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RESEARCH ARTICLE

An Integrated Framework for Early Differential Diagnosis of COVID-19 using Improved Fuzzy Cognitive Map Approaches

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Abstract

Background/Objectives: The COVID-19 pandemic has created an urgent need for rapid and accurate diagnosis to facilitate timely treatment and control spread. However, the initial symptoms can be non-specific, making early differential diagnosis challenging. **Methods:** This study proposes an integrated framework for COVID-19 diagnosis using improved Fuzzy Cognitive Map (FCM) approach for fast, intelligent screening of COVID-19 cases versus other respiratory conditions based on risk factors and clinical presentation. The integrated framework is designed based on combining fuzzy cognitive maps with different classifiers separately such as Random Forest (RF) classifier, Gradient Boosting (GB) classifier and Weighted Decision Tree (WDT) approach to model interrelationships between indicative symptoms and risk factors in COVID-19. The model is evaluated on a real time COVID-19 dataset of 600 patient details (i.e., 520 non-covid and 80 Covid). Due to the unbalanced nature of class labels, this work is evaluated based on balanced accuracy and Matthews's correlation coefficient to identify the appropriate model. **Findings:** Among the different combination of classifiers FCM-RF attains 95.91% which outperforms 15.14%, 5.05% and 7.69% higher than normal FCM, FCM-GB and FCM-WDT. **Novelty:** The interpretability of the fuzzy map supplemented by the high predictive performance of random forest provides an effective decision support system for frontline healthcare workers to make quick, reliable screening decisions and ensure optimal care pathways. The integrated approach demonstrates the potential of computational intelligence in addressing critical diagnosis challenges within complex, urgent medical scenarios.

Keywords: COVID-19; Ensemble Approach; Improved fuzzy cognitive maps; Balanced accuracy; Clinical dataset

1 Introduction

COVID-19, caused by the highly contagious SARS-CoV-2 virus, has rapidly spread globally, resulting in over 450 million cases and 6 million deaths as of March 2023 [1]. Timely and accurate diagnosis is critical to reduce COVID-19 severity and prevent fatalities. However, no single diagnostic test is 100% accurate, and traditional methods like RT-PCR testing, rapid antigen testing, and radiographic imaging have limitations such as long turnaround times, false negatives, and difficulty handling complex interdependencies [2]. Initially, several clinical and diagnostic methods were developed for COVID-19 disease include molecular approaches like RT-PCR for detecting viral genome markers [3], serological testing, laboratory devices, radiology detection, and viral cell cultures [4]. Rapid antigen/antibody tests and serological assays have also been developed for accurate detection of SARS-CoV-2 [5]. However, the accuracy of these clinical diagnostic tests is not guaranteed, and alternate tests are often necessary to confirm sensitivity and specificity. Additionally, factors such as the establishment of well-equipped laboratories, expensive testing machines, travel time to competent laboratories, and the scarcity of qualified medical personnel can impact the results and lead to potential false negatives.

To address these limitations, researchers have turned to innovative computational techniques combining cognitive modeling and optimization algorithms to improve diagnostic accuracy [6]. Several studies have demonstrated the efficacy of deep convolutional neural networks combined with classifiers like Support Vector Machines (SVM) for multi-class classification of COVID-19 from chest X-ray [7] and CT scan images [8], achieving accuracies exceeding 98% and outperforming other approaches. Other works have focused on optimizing model hyperparameters and feature selection using novel metaheuristic algorithms like Binary Sparrow Search for COVID-19 patient data classification, resulting in improved performance over unoptimized versions [9]. Hybrid models combining techniques like Sparger Wolf Hawk Optimization with deep neural networks have also shown promise for COVID-19 assessment [10]. For text data, weighting schemes have been employed to extract informative features from clinical notes for COVID-19 identification and mortality prediction [11]. Deep learning methods have effectively utilized both image and text data, proving superior to classical machine learning techniques. Additionally, Computer Aided Design (CAD) systems have been developed, implementing phases like segmentation, clustering, and visualization for automated CT scan COVID-19 screening [12].

However, most studies in the literature have focused on computational approaches using Computed Tomography (CT) images and X-ray images, with Deep Neural Networks being the most commonly used classifier [13]. These image-based approaches may not be suitable for early diagnosis of mild COVID-19 cases, where symptoms overlap with other respiratory diseases like influenza, pneumonia, and tuberculosis [14]. Furthermore, the computational models primarily focus on chest X-ray image data for COVID-19 diagnosis, neglecting other symptoms like fever, cough, and fatigue. These models are ineffective in the early stages of infection, as chest X-ray images may not accurately predict symptoms. No studies have explored the use of intelligence-based classifiers or combinations thereof for COVID-19 diagnosis using non-image-based datasets, including clinical symptoms and laboratory results.

There is a need for an integrated approach that leverages the strengths of both cognitive modeling and optimization algorithms to model complex diagnostic relationships and accurately classify COVID-19 from other respiratory conditions using non-image-based datasets. By incorporating clinical symptoms and laboratory results, such an approach could enable early detection, appropriate triage, and better patient outcomes [15].

The motivation of this study is to address the limitations of existing image-based approaches for COVID-19 diagnosis by developing an integrated approach that incorporates clinical symptoms and laboratory results. By leveraging the strengths of cognitive modeling and optimization algorithms [16], the proposed approach aims to model complex diagnostic relationships and accurately classify COVID-19 from other respiratory conditions, enabling early detection, appropriate triage, and better patient outcomes. The specific objective of this work is to carry out a controlled experiment using intelligence-based classifiers – Fuzzy Cognitive Maps (FCM), FCM with Random Forest (FCM-RF), FCM with Gradient Boosting (FCM-GB), and FCM with Weighted Decision Trees (FCM-WDT) – for early COVID-19 identification using clinical symptoms and laboratory results. The major area of application of this work is early diagnosis of COVID-19 using non-image-based datasets, including clinical symptoms and laboratory results. This approach aims to improve diagnostic accuracy and enable timely intervention, especially in cases of mild COVID-19 infections with non-specific symptoms. This work attempts to solve the following research questions:

RQ1: Which hybrid classifier approach performs better prediction rate for COVID-19 diagnosis?

RQ2: How accurately do the chosen classifiers for COVID-19 differential diagnosis perform in terms of metrics such as accuracy, precision, recall, F-measure, Matthews Correlation Coefficient, and balanced accuracy?

By addressing these research questions, this study aims to contribute to the existing state-of-the-art approaches by providing a comprehensive analysis and evaluation of intelligence-based classifiers for early COVID-19 diagnosis using non-image-based datasets. The integrated approach, combining cognitive modeling and optimization algorithms, is designed to leverage the strengths of both techniques to model complex diagnostic relationships and accurately classify COVID-19 from other

respiratory conditions. Improving diagnostic accuracy and efficiency can enable early detection, appropriate triage, and better patient outcomes, ultimately contributing to more effective management of COVID-19 and similar respiratory diseases.

2 Methodology

This section discusses the approaches used in this work, dataset description and the performance evaluation metrics.

2.1 Approaches

This section discusses in detail about the random forest, gradient boosting approach, weighted decision tree and fuzzy cognitive maps used for COVID-19 diagnosis.

(i) Random Forest

A random forest is a machine learning method for classification and regression, using ensemble learning to solve complex problems[17]. It uses decision trees and bagging to train a forest, increasing accuracy through bagging. The algorithm determines the result by averaging or averaging out different trees, with accuracy growing as the number of trees increases.

Bagging: Training set for kth tree:
Xk = {x1k, x2k,...,xnk} sampled with replacement from original training set X
Tree training:
hk(x) = learned tree prediction model for training set Xk
Forest prediction:
For classification:
$\hat{y}$ = majority vote {$\hat{h}$1(x), $\hat{h}$2(x),..., $\hat{h}$K(x)}
For regression:
$\hat{y} = (1/K) \sum \hat{h}k(x)$
Gini impurity:
$G = 1 - \sum pi2$
Where pi is proportion of class i samples at a node
Information gain:
Gain(T,f) = Impurity(Parent node T) - $\sum \sigma$i Impurity(Child node Ti)
Where f is the feature Split, σi is proportion of samples in child node i

(ii) Gradient Boost

Gradient boosting is an advanced method of boosting that turns several weak learners into strong learners[18]. Gradient descent is used to train each new model in this process to minimize the loss function of the previous model, which could mean squared error or cross-entropy. A boosting method would be gradient boosting. Each time a new weak model is trained, the technique computes the gradient of the loss function with respect to the predictions made by the current ensemble. The cycle continues until the gradient is decreased. Then, until a stopping requirement is met, the method is repeated as often as necessary, adding the new model's predictions to the ensemble each time.

$$f_m = f_{m-1} - \rho mgm \tag{1}$$

(iii) Weighted Decision Tree

The Decision Tree (Weight-Based) approach is a nested approach that creates attribute weights from the COVID - 19 dataset[19], applying this approach requires a rudimentary understanding of subprocesses. Instead of the information gain or gain ratio criteria, the Decision Tree (Weight-Based) approach uses an arbitrary attribute relevance test criterion.

(iv) Fuzzy Cognitive Maps

Fuzzy cognitive maps (FCMs) can model complex interrelationships between clinical variables using graphs with weighted nodes and edges[20]. For COVID-19 diagnosis, FCMs can connect symptom, risk and test nodes to outcome nodes signaling likelihood of COVID-19 infection. Edge weights represent the strength of influence between nodes based on symptom patterns in patient data. Appropriate training tunes the edge weights so the FCM mimics real clinical outcomes. A new patient's symptoms can then be input to the trained FCM to predict the likelihood of COVID-19 vs other respiratory diseases[21]. FCMs leverage their network structure and training to capture nuanced symptom interactions for accurate COVID-19 screening and diagnosis from presenting signs[22].

The FCM activation function is:

$$state\_i(t+1) = 1 / (1 + exp(-net\_input\_i(t))) \tag{2}$$

Where:

1. The net input for a concept is calculated as:
net_input_i(t) = Σ(weight_i,j * state_j(t)) for j in range(num_concepts)
2. The state of each concept is updated iteratively:
For each concept i in FCM:
state_i(t+1) = activation_function(net_input_i(t))
3. Convergence is checked as:
convergence = Σ(|state_i(t+1) - state_i(t)|) < convergence_threshold for i in range(num_concepts)
4. State_i(t) is the state or activation level of concept i at time t.
5. Weight_i,j is the weight between concept i and concept j in the FCM.
6. Activation_function maps the net input to the activation level of a concept.
7. Convergence-threshold is a predefined threshold to check for convergence.

2.2 Data Set Description

The data are obtained from [23] which contain 600 patient details having 18 features each. The dataset has 520 non covid findings and 80 are COVID-19 patient details. The detailed description of dataset is given in Table 1.

Table 1. Dataset Description

Variable	Description	Measured Values (Units)
C1: Patient age	Age of the patient	Numeric value (years)
C2: Hematocrit	Percentage of red blood cells in the total blood volume	Numeric value (%)
C3: Hemoglobin	Amount of hemoglobin in the blood	Numeric value (g/dL)
C4: Platelets	Number of platelets in the blood	Numeric value (10^9/L)
C5: Red blood Cells	Number of red blood cells per unit volume of blood	Numeric value (10^12/L)
C6: Lymphocytes	Percentage of lymphocytes in the total white blood cells	Numeric value (%)
C7: Leukocytes	Number of white blood cells in the blood	Numeric value (10^9/L)
C8: Eosinophils	Percentage of eosinophils in the total white blood cells	Numeric value (%)
C9: Monocytes	Percentage of monocytes in the total white blood cells	Numeric value (%)
C10: Neutrophils	Percentage of neutrophils in the total white blood cells	Numeric value (%)
C11: C Reactive Protein	Level of C-reactive protein	Numeric value (mg/dL)
C12: Decision	COVID-19 Stage	Low, Moderate, High

2.3 Performance Evaluation Measures

In this work, the metrics chosen for evaluating the performance of the proposed approaches are sensitivity, specificity, Matthews's correlation coefficient, F1 score, and balanced accuracy. As stated in much of the literature, calculating normal accuracy is not suitable for class imbalance problems. So, in this work, we calculate balanced accuracy [24] which gives the exact performance of the classifier on imbalanced data. Additionally, the Matthews correlation coefficient is used in many research works to calculate classifier performance, especially in disease diagnosis [25]. The detailed explanation of these metrics are as follows:

2.3.1 Specificity

Specificity is a metric that assesses the proportion of correctly detected negatives out of the total number of negative predictions a model can make. It is also referred to as the true negative rate.

$$Specificity = TN / (TN + FP) \tag{3}$$

2.3.2 Sensitivity

Sensitivity is a metric that measures the proportion of actual positives a model correctly predicts out of all positive predictions it can make. It is also known as the true positive rate or recall.

$$Sensitivity = TP / (TP + FN) \tag{4}$$

2.3.3 Matthews Correlation coefficient

The Matthews correlation coefficient (MCC) is a reliable statistical measure that produces high scores only if a model achieves good results across all four confusion matrix categories (true positives, false negatives, true negatives, false positives) in proportion to the positive and negative elements in the dataset. The MCC values range from -1 to +1.

$$MCC = TN\,x\,TP - FN\,x\,FP/\sqrt{(TP+FP)(TP+FN)(TN+FP)(TN+FN)} \quad (3)$$

2.3.4 F1 Score

The F1-score balances precision and recall. It is commonly used when there is class imbalance but can also quantify the accuracy of an individual test.

$$F1 = 2 * ([precision * recall] / [precision + recall]) \quad (5)$$

2.3.5 Balanced Accuracy

Balanced accuracy is the arithmetic mean of sensitivity and specificity. It is used with imbalanced datasets where one target class is much more frequent than the other.

$$Balanced\,accuracy = (Sensitivity + Specificity) / 2 \quad (6)$$

2.4 Integrated FCM-RF approach for COVID-19 diagnosis

This section discusses the proposed Integrated FCM-RF approach for COVID-19 diagnosis. The first step is to create fuzzy rules based on the expert's suggestion. After this next section discusses how the fuzzy cognitive maps integrated with random forest approach to diagnose COVID-19 effectively. The overall architecture of proposed approach diagrammatically represented in Figure 1.

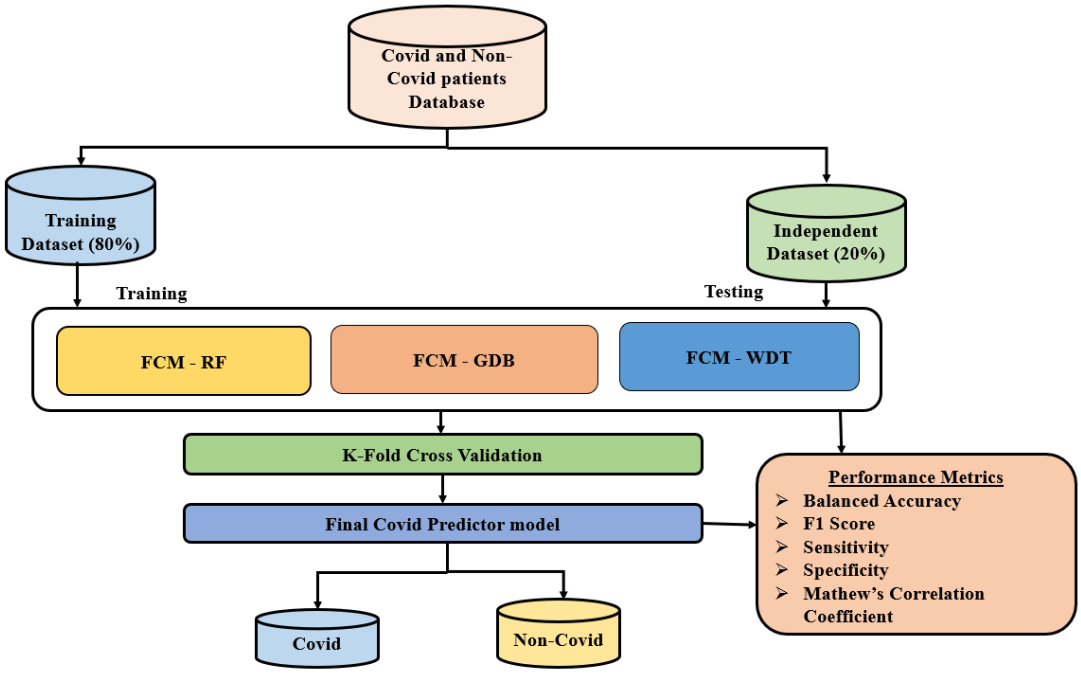

Fig 1. Overall architecture of Proposed System

2.4.1 Expert suggestion and rule creation

The first critical step in developing the COVID-19 diagnosis model was to select the important factors for future analysis. To assess the degree of connection between various elements and the decision idea, medical specialists were consulted.

A correlation analysis was also performed on the data to determine the most influential components in the diagnosing process. Previous studies were also considered for determining the most critical parameters, for example, stating that the best diagnostic results were obtained by taking into account characteristics such as patient age, hemoglobin, lymphocytes, leukocytes, neutrophils, and C Reactive Protein. These variables were discovered to have a substantial influence on COVID-19 diagnosis accuracy. Factors such as monocytes and hematocrit, on the other hand, had a low connection and were therefore excluded from the model. In addition to the choice idea, twelve elements were chosen for the creation of the COVID-19 diagnosis model. Experts are important in constructing the weight matrix since they have useful knowledge about the interdependencies between concepts. They contribute by using rules to define the links between concepts. These rules are then turned into precise weights using linguistic notions in a process known as defuzzification. To guarantee a thorough investigation, three experts were interviewed individually to characterize the relationships between concepts using If-Then logic. This method provided for a wide range of expert viewpoints. The methodologies used in this procedure are as follows:

First Expert: If there is a small change in C Reactive Protein (C11), then there is a moderate change in the Decision (C12).
It means: The influence from C11 to C12 is positively moderate.

Second Expert: If there is a small change in C Reactive Protein (C11), then there is a high change in the Decision (C12).
It means: The influence from C11 to C12 is positively high.

Third Expert: If there is a small change in C Reactive Protein (C11), then there is a very high change in the Decision (C12).
It means: The influence from C11 to C12 is positively very high.

To diagnose COVID-19, a comprehensive dataset of clinical and laboratory parameters is required. The dataset should contain diagnostic labels matching the clinical presentations and lab findings. Various preprocessing techniques are applied on the dataset including handling missing values, encoding categorical variables, and scaling numerical features. A Fuzzy Cognitive Map (FCM) model is then constructed to capture the complex interrelationships between the input features and output diagnosis labels. This model is represented clearly in the Figure 2. The FCM contains nodes representing input attributes like fever, cough etc. It also has output nodes corresponding to diagnostic labels like COVID-19 positive or negative. Fuzzy membership functions allow the nodes to take on continuous values between 0 and 1 at any time. Fuzzy rules encode meaningful correlations between the feature and diagnosis nodes based on clinical expertise or data-driven methods. The weight matrix was extracted from the dataset using the Hebbian Learning algorithm with sigmoid function. The FCM model's inference function parameters were used to scale the column values in the [0, 1] range of the imported data frame with the data and weight matrix. Thus, 480 records were used to train the weight matrix and 120 to test class imbalance. The inference results are stored in an array named fcm.inferences with 10 to 100 iterations separately. These results were compared to test data labels.

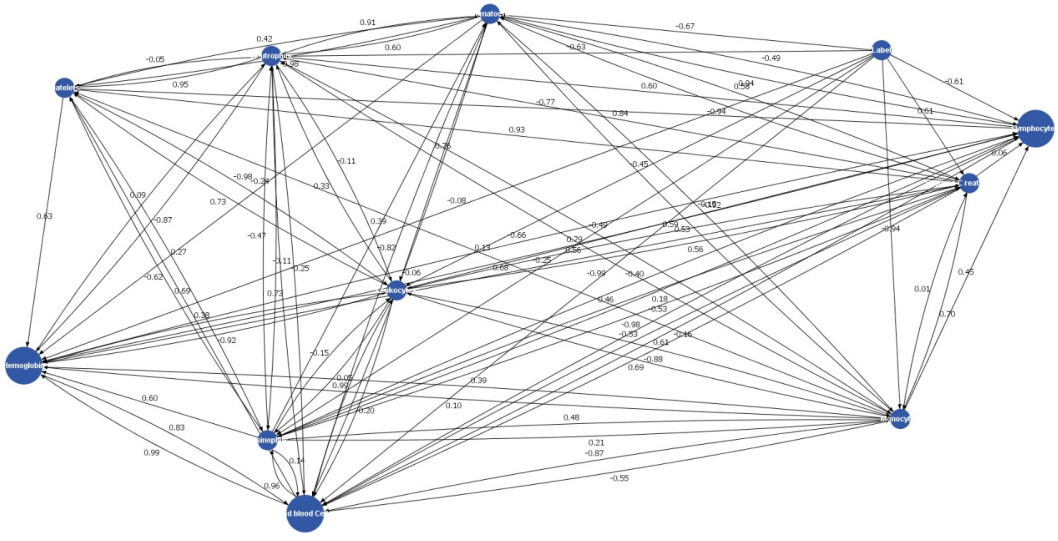

Fig 2. FCM Graphical Representation

For example, "IF fever is high AND cough is persistent, THEN COVID-19 test is likely positive". In parallel, a Random Forest classifier model is trained on the preprocessed dataset, using the diagnosis labels as targets and features as predictors for supervised learning. This enables the model to learn non-linear relationships between features for reliable classification. For a

new case, the feature values are passed through the FCM, which applies fuzzy rules to propagate values and obtain intermediate fuzzy outputs for the diagnosis nodes. These outputs are fed as inputs to the trained Random Forest model for final COVID-19 prediction. The integrated FCM-RF pipeline is evaluated on metrics like accuracy, sensitivity, and specificity. It is validated on new datasets for robustness. The fuzzy rules and Random Forest hyperparameters are tuned for optimal performance. Finally, the interpretable FCM integrated with the accurate Random Forest model is deployed for automated COVID-19 screening using clinical features.

There are a few reasons why mixing Fuzzy Cognitive Maps (FCMs) and Random Forest models might give better results than using either method alone: The hybrid model uses the fact that the FCM is easy to understand and the accuracy of the Random Forest. The FCM is easy to understand because it models the relationships between variables. Random forest makes predictions that are very correct. Together, they are better than either one alone. FCM lets you use expert knowledge: fuzzy rules in FCM can store domain experience and clinical insights on COVID-19 diagnosis. This information adds to the Random Forest model, which is based on facts. FCMs can show links and dependencies between symptoms and diagnoses that don't follow a straight line. This is better at handling complications. Customization is possible with a two-stage method because the FCM transformation of inputs can be tuned separately from the Random Forest model training. Each part can be changed to your liking. When techniques work together, they make up for each other's flaws. For example, FCMs are less accurate on their own. Random forests can be too good at fitting and not clear enough. The hybrid method makes up for the flaws. Validation of real-world performance is needed. Theoretically, combining FCM and Random Forest seems like a good idea, but it will take a lot of testing on different clinical datasets to prove that it works better in the real world.

Pseudocode:

// Data Collection and Preprocessing
1. Collect dataset with clinical and laboratory features for COVID-19 diagnosis.
2. Preprocess the dataset (cleaning, handling missing values, feature scaling, etc.).
// FCM Construction
3. Define FCM structure with input nodes for features and output nodes for diagnosis.
4. Determine fuzzy membership functions for each node.
5. Establish fuzzy rules based on expert knowledge or data-driven approaches.
6. Create FCM by connecting nodes and assigning fuzzy rules.
// Model Tuning
7. Split the dataset into training and testing sets.
8. Perform feature selection if necessary.
9. Train models using training dataset and corresponding diagnosis labels.
// Integration of FCM and Classifiers RF, WDT and GB
10. Pass input feature values through FCM to obtain intermediate values for the output node.
11. Feed intermediate values into trained classifier models for final diagnosis prediction.
// Evaluation
12. Evaluate performance using appropriate metrics (balanced accuracy, sensitivity, specificity, MCC, F1 Score.
// Validation and Optimization
13. Validate framework on independent dataset for generalization evaluation.
14. Optimize framework parameters (e.g., FCM weights, Random Forest, Gradient Boosting and Weighted Decision Tree hyperparameters) if necessary.
// Deployment
15. Deploy the integrated framework as a reliable tool for COVID-19 diagnosis.

In a similar way instead of the RF approach, GB and WDT are replaced, and the performance is calculated. Among the approaches which have highest balanced accuracy will be taken for further modeling. The above pseudocode is implemented in this proposed work with MATLAB software.

3 Results and Discussion

This section discusses the answers of two research questions RQ1 and RQ2 mentioned in introduction section.

3.1 Performance comparison of classifiers

The data present the model performance in terms of prediction performance for four different models: FCM, FCM-RF, FCM-GB, and FCM-WDT, across a range of different iteration counts is diagrammatically represented in Figure 3. The FCM has

the worst performance to begin with but gradually improves as the number of iterations increases, reaching 84.74 after 100 iterations. The FCM-RF and FCM-GB offer the best beginning performance, but their results gradually deteriorate as the algorithm is iterated. At 100 iterations, FCM-RF suffers the greatest drop in quality, falling to 95.67. Performance-wise, FCM-WDT falls somewhere in the middle. It gets better with each subsequent iteration, though not quite as quickly as FCM does. In all models, the most substantial changes in performance are observed in the first 30–50 iterations of the process. After that, there is an equilibrium in performance. The FCM earns the greatest final value of 84.74 after being run through 100 iterations, making it the model that performs the best overall. In contrast, the performance of FCM-RF and FCM-GB deteriorates when more iterations are applied. In conclusion, the FCM is the only model that continues to get better with additional iterations, whereas the others reach their peak early on and then start to decline significantly. If enough iterations are performed, the FCM is the optimal model to use.

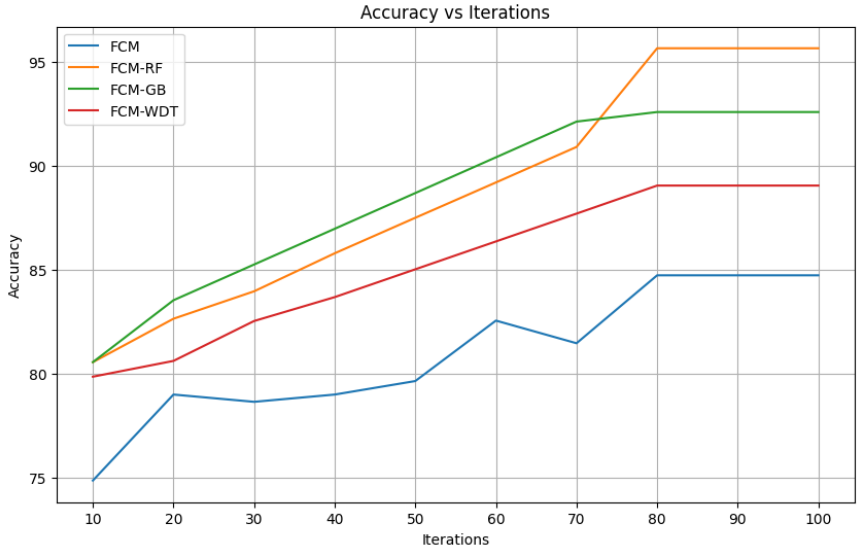

Fig 3. Prediction Accuracy

The data shows model performance in terms of error rate across different iteration counts for 4 models - FCM, FCM-RF, FCM-GB and FCM-WDT is diagrammatically represented in Figure 4. FCM starts off with the worst performance but improves slowly and steadily as iterations increase, ending with a value of 15.26 at 100 iterations. FCM-RF and FCM-GB have the best initial performance but improve rapidly in early iterations before plateauing in later iterations. FCM-RF levels off earliest at around 10 iterations. FCM-WDT has performance in between FCM and the other models. It improves steadily across iterations but not as quickly as FCM-RF/FCM-GB. The most dramatic performance improvements are seen in the first 20-40 iterations for all models. After this the rate of improvement decreases. The overall best performing model is FCM-RF which achieves the lowest final value of 4.33 at 100 iterations. FCM-GB is comparable at 7.40. In summary, iterative training leads to substantial performance gains in early iterations for all models, but with diminishing returns later on. FCM-RF is the overall best performing model given sufficient iterations.

3.2 Training Results and Testing Results

The Table 2 compares COVID-19 diagnosis categorization performance parameters for FCM, FCM-RF, FCM-GB, and FCM-WDT. FCM-RF has the highest sensitivity at 0.9760, followed by FCM-GB at 0.9615. FCM-RF accurately identifies the most COVID-19 positive cases, although FCM has the lowest sensitivity. FCM-RF again has the highest specificity at 0.9375, surpassing FCM's 0.7813. FCM-RF has the fewest false positives. FCM-RF has better balanced accuracy (sensitivity and specificity) at 0.9567 than FCM at 0.8474. Matthews Correlation Coefficient (MCC) accounts for all confusion matrix results. FCM-RF's maximum MCC is 0.8798, far above FCM's 0.6158. Finally, FCM-RF scores 0.9831 versus 0.9383 for FCM's F1. FCM-RF performs best across all evaluation measures, proving the hybrid model's COVID-19 diagnosis efficacy. FCM + Random Forest enhances diagnosis accuracy, precision, and dependability. The FCM-RF technique is predictive, according to the data.

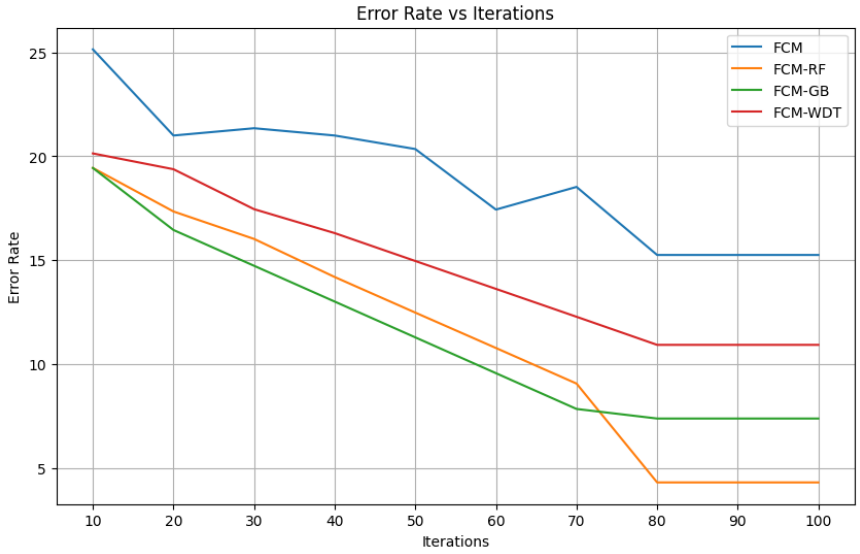

Fig 4. Error Rate

Table 2. Training Performance

Performance Metrics	FCM	FCM-RF	FCM-GB	FCM-WDT
Sensitivity	0.9135	0.9760	0.9615	0.9375
Specificity	0.7813	0.9375	0.8906	0.8438
Balanced Accuracy	0.8474	0.9567	0.9260	0.8906
MCC	0.6158	0.8798	0.8067	0.712
F1 Score	0.9383	0.9831	0.9721	0.9559

The Table 3 compares performance metrics for four models - FCM, FCM-RF, FCM-GB, and FCM-WDT on a COVID-19 diagnosis classification task. Looking at sensitivity, FCM-RF achieves the highest score of 0.9808, followed closely by FCM-WDT at 0.9519. This implies FCM-RF correctly identifies the greatest number of positive COVID-19 cases, while FCM alone has the lowest sensitivity. For specificity, FCM-RF again scores the best at 0.9375, significantly higher than FCM's 0.75. So FCM-RF makes the least false positive errors. In terms of balanced accuracy, which balances sensitivity and specificity, FCM-RF is superior at 0.9591 balance. FCM is much lower at 0.8077 balance. The Matthews correlation coefficient (MCC) accounts for all confusion matrix outcomes. Again, FCM-RF obtains the highest MCC of 0.8952, greatly exceeding FCM's 0.5078. Finally, for the F1 score, FCM-RF achieves the maximum score of 0.9855, compared to just 0.9091 for FCM. In summary, FCM-RF obtains the best performance across all evaluation metrics signifying the hybrid model's effectiveness for COVID-19 diagnosis. The integration of FCM with Random Forest improves diagnosis accuracy, precision and reliability compared to using only FCM. The findings highlight the predictive power of the proposed FCM-RF approach.

Table 3. Testing Performance

Performance Metrics	FCM	FCM-RF	FCM-GB	FCM-WDT
Sensitivity	0.8654	0.9808	0.9423	0.9519
Specificity	0.7500	0.9375	0.8750	0.8125
Balanced Accuracy	0.8077	**0.9591**	0.9086	0.8822
MCC	0.5078	0.8952	0.7455	0.6950
F1 Score	0.9091	0.9855	0.9608	0.9212

The FCM-RF outperforms predicted in every parameter on the training set: F1 score of 0.9855, top sensitivity of 0.9808, top specificity of 0.9375, balanced accuracy of 0.9591, and MCC of 0.8952. It accurately identifies COVID-19 cases with little false positives. FCM-RF continues to have the highest sensitivity (0.9760), specificity (0.9375), balanced accuracy (0.9567), MCC

(0.8798), and F1 score (0.9831) on the untested testing set. The persistent high performance of FCM-RF from training to testing shows its durability and generalization capabilities. The much weaker outcomes of FCM and Random Forest demonstrate its benefits. The fact that measurements scarcely changed from training to testing suggests that FCM-RF works effectively with new data. Its excellent training plan passes real-world testing. In conclusion, FCM-RF's excellent training and testing results support its COVID-19 prediction ability. The results show that Random Forest enhances FCM accuracy, precision, and reliability.

3.3 Comparison with existing state of the art approaches

In this section, we provide a comprehensive comparative analysis of our proposed integrated framework for early differential diagnosis of COVID-19 with existing methods and approaches reported in the literature. This analysis aims to clearly demonstrate the unique features and contributions of our work, as well as its advantages over previous studies.

Several existing studies have explored various methods for COVID-19 diagnosis, including machine learning techniques, deep learning models, and traditional statistical approaches. However, most of these works have focused on either clinical data or radiological data in isolation, failing to leverage the complementary information provided by both sources.

For instance, [(12)] have utilized machine learning algorithms or deep learning models to analyze chest X-ray or CT scan images for COVID-19 detection. While these approaches have shown promising results, they do not incorporate clinical data, which can provide valuable insights into the patient's symptoms, medical history, and risk factors. On the other hand, studies such as [(14)] have employed statistical models or machine learning techniques to analyze clinical data, including symptoms, demographic information, and radiological data, for COVID-19 diagnosis. However, these methods failed to consider laboratory test results which can reveal crucial information about the disease's manifestation and progression in the lungs.

From the analysis of comparison between training, testing and comparison between existing state-of-the art approaches the proposed integrated framework addresses the limitations of existing approaches by combining clinical and laboratory data, leveraging the strengths of improved fuzzy cognitive maps with machine learning algorithms. The key unique features and contributions of our work are as follows:

1. Integrated Approach: Our framework is one of the first to integrate clinical and laboratory data for early differential diagnosis of COVID-19, providing a more comprehensive and holistic perspective on the disease.
2. Improved Fuzzy Cognitive Maps: We have developed a novel variant of the fuzzy cognitive map approach, tailored specifically for the COVID-19 diagnosis problem. Our improved algorithm incorporates domain knowledge and expert insights, enabling more accurate modelling of the intricate relationships between symptoms, risk factors, and diagnostic indicators.
3. Interpretability and Explainability: Unlike many existing approaches that lack transparency, our framework prioritizes interpretability and explainability, ensuring that healthcare professionals can understand and trust the decision-making process.

4 Conclusion and Future directions

The proposed integrated framework combines fuzzy cognitive mapping with classifiers such as random forest to achieve rapid, accurate screening for COVID-19 relative to other respiratory conditions based on clinical features. The FCM-RF model obtains balanced accuracy of 95.91%, outperforming FCM, FCM-GB, and FCM-WDT by greater than 15%, 5%, and 7%, respectively. The integration of interpretable FCMs with high-precision random forests yields an efficient decision support system for COVID-19 diagnosis in the frontline. The framework highlights the potential for computational intelligence techniques to resolve diagnostic difficulties in emergency medical situations. While the results are encouraging, further improvements in computational efficiency and accuracy could help improve clinical applicability. It would be advantageous to test the framework on larger, more heterogeneous patient datasets and implement it with optimization techniques such as quantum annealing. Exploring alternative cognitive models and classifiers may provide additional benefits. Overall, the integrated approach demonstrates a diagnostic framework that is highly flexible and merits further research and development.

References

1) Hillary VE, Ceasar SA. An update on COVID-19: SARS-CoV-2 variants, antiviral drugs, and vaccines. *Heliyon*. 2023;9(3):1–25. Available from: https://doi.org/10.1016/j.heliyon.2023.e13952.
2) Battaglini D, Lopes-Pacheco M, Castro-Faria-Neto HC, Pelosi P, Rocco PRM. Laboratory Biomarkers for Diagnosis and Prognosis in COVID-19. *Frontiers in Immunology*. 2022;13:1–11. Available from: https://dx.doi.org/10.3389/fimmu.2022.857573.

3) Chu VT, Schwartz NG, Donnelly MAP, Chuey MR, Soto R, Yousaf AR, et al. Comparison of Home Antigen Testing With RT-PCR and Viral Culture During the Course of SARS-CoV-2 Infection. *JAMA Internal Medicine*. 2022;182(7):701–709. Available from: https://dx.doi.org/10.1001/jamainternmed.2022.1827.
4) Pu R, Liu S, Ren X, Shi D, Ba Y, Huo Y, et al. The screening value of RT-LAMP and RT-PCR in the diagnosis of COVID-19: systematic review and meta-analysis. *Journal of Virological Methods*. 2022;300:1–9. Available from: https://dx.doi.org/10.1016/j.jviromet.2021.114392.
5) Rivera-Olivero IA, Henríquez-Trujillo AR, Kyriakidis NC, Ortiz-Prado E, Laglaguano JC, Vallejo-Janeta AP, et al. Diagnostic Performance of Seven Commercial COVID-19 Serology Tests Available in South America. *Frontiers in Cellular and Infection Microbiology*. 2022;12:1–6. Available from: https://dx.doi.org/10.3389/fcimb.2022.787987.
6) Samee NA, El-Kenawy ESM, Atteia G, Jamjoom MM, Ibrahim A, Abdelhamid AA, et al. Metaheuristic Optimization Through Deep Learning Classification of COVID-19 in Chest X-Ray Images. *Computers, Materials & Continua*. 2022;73(2):4193–4210. Available from: https://doi.org/10.32604/cmc.2022.031147.
7) Hu R, Gan J, Zhu X, Liu T, Shi X. Multi-task multi-modality SVM for early COVID-19 Diagnosis using chest CT data. *Information Processing & Management*. 2022;59(1):1–15. Available from: https://dx.doi.org/10.1016/j.ipm.2021.102782.
8) Hemalatha M. A hybrid random forest deep learning classifier empowered edge cloud architecture for COVID-19 and pneumonia detection. *Expert Systems with Applications*. 2022;210:1–13. Available from: https://doi.org/10.1016/j.eswa.2022.118227.
9) Kumar A, Parihar A, Panda U, Parihar DS. Microfluidics-Based Point-of-Care Testing (POCT) Devices in Dealing with Waves of COVID-19 Pandemic: The Emerging Solution. *ACS Applied Bio Materials*. 2022;5(5):2046–2068. Available from: https://dx.doi.org/10.1021/acsabm.1c01320.
10) Mahdi AY, Yuhaniz SS. Automatic Diagnosis of COVID-19 Patients from Unstructured Data Based on a Novel Weighting Scheme. *Computers, Materials & Continua*. 2023;74(1):1375–1392. Available from: https://dx.doi.org/10.32604/cmc.2023.032671.
11) Hammad MS, Ghoneim VF, Mabrouk MS, Al-atabany WI. A hybrid deep learning approach for COVID-19 detection based on genomic image processing techniques. *Scientific Reports*. 2023;13(1):1–21. Available from: https://dx.doi.org/10.1038/s41598-023-30941-0.
12) Sadeghi A, Sadeghi M, Sharifpour A, Fakhar M, Zakariaei Z, Sadeghi M, et al. Potential diagnostic application of a novel deep learning- based approach for COVID-19. *Scientific Reports*. 2024;14(1):1–19. Available from: https://dx.doi.org/10.1038/s41598-023-50742-9.
13) Yenurkar G, Mal S. Future forecasting prediction of Covid-19 using hybrid deep learning algorithm. *Multimedia Tools and Applications*. 2023;82(15):22497–22523. Available from: https://dx.doi.org/10.1007/s11042-022-14219-7.
14) Schwab P, Schütte AD, Dietz B, Bauer S. Clinical Predictive Models for COVID-19: Systematic Study. *Journal of Medical Internet Research*. 2020;22(10):1–14. Available from: https://doi.org/10.2196/21439.
15) Sahin ME. Deep learning-based approach for detecting COVID-19 in chest X-rays. *Biomedical Signal Processing and Control*. 2022;78:1–10. Available from: https://doi.org/10.1016/j.bspc.2022.103977.
16) Ramón A, Torres AM, Milara J, Cascón J, Blasco P, Mateo J. eXtreme Gradient Boosting-based method to classify patients with COVID-19. *Journal of Investigative Medicine*. 2022;70(7):1472–1480. Available from: https://dx.doi.org/10.1136/jim-2021-002278.
17) Rostami M, Oussalah M. A novel explainable COVID-19 diagnosis method by integration of feature selection with random forest. *Informatics in Medicine Unlocked*. 2022;30:1–15. Available from: https://dx.doi.org/10.1016/j.imu.2022.100941.
18) Chumachenko D, Meniailov I, Bazilevych K, Chumachenko T, Yakovlev S. Investigation of Statistical Machine Learning Models for COVID-19 Epidemic Process Simulation: Random Forest, K-Nearest Neighbors, Gradient Boosting. *Computation*. 2022;10(6):1–22. Available from: https://dx.doi.org/10.3390/computation10060086.
19) Heidari A, Navimipour NJ, Unal M, Toumaj S. Machine learning applications for COVID-19 outbreak management. *Neural Computing and Applications*. 2022;34(18):15313–15348. Available from: https://dx.doi.org/10.1007/s00521-022-07424-w.
20) Groumpos PP. Modelling COVID-19 using Fuzzy Cognitive Maps (FCM). *EAI Endorsed Transactions on Bioengineering and Bioinformatics*. 2021;1(2):1–13. Available from: https://dx.doi.org/10.4108/eai.24-2-2021.168728.
21) Höhl W. COVID-19 and digital transformation: developing an open experimental testbed for sustainable and innovative environments using Fuzzy Cognitive Maps. *F1000Research*. 2021;10:1–33. Available from: https://doi.org/10.12688/f1000research.51357.1.
22) Wu K, Liu J. Learning large-scale fuzzy cognitive maps under limited resources. *Engineering Applications of Artificial Intelligence*. 2022;116. Available from: https://dx.doi.org/10.1016/j.engappai.2022.105376.
23) Meraihi Y, Gabis AB, Mirjalili S, Ramdane-Cherif A, Alsaadi FE. Machine Learning-Based Research for COVID-19 Detection, Diagnosis, and Prediction: A Survey. *SN Computer Science*. 2022;3(4):1–35. Available from: https://dx.doi.org/10.1007/s42979-022-01184-z.
24) Saqlain SM, Sher M, Shah FA, Khan I, Ashraf MU, Awais M, et al. Fisher score and Matthews correlation coefficient-based feature subset selection for heart disease diagnosis using support vector machines. *Knowledge and Information Systems*. 2019;58(1):139–167. Available from: https://dx.doi.org/10.1007/s10115-018-1185-y.
25) Sundaramurthy S, Jayavel P. A hybrid Grey Wolf Optimization and Particle Swarm Optimization with C4.5 approach for prediction of Rheumatoid Arthritis. *Applied Soft Computing*. 2020;94. Available from: https://dx.doi.org/10.1016/j.asoc.2020.106500.