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Heuristic and collaborative learning process for analyzing pathological image biomarkers

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Abstract:

A disease's existence, progression, or prognosis can be determined by analysing biomarkers found in pathological pictures. These images might depict micrographs, scans, or even real pieces of tissue. Early diagnosis and individualized treatment depend on accurate biomarker evaluation of abnormal images. Adapting to small changes in cell structure and biomarker expression is challenging for current approaches, which frequently depend on supervised machine learning and deterministic algorithms due to the absence of annotated data. To tackle these issues, this research suggests a network, HHC-CNN-ACO, combining hybrid heuristics and collaborative learning with Convolutional Neural Network (CNN) and ant colony optimization (ACO). This approach enhances the detection and understanding of illness biomarkers by combining ACO with collaborative learning and heuristic-based preprocessing. Regarding preprocessing, feature recognition is significantly improved by edge detection and Adaptive Histogram Equalization (AHE). Through the application of ant behaviour modelling to optimize feature selection, the ACO heuristic determines the most effective biomarkers. A strong, anonymous model is guaranteed by the collaborative method, which combines federated instruction with annotation from several experts. An ensemble of classifiers, guided by ACO-optimized features, fine-tunes the system's primary convolutional neural network (CNN), and the pre-processed images are enhanced. The experimental outcomes indicate that the HHC-CNN-ACO is more precise and easier to understand than the state-of-the-art biomarker classification and identification approaches. This system enhances diagnostic outcomes and advances personalized treatment by providing a precise, adaptable, and explicable pathological picture analysis solution.

Keywords: Heuristic-Collaborative learning, Convolutional Neural Network, Adaptive Histogram Equalization, Pathological image biomarkers.

1. Introduction

Computerized methods for medical picture analysis have been flourishing as of late, with the goals of providing clinical information, integrating second perspectives, and reducing the need for human involvement [1]. With the introduction of whole-slide imaging systems, new interactive simulators for pathology education have been accelerated, clinical workflows have been improved, and chances to create new tools and investigative methodologies for clinically actionable image analysis have been presented [2]. Many parameter-tuning strategies have emerged because of the tremendous advancements made in medical imaging using deep learning. These methods have limited generalizability because they are often developed to tackle disease-specific issues [3]. Pathologists use hematoxylin and eosin to stain slices of histopathological samples to conduct a pathological biopsy. This helps to reveal the intricate cellular structures between tissues, which are subsequently examined under a microscope [4]. The advancement of diagnosis and treatments in medicine relies heavily on biomarkers. Imaging biomarkers are defined by the National Institutes of Health (NIH) program on biomarkers and surrogate endpoints as metrics or indicators of normal biologic processes, pathogenic processes, or pharmaceutical reactions to a therapeutic intervention [5]. When applying ML algorithms to medical photos, important features are crucial. Most of the algorithms that came before it relied on manually analysed medical images to create characteristics. Having said that,

the limited information and discriminative capabilities provided by the handcrafted features are not very helpful [6].

Deep learning methods perform exceptionally well during the training phase when a vast quantity of data is available. For instance, medical image analysis has used deep learning because of significant advancements in computer vision. Improvements in accuracy and the opening of new horizons in medical image analysis have resulted from deep learning-based applications, which are emerging as the most cutting-edge computer tools [7]. The transformation of visually unstructured data into analyzable representations relies heavily on feature extraction techniques. Among these techniques are older ones that rely on hand-crafted features and newer ones that use deep learning architectures [8]. From picture segmentation and classification to numerous other fields, convolutional neural networks (CNNs) have proven to be the most applied and effective deep learning approach thus far. Convolutional neural networks (CNNs) may learn to accurately predict outcomes from datasets with little to no augmentation from humans [9]. The use of ML for picture classification and forecasting has grown substantially. CNNs are one type of Deep Learning algorithm among many others. After learning crucial characteristics of the image being used, such as its dimension, form, and intensity, the model's parameters, such as weights and bias, enable them to distinguish across images [10].

Adaptive histogram equalization (AHE) boosts contrast and highlights minute details, whereas edge recognition methods highlight the structural boundaries of the tissue. With ACO, the various aspects of the images can be narrowed down to those that most strongly indicate the presence of disease. Integrating distributed learning techniques and annotation from various individuals, the proposed HHC-CNN-ACO methodology guarantees a strong model that uses shared knowledge while protecting patient data. The convolutional neural network (CNN) can focus on the most essential parts of the images for biomarker identification by training it to operate in tandem with the preprocessing and feature selection systems. The system outperforms conventional biomarker identification and classification approaches by utilizing efficient feature selection, collaborative learning, and advanced preprocessing techniques. Improvements in biomarker analysis may lead to better disease diagnosis, prognosis, and therapy planning.

The main contribution is

- The HHC-CNN-ACO framework for pathological image processing will be utilized to improve the identification and interpretation of biomarkers in complicated medical imaging situations.
- This work combines edge detection approaches with AHE to improve the clarity of blurry photographs and draw attention to crucial details.
- To improve the precision and effectiveness of pathological image analysis, Ant Colony Optimization (ACO) presents a new feature selection method based on real-world events.
- To use an ensemble of classifiers guided by ACO-optimized features to enhance biomarker analysis/classification accuracy and reliability.
- To improve the accuracy and interpretability of prior biomarker identification and classification methods, according to experimental results.

Improving pathological image analysis with ACO, heuristic-based preprocessing, and collaborative learning is the goal of the HHC-CNN-ACO architecture. This approach helps discover biomarkers by addressing data availability issues and tissue architecture

variations. Improvements in feature recognition using edge detection and AHE, privacy-preserving expert collaboration through federated learning, and optimal feature selection through ACO are all significant developments. Optimised features for ACO guide a group of classifiers to improve the analysis. The experimental outcomes show that HHC-CNN-ACO is much more accurate and easier to understand than the current approaches, which improves diagnostic and customized medicine capacities.

2. Literature Review

Bankhead, P. [11] examined the challenges in translating novel image analysis methods in digital pathology from research to practical application. The review discusses various approaches and techniques for analyzing pathology images but doesn't focus on a specific method. Instead, it highlights the limitations in software availability, complexity, and dataset dependency that hinder widespread adoption. The result is a disconnect between the potential and actual capabilities in digital pathology. The advantage of addressing these issues would be increased adoption and practical application of novel algorithms. The main limitation is the lack of user-friendly, complete, and dataset-independent software implementations.

Li, F.et al., [12] developed and assessed the efficacy of a new deep learning (DL) biomarker for pCR prediction using pictures of H&E-stained tissue. The histopathological biomarker pCR-score was generated by automatically identifying tumour epithelium in H&E-stained pictures and then using DL techniques to predict pCR. Researchers compared the predictive effectiveness of the pCR-score to that of more conventional markers including subtype and stromal tumor-inflating lymphocytes (sTILs). Using the pCR-score from H&E staining for direct pCR prediction resulted in an AUC of 0.847.; after logistic regression processing, it yielded an F1 score of 0.853, an AUC of 0.822, and an accuracy of 0.503. The sample's demographic and geographical composition may introduce bias into the results.

An AI-based computer-aided diagnostic (CAD) pipeline for tumor grading was suggested by Lagree, A. et al. [13]. This retrospective analysis comprised 138 participants. Preparation, digitization, and pre-processing of breast core biopsy slides were carried out according to established laboratory protocols. In order to segment tumor nuclei and locate areas of interest with cancer cells, deep convolutional neural networks (CNNs) were created. Imaging-based characteristics linked to spatial parameters were retrieved from the ROIs that were segmented. The area under the curve (AUC) for the classification performance was 0.745 for imaging-derived indicators utilized alone and 0.836 when the same characteristics were modelled with additional pathologic biomarkers. Due to its retrospective design, the study runs the risk of selection bias and inadequate controls for potential confounding variables.

The goals of the study by Chen, Z., et al. [14] were twofold: first, to determine whether cognitive tests and biomarkers are adequately documented in electronic health records (EHRs) to serve as real-world endpoints; and second, to utilize Natural Language Processing (NLP) techniques to retrieve and harmonize various cognitive tests from clinical narratives into severity categories for Alzheimer's Disease (AD) as well as AD-Related Dementias (AD/ADRD). A rule-based natural language processing pipeline was created to extract biomarkers and cognitive tests from clinical narratives in electronic health records of patients with Alzheimer's disease and dementia with dementia (ADRD). The F1-score

for the NLP pipeline was 0.9059 across all seven measures. The study classified patients based on the outcomes of four out of the six tests for cognition, allowing us to provide specific demographic information about each patient. This may not give a full view of all AD/ADRD patients and restricts the quantity of data that can be analysed.

Yousef, R. et al. [15] critically assess the current advancements in this field by surveying the different medical picture modalities and DL approaches employed for distinct applications. For the public and those without medical training, this article is a great resource for learning about deep learning and its principles. Next, it provides several deep learning applications (such as segmentation, classification, detection, and so on) that are frequently utilized in clinical settings across various anatomical locations. Finally, the study defines key terms for attributes related to deep learning, such as basic architecture, improving data, transferred learning, and feature selection techniques. In the next years, medical images will be often used as input to deep learning architectures, and new deep learning approaches will likely form the basis of medical image analysis. Expanding to include many uses and approaches could make it difficult to explore any of them.

The application of Deep Learning for the automatic classification of lung disorders, such as COVID-19, using X-ray pictures was studied by Apostolopoulos, I. D. et al. [16]. On a massive X-ray picture dataset, we built the MobileNet v2 CNN. When tested against seven different classes, the approach achieved an accuracy of 87.66%; when tested against COVID-19, it achieved an accuracy of 99.18%. It was more beneficial to start at the beginning of the training process rather than rely on transfer learning. This approach limits exposure for medical professionals and provides speedy and economical detection. Additional research is necessary to determine the generated features' potential as biomarkers. The results show that computer-aided diagnosis can greatly help when dealing with complicated cases and making first evaluations.

A comprehensive analysis of the Deep Learning Approach (DLA) and instructions on building artificial neural networks were provided by Puttagunta, M., and Ravi, S. [17]. Medical imaging applications that utilize this method are intriguing. Most DLA deployments are around digital pictures from X-rays, CT scans, digital mammography, and digital histopathology. It provides an exhaustive review of the research on medical image classification, detection, and segmentation using DLA. Two goals are being pursued by using DLA in medical picture analysis. An overview of deep learning and its theoretical underpinnings is provided first. The second objective is to present a summary of a high-level DLA-based medical image analysis. The absence of tailor-made deep neural network designs is a major restriction.

Zhou, X., et al [18] presented a comprehensive overview of the Breast Histopathological Image Analysis (BHIA), techniques based on Artificial Neural Network (ANN). The authors first divided the BHIA systems into deep and traditional neural networks for further analysis. Subsequently, pertinent research utilizing BHIA systems is introduced. Following that, it examined the current models to determine the best algorithms. Most of the research uses texture and morphological features in feature extraction. The limitations include the need for new network models, lack of large, fully labelled datasets, and complex breast cancer classification.

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3. Proposed Work

a) Dataset Explanation

To investigate patterns in CT images, data linked to contrast and patient age, the dataset permits the testing of several methodologies. The primary goal is to detect statistical patterns, features, and image textures strongly correlated with these traits. Then, if these images have been misclassified, or if there are outliers, such as suspicious cases, inaccurate measurements, or poorly calibrated machines, the goal is to create simple tools that can automatically classify these images. A small selection of photos from the cancer imaging collection constitutes the data. All CT scans with usable age, modality, and contrast tags in the middle slice make up these sets. As a result, we get 475 series from 69 distinct patients.

b) Objective of this study

This project aims to build the HHC-CNN-ACO framework, which combines modern approaches to address critical issues in biomarker discovery to enhance the accuracy and efficacy of pathological-based image evaluation. Addressing issues such as variations in tissue structure and biomarker expression, as well as a dearth of annotated data, is the study's primary goal. The research accomplishes this by presenting a new method for optimizing biomarker discovery that selects features based on heuristics using Ant Colony Optimization (ACO). The work employs heuristic preprocessing methods, such as AHE and edge detection, to improve image quality and feature visibility. Collaborative learning that combines federated instruction with expert annotations allows for constructing trustworthy models while protecting sensitive data. To improve diagnostic accuracy and tailor treatment programs to each patient's unique needs, data is analysed and classified using an ensemble of classifiers driven by assets and costs optimization criteria. The pathological pictures of several tissues are displayed in Figure 1.

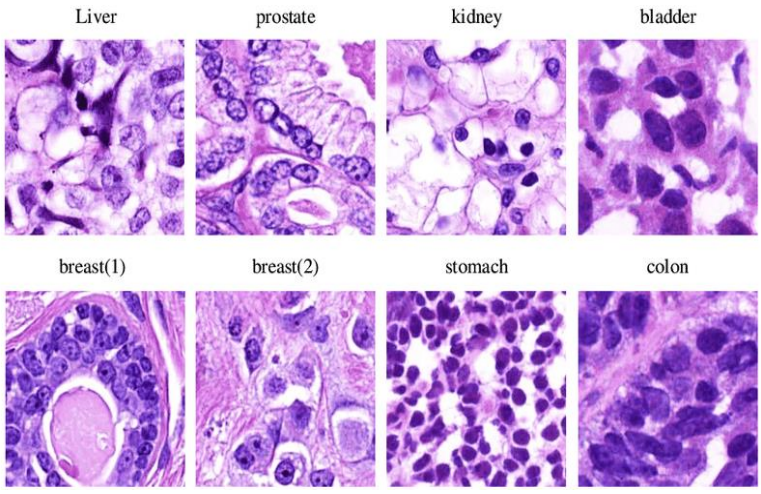

Fig.1. Pathological images of different tissues

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c) Working process of the proposed HHC-CNN-ACO method

The HHC-CNN-ACO system was developed for better pathology image processing and disease biomarker identification. Regarding biomarker discovery, the system employs many cutting-edge methods, such as heuristic-based preprocessing, Ant Colony Optimization (ACO), and collaborative learning. The proposed HHC-CNN-ACO method's workflow is shown in Figure 2. Before identifying the biomarker, the dataset's raw images must undergo pre-processing and fine-tuning. An AHE and an edge detection technique are the two main components of the picture preprocessing pipeline.

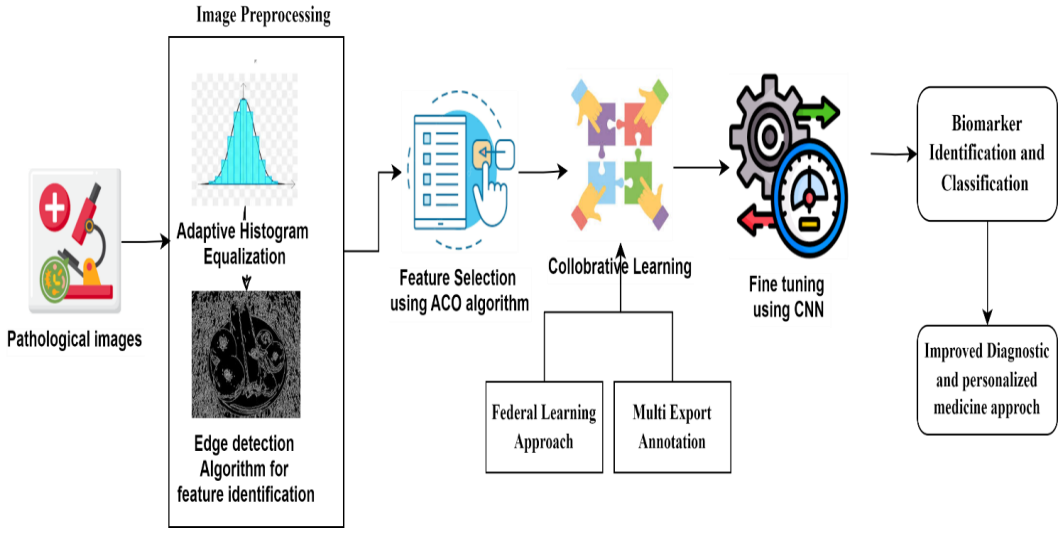

Fig.2. Working process of the proposed HHC-CNN-ACO method

Image Processing: The initial step is edge identification, a method for locating and emphasizing significant features and boundaries in diseased pictures. The boundaries of tissues, cellular structures, and areas of interest are some of the most important aspects of medical imaging, and these edges typically correlate to them. At the outset of the analysis, the system catches the most crucial details by improving these edges. An approach to improving contrast, AHE, is used in the images. To enhance the visibility of tiny details, AHE makes a contrast modification to certain image regions. For medical imaging, where even subtle changes in color or texture could reveal illness, this is of the utmost importance. These features stand out thanks to AHE's contrast enhancement, which improves feature recognition and analysis.

Feature Selection using ACO: Stochastic optimization approach An ant colony's natural foraging behaviours inspired ACO. An ant's capacity to utilize pheromone trails as an indirect interaction to determine the optimal route from the colony to food sources is fundamentally like the concept of ACO. ACO is employed to identify the most suitable biomarkers inside the image for feature selection. ACO is based on ants' ability to locate food by following pheromone trails. This system finds the most diagnostic set of features (biomarkers) by utilizing ACO, a heuristic optimization method, to navigate the massive

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picture feature space. This allows the system to quickly and easily detect the diagnostically important traits.

Collaborative Learning: To improve the system's accuracy and resilience, it employs federated learning, which allows multiple experts to work on the model independently. The data remains localized since federated training trains the algorithm across multiple remote nodes. The goal of this method is to safeguard private health information by combining the expertise of several experts. Along with user-generated content, the system takes expert annotations into account to enhance the model's ability to learn biomarker recognition and interpretation. Incorporating expert comments to obtain a more expansive and accurate recognition of the problem. This cooperative approach improves the model's performance and helps decrease biases that could arise from using just one annotation source.

Fine-tuning using CNN: After ACO applies its most relevant characteristics to the processed images, an ensemble of classifiers is used to improve them further. Use a collection of machine learning models to boost a system's efficiency. An ensemble of classifiers is utilised for more accurate and consistent biomarker categorization, wherein each classifier may concentrate on a distinct facet of the data. Despite the data's utility in medical imaging, the complexity and variety of the data make it unlikely that a single model could attain high accuracy. An image-processing subset of DL models, the CNN acts as the system's central processing unit (CPU). The CNN is adjusted by utilizing the enhanced and optimized data obtained from the ensemble of classifiers. To get optimal performance when analysing pathology images, it is necessary to fine-tune the CNN by adjusting its parameters. Here, it shows how well CNN can recognize different biomarkers and whether it can differentiate between them.

One of the strengths of the HHC-CNN-ACO system is the clarity and accuracy of the results it produces. The results of any diagnostic instrument are only as good as the doctor's ability to interpret and verify them. The system's design is to produce diagnostic results that emphasize and elucidate the biomarkers. The system's scalability is another significant feature since it processes big datasets and sick images. It is essential that the system be scalable so that it can be utilized in a diverse array of medical facilities, in hospitals large and small, and that it can be customized to screen for different types of diseases.

4. Result and discussion

By incorporating Collaborative learning, deep learning, and heuristic optimization into the enhanced preprocessing images, the HHC-CNN-ACO system achieves interpretable, scalable, and accurate results from pathological image analysis.

a) Experimental Setup

In this study, the HHC-CNN-ACO method is contrasted with more traditional methods. These methods include Deep Convolutional Neural Networks (CNNs) [13] for tumour nuclei verification and classification, MobileNet v2 CNN [16] for X-ray lung condition grouping, and Natural language processing (NLP) [14] methods for cognitive assessment extraction and harmonization from clinical narratives. The innovative HHC-CNN-ACO method is contrasted with the traditional methods using performance measures as sensitivity (recall), specificity, AUC-ROC, dice coefficient, or Jaccard index. The proposed HHC-CNN-ACO system outperformed numerous medical picture analysis methodologies in this

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comparison. It combines heuristic preprocessing, ACO, and collaborative learning. Section 3.1 describes the dataset.

b) Sensitivity (Recall) and Specificity:

A test or model's sensitivity, true positive rate, or recall is the percentage of real positive cases accurately identified. It can be calculated by the eq 1. Eq 2 provides Specificity, defined as the percentage of true negative cases accurately detected by the model or test.

$$Sensitivity = \frac{TP}{TP+FN} \quad \text{(Eq.1)}$$

$$Specificity = \frac{TN}{TN+FP} \quad \text{(Eq.2)}$$

where TN is the True Negatives as the quantity of healthy persons correctly recognized as healthy, the TP is to the True Positives as the quantity of sick people correctly identified as ill, and the FN refers to the False Negatives as the number of sick people wrongly recognized as healthy.

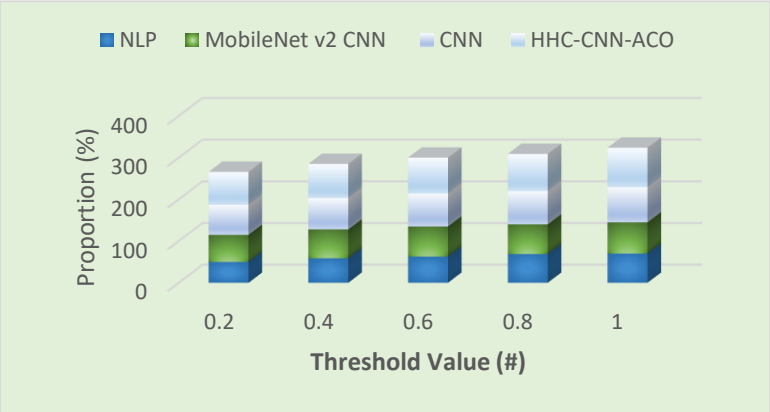

Fig.3. Sensitivity (Recall) and Specificity Analysis

Figure 3 compares the suggested and convolutional approaches to the Specificity and Sensitivity (Recall) measures. When the test's sensitivity is 100%, it detects all true positives. This means that every sick person gets a correct diagnosis. Because false negatives are expensive, applications requiring significant sensitivity are rare. One such application is screening for a life-threatening illness.

c) Area Under the Receiver Operating Characteristic Curve (AUC-ROC)

The AUC-ROC, or Area Under the Receiver Operating Characteristic Curve, is a crucial statistic for evaluating the accuracy of diagnostic tests in healthcare settings. The ROC curve can visually represent a diagnostic test's performance over a range of threshold levels. Eq 3 illustrates the True Positive Rate (TPR), a metric for the test's accuracy in detecting sick persons, and it shows how varying threshold values impact this rate. Eq 4 can compute the False Positive Rate (FPR), It assesses how often the test incorrectly evaluates healthy individuals as sick. A single scalar number that strikes a good balance between the test's sensitivity to detect illness and its specificity for recognizing the absence of disease demonstrates that it can differentiate between healthy and sick individuals. AUC-ROC measures can differentiate the patients between disease-positive and disease-negative.

$$TPR = \frac{TP}{TP+FN} \quad \text{(Eq.3)}$$

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$$FPR = \frac{FP}{FP+TN} \quad \text{(Eq.4)}$$

where TP is the number of sick people correctly identified as sick, TN alludes to the number of healthy persons whose health status was accurately reported, FP refers to the percentage of healthy individuals falsely diagnosed as ill, and FN refers to the incidence of false positives for health status among unwell individuals.

Figure 4 shows the comparative analysis of the AUC-ROC metric for the conventional and proposed HHC-CNN-ACO methods.

d) Dice Coefficient or Jaccard Index

The Jaccard Index and the Dice Coefficient are crucial for evaluating picture segmentation accuracy in medical imaging. These metrics compare the algorithm's predicted segmentation to the real ground truth provided by medical experts to determine how well an algorithm finds and locates abnormalities like tumours, organs, or lesions.

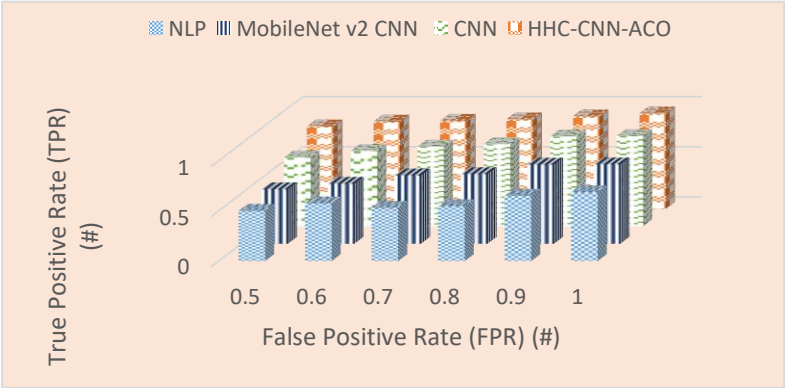

Fig.4. AUC-ROC Analysis

In the segmentation of medical images, the Dice Coefficient DC evaluates the degree to which the expected segmentation matches the actual data. It is commonly used for evaluating medical image processing tasks such as tumour boundary recognition. Eq 5 yields it.

$$DC = \frac{2\times|x\cap y|}{|x|+|y|} \quad \text{(Eq.5)}$$

where $|x \cap y|$ stands for the region where the predicted and real segmentation overlapper and $|x| + |y|$ denotes the dimensions of the actual and projected regions.

Another metric used to evaluate the precision of medical picture segmentation is the Jaccard Index or Intersection over Union (IoU). It verifies whether the cancer or organ in inquiry matches the predicted segmentation. It is deduced from eq 6.

$$JI = \frac{x\cap y}{x\cup y} \quad \text{(Eq.6)}$$

where $x \cap y$ is the surface area covered by the actual and predicted segmentation, and $x \cup y$ is the region where the two sets of segmentations overlap. Equation 7 can integrate these two.

$$DC = \frac{2\times JI}{1+JI} \quad \text{(Eq.7)}$$

Figure 5 shows the comparative analysis of the Dice Coefficient or Jaccard Index metrics for the proposed and conventional methods. The high value of these metrics using

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the proposed method indicates precise diagnosis, treatment planning, and patient monitoring. By offering clear and measurable insights into the effectiveness of different segmentation algorithms in reliably identifying regions of interest within medical pictures, these measures allow doctors and researchers to evaluate algorithms.

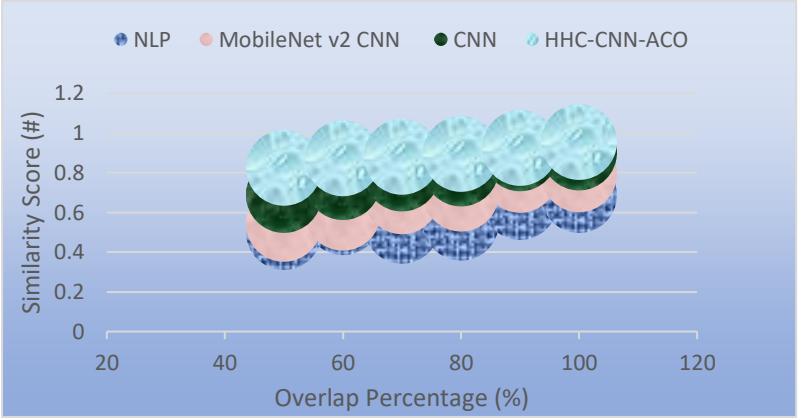

Fig.5. Dice Coefficient or Jaccard Index Analysis

5. Conclusion

The HHC-CNN-ACO framework has made significant progress in pathological image processing for biomarker identification and interpretation. This approach adapts to small differences in tissue architecture and biomarker expression, tackles the absence of annotated data, and combines heuristic-based preprocessing with Ant Colony Optimization and collaborative learning. An ensemble of classifiers is used to fine-tune the core CNN, and the framework's strength is in its multi-faceted approach, involving improved feature recognition with edge detection and Adaptive Histogram Equalization, optimized feature selection with ACO, privacy-preserving collaborative learning with federated learning, and more. The experimental results show that compared to other biomarker identification and classification methods, the HHC-CNN-ACO is the most accurate and easy to understand. This advancement could completely transform the way pathologists and other medical professionals assess, diagnose, and handle illnesses; it has far-reaching consequences for early detection and tailored treatment across many medical domains. As a result of the system's accurate, scalable, and explicable pathological image analysis solution, diagnostic results are improved and tailored therapy is advanced. Future work could aim to improve the system's interpretability, diversify datasets, and test its effectiveness in real-world scenarios through clinical trials, while still addressing computational complexity as a limitation.

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