class is low and this may be attributed to smaller number of samples in this category.

From the literature review conducted, the following research gaps were identified: (1) Most of the work review can only solve binary classification and (2) the work that implemented an approach for lung cancer multi-classification have low performance.

In light of the difficulty involved in classifying lung cancer and the constraints imposed by the practices that are currently in use, there is a pressing need for novel clinical data assessment tools that can complement biopsies and contribute to a more accurate description of disease characteristics.

Therefore, this paper presents a hybrid ensemble transfer learning approach combining three pre-trained models (AlexNet + VGG + GoogleNet) and support vector machine (SVM) classifier optimized with honey badger optimization algorithm (HBA) as classification algorithm for lung CT image classification. Transfer learning can lead to improved performance in lung cancer detection tasks by leveraging the knowledge and features learned from pre-training on large datasets. This can result in faster convergence during training and better generalization to new datasets. Transfer learning can also reduce the amount of labelled data required to train a deep learning model. This is particularly useful in the case of lung cancer detection, where annotated data can be limited. Transfer learning leads to faster model development; as pre-trained models can be fine-tuned for specific tasks rather than starting from scratch. This can save time and resources during the development process.

The remaining part of the paper is structured as follows: The methodology of the proposed hybrid method is presented in section 2. Results and discussion are detailed in section 3. Finally, conclusion and possible future research direction is given in section 4.

METHODOLOGY

The materials and methods employed in this study was presented in this section

Dataset Description

The lung cancer dataset utilized for both training and evaluation in this study was sourced from the Iraq-Oncology Teaching Hospital and the National Center for Cancer Diseases (IQ-OTHNCCD). The dataset was meticulously compiled over a span of three months during the autumn of 2019, as documented by Alyasriy, (2020). Comprising a total of 1190 images, the dataset encompasses 416 normal images, 120 images depicting benign lung tumors, and 561 images featuring instances of malignant tumors. All images within the dataset adhere to the JPEG (Joint Photographic Expert Group) grayscale format and exhibit a resolution of 512x512 pixels. To provide a visual representation, Fig. 1-3 showcases a representative example from the benign, malignant, and normal classes respectively. This dataset selection aligns with the comprehensive nature of the study, ensuring a diverse and well-annotated collection of lung cancer images for the purpose of model training and evaluation.

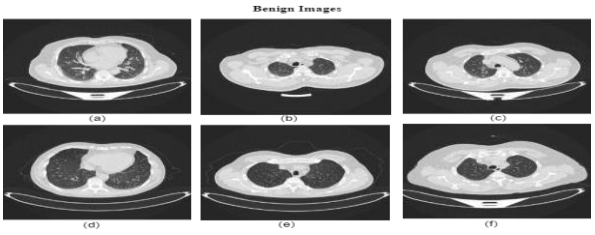

Figure. 1 Representative samples from the benign class

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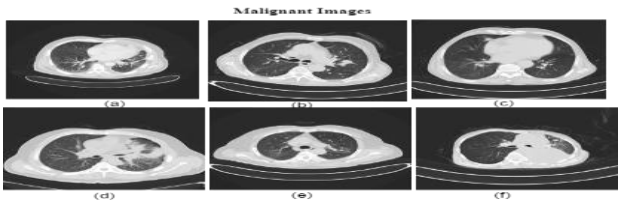

Figure. 2 Representative samples from the malignant class

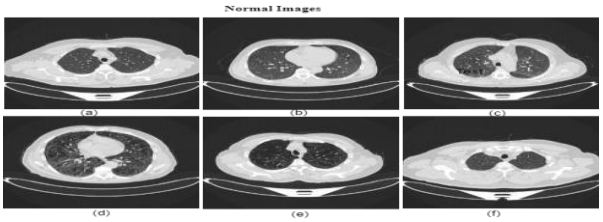

Figure. 3 Representative samples from the normal class

Support Vector Machine (SVM)

Support Vector Machine (SVM) stands as a mathematical model recognized for its efficacy as a universal approximator, well-suited for addressing classification and regression problems. Rooted in the principle of structural risk minimization, SVM diverges from the empirical error minimization concept inherent in Neural Network. A distinctive feature of SVM is its proficiency in both linear and nonlinear classification. This is achieved through a process of projection, involving a nonlinear mapping facilitated by the kernel trick, which elevates the training dataset to a higher-dimensional space. Within this augmented space, an optimal linear support vector, represented by a hyperplane, is determined to effectively separate the categories within the training data. Consequently, the overarching objective of the SVM learning process is to identify the optimal linear support vectors or hyperplane within this elevated dimension. The Support Vector Machine (SVM) algorithm possesses a notable merit in its immunity to the influence of local minima. Additionally, it remains resilient against the curse of high dimensionality owing to its reliance on support vectors. Regrettably, the efficacy of SVM is intricately tied to parameter configuration (C and gamma (γ)) and the judicious selection of its kernel (Bajaj, et al., 2023). The quality of SVM parameterization and the choice of kernel functions significantly impact the algorithm's learning and generalization performance. In general, the optimal performance of machine learning algorithms is contingent upon the meticulous tuning of their parameters. For the construction of a highly accurate classification model, the judicious selection of a robust machine learning algorithm is paramount, accompanied by the precise adjustment of its parameters. Manual parameter optimization can be a time-intensive process, particularly when dealing with learning algorithms characterized by a multitude of parameters. In establishing a Support Vector Machine (SVM) model, the primary challenges manifest in determining the suitable kernel function and its associated parameter values (C and gamma (γ)). Inadequate parameter configurations can result in suboptimal classification outcomes. In the literature, various techniques have been suggested for selection of this parameters such as using heuristic and metaheuristic methods. Figure 4 shows the SVM classification process.

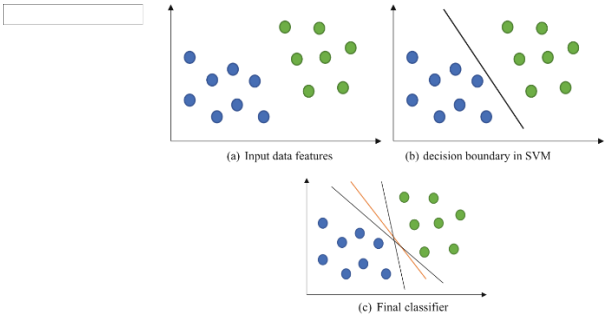

Figure. 4 SVM Classification process

Honey Badger Optimization Algorithm

The Honey Badger Algorithm (HBA) proposed by Hashim et al., (2022), is a population-centred metaheuristic optimization approach encouraged by the dynamic hunting conduct of honey badgers, utilizing honey and digging-seeking techniques. Since its introduction by Hashim et al. (2022), HBA has garnered widespread attention and has been applied across various domains. The notable appeal of HBA within the research community stems from its straightforwardness, ease of use, efficient computational time, accelerated convergence speed, high efficacy, and capability to address different kind of optimization issues, distinguishing it from the well-known optimization approaches presented. These creatures employ two primary senses; scent and digging, to identify food sources. In what is referred to as the "digging mode," the honey badger relies on its smell logic to locate prey. Once the prey is detected, it strategically circles it, determining the optimal location to dig for an increased chance of capturing it. In the "honey mode," the honey badger directly finds beehives by following the guidance of the honeyguide bird. This two-fold approach showcases the algorithm's inspiration drawn from the honey badger's self-motivated hunting conduct. The HBA adopts a structure akin to other metaheuristics. It utilizes a set of potential solutions for a given optimization problem, honing them via a variety of techniques like randomization and proximity to the problem's global optimum. The procedural components of HBA are expounded upon below

(a) Initialization phase

The honey badger optimization algorithm process typically begins with population initialization. Assuming that Nop is the total number of honey badgers. Location of h_{th} honey badger is initialized as in Eqn. (1).

$$Y_h = lower + (upper - lower) \times r_1,\ h = 1,\ 2,\ 3,\ \ldots Nop \quad (1)$$

where Y_h define location of h_{th} the honey badger, $lower$, and $upper$ define the lower and upper bounds of the hunting region. Whereas r_1 define a randomly chosen value within the interval of (0, 1). During the evaluation phase, the objective function of each agent is obtained using Eqn. (2).

$$f_h = f_{obj}(y_h) \quad (2)$$

(b) Digging phase (Exploration)

The way certain honey badgers approach their food using their sense of smell can help us determine which way the digging stage is going to go. At the digging step, the intensity operator, trend modifier, and density factor are defined together with the position update formula.

i. Digging phase location update

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The honey badger's keen ability to detect smell enables it to discover prey even in difficult conditions and make precise target identification decisions. This phase, known as the "digging phase," is achieved using Eqn. (3).

$$y_{new} = y_{prey} + F \times \beta \times IF \times y_{prey} + F \times r_2 \times \alpha \times d_h \times |\cos(2\pi r_3) \times [1 - \cos(2\pi r_4)]| \quad (3)$$

where y_{prey} represents the best position (prey position), β defines a constant value that is ≥ 1, which usually puts as 6 as suggested in the original paper, d_h represent differences among the best location y_{prey} and h_{th} honey badger. r_2, r_3, r_4 represent diverse random numbers in the range [1, 0] and F works as a flag that adjusts the exploration path to help the algorithm leave the local optimal zone. IF depicts the intensity variable.

ii. Defining Intensity Factor

The intensity variable shows the honey badger's controllable range to its prey, which is mostly influenced by the prey's caution and capacity for counter-reconnaissance. The definition of the intensity operator expression is given in Eqn. (4).

$$IF = r_5 \times \frac{S}{4\pi d_h^2} \quad (4)$$

$$S = (y_h - y_{h+1})^2 \quad (5)$$

$$d_h = y_{prey} - y_h \quad (6)$$

where d_h is the length separating the h_{th} honey badger and its target, S define the source strength, The number r_5 is a randomly generated value in the interval [0, 1] and y_{prey} represent the prey position, which is the greatest location so far obtained.

iii. Trend modifier (F) definition

Trend modifier (F) is a mechanism that permits the honey badger to alter the search trend and search the solution space completely. Typically, it is defined as Eqn. (7).

$$F = \begin{cases} 1, & if\ r_6 \leq 0.5 \\ -1 & else \end{cases}, \quad (7)$$

iv. Density variable (α) definition

The density variable (α) is a constant variable that adapts with time (a repetitive operation). When the operation continues, it will reduce randomly. Its goal is to guarantee the transition from the early phase of the iterative process stage toward the later development stage as defined in Eqn. (8).

$$\alpha = C \times \left(\frac{-curIt}{MaxIt}\right) \quad (8)$$

here C represents a fixed number ≥ 1 but is chosen as 2, and $curIt$ defines the existing iteration, $MaxIt$ signifies the total amount of iterations.

(c.) Honey phase (Exploitation)

The honey badger and honey guide bird are instances of mutually beneficial collaboration. Ultimately, the two depend on one another to discover the honey and honeycomb. The honeyguide bird's primary job is to point the honey badger in the direction of food. Eqn. (9), which is used to determine this stage, is identified as the "honey stage."

$$y_{new} = y_{prey} + F \times r_7 \times \alpha \times d_h \quad (9)$$

where r_7 represent a value generated randomly in the range [0, 1], y_{prey} represent the best location thus far discovered and y_h is the h_{th} Honey Badger's next position. α and F are obtained using Eqn. (7) and (6) respectively. It is evident from Eqn. (8) that a honey badger uses distance information d_h to undertake searches in the vicinity of the best location (prey location) y_{best} so far found. At this point, hunting is controlled by foraging behaviour differing by time (α). Additionally, a honey badger might discover disruption F. The complete HBA process algorithmically is presented in algorithm 1

Algorithm 1 HBA Pseudocode

Assign parametrs $MaxIt, \beta, C, Nop$
Initialize the population position randomly
Compute the fitness of the agent location based on the objective function and set to $f_h, h \in [1, 2, \dots, N]$
Store the best location y_{prey} *and set fitness to* f_{prey}
while $curIt \leq MaxIt$ **do**
  Update the decreasing factor α *based on Eqn.* (8)
  for $h = 1$ *to* Nop **do**
    Compute the IF based on Eqn. (4)
    if $r < 0.5$ **then** $\rightarrow (r)$*represent a random number in range* $[0, 1]$
      Update the position y_{new} *based on Eqn.* (3)
    else
      Update the position y_{new} *based on Eqn.* (9)
    end if
    Evaluate new position and set to f_{new}
    if $f_{new} \leq f_h$ **then**
      Assign $y_h = y_{new}$ *and* $f_h = f_{new}$
    end if
    if $f_{new} \leq f_{prey}$ **then**
      Assign $y_{prey} = y_{new}$ *and* $f_{prey} = f_{new}$
    end if
  end for
end while *Stopping condition met*
Return y_{prey}

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Proposed Hybrid Transfer Learning Model for Feature Extraction and Classification

The proposed approach for lung cancer classification encompasses several integral steps. Initially, raw lung CT images from the dataset undergo a resizing operation to standardize their dimensions. This operation, along with the subsequent partitioning of the dataset into training and testing sets, constitutes the pre-processing phase. Following this, an augmentation technique is applied to expand the size of the training data, serving as a preventive measure against model overfitting and enhancing overall model performance. Subsequently, the pre-processed images from the original dataset and the augmented images are inputted separately into three pre-trained base models within the transfer learning framework. This step aims to extract feature values from both the pre-processed and augmented images. The features obtained from individual pre-trained models are then combined to create hybrid feature values. These hybrid features are subsequently fed into a Support Vector Machine (SVM) optimized using the Honey Badger Optimization algorithm to perform the classification task on lung cancer CT images. A visual representation of the proposed lung cancer classification method is presented in Figure. 5, providing a comprehensive overview of the sequential processes involved in this innovative approach. This methodology leverages key concepts from transfer learning, data augmentation, and hybrid feature extraction, culminating in an optimized SVM-based classification system tailored for lung cancer image analysis.

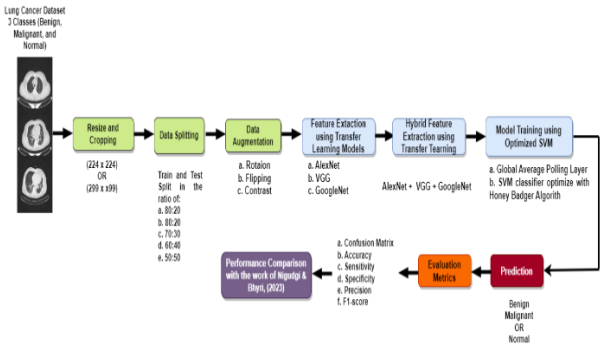

Figure. 5 Proposed hybrid transfer learning approach for lung cancer classification

Data Pre-processing

The lung cancer images within the dataset share a common size of 512x512 pixels. However, diverse neural network architectures impose varying input size requirements. For instance, the VGG architecture expects images of size 224 × 224, AlexNet architecture requires 256 x 256, and the GoogleNet architectures anticipate an input size of 299 × 299. To address this, a resizing operation is applied to conform all lung cancer images to the shape (224 × 224 x 3), ensuring compatibility with the diverse architectures employed in this study. This resizing not only aligns with the specific input requirements but also accelerates the training process. In addition to resizing, data partitioning is a pivotal aspect of image classification. During the initiation of the deep learning model's training phase, the image data is bifurcated into two subsets: training and testing. In this research, the dataset is partitioned into five different ratios, namely 80:20, 70:30, 60:40, and 50:50, for training and testing, respectively. This comprehensive approach to data partitioning facilitates a thorough evaluation of the model's performance under varying training and testing configurations.

Data Augmentation

Image augmentation techniques are implemented in this study to address potential overfitting challenges arising from limited data in the dataset. Additionally, augmentation serves to augment the size of the minority class, thereby enhancing the classification performance of the deep learning models. By augmenting existing data rather than acquiring new data, the efficacy of the deep learning model is notably improved. This research employs three distinct augmentation strategies to generate a new training set:

1. Rotation: Images are rotated by an angle of 90 degrees.
2. Horizontal Flipping: All images are horizontally flipped.
3. Random Contrast Adjustment: Random contrast adjustments are applied during training, introducing variability by randomly adjusting the contrast by a factor of 0.2.

Notably, to address imbalances, three augmented images are added for each image in the benign class, whereas one augmented image is added for the remaining two classes. This strategic augmentation approach contributes to a more balanced and enriched training dataset, mitigating the impact of class imbalances and further fortifying the model against overfitting.

Feature Extraction

Following the completion of the pre-processing phase on the original data and the augmentation process, convolutional feature values are extracted from the pre-processed lung cancer images. This is achieved by leveraging three distinct pre-trained Deep Convolutional Neural Network (DCNN) base models within the transfer learning paradigm. The chosen models include VGG-16, AlexNet, and GoogleNet. To facilitate feature extraction, the fully connected layer is removed from each of these architectures, retaining only the convolutional and pooling layers. These layers are instrumental in feature extraction, with deep dense convolutional layers characterizing all three base models. Specifically, the VGG-16 architecture comprises 16 convolutional layers organized into blocks with varying filter sizes and max pooling operations. The AlexNet architecture, on the other hand, is characterized by 201 layers, with each composition layer involving pre-activation Batch Norm (BN), Rectified Linear Unit (ReLU), and 3 × 3 convolutions. Notably, each layer receives feature maps from all preceding layers. The architectural details of VGG-16 and AlexNet are illustrated in Fig. 6 and 6, respectively. As for GoogleNet, its input layer is a convolutional layer with 64 filters of size 7 x 7 and a stride of 2. This is succeeded by a max pooling layer with a pool size of 3 x 3 and a stride of 2, tailored to handle images of size 224 x 224. The architectural configuration of GoogleNet is depicted in Fig. 8. Table 1 provides comprehensive details on the pre-trained models, encompassing information on input size and the number of extracted features. These extracted features serve as the foundation for subsequent stages in the proposed methodology, contributing to a robust and comprehensive approach to lung cancer image analysis.

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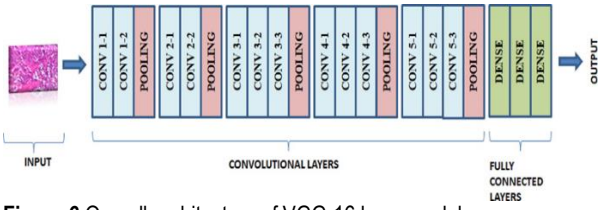

Figure 6 Overall architecture of VGG-16 base model.

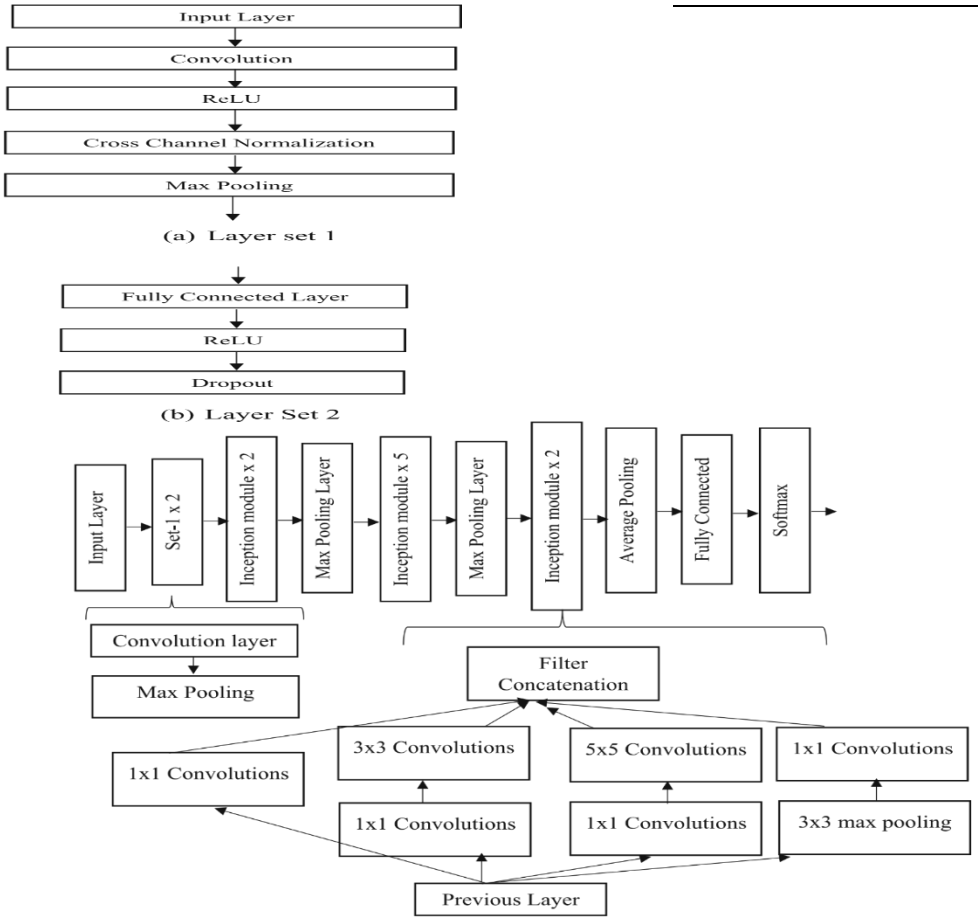

Figure. 8 GoogleNet architecture

Figure. 7 AlexNet architecture

Table 1 Details of the three models

Models	Input image size	Number of features extracted
VGG16	244 x 244	512
AlexNet	244 x 244	248
GoogleNet	244 x 244	248

Classification using SVM Optimized with Honey Badger Algorithm

In this research, solely the kernel weights of the pre-trained base models, namely AlexNet, VGG19, and GoogleNet, are transferred and employed for extracting convolutional feature values from lung cancer tumor images. The resulting feature maps generated by these three pre-trained base models are amalgamated to create hybrid feature maps, a strategy aimed at bolstering classification performance. Subsequently, these hybrid feature maps undergo processing through a global average pooling layer, serving as a superior alternative to the conventional flattening layer. The global average pooling layer transforms the (H × W × N) feature map into a (1 × N) feature map, where (H × W) denotes the image size, and N signifies the number of filters. The adoption of the global average pooling layer, as opposed to a fully connected layer, enhances interpretability by enforcing correspondence between feature maps and categories. This approach mitigates overfitting issues and establishes a direct mapping between output channels and feature categories. Additionally, it reduces the number of parameters and obviates the need for extensive parameter optimization, as advocated in prior studies (Maharjan et al., 2020; Rehman et al., 2021; Asif et al., 2023). Following the global average pooling layer, the lung cancer images are subjected to classification using a Support Vector Machine (SVM) optimized with the Honey Badger Algorithm (HBA). This optimized SVM categorizes the lung cancer CT images into benign, malignant, or normal classes. The optimization process for SVM using HBA is outlined in Algorithm 2.

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Algorithm 2 SVM + HBA pseodocode

```
Define the SVM objective function
function HoneyBadgerOptimizationForSVM(MaxIt, β, C, Nop)
    // Initialization
    Initialize random population positions for C and gamma
    // Evaluate initial fitness
Compute fitness for each agent based on SVM objective function and set to f_h, h ∈ [1, 2, …, N]
    Set y_prey as the best location and set fitness to f_prey
    // Main optimization loop
    curIt = 1
    while curIt ≤ MaxIt do
        // Update decreasing factor α
        Update decreasing factor α based on Eqn. (8)
        // Iterate over agents
        for h = 1 to Nop do
            // Compute the Influence Function (IF)
            Compute the Influence Function (IF) based on Eqn. (4)
            // Generate a random number
            r = random_number()
            // Update position based on Eqn. (3) or Eqn. (9)
            if r < 0.5 then
                Update position y_new based on Eqn. (3)
            else
                Update position y_new based on Eqn. (9)
            end if
            // Evaluate new position
            Evaluate new position and set to f_new
            // Update best positions
            if f_new ≤ f_h then
                Assign y_h = y_new and f_h = f_new
            end if
            if f_new ≤ f_prey then
                Assign y_prey = y_new and f_prey = f_new
            end if
        end for
        curIt = curIt + 1
    end while
    // Return the optimized SVM parameters
    Return y_prey as optimized SVM parameters
end function
```

Performance Evaluation Metrics

The evaluation of the proposed lung cancer CT image classification model incorporates a comprehensive analysis based on key performance indicators, encompassing accuracy, sensitivity, precision, specificity, and F1-score. Additionally, the assessment involves the introduction of a confusion matrix, which provides a visual representation of the diagnostic instances of lung cancer images as predicted by the proposed model. Equations 10, 11, 12, 13 and 14 as outlined, are employed to compute the accuracy, sensitivity, precision, specificity, and F1-score, respectively, of the trained model utilizing the proposed methodology. These performance metrics are calculated using test data and are derived from the information encapsulated within the confusion matrix (Agaba et al., 2022). This rigorous evaluation framework offers a nuanced understanding of the model's effectiveness in classifying lung cancer CT images, enabling a thorough assessment of its capabilities.

$$Accuracy = \frac{TP}{TP+TN+FP+FN} \quad (10)$$

$$Sensitivity = \frac{TP}{TP+FN} \quad (11)$$

$$Precision = \frac{TP}{TP+FP} \quad (12)$$

$$Specificity = \frac{TN}{TN+FP} \quad (13)$$

$$F1-score = 2 \times \frac{Precision \times Recall}{Precision+Recall} \quad (14)$$

In the equations above, TP means true positives, FP means false positives, TN means true negatives, and FN means false negatives.

Experimental settings

We trained the proposed deep transfer learning models using the Python programming language using TensorFlow and Keras framework. All experimental studies are performed on Kaggle. *Kaggle* is the world's largest data science community with powerful

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tools and resources which help to run python codes on cloud for free.

RESULTS AND DISCUSSION

This section presents the experimental results carried out to evaluate the proposed Hybrid transfer learning with honey badger algorithm optimized SVM model to classify the lung cancer images into benign, malignant and normal images using 80:20, 70:30, 60:40, and 50:50 training and testing sets respectively. Furthermore, a comparative analysis between the proposed method and other methods presented in the literature was also provide to gauge the effectiveness of the proposed approach.

Experimental Analysis for the Proposed Model

The dataset is divided into training and testing images in the following ratios of 80:20, 70:30, 60:40, and 50: 50%, respectively. The experimental results obtained during testing are as follows:

The confusion matrices that were acquired during testing was shown in Fig. 9, 10, 11 and 12 for 80:20, 70:30, 60:40, and 50:50 ratios respectively. A confusion matrix is a table that describes the performance of a classification model by comparing the predicted labels with the actual labels of a batch of data. This comparison is made using a confusion matrix. The number of correct positive, incorrect positive, correct negative, and incorrect negative predictions produced by the model is all shown on a confusion matrix.

The confusion matrix for a scenario with 80% training and 20% testing is shown in Figure 8. The results obtained for each class from the confusion matrix was shown in Table 2. The table indicates that the model with 80%:20% training and testing data achieved 97%, 90%, 98%, and 93% for the Benign class, 96%, 99%, 99%, and 97% for Malignant class, and 96%, 95%, 97%, and 95% for the normal class in terms of Sensitivity (Recall), Precision, Specificity, and F1-score respectively.

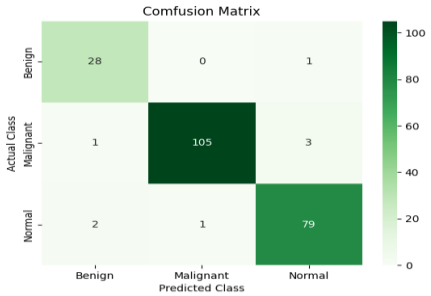

Figure. 9 Confusion matrix for the 80% training + augmented data and 20% testing

Table 2 Testing result: 80% training and 20% testing

	Benign	Malignant	Normal
TP	28	105	79
FP	3	1	4
FN	1	4	3
TN	188	110	134
Recall (Sensitivity)	0.97	0.96	0.96
Precision	0.90	0.99	0.95
Specificity	0.98	0.99	0.97
F1-score	0.93	0.97	0.95

Figure. 9 shows the confusion matrix with 70% training and 30% testing and the results of the individual classes was depicted in Table 3. The results indicate that, in the benign class, this scenario achieved 93% recall, 91% F1-score, which this shows a lower performance than the 80:20 scenarios in terms of this two metrics. However, the results indicate the same performance for the two scenarios in this class in terms of precision and specificity. Moreover, in the malignant class, in terms of sensitivity and F1-score, 70:30 is slightly higher than the 80:20 scenario obtaining 98% performance in the two metrics each. In addition, for the normal class, the 70:30 outperform the 80:20 scenarios in terms of all the metrics with a slim margin.

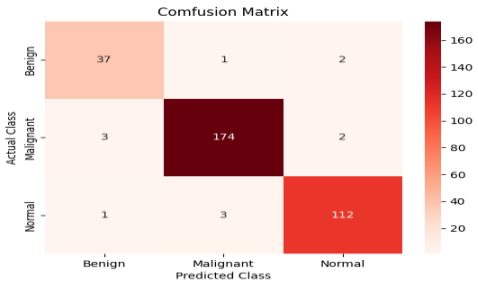

Figure. 10 Confusion matrix for the 70% training + augmented data and 30% testing

Table 3 Testing result: 70% training + augmented data and 30% testing

	Benign	Malignant	Normal
TP	37	174	112
FP	4	4	4
FN	3	4	4
TN	291	152	215
Recall (Sensitivity) (%)	0.93	0.98	0.97
Precision (%)	0.90	0.98	0.97
Specificity (%)	0.98	0.97	0.98
F1-score (%)	0.91	0.98	0.97

In the 60:40 training and testing ratio scenario, the results obtained was shown in Table 4 which is computed using confusion matrix presented in Figure 10. The results indicate a lower performance of this percentage in terms of Sensitivity and F1-score compared to 80:20 and 70:30 in the Benign class prediction with 89% in each of the two metrics. However, in predicting Malignant and Normal classes, this scenario has a very close performance with the two other scenarios in terms of all the metrics.

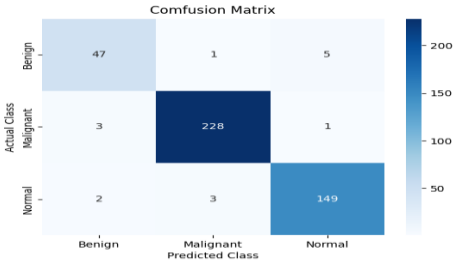

Figure. 11 Confusion matrix for the 60% training + augmented data and 40% testing

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Table 4 Testing result: 60% training + augmented data and 40% testing

	Benign	Malignant	Normal
TP	47	228	149
FP	5	4	6
FN	6	4	4
TN	381	203	279
Recall (Sensitivity) (%)	0.89	0.98	0.97
Precision (%)	0.90	0.98	0.96
Specificity (%)	0.98	0.99	0.98
F1-score (%)	0.89	0.98	0.96

Table 5 shows the result obtained in the 50:50 percentage ratio as computed from the confusion matrix shown in Figure11. The result from this table indicates that, this ratio obtained the least Sensitivity performance of 85% than all the other scenarios. However, in the Malignant, this scenario obtained almost similar result with the other scenarios with respect to all the metrics. Finally, the least performance was obtained in predicting the Normal class in the 50:50 ration in all the four metrics obtaining 95% Recall, 93% Precision, 96% Specificity, and 94% F1-score. Overall, the highest performance in terms of Sensitivity in predicting Benign class was obtained in 80:20 scenarios and the list is in 50:50.

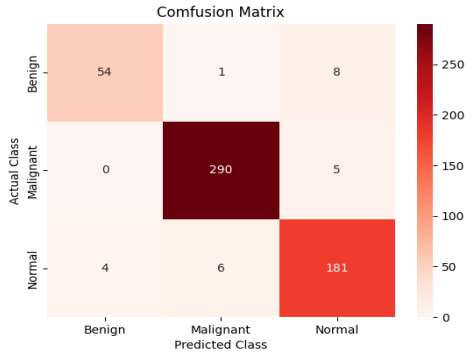

Figure. 12 Confusion matrix for the 50% training + augmented data and 50% testing

Table 5 Testing result: 50% training + augmented data and 50% testing

	Benign	Malignant	Normal
TP	54	290	181
FP	4	7	13
FN	9	5	10
TN	482	247	343
Recall (Sensitivity) (%)	0.85	0.98	0.95
Precision (%)	0.93	0.98	0.93
Specificity (%)	0.99	0.97	0.96
F1-score (%)	0.89	0.98	0.94

Comparison of the Proposed Model with other Models Presented in the Literature in Terms of Accuracy

The performance of the proposed model was compared with other models from the literature using accuracy measure to further validate the efficacy of the proposed model, which the results can be seen in Table 6 and graphically depicted in Fig. 13. The results demonstrated that the proposed method outperformed the other works with 98%, compared to Nigudgi & Bhyri (2023) having 93%, GoogleNet achieving, 91%, VGG19, 90%, and AlexNet having 87%.

Table 6 Comparison with other works in the literature

Models	Accuracy
Hybrid model (Nigudgi & Bhyri, 2023)	93%
AlexNet (Agarwal et al. 2021)	87%
DenseNet (Kalaivani et al. 2020)	86%
GoogleNet (Almas et al. 2019)	91%
ResNet (Saric et al., 2019)	88%
Proposed model	98%

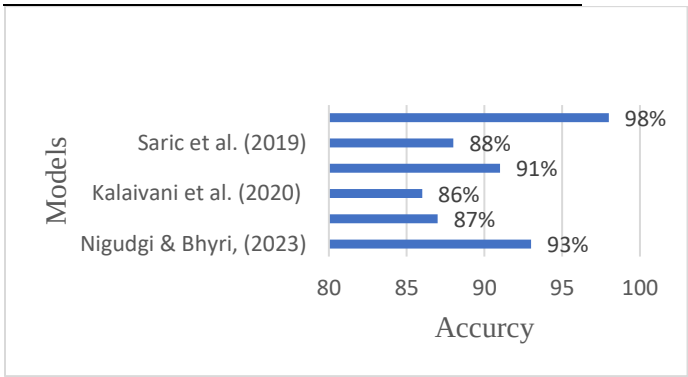

Figure 13 Comparison chart of the proposed model with other works in the literature

CONCLUSION

In this work, we developed a hybrid transfer learning model using three pre-trained models (GoogleNet, VGG19, and AlexNet) with optimized SVM using honey badger optimization algorithm for multi-class lung cancer classification. The model training and testing process is conducted utilizing the IQ-OTH/NCCD dataset, comprising a total of 1190 cases categorized into one of three classes: normal, benign, or malignant. First, analysis was conducted using four different training and testing ratios (80:20, 70:30, 60:40, and 50:50) to find out which of these ratios will give the best performance in terms of predicting the individual classes of the lung cancer CT images using precision, sensitivity, specificity, and F1-score performance measure. Furthermore, a comparative analysis was conducted to ascertain capability of this work in comparison with other works in the literature in terms of accuracy. The results indicated that the proposed work outperformed that of other compared approaches. In the future, the authors intent to employ other advanced techniques such as auto-encoder for enhanced lung cancer classification.

Conflict of Interest: The corresponding author, representing all authors, confirms the absence of any conflict of interest.

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