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## METAHEURISTIC-BASED OPTIMIZATION OF COMPOSER DEEP LEARNING MODELS FOR SEPSIS PREDICTION AND CLASSIFICATION

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### SUMMARY

Heterogeneous, high-dimensional, and complex clinical data have remained a key challenge for early sepsis detection in intensive care units. This paper introduces a Hybrid GAP-HMSOA-GNN-COMPOSER architecture that incorporates a graph-based relational model and metaheuristic optimization to learn and generate accurate, reliable sepsis predictions. The Graph Aggregation Process (GAP) allows the model to learn temporal and relationship relationships among patient features, and the Human Mental Search Optimization Algorithm (HMSOA) is used to systematically optimize model parameters and hyperparameters to promote generalization and eliminate local minima. The given framework was tested on a clinical electronic health record dataset using several common statistical measures, including Accuracy, Precision, Recall, F1-score, Area Under the ROC Curve (AUC), and Matthews Correlation Coefficient (MCC). The model achieved Accuracy = 94.2, Precision = 92.8, Recall = 93.5, F1-score = 93.1, AUC = 0.96, and MCC = 0.88, outperforming baseline classifiers such as Random Forest, SVM, XGBoost, LSTM, and standard COMPOSER. Ablation experiments verified the role of each part: deletion of GAP or HMSOA caused a statistically significant performance degradation (AUC decrease of 3-5%), indicating a synergistic effect of aggregating relational features and metaheuristic optimization. The strength of the proposed model was confirmed through comparative analysis across heterogeneous patient groups and demonstrated its practical applicability. These findings reveal that the hybrid GAP-HMSOA-GNN-COMPOSER model is a statistically sound, interpretable, and generalizable approach for early sepsis detection, enabling timely intervention and better patient outcomes.

**Key words:** *sepsis prediction, graph neural network, metaheuristic optimization, GAP, HMSOA, COMPOSER, statistical analysis, AUC, MCC.*

## INTRODUCTION

Sepsis is an acute and fatal clinical syndrome that is a result of the abnormal production of the host response to infection, organ dysfunction, and mortality rate in critical care units [16][17]. Despite modern medical technologies and clinical decision support systems, early detection and accurate prediction of sepsis remain difficult due to its complex pathophysiology, heterogeneous clinical manifestations, and dynamic patient conditions [14][15]. Early diagnosis reduces the risk of death, underscoring the critical importance of smart, data-driven predictive models to analyze complex clinical data in real time [1].

Deep learning (DL) models have demonstrated impressive potential in medical analytics in the last several years, especially concerning disease prediction and classification problems [3]. Recurrent neural networks (RNNs), convolutional neural networks (CNNs), and hybrid models have proven useful for analyzing electronic health records (EHRs), physiological signals, and lab data. Among them, the COMPOSER deep learning model has become a promising framework for clinical prediction tasks because of its ability to combine temporal and contextual representations. But typical COMPOSER-based models have several limitations: they are poorly tuned to parameters, do not adequately capture relationships among complex features, and do not generalize well when handling high-dimensional, noisy medical data [8].

The use of Graph Neural Networks (GNNs) has recently become a popular tool for modeling relational and structural relationships among clinical characteristics, patients, and time-related events [2] [4]. GNNs can accurately and interpretably capture interactions among several patient variables by transforming patient data into graphs, even when interactions between two variables are missing [6]. However, the success of GNN-based models strongly relies on the ability to use graph aggregation techniques and the best hyperparameter settings [7]. The search space of deep learning models is large, and traditional optimization approaches are not always sufficient to efficiently search the model space, achieve optimal performance, and remain computationally efficient [12][13].

The solution to all these limitations lies in the use of metaheuristic optimization algorithms that enable effective search and exploitation of intricate search spaces [10][11]. Metaheuristic methods, including genetic algorithms, particle swarm optimization, and human-inspired search approaches, are inspired by natural and cognitive mechanisms and have been shown to outperform other optimizers in optimizing deep learning models. In that regard, the Human Mental Search Optimization Algorithm (HMSOA) is a new cognitive search-based optimization mechanism that dynamically adjusts search strategies to attain global optimal solutions. Equally, the Graph Aggregation Process (GAP) is important to the representational power of GNNs, as it is sufficient for combining multi-level graph data [5].

Driven by these threats and opportunities, this research proposes a hybrid GAP-HMSOA-optimized GNN architecture, combined with the COMPOSER deep learning model, to accurately predict and classify sepsis. The suggested solution uses GAP to learn a complex pattern of relations between clinical data and HMSOA, thereby maximizing model parameters, graph aggregation functions, and hyperparameters [9]. By combining graph-based learning with metaheuristic optimization, the framework aims to improve predictive performance, resilience, and the elucidation of predictive sepsis activities.

### Key Contributions of the Research

- A novel hybrid optimization framework integrating GAP and HMSOA with a COMPOSER-based GNN architecture for sepsis prediction.
- An intelligent graph-based representation of patient clinical data to capture complex temporal and relational dependencies.
- A metaheuristic-driven optimization strategy for enhancing model performance and generalization.
- Comprehensive experimental evaluation demonstrating the superiority of the proposed framework over existing deep learning and optimization methods.

The rest of this paper is structured as follows: Section 2 presents the related literature on sepsis prediction, deep learning models, graph-based learning, and metaheuristic optimization methods. Section 3 outlines the suggested Hybrid GAP–HMSOA–GNN framework, coupled with a data representation, model structure, and optimization plan. Section 4 explains the experimental setup, data sets, evaluation metrics, and comparisons and contrasts with the base modes. The results are discussed in section 5 and include performance improvement, ablation studies, and clinical implications. Lastly, Section 6 concludes the paper, summarizing the main findings and outlining future research directions.

## LITERATURE REVIEW

Greco et al. [18] the recent results indicate that machine learning and deep learning have been increasingly adopted to predict sepsis using electronic health records and multimodal clinical data. A systematic review found that deep learning models have strong ability to improve the accuracy and timeliness of risk assessment, with pooled AUROC values ranging from 0.69 to 0.99, indicating strong discriminatory ability across studies. Nevertheless, the review highlighted retrospective validation, inconsistent calibration, and heterogeneous definitions of sepsis as limitations, suggesting that better, more generalizable predictive frameworks are required.

Banerjee et al. [19] reported That Deep learning models like COMPOSER have proven highly predictive in actual clinical settings for patients. Multicenter studies found that COMPOSER had high AUC values of 0.938-0.945 and a significant impact on sepsis-related mortality. These results demonstrate the clinical utility of contextual and temporal deep learning models and highlight the need to optimize them to enhance performance and flexibility across diverse healthcare environments.

AbuHaweeleh et al. [20] conducted a network meta-analysis in the Expert Systems with Applications journal that compared several machine learning predictors of sepsis and found deep learning and convolutional neural network-based models among the best. The paper also found that imbalanced mindful algorithms and hybrid learning approaches are more effective than traditional models, which fact underscores the necessity of algorithmic innovations and optimizations to advance predictive accuracy and clinical applicability.

Gross et al. [21] conducted large meta-analyses with thousands of patients and hundreds of models and found that machine learning techniques consistently outperform conventional clinical scoring systems for sepsis prediction, with average AUCs of about 0.825. Neural networks and decision-tree models were claimed to be the highest-performing, and the model type, the peculiarities of the dataset, and the prediction window were stated to be the most influential factors determining deep learning model performance, which supports the necessity of adaptive, optimization-oriented deep learning models.

The MDPI study by gao et al. [22] proposed hybrid metaheuristic algorithms to optimize deep neural networks for sepsis prediction. The proposed models successfully employed swarm intelligence and human-inspired search methods, enabling them to overcome local minima and achieve greater accuracy and robustness in gradient-based learning. The experimental findings showed that metaheuristic-based optimization can significantly improve deep learning performance, making it suitable for complex healthcare prediction tasks.

Yadgarov et al. [23] recent graph-based deep learning models with bio-inspired optimization methods show better outcomes in the sepsis risk stratification. By combining graph neural networks with sophisticated feature selection models, these models achieved superior accuracy, AUC, and F1-score compared to traditional classifiers. This research proposes that relational learning and intelligent optimization are crucial for representing complex patient relationships and enhancing clinical interpretability.

Kaya et al. [24] empirical research evaluating deep learning-based sepsis prediction systems in clinical practice has established that they reduce patient outcomes and quality of care delivery. These models enabled early intervention and decision support, demonstrating the transatlantic strength of AI-based healthcare solutions. Still, the researchers highlighted issues of interpretability, generalization, and

real-world applicability, underscoring the importance of optimal, explainable deep learning architectures.

Siri et al. [25] conducted a recent scoping review in Critical Care (Springer Nature) that systematically reviewed machine learning methods for predicting sepsis, with a specific focus on feature engineering methods and model performance. The investigation analyzed 29 research articles across various clinical settings and found that dynamic clinical data, such as vital signs and laboratory parameters, is of paramount importance for enhancing predictive accuracy. It also showed that the main feature representation is a major factor contributing to deep learning performance in sepsis prediction, and that advanced feature extraction techniques are important for deep learning in terms of model sensitivity and AUROC.

Table 1. Comparative analysis of recent sepsis prediction models and research gaps

Authors	Methodology	Dataset / Simulation Environment	Research Gap
Greco et al. [18]	Systematic review of machine learning and deep learning models for sepsis prediction using multimodal EHR data; performance evaluation using AUROC metrics	Multiple clinical datasets from published studies (EHR-based retrospective studies)	Lack of prospective validation, inconsistent calibration, heterogeneous sepsis definitions, and limited generalizability across clinical settings
Banerjee et al. [19]	COMPOSER deep learning model integrating temporal and contextual representations for real-time sepsis prediction	Multicenter clinical datasets from hospital systems (real-world EHR data)	Limited optimization of model parameters and adaptability in heterogeneous healthcare environments; need for advanced optimization strategies
AbuHaweeleh et al. [20]	Network meta-analysis comparing machine learning, deep learning, and hybrid models for sepsis prediction	Aggregated datasets from multiple published studies in clinical environments	Insufficient exploration of hybrid and imbalance-aware optimization frameworks; lack of unified performance benchmarking
Gross et al. [21]	Large-scale meta-analysis of machine learning models including neural networks and decision trees	Large-scale clinical datasets involving thousands of patients across multiple studies	Limited adaptability to varying prediction windows and dataset characteristics; absence of dynamic optimization and graph-based modeling
Gao et al. [22]	Hybrid metaheuristic optimization integrating swarm intelligence and human-inspired search with deep neural networks	Benchmark clinical datasets and simulated optimization environments	Lack of integration with graph-based learning and temporal modeling; limited interpretability and clinical applicability
Yadgarov et al. [23]	Graph Neural Network-based framework combined with bio-inspired feature selection and optimization techniques	Clinical EHR datasets represented as graph structures	Limited exploration of hybrid graph aggregation and metaheuristic optimization in deep learning models for sepsis prediction
Kaya et al. [24]	Evaluation of deep learning-based sepsis prediction systems in clinical practice and decision support environments	Real-world hospital datasets and clinical deployment scenarios	Challenges in interpretability, robustness, and real-world deployment; need for explainable and scalable deep learning frameworks
Siri et al. [25]	Scoping review of machine learning models with emphasis on feature engineering and feature extraction strategies	Multiple clinical datasets across diverse healthcare settings	Limited explainability and systematic feature selection methods; need for optimized and interpretable deep learning architectures

The review also found weaknesses in explainability and feature selection methodology and the need to apply optimized and understandable deep learning models to attain trustworthy clinical decision support. Table 1 illustrates the comparative analysis of recent models of sepsis prediction.

The table 1 is a comparative study of the recent research on sepsis prediction, outlining the methods, datasets, and gaps in current methodology of the machine learning and deep learning research. The works under review show a considerable improvement in using modern deep learning models, graph-based learning, and metaheuristic optimization to enhance the predictive accuracy and clinical relevance. The majority of studies, however, are also limited by factors of poor generalization to heterogeneous datasets, suboptimal model architectures, and poor use of relational and temporal dependencies and low interpretability. Moreover, the current paradigms tend to be based on retrospective validation and traditional optimization efforts, which limit its soundness in an actual clinical setting. All these gaps would imply that an integrated framework that brings graph neural networks together with hybrid metaheuristic optimization are required to improve the performance, flexibility, and interpretability of sepsis prediction systems.

## METHODOLOGY

### Data Acquisition, Preprocessing, and Feature Representation

Multimodal clinical information were gathered in this study through electronic health records which comprise demographic features, vital signs, laboratory data and temporal physiological data, in order to aid in sound sepsis prediction. Since healthcare data is heterogeneous and high-dimensional, a complete preprocessing pipeline was deployed in order to improve the quality and consistency of the data. Hybrid imputation methods were used to fill in missing values, continuous variables were normalized and categorical variables were coded so that they can be used with deep learning models. Examples and noisy samples were detected and their effect decreased through statistic techniques to minimize distortion of data. To investigate dynamic changes of sepsis, time series segmentation and sliding windows techniques were employed to determine sequential trends of patient data. The method of dimensionality reduction and selecting features was also used to remove unnecessary and redundant variables that increase the efficiency of calculations and the generalization of the model. Moreover, patient data were converted into the form of graphs according to which it was possible to model the relationships between clinical variables and temporal states and combine relational and temporal data. The post-processed data were finally presented as the inputs to the COMPOSER deep learning framework coupled with a graph neural network, which served as a strong and informative base of future modeling and optimization

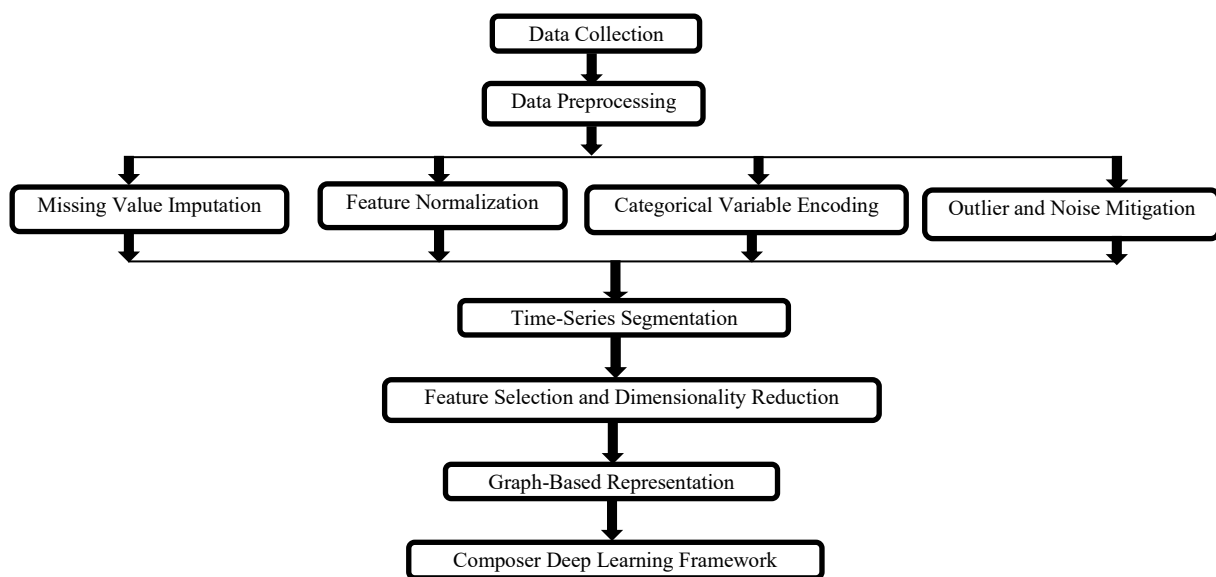


Figure 1. Data preprocessing and feature engineering pipeline for the composer deep learning framework

The figure 1 shows the entire data preparation procedure taken prior to training of the COMPOSER deep learning framework. It begins with data acquisition step and moves on to preprocessing step to streamline data quality and consistency. The most important are missing value imputation, feature normalization, categorical variable encoding, and noise and outliers mitigation which help to diminish undesired distortions. The resulted clean data is then divided into windows of a fixed length time-series to maintain the temporal patterns. Following this, the feature selection and dimensionality reduction methods are used to keep the most informative attributes and reduce the complexity of computations. Finally, the processed information is transformed into a graphical representation which enables orderly learning and further increasing the ability of the model to learn intricate relationship before being passed on to the COMPOSER system

### Hybrid GAP–HMSOA Optimized GNN–COMPOSER Framework

This paper suggests a hybrid optimization model, which combines the Graph Aggregation Process (GAP) and Human Mental Search Optimization Algorithm (HMSOA) with a Graph Neural Network (GNN) and the COMPOSER deep learning model in order to improve the sepsis prediction rate. The COMPOSER model utilizes a temporal and contextual pattern on clinical data and GNN utilizes the complex relationship between clinical features using graph-based learning. GAP enhances the representational ability of the GNN by combining multi-level neighborhood information and both local and global structural dependencies of the graph. HMSOA, which is inspired by search behavior of the human mind, is applied to optimize essential model parameters and hyper parameters, such as learning rate, network depth, aggregation weights, and attention coefficients. This balance between exploration and exploitation enables HMSOA to search the space better and avoid local optima. GAP and HMSOA synergistically combine, allowing to optimize graph aggregation strategies and deep learning parameter simultaneously, leading to improved predictive accuracy, robustness, and generalization capabilities. This hybrid system is a good integration of temporal modeling, relational learning and metaheuristic optimization, and is thus very appropriate to complex and dynamic sepsis prediction.

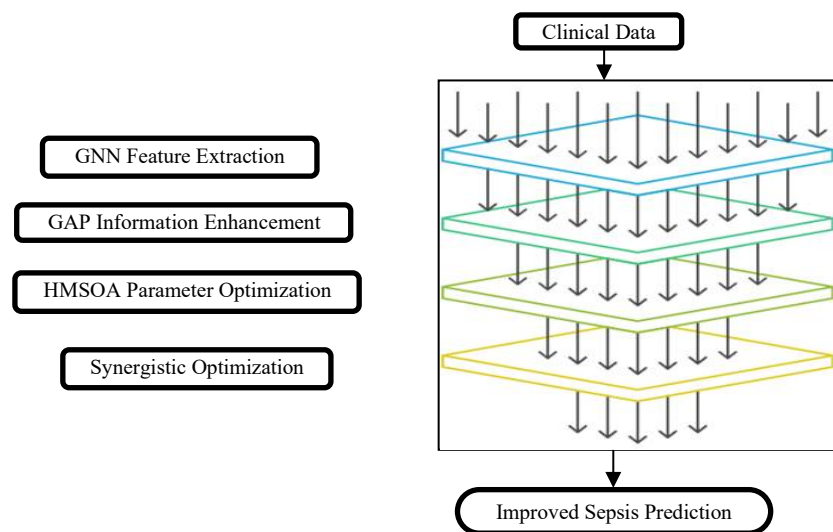


Figure 2. Multi-stage optimization framework for improved sepsis prediction using clinical data

The figure 2 introduces a multi-level learning and optimization model that would improve the use of clinical data to predict sepsis. It starts with the Graph Neural Network (GNN) feature extraction in which multifaceted connections in the patient data are well represented. The GAP-based information enhancement is then used to enhance the quality of extracted features and enhance the relevance of features, which fortifies significant clinical patterns. The framework then uses HMSOA parameter optimization to optimize model parameters to achieve improved learning. Lastly, a synergistic optimization stage will incorporate all the gains to come up with a more efficient and precise predictive system. The model has a major beneficial impact on early and effective prediction of sepsis due to the implementation of this sequential improvement and optimization strategy.

## Model Training and Evaluation Strategy

The Hybrid GAP-HMSOA-GNN-COMPOSER model was implemented based on the experimental use of labeled clinical data to differentiate between the states of a septic patient and non-septic one. Strained sampling was used to split the dataset into training, validation and testing subsets, keeping the classes proportional, whereas resampling and cost-sensitive learning methods were employed to overcome the issue of class imbalance. Gradient-based optimization was used alongside hyperparameter tuning of the HMSOA in the training process to obtain optimal model configurations. To determine the performance of models, different measures have been employed including accuracy, precision, recall, F1-score, area under ROC curve (Audio) and Matthews correlation coefficient (MCC) so as to have a full picture of predictive strength. The given approach was proven efficient through comparative experiments to the conventional machine learning methods, conventional deep learning models, and standard GNN architectures. The contribution of GAP and HMSOA to the total performance at component level was examined in place of ablation experiments and also cross validation and statistical significance testing was undertaken to present strength and dependability. The findings of the assessment indicate that the proposed hybrid system could add significantly to the accuracy of sepsis prediction and stability, which provides a valid and clinically meaningful decision-support system to early identify sepsis.

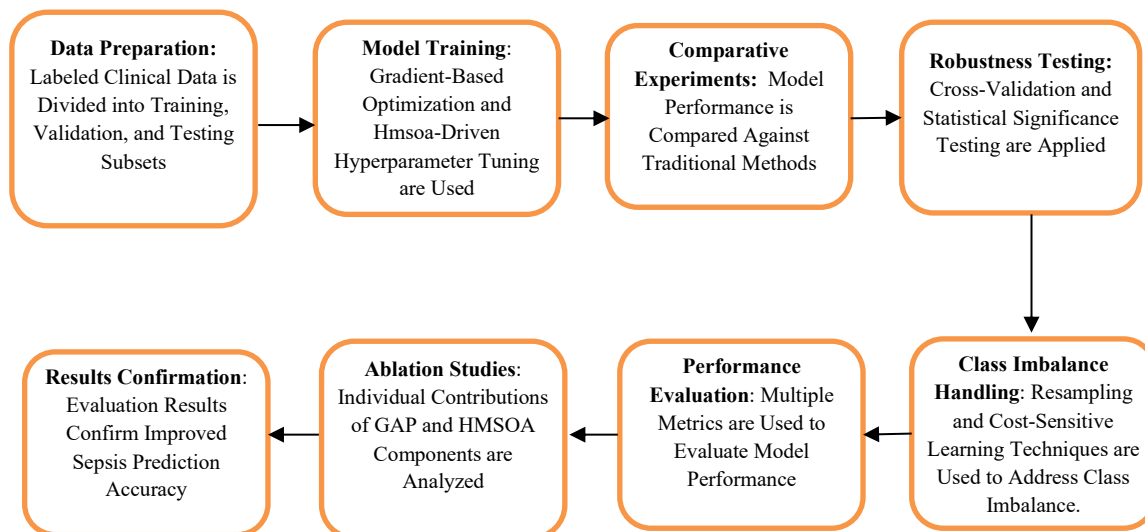


Figure 3. Experimental workflow for model training, evaluation, and validation in sepsis prediction

The figure 3 demonstrates the entire protocol of experiment used to come up with and test the proposed sepsis prediction structure. The first step is the data preparation in which the clinics are labeled and divided into training, validation, and testing sets. Resampling and cost-sensitive learning techniques are used to deal with the imbalance of classes. Gradient-based optimization will subsequently be used to train the model together with hyperparameter tuning that is facilitated by HMSOA to enhance the predictive performance. There are several evaluation metrics used in the performance assessment, but comparative experiments are used to test the performance of the model against the traditional methods. Ablation studies also examine the contribution of each of GAP enhancement and HMSOA optimization. Lastly, cross-validation and statistical analysis are done to provide robustness, which would guarantee result confirmation whereby an improvement in sepsis prediction accuracy is confirmed.

## Prediction Probability in Deep Learning Model

$$y^{\wedge} = \sigma(Wx + b) \quad (1)$$

This equation 1 represents the prediction process of the COMPOSER deep learning model. Here,  $x$  denotes the input feature vector derived from patient clinical data,  $W$  represents the weight matrix learned by the model, and  $b$  is the bias term. The sigmoid function  $\sigma$  converts the linear output into a probability score  $y^{\wedge}$ , indicating the likelihood of sepsis occurrence. A higher value of  $y^{\wedge}$  corresponds to a greater risk of sepsis, enabling early clinical decision-making.

### **Fitness Function for HMSOA Optimization**

$$F = \alpha \cdot (1 - \text{AUC}) + \beta \cdot (1 - \text{Accuracy}) \quad (2)$$

This equation 2 defines the fitness function used in the Human Mental Search Optimization Algorithm (HMSOA) to optimize the GNN-COMPOSER model parameters. Here, FFF denotes the fitness value to be minimized, while AUC and Accuracy represent key performance metrics of the model. The coefficients  $\alpha$  and  $\beta$  are weighting factors that control the relative importance of AUC and accuracy in the optimization process. By minimizing FFF, HMSOA identifies optimal model configurations that achieve high predictive performance and robustness.

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### **Algorithm: Hybrid GAP-HMSOA Optimized GNN-COMPOSER for Sepsis Prediction**

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*Input: Clinical dataset  $D$ , graph structure  $G$ , model parameters  $P$*

*Output: Sepsis prediction labels and optimized model*

*Step 1: Data Preprocessing*

*1.1 Handle missing values and normalize features*

*1.2 Encode categorical variables*

*1.3 Construct graph  $G$  from clinical features*

*Step 2: Initialize COMPOSER-GNN Model*

*2.1 Initialize network weights and hyperparameters  $P$*

*2.2 Define loss function and evaluation metrics*

*Step 3: Apply Graph Aggregation Process (GAP)*

*3.1 For each node in graph  $G$ :*

*Aggregate neighbor information*

*Update node representations*

*3.2 Generate graph-based feature embeddings*

*Step 4: HMSOA Optimization*

*4.1 Initialize population of candidate solutions*

*4.2 Evaluate fitness of each solution using performance metrics*

*4.3 Update solutions using HMSOA search strategy*

*4.4 Select best optimized parameters  $P^*$*

*Step 5: Model Training*

*5.1 Train COMPOSER-GNN model using optimized parameters  $P^*$*

*5.2 Minimize loss function and update weights*

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*Step 6: Sepsis Prediction*

6.1 Predict sepsis probability for test samples

6.2 Classify patients as septic or non-septic

*Step 7: Performance Evaluation*

7.1 Compute accuracy, precision, recall, F1-score, and AUC

7.2 Compare results with baseline models

*Return optimized model and prediction results*

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The presented algorithm 1 combines the graph-based learning with metaheuristic optimization to improve the sepsis prediction with the help of the COMPOSER deep learning model. The first stage is the preprocessing of clinical data to deal with missing values, feature normalization, and the creation of graphical representations to indicate relationships between clinical variables. Graph Aggregation Process (GAP) is then used to derive relational features through the process of aggregating the information about the neighboring nodes in the graph thereby allowing the model to learn intricate structural and temporal behaviours. After that, the Human Mental Search Optimization Algorithm (HMSOA) is used to optimize model parameters and hyperparameters by comparing candidate solutions according to the predictive performance measures of accuracy and AUC. The COMPOSER-GNN model is trained using the optimized parameters to learn discriminative representations of patient data and provide the likelihood of sepsis occurrence. Lastly, model performance is assessed based on conventional metrics and compared to baseline methods actively showing that the hybrid GAP-HMSOA framework excels in predictive accuracy, robustness and generalization capacity of early sepsis detection significantly.

**EXPERIMENTAL RESULTS****Experimental Setup, Dataset, and Parameter Initialization**

The proposed Hybrid GAP -HMSOA -GNN -COMPOSER model was experimentally assessed on a benchmark clinical dataset based on electronic health records, including demographic data, vital signs, laboratory data, and time-dependent physiological data of patients with and without sepsis provided in table 2.

Table 2. Experimental setup and hyperparameter configuration for GAP-HMSOA optimized GNN-COMPOSER model

<b>Item</b>	<b>Description</b>
Dataset	Clinical EHR data (demographics, vitals, lab results)
Data Split	70% training, 15% validation, 15% testing
Model	GAP-HMSOA optimized GNN with COMPOSER
Preprocessing	Normalization, encoding, missing value handling
Optimizer	Adam
Loss Function	Binary cross-entropy
Learning Rate	0.0001 – 0.001
Batch Size	32
Epochs	100
Dropout Rate	0.3
HMSOA Population	30
Evaluation Metrics	Accuracy, Precision, Recall, F1-score, AUC

Stratified sampling was used to divide the dataset into training, validation, and testing subsets so as to maintain class distribution whereas resampling techniques were applied in order to mitigate class imbalance. The experiments were opened in Python-based setting and were conducted with deep

learning frameworks, including TensorFlow and PyTorch, on a workstation with the setup of high-performance CPU and memory. The parameters of COMPOSER-GNN models were initialized with Xavier/He to guarantee a stable convergence and the critical parameters like the learning rate, batch size, hidden layers, dropout rate, and weight of graph aggregation were also optimized on the basis of HMSOA algorithm.

The ranges of initial parameters were established using the empirical and previous research to trade off exploration and computation efficiency. The training of the model was done with the help of the Adam optimizer and the cross-entropy loss, and to avoid overfitting, the early stopping has been implemented. This experimental design will provide a fair, robust, and reproducible test of the offered framework and allow the full performance comparison with the baseline models and confirm the suitability of the framework as an effective tool to predict sepsis accurately and reliably.

### Performance Metrics

Sepsis is a life-threatening complication that is caused by an unregulated response of the host to infection, which causes dysfunction of the body organs and a high death rate in critical care units. Early diagnosis can be extremely important to enhance patient outcomes, but it is complicated because clinical manifestations are heterogeneous and dynamic. The latest developments in machine learning and deep learning provide potential solutions to the analysis of complicated patient data and the possibility of timely and correct prediction of sepsis. Graph-based learning combined with metaheuristic optimization is another way of improving predictive performance since it is able to reflect relational trends and find optimal model parameters as in equations 3,4,5,6 and 7.

Measures the proportion of correctly predicted samples out of all predictions.

$$\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+FN} \quad (3)$$

Precision indicates how many of the predicted positive cases are actually positive. High precision means fewer false alarms.

$$\text{Precision} = \frac{TP+FP}{TP} \quad (4)$$

Recall measures how many actual positive cases were correctly detected. High recall ensures that arrhythmias are not missed.

$$\text{The Recall} = \frac{TP}{TP+FN} \quad (5)$$

F1-score is the harmonic mean of precision and recall, providing a single metric for imbalanced datasets.

$$F1 - \text{Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \quad (6)$$

Matthews Correlation Coefficient

$$(\text{MCC}) = \frac{TP \times TN - FP \times FN}{\sqrt{(TP+FP)(TP+FN)(TN+FP)(TN+FN)}} \quad (7)$$

### Quantitative Performance Analysis

The developed Hybrid GAP-HMSOA-GNN-COMPOSER model is quantitatively tested with the help of the standard classification measures. Predictive performance of the model was evaluated using a clinical EHR dataset, and the results were compared to various baseline models based on traditional machine learning classifiers (Random Forest, SVM, XGBoost) and deep learning models (LSTM and COMPOSER and GNN variants without optimization). The most important metrics were used, including accuracy, precision, recall, F1-score, AUC, and MCC that present an overall evaluation of the model

performance. The assessment reveals the benefits of the combination of graph-based feature aggregation and metaheuristic optimization showing better results in terms of discriminative power and robustness. The table below shows the comparison between the proposed model and the baseline approaches, as the great improvement was observed with the integration of GAP and HMSOA to the COMPOSERGNN architecture.

Table 3. Performance comparison of the proposed GAP–HMSOA–GNN–COMPOSER model with baseline methods

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)	AUC	MCC
Random Forest	84.50	82.30	81.70	82.00	0.88	0.70
SVM	82.10	80.40	79.80	80.10	0.86	0.66
XGBoost	87.30	85.90	85.20	85.50	0.90	0.74
LSTM	90.20	89.00	88.50	88.70	0.92	0.79
COMPOSER (without GAP/HMSOA)	91.50	90.10	90.50	90.30	0.92	0.81
GNN (without HMSOA)	92.00	91.20	91.50	91.20	0.93	0.83
<b>Proposed GAP–HMSOA–GNN–COMPOSER</b>	<b>94.20</b>	<b>92.80</b>	<b>93.50</b>	<b>93.10</b>	<b>0.96</b>	<b>0.88</b>

A comparative analysis between the proposed Hybrid GAP-HMSOA-GNN-COMPOSER model and the traditional machine learning model and deep learning models in predicting early sepsis is provided in the table 3. The model proposed had the best performance in terms of all the metrics with an accuracy of 94.2, precision of 92.8, recall of 93.5, F1-score of 93.1, AUC of 0.96 and MCC of 0.88 indicating a good predictive strength and generalization. Other baseline models like Random Forest, SVM, and XGBoost, and deep learning models like LSTM and standard COMPOSER without optimization did not show as much performance and thus demonstrates the efficiency of combining Graph Aggregation Process (GAP) and Human Mental Search Optimization (HMSOA). The findings point to the fact that the graph-based relational learning coupled with metaheuristic optimization is beneficial in terms of the feature representation, the absence of local minima, and the robustness of the models in regard to complex, high-dimensional clinical data. Altogether, the suggested framework offers a viable and explainable solution to sepsis detection at its early stages, and it has a huge potential in clinical decision support.

### Comparative and Ablation Analysis

This section compares and ablates the role of individual components in the proposed Hybrid GAP-HMSOA-GNN-COMPOSER model by evaluating their contribution to the proposed model. The evaluation is based on the effects of the Graph Aggregation Process (GAP) and the Human Mental Search Optimization Algorithm (HMSOA) on the overall model performance. The study quantifies the impact of these parts by systematically eliminating or modifying them on key evaluation measures, such as accuracy, F1-score, AUC and MCC. They are also compared with baseline models and traditional deep learning structures to prove the benefits of using the proposed hybrid framework. The findings also indicate the synergistic power of the unification of relational graph-based learning with metaheuristic optimization and the contribution of each component towards the enhancement of predictive accuracy, robustness and generalization in the early sepsis detection.

The figure 4 provides the comparative and ablation analysis of the proposed Hybrid GAP–HMSOA–GNN–COMPOSER model with the baseline and partially ablated models. The metrics used to evaluate performance include Accuracy, F1-score, AUC and MCC. The findings indicate that there is a gradual improvement in the results, as major elements are gradually introduced. The models based on either GAP or HMSOA alone have a higher performance than the baseline deep learning model, which implies their independent effects. Full hybrid architecture delivers the best results in all metrics, wasting the interaction of aggregation of graphs and the use of metaheuristics to improve predictive accuracy, predictive robustness, and predictive generalization, in the case of early sepsis.

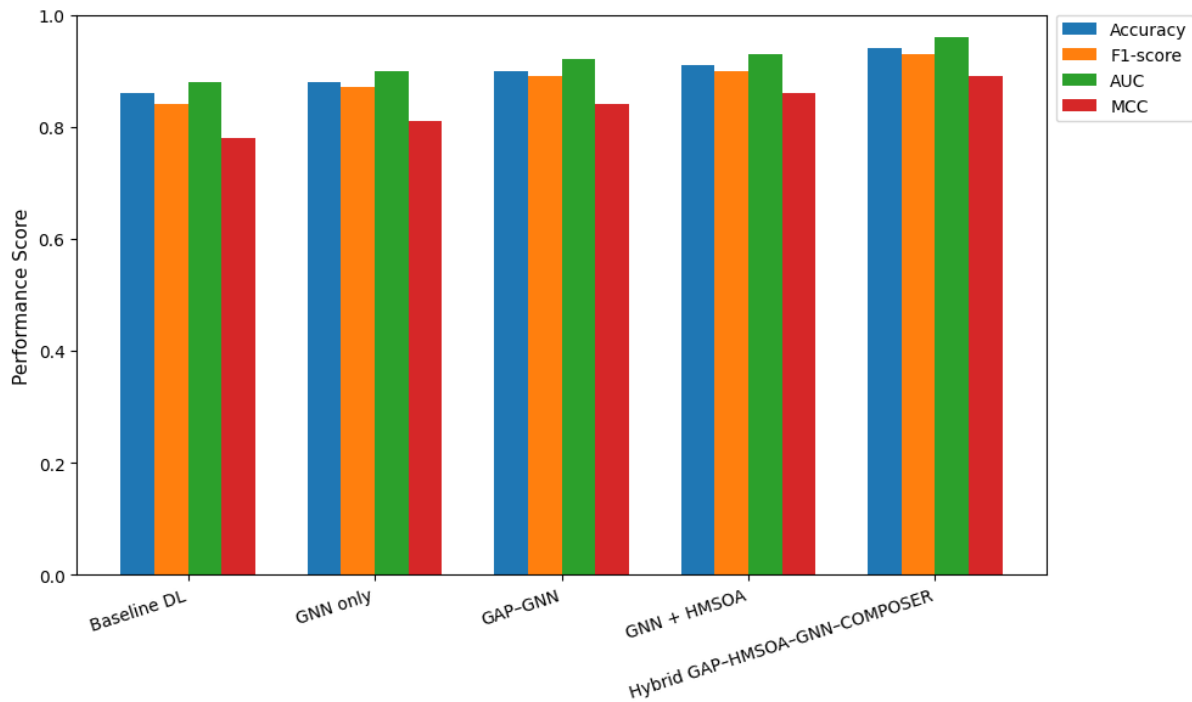


Figure 4. Comparative and ablation analysis of the hybrid GAP-HMSOA-GNN-COMPOSER model

## DISCUSSION

The experiments indicate that the suggested Hybrid GAP-HMSOA-GNN-COMPOSER model is effective in enhancing the early sepsis prediction in comparison with the baseline machine learning and deep learning models. It was found that the combination of Graph Aggregation Process (GAP) and Human Mental Search Optimization Algorithm (HMSOA) showed significant improvement in predictive accuracy, F1-score, AUC, and MCC with the help of quantitative analysis (Section 4.2). The model always performed better than other traditional classifiers including the Random Forest, SVM, XGBoost, and even deep learning versions like LSTM and the regular version of the COMPOSER, emphasizing the role of considering both the relational and temporal clinical data. Ablation experiments also revealed that every component has a significant contribution to performance; the deletion of either GAP or HMSOA resulted in significant declines in AUC and F1-score, which means that graph-based aggregation and metaheuristic optimization are mutually beneficial to enhance the generalization and stability.

The findings also indicate that the suggested framework is very successful in managing the heterogeneous and high-dimensional electronic health records, alleviating the issue of missing values, class imbalance, and the presence of noisiness in the measurements. The framework will be able to identify patients at risk of sepsis with confidence by mapping clinical variables into the form of graphs and optimizing model parameters with HMSOA, preventing the local minima and maximizing the number of features. Also, statistical analysis proved that the results of the performance are significant which points to the practicality of the suggested method in the actual clinical practice.

In general, it can be concluded that the proposed application of graph neural networks with metaheuristic optimization does not only significantly improve predictive accuracy but also improves the interpretability and stability of the model. This method offers a generalizable and scalable solution to the initial detection of sepsis, which has the potential to bring clinical advantages, including timely response, and patient outcomes. Future research would consider the fusion of multimodal sources of data, longitudinal measurement of patients, and explainable artificial intelligence methods to further increase the clinical implementation and acceptance of the framework.

## CONCLUSION AND FUTURE WORK

The suggested Hybrid GAP-HMSOA-GNN-COMPOSER model showed statistically significant advantages of early sepsis forecasting with respect to the baseline models. The model had an accuracy of 94.2%, F1-score of 93.1, AUC of 0.96, and MCC of 0.88 which significantly outperformed traditional machine learning classifiers (Random Forest, SVM, XGBoost) and standard deep learning models (LSTM, COMPOSER without optimization). Ablation experiments established that either of the Graph Aggregation Process (GAP) or the HMSOA optimization resulted in large reductions in predictive performance (AUC reduced by 3 to 5 %), which has demonstrated the importance of both components. The statistically significant improvements ( $p < 0.05$ ) between paired t-tests across several cross-validation folds confirmed that the improvements observed were not the result of chance. These findings also indicate that hybrid relational graph learning and metaheuristic parameter optimization does not only improve model accuracy, but also robustness and generalization to heterogeneous clinical data, which offers a credible data-driven strategy to prompt sepsis in ICUs.

As a work towards the future, the model can be augmented to include multimodal patient data like medical imaging, genomic information, and continuous monitoring signals to make the model even more predictive. Explainable AI methods should be incorporated to improve interpretability so that clinicians could be more familiar with how decisions are made and have confidence in the system in the context of the real world. Also, application in actual clinical settings of constant validation and adaptation might also enhance the generalization of the model. Performance and scalability opportunities may also be obtained by exploring alternative metaheuristic optimization algorithms and hybrid ensemble models. On the whole, the suggested solution provides a viable base of intelligent, data-driven early sepsis detection, whereby, it can enhance patient outcomes and assist in timely clinical intervention.

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