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Liver tumour segmentation and classification using MV3CNN-KHO: a combination of multiparameterised inception V3 CNN and Krill Herd optimisation

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Abstract: The segmentation and classification of liver tumours are crucial in medical imaging, aiding early detection and treatment planning for liver diseases. Deep learning-based liver lesion segmentation has the potential to enhance the precision and effectiveness of liver disease detection. Recent studies have shown promising results in liver cancer prediction using convolutional neural network (CNN)-based techniques. This work proposes a Multiparameterised Inception v3 CNN to improve feature extraction for liver cancer prediction. Additionally, Krill Herd optimisation (KHO) optimisation can be applied to identify ideal hyperparameters, further enhancing the system's performance. By integrating KHO, the proposed model can achieve higher accuracy in predicting liver cancer, benefiting both patients and medical professionals. The study, conducted on the liver tumour segmentation (LiTS) dataset, evaluates accuracy, sensitivity, and specificity, with the MIV3CNN-KHO model achieving 96% accuracy, 0.96 sensitivity, and 0.94 specificity. The implementation was done using Jupyter Notebook, with Python as the programming language. The optimised system offers an improved solution for liver cancer detection and prognosis, making it a valuable tool in medical imaging.

Keywords: segmentation classification; multiparameterised inception V3; KHO; Krill Herd Optimisation; convolutional neural network; medical imaging; feature extraction; model evaluation; accuracy analysis.

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Biographical notes: A. Bathsheba Parimala holds an MSc from Manonmaniam Sundarnar University (2007) and an MPhil from Vinayaka Missions University (2009). She received the Research Excellence award from the *International Journal of Modern Trends in Science and Technology (IJMTST)* in 2019. She has contributed to books on Research Methodology and Computer Networks. Currently, she is pursuing her PhD in Computer Science at Vinayaka Missions Kirupananda Variyar Arts and Science College, Salem. Her research interests focus on Medical Image Processing and Machine Learning.

R.S. Shanmugasundaram holds a BE in Electronics and Communication Engineering from the University of Madras (1996), an ME from Bharathidasan University (2001), and a PhD from Anna University (2015). His research focuses on medical image processing, deformable models, and segmentation. He is also a life member of ACS and ISTE, and currently serves as the Director of Students Welfare at Vinayaka Mission's Research Foundation (Deemed to be University), Salem, Tamil Nadu.

1 Introduction

Medical picture segmentation, which is crucial in the analysis of image studies, is critical for clinicians making computer-aided diagnoses in the field of medicine (Bogovic et al., 2013). Segmenting the appropriate organ or region from pictures from several medical fields, particularly radiology, is critical in planning the early diagnosis and treatment of disorders. Compared to other methods, the use of AI in radiation has grown fast in recent years (Özcan et al., 2023). Liver cancer, namely hepatocellular carcinoma, occurs as a result of an assortment of risk factors. Chronic hepatitis B or C virus infections and inflammation may result in liver cell mutations. Prolonged alcohol misuse can result in liver cirrhosis, which increases the risk of cancer substantially. Non-alcoholic fatty liver disease (NAFLD) and its progressive variant, NASH, both associated with obesity, raise the risk. Another important concern is exposure to aflatoxins, poisons from moulds in contaminated food (Angeline et al., 2023). Diabetes, probably due to its association with fatty liver disease, contributes, as may genetic susceptibility, tobacco use, and long-term exposure to toxins like vinyl chloride. While not everybody with these risk factors obtains liver cancer, identifying and minimising these risks through prevention and early detection are critical in dealing with this major health issue (Chitra et al., 2024).

Employing computing tools to segment liver tumours entails employing various computational approaches and algorithms to process medical pictures and detect tumour locations within the liver. The liver organ is the second-largest component in the human body, and the one that weighs the most is situated on the right side of the belly. The gallbladder, pancreas, and intestines interact with the liver's right and left lobes (Gharban et al., 2024). The liver interacts with several other organs (Ghozali, 2023). The cells that create the liver can produce primary, secondary, or metastatic cancer, brought on by malignant cells from other body parts (Gandhi et al., 2024). Among all liver malignancies, malignant HCC (Hepatocellular Carcinoma) is the most prevalent primary liver disorder (Rahman et al., 2022). The third most common reason for cancer-related demisesuniversal is the liver tumour, which is also the sixth most often diagnosed cancer (Sung et al., 2021). HCC is a primary liver tumour that includes a variety of cancers with genetic and molecular diversity and accounts for between 70% and 85% of all liver cancer cases worldwide (Ferlay et al., 2010).

Pathological diseases such as fatty liver, iron accumulation, fibrosis, and malignancies can also cause anatomical degeneration of the liver in terms of tissue and signal intensity (Gotra et al., 2017). Despite these challenges, substantial research has been conducted to divide the liver and hepatic lesions into CT volumes (Ghozali et al., 2023). Various dynamic, automatic, and semi-automatic approaches have been developed

in this manner. Determining liver tumours using computational techniques is a major field of medical imaging analysis investigation that is crucial for effective diagnosis and therapy planning (Gnanaguru et al., 2024). Traditional image processing techniques such as thresholding, region expanding, and edge detection are used, as are complex computing algorithms such as ML and DL (Ghozali et al., 2022). Machine learning algorithms, which include supervised techniques such as support vector machine (SVM) and unsupervised methods such as clustering, allow for the automated classification of pixels or image segments as tumour or non-neoplastic (Komperla et al., 2024). Deep learning models, particularly convolutional neural network (CNN), have proven excellent capabilities in feature extraction and sophisticated pattern recognition, making them ideal for segmenting liver tumours (Gharban et al., 2019).

The ability to effectively diagnose and treat liver cancer is made possible by the classification of liver tumours (Kler et al., 2024). An essential organ, the liver is responsible for several internal processes like metabolism, digestion, and detoxification. Prevention and treatment of liver cancer are crucial to enhancing patient outcomes because it can be fatal (Jeba et al., 2024). The classification of liver tumours entails determining a particular kind of liver cancer by considering the size, place of residence, amount of tumours and the histological and molecular characteristics of the tumour cells (Kumar et al., 2024). Furthermore, graph-based techniques such as graph cuts, level set methods such as active contour models, and fuzzy logic approaches are useful for properly outlining tumour boundaries (Jasper et al., 2024). Hybrid strategies that combine various methodologies are frequently investigated to capitalise on their complementary qualities (Hariharan et al., 2024). The approach chosen is determined by the characteristics of the imaging data and the demand for precision, and researchers are always innovating to improve the efficiency and accuracy of liver tumour segmentation by utilising various computational techniques (Harendharan and Boussi Rahmouni, 2023).

Due to their ability to consistently and effectively handle vast volumes of data, computing techniques are essential in classifying diseases (Karthikeyan et al., 2024). To uncover trends and diagnose diseases, categorising disease entails analysing and classifying patient data, including symptoms, medical history, test findings, and demographic data (Kuppam et al., 2024). Improved medical care and patient outcomes result from using computing tools by researchers and medical professionals to analyse and interpret this data more impartially and exactly (Kumar Nomula, 2023). Previous studies had limitations since they used images from better MRI and CT (Nagaraj, 2023). In addition, the CNN technique was only applied to a subset of liver cancers (Maraju, 2024). In recent years, research has focused on developing a completely automated system for accurate and timely prediction of liver tumours while conserving time and resources (Mudunuri, 2024). The benefit of automated procedures is that they evolve due to their performance and the incorporation of diverse situations and inputs (Rahman et al., 2022). Recent research has investigated the effectiveness of ML and DL models for pre-screening, assessing, and treating liver tumour sufferers using investigative evaluation of images, biomarker exploration, and forecasting adapted medical outcomes (Bakrania et al., 2023).

DL models are being used to classify liver cancer, and there have been numerous studies on this subject. The classification of liver cancer can be aided by applying DL models to analyse medicinal pictures such as Computed Tomography (CT) scans or

magnetic resonance imaging (MRI). Investigators have utilised a variety of CNN structures to categorise liver cancer, including VGG, ResNet, and Inception (Lodha et al., 2023).

DL is an effective method for classifying liver cancer because it offers excellent accuracy and efficacy in examining medical images (Obeta et al., 2024). Deep learning methods are likely to become more crucial for identifying and managing liver cancer as they grow in advance (Singh et al., 2024). DL with optimisation algorithms for liver tumour segmentation is a novel approach to analysing medical images (Paramasivan et al., 2024). Investigators can dynamically understand complicated patterns and features inside medical images by utilising the power of DL models, particularly CNNs. These DL architectures excel in capturing complicated correlations in data, which is critical in determining tumour edges (Pranav et al., 2023). Optimisation strategies improve classification accuracy and speed up the training process. The DL framework incorporates many optimisation strategies, such as biological algorithms, particle swarm optimisation (PSO), and gradient-based methods (Shalom Soji et al., 2024).

The segmentation of liver tumours utilising the Multiparameterised Inception V3 CNN and Krill Herd Optimisation (KHO) algorithm is an exciting revolution in healthcare imaging (Sengupta et al., 2023). Combining Inception V3 CNN's sophisticated pattern recognition skills with KHO finesse yields unprecedented precision in recognising liver cancers. This integration ensures great accuracy in tumour boundary segmentation, allowing for early and precise diagnosis. Furthermore, combining these techniques improves computational efficiency, allowing for the speedy analysis of complicated medical pictures (Parveen Roja et al., 2024). The model's resilience guarantees constant performance over various imaging settings, resulting in accurate results critical for treatment planning and monitoring (Regin et al., 2023). Furthermore, the automated aspect of this technique saves healthcare practitioners time and effort, supporting streamlined workflows and potentially lowering healthcare expenditures (Rajest et al., 2023). Finally, this enhanced segmentation technology improves patient care by enabling tailored treatment methods (Saxena et al., 2023). It advances the field of medicine by supplying high-quality, standardised data for in-depth analysis and therapeutic developments (Nirmala et al., 2023).

The remainder of the research paper is designed as follows. Section 2 explores the existing literature, critically examining previous datasets and approaches while highlighting their limitations and drawbacks. This in-depth examination sheds light on the research gap the current study seeks to fill. Section 3 exhaustively details the novel methodology, offering a clear process and outlining the complex techniques, such as integrating Optimised Multiparameterised Inception V3 CNN with KHO. Section 4 thoroughly evaluates, focusing on implementing the improved model on a specific dataset. This section's explanation explores the dataset's complexities, offering insight into the findings. The work unpacks the significance of the results through thorough analysis and interpretation, providing light on fresh insights from using the Optimised Multiparameterised Inception V3 CNN with KHO. The final section summarises the proposed technique, summarising the study's important contributions and emphasising their significance in liver tumour segmentation. Furthermore, it lays the groundwork for future research initiatives, indicating potential routes for investigation and recommending strategies to develop the subject. It smoothly transitions from the current study to more inventive medical imaging analysis and DL inquiries.

2 Related works

Zhen et al. (2020) applied CNN to construct a DL system (DLS). Even in the nonexistence of agents of contrast, DLS that combine these systems could be trained using data from varied acquisition situations and employed as a precise and time-saving assisted-diagnosis technique for liver tumours in medical settings. Therefore, DLS can help patients with liver tumours reduce contrast-related adverse properties and lower the financial costs connected to existing routine MRI inspection practices.

Naeem et al.'s (2020) goal is to use a fused dataset of 2DCT scans and MRI to show the effectiveness of ML algorithms for classifying liver cancer. At Bahawal Victoria Hospital (BVH), Bahawalpur, Pakistan, benign and malignant liver cancer datasets were collected. The final dataset for each malignancy was created using 1200 ($100 \times 6 \times 2$) MR and CT-scan pictures and 200 (100×512) images. The collected dataset has been pre-processed using Otsu thresholding-based classification and the Gabor filters to automatically capture RIOs (Regions of Interest) and decrease noise. The pre-processed dataset obtained 254 hybrid features—a mixture of the histogram, wavelet, co-occurrence, and run-length attributes—for each ROI. The attribute collection method chose 10 optimised hybrid attributes. Using a tenfold cross-validation process, they installed this optimised hybrid-feature dataset to four ML models for categorisation: the multilayer perceptron (MLP), SVM, Random Forest (RF), and J48. MLP displayed a total accuracy of 95.78% and 97.44% on MRI and CT, respectively. Regrettably, the outcomes were not encouraging, and there were some restrictions because the sample had multiple modalities. The fused optimised hybrid-feature dataset was then formed by merging the MRI and CT-scan image datasets. Among all the implemented classifiers, the MLP has demonstrated an impressive accuracy rate of 99%.

The process is a complete and total flop in other situations. If not removed, tissue of damaged or diseased cells expelled from the human body may give rise to nodules and lumps. Both of these types of tumour forms can grow in the liver. Compared to benign tumours, malignant lumps are more harmful to one's well-being. A method for categorising and identifying liver swellings based on image processing and ML was presented by Jasti et al. (2020). The fuzzy histogram equalisation approach is used to reduce noise in images during the pre-processing step of the generation of pictures. The images are then separated into numerous sections to focus on the ROI. The RBF-SVM strategy, the ANN technique, and the RF(Random Forest) models are all used for this categorisation task.

Kiani et al. (2020) established a DL-based assistant and examined its influence on the analytic abilities of 11 physicians with dissimilar degrees of experience. On the validation set of 26 WSI, the current model's accuracy was 0.885; on a standalone test set of 80 WSI, it was 0.842. Their findings emphasise the difficulties in applying AI models in healthcare environments and the significance of considering any unplanned negative effects of model support when developing and testing healthcare AI-based methods 9.

Radiologists and doctors can diagnose liver lumps more accurately using the suggested innovative architecture. Zou et al. (2021) recapitulate the literature on ML algorithms to summarise the benefits and drawbacks of ML and its probable application in forecasting prognosis following various HCC treatment schedules.

By gathering retrospective information, Wang et al. (2022) suggest an end-to-end DL structure for forecasting microvascular invasion in hepatocellular cancer. Only by using the patient's radiomic data can this structure produce noninvasive, precise, and effective

preoperative forecasting, particularly useful for clinicians when making treatment decisions regarding patients suffering from HCC.

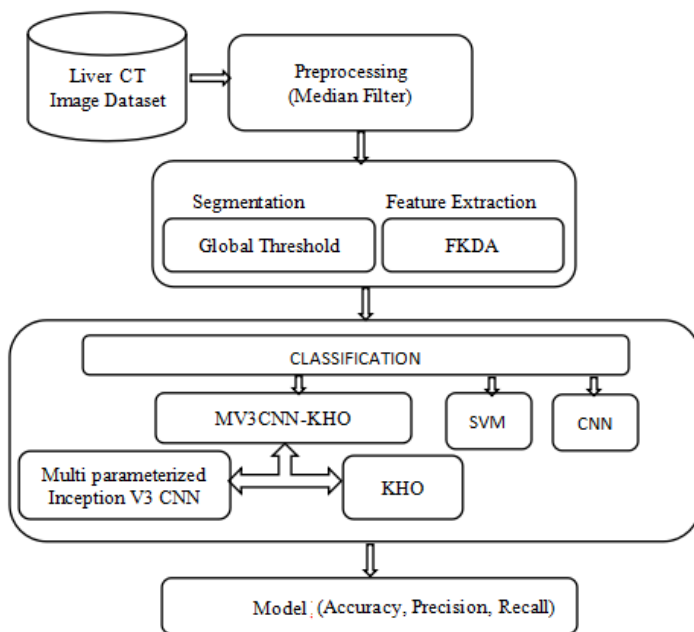
Chen et al. (2022) used the SENet DL to intelligently classify all types of distinguished tumours in liver histopathological photographs for the first time. They compare it to the four DL models of VGG16, ResNet50, ResNet_CBAM, and SKNet based on creating a comprehensive data procurement scheme. The current study used evaluation indices such as the confusion matrix, precision, recall, and F1 Score. Identified assessment indices can be influenced to assess the model thoroughly and precisely. The study also demonstrates the enormous practical utility of DL in addressing the time-consuming and arduous issues associated with physical film reading, and it has some relevance for the smart categorisation of various cancer histological pictures.

To classify multiclass liver tumours, Hussain et al. (2022) offered a work concentrating on the ML techniques RF, J48, LMT (Logistic Model Tree) and RT (Random Tree) with several autonomous ROIs. Hemangioma, cyst, HCC, and metastasis are the four tumour classes represented in the dataset. The photos were changed to greyscale, and histogram normalisation was used to enhance the dissimilarity of the photographs. The Gabor filter was used to minimise disturbances, and an image refinement technique was used to improve the worth of the images. In addition, for each ROI, 55 attributes were collected using rotational, scalability, and translational (RST) approaches, texture, binary, histogram, and histograms of varied pixel diameters. From these 55 features, 20 optimised features for categorisation were obtained using the correlation-based feature selection (CFS) technique. According to the data, with an accuracy of 97.48% and 97.08%, respectively, RF and RT fared more than J48 and LMT.

According to Bhattacharyya et al. (2023), the liver tumour is the foremost cause of mortality universal. Medical pictures require interpretation to detect liver cancer. Adaptive thresholding with a watershed transform technique distinguishes the liver organ from other bodily sections. Some techniques to distinguish the liver's cancerous region include optimal policies and the swarm optimisation model. Two hundred twenty-five photos from individuals with various kinds of liver cancer were included in the data. The grey level matrix (GLM) and local binary pattern (LBP) were utilised to construct a large dataset and uncover vital characteristics. Then, it is divided into various cancer types using NN (Neural Network), SVM, RF, and DNN (Deep Neural Network) classifiers. Hepatocellular carcinoma and hemangioma are examples of these. The suggested approaches are evaluated based on their sensitivity, specificity, accuracy rate, and Jaccard index value. It has been discovered that liver cancers can be detected by using watershed Gaussian-based DL algorithms. The top classifiers were DNNs, with a Jaccard index value of 0.97 across 300 epochs and an accuracy of 99.25% with less validation loss of 65.73%.

3 Proposed methodology

Radiological pictures from CT or MRI scans are frequently used to categorise liver tumours. The workflow of the suggested tumour segmentation model is shown in Figure 1.

Figure 1 Proposed architecture of liver tumour segmentation model using multiparameterised inception V3 CNN

The key phases of liver segmentation are explained in the sections below.

3.1 Data acquisition

The liver's CT scans and the related liver and tumour segmentations are included in the LiTS dataset, a publicly accessible resource. The dataset can be utilised for activities like segmenting the liver and its tumours.

3.2 Pre-processing – median filter

This filter reduces image noise without distorting the image's edges (Maheshan and Kumar, 2020). The median is determined by arranging the neighbouring window's pixel values in the correct numerical sequence, then swapping out the pixel being considered for the middle pixel result. Equation (1) illustrates the mathematical formula for the median filtered picture $J(x, y)$ of the picture $K(u, v)$.

$$J(x, y) = \underset{(u, v) \in R_{xy}}{\text{median}} \{K(u, v)\} \quad (1)$$

3.3 Image segmentation – global thresholding technique

In this kind of segmentation, the liver region's unique pixels are calculated first and then combined until the entire image has been segmented. A region or segment is created from the relevant pixels to the threshold. After every grouping procedure, a rule checks the homogeneity of the feature locations.

Calculating the new threshold by using equation (2)

$$T = \frac{\mu_1 + \mu_2}{2} \quad (2)$$

The group's homogeneity was confirmed using the following method.

$$\text{If (pixel intensity is close to the mean value } |I(i, d) - M(i)| \leq T(i))$$

The threshold T changes depending on the brightness of the pixel $I(i, d)$, and the area R_n . Homogeneity validation is used in the lesion segment of the segmented CT picture.

3.4 Feature extraction – fast kernel discriminant analysis (FKDA)

Feature vectors describing the characteristics of the lesion elements make up the feature extraction technique's output. When a CT picture of size $N \times N$ is given, it first refers to the image as a vector with high variance values representing a 1D vector U . The lesion traits. This is how variation for an image's obtained feature X is calculated:

$$\text{Standard Deviation}(y) = \frac{\sum_{i=1}^n b(y_i - y)(y_i - y)}{n - 1} \quad (3)$$

The formula for the calculation of the scatter matrix, which produces the mean and SD for the features for the big global sections and differs in the calculation of the mean for each region, is as follows:

$$\text{Mean}(x, y) = \frac{\sum_{i=1}^n a(y_i - y)(x_i - x)}{n - 1} \quad (4)$$

The feature vector of F_{ij} is a feature in this calculation that consists of the primary feature cluster that is utilised to categorise the characteristics of liver lesions.

3.5 Multiparameterised inception V3 CNN

The multiparameterised inception, V3 CNN structure, uses the characteristics collected from the FKDA analysis. It processes the feature vector to produce the illness's classes and phases, including fibrosis, cirrhosis, basal hepatocellular carcinoma, hemangioma, and liver metastases. As a combination of the convolution layer, pooling type layer, loss layer, and fully connected type layer—which reflects the categorisation layer – Inception v3 architecture is designed to produce a set of feature maps with the lowest possible resolution.

3.6 Convolution layer

The features in this convolution layer have been processed using a kernel size of 7×7 . Using V4 Inception, it creates the feature map from the feature vectors.

Consider a layer of $N \times N$ square neurons followed by a convolutional layer. If so, employ a $m \times m$ filter ω . The output of the convolutional layer will be $(N - m + 1) \times (N - m + 1)$ in size. The inputs from the preceding layer cells must be added up to determine the pre-nonlinearity input to some unit x_{ij}^l in the layer.

$$x_{ij}^l = \sum_{a=0}^{m-1} \sum_{b=0}^{m-1} \omega_{ab} y_{(i+a)(j+b)}^{l-1} \quad (5)$$

The convolutional layer then employs nonlinearity:

$$y_{ij}^l = \sigma(x_{ij}^l) \quad (6)$$

3.7 Max pooling layer

In this pooling layer, the feature vector in the structure of a feature map is down-sampled to provide top-level characteristics after determining the link between the attributes and producing a pooling index for the variables to eliminate over-fitting problems. The pooling technique obtains the small grid segment representing the downsampling. The maximum pooled layer selects features from the feature vector with high-level descriptions.

The simple max-pooling layers do not learn for themselves. They produce a single value, the greatest in the given $k \times k$ rectangle. For instance, if their input layer is an $N \times N$ layer, they will output a $\frac{N}{k} \times \frac{N}{k}$ layer since the max method reduces each $k \times k$ block to a single number.

3.8 Activation layer

The rectified linear units (ReLU) activation method used by the architecture increases training efficiency by reducing mistakes and generates nonlinearity in the maximum pooling feature vector. The output of each activation function is normalised with the convolution operation of illnesses for organising labels, which reduces overfitting and enhances system generalisation.

3.9 Fully connected layer

A fully connected layer is depicted as the classifier dividing the classes from the feature map acquired from earlier layers by flattening and removing the features. The Softmax layer will learn the most discriminating features from the feature map to create a class.

A DL model called Multiparameterised Inception V3 CNN has been used for forecasting liver malignancy. The Inception V3 design, a CNN architecture that has been demonstrated to perform well in identifying tasks, forms the foundation of this model. The CT or MRI scans of the liver are two medical scans that can be used as input in the Multiparameterised Inception V3 CNN model.

3.10 Pseudo code of MV3CNN-KHO approach

- 1 Load liver tumour dataset (X, y) where X represents images and y represents labels (tumour or non-tumour).
- 2 Pre-process images – Apply Median Filter to the images to reduce noise and enhance features.
- 3 Apply fast KDA (FKDA) for feature extraction – reduce dimensionality while preserving essential information.
- 4 Define Multiparameterised Inception V3 CNN architecture.
- 5 Integrate Fast KDA features with Inception V3 features.
- 6 Apply KHO for model optimisation:
 - Initialise a population of candidate solutions (model parameters).
 - Define an objective function evaluating model performance using combined features.
 - Use KHO to optimise the model parameters, iterating until convergence.
- 7 Split the dataset into training and testing sets.
- 8 Train and validate the optimised model.
- 9 Evaluate the model on the test dataset.
- 10 Visualise segmented regions and classification results for analysis and interpretation.

3.11 Krill Herd optimisation (KHO)

Generally speaking, the established motions often shift a krill individual's location towards the best fitness. Two global and two local techniques are used in the motion other krill individuals generate and when they are foraging. KH is a powerful algorithm because these are running concurrently. The subsequent equation provides the position vector value of a krill individual over the period t to $t + \Delta t$ using various effective variables of how it moves within the time:

$$X_i(t + \Delta t) = X_i(t) + \Delta t \frac{dX_i}{dt} \quad (7)$$

Δt is one of the most crucial constants that should be properly adjusted by the optimisation issue, it should be emphasised. This is because this attribute acts as a speed vector scale factor. Δt can be easily calculated using the equation provided below.

$$\Delta t = C_i \sum_{j=1}^{NV} (UB_j - LB_j) \quad (8)$$

where LB_j , UB_j are the lower and upper limits of the i th identifier ($j = 1, 2, \dots, NV$), accordingly, and NV is the overall number of parameters. The constant number in the range $[0, 2]$ is C_i .

4 Results and discussion

4.1 Liver tumour segmentation (LiTS) dataset description

The liver tumour segmentation (LiTS) dataset is a medical imaging dataset commonly used for medical image analysis research, particularly for liver and liver tumour segmentation tasks. Here is a brief description of the LiTS dataset:

Purpose: The primary purpose of the LiTS dataset is to facilitate the development and evaluation of algorithms for the segmentation of liver lesions, specifically tumours, in medical images. This dataset is valuable for liver cancer diagnosis and treatment planning research.

Data source: The dataset contains medical images derived from computed Tomography (CT) scans. These CT scans are typically used for diagnosing liver conditions, including tumours.

Size: The dataset includes a collection of 201 abdominal CT scans with varying resolutions and qualities and corresponding liver and tumour segmentation masks.

Several benefits come from using the multi-parameterised Inception V3 CNN architecture to segment liver cancer, including its capacity to capture multi-scale features and parallel convolutions with various filter sizes. The findings of this work indicate that multi-parameterised Inception V3 CNN architecture and CNN can be efficient methods for segmenting liver cancer in medical imaging. The following figures represent the output obtained during different stages of execution.

Figure 2 represents the loading of the input image, where one image is uploaded from the database for testing. Figure 3 represents the pre-processing stage. In this stage, the input image will be resized, and noise inside the image will be removed using a filtering technique.

Figure 2 Load input image

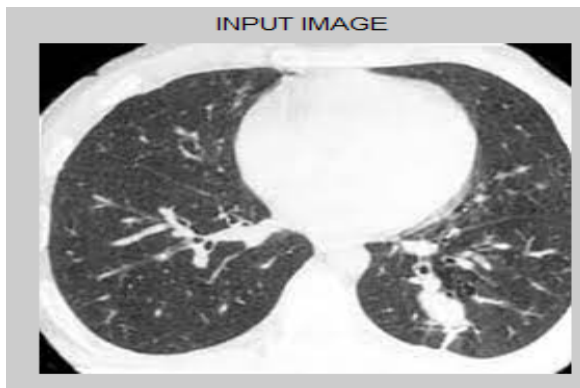


Figure 4 represents the segmentation process of dividing the input image into pixels. Figure 4(a) shows the segmented areas in different colours, such as red, blue and yellow. Figure 4(b) shows the segmentation during 100 iterations.

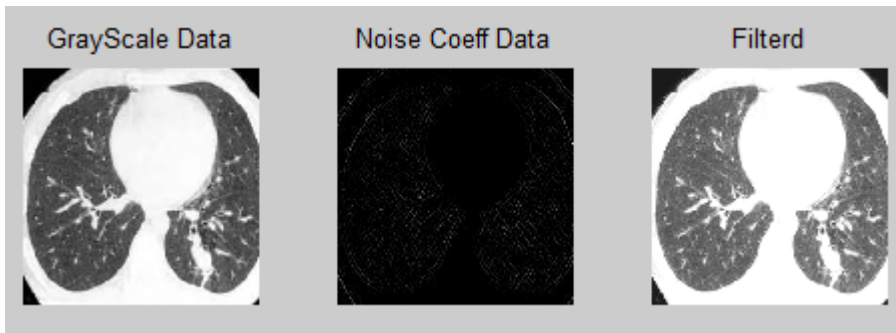
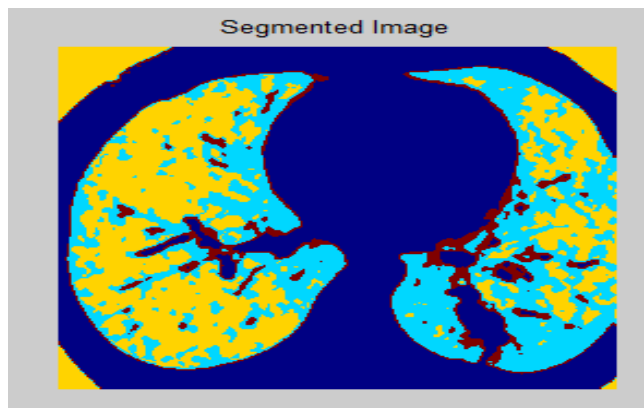
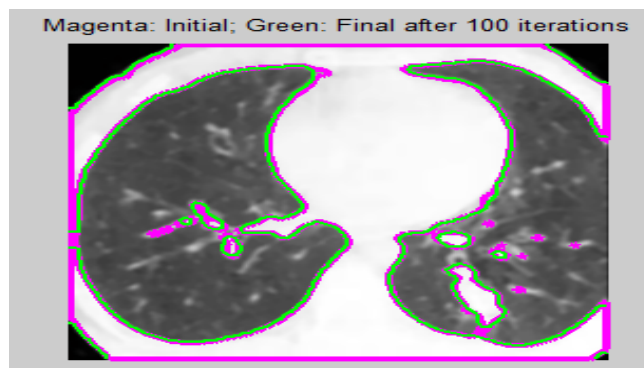
Figure 3 Pre-processing stage**Figure 4(a)** Segmented output image (see online version for colours)**Figure 4(b)** Segmented output image after 100 iterations (see online version for colours)

Figure 5 represents the Feature Extraction stage and Feature Selection. Well-known features such as Contrast, Correlation, Cluster Prominence, Cluster shade, Dissimilarity, Energy, Entropy, Homogeneity, Maximum probability, Variance and Autocorrelation are considered.

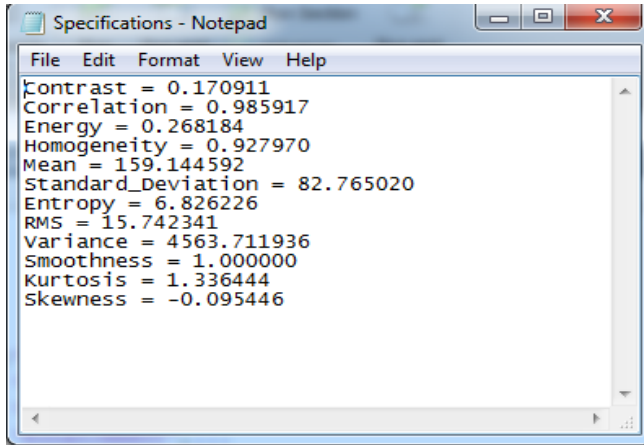
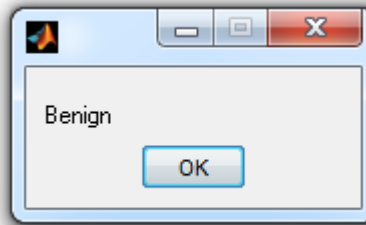
Figure 5 Feature extraction and selection stage (see online version for colours)

Figure 6 represents the Classification stage. Here, the input image will be classified as whether the input image stage is benign or malignant.

Figure 6 Classification stage (see online version for colours)

The following metrics for assessment were chosen to help validate the suggested model: Accuracy, Sensitivity and Specificity. These metrics are described as follows:

4.2 Accuracy analysis

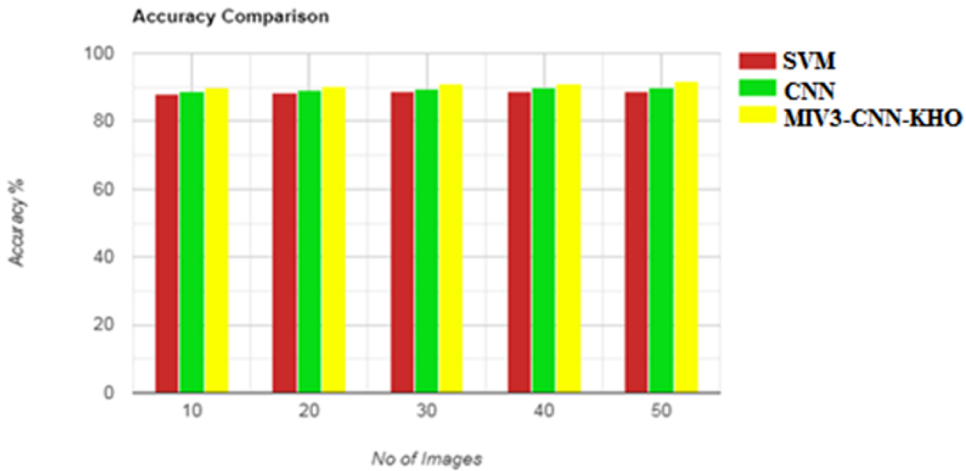
A model's capability to accurately anticipate a task's outcome is measured by the accuracy metric, frequently employed in deep learning (DL). It is the proportion of the model's right predictions to all its other forecasts.

$$Acc = \frac{TP + TN}{TP + TN + FP + FN} \quad (9)$$

Table 1 and Figure 7 present the accuracy analysis comparing the proposed MIV3-CNN-KHO algorithm with other existing algorithms. The results show that MIV3-CNN-KHO achieves an accuracy ranging from 90% to 91%, slightly outperforming CNN, which has an accuracy range of 89% to 91%. Meanwhile, SVM produces a lower accuracy, ranging from 88% to 90%. This analysis demonstrates the superior classification performance of MIV3-CNN-KHO, as it consistently delivers higher accuracy than both CNN and SVM in the given context (Priya and Khanaa, 2024).

Table 1 Accuracy analysis of MIV3-CNN-KHO with other existing algorithms

No. of images	SVM accuracy (%)	CNN accuracy (%)	MIV3-CNN-KHO accuracy (%)
10	88.98	89.90	90.88
20	89.23	90.22	91.26
30	89.68	90.55	91.87
40	89.89	90.78	91.18
50	89.95	90.93	91.63

Figure 7 Accuracy analysis of MIV3-CNN-KHO with other existing algorithms graph (see online version for colours)

4.3 Sensitivity analysis

It, also known as true positive rate (TPR) or recall, is a performance indicator used in deep learning (DL) to assess a model's ability to detect positive data properly. Sensitivity quantifies the percentage of genuine positive samples among all positive samples, including those mistakenly categorised as negative (false negatives).

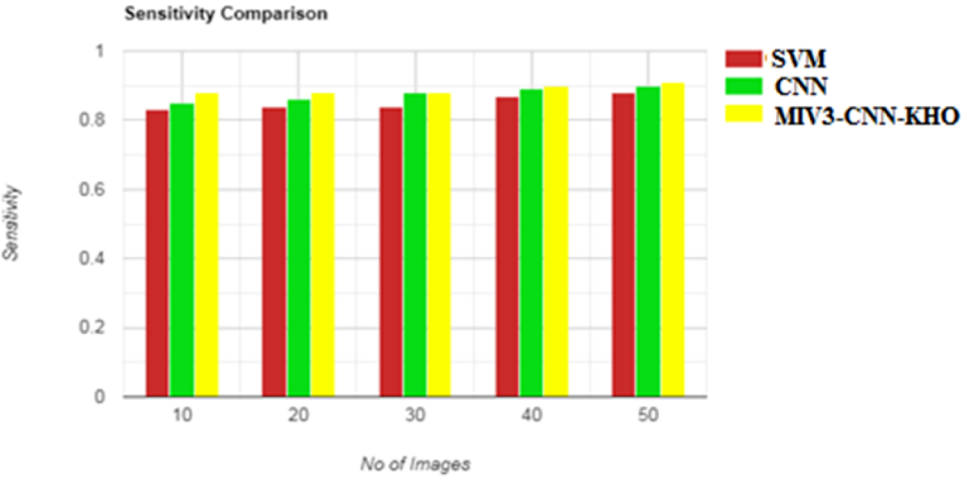
$$\text{Sensitivity} = \frac{TP}{\text{Total Disease}} \times 100 \quad (10)$$

Table 2 and Figure 8 display the sensitivity analysis comparing the proposed MIV3-CNN-KHO algorithm with other existing algorithms. The findings demonstrate that MIV3-CNN-KHO achieves a sensitivity ranging from 0.88 to 0.91, surpassing the performance of CNN and SVM. Specifically, CNN yields a sensitivity between 0.87 and 0.90, while SVM delivers a slightly lower range of 0.86 to 0.89. This comparison highlights the superior ability of MIV3-CNN-KHO in accurately identifying true positive cases, making it more effective than the other algorithms in terms of sensitivity (Priya and Khanaa, 2024).

Table 2 Sensitivity analysis of MIV3-CNN-KHO with other existing algorithms

<i>No. of images</i>	<i>SVM sensitivity</i>	<i>CNN sensitivity</i>	<i>MIV3-CNN-KHO sensitivity</i>
10	0.86	0.87	0.88
20	0.86	0.88	0.89
30	0.86	0.89	0.89
40	0.89	0.90	0.90
50	0.89	0.90	0.91

Figure 8 Sensitivity analysis of MIV3-CNN-KHO with other existing algorithms graph (see online version for colours)



4.4 Specificity analysis

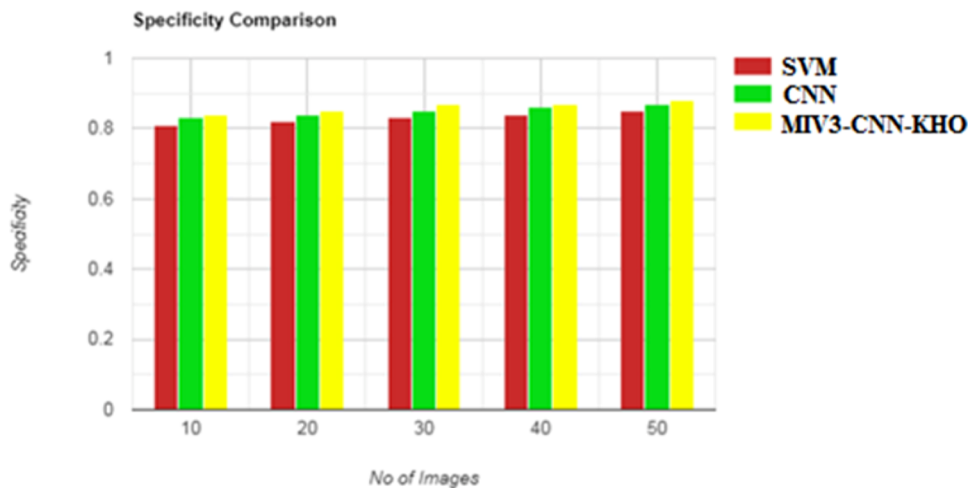
A specificity performance parameter assesses a model's accuracy in identifying negative samples. Specificity, also called the true negative rate (TNR), measures the percentage of true negative cases that the model properly identifies.

$$Specificity = \frac{TN}{Total\ Healthy} \times 100 \quad (11)$$

Table 3 and Figure 9 present the specificity analysis comparing the proposed MIV3-CNN-KHO algorithm with existing algorithms. The results show that MIV3-CNN-KHO achieves a specificity ranging from 0.84 to 0.88, which outperforms both CNN and SVM. In comparison, CNN produces a specificity between 0.84 and 0.87, while SVM lags with a range of 0.82 to 0.85. This analysis highlights the improved performance of MIV3-CNN-KHO over the other algorithms, particularly in distinguishing between true negatives and false positives. The superior specificity of MIV3-CNN-KHO demonstrates its effectiveness in achieving more accurate classification results in this context.

Table 3 Specificity analysis of MIV3-CNN-KHO with other existing algorithms

No. of images	SVM specificity	CNN specificity	MIV3-CNN-KHO specificity
10	0.82	0.84	0.84
20	0.82	0.84	0.85
30	0.83	0.85	0.87
40	0.83	0.86	0.88
50	0.85	0.87	0.88

Figure 9 Specificity analysis of MIV3-CNN-KHO with other existing algorithms graph (see online version for colours)

Liver tumour segmentation using CNNs is a significant advancement in medical image analysis. CNNs are deep learning models designed to automatically identify and delineate the boundaries of liver tumours in medical images, primarily in computed tomography (CT) scans. The use of CNNs in this context offers several benefits. These networks can learn and represent complex image features, enabling accurate and robust tumour segmentation. The ability to capture fine-grained details and adapt to tumour shape and size variations makes CNNs a valuable tool for radiologists and oncologists.

One of the key advantages of employing CNNs for liver tumour segmentation is their ability to reduce the manual effort required for image analysis. Traditional segmentation methods often involve tedious and time-consuming manual delineation of tumour boundaries. CNNs automate this process, saving valuable time for healthcare professionals and potentially reducing human error. Moreover, CNN-based segmentation models can provide quantitative tumour size and shape measurements, aiding in treatment planning and monitoring the progress of liver cancer patients.

However, challenges remain in optimising CNNs for liver tumour segmentation, such as sufficient and high-quality training data and the risk of false positives or negatives. Research in this area continues to evolve, focusing on enhancing the accuracy and generalisability of CNN-based segmentation models. As technology and algorithms advance, CNNs are poised to play a vital role in improving the diagnosis and treatment of liver tumours, ultimately benefiting patients and healthcare providers.

The findings demonstrate that the proposed MIV3-CNN-KHO algorithm outperforms both CNN and SVM in terms of accuracy, sensitivity, and specificity. Specifically, the MIV3-CNN-KHO achieves an accuracy ranging from 90% to 91%, while CNN's accuracy is between 89% and 91%, and SVM's is slightly lower, at 88% to 90%. When it comes to sensitivity, MIV3-CNN-KHO performs better with a range of 0.88 to 0.91, compared to CNN's 0.87 to 0.90 and SVM's 0.86 to 0.89. Regarding specificity, MIV3-CNN-KHO again leads with a range of 0.84 to 0.88, while CNN achieves 0.84 to 0.87, and SVM lags with 0.82 to 0.85. These metrics indicate that the MIV3-CNN-KHO outperforms both CNN and SVM across all evaluation criteria, such as accuracy, precision, and recall. The results prove the superiority of the MIV3-CNN-KHO in delivering more consistent and reliable outcomes, making it the best choice among the tested algorithms for improving classification performance in the given context.

5 Conclusion

Advanced techniques such as deep learning models like Inception V3 CNN and optimisation algorithms like KHO can dramatically enhance tumour detection, classification accuracy, and efficiency. The combination of Multiparameterised Inception V3 CNN with the KHO method in liver tumour segmentation provides a powerful solution that combines the strengths of deep learning for image processing with advanced optimisation approaches for model improvement. This method improves the precision and efficiency of liver tumour segmentation and has important implications for customised medicine, research, and healthcare cost management. In the matrices of accuracy sensitivity and specificity, the segmentation of liver cancer utilising CNN and the multi-parameterised Inception V3 CNN technique demonstrated good results. According to the study, the liver segmentation job had a whole accuracy rate of 92.75%, sensitivity of 0.91 and specificity value of 0.88. These findings show that the model successfully distinguished between positive and negative liver cancer cases in the LiTS dataset. This shows that the model successfully captured the intricate patterns and features in the liver cancer photos. The segmentation of liver cancer using the multi-parameterised Inception V3 CNN architecture produced encouraging results and may have applications in clinical settings. Integrating modern deep learning architectures, such as attention mechanisms or capsule networks, can capture complicated spatial connections within medical pictures, potentially leading to more precise tumour delineation. Furthermore, focusing on transfer learning methodologies, such as utilising pre-trained models on large-scale medical imaging datasets, could enable the system to learn detailed tumour traits, especially when data availability is limited. Furthermore, using unsupervised learning approaches like variational autoencoders to uncover intrinsic tumour representations from unlabelled data holds promise for understanding complicated tumour patterns without explicit labels.

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