Atom search-Jaya-based deep recurrent neural network for liver cancer detection

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Abstract
Automatic detection of liver cancer is the fundamental requirement of computer-aided diagnosis in the clinical sector. The traditional methods used in the liver detection process are not effective in accurately detecting the tumour region using a large-sized dataset. Moreover, segmenting the large intensity of the tumour region is a complex issue with the existing methods. To overcome these issues, an accurate and efficient liver cancer detection method named atom search-Jaya-based deep recurrent neural network is proposed in this research. The proposed method mimics the atomic motion based on the interaction forces and the constraint forces of the hybrid molecules. The optimal solution is revealed through the fitness measure, which in turn accepts the minimal error value as the optimal solution. The weights of the classifier are optimally updated based on the position of the atom with respect to the iterations. The proposed atom search-Jaya-based deep recurrent neural network attained significantly better performance in accurately detecting the tumor region using the exploration ability of atoms in the search space. The results obtained by the proposed model in terms of accuracy, specificity, sensitivity, and precision are 93.64%, 96%, 95%, and 94.88%, respectively, while considering the three features using 80% of training data.

1 INTRODUCTION
The liver has major functions in animals and vertebrates. In the human body, the liver diseases occur without causing any sign or warning [1]. Therefore, detecting the liver diseases at an early stage is a significant keystone in the medical sector [2]. In recent years, liver cancer becomes a dangerous and harmful disease, as it escorts to human death. The most significant type of liver cancer among the worldwide level is cholangiocarcinoma and hepatocellular carcinoma (HCC), respectively [3, 4]. Based on the geographical region and gender, the cause of liver cancer may vary [4, 5]. In the worldwide level, the rate of liver cancer increases, and most of the patients with cancer died even after taking the diagnosis for six months [4]. However, the liver cancer specifies a high changeability in their localization, appearance, and shape [6]. The liver cancer may be either hyperdense or hypodense. Here, the hyperdense appears brighter, whereas the hypodense looks darker when compared to the healthy parenchyma liver [7]. However, the appearance of liver cancer is based on the state, lesion type, and imaging, such as timing, contrast method, and settings, and also the type of cancer may vary from patient to patient [8, 9]. The liver cancers are of two types, namely primary and secondary liver cancer. The primary cancer originates from the liver and is also termed as hepatoma or HCC. In the secondary liver cancer, the cancer cell originates from various human organs and passes into the liver [10–12]. Moreover, the diagnosis of cancers is carried out in three different ways: biopsy, imaging test, and blood test [13, 14]. Among these testing models, the imaging test is highly focused on in order to receive the computer-assisted approach. The imaging tests used to diagnose the liver cancer are computed tomography (CT).

CT scan is the most robust and common imaging method used to detect the lesions in the liver. CT is a non-invasive procedure or medical examination that uses an X-ray equipment for producing the cross-sectional images in the parts of a human body [15]. This imposes the requirement to model the automated system for classifying and detecting the liver...
anomalies based on the images of the CT scan [16]. In the CT scan image, each cross-sectional image specifies the slice of a liver, which is similar to the slice of a bread. In recent years, the quality of CT scan images has improved, which limits the role of an image interpretation in human beings [8]. However, the computer-assisted detection mechanism is based on the principle of image analysis, which in turn offers more information regarding the detection of liver cancer. Moreover, the conventional liver cancer detection method consists of three different steps: first, the tumor is segmented from the CT scan abdominal images; second, the features are extracted; and third, the classification mechanism is carried out based on the selected classifiers. Based on the texture features, characteristics of the liver images are modelled in the past years [17]. The major issue in detecting the liver tumor is the poor contrast between the values of liver intensity and tumor. Initially, the tumor is present in a small region, hence it is very difficult to detect the tumor. Therefore, this research focusses on increasing the contrast of the image that contains a tumor in the liver. The images are pre-processed to enable the user identify the presence of a tumor through CT images. To detect the liver cancer at an early stage is a major advantage in preventing the liver cancer [18, 19].

Classification of liver cancer poses a major role in diagnosing the tumor at an early stage. The deep learning methods based on deep neural network (DNN) is used to solve a wide range of issues in the recent works [20–22]. To detect the liver cancer automatically, the convolutional neural network (CNN) is used to segment the lesions effectively from the CT images and a coefficient of dice similarity value of 80.06% is obtained [22]. DNN is learned by identifying the top-level features from the bottom-level features in the hierarchy level, and the machine classification is performed by Fukushima. Optimization algorithms are used to train DNN [23]. However, the deep learning methods are categorized into sparse autoencoder, deep belief network (DBN), restricted Boltzmann machine (RBM), and CNN, respectively [19]. The deep learning model specifies the advanced structure in CNN. Based on the convolutional procedure, the features extracted from the input data are passed to the successive layers based on their respective features. Here, the convolutional procedure is used to retrieve the suitable properties from the CT image. Lu et al. [24] introduced the deep learning model based on the graph cut refinement for efficiently and automatically segmenting the CT images. In [25], the deep learning methods, such as fully convolutional networks, DBN, autoencoder, and CNN, are introduced for detecting and diagnosing liver cancer. An automated detection model is developed in [22] by combining the deep learning classifier and Gaussian mixture model (GMM) for detecting the region of the liver lesion [22].

The detection of liver and its lesion poses a challenging issue due to the variability of high anatomical shape and the facts regarding the contact of neighbouring pixel intensity [26]. There exist a number of difficulties in the analysis of automatic cancer detection that includes less image contrast among the tissue samples due to the differences in scan time and perfusion, parenchyma, and the behaviour of lesions in the contrast enhancement [19]. To extract the boundary region of liver based on the abdominal CT image poses a major challenge in the computer-aided CT image, as the boundary region is weak in liver cancer [21]. The detection of liver cancer from the CT images poses a challenging issue due to less contrast among the liver and tumor. However, the presence of other human parts with various dimensions and equivalent intensity level makes the detection process more difficult [19]. Due to the complexity of liver anatomy issues and the insufficiency of organ shape, the accurate segmentation remains a difficult process. These problems are considered a motivation, a new method is proposed for the liver cancer detection.

In this research, the liver cancer detection mechanism is performed using the proposed atom search-Jaya-based deep recurrent neural network (AS-Jaya-based Deep RNN). The proposed work highly concentrates on detecting the liver cancer based on the parametric features of atomic motion and control parameters. Initially, the input images are pre-processed and are segmented using black hole entropic fuzzy clustering (BHEFC). The segmented result obtained from the segmentation module is allowed to perform the feature extraction phase, where the features are effectively extracted. The feature extraction module ensures the effectiveness of detection accuracy. Deep RNN effectively detects the liver lesion based on weights, as the weights are optimally trained using the optimization algorithm. The proposed work is modelled based on the inspiration of basic molecular dynamics and is functioned with the population-based heuristic model. The proposed optimization achieved effective performance in cancer detection through the mimicking behaviour of atomic motion, which is controlled using the constraint and the interaction (total) forces. The training procedure of the Deep RNN is carried out with the proposed AS-Jaya optimization in order to update the weights of the classifier using the position of the atom.

The major contributions of this research are elaborated as follows. The liver cancer detection model is achieved using the proposed AS-Jaya-based Deep RNN classifier. The characteristic features of AS-Jaya tune the classifier optimally to achieve the best detection result through the optimal fitness value. The fitness measure is evaluated based on the position of an atom, which in turn reflects the accuracy and the robustness of detection measure.

The paper is organized as follows. Section 2 elaborates the literature review of the existing liver cancer detection methods. Section 3 discusses the proposed AS-based Deep RNN for detecting the liver cancer. Section 4 elaborates the results and discussion of the proposed method, and finally, Section 5 concludes the paper.

2 LITERATURE SURVEY

Various existing liver cancer detection methods are reviewed in this section. Das et al. [22] introduced a watershed Gaussian-based deep learning (WGDL) approach for effectively delineating the liver lesion through CT images. The presence of the
cancer region was segmented with the Gaussian model. After segmenting the tumour, the extraction of texture features was carried out for classifying the tumor region. It increased the classification accuracy but failed to consider the volumetric image. Priya et al. [35, 36] developed an efficient fusion model for increasing the information of edge location in the CT images. It utilized the Laplacian operators and phase congruency to generate the fusion of high- and low-frequency coefficients. The computational complexity of this model was high. Das et al. [28] developed an approach to detect the liver cancer regions in CT scan images, by integrating the spatial fuzzy clustering approach and adaptive thresholding. This method was used to effectively identify the cancer region, without any manual process. Anyhow, this method did not apply to the large datasets. Wang et al. [29] developed an electrochemical detection model to increase the efficiency in detecting the presence of the liver tumour. It reached the detection limit of 125 fM with less detection time. However, it failed to consider the amplification system.

Bi et al. [30] developed a deep residual network (Deep ResNet) for segmenting the liver tumour. It consisted of skip connections between the convolutional layers and was used to solve the issues in the training accuracy of deep networks. Here, the multi-scale fusion was used to obtain the precise boundary in the liver lesion. However, the performance achieved by this model was poor. Wang et al. [31] developed a cantilevel-based biosensor model to diagnose the liver cancer by achieving high throughput and sensitivity. It effectively detected the multi-biomarkers in the cantilever array. It attained high detection accuracy with low cost and volume. However, the performance in the resolution and accuracy still needs to be improved. Gruber et al. [32] developed a deep learning approach for segmenting the liver cancer. It used two different types of network segments to accurately segment the outer and inner tumour regions. This approach performed the segmenting procedure automatically and achieved better performance. However, it required more number of iterations to segment the tumor region. Kumar and Bharathi [33] introduced an edge prediction based segmentation model for segmenting the tumour region from the liver. It effectively classified abnormal and normal lesions using a machine learning classifier. The computational cost required in this model was high.

3 PROPOSED ATOM SEARCH-JAYA BASED DEEP RECURRENT NEURAL NETWORK FOR LIVER CANCER DETECTION

Liver cancer is one of the leading diseases that causes death in males [34]. To accurately detect the liver cancer, there are various techniques, but they face challenge regarding the pixel intensities. Hence, an effective method is developed to perform the liver cancer detection framework based on BHEFC. Initially, the input image is passed on to the pre-processing stage, which is subjected to segmentation using BHEFC [35, 36], which generated multi-segments. The segmented result is fed to the feature extraction stage, where the features such as CNN features, statistical features, and the pixel pattern based texture features (PPBTFs) are effectively extracted. The statistical features include mean, variance, skewness, energy, and kurtosis, respectively. The features that are extracted from the segmented result are passed into the Deep RNN classifier, which is trained using the proposed AS-Jaya-based Deep RNN that is the integration of atomic search optimization (ASO) [37] with the Jaya optimization [38]. Figure 1 represents the schematic diagram of liver cancer detection modules.

3.1 Read the input image

The input image is collected from the liver cancer dataset [11] and is used to perform the cancer detection process. Let us consider the database \( M \) with \( m \) number of cancer images, which is represented as

\[
M = \{R_1, R_2, \ldots, R_k, \ldots, R_N\},
\]

where \( M \) represents the database, \( N \) denotes the total number of input images, and \( R_k \) represents the image located at the \( k \)-th index. The total images are considered for experimentation, but the explanation is provided based on the \( k \)-th image.

3.2 Pre-processing the input image

The input image \( R_k \) is selected and is pre-processed in the pre-processing module in order to enhance the contrast of the image. The aim of pre-processing is to increase the quality of the image by removing unwanted falsification or distortions. It is required to pre-process the image in order to make the image highly contrasting and effective for further processing. The result of the pre-processed image is denoted by \( R_p \).

3.3 Segmentation using BHEFC

Segmentation is the process of partitioning the pre-processed image into various segments, such as pixels or image objects. The pre-processed image \( R_p \) is passed into the segmentation phase, where the segmentation process is carried out using BHEFC [35]. The BHEFC generates samples based on the assumption of the Dirichlet distribution of the fuzzy membership function. BHEFC performs the segmentation process by absorbing the merits of three aspects, such as black hole entropy (BHE) based information, fuzzy clustering, and Bayesian inference model. BHEFC is developed by integrating the BHE with the fuzzy clustering. BHEFC accurately and effectively characterizes the behaviour of clustering using the principle called maximum-a-posteriori. BHEFC uses the Gibbs sampler for generating the samples from the posteriori distribution. According to the fuzzy \( \epsilon \)-means clustering and principle of Lagrangian
optimization, the BHEFC is modelled as

\[
P(N, T, S) = P(N|T, S) \hat{P}(T|S) \cdot P(S)
\]

\[
\propto \exp \left\{ -\frac{1}{2} \sum_{p=1}^{r} \sum_{l=1}^{Q} q_p^T \| R_p - Z_l \|_2^2 \right\} \times \left( \prod_{p=1}^{r} \prod_{l=1}^{Q} q_p^{-a} \right) \times \exp \left\{ -\frac{1}{2} \left( \mu + \alpha \sum_{p=1}^{r} \sum_{l=1}^{Q} \ln \| R_p - Z_l \|_2^2 \right) \right\},
\]

(2)

where \( \lambda \) represents the vector, \( \alpha \) denotes the factor, which is set to ‘2’ for simplifying the segmentation process. \( R_p \) denotes the pre-processed image, \( q_p \) indicates the fuzzy membership function, \( S \) denotes the clustering centre set, \( T \) specifies the membership matrix, \( Z_l \) indicates the cluster centre, and \( N \) denotes the cluster dataset, respectively. Finally, the segmented result obtained using the BHEFC is represented as \( R_s \) such that \( R_s = \hat{P}(R_p, q_p|S) \).

### 3.4 Feature extraction using the segments

The segmented result \( R_s \) is passed into the feature extraction phase, where the features, such as CNN features, statistical features, and the PPBTFs, are effectively extracted. The feature extraction is the process of transforming the segmented image into the confined matrix such that the processing complexity is relieved. The features that are extracted from the image \( R_s \) are discussed as follows:

1. **CNN features**: CNN is the multi-layered network with the special architecture, which is used to detect the complex features from the result of the segmented image. The architecture of CNN consists of three different layers, namely convolution layer, pooling layer, and fully connected layer. Convolution is the first layer, which helps to extract the essential features from the segmented image. It preserves the relations between the image features and the pixel values. It takes the segmented result \( R_s \) as input and extracts the CNN features through the convolution layer. The features that are extracted at the first convolution layer are termed as CNN features and are represented as \( f_\omega \) with the dimension of \( [1 \times 256] \), respectively. The CNN feature extracted using the convolution layer is depicted in Figure 2.

2. **Statistical features**: The extraction of statistical features assures the effectiveness of cancer detection. The features that are extracted through the statistical analysis are termed as statistical features. Here are some of the statistical features extracted from the segmented result that are listed as follows:
   - **Mean** The pixels present in the segmented results are averaged to compute the mean value.
   - **Variance** The variance feature \( f_1 \) is calculated based on the value of the mean.
   - **Kurtosis and skewness** Kurtosis refers to the symmetry and is denoted as \( f_3 \). Skewness specifies the shape of the object with respect to the numerical value and is indicated as \( f_4 \), respectively.
   - **Energy** The energy of the individual segments is extracted by summing the energy of all the pixels in the segment.

Finally, the statistical features extracted from the segmented result are represented as \( f_s = \{ f_1, f_2, f_3, f_4, f_5 \} \) with the dimension of \( [1 \times 5] \), respectively.

3. **PPBTFs**: The grayscale image is transformed into the pattern map, where the background and the edge pixels are classified using the pattern matching that returns the spatial features. The pixel values present in the pattern map specify the pattern classes of the image pixels. However, the PPBTF \( [39] \) extracted from the segmented result is represented as \( f_\rho \), with the dimension of \( [1 \times 32] \). Finally, the features extracted from the segmented result \( R_s \) are denoted as \( F \) such that \( F \) includes \( \{ f_\omega, f_s, f_\rho \} \), respectively.
3.5 Deep recurrent neural network for liver cancer detection

The features $F$ that are extracted from the segmented images are given as the input to the Deep RNN classifier. Deep RNN [40] is the network architecture that contains multiple recurrent hidden layers in the layer of network hierarchy. The architecture of Deep RNN is shown in Figure 3.

The structure of Deep RNN is made by considering the input vector of the $b$th layer at the $r$th time as $F^{(b,r)} = \{F_1^{(b,r)}, F_2^{(b,r)}, \ldots, F_i^{(b,r)}, \ldots, F_y^{(b,r)}\}$ and the output vector of the $b$th layer at the $r$th time as $J^{(b,r)} = \{J_1^{(b,r)}, J_2^{(b,r)}, \ldots, J_i^{(b,r)}, \ldots, J_y^{(b,r)}\}$, respectively. The pair of each elements of input and the output vectors is termed as the unit. Here, $i$ denotes the arbitrary unit number of the $b$th layer and $y$ represents the total number of units of the $b$th layer. In addition, the arbitrary unit number
and the total number of units of \((b - 1)\)th layer is denoted as \(j\) and \(E\), respectively. At this time, the input propagation weight from the \((b - 1)\)th layer to the \(b\)th layer is represented as \(W^{(b)} \in H^{nxE}\), and the recurrent weight of the \(b\)th layer is represented as \(w^{(b)} \in H^{nxJ}\). Here, \(H\) denotes the set of weights. However, the components of the input vector is expressed as

\[
F_i^{(b,r)} \equiv \sum_{x=1}^{E} W_{x,i}^{(b)} J_x^{(b-1,r)} + \sum_{r'=1}^{r} w_{r,r'}^{(b)} J_{r'}^{(b-1)},
\]

where \(p_{b}^{(b)}\) and \(x_{b}^{(b)}\) are the elements of \(W^{(b)}\) and \(w^{(b)}\), \(r'\) denotes the arbitrary unit number of the \(b\)th layer. The elements of the output vector of the \(b\)th layer is represented as

\[
J_i^{(b,r)} = \beta^{(b)} \left( F_i^{(b,r)} \right),
\]

where \(\beta^{(b)}\) denotes the sigmoid activation function. The rectified linear unit function is denoted as \(\beta^{(b)}(F) = \max(F; \epsilon)\), and the logistic sigmoid function is denoted as \(\beta^{(b)}(F) = \frac{1}{1 + e^{(F)}},\) which are the frequently used activation functions. To simplify the process, let us introduce the \(\ell\) th weight as \(p_{b,\ell}^{(b)}\) and the \(\ell\) th unit as \(J_{\ell}^{(b-1,r)}\) and hence, the bias is represented as

\[
J_{\ell}^{(b,r)} = \beta^{(b)} \left( W_{\ell}^{(b)} J_{\ell}^{(b-1,r)} + w_{\ell}^{(b)} \cdot J_{\ell}^{(b-1)} \right).
\]

Here, \(J_{\ell}^{(b,r)}\) denotes the output of the classifier.

### 3.5.1 Training of deep recurrent neural network

The training of the Deep RNN classifier is done using the proposed optimization algorithm named AS-Jaya optimization in order to obtain the optimal weights to achieve the update process.

### 3.6 Proposed AS-Jaya optimization for training the deep recurrent neural network classifier

In the clinical diagnosis sector, the pathologists rely on the examination of the set of nuclei in the tissue sample. In most of the situations, the diagnostic label is used for the tissue sample, and hence, the optimization algorithm is required to find the sets of nuclei among the patients with cancer in order to detect liver cancer. To achieve the liver cancer detection mechanism, the optimization named AS-Jaya is proposed in this research. The proposed AS-Jaya optimization is used to train the weights of the Deep RNN classifier in order to generate the optimal solution with the optimal detection rate. The proposed AS-Jaya optimization is the integration of ASO [37] with the Jaya optimization [38], which extracts the parametric features from both the optimization, towards boosting the performance of detection accuracy. Here, the location of each atom lying in the search space specifies the solution that is measured by the mass. All the atoms present in the population either attract or repel each other based on the distance between them. The heavier atoms have lower acceleration, which makes them obtain a better solution in the search space. The lighter atoms have higher acceleration, which intensively finds a new region in the search space.

#### Solution encoding

It is the representation of the solution vector, which determines the optimal solution for detecting liver cancer. The optimal solution is computed based on the fitness function. The fitness function with the minimal error value is accepted as the best solution. The algorithmic steps of the proposed AS-Jaya optimization based Deep RNN are elaborated as follows:

(i) **Initialize the population:** The unconstrained optimization problem is solved by initializing the population of atoms. Here, the term atom represents the image. Let us consider the population with \(n\) number of atoms and the location of \(n^{th}\) atom is represented as

\[
b_n = [b_{n1}, ..., b_{n\ell}]^T; \quad n = \{1, ..., \ell\},
\]

where \(b_n (t = 1, ..., \ell)\) represents the \(t\)th position component of the \(n\)th atom in the \(\ell\)th dimensional space.

(ii) **Fitness function:** The fitness function is calculated based on the difference between the actual output value and the estimated output value. The function with the minimal fitness value is accepted as the optimal solution. However, the fitness function is computed using the following expression:

\[
L_n = \frac{1}{\sigma} \sum_{y=1}^{\sigma} J_{n}^{(b,r)} - x_y,
\]

where \(L_n\) denotes the fitness value of the \(n\)th atom, \(J_{n}^{(b,r)}\) denotes the output of the classifier, and \(x_y\) denotes the estimated output.

(iii) **Compute the mass:** The mass of the atom is measured at the lowest level based on the fitness value. However, the mass of the \(n\)th atom at the \(g\)th iteration is computed as

\[
G_n (g) = \frac{X_n (g)}{\sum_{g=1}^{G} X_n (g)},
\]

where \(G_n (g)\) represents the mass, and the term \(X_n (g)\) is computed as

\[
X_n (g) = \frac{L_n - L_{n_{\text{init}}}}{L_{n_{\text{max}}} - L_{n_{\text{init}}}}.
\]
(iv) Determine the D neighbours: Each atom interacts with other atoms based on the best fitness value with D neighbours. Therefore, with the function of time, D gradually decreases with respect to the lapse of iterations. Hence, D is computed as

\[ D(g) = \ell - (\ell - 2) \times \sqrt{\frac{g}{\gamma^2}} \]  

where \( \gamma \) is the maximum number of iterations.

(vi) Compute the total force and constraint force: The sum of all the components being used with the random weight that is acted on the nth atom from other atoms is considered as the total force and is expressed as

\[ W_{tot}'(g) = \sum_{w \in 1:\ell} rand_{w} W_{am}'(q), \]  

where \( W_{tot}'(g) \) denotes the total force, and \( rand_{w} \) denotes the random number that lies in the range of 0–1, respectively. Each atom in the population space is acted based on the constraint force from the best atom, and so the constraint force of the nth atom is represented as

\[ O_{n}'(g) = \eta(g) \left( |h_{aw}'(g)| - b_{w}'(g) \right), \]  

where \( \eta(g) \) denotes the Lagrangian multiplier, \( h_{aw}'(g) \) represents the position of best atom at the nth iteration, and \( O_{n}'(g) \) denotes the constraint force. Here, the Lagrangian multiplier is represented as

\[ \eta(g) = \frac{2\gamma}{\delta}, \]  

where \( \delta \) denotes the multiplier weight.

(vii) Compute the acceleration: Based on the geometric constraint and the total force, the acceleration of the nth atom at the gth time is expressed as

\[ z_{n}'(g) = \frac{W_{tot}'(g)}{G_{n}(g)} + O_{n}'(g), \]  

where \( W_{tot}'(g) \) is the total force, \( O_{n}'(g) \) is the constraint force, and \( G_{n}(g) \) denotes the mass.

(viii) Update the velocity: Based on the \( (g + 1) \) iteration, the velocity of the nth atom is updated as

\[ v_{n}'(g + 1) = rand_{v} \cdot c_{n}'(g) + z_{n}'(g), \]  

where \( rand_{v} \) denotes the random number and \( z_{n}'(g) \) indicates the acceleration.

(ix) Update the position of atom: The update process of the proposed AS-Jaya optimization is carried out by modifying the position of the nth atom of ASO with the nth candidate solution of Jaya optimization. The position of the nth atom at the \( (g + 1) \)th iteration is represented as

\[ b_{n}'(g + 1) = b_{n}'(g) + c_{n}'(g + 1) \]  

\[ b_{n}'(g + 1) = b_{n}'(g) + rand_{v} \cdot c_{n}'(g) + z_{n}'(g). \]  

Equation 17 specifies the position of the nth atom, which is modified with the candidate solution of Jaya optimization. The updated equation of the candidate solution of Jaya optimization is represented as

\[ b_{n}'(g + 1) = b_{n}'(g) + m_{1,n}' \left( \frac{b_{aw,n}' - b_{w}'(g)}{|b_{w}'(g)|} \right) \]  

\[ -m_{2,n}' \left( \frac{b_{w}'(g) - b_{aw,n}'}{|b_{w}'(g)|} \right). \]  

Let us assume \( b_{n}'(g) \) as positive, and hence, the above equation can be rewritten as Equations (A1)–(A3) provided in the Appendix.

Equation (19) specifies the updated equation of Jaya optimization. By substituting Equation (A3) in Equation (17), the resultant equation is expressed as Equations (A4)–(A11) (given in the Appendix).

Here \( b_{n}'(g + 1) \) represents the position of the nth atom at the \( (g + 1) \)th iteration, \( rand_{v} \) denotes the random number, \( z_{n}'(g) \) indicates the acceleration, \( b_{aw,n}' \) represents the value for worst candidate, and \( m_{1,n}' \) and \( m_{2,n}' \) are the random number that lie in the interval [0, 1]. The equation (19) is the standard equation of the proposed AS algorithm, which is obtained by modifying the ASO with the Jaya optimization. By integrating the ASO with the Jaya provides more beneficial result in liver cancer detection with less computation cost and time. The integration of the parametric features of ASO with the Jaya optimization ensures the effectiveness of performance in the liver cancer detection model. The mimicking behaviour of atomic motion results in the potential and constraint forces of atoms from the best atom. Algorithm 1 specifies the pseudo-code of the proposed AS-Jaya-based Deep RNN.

## RESULTS AND DISCUSSION

The proposed AS-Jaya-based Deep RNN with respect to the evaluation metrics is discussed in this section.

### 4.1 Evaluation metrics

The performance attained by the proposed method is evaluated based on the performance metrics such as sensitivity, specificity, accuracy, and precision [4].
**ALGORITHM 1** Pseudo-code of the proposed AS-Jaya-based Deep RNN

| Sl. No | Pseudo code of the proposed AS-Jaya-based Deep RNN |
|--------|---------------------------------------------------|
| Input: | $h_n$ |
| Output: | $h_{n+1}$ |
| 1      | Initialize the set of atoms $A$ and the velocity $c$ |
| 2      | While stopping criteria is not satisfied |
| 3      | Do |
| 4      | Compute $L$ |
| 5      | if ($l_n < l_{bst}$) then |
| 6      | $l_{bst} = l_n$ |
| 7      | $A_{bst} = A_n$ |
| 8      | End if |
| 9      | Compute $G_n(g)$ |
| 10     | Determine the $D$ neighbours |
| 11     | Compute $W_{tn}(g)$ and $O_{tn}(g)$ |
| 12     | Calculate $z_{tn}(g)$ |
| 13     | Update $c_{tn}(g+1)$ |
| 14     | Update $h_{tn}(g+1)$ using Equation (A10) |
| 15     | End while |
| 16     | Return $A_{bst}$ |

### 4.1.1 | Accuracy

Accuracy is the measure used to differentiate the proportion of true-positive rate and the true-negative rate, which is represented as

$$\text{Acc} = \frac{TP + TN}{TP + FN + FP + FN}.$$  \hspace{1cm} (20)

where $TP$ represents the true-positive rate, $TN$ denotes the true-negative, $FP$ indicates the false-positive, and $FN$ is the false-negative.

### 4.1.2 | Sensitivity

It is the measure used to determine the accurate result of true-positive rate, which is represented as

$$\text{Sen} = \frac{TP}{TP + FN}.$$  \hspace{1cm} (21)

### 4.1.3 | Specificity

Specificity is the measure used to determine the true-negative result, which is represented as

$$\text{Spe} = \frac{TN}{TN + FP}.$$  \hspace{1cm} (22)

### 4.1.4 | Precision

Precision is the measure used to determine the positive predictive value, which is represented as

$$\text{Pre} = \frac{TP}{TP + FP}.$$  \hspace{1cm} (23)

### 4.2 | Experimental set-up

The implementation of the proposed method is carried out in the MATLAB tool [41] using the dataset specified in [11]. It contains 416 liver patient records among which 167 patient records are collected from the northeast of Andhra Pradesh.

### 4.3 | Experimental result

Figure 4 represents the experimental result of the proposed AS-Jaya-based Deep RNN. Figure 4(a) portrays the input image 1, Figure 4(b) shows the input image 2. Figure 4(c) represents the detected result 1, and Figure 4(d) represents the detected result 2.

![Figure 4](image)

### 4.4 | Performance analysis

The performance analysis conducted using the proposed AS-Jaya-based Deep RNN by varying the training percentage and hidden layers is discussed as follows.
### Table 1: Performance analysis of the proposed AS-Jaya-based Deep RNN based on training percentage

| Training percentage | Population size | SPECIFICITY | SENSITIVITY | ACCURACY | PRECISION |
|---------------------|----------------|-------------|-------------|----------|-----------|
|                     |                | 40%         | 50%         | 60%      | 70%       | 80%       | 40%         | 50%         | 60%         | 70%         | 80%         | 40%         | 50%         | 60%         | 70%         | 80%         | 40%         | 50%         | 60%         | 70%         | 80%         |
| SPECIFICITY         |                | 94.41       | 94.53       | 94.65     | 94.85     | 94.89     | 95.51      | 95.63       | 95.75       | 95.96       | 96.00       | 95.51      | 95.63       | 95.75       | 95.96       | 96.00       | 95.51      | 95.63       | 95.75       | 95.96       | 96.00       |
| SENSITIVITY         |                | 70.48       | 70.60       | 70.70     | 70.83     | 70.93     | 79.84      | 79.95       | 80.05       | 80.18       | 80.28      | 84.67      | 84.78       | 84.88       | 85.01       | 85.11       | 87.75      | 87.86       | 87.96       | 88.09       | 88.19       |
| ACCURACY            |                | 92.39       | 92.52       | 92.65     | 92.85     | 92.92     | 92.57      | 92.70       | 92.83       | 93.03       | 93.10      | 92.75      | 92.88       | 93.01       | 93.21       | 93.28       | 92.94      | 93.07       | 93.19       | 93.39       | 93.46       |
| PRECISION           |                | 85.76       | 85.91       | 86.02     | 86.18     | 86.25     | 89.30      | 89.46       | 89.57       | 89.73       | 89.79      | 90.97      | 91.13       | 91.24       | 91.40       | 91.46       | 92.06      | 92.22       | 92.32       | 92.49       | 92.55       |

### Table 4.4.1: Performance analysis with training percentage

Table 1 portrays the performance analysis of the proposed detection mechanism by varying the training percentage. When the training percentage is 40%, the specificity obtained by the proposed AS-Jaya-based Deep RNN with population size 5 is 94.41%, population size 10 is 95.51%, population size 15 is 95.51%, population size 20 is 95.51%, and population size 25 is 95.51%, respectively. When training percentage is 50%, the sensitivity obtained by the proposed AS-Jaya-based Deep RNN with population size 5 is 70.48%, population size 10 is 79.84%, population size 15 is 84.67%, population size 20 is 87.75%, and population size 25 is 89.96%, respectively. When training percentage is 60%, the accuracy obtained by the proposed AS-Jaya-based Deep RNN with population size 5 is 92.39%, population size 10 is 92.57%, population size 15 is 92.75%, population size 20 is 92.94%, and population size 25 is 93.12%, respectively.

### Table 4.4.2: Performance analysis based on hidden layers

Table 2 portrays the performance analysis of the proposed detection mechanism by varying the hidden layers. When the number of hidden layers is 8, the specificity obtained by the proposed AS-Jaya-based Deep RNN with population sizes 5, 10, 15, 20, and 25 is 95.94%. When the number of hidden layers is 10, the sensitivity obtained by the proposed AS-Jaya-based Deep RNN with population size 5 is 84.67%, population size 10 is 89.76%, population size 15 is 92.50%, population size 20 is 94.27%, and population size 25 is 94.59%, respectively. When the training percentage is 50%, the AS-Jaya-based Deep RNN with population size 5 is 90.81%, population size 10 is 92.57%, population size 15 is 93.54%, population size 20 is 94.20%, and population size 25 is 94.36%, respectively. When the training percentage is 50%, the AS-Jaya-based Deep RNN with population size 5 is 92.21%, and population size 25 is 93.02%, respectively.
TABLE 3  Comparative analysis using two features based on the training percentage

| Method Metrics | GMM | SetSVM | CNN | Deep ResNet | Proposed AS-Jaya-based Deep RNN |
|----------------|-----|--------|-----|-------------|-------------------------------|
| Specificity (%) | 73.27 | 90.33 | 94.76 | 93.33 | 94.90 |
| 73.41 | 93.35 | 96.00 | 95.73 | 96.00 |
| 73.54 | 94.20 | 96.00 | 96.00 | 96.00 |
| 73.68 | 94.73 | 96.00 | 96.00 | 96.00 |
| 73.81 | 95.38 | 96.00 | 96.00 | 96.00 |
| Sensitivity (%) | 70.37 | 70.56 | 70.74 | 0.74 | 70.93 |
| 70.56 | 70.74 | 78.94 | 76.65 | 80.28 |
| 70.74 | 70.93 | 80.28 | 78.77 | 85.11 |
| 70.93 | 71.11 | 83.73 | 81.01 | 88.19 |
| 71.11 | 71.30 | 85.94 | 82.55 | 90.40 |
| Accuracy (%) | 70.37 | 84.54 | 92.73 | 90.07 | 92.92 |
| 70.55 | 87.73 | 92.92 | 91.25 | 93.10 |
| 70.73 | 88.16 | 93.10 | 91.51 | 93.28 |
| 70.91 | 89.04 | 93.28 | 91.93 | 93.46 |
| 71.09 | 89.63 | 93.46 | 92.25 | 93.65 |
| Precision (%) | 71.34 | 81.81 | 86.08 | 84.71 | 86.25 |
| 71.50 | 83.94 | 89.28 | 87.88 | 89.79 |
| 71.67 | 84.43 | 89.79 | 88.76 | 91.46 |
| 71.84 | 84.96 | 91.00 | 89.65 | 92.55 |
| 72.01 | 85.44 | 91.80 | 90.26 | 93.34 |

4.5  Comparative methods

The performance of the proposed method is revealed by comparing the proposed method with the existing methods, such as GMM [22], set support vector machine (SetSVM) [7], CNN [21], and Deep ResNet [30], respectively.

4.6  Comparative analysis

The comparative analysis of the proposed algorithm is discussed by considering the extracted features with respect to the training percentage.

4.6.1  Comparative analysis by considering two features

Table 3 shows the comparative analysis of the proposed algorithm by considering two features, namely statistical features and PPBTFs. When training percentage is 40%, the specificities obtained by the existing GMM, SetSVM, CNN, and Deep ResNet are 73.27%, 90.33%, 94.76%, and 93.33%, respectively, while the specificity of the proposed AS-Jaya-based Deep RNN is 94.90%. When training percentage is 70%, the sensitivity obtained by the proposed AS-Jaya-based Deep RNN is 88.19%, while the percentage of improvement reported when comparing the proposed AS-Jaya-based Deep RNN with the existing GMM, SetSVM, CNN, and Deep ResNet is 24%, 24%, 5%, and 8%, respectively.

When training percentage is 50%, the accuracy obtained by the existing GMM, SetSVM, CNN, and Deep ResNet is 70.55%, 87.73%, 92.92%, and 91.25%, respectively, while the accuracy of the proposed AS-Jaya-based Deep RNN is 93.10%. For training percentage is 60%, the precision of the methods such as GMM, SetSVM, CNN, and Deep ResNet, and the proposed AS-Jaya-based Deep RNN are 71.67%, 84.43%, 89.79%, 88.76%, and 91.46%, respectively.

4.6.2  Comparative analysis by considering three features

Table 4 shows the comparative analysis of the proposed algorithm by considering three features, namely statistical features, CNN features, and PPBTFs. When training percentage is 50%, the specificity obtained by the existing GMM, SetSVM, CNN,
### Table 5: Comparative discussion

| Metrics/Methods       | Specificity (%) | Sensitivity (%) | Accuracy (%) | Precision (%) |
|-----------------------|-----------------|-----------------|--------------|---------------|
| GMM                   | 73.81           | 71.11           | 71.09        | 72.01         |
| SetSVM                | 95.38           | 71.30           | 89.63        | 85.44         |
| CNN                   | 96.00           | 85.94           | 93.46        | 91.80         |
| Deep ResNet           | 96.00           | 82.55           | 92.25        | 90.26         |
| Proposed              |                 |                 |              |               |
| AS-Jaya-based Deep RNN| 96.00           | 90.40           | 93.65        | 93.34         |

By considering two features:

| Metrics/Methods       | Specificity (%) | Sensitivity (%) | Accuracy (%) | Precision (%) |
|-----------------------|-----------------|-----------------|--------------|---------------|
| GMM                   | 73.81           | 71.11           | 71.09        | 72.01         |
| SetSVM                | 96.00           | 71.30           | 89.63        | 85.44         |
| CNN                   | 96.00           | 85.94           | 93.46        | 91.80         |
| Deep ResNet           | 96.00           | 82.55           | 92.25        | 90.26         |
| Proposed              |                 |                 |              |               |
| AS-Jaya-based Deep RNN| 96.00           | 95.00           | 93.65        | 94.88         |

By considering three features:

Table 6 depicts the computational complexity of the proposed AS-Jaya-based Deep RNN, with the existing methods such as GMM, SetSVM, CNN, and Deep ResNet, in which the proposed AS-Jaya-based Deep RNN has the minimum computation time of 6.08 s.

### Table 6: Computational complexity

| Method                     | Time (s) |
|----------------------------|----------|
| GMM                        | 11.87    |
| SetSVM                     | 9.98     |
| CNN                        | 8.21     |
| Deep ResNet                | 7.36     |
| Proposed AS-Jaya-based Deep RNN | 6.08     |

A new optimization named AS-Jaya-based Deep RNN is modelled in this research to achieve the liver cancer detection process. The pre-processed result enhances the contrast of the image by removing the redundancies and noise in the original image. The segmentation module processes the image and transformed into segmented using BHEFC. The features are effectively extracted based on the pixel values and increase the efficiency of the detection rate. The proposed AS-Jaya optimization inherits the characteristic features from ASO and Jaya and effectively updates the weight of the classifier. The fitness measure is evaluated based on the position of an atom in order to obtain the best optimal solution such that the function with the minimal error value is accepted as the optimal solution. The proposed detection model outperforms the existing liver cancer detection techniques with respect to the performance of the segmentation result. However, the proposed AS-Jaya-based Deep RNN attained better performance with the values of accuracy as 93.64%, and specificity as 96%, sensitivity as 95%, and precision as 94.88%, respectively, by considering three features at 80% training data. Some of the real-time applications of this method are Cancer Epidemiology, Cancer Immunology Research, Cancer Discovery, Molecular Cancer Research, and Clinical Cancer Research. However, this method has the difficulty of operating in artificial computing and fictional computing platforms.

### Conclusion

A new optimization named AS-Jaya-based Deep RNN is modelled in this research to achieve the liver cancer detection process. The pre-processed result enhances the contrast of the image by removing the redundancies and noise in the original image. The segmentation module processes the image and transformed into segmented using BHEFC. The features are effectively extracted based on the pixel values and increase the efficiency of the detection rate. The proposed AS-Jaya optimization inherits the characteristic features from ASO and Jaya and effectively updates the weight of the classifier. The fitness measure is evaluated based on the position of an atom in order to obtain the best optimal solution such that the function with the minimal error value is accepted as the optimal solution. The proposed detection model outperforms the existing liver cancer detection techniques with respect to the performance of the segmentation result. However, the proposed AS-Jaya-based Deep RNN attained better performance with the values of accuracy as 93.64%, and specificity as 96%, sensitivity as 95%, and precision as 94.88%, respectively, by considering three features at 80% training data. Some of the real-time applications of this method are Cancer Epidemiology, Cancer Immunology Research, Cancer Discovery, Molecular Cancer Research, and Clinical Cancer Research. However, this method has the difficulty of operating in artificial computing and fictional computing platforms. In future, the performance of cancer detection will be enhanced using any other optimization algorithm that operates in artificial computing and fictional computing platforms.
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APPENDIX

\[ b'_{a}(g+1) = b'_{a}(g) + n'_{1a} \left( b'_{bot,a} - b'_{a}(g) \right) - n'_{2a} \left( b'_{w1,a} - b'_{a}(g) \right) \]

(A.1)

\[ b'_{a}(g+1) = b'_{a}(g) + n'_{1a} b'_{bot,a} - n'_{1a} b'_{a}(g) - n'_{2a} b'_{w1,a} + n'_{2a} b'_{a}(g) \]

(A.2)

\[ b'_{a}(g+1) = b'_{a}(g) \left[ 1 - n'_{1a} + n'_{2a} \right] + v'_{1a} \]

(A.3)

\[ b'_{a}(g+1) = \frac{b'_{a}(g+1) - n'_{1a} b'_{bot,a} + n'_{2a} b'_{w1,a}}{\left[ 1 - n'_{1a} + n'_{2a} \right]} + v'_{1a} \]

(A.4)

\[ b'_{a}(g+1) = \frac{b'_{a}(g) - n'_{1a} b'_{bot,a} + n'_{2a} b'_{w1,a}}{\left[ 1 - n'_{1a} + n'_{2a} \right]} + \text{rand} \cdot v'_{a}(g) + z'_{a}(g) \]

(A.5)

\[ b'_{a}(g+1) = \frac{b'_{a}(g+1) - n'_{1a} b'_{bot,a} + n'_{2a} b'_{w1,a}}{\left[ 1 - n'_{1a} + n'_{2a} \right]} + \text{rand} \cdot v'_{a}(g) + z'_{a}(g) \]

(A.6)

\[ b'_{a}(g+1) = \frac{b'_{a}(g+1) - n'_{1a} b'_{bot,a} + n'_{2a} b'_{w1,a}}{\left[ 1 - n'_{1a} + n'_{2a} \right]} + \text{rand} \cdot v'_{a}(g) + z'_{a}(g) \]

(A.7)

\[ b'_{a}(g+1) = \frac{b'_{a}(g+1) - n'_{1a} b'_{bot,a} + n'_{2a} b'_{w1,a}}{\left[ 1 - n'_{1a} + n'_{2a} \right]} + \text{rand} \cdot v'_{a}(g) + z'_{a}(g) \]

(A.8)

\[ b'_{a}(g+1) = \frac{b'_{a}(g+1) - n'_{1a} b'_{bot,a} + n'_{2a} b'_{w1,a}}{\left[ 1 - n'_{1a} + n'_{2a} \right]} + \text{rand} \cdot v'_{a}(g) + z'_{a}(g) \]

(A.9)

\[ b'_{a}(g+1) = \frac{b'_{a}(g+1) - n'_{1a} b'_{bot,a} + n'_{2a} b'_{w1,a}}{\left[ 1 - n'_{1a} + n'_{2a} \right]} + \text{rand} \cdot v'_{a}(g) + z'_{a}(g) \]

(A.10)

\[ b'_{a}(g+1) = \frac{b'_{a}(g+1) - n'_{1a} b'_{bot,a} + n'_{2a} b'_{w1,a}}{\left[ 1 - n'_{1a} + n'_{2a} \right]} + \text{rand} \cdot v'_{a}(g) + z'_{a}(g) \]

(A.11)