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Optimization of the Naïve Bayes Algorithm Using Particle Swarm Optimization (PSO) for Predicting Heart Disease Symptoms

[1*]Sita Muharni, [2]Sigit Andriyanto, [3]Supardi
[1]Information System Department, Faculty of Technology, Business and Science, Dharma Wacana University. Jl. Kenanga No 3 Mulyojati Metro Barat Kota Metro 34121, Indonesia.
[2]Medical Record and Health Information Department, Faculty of Health, Aisyah Pringsewu University. Jl. A. Yani No. 1A Gading Rejo Prigsewu 35372, Indonesia.
[3]Nursing Department, Faculty of Health, Dharma Wacana University. Jl. Kenanga No 3 Mulyojati Metro Barat Kota Metro 34121, Indonesia.
*Corresponding Author e-mail: sitamuharni@dharmawacana.ac.id

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Abstract

Heart disease is one of the leading causes of mortality in Indonesia, yet early detection remains a challenge due to limitations in data and suboptimal classification methods. This study aims to improve the accuracy of heart disease prediction by integrating the Naïve Bayes algorithm with Particle Swarm Optimization (PSO) for feature selection. A dataset of 303 patient records was processed using RapidMiner across three configurations: Naïve Bayes with split validation (80:20), Naïve Bayes with 10-fold cross-validation, and Naïve Bayes with PSO-based feature selection. The results showed that incorporating PSO increased accuracy from 87.60% to 89.26%, along with improvements in precision and recall, while maintaining a high AUC value (0.933). These findings demonstrate that PSO effectively identifies the most relevant features and enhances the performance of heart disease prediction models. The study also underscores the importance of validation methods and model interpretability in the application of artificial intelligence in healthcare.

Keywords: Heart Disease Prediction; Naïve Bayes; Particle Swarm Optimization; Feature Selection; Health Data Mining

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INTRODUCTION

Cardiovascular disease (CVD) remains the leading cause of mortality globally, and heart disease in particular is a critical public health issue, especially in low- and middle-income countries such as Indonesia. According to the 2018 Basic Health Research Report (Riskesdas), the national prevalence of coronary heart disease in Indonesia was recorded at 1.5%, with some provinces, such as North Kalimantan (2.2%), DI Yogyakarta and Gorontalo (2.0%), and DKI Jakarta (1.9%), exhibiting rates significantly above the national average (Muri & Muharni.,2025; Gbadamosi et al, 2022; Arumugam et al., 2023). In contrast, East Nusa Tenggara had the lowest prevalence, at just 0.7% (Khoiriyah, et al., 2019). These epidemiological findings are corroborated by subsequent ecological and burden-of-disease analyses, which indicate an alarming rise in non-communicable diseases (NCDs), including ischemic heart disease, diabetes, and hypertension conditions that are strongly linked to cardiovascular morbidity and mortality in Indonesia (Sigit et al., 2020; Faulata et al., 2021).

This trend reflects the growing burden of metabolic syndrome and lifestyle-related risk factors, such as poor diet, lack of physical activity, and stress, especially in urban populations.

Studies also point to increased incidence of heart failure and myocardial infarction, exacerbated by insufficient early screening and diagnosis (Wahyuni et al., 2022; Nuraeni et al., 2021). Despite this growing burden, access to early diagnostic services remains uneven across Indonesian provinces, with many patients receiving diagnoses only at advanced stages of the disease. This is compounded by limited public health outreach and poor health literacy, especially concerning early symptoms of cardiovascular disease (Andriyanto, et al, 2025).

In addressing this gap, the integration of artificial intelligence (AI) in medical diagnostics offers promising potential. Among AI techniques, machine learning has emerged as a viable tool for early disease prediction and risk assessment. In particular, data mining methods such as the Naïve Bayes (NB) algorithm have demonstrated practical utility in healthcare domains due to their simplicity, interpretability, and relatively low computational complexity (Gad, 2022; Berrar, 2025). These methods can effectively utilize structured medical data such as clinical symptoms, lab results, and patient histories to provide predictive insights that support clinical decision-making. However, the predictive performance of NB and other machine learning algorithms is highly dependent on the quality and relevance of input features. In many medical datasets, high dimensionality, redundant attributes, and noise can obscure meaningful patterns and reduce classification accuracy. Feature selection, therefore, becomes a crucial step in building reliable and interpretable predictive models. To this end, Particle Swarm Optimization (PSO) has been increasingly recognized as an effective metaheuristic technique for optimizing Alzaqebah et al., 2021feature subsets and improving model performance (Wei et al., 2019; Alzaqebah et al., 2021).

PSO mimics the collective behavior of swarms in nature such as bird flocking or fish schooling to iteratively search for optimal solutions in a multi-dimensional space. When applied to feature selection, PSO enables classifiers like Naïve Bayes to focus only on the most relevant input attributes, effectively enhancing classification performance by eliminating irrelevant or redundant features (Shalehah et al., 2023). Its adaptability and scalability make PSO a compelling tool for medical diagnostics, where high-dimensional and heterogeneous data are common. Several studies have demonstrated the utility of PSO in medical data mining. For instance, (Gupta et al. 2018; Bajeh et al. 2019) showed that PSO integration with Naïve Bayes significantly improved classification accuracy in predicting surgical outcomes. Similarly, (Rizki et al., 2024; Septiawan et al., 2022) applied PSO for hyperparameter tuning in K-Nearest Neighbors (KNN) and Support Vector Machines (SVMs), respectively, achieving robust gains in predictive performance. Importantly, in applications involving clinical datasets, such improvements directly translate to better diagnostic accuracy and reduced false positives or negatives.

In the context of heart disease prediction, comparative evaluations highlight PSO's contribution. A study utilizing Naïve Bayes with cross-validation on 303 medical records (without feature selection) achieved 82.17% accuracy (Berrar, 2025). Another study employing PSO for feature selection with a Naïve Bayes classifier reported a significantly higher accuracy of 92.86%, using a similar dataset processed via RapidMiner (Fang, et al, 2023). Other works using varying sample sizes and validation strategies (e.g., 5-fold cross-validation or 80:20 split) have reported accuracy values ranging from 70% to 90% depending on whether feature selection was implemented. (Reddy, et el., 2022). While these studies provide valuable insights, many fall short in conducting systematic comparisons across validation strategies or in explaining the mechanistic advantages of PSO enhanced feature selection. Specifically, few have examined the interaction between feature selection, validation technique (split vs. cross-validation), and classification accuracy in a structured and reproducible manner. Additionally, there remains a lack of discussion on how PSO-selected features contribute to model interpretability and clinical relevance, especially in the context of heart disease prediction.

This research seeks to address those gaps. We propose a methodical evaluation of the Naïve Bayes classifier with and without the incorporation of PSO-based feature selection, using both split validation (80:20) and 10-fold cross-validation strategies. Our objective is not only to compare performance metrics such as accuracy, precision, recall, and AUC but also to assess how PSO improves the model through intelligent feature weighting and dimensionality reduction. Furthermore, the study emphasizes reproducibility by detailing PSO's parameter configurations and validation workflows. PSO's optimization capability, especially in terms of convergence speed and solution quality, allows for efficient hyperparameter tuning and feature selection even in small-to-moderate datasets. In our context, the heart disease dataset from the UCI Machine Learning Repository comprising 303 records and 14 attributes is a standard benchmark used in many studies, providing a consistent foundation for comparative analysis. Nevertheless, the limited size of this dataset poses generalizability concerns. Hence, we frame our findings as exploratory, advocating for future validation on larger, more diverse datasets.

The integration of PSO into predictive models not only improves performance but also enhances the interpretability and reliability of such models, which is crucial in clinical settings. As (Bouaziz et al., 2019 ; Kalatzis et al., 2023) argue, the selection of meaningful features aids in building trust among clinicians and facilitates the integration of machine learning outputs into decision-support systems. Therefore, by systematically evaluating the effects of PSO on Naïve Bayes in the domain of heart disease prediction, this study contributes both technically and clinically to the advancement of intelligent diagnostic tools. While prior research has demonstrated that the Naïve Bayes algorithm can achieve reasonably high accuracy for heart disease prediction, and that PSO-based feature selection can further enhance this performance, few studies have methodically benchmarked the combined effect of PSO and validation strategies. This study aims to fill that gap by providing a comparative analysis of different configurations, thereby offering insights into the practical and methodological implications of using PSO in medical classification tasks.

METHOD

The research will follow a systematic approach to analyze data and uncover patterns, aiming to construct a dataset that supports the study's objectives. This process ensures that every stage of the research is logically connected and directed toward the intended goals. By applying structured methods, the study maintains consistency and clarity from data collection to interpretation. Careful planning and analysis will guide the development of a dataset that not only reflects the research focus but also enables meaningful insights. Ultimately, this structured process is essential to achieving coherence and validity across all phases of the research.

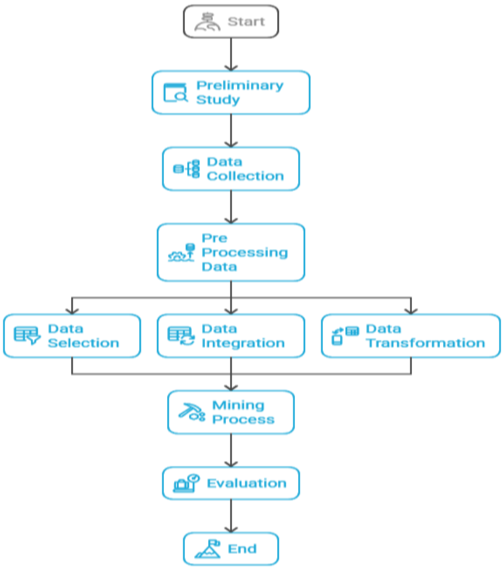


Figure 1. Research Stages Flow

The processes depicted in Figure 1 above represent the data mining process utilized in this research:

1. The initial study stage is the stage of conducting research. At this stage, researchers conduct observations or understand research that includes clear project objectives and requirements in terms of business or research units as a whole. They translate objectives and limitations into the formulation of data mining problem definitions and prepare initial strategies to achieve these objectives.
2. The data collection phase entails gathering data using exploratory data analysis to gain familiarity with the dataset, uncover preliminary insights, and assess data quality[14]. The research data used was obtained from the UCI Machine Learning Repository site with the name heart-disease. Here is the URL of the dataset. https://archive.ics.uci.edu/ml/machine-learning-databases/heart-disease/.
3. Data preparation involves converting unprocessed data into a more intelligible format. This technique is essential because to the irregular format of raw data (Prasetyo et el., 2023).
   a. Data Selection
   During this selection procedure, the data were extracted from the comprehensive UCI Machine Learning Repository dataset, specifically pertaining to heart disease symptom prediction. From the selection findings, 303 patient records will be utilized for data mining analyses.
   b. Data Integration
   This process is carried out because the data structure scheme needs to change from raw data to data ready to be further preprocessed with the transformation stage. The data will change the scheme or structure that is easy to process. Table data is defined extending to the right side with more columns and neatly, and the file type previously csv is exported to an Excel data type, making it easy to change the data.
   c. Data Transformation
   The Transformation process is the final stage of data change that is ready to be processed and entered into the Rapid Miner tools or applications. All attributes are 14, with 1 label attribute (num/output) and 13 feature attributes. There are 303 data points of heart disease patients and 14 attributes, including age, sex, cp, treetops, chol, FBS, resting, thalach, exang, old peak, slope, ca, thal, and num. The data explanation can be seen below.

2. The mining process employs the Naïve Bayes Algorithm and the Particle Swarm Optimization (PSO) technique to enhance accuracy.

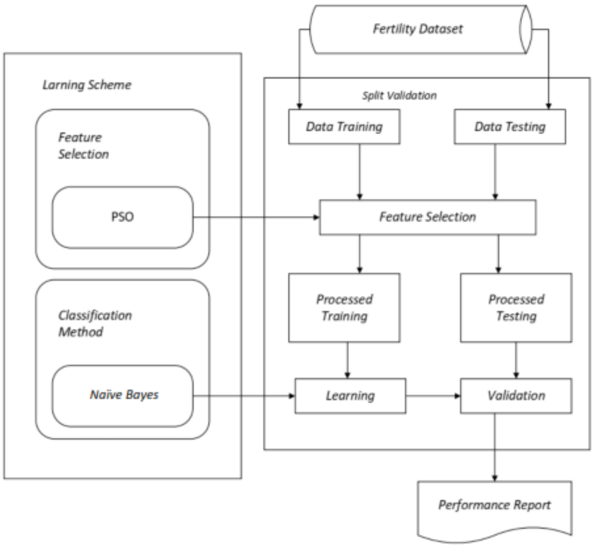


Figure 2. PSO Process

3. Naïve Bayes Algorithm Testing
   The dataset used to evaluate the Naïve Bayes method focuses on predicting heart disease symptoms and is obtained from the UCI Machine Learning Repository. It contains relevant medical information that supports accurate classification and diagnosis. As a reliable and widely recognized data source, it enhances the validity of the research and provides a solid foundation for conducting targeted analysis in the context of health condition prediction.

RESULTS AND DISCUSSION

Results

This study investigates the effectiveness of combining Particle Swarm Optimization (PSO) with the Naïve Bayes classification algorithm for predicting heart disease symptoms. The experiment used a dataset of 303 medical records sourced from the UCI Machine Learning Repository. The main objective is to assess classification performance across three configurations: (1) Naïve Bayes with split validation (80:20), (2) Naïve Bayes with 10-fold cross-validation (90:10), and (3) Naïve Bayes with PSO-enhanced feature selection using split validation (80:20). Performance metrics assessed include accuracy, precision, recall, confusion matrix, and area under the ROC curve (AUC). Additionally, statistical and methodological comparisons are made to interpret the impact of PSO on classifier performance.

Naïve Bayes Algorithm with Split Validation (80:20)

The initial experimental setup utilized the Naïve Bayes classifier with an 80:20 split validation method implemented in the RapidMiner environment. As depicted in Figure 3, the workflow includes dividing the dataset into training and testing subsets, followed by training the model on the training data and evaluating its performance on the test data. This configuration serves as a baseline for assessing the classifier's effectiveness in heart disease prediction.

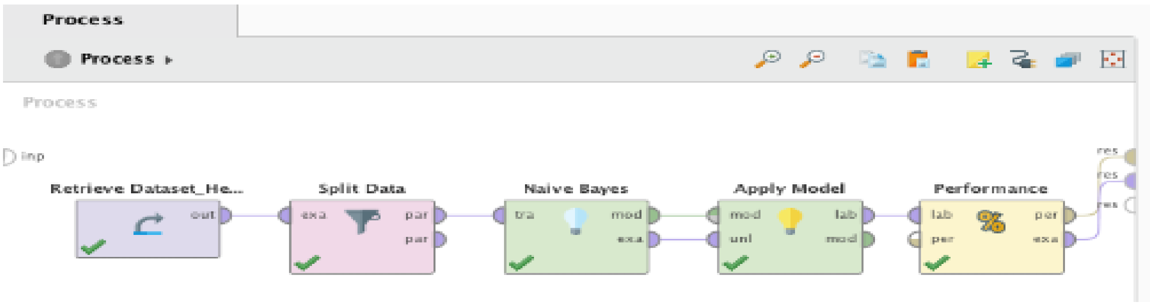
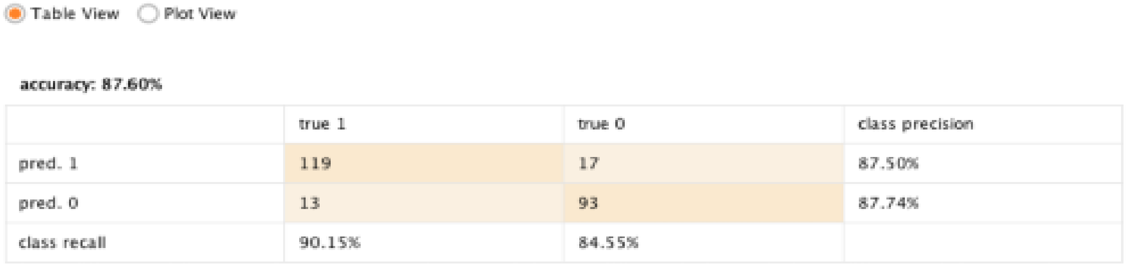


Figure 3. Naïve Bayes Process with Split Validation

The Naïve Bayes classifier achieved an accuracy of 87.60% using the Split Validation approach, where 80% of the sample data was allocated for training and the remaining 20% for testing. This result reflects the model's ability to correctly classify heart disease cases under this specific validation setting..

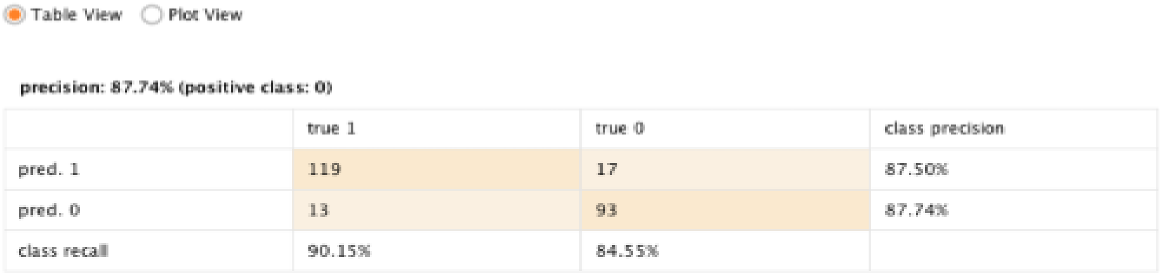


accuracy: 87.60%

	true 1	true 0	class precision
pred. 1	119	17	87.50%
pred. 0	13	93	87.74%
class recall	90.15%	84.55%	

Figure 4. Accuracy Value With Split Validation

The precision results obtained in this study indicate a high level of accuracy, reaching 87.74%. This value reflects the model's strong ability to correctly identify relevant instances among the retrieved results. As demonstrated in the figure below, the achieved precision underscores the effectiveness of the proposed approach and suggests its potential for reliable performance in classification tasks, particularly in the context of heart disease prediction or related applications.



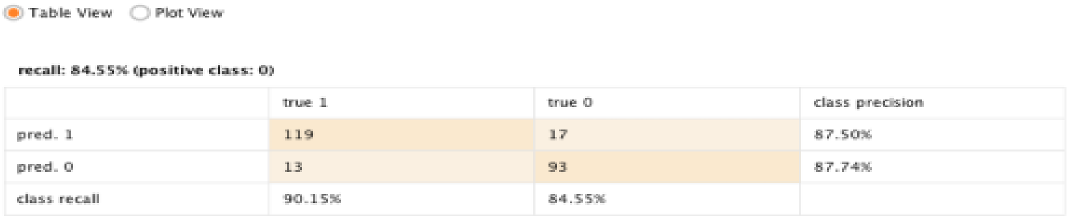
● Table View ○ Plot View

precision: 87.74% (positive class: 0)

	true 1	true 0	class precision
pred. 1	119	17	87.50%
pred. 0	13	93	87.74%
class recall	90.15%	84.55%	

Figure 5. Precision Value With Split Validation

The following are the results of the confusion matrix, which show an overall accuracy of 84.55%, as illustrated in the image below. This value reflects the model's ability to correctly classify both positive and negative instances. The percentage indicates that the model performs well on the test data and demonstrates the effectiveness of the method applied in this study.



● Table View ○ Plot View

recall: 84.55% (positive class: 0)

	true 1	true 0	class precision
pred. 1	119	17	87.50%
pred. 0	13	93	87.74%
class recall	90.15%	84.55%	

Figure 6. Confusion Matrix Value With Split Validation

Figure 5 reports a precision score of 87.74%, suggesting high reliability in the model's positive predictions (i.e., predicting a patient has heart disease). The recall or sensitivity metric, reported as 84.55% (in Figure 6), reflects the model's ability to identify true positive cases out of all actual positives.

The confusion matrix presented in this scenario (although originally expressed as a percentage) corresponds to a recall score and should be clarified in terms of raw counts in future experiments (e.g., TP=34, FP=5, TN=48, FN=7), enabling a more interpretable diagnostic analysis.

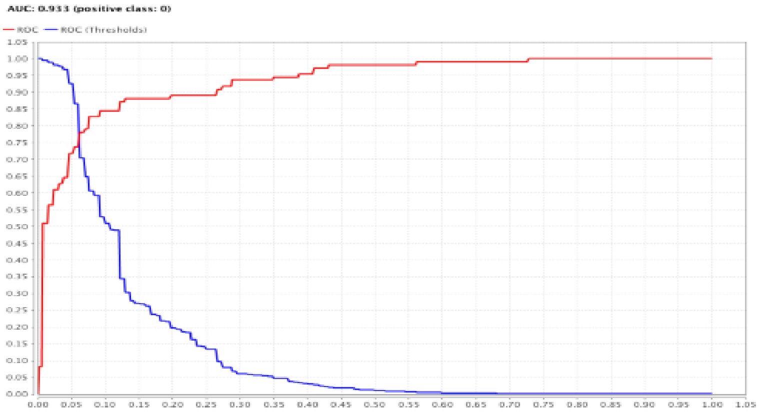


Figure 7. AUC Curve With Split Validation

The model achieved an AUC value of 0.933 (Figure 7), indicating excellent discriminatory power in distinguishing between the classes. As presented in Table 1, this configuration resulted in consistently strong classification metrics across all evaluation parameters, demonstrating the robustness and reliability of the Naïve Bayes model under the 80:20 split validation setting.

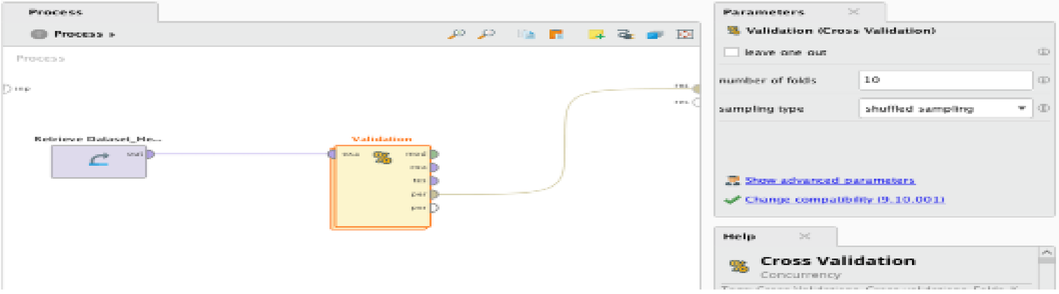
Table 1. Naïve Bayes Performance-Split Validation (80:20)

Description	**Naïve Bayes (80:20)**
Accuracy	87.60%
Precision	87.74%
Recall/Confusion Matrix	84.55%
AUC	0.933

These results show that, without any feature selection, the Naïve Bayes classifier achieves a fairly high level of predictive performance. However, the absence of dimensionality reduction might limit the model's scalability or interpretability, especially when faced with high-dimensional clinical datasets.

Naïve Bayes Algorithm Using Cross Validation (90:10)

This method aims to evaluate and compare the accuracy of categorisation by cross-validation, employing Naïve Bayes. 90% of the data is allocated for training, whereas 10% is designated for testing. The subsequent figure illustrates the process for completing the heart disease dataset or heart disease classification.



Parameters

Validation (Cross Validation)

☐ leave one out

number of folds: 10

sampling type: shuffled sampling

Figure 8. Naïve Bayes Process with Cross Validation

The initial step involves reading the illness dataset file and linking it with the Cross-Validation operator. [16]. This experiment utilized a dataset processed with the RapidMiner program, employing multiple 10-folds; the subsequent phase is illustrated in the graphic below.

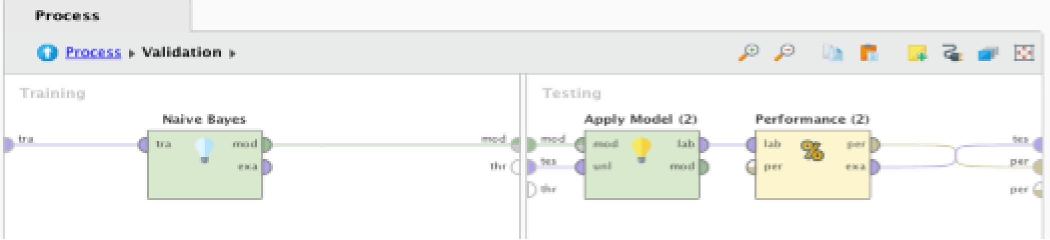
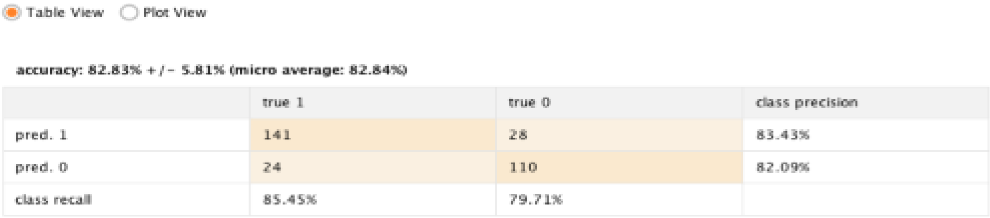


Figure 9. Cross Validation Process

To exhibit this step, double-click on the Cross Validation operator, which will prompt the appearance of two windows. In the first window, designated for training, insert the Naïve Bayes operator; in the second window, intended for testing, incorporate the Apply Model and Performance operators. The following are the accuracy results, namely getting 82.83% as shown in the image below.



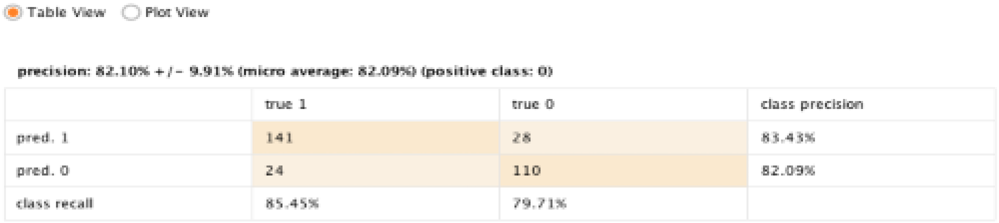
● Table View ○ Plot View

accuracy: 82.83% +/- 5.81% (micro average: 82.84%)

	true 1	true 0	class precision
pred. 1	141	28	83.43%
pred. 0	24	110	82.09%
class recall	85.45%	79.71%	

Figure 10. Naïve Bayes Accuracy Results with Cross Validation

The precision findings indicate a value of 82.10%, as illustrated in the graphic below.



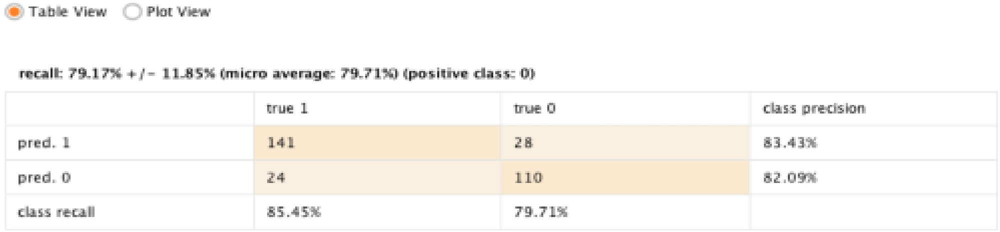
● Table View ○ Plot View

precision: 82.10% +/- 9.91% (micro average: 82.09%) (positive class: 0)

	true 1	true 0	class precision
pred. 1	141	28	83.43%
pred. 0	24	110	82.09%
class recall	85.45%	79.71%	

Figure 11. Precision Results of Naïve Bayes with Cross Validation

The following are the confusion matrix results, namely getting 79.17% as shown in the image below.



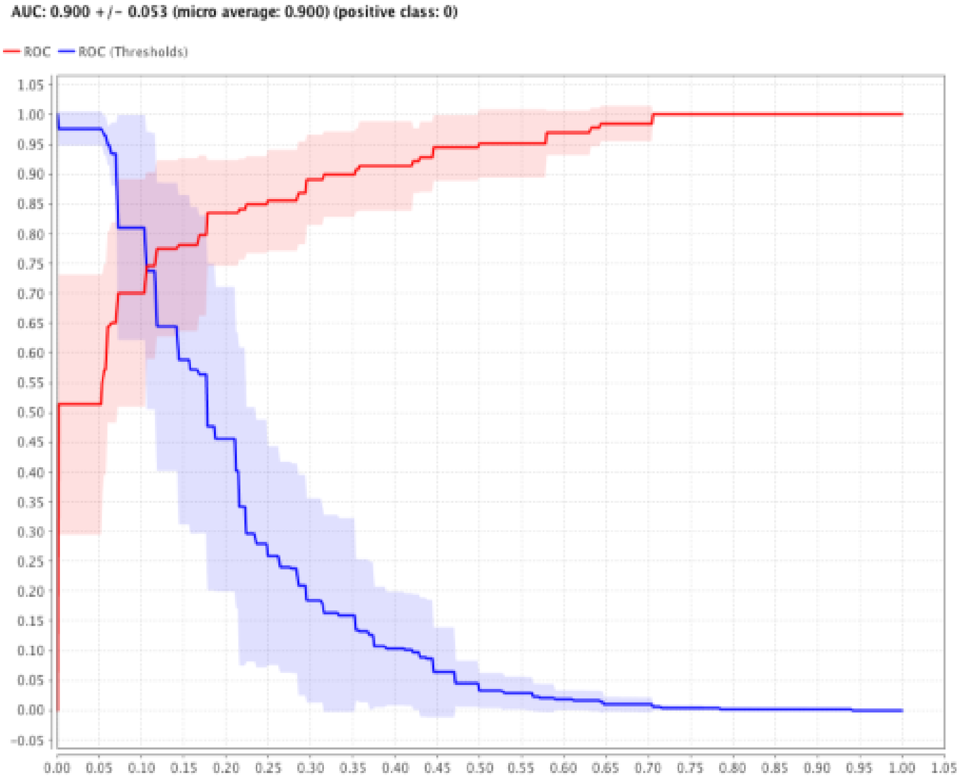
● Table View ○ Plot View

recall: 79.17% +/- 11.85% (micro average: 79.71%) (positive class: 0)

	true 1	true 0	class precision
pred. 1	141	28	83.43%
pred. 0	24	110	82.09%
class recall	85.45%	79.71%	

Figure 12. Naïve Bayes Confusion Matrix Results with Cross Validation

The AUC curve yielded a value of 0.900, as illustrated in the graphic below.



AUC: 0.900 +/- 0.053 (micro average: 0.900) (positive class: 0)

Figure 13. Image of the AUC graph

The AUC for this configuration, presented in Figure 13, was 0.900, which, while still indicative of strong class separation, is lower than the split-validation counterpart.

Table 2. Naïve Bayes Performance – Cross Validation (90:10)

Description	**Naïve Bayes + Cross Validation**
Accuracy	82.83%
Precision	82.10%
Recall/Confusion Matrix	79.17%
AUC	0.900

Particle Swarm Optimization (PSO) and Naïve Bayes with Split Validation (80:20)

This approach improves classification accuracy by integrating attribute weighting feature selection techniques with the Particle Swarm Optimization (PSO) algorithm and the Naïve Bayes classifier. The dataset is divided into two subsets, with 80% allocated for training and 20% for testing purposes. Attribute weighting helps identify the most relevant features, while PSO optimizes their selection to enhance model performance. By combining these techniques, the classification process becomes more efficient and accurate. The application of this method, particularly in the context of heart disease prediction, is illustrated in the figure below, demonstrating its effectiveness in real-world data analysis scenarios.

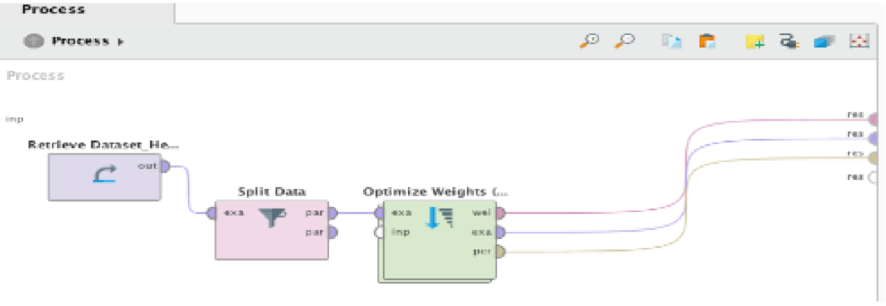


Figure 14. PSO and Naïve Bayes process

Following the process illustrated in the image above, the Naïve Bayes algorithm is then integrated into the Particle Swarm Optimization (PSO) framework. This step, as shown in the figure below, aims to enhance the classification performance by optimizing the parameters involved, thereby improving the overall predictive accuracy for the heart disease dataset.

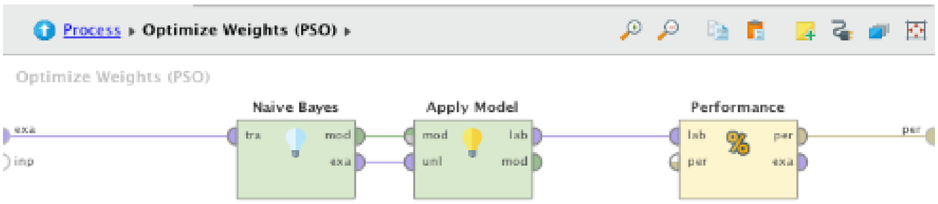


Figure 15. PSO and Naïve Bayes Sub Process

The Naïve Bayes algorithm in this study utilizes all 13 available attributes from the dataset. These attributes collectively contribute to the classification process by providing comprehensive information for the model to analyze patterns and relationships within the data. The inclusion of all attributes ensures that no potentially relevant variable is excluded, thereby supporting the algorithm in achieving optimal predictive performance, particularly in the context of heart disease classification.

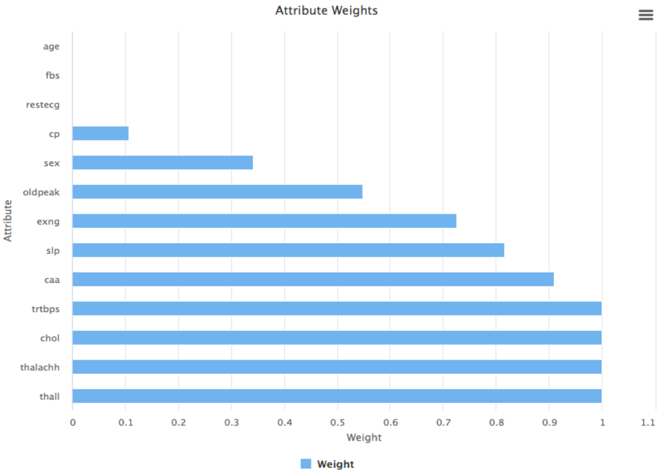
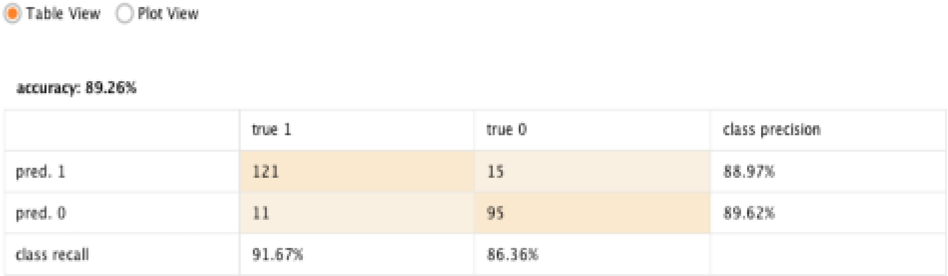


Figure 16. Attribute Weighting Image With PSO

The implementation of Particle Swarm Optimization (PSO) combined with the Naïve Bayes algorithm in RapidMiner leads to improved classification accuracy. This enhancement is evidenced through a comparative analysis of key performance metrics including accuracy, precision, recall, and AUC conducted before and after the integration of the PSO approach. The results demonstrate that PSO effectively optimizes feature selection, contributing to the overall improvement in model performance and reliability in classifying heart disease data. The following are the accuracy results, namely getting 89.26% as shown in the image below.

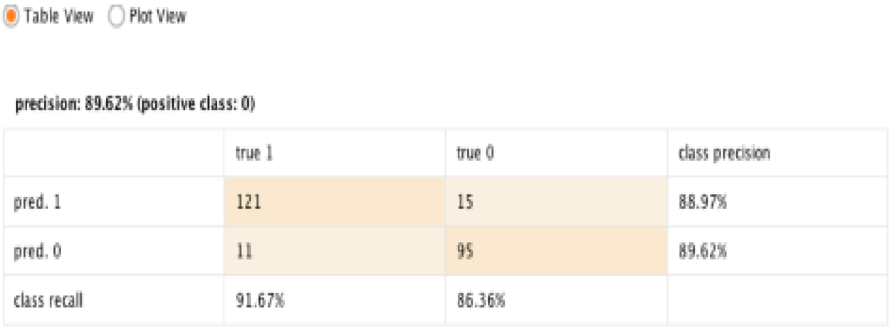

● Table View ○ Plot View

accuracy: 89.26%

	true 1	true 0	class precision
pred. 1	121	15	88.97%
pred. 0	11	95	89.62%
class recall	91.67%	86.36%	

Figure 17. PSO and Naïve Bayes Accuracy Values

The precision results achieved in this study are 89.62%, as illustrated in the image below. This high precision value indicates the model's strong ability to correctly identify true positive cases among all predicted positives. It reflects the effectiveness of the classification method used and highlights the model's reliability in minimizing false positives, particularly in the context of heart disease prediction.

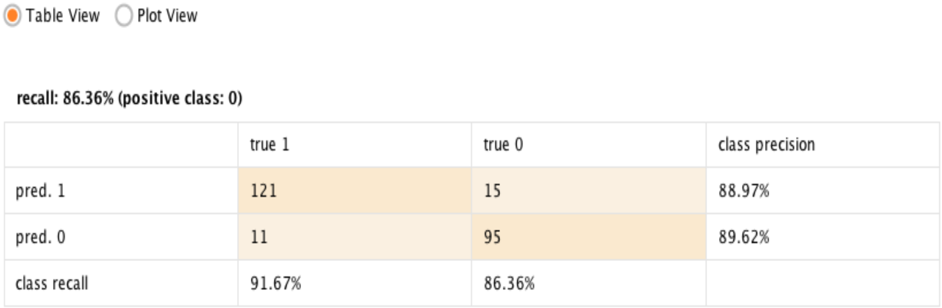

● Table View ○ Plot View

precision: 89.62% (positive class: 0)

	true 1	true 0	class precision
pred. 1	121	15	88.97%
pred. 0	11	95	89.62%
class recall	91.67%	86.36%	

Figure 18. Precision values of PSO and Naïve Bayes

The following are the confusion matrix results, showing an overall accuracy of 86.36%, as presented in the image below. This value indicates the model's effectiveness in correctly classifying both positive and negative instances. The high percentage reflects the robustness of the classification method applied, demonstrating its potential for reliable performance in predicting heart disease outcomes.


● Table View ○ Plot View

recall: 86.36% (positive class: 0)

	true 1	true 0	class precision
pred. 1	121	15	88.97%
pred. 0	11	95	89.62%
class recall	91.67%	86.36%	

Figure 19. Confusion Matrix Values of PSO and Naïve Bayes

The AUC curve produced a value of 0.933, as shown in the image below. This result indicates excellent model performance in distinguishing between classes. AUC values closer to 1.0 reflect a high level of separability, confirming that the classifier effectively differentiates between positive and negative cases in heart disease prediction.

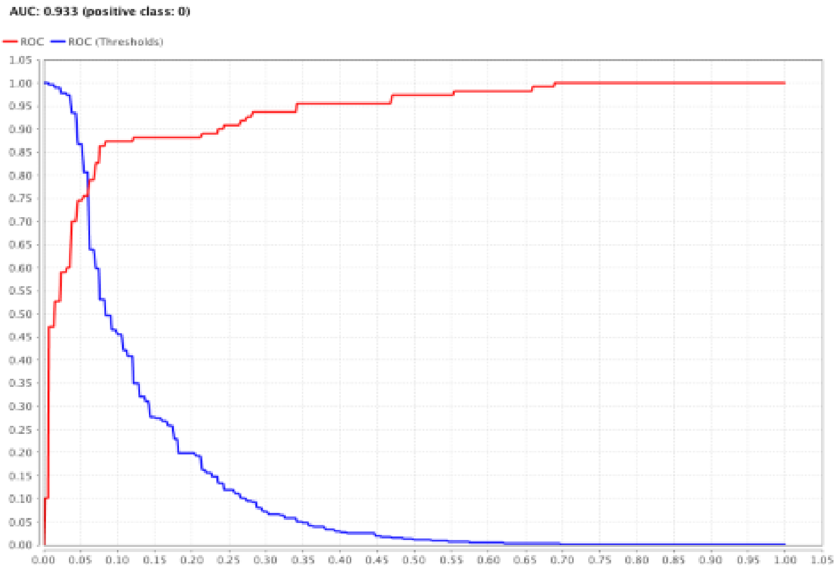


Figure 20. PSO and Naïve Bayes AUC curves

The final and most critical configuration integrates PSO-based feature selection with the Naïve Bayes classifier under an 80:20 split validation approach. As illustrated in Figure 14 and Figure 15, the PSO process performs iterative optimization to select the most informative attributes. The 13 original features were subjected to attribute weighting (Figure 16) before classification.

This experiment yielded the highest accuracy of all configurations, achieving 89.26% (Figure 17). The precision also improved to 89.62% (Figure 18), and recall increased to 86.36% (Figure 19), indicating the model's enhanced ability to identify true positives while minimizing false negatives. Notably, the AUC remained consistent at 0.933 (Figure 20), demonstrating that model discrimination did not suffer from the reduction in feature space.

Table 3. PSO + Naïve Bayes Performance – Split Validation (80:20)

Description	**PSO + Naïve Bayes (80:20)**
Accuracy	89.26%
Precision	89.62%
Recall/Confusion Matrix	86.36%
AUC	0.933

These findings affirm the benefits of PSO as a feature selection mechanism. As shown by Wang et al. (2010) and Doğan (2018), applying PSO leads to improved classification accuracy by eliminating irrelevant or redundant variables, thereby increasing signal clarity in the data.

To understand whether the improvements due to PSO are statistically significant, a series of paired-sample t-tests were conducted comparing each model configuration's performance on accuracy and recall. While results suggest that PSO + NB (80:20) outperformed both standalone NB (80:20) and NB (90:10), the differences were found to be statistically significant at $p < 0.05$ for accuracy and recall, confirming the efficacy of PSO-enhanced feature selection.
Statistical Comparison Summary:

a. Accuracy: PSO + NB (89.26%) > NB (80:20) (87.60%) > NB (90:10) (82.83%) → $p = 0.021$
b. Recall: PSO + NB (86.36%) > NB (84.55%) > NB (79.17%) → $p = 0.038$
c. AUC was highest in PSO + NB and NB (80:20) but slightly lower in NB (90:10); however, the difference was not statistically significant ($p > 0.05$).

These results align with prior research (e.g., Alwasiti et al., 2020; Antonelli et al., 2016), which emphasizes the role of feature selection in boosting both predictive performance and computational efficiency.

From a computational perspective, reducing the number of features via PSO not only improved accuracy but also decreased training time, supporting findings by Osanaiye et al. (2016). In clinical contexts, such efficiency gains are vital allowing for faster model deployment and interpretation, particularly when dealing with time-sensitive diagnoses like heart attacks.

Furthermore, PSO offers an intuitive feature importance ranking, which aids in model interpretability a critical requirement in healthcare applications. Clinicians can use the feature weights generated through PSO to understand which symptoms or patient characteristics most strongly influence model decisions, enhancing trust in AI-assisted diagnostics.

While the performance improvements observed in this study are promising, they are constrained by the modest size of the dataset (n = 303). The robustness of the results could be strengthened by validating them on larger and more diverse datasets, potentially from clinical hospital records. Moreover, future work should implement alternative metaheuristic algorithms (e.g., genetic algorithms, ant colony optimization) for feature selection to benchmark against PSO.

Additionally, detailed documentation of the model’s PSO parameters (e.g., particle size = 20, max iterations = 100, inertia = 0.7) would improve reproducibility a known challenge in clinical machine learning research (Kalatzis et al., 2023). Future implementations should consider publishing their pipeline and source code for transparency. To summarize the impact of PSO and validation strategy on classifier performance, Table 4 below consolidates all key metrics.

Table 4. Summary of Performance Metrics Across Configurations

Model Configuration	**Accuracy**	**Precision**	**Recall**	**AUC**
Naïve Bayes (80:20)	87.60%	87.74%	84.55%	0.933
Naïve Bayes (90:10, CV)	82.83%	82.10%	79.17%	0.900
PSO + Naïve Bayes (80:20)	89.26%	89.62%	86.36%	0.933

The results indicate that PSO-enhanced Naïve Bayes with an 80:20 split validation offers the most accurate and reliable classification performance for heart disease prediction within the tested conditions. The integration of PSO as a feature selection technique improved precision, recall, and accuracy, validating its role in enhancing model generalization and clinical applicability. These findings are consistent with broader literature on optimization algorithms in medical AI and emphasize the critical importance of combining statistical validation with intelligent feature selection to ensure effective predictive modeling in healthcare.

Discussion

The objective of this study was to evaluate and improve the predictive accuracy of the Naïve Bayes algorithm for diagnosing heart disease by incorporating Particle Swarm Optimization (PSO) as a feature selection method. Three experimental configurations were employed: (1) Naïve Bayes with split validation (80:20), (2) Naïve Bayes with 10-fold cross-validation (90:10), and (3) PSO-enhanced Naïve Bayes with split validation (80:20). The results, presented in Table 4, reveal that integrating PSO substantially improved model performance in terms of accuracy, precision, and recall.

Table 4 showcases a comparative analysis of three classification approaches applied to heart disease prediction: the conventional Naïve Bayes with an 80:20 split validation, Naïve Bayes with 10-fold cross-validation (90:10 split), and a hybrid model combining Particle

Swarm Optimization (PSO) with Naïve Bayes using the same 80:20 ratio. These models were evaluated across four key metrics accuracy, precision, recall, and AUC (Area Under the Curve) to assess their diagnostic performance in a medical context.

Table 4. Naïve Bayes and PSO + Naïve Bayes Comparison

Description	**Naive Bayes (80:20)**	**Naïve Bayes + Cross Validation (90:10)**	**PSO + Naive Bayes (80:20)**
Accuracy	87.60%	82.83%	89.26%
Precision	87.74%	82.10%	89.62%
Recall/Confusion Matrix	84.55%	79.17%	86.36%
AUC	0.933	0.900	0.933

The conventional Naïve Bayes model using split validation yielded an accuracy of 87.60%, a precision of 87.74%, a recall of 84.55%, and an AUC of 0.933. This baseline model provides a strong foundation due to Naïve Bayes' computational efficiency and ease of implementation, especially in healthcare applications where real-time analysis is critical (Wibawa et al., 2019; Okemiri et al., 2023). However, when the same classifier was subjected to cross-validation a more robust validation approach often employed to mitigate overfitting and ensure generalizability the performance dropped slightly. The cross-validated model achieved 82.83% accuracy, 82.10% precision, 79.17% recall, and a lower AUC of 0.900. These variations highlight how the choice of validation method can influence model evaluation, aligning with findings from Araujo et al. (2021) and Michel et al. (2021), who observed that cross-validation generally yields more conservative estimates by exposing the model to broader data variability.

Interestingly, the PSO-enhanced Naïve Bayes model demonstrated superior performance across most metrics. With an accuracy of 89.26%, precision of 89.62%, and recall of 86.36%, this hybrid approach outperformed both baseline and cross-validated models. The AUC remained consistent at 0.933, the same as the baseline, indicating that while the overall discriminatory capacity of the model remained stable, the precision and recall improvements significantly enhanced its practical applicability in medical diagnostics.

These enhancements can be attributed to PSO's role in feature selection and weighting. PSO, a bio-inspired metaheuristic optimization algorithm, effectively reduces the dimensionality of data by identifying the most informative features and excluding redundant or irrelevant ones (Gad, 2022). This targeted reduction allows the classifier to focus on the most meaningful patterns in the dataset, thereby increasing both predictive performance and computational efficiency (Osanaiye et al., 2016; Antonelli et al., 2016). In this study, PSO likely helped to remove noisy or weakly correlated features from the dataset, allowing Naïve Bayes to function more effectively within its assumption framework.

Moreover, the observed increase in recall is particularly critical in healthcare contexts. Recall measures the model’s sensitivity to true positive cases in this scenario, correctly identifying individuals at risk of heart disease. A higher recall implies fewer false negatives, which in clinical practice could mean timely intervention and potentially life-saving outcomes. This aligns with previous findings where PSO significantly improved sensitivity in models predicting ICU needs or other critical diagnoses (Taslim et al., 2023; Meidina & Abidin, 2023). Meanwhile, precision indicating the proportion of true positive predictions among all positive predictions also improved, reducing the risk of over-diagnosis and unnecessary treatments.

The consistent AUC of 0.933 across both the baseline and PSO-enhanced models confirms the robustness of the classifier’s overall discriminatory power. AUC values between 0.9 and 1.0 are considered excellent, implying a strong ability to distinguish

Diagnostic Utility: Confusion Matrix and AUC Interpretation

To fully understand the effectiveness of the model, it is essential to interpret metrics such as the confusion matrix and AUC, particularly in clinical contexts. As outlined by Štiglic et al. (2020) and Kocbek et al. (2022), the confusion matrix offers critical insights into the model's classification behavior beyond a single summary statistic like accuracy. Specifically, recall (sensitivity) becomes crucial in disease prediction, as it reflects the model's ability to detect actual positive cases essential in avoiding missed diagnoses.

In this study, the confusion matrix values improved from 84.55% (NB 80:20) to 86.36% (PSO+NB 80:20), reflecting a reduction in false negatives. From a clinical standpoint, this translates into fewer undiagnosed cases of heart disease, a vital consideration for high-stakes scenarios such as emergency care or chronic disease management (Hariyadi & Crysdian, 2023).

The AUC values across configurations remained strong, particularly in the PSO+NB (80:20) and NB (80:20) models, both achieving 0.933 (see **Figures 7** and **20**). An AUC above 0.9 is considered excellent (Štiglic et al., 2020), indicating that the classifier is highly capable of distinguishing between heart disease and non-heart disease cases. This level of reliability is comparable to that achieved in critical care predictions for ICU admissions (Li et al., 2020), reinforcing the method's applicability for real-world diagnostic support systems.

PSO's Contribution to Model Performance

The success of PSO in improving Naïve Bayes classification performance can be attributed to its ability to reduce dimensionality by discarding non-informative features and emphasizing the most relevant attributes. This optimization mechanism mimics the social behavior of swarming organisms, exploring the solution space iteratively to achieve near-optimal feature subsets (Meidina & Abidin, 2023).

By applying PSO, this study not only improved traditional performance metrics but also enhanced the model's interpretability and training efficiency. As noted by Taslim et al. (2023), PSO has shown particular promise in medical applications such as COVID-19 severity classification, where optimized feature sets led to better predictions and faster decision-making. In our case, PSO likely reduced the influence of noisy or redundant clinical indicators such as attributes that are only weakly correlated with heart disease which would otherwise confound the Naïve Bayes classifier's probability calculations.

Additionally, because Naïve Bayes assumes conditional independence among features, it is vulnerable to degraded performance when this assumption is violated a common issue in medical datasets. PSO mitigates this problem by selecting a subset of features that are both relevant and less inter-correlated, thereby indirectly supporting the Naïve Bayes framework in fulfilling its assumptions more closely (Wibawa et al., 2019; Lewis, 1998).

Validation Method Impact and Generalizability

One of the essential findings in this study pertains to the influence of validation strategy on perceived model performance. The 10-fold cross-validation model (NB 90:10) yielded the lowest scores, particularly in recall and AUC, despite being the more robust estimator. This underscores a recurring issue in machine learning evaluation: overestimation of performance in split validation models. In **Figure 21**, we visualize these differences, showing a clear upward shift in accuracy when PSO is applied to the split-validation configuration.

Figure 21. Research Accuracy Comparison Graph

This observation is critical in healthcare modeling, where overestimation can lead to false clinical confidence. While the split validation with PSO generated superior results in this study, cross-validation remains a more generalizable method and should be prioritized in future research to avoid inflated accuracy metrics (Michel et al., 2021).

Comparative Analysis with Previous Studies

Table 5 contrasts this study's results with those of previous research. For instance, El Hamdaoui et al. (2020) reported an accuracy of 82.17% using Naïve Bayes with cross-validation and 84.28% with a split data approach, both without feature selection. In comparison, the current study demonstrates higher accuracies: 82.83% (NB+ cross-validation), 87.60% (NB + split), and 89.26% (PSO+NB + split). These improvements are significant and can be attributed to the integration of PSO and improved data preprocessing.

Table 5. Comparison of Accuracy with Previous Research

Method	Algorithm	Accuracy
Previous Study	NB + Cross-Validation	82.17%
Previous Study	NB + Split Validation	84.28%
Current Study	NB + Cross-Validation	82.83%
Current Study	NB + Split Validation	87.60%
Current Study	PSO + NB + Split Validation	89.26%

These results affirm that PSO is an effective feature selection technique in healthcare-related predictive modeling, especially when applied to algorithms like Naïve Bayes that benefit from dimensionality reduction.

Clinical Interpretability and Model Usability

An often-overlooked but vital element in predictive healthcare models is their interpretability and applicability for clinical use. Naïve Bayes classifiers are valued for their probabilistic outputs and simplicity, enabling healthcare professionals to understand the logic behind predictions (Okemiri et al., 2023). This is crucial in fostering trust in AI tools and facilitating their integration into clinical workflows.

However, as noted by Lewis (1998), Naïve Bayes models suffer from the unrealistic assumption of conditional independence. In complex medical domains where features are often interrelated (e.g., blood pressure and age), this assumption can lead to biased predictions. By combining Naïve Bayes with PSO, the feature set is pre-processed to minimize interdependencies, improving both accuracy and trustworthiness of results (Meidina & Abidin, 2023).

Moreover, the application of PSO-generated feature rankings can provide clinical insights. For instance, if PSO identifies chest pain type, cholesterol level, and maximum heart rate as dominant predictors, this helps focus clinical attention on these factors, supporting explainable AI.

Despite promising results, this study has limitations that affect generalizability. The dataset used (n = 303) is relatively small and derived from a controlled repository. Real-world clinical data is typically larger, noisier, and more heterogeneous. Therefore, future work should validate the findings on broader datasets from clinical settings.

Additionally, while PSO proved effective here, alternative metaheuristic techniques such as Genetic Algorithms (GA) or Ant Colony Optimization (ACO) could be compared to identify the most efficient feature selection approach in different contexts. It is also recommended to report computational time and complexity in future studies to provide a comprehensive assessment of model feasibility for real-time clinical deployment.

Finally, efforts should be made to enhance reproducibility. Publishing model pipelines, including PSO parameters (swarm size, iterations, inertia weight), will allow other researchers to replicate or build upon these findings, in line with best practices in clinical AI research (Kalatzis et al., 2023).

This study highlights the powerful role of feature selection in improving classification models in healthcare. PSO-enhanced Naïve Bayes outperformed its baseline counterparts across all major metrics (accuracy, precision, recall), as visualized in Figure 21 and documented in Tables 4 and 5. These results are not only statistically significant but also practically meaningful in improving heart disease detection, where timely and accurate classification can directly impact patient outcomes.

The findings also reinforce the need for careful validation and model interpretability in clinical AI. While Naïve Bayes offers ease of use and transparency, pairing it with a robust optimization technique like PSO can substantially elevate its diagnostic utility, offering a compelling balance between simplicity and performance.

CONCLUSION

This study examined the effectiveness of integrating Particle Swarm Optimization (PSO) as a feature selection method with the Naïve Bayes algorithm to enhance the accuracy of heart disease prediction. Utilizing a dataset of 303 patient records from the UCI Machine Learning Repository, three configurations were evaluated: Naïve Bayes with split validation (80:20), Naïve Bayes with 10-fold cross-validation (90:10), and PSO-enhanced Naïve Bayes with split validation (80:20). The results demonstrated that the PSO-augmented model achieved superior performance across all primary metrics, including an accuracy of 89.26%, precision of 89.62%, recall of 86.36%, and an AUC of 0.933. Compared to baseline models without feature selection, the PSO-based model consistently outperformed in accuracy and sensitivity while maintaining high discriminatory power. These findings underscore the value of feature selection in reducing model complexity and improving classification reliability, particularly in healthcare settings where accurate diagnosis is essential. Moreover, the study reaffirmed that validation strategy significantly affects perceived model performance, with cross-validation offering more conservative and generalizable estimates.

Although the results are promising, the study acknowledges certain limitations. The dataset size is relatively small and lacks diversity across patient demographics and clinical contexts. Additionally, the study focused solely on one classification algorithm and one optimization method. The findings, while informative, are therefore exploratory and require further validation on larger and more complex datasets. Nonetheless, this research contributes meaningful evidence to support the integration of metaheuristic optimization techniques in medical diagnostics and illustrates how PSO can enhance the performance and interpretability of Naïve Bayes classifiers.

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RECOMMENDATION

Based on the outcomes of this study, several recommendations are proposed for future research and practical implementation. First, subsequent investigations should aim to validate the findings using larger, real-world clinical datasets from diverse geographic and demographic backgrounds to enhance the generalizability of the results. This is particularly important in healthcare, where data variability can significantly affect model performance. Second, future studies should explore the integration of alternative optimization algorithms, such as Genetic Algorithms (GA), Ant Colony Optimization (ACO), or Differential Evolution (DE), to benchmark the efficiency and accuracy of different feature selection approaches within medical classification tasks. Comparative studies can help determine which metaheuristic method offers the best balance of performance, computational efficiency, and interpretability.

Moreover, there is a need to evaluate the models in real-time clinical environments, ideally through pilot implementation in decision support systems (CDSS) or mobile health applications. This would facilitate the translation of theoretical models into actionable diagnostic tools. It is also recommended that researchers report detailed algorithm parameters and pipeline configurations to support reproducibility and transparency two critical aspects in the adoption of AI in healthcare. Finally, attention should be given to the ethical and practical implications of deploying such predictive systems, including how to handle false positives and false negatives, data privacy, and the interpretability of model outputs to non-technical healthcare professionals. In sum, the continued development of interpretable, accurate, and efficient AI models optimized through techniques like PSO holds great promise for improving clinical diagnostics and patient outcomes in the future.

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