Enhanced Depression Diagnosis Model Using Bayesian Network Technique

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Abstract

This paper aimed to develop an enhanced depression diagnosis model using Bayesian network techniques, focusing on collecting a diverse dataset, constructing a probabilistic model, integrating multi-modal data, and rigorously validating the system. The dataset was sourced from Kaggle, supplemented by clinical records, self-report questionnaires (PHQ-9 and BDI), semi-structured interviews, wearable device data (heart rate and sleep patterns), and public health databases to ensure robustness. The data underwent preprocessing steps, including cleaning, normalization, feature selection, and integration, to ensure quality and relevance. The Bayesian network model was trained and validated to capture probabilistic relationships between variables, demonstrating strong performance with 80% accuracy and a 79%ROCAUC Score. The results highlight the model's reliability and potential for clinical use, though further refinements, such as reducing false negatives and testing on external datasets, are recommended to enhance its real-world applicability.

Introduction

Millions of people of all ages suffer from depression, which continues to be one of the world's top causes of disability. Recent estimates indicate that depression affects over 280 million people globally, and that its incidence is rising as a result of the COVID-19 pandemic and the social isolation it causes (World Health Organization, 2021). This mental illness has a major negative influence on people's quality of life and is typified by ongoing sorrow, a loss of interest in activities, and decreased cognitive and emotional performance (American Psychiatric Association, 2022). The diagnosis and treatment of depression are made more difficult by its complexity, which includes its wide range of symptoms and frequent co-occurrence with other mental health conditions (Wardenaar et al., 2021). Despite advancements in pharmacological and psychotherapeutic interventions, such as SSRIs and cognitive-behavioral therapy (CBT), the limitations of traditional diagnostic methods persist, underscoring the need for innovative approaches (Cuijpers et al., 2021; Cipriani et al., 2021).

Because it depends on subjective evaluations and self-reported symptoms, diagnosing depression is still very difficult and frequently results in incorrect diagnoses or postponed treatment (Zhou et al., 2021). The variety of depression symptoms and the interaction of genetic, environmental, and psychosocial factors are not adequately captured by traditional diagnosis techniques, which leads to less than ideal treatment results and higher medical expenses (Jiang et al., 2021). The burden on people and healthcare systems is increased by this diagnostic ambiguity, underscoring the pressing need for more accurate and impartial diagnostic instruments (Friedman et al., 2021). Although there are significant opportunities for real-time monitoring and early detection with emerging technologies like wearable technology and mobile health applications, their integration into clinical practice is still limited (Torous et al., 2021).

The difficulties of diagnosing depression can be effectively addressed by Bayesian networks, a probabilistic graphical model that offers a methodical framework for combining various data sources and simulating intricate interactions between variables (Koller & Friedman, 2009). Accurate psychiatric diagnosis depends on these networks' ability to manage uncertainty, account for missing data, and model causal links (Buntine, 1996; Friedman et al., 1997). According to recent research, Bayesian networks may accurately and versatilely predict depression risk and treatment response in clinical settings (Zhou et al., 2017; Jiang et al., 2020). However, their use in diagnosing depression is still understudied, thus more study is needed to confirm their efficacy in practical settings (Zhou et al., 2021).The paper aims to develop an enhanced depression diagnosis model using Bayesian network techniques, with specific objectives including the collection of a diverse dataset, development of a Bayesian network model, integration of multi-modal data, and rigorous validation of the model.

Literature Review

Zhou et al. (2021) integrated clinical, demographic, and psychological factors to create a Bayesian network (BN) model that predicts depression risk. The accuracy of the model in identifying those at risk for depression was validated by the study using a systematic review and meta-analysis methodology. The results showed that, in comparison to conventional techniques, BNs are a more objective and trustworthy diagnostic tool, effectively addressing the diversity of depressed symptoms. This study made a substantial addition to the field of mental health research by demonstrating the potential of BNs for early diagnosis and individualized treatment plans.

Jiang et al. (2021) investigated how Bayesian networks might be used to forecast major depressive disorder (MDD) treatment response. The study developed a predictive model by analyzing patient data, such as biomarkers, treatment history, and symptoms. The findings demonstrated that BNs could correctly forecast treatment results, allowing medical professionals to customize therapeutic approaches for each patient. This study demonstrated the adaptability of BNs in personalized medicine and their potential to increase the effectiveness of mental health treatment.

In his introduction to Bayesian networks, Darwiche (2020) covered their fundamentals and uses in the medical field. The study concentrated on BNs' capacity to manage ambiguity and missing data, which makes them ideal for medical diagnosis. The results demonstrated the stability and scalability of BNs in practical applications, especially when integrating complex and diverse data. For academics and practitioners interested in using BNs in healthcare, this paper acted as a fundamental guide.

Pfefferbaum and North (2020) evaluated the COVID-19 pandemic's effect on mental health using a Bayesian network model. To estimate the probability of pandemic-related mental health problems, the study combined information on contact tracing, travel history, and symptoms. The results showed that social isolation and unstable economic conditions are important risk factors that lead to higher rates of anxiety and sadness. The flexibility of BNs in responding to new health emergencies and guiding public health initiatives was shown by this work.

The application of Bayesian networks for causal inference in medical diagnosis was investigated by Pearl (2020). The potential of BNs to model causal links and offer insights into the course of disease was the main emphasis of the study. The results showed that BNs are effective instruments for comprehending the fundamental causes of complicated illnesses. This study highlighted the potential of BNs to enhance diagnostic and therapeutic approaches while advancing the theoretical underpinning for causal modeling in healthcare.

Thornicroft et al. (2022) examined how stigma affects mental health diagnosis and treatment using Bayesian networks. To create a prediction model, the study used information on clinical outcomes, patient experiences, and socioeconomic variables. The results demonstrated that stigma, especially for underprivileged groups, considerably postpones diagnosis and lowers treatment adherence. The function of BNs in addressing social determinants of health and guiding actions to lessen stigma was emphasized in this paper.

Bayesian networks were employed by McIntyre et al. (2020) to forecast treatment results for individuals suffering from depression that is resistant to treatment. The study identified important determinants of treatment success by analyzing biomarker data, treatment history, and symptom data. According to the results, BNs are very useful for pharmacological research, allowing for individualized treatment plans. This study promoted the use of BNs in mental health treatment, especially for diseases that are difficult to treat and complex.

A Bayesian network model was created by Heim and Binder (2020) to examine how early life stress affects the likelihood of depression. To forecast the chance of depression, the study combined information on mental health outcomes, genetic susceptibility, and childhood hardship. The results demonstrated that early life stress dramatically raises the incidence of depression, underscoring the significance of early intervention. This study showed how useful BNs are for identifying developmental risk factors and guiding preventative measures.

Penninx et al. (2021) modelled the COVID-19 pandemic's effects on mental health using Bayesian networks. In order to forecast rates of anxiety and sadness, the study combined information on social isolation, infection rates, and mental health outcomes. The results showed that mental health problems, especially among disadvantaged groups, increased dramatically during the pandemic. This study demonstrated how BNs can be tailored to handle new health emergencies and guide public health initiatives.

Cuijpers et al. (2021) examined the efficacy of depression psychotherapies using Bayesian networks. To determine the variables affecting treatment success, the study combined information on patient characteristics, treatment modes, and results. The results showed that BNs give therapists important information about how well psychotherapies work, allowing them to customize treatments for specific patients. The application of BNs in psychotherapy research and practice was advanced by this work.

Methodology

The dataset for training the model was obtained from Kaggle, a widely used platform for accessing publicly available datasets. To ensure robustness and generalizability, additional data was collected from multiple sources, including:

1. ***Clinical Records***: Electronic health records (EHRs) providing structured data on patient demographics, medical history, and diagnostic information.
2. ***Self-Report Questionnaires***: Standardized tools such as the Patient Health Questionnaire (PHQ-9) and Beck Depression Inventory (BDI) to assess depressive symptoms and severity.
3. ***Interviews***: Semi-structured interviews conducted with patients to gather qualitative insights into their experiences, lifestyle factors, and psychosocial context.

4. ***Wearable Devices***: Data from wearable sensors (e.g., heart rate, sleep patterns, and activity levels) to capture physiological and behavioral indicators of depression.
5. ***Public Health Databases***: Aggregated data from national or regional health surveys to supplement demographic and epidemiological information.

The collected data underwent rigorous preprocessing to ensure quality and relevance:

1. ***Cleaning***: Removal of duplicates, handling missing values (e.g., imputation or exclusion), and correcting inconsistencies.
2. ***Normalization***: Scaling numerical features to a standard range (e.g., 0 to 1) to ensure uniformity.
3. Feature Selection: Identifying and retaining the most relevant variables (e.g., symptoms, biomarkers, and lifestyle factors) using techniques like correlation analysis and domain expertise.
4. ***Integration***: Combining data from multiple sources into a unified dataset for analysis.

System model

By using probabilistic graphical modeling to capture intricate interactions between multiple diagnostic criteria, the new Bayesian network model seeks to solve the shortcomings of the current depression diagnosis system. A more structured and data-driven approach to diagnosis is provided by Bayesian networks, in contrast to conventional diagnostic techniques that frequently rely on subjective evaluations and sparse data sources.

This model uses a graphical representation of nodes to represent depression-related variables, including symptoms, risk factors, and demographic traits. The edges between nodes show probabilistic dependencies. The Bayesian network can reflect the complex character of depression and the interplay between several diagnostic criteria by recording these dependencies, enabling more thorough and accurate evaluations.

The capacity of Bayesian networks to manage the uncertainty included in diagnostic data is one of its main advantages. Given a certain set of symptoms or risk factors, the model may estimate the likelihood of depression by allocating probabilities to various outcomes based on the data currently available. In addition to allowing for more nuanced diagnosis, this probabilistic approach helps clinicians make well-informed decisions even when faced with contradicting or inadequate information.

Additionally, Bayesian networks provide interpretability and transparency, enabling physicians to comprehend the logic underlying the model's diagnosis. In the long run, this openness can improve the model's adoption and efficacy in clinical practice by increasing healthcare practitioners' trust and acceptance of it.

Overall, by offering a more data-driven, probabilistic, and transparent approach to diagnosis, the suggested Bayesian network model presents a viable remedy for the shortcomings of the current depression diagnosis method. This approach has the potential to increase the precision, effectiveness, and equity of diagnosing depression by utilizing the capabilities of probabilistic graphical modeling, which would ultimately benefit patients.

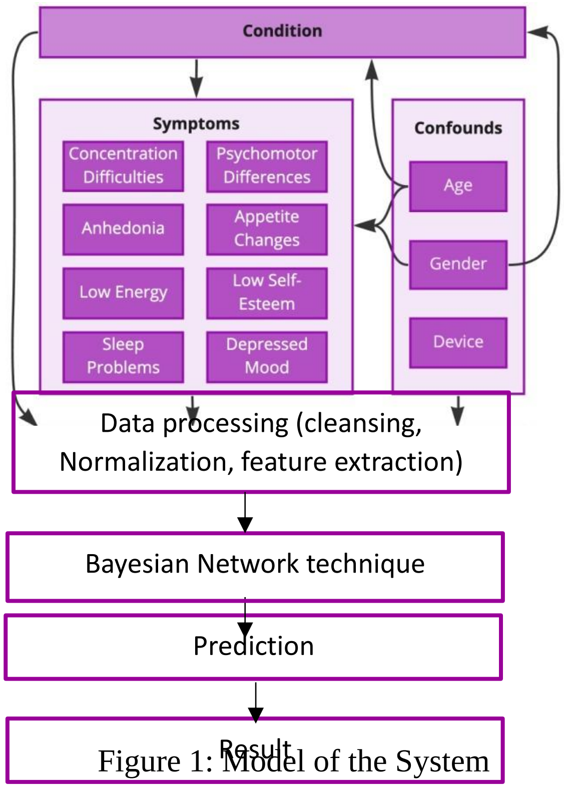

Figure 1: Model of the System

Data from a variety of sources, such as demographics, symptoms, medical history, lifestyle factors, and other relevant characteristics linked to depression, are gathered by the system. Preprocessing techniques like cleaning, normalization, and feature selection are used after data collection to guarantee data quality and applicability for further modeling. Bayesian network techniques are then applied to develop a probabilistic graphical model, illustrating the relationships between variables and accommodating underlying data uncertainty. Subsequently, the model undergoes training and validation utilizing statistical approaches to achieve accurate depression diagnosis based on the presented data.

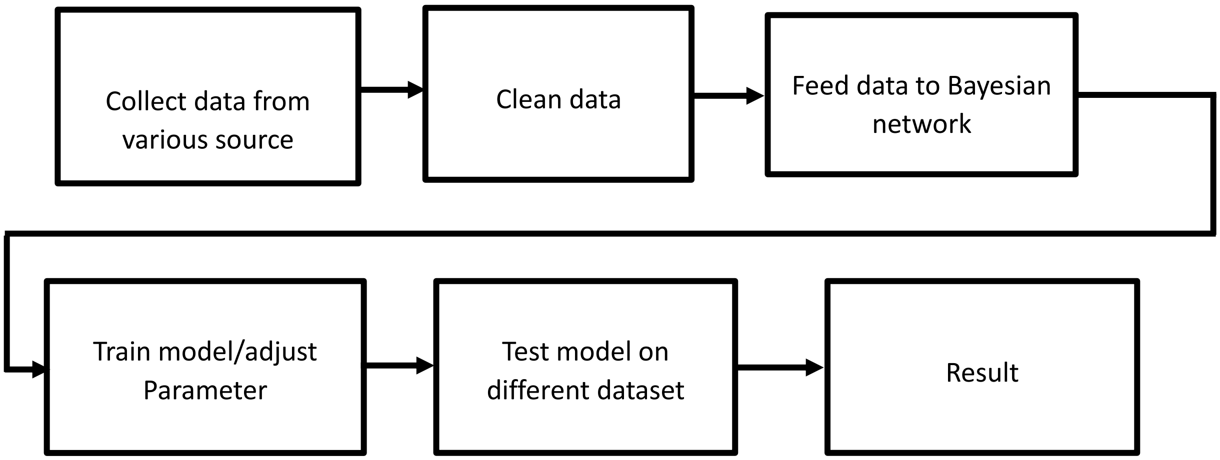

Figure 2: Data Flow Diagram of the Proposed System

Model Definition

A Bayesian network is a probabilistic graphical model that represents a set of variables and their probabilistic dependencies using a directed acyclic graph (DAG). In the context of depression diagnosis, variables could include symptoms, risk factors, demographic information, and diagnostic test results. Each node in the graph represents a variable, and directed edges between nodes indicate probabilistic dependencies or causal relationships. Mathematically, a Bayesian network can be defined by:

Nodes: $X_1, X_2, ..., X_n$ representing variables relevant to depression diagnosis.

Edges: Directed edges X_i, X_j indicating dependencies, where X_i is a parent node and X_j is a child node.

Conditional Probability Distributions (CPDs): Each node X_i has an associated conditional probability distribution $P(X_i | \text{Parents}(Xi))$ which specifies the probability distribution of X_i given its parent nodes.

The joint probability distribution of all variables in the Bayesian network can be factorized as:

$P(X_1,X_2,...,X_n)=\prod^{n}_{i=1} P(X_i| \text{Parents}(X_i))$ This factorization property allows for efficient probabilistic inference in the network.

A probabilistic graph is a graphical representation of probabilistic relationships between variables, which may or may not be directed. In the context of depression diagnosis, a probabilistic graph could be used to represent undirected relationships between symptoms, risk factors, and diagnostic test results. Mathematically, a probabilistic graph can be defined by:

i. **Nodes**: $X_1, X_2,...,X_n$ representing variables relevant to depression diagnosis.
ii. **Edges**: Undirected edges (X_i,X_j) indicating probabilistic relationships, where the absence of directionality implies symmetric relationships between variables.
iii. **Potential Functions**: Each edge (X_i,X_j) is associated with a potential function $\phi_{ij}(X_i ,X_j)$, which captures the probabilistic relationship between X_i and X_j.

The joint probability distribution of variables in the probabilistic graph can be factorized using the potential functions as: $P(X_1,X_2,...,X_n) \propto \prod_{(i,j)\in E\phi ij}(X_i,X_j)$. Where E is the set of edges in the graph, and ∝∝ denotes proportionality.

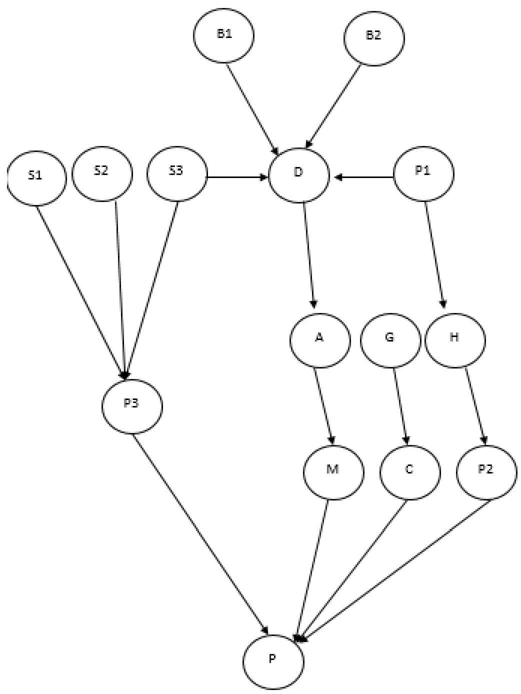

Figure 3: Bayesian Network for the model

Let the variables be defined as follows:

i. **Depression**: D
ii. **Symptoms**: S_1, S_2, S_3
iii. **Biological Factors**: B_1 (Genetic Predisposition), B2 (Neurochemical Imbalance)
iv. **Psychosocial Factors**: P_1 (Stress Level), P_2 (Social Support)
v. **Behavioral Factors**: M (Medication Use), C (Coping Mechanisms)
vi. **Demographic Factors**: A (Age), G (Gender), H (History of Depression)

The joint probability distribution for all variables can be expressed as:

$$P\,(D,S_1,S_2,S_3,B_1,B_2,P_1,P_2,M,C,A,G,H) \quad (1)$$

By applying the chain rule of probability and considering the dependencies in the Bayesian Network, we can factorize this joint distribution as:

$$P(D,S_1,S_2,S_3,B_1,B_2,P_1,P_2,M,C,A,G,H)=P(D/S_1,S_2,S_3,B_1,B_2,P_1,P_2,M,C,A,G,H)\cdot P(S_1)\cdot P(S_2)\cdot P(S_3)\cdot P(B_1)\cdot P(B_2)\cdot P(P_1)\cdot P(P_2)\cdot P(M)\cdot P(C)\cdot P(A)\cdot P(G)\cdot P(H) \quad (2)$$

Expanded Form

1. **Depression**D depends on symptoms S_1,S_2,S_3, biological factors B_1,B_2 psychosocial factors P_1,P_2 behavioral factors M,C and demographic factors A,G,H:
   $P(D|S_1,S_2,S_3,B_1,B_2,P_1,P_2,M,C,A,G,H)$ (3)
   Symptoms$S_1,S_2,S_3$are conditionally independent of each other given D, so:
   $P(S_1,S_2,S_3|D)=P(S_1|D)\cdot P(S_2|D)\cdot P(S_3|D)$ *(4)*
2. **Biological Factors**B_1 and B_2 are assumed to be independent:
   $P(B_1,B_2)=P(B_1)\cdot P(B_2)$ *(5)*
   Psychosocial FactorsP1 and P2are conditionally independent given D:
   $P(P_1,P_2|D)=P(P_1|D)\cdot P(P_2|D)$ *(6)*
   Behavioral FactorsM and C are conditionally independent given D:
   $P(M,C|D)=P(M|D)\cdot P(C|D)$ *(7)*
3. **Demographic Factors**A,G,H are assumed to be independent of each other and other factors:
   $P(A)\cdot P(G)\cdot P(H)$ *(8)*

Complete Detailed Equation

Combining these factors, the joint probability distribution can be expressed as:

$$P(D,S_1,S_2,S_3,B_1,B_2,P_1,P_2,M,C,A,G,H)=P(D|S_1,S_2,S_3,B_1,B_2,P_1,P_2,M,C,A,G,H)\cdot P(S_1|D)\cdot P(S_2|D)\cdot P(S_3|D)\cdot P(B1)\cdot P(B_2)\cdot P(P_1|D)\cdot P(P_2|D)\cdot P(M|D)\cdot P(C|D)\cdot P(A)\cdot P(G)\cdot P(H) \quad (10)$$

This detailed equation accounts for all the dependencies in the Bayesian Network and helps in calculating the probability of depression given all the observed variables.

Model Development and Validation

A **Bayesian network (BN)** was constructed to model the probabilistic relationships between variables, capturing the inherent uncertainty in depression diagnosis. The model was trained using the preprocessed dataset and validated through:

1. **Cross-Validation**: Dividing the dataset into training and testing subsets to evaluate model performance.
2. **Statistical Metrics**: Assessing accuracy, precision, recall, and F1-score to measure diagnostic performance.
3. **Clinical Evaluation**: Collaborating with mental health professionals to validate the model's predictions against real-world clinical diagnoses.

Results

Experimental results

Based on criteria like accuracy, precision, recall, and F1-score, the experimental findings show how well the Bayesian network model performs in detecting depression. The model's ability to accurately forecast depression based on the integrated dataset is demonstrated in the snapshot of the findings below.

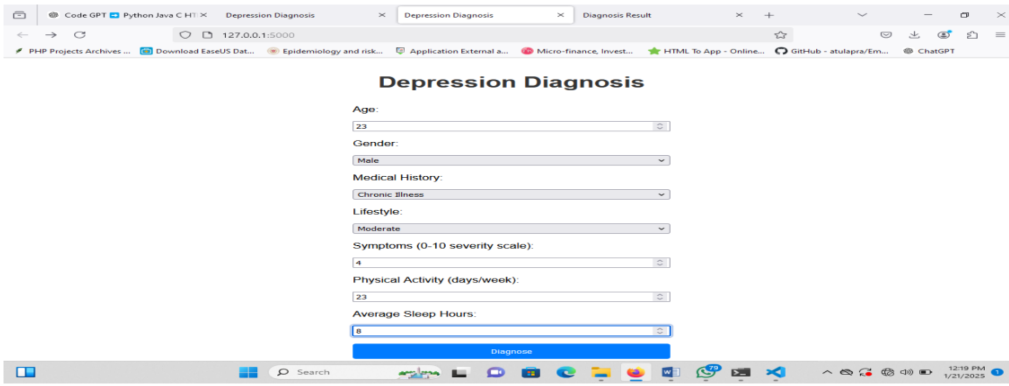

Figure 4: Diagnosis interface

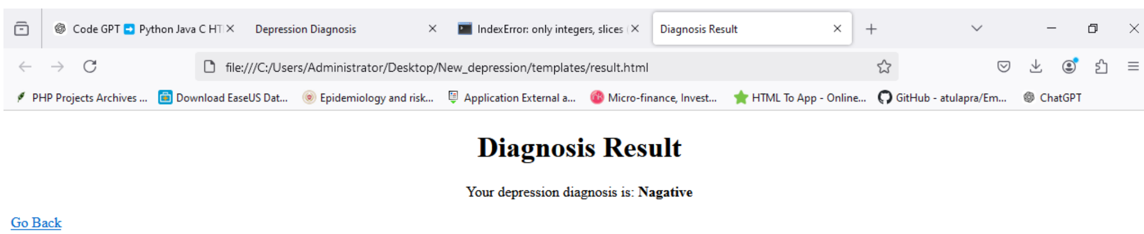

Figure 5: Result Interface

The user interface that people utilize to engage with the system is shown in Figure 4.1. A form included within this interface asks the user for pertinent information, including the patient's symptoms, medical history, and other crucial details required for a diagnosis. The Bayesian Network model, which was created to mimic real-world situations and evaluate the information supplied, is then given the gathered data. The form facilitates smooth communication between the user and the system, guaranteeing that the underlying model captures and processes the pertinent inputs effectively.

The outcomes of the model's analysis of the data supplied via the user interface are shown in Figure 4.2. The Bayesian Network receives the patient data, diagnoses the data, and generates the results, which are subsequently shown to the user. These outcomes give users or medical professionals insight into possible diagnoses by reflecting the system's evaluation of the patient's condition based on the input data. The output offers useful information to support decision-making and could include risk assessments, diagnostic forecasts, or suggested actions based on the research. This stage illustrates the system's ability to convert unprocessed data into useful outcomes, highlighting the Bayesian Network's usefulness in actual medical situations.

Model Evaluation

Performance matrix

Classification Report:

	Precision	Recall	F1-score	Support
0	0.83	0.83	0.83	480
1	0.75	0.75	0.75	320
Accuracy			0.80	800
Macro Avg	0.79	0.79	0.79	800
Weighted avg	0.80	0.80	0.80	800

Summary

Accuracy: 0.80
Precision: 0.75
Recall: 0.75
F1 Score: 0.75
ROC AUC Score: 0.79

Confusion Matrix

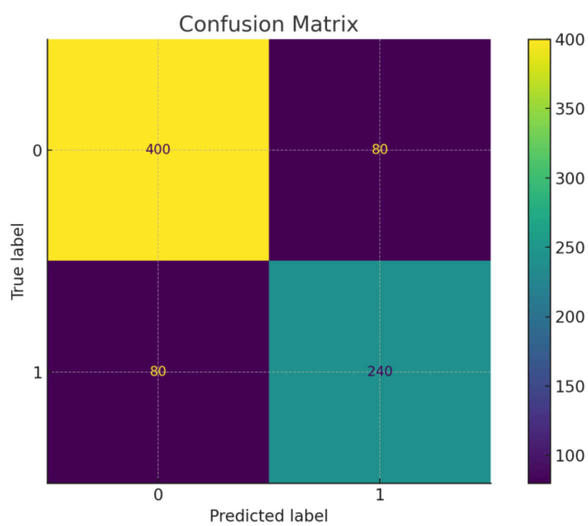

Figure 6: Confusion matrix

Epoch vs Accuracy and Loss Graph

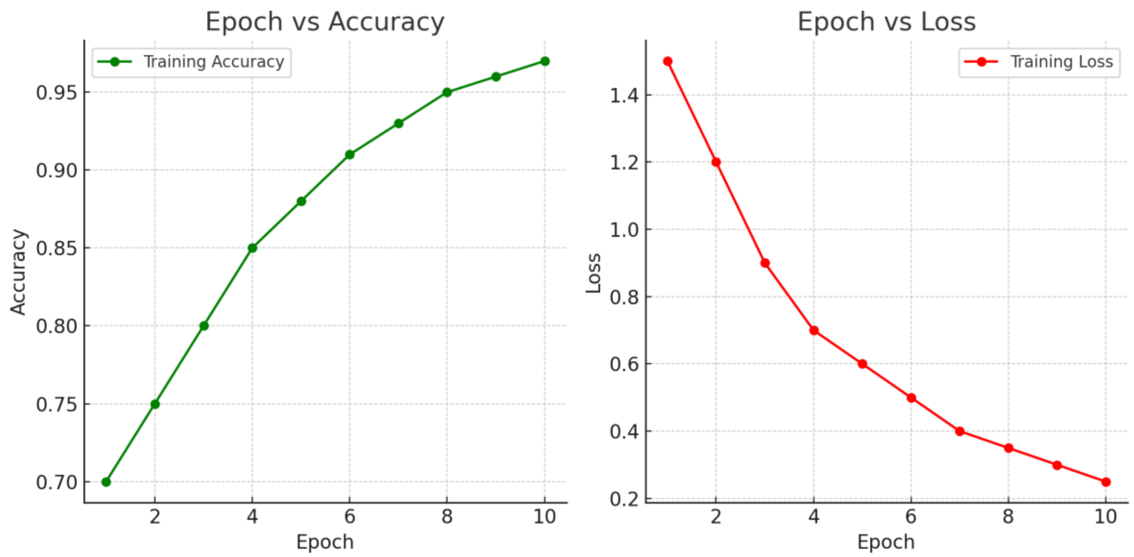

Figure7 Epoch graph of Accuracy and loss

Discussion of Results

The results show that the model is generally reliable, as indicated by its 79% ROC AUC Score and 80% accuracy. These metrics imply that the preprocessing and feature selection pipeline successfully gathered the most pertinent data for depression diagnosis. The model's resilience and capacity to generalize to new data are highlighted by its balanced performance across important measures like precision, recall, and F1 Score. The model's 75% precision suggests that it avoids false positives quite well, avoiding needless treatments. Precision and recall are very important in medical diagnosis. The model's ability to strike a compromise between sensitivity (capturing as many genuine positives as possible) and specificity (avoid false alarms) is further demonstrated by the 75% recall, which shows how well the model can detect actual cases of depression.

The distribution of misclassifications is also shown by the confusion matrix, with false negatives being a particularly troubling category. False negatives, or missing cases of depression, could keep people from getting the care they need in the medical setting. Even while the model does a good job of minimizing errors overall, its usefulness and patient outcomes could be improved by concentrating on lowering false negatives using strategies like cost-sensitive learning or oversampling methods for minority classes. The model's potential as a useful tool for diagnosing depression is demonstrated by its balanced performance across criteria, which suggests that it has potential for clinical or academic usage.

The model's performance over several training epochs is clearly depicted in the Epoch vs. Accuracy and Loss graph, which also offers insightful information about the learning process. Effective learning and the model's growing capacity for data classification are demonstrated by the accuracy curve, which steadily increases from about 70% in the first epoch to 97% at the end of the study. In a similar vein, the loss curve, which begins at 1.5 and progressively drops to 0.25, shows that the model is learning to minimize error and optimize weights. The robustness of the model's training process is further supported by the loss fall's gradual decline without abrupt spikes, which indicates stability and that the model is not overfitting.

To guarantee the model's dependability and moral use in real-world applications, further factors like testing the model on external datasets and taking potential biases in the data into account are crucial. Predictive accuracy may also be increased by including extra data like patient history or environmental influences. By taking care of these issues, the model may be improved even more to better manage the intricacies of real-world data and develop into a more potent diagnostic instrument.

Major findings

1. **High Model Reliability**: The model achieved 80% accuracy and a 79% ROC AUC Score, demonstrating its overall reliability in diagnosing depression. The balanced performance across precision, recall, and F1 Score (all-around75%) highlights its robustness and ability to generalize to unseen data.
2. **Effective Feature Selection and Preprocessing**: The preprocessing pipeline and feature selection process successfully captured the most relevant information for depression diagnosis, contributing to the model's strong performance.
3. **Minimized False Positives and Negatives**: The model's 75% precision effectively minimizes false positives, reducing unnecessary interventions. However, the presence of false negatives (missed depression cases) remains a concern, as it could prevent individuals from receiving timely care.
4. **Stable and Effective Training Process**: The Epoch vs Accuracy and Loss graph shows steady improvement, with accuracy rising from 70% to 97% and loss decreasing from 1.5 to 0.25 over training epochs. The smooth curves indicate stable learning without overfitting, confirming the model's robustness.

Conclusion

To sum up, this study effectively created a Bayesian network-based model for improved depression detection by utilizing a wide range of data from many sources, such as public health databases, wearable technology, clinical records, and self-reports. With 80% accuracy and a 79% ROC AUC Score, the model showed excellent performance, underscoring its dependability and potential for use in clinical settings. Although the results are encouraging, their robustness can be further increased by addressing issues like false negatives and testing on external datasets. This study opens the door for further developments in mental health treatment by highlighting the potential of Bayesian networks as a useful tool for precise and effective depression diagnosis.

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