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Performance Comparison of Breast Cancer Classification Methods: Naive Bayes vs. Support Vector Machine

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Abstract — Breast cancer is a global health issue where early detection and accurate diagnosis play a key role in improving patients' chances of successful recovery. Despite their widespread use and proven effectiveness, traditional diagnostic methods have limitations that have prompted the development of computational approaches. Machine learning is one such approach. Numerous prior studies have investigated various algorithms, including Naive Bayes and Support Vector Machine (SVM), for breast cancer classification; however, research directly comparing their performance on the same dataset is still limited. This study evaluates the efficacy of Naive Bayes and SVM methods for classifying breast cancer diagnoses as benign or malignant using the publicly available Wisconsin Diagnostic Breast Cancer (WDBC) dataset. The research stages include data collection, preprocessing, splitting the dataset into training and test sets at 70% to 30%, standardizing features for the SVM model, applying both algorithms, and evaluating performance using metrics such as accuracy, precision, recall, and F1-score. The test results indicate that the SVM algorithm achieved an accuracy of 98.25%, precision of 100%, recall of 95%, F1-score of 98%, and MCC of 0.96. Conversely, the Naive Bayes algorithm achieved 94.15% accuracy, 94% precision, 91% recall, a 93% F1-score, and 0.88 MCC. The comparison results indicate that SVM outperforms Naive Bayes on this dataset, especially in reducing false- positive and false-negative rates. This research is expected to serve as a valuable resource for medical professionals and researchers seeking to select the appropriate machine learning algorithm for early breast cancer detection.

Keywords – accuracy, breast cancer, classification, naive bayes, support vector machine (SVM)

I. INTRODUCTION

Cancer is a non-communicable disease characterized by abnormal cells that grow uncontrollably and can attack and spread between cells and even between body tissues [1]. In 2022, the GLOBOCAN 2022 database recorded that no less than 2.3 million women were diagnosed with breast cancer, representing approximately 11.6% of all cancer cases globally [2]. This fact shows that breast cancer is the most common type found in women worldwide. Breast cancer occurs when cells in breast tissue grow uncontrollably and abnormally. The development of these cancer cells can lead to the attack and domination of the healthy tissue surrounding the breast [3]. In Indonesia, breast cancer is also the leading cause of cancer deaths in women [4][5]. According to data released by the International Agency for Research on Cancer (IARC) through the GLOBOCAN database, an estimated 19,292,789 new cancer cases and 9,958,133 cancer-related deaths occurred worldwide in 2020 [2].

Breast cancer, which affects women, is considered one of the most dangerous types of cancer[3]. Various factors, including abnormalities in blood cells and the supporting tissues around breast ducts, contribute to the causes. This cancer can be benign or malignant [6]. Although conventional diagnostic procedures such as biopsies, mammograms, and Magnetic Resonance Imaging (MRI) remain the gold standard, they are often time-consuming and require a high level of medical expertise. These limitations can lead to delayed diagnoses and delayed treatment initiation. Consequently, the development of faster, non-invasive, and more accurate diagnostic techniques has become a key focus in both medical and computational research.

In this era of globalization, the rapid development of machine learning offers new opportunities to apply technology to medical diagnosis and prediction in the healthcare sector. Machine learning can analyze complex datasets, including clinical, demographic, and pathological variables, and uncover hidden patterns that might not be detected by human observation. This approach offers significant potential for more accurate and efficient medical decision-making. Machine learning can also be applied to breast cancer prediction due to its ability to detect complex relationships among data variables. This allows for greater accuracy in classifying tumor types as benign or malignant [7]. Various machine learning methods are often used to address breast cancer prediction problems, particularly classification algorithms such as Artificial Neural Networks (ANNs), SVMs, Neural Networks, and Naive Bayes [7]. Support Vector Machine (SVM) is a classification algorithm that separates data into distinct classes by constructing a maximum-margin hyperplane (MMH) based on the closest data points, known as support vectors [8]. Artificial Neural Networks (ANNs) are highly effective methods that have been applied in various fields, including pattern recognition, classification, prediction, and regression of analyzed data [9]. Unlike Naive Bayes, which calculates probabilities using the independence assumption [10]. Each of these methods has its strengths, weaknesses, and levels of accuracy.

In previous studies, the Support Vector Machine (SVM) method has been applied to classify breast cancer types, distinguishing between malignant and benign cases. The findings revealed that SVM achieved a high classification accuracy of approximately 95% [11]. In a study by Barus et al. (2023) [12], classification accuracy was evaluated using the Naïve Bayes algorithm without feature selection, yielding 74.586% [12]. Meanwhile, in the study conducted by Fahrurrozy (2023) [13] , the results indicate that KNN achieved the highest accuracy, outperforming the Decision Tree algorithm. In the subclass prediction task, SVM achieved 80% accuracy, slightly outperforming CatBoost [14]. In addition to domestic research, there is significant international research on brain tumors using machine learning. SVM, Random Forest, and ANN methods to analyze MRI images, concluding that each technique has unique advantages and its application should be tailored to specific clinical scenarios [15].

The difference between this research and previous studies lies in the focus on direct comparison and head-to-head accuracy between two fundamental yet philosophically different classification methods: Naive Bayes, which is based on Bayes' theorem and the assumption of feature independence, and SVM, which finds the optimal decision boundary (hyperplane) in high-dimensional space. The Naive Bayes classification method assumes that the identified class category affects every attribute in the data. This method has several advantages over other classification techniques, including its ability to handle both qualitative and quantitative data, its computational efficiency, and its ease of implementation and understanding [16].

Although many previous studies have used these two algorithms separately or as part of broader comparative analyses, this research will specifically evaluate the performance of each method individually on the same breast cancer dataset. The goal is to determine which algorithm empirically demonstrates superior accuracy. To ensure a fair comparison, the data preprocessing and basic model parameter settings were standardized.

The primary objective of this research is to compare the accuracy of the Naive Bayes and Support Vector Machine (SVM) methods in classifying breast cancer diagnoses as either benign or malignant using a public dataset. Through this comparison, the study seeks to identify and rank the algorithm that demonstrates superior performance. This work provides deeper insights into the relative effectiveness of these two algorithms in breast cancer diagnosis. It serves as a valuable reference for researchers and medical practitioners in selecting the most suitable machine learning approach for early detection and accurate diagnosis.

II. RESEARCH METHOD

This research comprises interconnected, mutually supportive stages that contribute to the overall data analysis process, as shown in Figure 1.

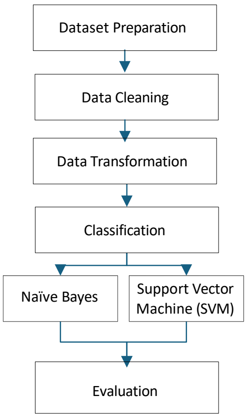


Fig.1. Research Framework

This research began by downloading the WDBC dataset, which consists of 569 records and has 32 attributes. The CSV operator in Python is used to read datasets for processing in subsequent stages. After the data is successfully read, the next step is data preprocessing to ensure data quality and readiness for machine learning analysis, such as column identification, data cleaning, and encoding categorical variables. Next, the data is split into two groups: training and test. 70% of the data is used to train the model, and the other 30% is used to test how well the model works. Then, the algorithms Naïve Bayes and SVM were applied individually. The Gaussian Naïve Bayes model was initialized and trained using the feature-selected training data (X_train) and target (y_train). SVM, on the other hand, will use the Radial

Basis Function (RBF) kernel with *C=1*. It will be set up and trained using the scaled training data (X_train_scaled) and target (y_train). Using class_weight="balanced" also helps address potential class imbalance in the dataset.

After both models are trained, an evaluation phase is conducted to assess each model's performance on the test data. The evaluation metrics used include accuracy, precision, recall, F1-score, and the confusion matrix. The final step is to compare the accuracy results of the two methods directly. From this comparison, it will be determined which algorithm demonstrates superior classification performance on the breast cancer dataset used.

A. Dataset Preparation

The first step in this research is the data collection phase. The dataset is loaded using the Python code pd.read_csv('wdbc.data', delimiter=','). The dataset used is wdbc.data. The dataset used is breast cancer data taken from the UCI Machine Learning Repository. The dataset consists of 569 patient entries with 32 attributes, including patient ID and diagnosis label, where 'M' indicates malignant and 'B' indicates benign. After the loading process is complete, the columns in the dataset are named manually using the command df.columns = names, as the wdbc.data file does not include a header row by default.

B. Data Cleaning

The data cleaning stage involves removing irrelevant information and correcting problematic entries, such as null values or data inconsistencies [17]. This process is essential for eliminating noise and inconsistencies, ensuring the data are adequately prepared for subsequent analysis. At this stage, two main procedures are performed: removing redundant columns and checking or handling missing values. In the redundant column removal process, the ID column is excluded from the dataset, as it serves only as a unique identifier for each sample and does not contribute predictive information relevant to cancer diagnosis classification. Removing this column reduces data dimensionality and minimizes the risk of overfitting. Meanwhile, the checking and handling of missing values are conducted to identify and, if necessary, address incomplete data across all columns.

C. Data Transformation

At the data transformation stage, the preprocessed data will be converted into a format more suitable for analysis. This process involves changing the format or scale of the data to optimize the performance of machine learning algorithms. The data transformation stages are presented in Figure 2.

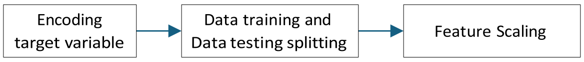


Fig. 2. Process at the Data Transformation Stage

Based on Figure 2, during the encoding process, the categorical variable diagnosis—initially represented by the characters ‘M’ and ‘B’—is converted to a binary numerical format, where 1 denotes Malignant and 0 denotes Benign. This transformation is essential because machine learning classification algorithms require target labels in numerical form. Subsequently, the preprocessed dataset is divided into two subsets: 70% for training and 30% for testing. This data split ensures that the model can learn from a sufficient portion of the data while retaining an independent set for evaluating its performance [18]. The parameter random_state=42 ensures that the data splitting process remains consistent and can be replicated across executions. It is to provide controlled randomness, which is essential for comparing models [19]. The final step is feature scaling, a crucial step in the SVM algorithm. This process scales each feature so that it has a mean of zero (μ=0) and a standard deviation of one (σ=1). This uniform scale is essential for SVM because the algorithm calculates distances between data points, and features with larger value ranges can disproportionately dominate these calculations, resulting in suboptimal model performance.

D. Classification

Classification refers to the process of grouping object data using models or functions that accurately distinguish each class [20]. The classification phase is the central component of the modeling process, in which machine learning algorithms are applied to construct predictive models. In this stage, two algorithms—Naïve Bayes and Support Vector Machine (SVM)—are employed. The GaussianNB class from the Scikit-learn library is used to implement the Naïve Bayes classifier, while the SVC (Support Vector Classifier) from the sklearn.The SVM module is used for the SVM model. The overall classification process for both methods is depicted in Figure 3.

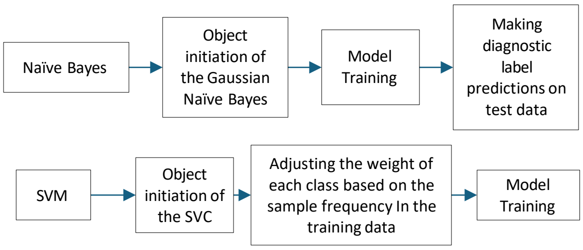


Fig. 3. Classification Process

In the Naïve Bayes method, the initial process is to initialize a Gaussian Naïve Bayes model object, followed by training the Naïve Bayes model using the training data (X_train) and the corresponding diagnostic labels (y_train). In the training, the learning model estimates the probability parameters for each feature and each class (benign or malignant) under the assumption of feature independence. The final step is to predict the diagnostic labels for the test data (X_test). These prediction results (prediks) are then compared to the actual labels (y_test) to evaluate the model's performance.

In contrast, in the SVM method, the model initialization is performed by configuring the SVM parameters, namely the kernel using the Radial Basis Function (RBF), parameter C=1, random_state=42, and class_weight='balanced'. The next step is to adjust the weights for each class based on the sample frequency in the training data. This is very useful when there is class imbalance (e.g., more benign than malignant samples) because it helps the model pay equal attention to both classes, preventing it from being overly biased toward the majority class. Next, the SVM model will be trained using the scaled training data (X_train_scaled) and the corresponding target labels (y_train). During this process, SVM searches for the optimal hyperplane that best separates the classes in the feature space transformed by the kernel.

E. Evaluation

The evaluation stage assesses and validates the performance of the Naïve Bayes and SVM models trained on the test dataset. Several evaluation metrics are employed to measure model performance, including accuracy [21], precision [22], recall [23], F1-score [22], confusion matrix [24], and the Matthews Correlation Coefficient (MCC) [25].

Accuracy represents the ratio of correctly predicted instances to the total number of predictions, reflecting the model's overall correctness. Precision measures the proportion of correctly predicted positive cases among all predicted positive cases. Recall (or sensitivity) denotes the ratio of correctly predicted positive cases to the total number of actual positive cases [14]. The F1-score is the harmonic mean of precision and recall, indicating the balance between the two metrics. Furthermore, the confusion matrix provides a comprehensive summary of the model's classification results by displaying the number of True Positives (TP), True Negatives (TN), False Positives (FP), and False Negatives (FN). Additionally, the Matthews Correlation Coefficient (MCC) is calculated to evaluate the correlation between predicted and actual class labels, with values ranging from −1 to +1. An MCC value of +1 indicates perfect prediction, 0 represents random prediction, and −1 indicates total disagreement between predictions and actual outcomes. The MCC value is computed using Equation (1).

$$MCC = \frac{(TP*TN)-(FP*FN)}{\sqrt{(TP+FP)(TP+FN)(TN+FP)(TN+FN)}} \tag{1}$$

Where TP = True Positive, TN = True Negative, FP = False Positive, FN = False Negative

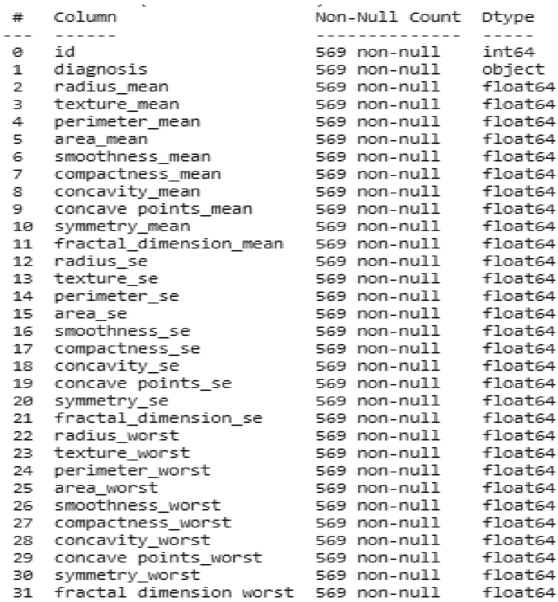
III. RESULTS

A. Breast Cancer Dataset

This study utilizes the Breast Cancer dataset from the UCI Machine Learning Repository. The dataset comprises 569 patient records with 32 attributes, including patient ID and diagnosis labels, where M denotes Malignant and B denotes Benign. The complete list of attributes is presented in Figure 4.

B. Model Development Environment

The implementation and testing of both models were conducted on a system configured with an 11th Gen Intel(R) Core (TM) i5-1155G7 processor running at 2.50 GHz, 8 GB of RAM, and Intel(R) Iris(R) Xe Graphics with 4 GB of memory. The software setup comprised Windows 11 Pro 64-bit, Google Chrome Browser version 138.0.7204.97, and Google Colab (version 2025-06-16) as the Python execution environment.



```
 #   Column                   Non-Null Count  Dtype  
---  ------                   --------------  -----  
 0   id                       569 non-null    int64  
 1   diagnosis                569 non-null    object 
 2   radius_mean              569 non-null    float64
 3   texture_mean             569 non-null    float64
 4   perimeter_mean           569 non-null    float64
 5   area_mean                569 non-null    float64
 6   smoothness_mean          569 non-null    float64
 7   compactness_mean         569 non-null    float64
 8   concavity_mean           569 non-null    float64
 9   concave points_mean      569 non-null    float64
 10  symmetry_mean            569 non-null    float64
 11  fractal_dimension_mean   569 non-null    float64
 12  radius_se                569 non-null    float64
 13  texture_se               569 non-null    float64
 14  perimeter_se             569 non-null    float64
 15  area_se                  569 non-null    float64
 16  smoothness_se            569 non-null    float64
 17  compactness_se           569 non-null    float64
 18  concavity_se             569 non-null    float64
 19  concave points_se        569 non-null    float64
 20  symmetry_se              569 non-null    float64
 21  fractal_dimension_se     569 non-null    float64
 22  radius_worst             569 non-null    float64
 23  texture_worst            569 non-null    float64
 24  perimeter_worst          569 non-null    float64
 25  area_worst               569 non-null    float64
 26  smoothness_worst         569 non-null    float64
 27  compactness_worst        569 non-null    float64
 28  concavity_worst          569 non-null    float64
 29  concave points_worst     569 non-null    float64
 30  symmetry_worst           569 non-null    float64
 31  fractal dimension worst  569 non-null    float64
```

Fig. 4. Breast Cancer Atributes Dataset

C. Experimental Results

Performance measurement assesses the model's ability to distinguish between malignant and benign samples. In this subsection, the performance of breast cancer classification methods is measured and compared using several standard evaluation metrics—namely, accuracy, precision, recall, F1-score, and the confusion matrix (true negatives, false positives, false negatives, and true positives). The test results will be presented quantitatively and analyzed to assess the reliability of both methods, Naïve Bayes and Support Vector Machine (SVM), as shown in Table 1.

Table 1. Performance Results Comparison

No	***Evaluation Metrix***	***Naïve Bayes***	***Support Vector Machine (SVM)***
1	Accuration	94,15%	98,25%
2	Precision	94%	100%
3	Recall	91%	95%
4	F1-Score	93%	98%
5	True Negatives	99	107
6	False Positives	4	0
7	False Negatives	6	3
8	True Positives	62	61

Beyond the standard evaluation metrics—accuracy, precision, recall, and F1-score—this study also uses the Matthews Correlation Coefficient (MCC) to evaluate model performance further. The MCC provides a robust measure of the correlation between predicted and actual classifications, effectively balancing true positives and false negatives [25]. This makes it especially suitable for datasets with imbalanced class distributions. The corresponding MCC results are presented in Table 2.

Table 2. MCC Measurement

Method	***FN***	***FP***	***TN***	***TP***	***MCC***
Naïve Bayes	6	4	99	62	0,88
SVM	3	0	107	61	0,96

The explanation and analysis of the experimental results will be discussed in the discussion section.

IV. DISCUSSION

From Table 1 above, the evaluation results indicate that the Support Vector Machine (SVM) algorithm consistently outperforms Naïve Bayes across all testing metrics. The SVM achieved 98.25% accuracy, while Naïve Bayes achieved only 94.15%. This difference indicates that SVM has better capabilities in recognizing data patterns and minimizing overall classification errors. SVM achieved 100% precision, meaning all its predictions for malignant classes were correct. Conversely, Naïve Bayes achieved only 94% accuracy, due to 4 false positives (cases predicted as malignant when they were not). This means that SVM is better at distinguishing between malignant and non-malignant classes.

The recall value also demonstrates the superiority of SVM, which is 95% compared to 91% for Naïve Bayes. This means that SVM can detect more actual malignant cases, thereby reducing the number of potentially dangerous false negatives in the context of early detection. This increase indicates that the SVM model is more sensitive to positive data.

The F1-score, which combines precision and recall into a single balanced measure, showed that SVM achieved 98% and Naïve Bayes only 93%. The high F1-score for SVM indicates that this model is not only accurate but also consistent in classifying both classes without significant bias.

Analysis of the confusion matrix reinforces these results. SVM showed no false positives and only three false negatives (Figure 5), while Naïve Bayes produced four false positives and six false negatives (Figure 6). This condition confirms that SVM has a lower error rate and higher classification reliability. Overall, these results demonstrate that SVM provides an optimal balance between accuracy, precision, and sensitivity, making it the most suitable method for this dataset. The slightly lower performance of Naïve Bayes is thought to be due to the data not fully satisfying the assumption of feature independence, leading to less accurate predictions.

Based on Table 2, the SVM model achieves an MCC of 0.96, while the Naïve Bayes model achieves 0.88. Both values fall into the very high category, indicating a strong correlation between the model's predictions and the actual labels. However, the difference of 0.08 between the two models provides an important indication of performance stability and reliability. An MCC value of 0.96 for SVM indicates that this model is almost achieving perfect classification. The absence of false positives (FP = 0) strengthens the previously obtained precision by 100%. Additionally, there were only three false negatives, indicating that SVM is not only accurate in identifying positive classes but also highly sensitive in detecting all actual cases. Thus, SVM demonstrates an optimal balance between precision and sensitivity—two aspects that are often difficult to achieve simultaneously.

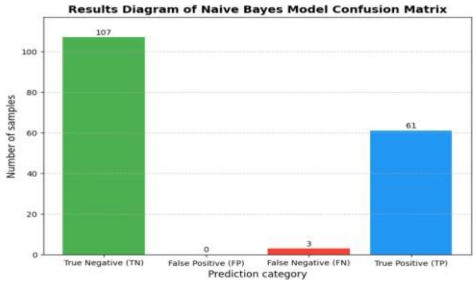


Fig. 5. Diagram of the confusion matrix model SVM

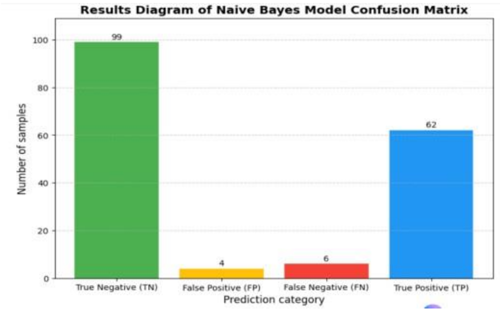


Fig.6. Diagram of the confusion matrix model, naive Bayes

Conversely, Naïve Bayes with an MCC of 0.88 still performed well, but slightly lower. The presence of four false positives and six false negatives indicates that this model tends to misclassify at the boundaries between classes. This aligns with Naïve Bayes, which assumes that features are independent. This isn't always true for image datasets or medical data. As a result, the overall correlation value between the predicted results and the actual labels decreased slightly compared to SVM.

Generally, the high MCC values in both models reinforce the classification system's reliability. Still, the superiority of SVM indicates that this margin-based approach is more robust to data variations. In other words, SVM produces more consistent classification decisions for both positive and negative classes, making it a more suitable algorithm for this research. Based on the analysis of MCC values, it can be concluded that the SVM algorithm shows a stronger correlation between predicted labels and actual labels than Naïve Bayes. This confirms that SVM not only excels in accuracy but also demonstrates high performance stability and consistency in recognizing data patterns across both classes. This result aligns with previous studies that note that SVMs excel at handling high-dimensional data and have outstanding generalization capabilities for non-linear data.

V. CONCLUSION

The results indicate that the Support Vector Machine (SVM) performs more consistently than Naïve Bayes for breast cancer classification. This confirms the effectiveness of the maximum margin method in handling data complexity and feature relationships. This finding underscores the importance of selecting algorithms that balance accuracy and generalization, especially in medical image-based applications that demand high precision. In practice, this proven, reliable SVM model can serve as the basis for developing precise, adaptive artificial intelligence-based decision-support systems. Looking ahead, research can be directed toward optimizing SVM parameters using metaheuristic algorithms, integrating with adaptive contrast enhancement methods or deep learning models, and testing on more complex datasets to strengthen generalization capabilities and enhance application potential across various image analysis domains.

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