Methodology for Automatic diagnosing Colon and Lung Carcinoma using TSA- PSODL Algorithm

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***Abstract*—Artificial Intelligence (AI) has significantly advanced in biomedical diagnostics and research, particularly in disease evaluation, medication development, and therapeutic interventions. This technology is revolutionizing the field, and one of its most critical applications is in the identification of cancer, which kills one in six people worldwide and is the leading cause of mortality. Among the various types of cancer, colon and lung cancers are particularly prevalent and lethal. Early detection of these cancers can greatly improve survival rates. ML and DL methods are being utilized with growing frequency to expedite the process of cancer detection. These methods enable researchers to analyze vast amounts of patient data more efficiently and cost-effectively. A promising new approach involves using the Tuna Swarm Algorithm (TSA) and Particle Swarm Optimization (PSO) using a deep learning model referred to as the TSA-PSODL approach, advanced analysis of biomedical images is being developed to detect colon and lung cancer. The TSA-PSODL technique preprocesses input images with Laplacian of Gaussian filtering (LoG) to enhance image quality and highlight key features necessary for accurate cancer detection. In addition, the TSA-PSODL approach employs InceptionNetV5 feature extractor to generate a comprehensive set of feature vectors. The Adaptive Fuzzy Adam Optimizer (AFAO) is then used to fine-tune the hyperparameters of these feature extractors, improving their performance. Finally, the TSA-PSODL approach is utilized to use an Echo State Network (ESN) classifier to identify lung and colon cancer, providing a robust and effective solution for early diagnosis. This innovative methodology showcases the immense potential of AI in revolutionizing cancer detection and treatment, paving the way for more efficient and accurate diagnostic tools. An comprehensive experimental result is conducted in order to illustrate the more amazing consequence of the TSA-PSODL system. With a maximum accuracy of 99.44%, when compared to other approaches, the comprehensive comparison study showed that the TSA-PSODL strategy was more efficient.**

Keywords—Cancer, Artificial Intelligence, Biomedical Imaging, Particle Swarm Optimization, Tuna Swarm Algorithm, Laplacian of Gaussian Filtering, InceptionResNetV5.

I. INTRODUCTION

Cancer arises from the unchecked proliferation of aberrant cells originating from the body's tissues or organs. According to statistical analysis conducted in the United States in 2020, lung and colon cancers were projected to be among the three most widespread kinds of cancer. If not detected early, there is a possibility that tumour cells may spread to other organs [1]. Lung tumours are the second most common malignancy in the US, following colon cancer. A patient can be affected by coexistence of lung and colon cancer, making it crucial to assess and identify these cancers early. Coughing, fatigue, muscle aches, and other syndromes are typical symptoms. Histopathological imaging, Ultrasound mammography, MRI, CT, and PET are advanced diagnostic imaging techniques. Hierarchical hyperparameters, sometimes referred to as multi-level hyperparameters, can be used to control the behaviour and design of complicated DL models [2]. A classifier's capacity to recognize intricate patterns is greatly influenced by the quantity of hidden units in its layers. PET (Positron Emission Tomography) scans [3] are frequently used to identify cancer. The earliest phases of tumour identifications are the main challenges that can be addressed through medical applications of artificial intelligence (AI), which include disease forecasting, biomedical imaging, and early health disease detection. Deep Learning (DL) techniques are particularly effective at analysing high- dimensional images and anatomical representations, extracting this work creates a novel Tuna Swarm Algorithm and Particle Swarm Optimization with Deep Learning (TSA- PSODL) model for the identification and assessment of lung and colon cancer using Biomedical Image analysis. The primary findings and advancements of the study are summarized below:

- Create automated model for colon and lung cancer diagnosis that includes TSA-based approaches parameter optimization, AFAO-

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based hyperparameter tuning, LoG preprocessing, InceptionNetV5 feature extraction and ESN classification. The TSA-PSODL approach has never been documented in the literature, as far as we are aware.

- Use AFAO in conjunction with the InceptionNetV5 model to extract features, which helps to accurately depict picture data related to lung and colon cancer.
- To help with reliable cancer detection, use the ESN model to efficiently identify and categorize Non-malignant and malignant patterns in pictures of lung and colon cancer. The AFAO and TSA-PSO hyperparameter tuning procedure enhances the TSA-PSODL model's capacity for cancer diagnosis.

II. Related Works

Garg and Garg modified the current prior for training CNN-driven techniques in HPI-based colon and lung cancer diagnosis, incorporating improved augmentation techniques. Here, LC25000 data was used to train eight different pre-trained CNN algorithms: InceptionResNetV2, InceptionV3, VGG16, ResNet50, NASNetMobile, DenseNet169, MobileNet, and Xception. Adu et al. [4] presented an innovative DHS-CapsNet in order to categorize HPI in colon and lung cancer. Sakr et al. introduced a novel lightweight deep learning method that uses a CNN for potential colon recognition. This approach establishing a system for dividing colon cancer into two categories such as adenocarcinomas and polyps by utilizing the CNN methodology and the MobileNet architecture. A DL method was introduced by Mohalder et al. to predict CRC tumours in HPI. The CNN system is used to examine complex data. CNN uses the VGG19, ResNet152, DenseNet201, ResNet101, MobileNetV2, VGG16, and InceptionV3 structures to enhance its performance for lung and colon cancer. Simultaneously, several hyperparameters significantly impact the efficiency of the CNN model [5]. Bhattacharya examined a framework that predicts lung or colon cancer, or both, in HPIs using either DL or meta-heuristic approaches [6] with almost perfect accuracy. As a result, we use the IAFO and TSA algorithms in this study to choose the parameters for the GhostNet model and ESN model respectively. Recognizing the critical role that histology diagnosis plays in improving cancer treatment approaches. M.S.N. Raju and B.S. Rao want to establishing an effective computer aided diagnosis system is the aim of this study.

III. Proposed Methodology

The TSA-PSODL approach leverages the strengths of multiple advanced techniques to achieve high accuracy in cancer detection. Initially, the method preprocesses the input biomedical images using Laplacian of Gaussian (LoG) filtering. For feature extraction, the TSA-PSODL system employs powerful neural network architectures namely InceptionNetV5.These models are known for their ability to capture intricate details and patterns within images, there by generating robust feature [7] vectors that are essential for accurate classification. To further optimize the system, the Adaptive Fuzzy Adam Optimizer (AFAO) is used to fine tune the hyperparameters of the feature extractors. Finally, the TSA-PSODL method uses an Echo State Network (ESN) for classification, supported by the TSA-PSO algorithm for parameter tuning. By combining these advanced techniques, the TSA-PSODL methodology offers a thorough and effective way to identify and classify colon and lung cancer early on, perhaps leading to better patient outcomes through prompt management.

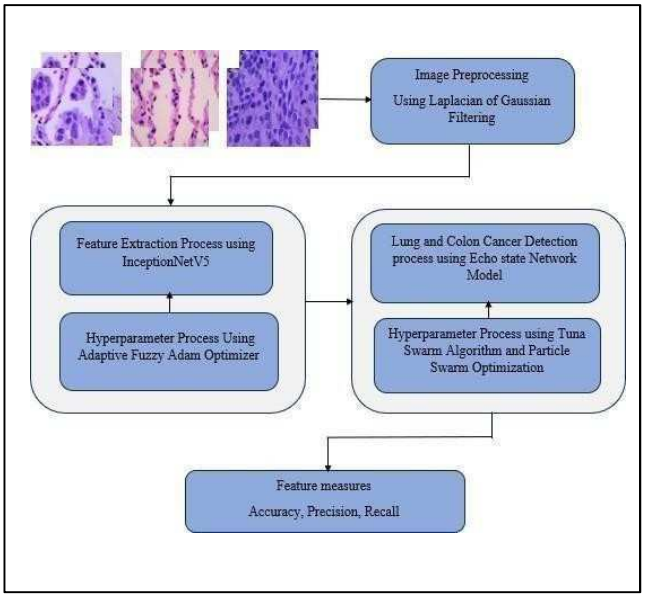

Fig 1. Workflow of TSA-PSODL Approach

A. Data Preprocessing

Gaussian Smoothing (Noise Reduction):

- Medical images often contain noise due to factors like sensor limitations, patient movement, or environmental conditions during image acquisition.
- Gaussian filtering is used to smooth the image by reducing noise while preserving essential structural details.

Laplacian Operator (Edge Enhancement):

- The Laplacian operator is used to identify edges after the image has been smoothed edges.
- Regions of abrupt intensity shift, usually connected to edges in a picture, are highlighted by the Laplacian function, a second-order derivative operator image.
- Since the Laplacian operator is sensitive to noise, applying it directly to raw images can lead to undesirable artifacts. However, when combined with Gaussian smoothing, the result is a more robust edge detection method.

Laplacian of Gaussian (LoG) filter is a powerful image processing technique used in preprocessing for colon and lung cancer detection. It combines Gaussian smoothing to reduce noise and a Laplacian filter to highlight edges and boundaries. By applying LoG [8] to medical images, subtle features like polyps in colonoscopy images and nodules in lung CT scans become more prominent.

B. Optimal InceptionNetV5 Feature Extractor

InceptionNetV5, a sophisticated convolutional neural network architecture, builds upon previous advancements by Incorporating cutting-edge techniques to improve its efficiency and performance. Using a sizable dataset of medical images, the pre-trained InceptionNetV5 model was refined, it can learn to extract highly discriminative features that capture the subtle differences between healthy and cancerous tissues to make accurate predictions about the presence and type of cancer.

a) *Inception Module*: InceptionNetV5 is composed of modular units that serve as its fundamental building blocks.

b) *Stem Block:* The initial layers of the network, typically convolutional and pooling layers, analyze the input image and extract fundamental features.

c) *Reduction Blocks:* These blocks reduce the feature maps' spatial dimensions while deepening their channels. The network can now concentrate on more abstract traits as a result.

d) *Auxiliary Classifiers*: These classifiers are added at intermediate layers to provide additional training signals, during backpropagation, helping to stabilize training and improve performance.

e) *Global Average Pooling:* This feature maps are averaged across spatial dimensions in this layer, reducing the dimensionality of the feature representation.

f) *Fully Connected Layer:* Based on the features that have been retrieved, the input image is classified using a fully connected layer.

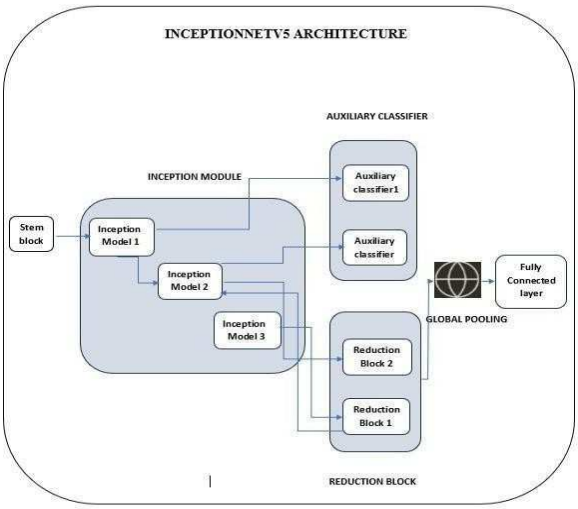

Fig.2 InceptionNetV5 Architecture

InceptionNetV5 has Demonstrated excellent performance in various image classification applications, including medical imaging for colon and lung cancer detection cancer.

C. Detection of Cancer using ESN Model

To diagnose and categorize cancer, the ESN model is employed. Although quantitative approaches make modelling easier, their capacity for forecasting is frequently restricted. On the other hand, because of its quick training time and simplicity of use, the ESN is regarded as a very successful method for training RNNs. $[v_1(n)\cdots v_k(n)]T = v(n)T$, at particular time, the input instance, represents the consequence equal to (n) [10].

$$f(Q_{in}\, v(n+1) + \sim Q\, x(n)) = x(n+1) \qquad (1)$$

where, $\sim Q$: Reservoir state connection matrix.

$$f_{out}\,(Q_{out}\, x(n+1)\,) = y(n+1) \qquad (2)$$

where, f_{out} : Resultant excitation function,
Q_{out} : Consequent connection

In contrast, −1 indicates the inverse of a matrix. The superscript T denotes the transposition of matrix [9]. Y displays the final matrix method, whereas X explains the matrix operation of the input reservoir layer. An optimal solution is initiated using solely MSE or least squares.

D. Using TSA and PSO to modify the parameters

Finally, the TSA and PSO are used to choose the optimal parameters for the ESN model. The TSA approach initiates the refinement process [9], and PSO then generates the starting population uniformly and randomly within the search area. The following is a formulation of the TSA mathematical expression:

$$Y^{(0)} = rand \cdot (va - sa) + sa,\ j = 1,2,\ N(P) \qquad (3)$$

- **Y(0)** → A candidate solution's (tuna) initial location in the search space. .
- **rand** → A value between 0 and 1 that is produced at random to provide initialization diversity.
- **va (Upper Bound)** → The maximum possible value for the position of a tuna in the search space. This defines the highest limit for the initialized solution.
- **sa (Lower Bound)** → The minimum possible value for the position of a tuna in the search space. This defines the lowest limit for the initialized solution.
- **N(P)** → The total number of candidate solutions (population size) in the algorithm.
- **j** → The index representing a specific candidate solution in the population.

Tuna exhibits a primary foraging behaviour known as spiral foraging, where they pursue prey by creating tight spirals. Additionally, schools of tuna exchange information with one another.

a) Fitness Assessment: Determine the fitness of each individual solution within the population by evaluating its performance based on the defined objective function.

b) Position Adjustment: The position of each tuna is updated using the spiral foraging approach.

$$Y_i(t+1) = Y_i(t) + A \cdot \sin(\theta) \cdot \exp(B \cdot \theta) \qquad (4)$$

In this equation,

- $Y_i(t+1)$ is the i-th individual's updated position at iteration t+1
- $Y_i(t)$ is the individual's current position at iteration

c) Information Sharing: The information

sharing formula is expressed as follows,

$$Y_i(t+1) = Y(t+1) + c \cdot rand \cdot (Y_{best} - Y_i(t+1)) \quad (5)$$

In the expression,

- $Y_i(t+1)$ is the updated position respective individual and c is a coefficient that controls the influence of the best position.
- rand function generates a random number ranging from 0 to 1.
- The parameter Y_{best} represents the optimal position discovered by the entire swarm. [9].

d) Iteration and Convergence: Repeat the fitness evaluation and position update steps for a set The process runs for a set number of iterations or until a termination criterion is met (e.g., when no significant improvement is observed) best solution.

TABLE I. DETAILS OF DATABASES

Class Name	Description	No. of Samples
LunAd	Lung Adenocarcinoma	5000
LunBe	Lung Benign Tissue	5000
LunSC	Lung Squamous Cell Carcinoma	5000
ColAd	Colon Adenocarcinoma	5000
ColBe	Colon Benign Tissue	5000
Total Number of Samples		25000

The process of Particle Swarm Optimization can be carried out by following these steps:

a) *Initialization Formula:* The initialization formula as follows,

$$X_i(0) = rand \cdot (vb - sb)\, lb,\ i = 1,2,,\ NP \quad (6)$$

- $X_i(0)$ is the i- th flyspeck's starting position,
- rand is a aimlessly distributed value between 0 and 1.
- The hunt space's higher and lower boundaries are represented by the parameters vb and sb, independently [9].
- The mass's flyspeck count is denoted by NP.

b) Fitness Evaluation Formula:

$$f(X_i) = Accuracy(X_i) \quad (7)$$

In this expression,

- $f(X_i)$ is the fitness value of the i-th flyspeck.
- Delicacy (X_i) is the delicacy of the model with hyperparameters represented by X_i.

This formula measures how well the hyperparameters represented by X_i perform in terms of delicacy, which is pivotal for assessing and optimizing the model.

c) Velocity Update Formula: The Expression for calculating the velocity update is as follows,

$$v_i(t+1) = w \cdot v_i(t) + c_1 \cdot r_1 \cdot (pbest_i - X_i(t)) + c_2 \cdot r_2 \cdot (gbest - X_i(t)) \quad (8)$$

- $v_i(t+1)$ represents the i-th flyspeck's streamlined haste
- $v_i(t)$ is its current haste

acceleration portions are represented by the parameters c1 and c2. also, r1 and r2 are arbitrary values in the range between 0 and 1.

d) Position Update Formula:

$$Y_i(t+1) = Y_i(t) + v_i(t+1) \quad (9)$$

Here,

- $Y_i(t+1)$ is the updated position of the i-th particle
- $Y_i(t)$ is where the i-th particle is at the moment.
- The parameter $v_i(t+1)$ is the updated velocity of the i-th particle.

This formula updates the position of each particle based on its current position and its newly calculated velocity.

a) *Iteration and Convergence:* For a predetermined Steps two through four are repeated after the process has run for a predefined number of iterations or until a stopping criterion is fulfilled (for example, the best solution has not improved after a predetermined number of iterations).

b) *Optimization:* The best hyperparameters found by the PSO algorithm are used to configure the model for optimal performance in detecting lung and colon cancer [10].

IV. EXPERIMENTAL RESULTS

On a PC with the following parameters, the suggested TSA-PSODL model was implemented using a Python 3 tool: Disk: 32.6 / 107.7 GB, System RAM: 1.3/12.7 GB, Total SSD: 107 GB, and HDD: 0.11 TB [10]. The model was run with The parameters are set as follows: batch size of 5, 50 epochs, learning rate of 0.001, dropout rate of 0.45, and activation function ReLU (Rectified Linear Unit). The LC25000 database, which comprises five classes with 5,000 samples each, was used to experimentally validate the TSA-PSODL algorithm, as shown in Table 1. Samples of lung and colon pictures are shown in Fig.3 and Fig.4. Benign lung tissues, lung adenocarcinomas, colon adenocarcinomas, and benign colon tissues. The five classes [10] include benign colonic tissues, colon adenocarcinomas, lung adenocarcinomas, benign lung tissues, and squamous cell lung carcinomas. For experimental validation, the data was divided into A 70% for train and 30% for test.

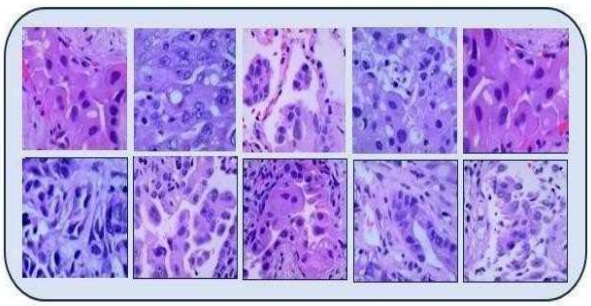

Fig 3. Lung Images

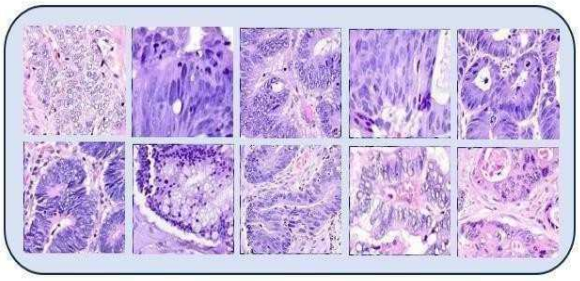

Fig 4. Colon Images

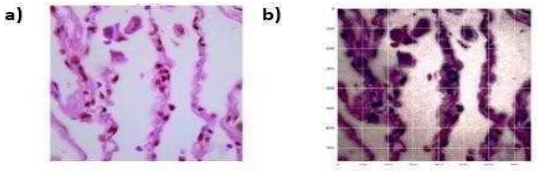

Fig 5. Lung colon image a) before preprocessing b) after preprocessing

Fig 6. Accuracy curve of TSA-PSODL Approach after 5 epoch

TABLE II. DETAILS OF ACCURACY AFTER 5 EPOCH

	Precision	Recall	F1-score	Support
0	0.99	1.00	1.00	479
1	1.00	0.99	1.00	519
2	1.00	1.00	1.00	516
3	1.00	1.00	1.00	498
4	1.00	1.00	1.00	488
Accuracy			1.00	2500
Macro avg	1.00	1.00	1.00	2500
Weighted avg	1.00	1.00	1.00	2500

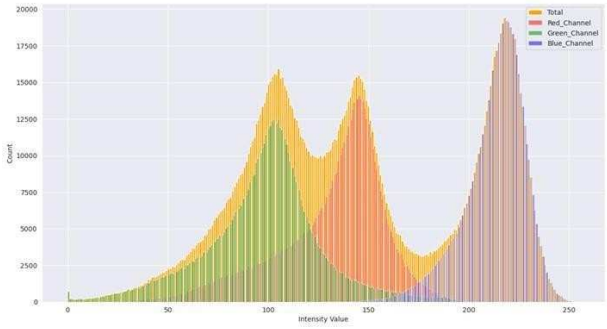

Fig 7. Intensity ranges

The machine learning model's training and validation accuracy across several epochs is depicted in the provided graph. The y- axis shows accuracy, and the x-axis shows the number of epochs. The model's performance on the training dataset (blue line) and the validation dataset (red line) is depicted by the two curves. Both accuracies initially rise quickly, suggesting that the model is successfully learning from the input. Convergence is indicated by the accuracy levelling out at about 99% to 100% around the five epoch. The model's strong generalization to unknown data is indicated by the tight alignment of training and validation accuracy, which points to little overfitting. Accuracy stabilizes as training goes on, showing that more instruction has no discernible effect on performance. The graph shows a well- optimized model with good generalization abilities overall.

Fig 8. Accuracy Curve of the TSA-PSODL Approach after 30 epoch

The graph of "Training & Validation Accuracy" illustrates how the TSA-PSODL model consistently achieves near-perfect accuracy throughout the training process. The accuracy values for both training and validation remain close to 1.000, showcasing the model's strong learning capability and quick convergence within a few epochs. The minimal gap between the two curves highlights excellent generalization, ensuring robust performance on unseen data. The TSA-PSODL methodology combines advanced preprocessing, such as Laplacian of Gaussian (LoG) filtering, with feature extraction using InceptionNetV5. Parameter optimization through the Tuna Swarm Algorithm (TSA) and Particle Swarm Optimization (PSO) further fine-tunes the model for efficient classification. Using the LC25000 dataset, the method achieves exceptional results, with a high accuracy of 99.44%, indicating its potential for trustworthy early lung and colon cancer diagnosis.

TABLEIII. DETAILS OF ACCURACY AFTER 30EPOCH

	Precision	Recall	F1-score	Support
0	1.00	1.00	1.00	479
1	1.00	1.00	1.00	519
2	1.00	1.00	1.00	516
3	1.00	1.00	1.00	498
4	1.00	1.00	1.00	488
Accuracy			1.00	2500
Macro avg	1.00	1.00	1.00	2500
Weighted avg	1.00	1.00	1.00	2500

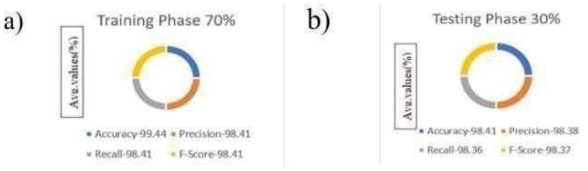

Fig.9. a) Average outcome of 70% TRP b) Average outcome of 30% TSP

The TSA-PSODL achieves impressive results, with a maximum accuracy of 99.44%, A precision of 98.41%, a recall of 98.41%, and an F1 score of 98.41%. These metrics highlight the enhancement of the TSA-PSODL medical image analysis system that leverages both PSO

and TSA models proposed in this technique are responsible for selecting the optimal ESN and InceptionNetV5 model hyperparameter values. Since they are not learned during training, hyperparameters are settings that must be decided upon before to the training process. Model performance can be considerably enhanced by choosing them optimally. Through the use of PSO and TSA algorithms, the TSA- PSODL model can optimize the algorithm's parameters to produce even better results. These findings support the TSA- PSODL technique's superior performance over other approaches currently in use.

TABLEIV. RELATIVE ANALYSIS OF TSA-PSODL APPROACH WITH RECENT ALGORITHMS

Methods	$Accu_y$	$Prec_n$	$Reca_l$	F_{Score}
TSA-PSODL	99.44	98.41	98.41	98.41
BICLCD-TSADL	99.33	98.31	98.31	98.31
MPADL-LC3	98.81	97.92	97.87	97.91
mSRC	88.25	85.20	91.74	86.66
Faster RCNN	98.70	96.44	97.84	97.28
DAELGNN	98.56	98.08	96.56	96.65
RESNET50	93.96	96.28	97.48	96.95
CNN Model	97.05	96.92	97.41	97.74
DL Model	96.29	96.96	96.14	98.03

V. CONCLUSION

The key evaluation measures, including accuracy, precision, recall, and F-score, have been used to analyze the effectiveness of several deep learning and machine learning algorithms in the diagnosis of lung and colon cancer. The comparative analysis includes well-established models such as RESNET50, Faster CNN, CNN Model, and DL Model, along with recently introduced approaches like BICLCD TSADL, MPADL LC3, and DAELGNN. The proposed TSA- PSODL algorithm has demonstrated superior performance across all metrics, achieving an outstanding accuracy of 99.44%, which outperforms other contemporary models.

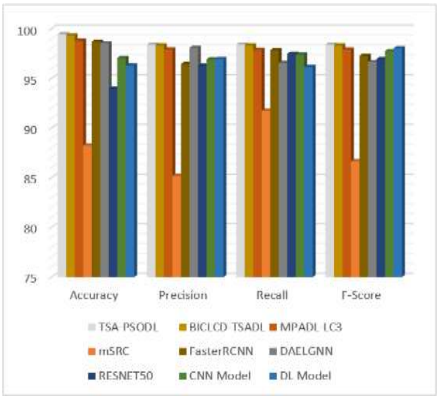

Fig 10. TSA-PSODL approach's comparative results with new algorithm

From the graph, it is evident that the TSA-PSODL method achieves consistently high values in all evaluation parameters, indicating its ability to effectively classify and detect cancerous regions in biomedical images. While some models such as RESNET50 and Faster CNN show competitive performance, they fall slightly lacking in memory and precision, two critical components in lowering false positives and false negatives in medical diagnosis. The TSA-PSODL algorithm surpasses existing methods in diagnosing colon and lung cancer, achieving a remarkable 99.44% accuracy due to optimized preprocessing (LoG filtering), advanced feature extraction (InceptionNetV5), and robust classification (AFAO and ESN). The integration of TSA and PSO for parameter tuning further enhances performance, making it a reliable approach for biomedical image analysis.

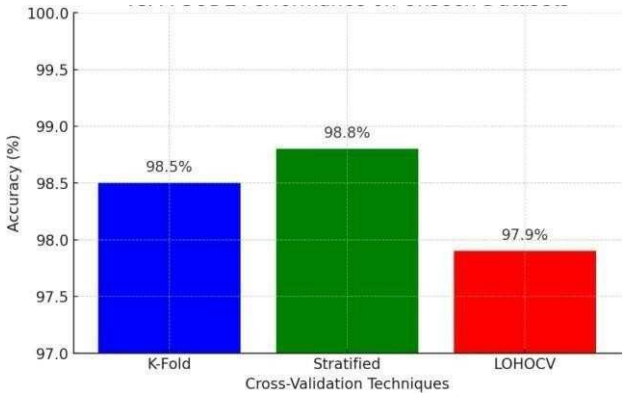

Fig.11. TSA-PSODL's performance on datasets

The bar graph comparing TSA-PSODL's performance on datasets using different cross-validation techniques. It demonstrates that Stratified Cross-Validation achieves the highest accuracy (98.8%), followed by K-Fold (98.5%), while Leave-One-Hospital-Out Cross-Validation (LOHOCV) has slightly lower accuracy (97.9%) due to real-world dataset variability. To increase its scalability and usefulness in medical diagnostics, future studies should concentrate on feature fusion, ensemble learning, and computational optimization.

REFERENCES

[1] Marwa Obayya, Muniya A. Aarasi,Nuha Alruwais,Raed Alsini,Abdullah Mahamed and Ishfaq yaseen,"Biomedical Image Analysis for Colon and Lung Cancer Detection Using Tuna Swarm Algorithm with Deep Learning Model"24 Aug,2023.

[2] M.S.N. Raju and B.S. Rao, "Lung and colon cancer classification using hybrid principle component analysis network-extreme learning machine." Concurrency Comput., Pract. Exper., vol. 35, no. 1, Jan. 2023.

[3] Nazmuk Shahadat, Ritika Lama Anna Nguyen and , "Lung and Colon cancer Detection using a Deep AI Model",20, Nov.2024.

[4] Nuha Alruwais, Raed Alsini,Abdullah Mohamed and Ishfaq Yaseen,"Biomedical Image Analysis for Colon and Lung Cancer Detection Using Tuna Swarm Algorithm With Deep Learning Model",29 Aug,2023.

[5] Sheikh Ridwan Raihan,Hirak Modal and Anindya Nag," Identification of Lung Cancer Using Particle Swarm Optimization and Machine Learning Technique",Oct,2024.

[6] Omer Turk, Emrullah Acar, Emrah Irmak and Enes Bakis, "A Hybrid 2D Gaussian Filter and Deep Learning Approach with Visualization of Class Activation for Automatic Lung and Colon Cancer Diagnosis" Jan,2024.

[7] Rauel Ochoa-Ornelas, Alberto Gudino-Ocho, Garcia-Radriguez and Sofia Uribe Toscana," Lung and colon cancer detection with InceptionResNetV2: a transfer learning approach", Dec,2024.

[8] M.A. Talukder, M. M. Islam, M. A. Uddin, A. Akhter, K. F. Hasan, and M. A. Moni, ''Machine learning-based lung and colon cancer detection using deep feature extraction and ensemble learning,'' Nov. 2022.

[9] O.Attallah, M. F. Aslan, and K. Sabanci, ''A framework for lung and colon cancer diagnosis via lightweight deep learning models and transformation methods,'', Nov. 2022.

[10] M.A.Fahami, M. Roshanzamir, N. H. Izadi, V. Keyvani, and R. Alizadehsani, ''Detection of effective genes in colon cancer: A machine learning approach,'' 24, 2021.