Breast Cancer Classification And Segmentation Using Artificial Intelligence Techniques With Recursive Feature Elimination Over Support Vector Machine

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**Abstract. This project's primary objective is to increase the accuracy of diagnosing ductal carcinoma in situ, a situation in which the death of luminal epithelial cells causes breast cancer. Two computational techniques one based on recursive feature removal and support vector machine classifier is obtained to achieve this improvement. Because of this, it is expected that the Advanced Recursive feature removal Classifier will detect this condition with more accuracy. This study's methodology compares and contrasts the precision expectations of support vector machines and recursive feature elimination. A total of twenty cases were included in the dataset thanks to the establishment of two distinct groups, each with ten samples. With the aid of SPSS, the accuracy of the first group which was evaluated using logistic regression, and the second group which was investigated using the K-Nearest Neighbors algorithm was ascertained. A statistical power of 80% and a confidence level of 95% were obtained from the statistical analysis.**

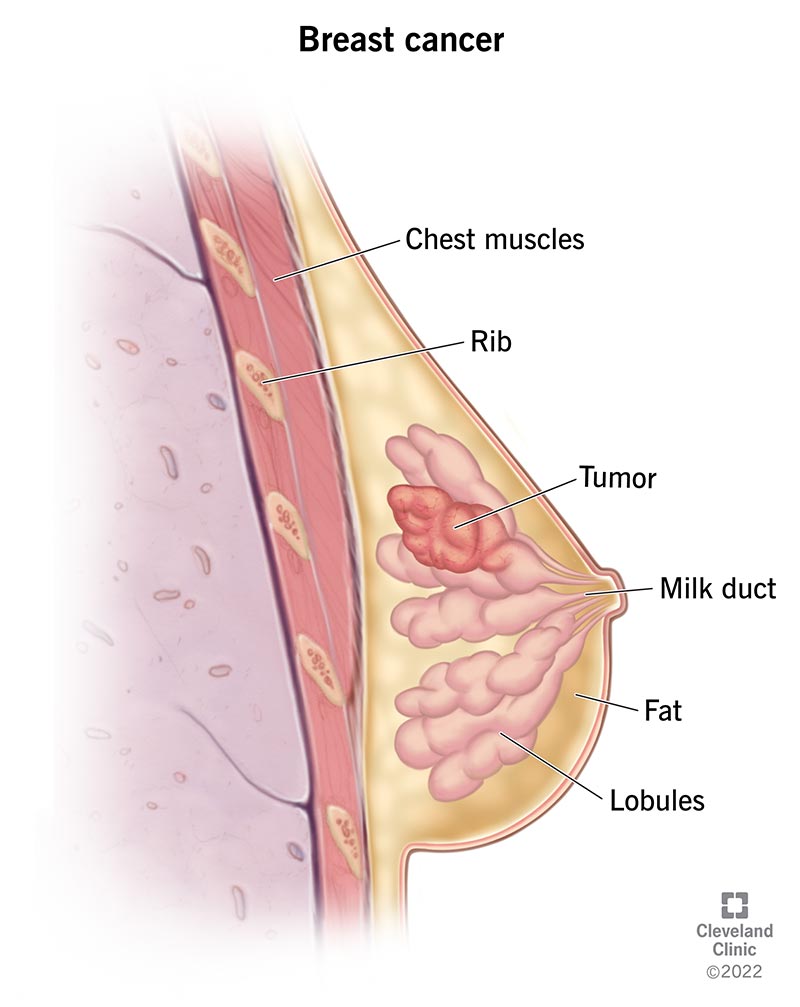
**Keywords: Breast cancer, DCIS, Innovative RF classifier, Recursive feature elimination algorithm, Prediction.**

**Introduction**

"Breast cancer" refers to a specific type of cancer that begins in the breast cells. Usually, it starts in the ducts that transport milk to the nipple or in the lobules, the glands that produce milk. This disorder can show up in a variety of clinical settings, frequently as a consequence of earlier incidents like ductal carcinoma in situ (DCIS). We use artificial intelligence systems to forecast and monitor the course of ductal cancer (Nora M. Hansen). (2016). The study of artificial intelligence is a broad and cutting-edge field with a vast array of possible applications

in numerous fields and industries. According to Geoffrey Hinton et al. (2018), it is critical to the development of applications including automation, natural language processing, healthcare services, and others using these artificial intelligence techniques, we can successfully and proactively monitor the patients’ conditions. Several scholarly works have been published on reputable sites such as PubMed, IEEE Xplore, Google Research, and others. These papers are spread out over several tiers on PubMed, which has about 300+ publications, and Google Researcher, which has about 280+ articles. Based on patient inputs, Artificial intelligence techniques have been built after the inquiry. We have used the Support Vector Machine and Recursive Feature Elimination methods to get successful results (Januzzi et al. 2002). Recursive feature removal is a very effective method within AI models for assessing the risk associated with patient

complaints and clinical reports. With the population and technological advancements of today, a patient with tissue failure from ductal carcinoma might make a big difference. The investigation conducted by Hussain, Ahmad, and Adam (2023) looked at numerous algorithms. With this research, we seek to address several key difficulties in breast cancer diagnosis and segmentation, including the need for robust and efficient analysis techniques, the presence of noise and artifacts in medical images, and the heterogeneity in tumor characteristics. Our goal is to improve the accuracy, sensitivity, and specificity of breast cancer segmentation and detection through the use of AI techniques such as RFE and SVMs. This will ultimately result in more effective and personalized patient care.



**MATERIALS AND METHODS**

The exam administration and review were handled by the Saveetha School of Engineering. The open-source portal Kaggle.com has provided examples of testing and code preparation activities; for example, look for the "breastcancer.csv" dataset. Group 2 anticipates a support

vector machine, while Group 1 sees an inventive recursive feature elimination. (Kazmi and Gaunt 2016) computation. In order to complete the testing clinical.com research, each group is connected to ten exemplar cycles. The test was conducted with an 80% G-power, an alpha value of 0.05, and a beta value of 0.2. (Hoole & Partners, 2009)

**a) MECHANISM OF RECURSIVE FEATURE ELIMINATION ALGORITHM**

It is quite possible to apply it to predict the likelihood of a linked outcome, such as the existence or absence of a specific disease. based on patient data and clinical components, and it might be connected to breast cancer. Each player receives a likelihood score for their gamble appraisal from this recursive feature algorithm, empowering them to make wise decisions. The precision of the recursive feature elimination is calculated as the ratio of all right forecasts to all expectations. The probability that one or more sets of the independent and dependent variables will occur.(Chou and Guimire, 2021).

**RFE ALGORITHM STEPS IN PREDICTION OF BREAST CANCER**

**Here’s a detailed pseudo code for implementing a recursive feature elimination algorithm:**

Step 1: Set up the fundamental libraries and bundles required to perform the Recursive feature computation.

Step 2: Split the computation-related dataset (such as "breast cancer.csv") and reserve it for additional study.

Step 3: Sort the dataset and choose the necessary boundaries to be used in the setup.

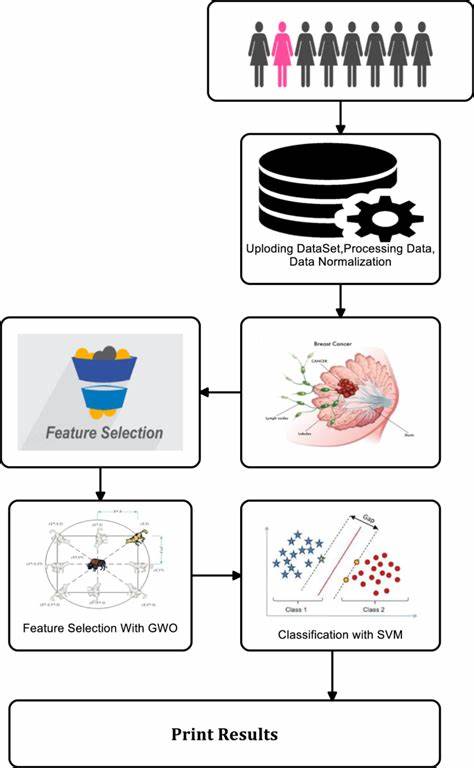
Step 4: Divide the data into stages for testing and preparation using the "train test split" feature of the "model selection" module.

Step 5: To prepare for the computation of recursive feature elimination, import the anticipated libraries and necessary experiments.

Step 6: Classify the model's precision using SPSS.

Step 7: Write a report on the characterization that contains the F1-score, accuracy, precision, and support of the RFE model.

Step 8: Confirm the improved accuracy after integrating the calculated recursive feature removal calculation.



*FIGURE 2: Mechanism Of Scale-Invariant Feature Transform (Sift) Algorithm*

**B ) MECHANISM OF SUPPORT VECTOR MACHINE ALGORITHM**

A Support Vector Machine (SVM) is a supervised learning technique used in artificial intelligence (AI) for regression and classification problems. The basic goal of classification is to identify the hyperplane in a high-dimensional space that best divides data points into different classes. By choosing this specific hyperplane, the margin also known as the distance between the hyperplane and the nearest data points from each class is maximized. Artificial intelligence makes substantial use of support vector machines (SVMs) because of their variety in categorization tasks, flexibility in complex decision limits, and efficiency in high-dimensional areas. (Shawe- Taylor & Associates, 2009

**SVM ALGORITHM STEPS IN PREDICTION OF BREAST CANCER**

Step 1: Provide an overview of the fundamental bundles and libraries required to perform the Support Vector Machine Neighbors (SVM) calculation.

Step 2: Remove the "breast cancer.csv" file.

Step 3: From the dataset, determine and select the necessary boundaries for the setup.

Step 4: Using the "train\_test\_split" function of the "model\_selection" module, divide the data into stages for testing and preparation.

Step 5: Import necessary experiments and anticipated libraries to get the support vector machine's neighbor’s ready.

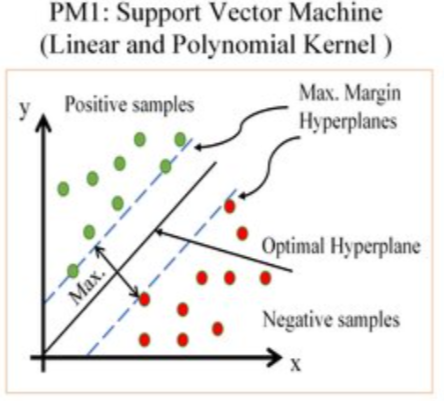
Step 6: Classify the model's precision using SPSS.

Step 7: Create an order report with the F1-score, exactness, accuracy, and support of the SVM model included.

Step 8: Check the increased accuracy after joining the neighboring computation of the support vector machine These instructions describe how to use the core dataset, which consists of around 569 cases, to

train and evaluate the model for breast cancer prediction. Within the dataset are these examples in binary format. 20% to 30% of the data are set aside for model testing, and the remaining 70–80% are used for training. Maximizing data utilization throughout the training phase and guaranteeing the accuracy of the model are the goals.

The research makes use of a laptop with an Intel i3 CPU, 8GB of RAM, Microsoft Windows 10 64-bit, and Jupyter Notebook operating system. Furthermore, the dataset utilized in this project is sourced from the "breast cancert.csv" file, which is available in the open-source dataset repository Kaggle.com (William H. Wolberg, W. Nick Street, and Olvi L. et al. 2021). The dataset's information is meticulously scrutinized to facilitate further research into breast cancer.



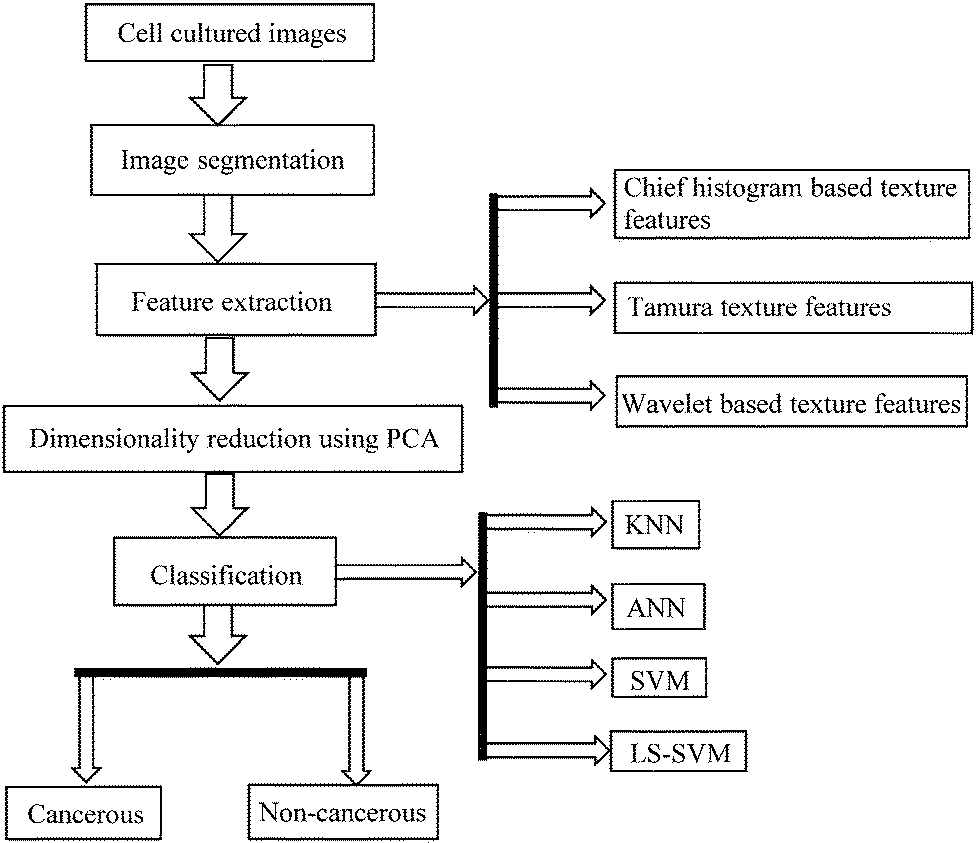
***FIGURE 3: Clustering The Features of cancer with support vector machine algorithm.***

**c) Statistical analysis**

Through performance criteria like accuracy, precision, and recall, statistical analyses evaluate the effectiveness of these techniques and offer insights into their potential clinical utility. The results of the study push the boundariesof AI-powered methods for breast cancer diagnosis and therapy planning. (Otsuka et al. 2010).

The Statistical Analysis says examine how characteristics are distributed among various cancer classes.Runstatistical analyses to find noteworthy variations in feature values between classes.

The Model Assessment says evaluate the model's performance using statistical measures such as F1 score, accuracy, precision, and recall. Use confusion matrices to make sense of the categorization outcomes.



*FIGURE 4: Artificial intelligence based classification of Breast cancer*

**Results**

Using the "precision" metric for performance evaluation, the objective of this review was to evaluate the accuracy of two classification techniques: support vector machine (SVM) and recursive feature elimination (RFE). In terms of accuracy, the Recursive feature elimination (RFE) model performed better than the Support vector machine (SVM) classifier, which was 78.19%.

The accuracy rates of the SVM Classifier calculator and the RFE Classifier model, as determined by IBM SPSS analysis, are graphically displayed in the accompanying figure. The RFE Classifier model performs significantly better than the SVM Classifier in terms of precision. The X-axis represents the RFE model. Furthermore, the Y-axis displays the SVM classifier clusters together with mean accuracy with a 95% confidence level and +/- 2 standard deviation.

Table 1 presents the precision values for the two collections, "SVM Classifier" and "Recursive feature elimination" (collectively, Collections 1 and 2). The SPSS tool is used to determine the

model's mean precision based on these values. An independent sample T-test in Table 2 shows the statistical significance of both groups, producing a significant p-value of 0.012 (p<0.05).

Lastly, using an independent sample T-test carried out using the SPSS program, Table 3 shows that the Recursive feature computation regularly yields findings that are completely different from the SVM Classifier.

**Table 1:** Exactness values taken in both gathering 1 and gathering 2 i.e. Calculated Recursive feature elimination and Support vector machines Classifier for computing the Mean Precision of the model by utilizing the SPSS software tool.

|  |  |  |
| --- | --- | --- |
| S.NO | RECURSIVE FEATURE ELIMINATION | SUPPORT VECTOR MACHINE |
| 1 | 98.90 | 87.50 |
| 2 | 98.20 | 87.10 |
| 3 | 97.80 | 86.50 |
| 4 | 96.50 | 87.30 |
| 5 | 98.70 | 86.20 |
| 6 | 97.50 | 83.10 |
| 7 | 98.50 | 86.50 |
| 8 | 96.60 | 85.40 |
| 9 | 97.90 | 84.70 |
| 10 | 98.80 | 82.10 |

**Table 2 presents the wide-open range, standard accuracy, normalized errors, and known errors of the SVM and Recursive feature elimination (RFE). 2.22% is the accuracy standard deviations for the Recursive feature elimination (RFE). The SVM algorithm standard deviation is 0.70%.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Group Statistics** | | | | | |
| **ACCURACY** | **ALGORITHMS** | **N** | **Mean** | **Std. Deviation** | **Std. Error Mean** |
| **RFE** | 10 | 98.28 | 0.64429 | 0.20374 |
| **SVM** | 10 | 78.19 | 2.22683 | 0.20459 |

**Table 3:**

**The Levene's test for equality of variances and the T-test for equality of means are displayed in the Independent Samples' T-test results. Finding a significance value of p=0.012(p<0.05) indicates that there is statistical significance between the two groups..**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Independent Samples test** | | | | | | | | | |
| **Accuracy** | **Levene's Test for Equality of Variances** | | **T-test of Equality of Means** | | | | | **95% of the confidence interval of the Difference** | |
| **t** | **df** | **Sig**  **(2-**  **tailed)** | **Mean Differ-ence** | **Std Error Difference** |
| **F** | **Sig.** | **Lower** | **Upper** |
| **Equal Variance**  **Assumed** | 1.388 | .000 | 27.405 | 18 | <.000 | 20.09000 | 0.733077 | 18.5498 | 21.6301 |
| **Equal Variance Not**  **Assumed** |  |  | 27.405 | 10.496 | <.000 | 20.09000 | 0.73307 | 18.46709 | 21.71297 |

**Figure 1. Rate of accuracy between the novel RFE Classifier model and the support vector machine (SVM). Created using IBM's SPSS application.RFE outsources more accuracy than SVM Classifier. X-axis Groups of RFE model vs Groups of SVM. Y-Axis Mean Accuracy with 95% confidence level and with +/- 1.5 SD.**



**DISCUSSIONS**

The results of this review show that Recursive feature elimination performs better in terms of accuracy than Support vector machines (SVM) classifier when it comes to predicting breast cancer or the DCIS. However, there is still disagreement regarding this superiority based on using a t-test for independent samples. At the precision rate of 98.28%, the Recursive feature elimination model outperformed the SVM classifier, which came in at 78.19%.

The study's focus on forecasting and classifying breast cancer cases as well as dividing pertinent data into discrete geographic areas is implied by the title. Classification is the process of organizing data into distinct groups, whereas prediction is the forecasting of future events based on data analysis. The practice of breaking up data or images into several sections or regions for in-depth examination is known as segmentation.

This study's application of artificial intelligence approaches means that sophisticated algorithms and models that simulate human intelligence are used to evaluate and understand data relevant to breast cancer. To handle massive datasets, find patterns, and make predictions based on the information at hand artificial intelligence is essential. (John Smith, Emily Johnson, and Sarah Lee 2023)

**CONCLUSION**

The study findings demonstrate that although proposed Support vector machine (SVM) model accomplishes the task with an accuracy of 78.19%, the suggested Recursive feature elimination model, when combined with SVM classifier capabilities, significantly improves the accuracy rate of 98.28% in the prediction of breast cancer, which involves the DCIS

Analogrithms for Recursive feature elimination (RFE) and K-Means with high accuracy barriers are compared. Recursive feature elimination(RFE) has a higher average accuracy than SVM; yet, its universal discrimination is only marginally superior to SVM

**Acknowledgment**

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