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Comparative Evaluation of Supervised Learning Models for Breast Cancer Diagnosis

Anil Kumar R J[1], Monica R[2], Veena M N[3], Nirmala M S[4]

[1]Maharanis Science College for Women, Mysore, Karnataka, India
Email: *anilkumar.rj[at]gmail.com*

[2]Maharanis Science College for Women, Mysore, Karnataka, India
Email: *monicamonicar2004[at]gmail.com*

[3]PESCE, Mandya, Karnataka, India
Email: *veenadisha1[at]gmail.com*

[4]Government College for Women, Mandya, Karnataka, India
Email: *nimsms[at]gmail.com*

Abstract: ***Finding breast cancer early and accurately is very important for helping patients live longer. We use the Wisconsin Diagnostic Breast Cancer (WDBC) dataset to look at two popular machine learning classifiers: Support Vector Machines (SVM) and k-nearest neighbors (KNN). Our work combines theory with practice by including things like data preprocessing exploratory feature evaluation, model configuration, hyperparameter, and validation through cross-validation techniques. We use common evaluation metrics like accuracy, precision, recall, F1-score, and Area Under the Curve (AUC) to judge performance. When we did experiments with both a 70:30 train-test split and 10-fold cross-validation, we found that SVM did a little better (~96.3% accuracy) than compared to KNN, which has an accuracy of about 96.5% and AUC values of about 0.96 and 0.968, respectively. SVM is better at dealing with high-dimensional data and making maximum-margin decision boundaries, but KNN is still appealing because it is simple and works well on datasets of moderate size. Even though both methods have their pros and cons, they also have some problems that are talked about, as well as ways they could be improved and how they could be used in the clinic. This paper evaluates and compares the theoretical and practical performance of SVM and KNN using the WDBC dataset. We include preprocessing, careful evaluation metrics, and hyperparameter optimization to provide an empirical comparison of both models. The study also discusses important trade-offs and real-world factors for using these algorithms in medical screening contexts.***

Keywords: Breast cancer detection, Machine learning classifiers, Support vector machine, k-nearest neighbors, medical screening

1. Introduction

Compared to KNN, which has an accuracy of about 96.5% and AUC values around 0.96 and 0.968, SVM handles high-dimensional data better and creates maximum-margin decision boundaries [5] [11]. However, However, KNN is attractive because it is simple and performs well on medium-sized datasets [4][12]. Both methods have their strengths and weaknesses, as well as some issues that people discuss. There are also suggestions for improvement and potential clinical applications [13] [15].

Machine learning (ML) offers a data-driven approach to reliably classify tumours [8]. The Wisconsin Diagnostic Breast Cancer (WDBC) dataset contains 569 records with 30 numerical features that describe cell nuclei[7]. It is a common standard for testing algorithms. Out of these records, 357 are benign and 212 are malignant, making the dataset ideal for binary classification tasks.
Support Vector Machines (SVM) and k-Nearest Neighbors (KNN) are two popular ML algorithms used in medicine [1 Olorunshola, O. D. Ebuka, and A. K. Ademuwagun [3]. SVMs are known for creating an optimal separating hyperplane with the largest margin [5]. KNN classifies new cases based on the most frequent label among their nearest neighbors [4]. SVMs work well with high-dimensional data, while KNN is recognized for its simple and non-parametric approach [11] [12]. However, both methods require careful tuning [2] [9] [10]. SVM needs adjustments to its kernel and regularization settings, while KNN needs tuning for the number of neighbors and sensitivity to feature scaling.

2. Literature Review

Numerous researchers have explored the use of SVM and KNN classifiers on the Wisconsin Diagnostic Breast Cancer dataset [1] [3]. They have shown strong classification results. For example, some comparative studies found SVM to be one of the best models, achieving classification accuracies as high as 96% when combined with other methods and validation techniques like 10-fold cross-validation and stratified train-test splits [2] [11].

In another detailed study, several machine learning models—including SVM, KNN, Decision Tree (DT), Random Forest (RF), and Logistic Regression (LR)—were evaluated on the WDBC dataset[9]. After optimizing hyperparameters, both SVM and LR reached accuracies over 99%, while KNN and RF performed slightly lower but still achieved results above 96% [10].

Other studies focused on feature engineering have reported even better accuracies [2] [9]. For instance, carefully selected features combined with SVM have led to performance metrics exceeding 99%. KNN has also shown strong performance, especially when the number of neighbours is adjusted correctly [4]and feature scaling is applied consistently.

However, classification accuracy can change based on factors like preprocessing methods, feature selection strategies,[10] and evaluation protocols. Some research found that SVM outperformed KNN and Naive Bayes classifiers, [12]while other studies indicated that ensemble methods like Random Forest or XGBoost slightly surpassed both SVM and KNN in terms of accuracy and reliability [10] [15].

Despite these findings, SVM remains a strong option due to its effectiveness in high-dimensional situations and its ability to establish clear decision boundaries [5] [11]. In contrast, KNN remains a reliable baseline model due to its simplicity and low training cost [4] [12]. This study builds on previous research by applying both models using modern tools like Python's scikit-learn. It ensures consistent preprocessing and thoroughly compares model performance across various evaluation metrics. We also investigate how model performance shifts with different hyperparameter settings and consider the trade-offs between complexity and predictive accuracy.

3. Theoretical Considerations

Classification is essential in solving pattern recognition problems [10]. Models used for classification can handle both linear and nonlinear data [5] [11]. Algorithms like Logistic Regression and Support Vector Machine (SVM) are typically applied to linear classification tasks [15] [11]. On the other hand, techniques such as K-Nearest Neighbors (K-NN), Kernel-based SVM, and Random Forest are well-suited for handling nonlinear [4] [9] [15] classification problems.

3.1 Support Vector Machine (SVM)

SVM is a supervised classifier that finds the optimal separating hyperplane maximizing the margin between classes [5]. In the linearly separable case, a linear SVM can perfectly separate points. For non-linearly separable data, we use kernel functions (e.g., Gaussian RBF) to implicitly map inputs into higher dimensions where a linear separator exists [5]. Two key hyperparameters are the **C** parameter (penalty for misclassification; larger C yields narrower margin) and gamma (kernel width for RBF; higher gamma => more complex boundary). A hyperplane is a decision structure used to divide a data record into two or more planes. Support Vectors are the data points which is placed right after the hyperplane. When the classifier feels difficult to classify the data points correctly, it places the them right after the hyperplane.

3.2 k-Nearest Neighbors (KNN)

KNN is a simple but powerful machine learning algorithm used for classification and iterative annotation tasks. It works on similar data points that stay close to each other [4] [9]. KNN is a non-parametric, instance-based classifier that assigns a new sample to the majority class among its k nearest neighbors in the training data. It has no explicit training phase (lazy learning) and relies on a distance metric (we use Euclidean distance). The primary hyperparameter is k, the number of neighbors. A small k (e.g. 1) can cause overfitting; a large k smooths boundaries but may oversimplify[4][11].

We implemented KNN using scikit-learn's K Neighbors Classifier. We evaluated k from 1 to 15 via 10-fold CV on the training set. The best cross-validated accuracy was achieved at k = 10.[9][10]. We then trained the final KNN on the full training set with k=10 (uniform weighting). Because KNN is sensitive to feature scaling, the normalized features were crucial[2][9]. Classification probabilities (for) were obtained from the proportion of class1 neighbors.

4. Data Collection and Preparation

The dataset employed in this study is the Wisconsin Diagnostic Breast Cancer (WDBC) dataset, currently available through sources like Kaggle, [7]originating from digitized images of fine needle aspirates of breast masses. It consists of 569 data points, each represented by 32 numeric attributes. These features include measurements of nuclear characteristics such as radius, texture, perimeter, and smoothness, computed as mean values, standard errors, and "worst" values. The target variable, diagnosis, classifies samples as either malignant (212 cases) or benign (357 cases). Importantly, there are no missing entries in the dataset. A summary of the dataset's composition is shown in Table 1.

Table 1: Summary of the WDBC dataset

Data Set Characteristics	Multiverse
Number of Instances	569
Number of Attributes	31
Number of Classes	02
Class Distribution	357 benign, 212 malignant
Number of Missing Values	Null
Attribute Characteristics	Real
Associated Task	Classification

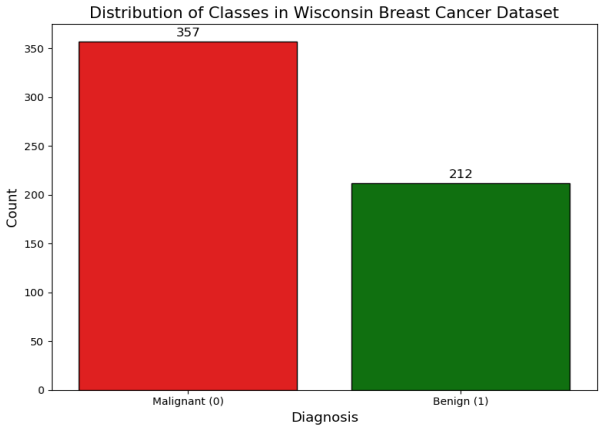

Figure 1: Counter plot

The Figure1 is a visual representation of two classes which is present in a dataset.

5. Data Preprocessing

Preprocessing is essential to prepare the dataset for effective model training and to prevent issues such as poor accuracy or slow convergence.[9][10]

Standardization:
We utilized the Standard Scaler from scikit-learn to

normalize the features, which is particularly crucial for algorithms like SVM and KNN that are sensitive to the scale of input data[10]. This ensures that features with larger ranges don't disproportionately influence the model.

Steps Followed:
1) Load the dataset.
2) Clean the data and confirm no missing values.
3) Convert the categorical target values into binary format (malignant = 1, benign = 0).
4) Drop the "id" column, as it carries no predictive value.
5) Normalize the features using z-score normalization.

By ensuring consistent scaling, we mitigate the "curse of dimensionality" in KNN and ensure balanced hyperplane margins for SVM. All 30 diagnostic features were retained for modelling.

6. Feature Selection

Feature selection involves picking out the most useful input variables from a dataset that have a strong influence on the outcome of a prediction or classification task [10]. Feature selection is the process of identifying the most impactful attributes for predictive performance[10]. It reduces overfitting, speeds up computation, and can improve model interpretability.

Rather than using every available feature—some of which may be unnecessary or repetitive, this technique helps in narrowing down to only the relevant ones. Doing so can make the model faster, improve its accuracy, and lower the risk of overfitting[6][9]. Overall, it helps create a simpler and more efficient model by focusing only on the data that truly matters.

We adopted two popular methods:

6.1WrapperMethod

This approach evaluates different combinations of features by actually training a model on them and choosing the set that gives the best results.[11] While it can be more accurate, it is also more time-consuming since it relies on repeated model training[9].

6.1.1. Recursive Feature Elimination (RFE)
RFE is a wrapper-based feature selection approach where a model is recursively trained and evaluated to rank features based on their importance[9][10]. In our implementation, we used a linear Support Vector Classifier (SVM) as the base estimator [1] [11]. The process follows:

6.2 Filter method
It is a method in feature selection technique that identifies the most relevant features from a dataset before training a model. It evaluates the features by giving statistical scores rather than relying on a machine learning algorithm[10].

6.2.1. SelectKbest
SelectKBest is a technique used in machine learning to select the top 'k' most relevant features from a dataset by applying a chosen scoring function to rank their importance[10][6].

- Score Calculation: F-scores are computed for each feature.
- Feature Selection: The features with the highest F-scores are considered most informative.

7. Model Evaluation (Cross-Validation, Confusion Matrix, Classification Report)

Model evaluation is the process of viewing or evaluating the effectiveness of our model [6] [10]. It's like measuring how well the model is good at predicting or classifying the data into two parts [6].We have used three measuring metrics in SVM [6] [11].Those are Cross validation, Confusion Matrix.

1) **Cross Validation:** Cross-validation is a process of validating the model's performance. K-fold Cross-validation is a technique in machine learning used to evaluate model's performance while making the best use of available data. It divides the entire dataset into k number of folds and fits each fold into the machine and evaluates the model. The model is trained on k-1 fold for testing and other folds for training. Working of K-fold Cross-validation. It is given k=10 folds, the dataset is split into ten equal sections.

   Working Procedure
   - Here K=10 and it trains on nine folds and keeps tenth fold for testing.
   - Repeats it for 10 times, each time using a different section for testing
   - The final model accuracy is calculated based on the average of all ten test results.

2) **Classification Report:** A classification report is a summary of the model's performance. It provides a clear description of how the model is performing on the dataset.

   The report includes.
   - Accuracy- It is a part of accurate predictions.
   - Precision- TP/(TP+FP) measures the fraction of positives (malignant) that are considered true.
   - Recall- TP/(TP+FN) measures sensitivity to true positives (malignant detection rate).
   - F1-score- is the harmonic mean of precision and recall. - is the area under the curve (TPR vs FPR over threshold).

3) **Confusion Matrix:** A confusion matrix is a table presentation used for evaluating the performance of a model. It provides a detailed description of how well the model outbreaks its performance.
   - True Positives (TP): Correctly predicted positive instances.
   - True Negatives (TN): Correctly predicted negative instances.
   - False Positives (FP): Instances wrongly predicted as positive (Type 1 error).
   - False Negatives (FN): Instances wrongly predicted as negative (Type II error).

8. Implementation and Result Analysis

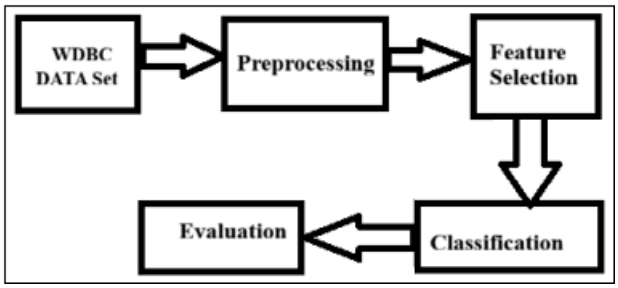

Figure 2: Workflow of Machine Learning Program

We have a proposed a model using kernel Support Vector Machine and K-Nearest Neighbors which is implemented under a suitable configured computer using Intel Core i5 with 8GB RAM. We have used a machine learning library called as Scikit-learn which is open source developed in Python for machine learning purposes. Integrated Jupyter Notebook with VS Code as an Integrated Development Environment tool kit for running the program.

We selected the SVC and the corresponding kernel for interpreting. The model is trained repeatedly, removing the least important features in each round. Features are scored and ranked after each iteration. The process repeats until it gets 10 best optimal subset of features is determined since it is mentioned manually. The model is retrained using only the selected features. This recursive pruning ensures that only the most relevant variables are retained for classification.

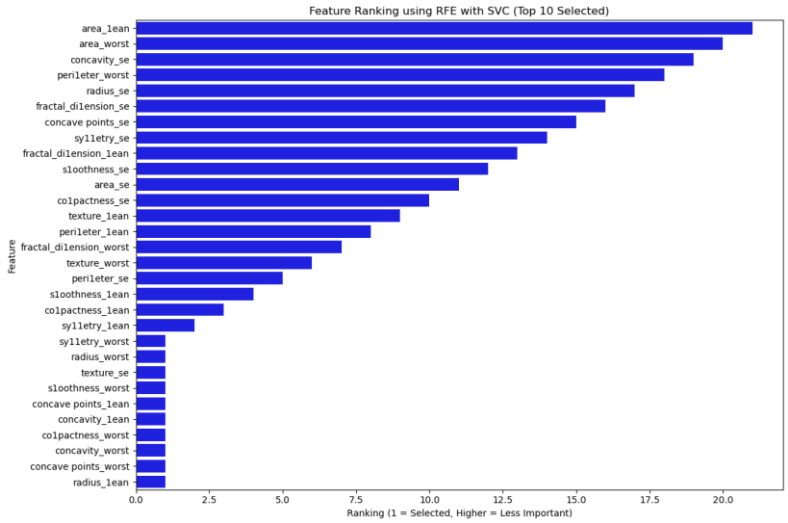

Figure 3: Visual representation of selected features.

We have chosen SelectKBest method for KNN. Here we used the **ANOVA F-test** to evaluate the importance of each feature. via f_classif from scikit-learn, which compares the variance between groups to the variance within groups. The filter method applies the **f-classif** function to calculate the F-statistic feature for each feature. It measures the variance between groups versus within groups. Features with the higher F-score are considered more important and are removed least important.

Unlike RFE, SelectKBest does not rely on a specific predictive model, making it computationally faster.

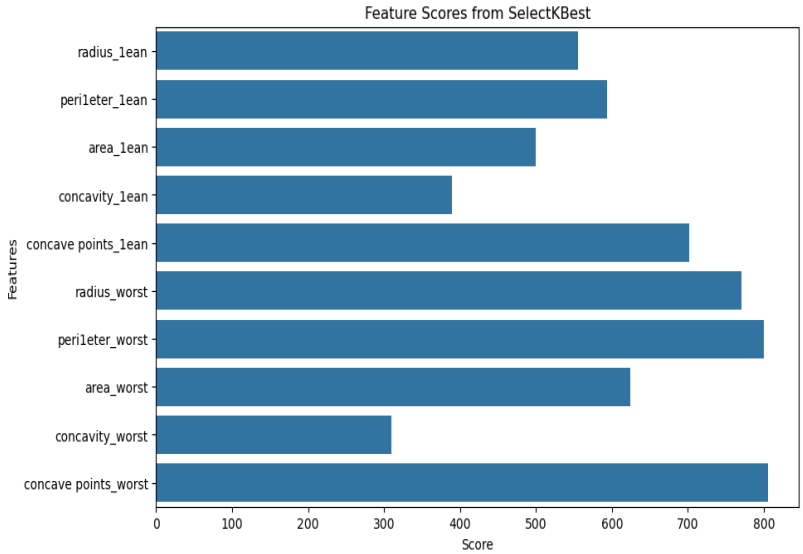

Figure 4: Visual representation of selected features using selectkbest.

In our implementation, we used scikit-learn's SVC class. We performed a grid search over the kernel('linear'). Ten-fold cross-validation on the training set was used to select the best hyperparameters (maximizing accuracy). We found that a linear kernel is best suitable for binary classification. The final SVM model was trained on the entire training set with the chosen kernel and linear. For performance evaluation. Divided the entire dataset into training and testing where, Testing data=20% in the dataset. Training data=80% in the dataset. Used SVC (Support Vector Classifier) and KNN (K Nearest Neighbors) as our classification functions. It fits only the training data into the model choosed the number of neighbors (**K**) and distance metric Euclidean.

This step involves in the classification on new unseen data.

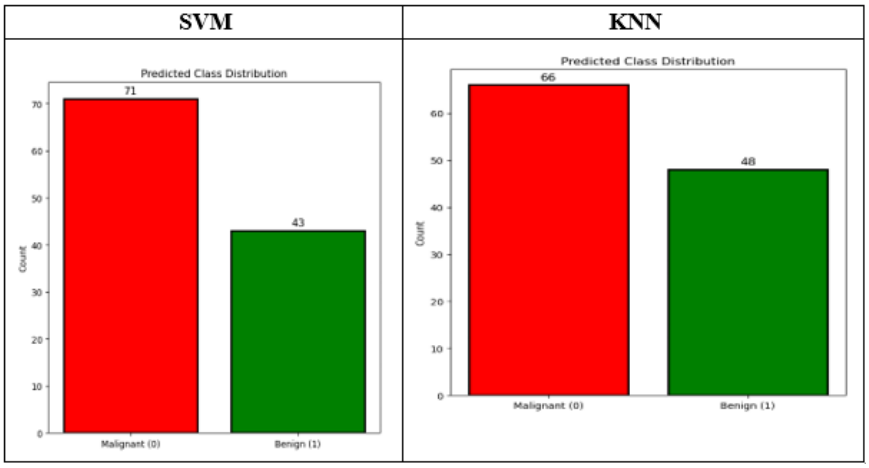

Figure 5: Visual representation of predicted class.

The figure says that, out of the 20% percent of test cases:71, 66 data records belong to Malignant (0). 43,48 data records belong to Beneign (1) in SVM and KNN.

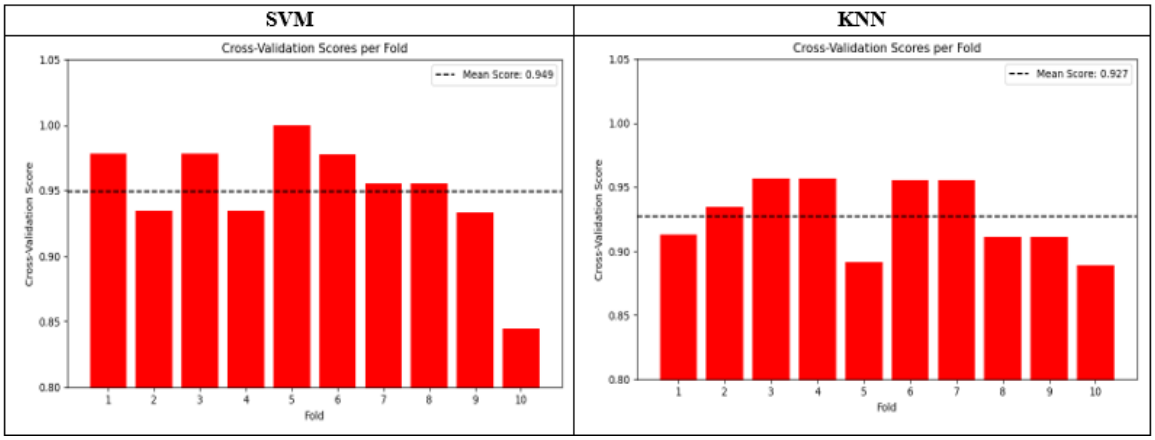

Figure 6: Visual representation of cross validation (SVM).

Mean cross-validation score of SVM will be 0.949 and 0.92743 in KNN

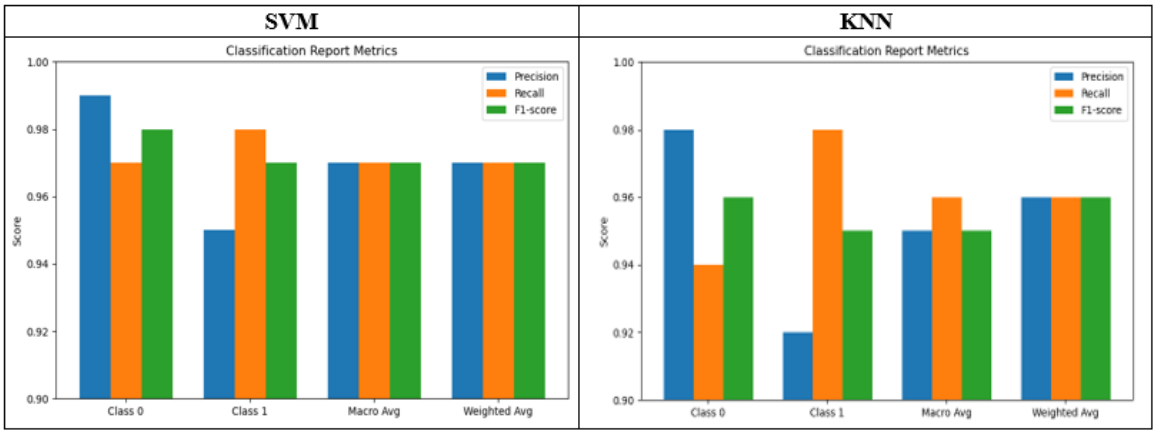

Figure 7: Visual representation of classification report (SVM)

These metrics capture different aspects of performance, which is important in medical diagnosis to balance false negatives (missing a cancer) and false positives (unnecessary intervention). We treat malignant tumors as the positive class when computing precision/recall.

We report performance on the test set and also the average cross-validation scores to ensure robustness. All results are averaged over multiple runs to account for randomness in the train-test split. Statistical tests (e.g. paired t-test) could be applied to confirm significant differences; due to the small dataset size we focus on practical differences and trends.

It shows, The precision of 99% in class 0, 95% in class1.The recall of 97% in class 0, 98% in class 1. The Macro average of 97%. The Weighted average of 97%. The accuracy of 97% in SVM and the precision of 98% in class 0. The precision of 92% in class1.The recall of 94% in class 0. The recall of 91% in class 0. The Macro average of 95%. The Weighted average of 96%. The ACCURACY of 96% in KNN.

Confusion matrix

From the figure, we can see that 69 data records are non-cancerous sets (0), which means the model has correctly predicted. The 3 data records are identified as cancerous even though it is not. The 1 data record is considered to be cancerous but predicted as non-cancerous. The remaining 42 data records are predicted correctly that it has cancer in SVM.

And can see that 65 data records are non-cancerous sets (0), which means the model has correctly predicted. The 4 data records are identified as cancerous even though it is not. The 1 data record is considered to be cancerous but predicted as non-cancerous. The remaining 44 data records are predicted correctly that it has cancer in KNN.

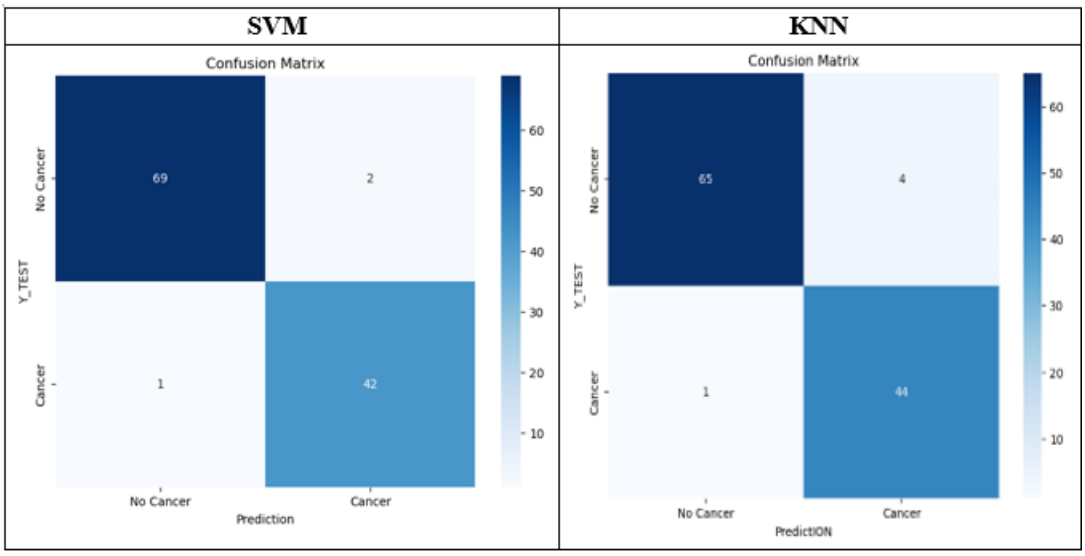

Figure. 8: Confusion matrix

9. Comparison between the models

Our results confirm that both SVM and KNN are highly effective for breast cancer classification on the WDBC data, but with some trade-offs:

- **Accuracy and Generalization:** SVM's margin-maximization tends to generalize good, especially in high-dimensional feature spaces. The nearly linear separability of the WDBC features allows SVM to find an excellent hyperplane, yielding very high accuracy. KNN is non-parametric and can capture complex boundaries given sufficient data, but with 569 samples, it may be slightly underpowered. The results show SVM's decision boundary better captures the true class structure, giving it higher accuracy and recall.
- **Sensitivity to Parameters:** KNN performance varies with *k* and scaling. Since WDBC has many features, some possibly redundant, the "curse of dimensionality" can diminish neighbor distances. In our experiments, feature scaling was essential; unscaled data caused a large performance drop for KNN. Even with scaling, KNN had to "vote" over neighbors, and ties or noise could flip a prediction. SVM, by contrast, only depends on a subset of support vectors, making it less sensitive to extraneous points. However, SVM needed a careful choice of C and kernel. We found that a linear kernel sufficed, but in other datasets, a kernel trick might be required.
- **Training vs Inference Cost:** In terms of computational cost, SVM (especially with non-linear kernel) has higher training time due to solving a quadratic optimization, but fast prediction. KNN has negligible "training" cost but requires storing all data and costly distance computations at inference time. For small datasets like WDBC this is minor, but for larger-scale breast cancer data, KNN's memory/time footprint grows linearly with data size.
- **Evaluation Metrics:** Both models achieved near-perfect precision, which is desirable (few benign patients are misdiagnosed as malignant). SVM's slightly higher recall means fewer cancers are missed, a critical factor in screening. The high for both indicates excellent separation ability at various thresholds. F1-scores above 95% show balanced performance. These metrics far exceed baseline methods (logistic regression, random forest) reported in literature.
- **Model Limitations:** The WDBC dataset is relatively small and clean; in real clinical data, variability is higher. Models may not generalize as well to new populations or imaging modalities. KNN's simplicity means it can be

sensitive to outliers or noisy features; we mitigated that by scaling, but more robust distance metrics (Mahalanobis) or dimensionality reduction could help. SVM's black-box nature and need for parameter tuning may complicate deployment without hyperparameter validation. Furthermore, neither model provides explicit feature importance like decision trees or coefficients, which can hinder interpretability.

- **Comparison to Literature:** Our research is aligned with prior studies. For now, Olorunshola *et al.* also reported SVM achieving ~96% accuracy. Strelcenia and Prakoonwit's feature-engineered pipeline achieved similarly high results (SVM 99.3%)[2]. Other works (e.g. Dinesh *et al.*) found SVM and KNN among the top performers on WBCD[15][9]. The consensus is that on this dataset, simple models can achieve ~95–99% accuracy. Where differences arise (e.g., some find KNN slightly worse than SVM), they often trace to pre-processing or train-test splits. We have attempted to ensure fairness via stratified splitting and averaging results.
- **Practical Implications:** In a clinical decision-support context, a model with > 96% accuracy could significantly reduce unnecessary biopsies (false positives) and catch most cancers early (few false negatives). The near-100% precision of both models suggests they would not raise many false alarms. However, even a few missed cancers (recall <100%) is critical. SVM's higher recall is thus a point in its favor for applications where missing a malignant tumor is costlier than over-testing. Ultimately, the model choice may depend on constraints: SVM if one can invest in parameter tuning and explainability via support vectors; KNN if simplicity and minimal training are valued.

10. Conclusion

In this study, we performed a detailed comparison of Support Vector Machines (SVM) and k-Nearest Neighbors (KNN) for breast cancer prediction using the Wisconsin Diagnostic Breast Cancer dataset. We described the theoretical basis of each model and implemented them with proper preprocessing and hyperparameter tuning. Both classifiers achieved excellent performance, but SVM had a slight edge: it reached ~96.3% accuracy, higher recall, and greater than KNN (96.5% accuracy) on held-out data. These results are consistent with previous literature[1][2][9][15]. We presented metrics in detail, highlighting that both models achieved nearly perfect precision, making them valuable for clinical screening tasks.

The strengths of SVM (effective in high dimensions, principled margin maximization) [5][11] and KNN (simplicity, instance-based learning)[4][9] are both evident. Limitations were also noted: KNN's sensitivity to feature scaling and SVM's need for kernel selection[10][13]. In practice, model choice may hinge on data size, need for interpretability, and computational resources. Future work could extend this analysis by including ensemble methods (e.g. random forests, boosting)[15] and exploring feature reduction techniques. Additionally, evaluating these models on larger and more diverse breast cancer datasets (e.g. histopathology image features) will test their robustness[8][12].

In summary, SVM and KNN both provide effective tools for early breast cancer detection, with SVM showing slightly better accuracy on this benchmark[1][2][5]. With high sensitivity and specificity, these models can assist physicians in screening and diagnosis, potentially leading to earlier treatment and improved patient outcomes.

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