DETECTION OF BREAST CANCER BY ASSOCIATION RULE MINING AND GIANT FEATURE SELECTION WITH CONVOLUTIONAL NEURAL NETWORKS

IT233 PROJECT

A PROJECT REPORT

Submitted To

PUDUCHERRY TECHNOLOGICAL UNIVERSITY

BY

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Under the Guidance of
Dr. V. GEETHA
(Associate Professor)

IN PARTIAL FULFILMENT FOR THE AWARDING OF THE DEGREE OF

BACHELOR OF TECHNOLOGY
in
INFORMATION TECHNOLOGY

PUDUCHERRY TECHNOLOGICAL UNIVERSITY

PUDUCHERRY - 605014

JUNE 2022

DEPARTMENT OF INFORMATION TECHNOLOGY

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BONAFIDE CERTIFICATE

This is to certify that the Project work titled "**Detection of Breast Cancer by Association Rule Mining and GIANT Feature Selection with Convolutional Neural Networks**" is a bonafide work done by **Ellen Daniel (18IT1012), Manigandan .G (18IT1027), Sushma .T (18IT1050)** of **VIII** semester **B.TECH** class of **Information Technology** Department for the **Project (IT233)** during the year **2021-2022**.

Project Guide
(DR. V. GEETHA)

Head of the department
(DR. V. GOVINDASAMY)

Place: Puducherry
Date : 01.06.2022

Submitted for the University Examination held on _____

Internal Examiner

External Examiner

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ABSTRACT

Breast cancer is the growth of a malignant tumor in the breast. The incidence of this disease in women has increased significantly in recent years. Currently, early detection is an important factor in cancer treatment. In this paper we propose a method based on feature selection with convolutional neural network (CNN). First, we do rule conversion by applying association rule mining. Second, we build a feature set with features of high priority using GIANT (genetic investigation of anthropometric traits) feature selection. Third, we use convolution neural network to classify benign and malignant breast masses. The performance of our proposed detection of breast cancer is found based on less number of features, reduced time and memory space and accuracy.

CHAPTER 1: INTRODUCTION

1.1 OVERVIEW

Breast cancer is a serious threat to women's life and health, and the morbidity and mortality of breast cancer are ranked first and second out of all female diseases. Breast cancer starts when malignant, cancerous lumps start to grow from the breast cells. The reason for increasing death rate is due to detection of disease at later stage. Hence, early detection may save life. Early detection of lumps can effectively reduce the mortality rate of breast cancer. Data mining techniques are clearly predictable in the medical care field. The patient information is very confidential and sensitive. Handling of patient data input needs time management and accuracy. Human errors are to be avoided. Diagnosis is often challenging, because signs and symptoms are nonspecific for several diseases especially for cancer in which abnormal gene grows uncontrollably and destroys body tissue. Data mining techniques is useful in diagnosing distinct cancer types such as breast cancer. Scientists developed screening mammography to provide early detection and to save lives from breast cancer. One major limitation of mammography screening: prognostically significant breast cancers are underdiagnosed. Researchers and clinicians have implemented several strategies to improve screening mammography's performance, including double reading, screening at yearly interval, obtaining two views per breast and analyzing prior mammograms for comparison. Radiologists aim to detect critical features like microcalcifications (MCs), architectural distortions (ADs), and asymmetries as biomarkers for cancer or cancer risk. Manually detecting these features leads to additional economic costs and strains on an already scarce breast imaging radiologist workforce. Computer-aided detection systems (CAD) automatically detect and classify breast lesions in mammograms. Still, these traditional CAD systems fail to significantly improve screening performance, mainly due to their low specificity. Specificity connects to how well algorithms detect and classify abnormalities in

mammograms. This differs from diagnosis, which involves causal inference regarding an abnormality's origin. Detecting anomalies in mammographs is essential. Novel algorithms based on Convolutional Neural Networks (CNNs) improve screening mammography's performance and increase breast imaging radiologists' efficiency. Researchers have developed several CNN-based algorithms for automated mammographic analysis. Feature selection is necessary to identify high priority features among clump thickness, uniformity of cell shape and size, marginal adhesion, single epithelial cell size, bare nuclei, bland chromatin, normal nuclei and mitosis. The purpose is to improve the prediction of tumour prognosis at greater accuracy.

1.2 PROBLEM DEFINITION

- To design an efficient feature selection scheme for the diagnosis of breast cancer.
- Avoidance of irrelevant features and reduction of data dimensionality.
- Avoid over fitting of genetic data by feature selection.
- Perform genetic metric to measure the genome.
- To propose a work based on anthropometric traits which leads to identify the unique set of features to diagnose disease.
- Reduction of the time consumption and error rate.

1.3 MOTIVATION

- Design a Recommender system for optimal feature selection for health care system.
- Detection of breast cancer with proposed feature selection.
- Reduce the number of expert rules for diagnosing diseases.
- Devise an efficient algorithm to cope with continuous attributes in the preprocessing step.

1.4 DOMAIN SPECIFICATION

Domain: DATA MINING:

- Data Mining is needed to extract knowledge from raw data. Some of the commonly used DM techniques are: Associative rule mining, Classification, Clustering, Regression and Prediction.
- Data mining techniques helps very well in prediction in the medical field.
- Helps to reduce time overhead, improve accuracy and avoid human errors.
- Phases in data mining: Data Pre-processing, Data Modelling, Data Post-processing.
- Data pre-processing: step towards obtaining general overview of data preparation (Data cleaning, Data integration, Data transformation, Data reduction by feature selection) and obtain a general overview of data.
- Data modeling: step towards predictive and descriptive categories.
- Predictive algorithms are further divided into classification and regression based on type of target variable (discrete or continuous).
- Descriptive algorithms are also classified as clustering and association rule mining.
- Data post-processing: step consider visualization and evaluation of extracted knowledge.

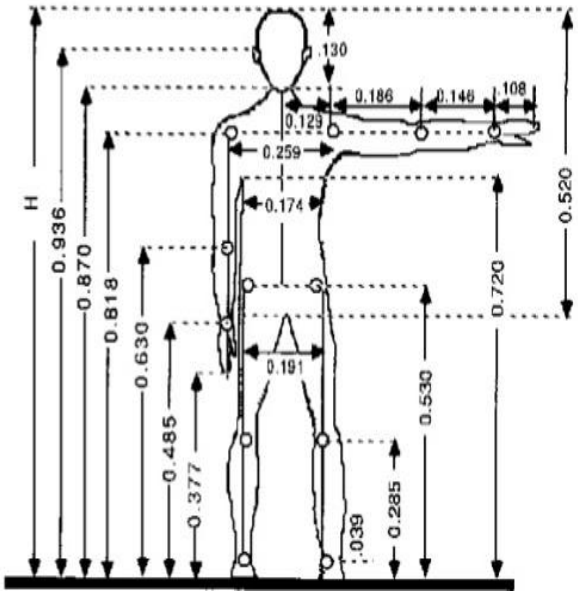
Sub Domain: FEATURE SELECTION

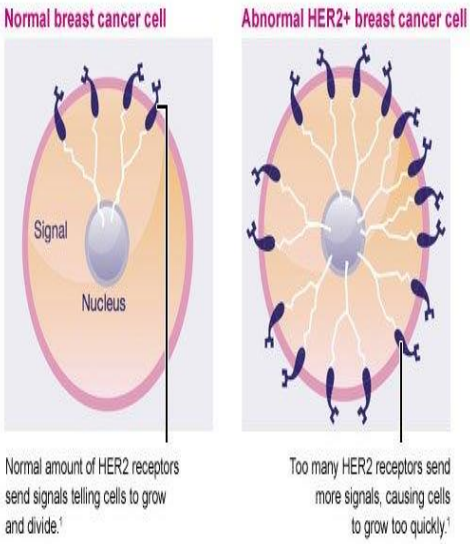
- Feature selection is an important part of data pre-processing phase in data mining.
- It refers to the process of reducing the data size for analysis or of finding the most meaningful input.
- Improves the quality of the model.
- Helps to reduce the computational cost and to improve the performance of the learning algorithm.
- Improve efficiency and decreasing human errors.

- Reducing the number of irrelevant or redundant features drastically reduces the running time of the learning algorithm.
- Facilitated data visualization and data understanding.
- Reduces the measurement and storage requirements, the training and utilization time.
- Solves high dimensional data.

Domain: ANTHROPOMETRY

- The word “anthropo” refers to human and “metric” refers to measurement.
- Used for the purpose of identification by using human physical variations.
- Common anthropometrics: Human body metrics, Facial metrics and Genetic metrics.
- The GIANT (Genetic Investigation of Anthropometric Traits) consortium made of many different groups of institutions, countries and the studies about large scale genetic datasets.
- Genome Wide Association Study (GWAS) performed a study across a population’s genomes to find markers that track with particular traits and spots the genome based heritability of height.
- Anthropometric measures on the human body Biomarkers measure





CHAPTER 2: LITERATURE SURVEY

2.1 LITERATURE REVIEW

"Classification of Breast Cancer Based on Histology Images Using Convolutional Neural Networks" by Dalal Bardou, Kun Zhang and Sayed Mohammad Ahmad, IEEE ACCESS, May 24, 2018.

Two machine learning approaches for the automatic classification of breast cancer histology images into benign and malignant and into benign and malignant sub-classes are compared. The first approach is based on the extraction of a set of handcrafted features encoded by two coding models (bag of words and locality constrained linear coding) and trained by support vector machines, while the second approach is based on the design of convolutional neural networks. Dataset augmentation techniques are experimentally tested to enhance the accuracy of the convolutional neural network as well as handcrafted features C convolutional neural network and convolutional neural network features C classifier' configurations. The results show convolutional neural networks outperformed the handcrafted feature based classifier.

"Breast Cancer Detection Using Extreme Learning Machine Based on Feature Fusion With CNN Deep Features" by Zhiqiong Wang, Mo Li, Huaxia Wang, Hanyu Jiang, Yudong Yao and Junchang Xin, IEEE ACCESS, August 14, 2019.

A breast CAD method based on feature fusion with convolutional neural network (CNN) deep features is explored. First, a mass detection method based on CNN deep features and unsupervised extreme learning machine (ELM) clustering is proposed. Second, a feature set fusing deep features, morphological features, texture features, and density features is built. Third, an ELM classifier is developed using the fused feature set to classify benign and

malignant breast masses. Extensive experiments demonstrate the accuracy and efficiency of our proposed mass detection and breast cancer classification method.

"Multi-View Feature Fusion Based Four Views Model for Mammogram Classification Using Convolutional Neural Network" by Hasan Nasir Khan, Ahmad Raza Shahid, Basit Raza, Amir Hanif Dar and Hani Alquhayz, IEEE ACCESS, November 13, 2019.

A Multi-View Feature Fusion (MVFF) based CADx system using feature fusion technique of four views for classification of mammogram is proposed. The complete CADx tool contains three stages, the first stage have the ability to classify mammogram into abnormal or normal, second stage is about classification of mass or calcification and in the final stage classification of malignant or benign classification is performed. Convolutional Neural Network (CNN) based feature extraction models operate on each view separately. These extracted features were fused into one final layer for ultimate prediction. The proposed system is trained on four views of mammograms, after data augmentation. The experiments were performed on publicly available datasets such as CBIS-DDSM (Curated Breast Imaging Subset of DDSM) and mini-MIAS database of mammograms. In comparison with literature the MVFF based system performed better than a single view-based system for mammogram classification.

"Deep Learning Assisted Efficient AdaBoost Algorithm for Breast Cancer Detection and Early Diagnosis" by Jing Zheng, Denan Lin, Zhongjun Gao, Shuang Wang, Mingjie He and Jipeng Fan, IEEE ACCESS, June 04, 2020.

Deep Learning assisted Efficient Adaboost Algorithm (DLA-EABA) for breast cancer detection has been mathematically proposed with advanced computational techniques. In addition to traditional computer vision approaches, tumor classification methods using

transfers are being actively developed through the use of deep convolutional neural networks (CNNs). This study starts with examining the CNN based transfer learning to characterize breast masses for different diagnostic, predictive tasks or prognostic or in several imaging modalities, such as Magnetic Resonance Imaging (MRI), Ultrasound (US), digital breast tomosynthesis and mammography. The deep learning framework contains several convolutional layers, LSTM, Max-pooling layers. The classification and error estimation that has been included in a fully connected layer and a softmax layer. This paper focuses on combining these machine learning approaches with the methods of selecting features and extracting them through evaluating their output using classification and segmentation techniques to find the most appropriate approach.

"A Review on Recent Progress in Thermal Imaging and Deep Learning Approaches for Breast Cancer Detection" by Roslidar Roslidar, Aulia Rahman, Rusdha Muharar, Muhammad Rizky Syahputra, Fitri Arnia, Maimun Syukri, Biswajeet Pradhan and Khairul Munadi, IEE ACCESS, July 02, 2020.

Thermography, a non-invasive and non-contact cancer screening method, can detect tumors at an early stage even under precancerous conditions by observing temperature distribution in both breasts. The thermograms obtained on thermography can be interpreted using deep learning models such as convolutional neural networks (CNNs). CNNs can automatically classify breast thermograms into categories such as normal and abnormal. Despite their demostrated utility, CNNs have not been widely used in breast thermogram classification. In this study, it is aimed to summarize the current work and progress in breast cancer detection based on thermography and CNNs. First breast thermography potential in early breast cancer detection is discussed, providing an overview of the availability of breast thermal datasets together with publicly accessible. The characteristics of breast thermograms

and the differences between healthy and cancerous thermographic patterns are also discussed. Breast thermogram classification using a CNN model is described step by step including a simulation example illustrating feature learning. Most research related to the implementation of deep neural networks for breast thermogram classification is covered and proposes future research directions for developing representative datasets, feeding the segmented image, assigning a good kernel, and building a lightweight CNN model to improve CNN performance.

"Breast Cancer Classification From Histopathological Images Using Patch-Based Deep Learning Modeling" by Irum Hirra, Mubashir Ahmad, Ayaz Hussain, M. Usman Ashraf, Iftikhar Ahmed Saeed, Syed Furqan Qadri, Ahmed M. Alghamdi and Ahmed S. Alfakeeh, IEEE ACCESS, February 11, 2021.

A novel patch-based deep learning method called Pa-DBN-BC is proposed to detect and classify breast cancer on histopathology images using the Deep Belief Network (DBN). Features are extracted through an unsupervised pre-training and supervised fine-tuning phase. The network automatically extracts features from image patches. Logistic regression is used to classify the patches from histopathology images. The features extracted from the patches are fed to the model as input and the model presents the result as a probability matrix as either a positive sample (cancer) or a negative sample (background). The proposed model is trained and tested on the whole slide histopathology image dataset having images from four different data cohorts. Consequently, the proposed method is better than the traditional ones, as it automatically learns the best possible features and experimental results show that the model outperformed the previously proposed deep learning methods.

"A Novel Deep-Learning Model for Automatic Detection and Classification of Breast Cancer Using the Transfer-Learning Technique" by Abeer Saber, Mohamed Sakr, Osama M. Abo-Seida, Arabi Keshk and Huiling Chen, IEEE ACCESS, May 19, 2021.

A new deep-learning (DL) model based on the transfer-learning (TL) technique is developed to efficiently assist in the automatic detection and diagnosis of the BC suspected area based on two techniques namely 80-20 and cross-validation. DL architectures are modeled to be problem-specific. TL uses the knowledge gained during solving one problem in another relevant problem. In the proposed model, the features are extracted from the mammographic image analysis- society (MIAS) dataset using a pre-trained convolutional neural network (CNN) architecture such as Inception V3, ResNet50, Visual Geometry Group networks (VGG)-19, VGG-16, and Inception-V2 ResNet. Six evaluation metrics for evaluating the performance of the proposed model in terms of accuracy, sensitivity, specificity, precision, F-score, and area under the ROC curve (AUC) has been chosen. Experimental results show that the TL of the VGG16 model is powerful for BC diagnosis by classifying the mammogram breast images with overall accuracy, sensitivity, specificity, precision, F-score, and AUC respectively for 80-20 method 10-fold cross-validation method.

"Identifying biomarkers for breast cancer by gene regulatory network rewiring" by Yijuan Wang and Zhi-Ping Liu, Springer, July 16, 2021.

A new bioinformatics method of identifying biomarkers based on network rewiring in different states is proposed. It firstly reconstructs GRN in different phenotypic conditions from gene expression data with a priori background network. We employ the algorithm based on path consistency algorithm and conditional mutual information to delete false-positive regulatory interactions between independent nodes/genes or not closely related gene pairs. And then a differential gene regulatory network (D-GRN) is constructed from the rewiring

parts in the two phenotypespecific GRNs. Community detection technique is then applied for D-GRN to detect functional modules. Finally, logistic regression classifier is applied with recursive feature elimination to select biomarker genes in each module individually. The extracted feature genes result in a gene set of biomarkers with impressing ability to distinguish normal samples from controls. The identified biomarkers are verified in external independent validation datasets. For a proof-of-concept study, the framework is applied to identify diagnostic biomarkers of breast cancer.

"Deep Learning based Early Prediction Scheme for Breast Cancer" by N. Hemavathi, R. Sriranjani, Parvathy Arulmozhi, M. Meenalochani, R. U. Deepak, Springer, August 20, 2021.

The proposal aims at predicting the presence of breast cancer at early stage through deep learning. To identify suitable model for deep learning, initially machine learning algorithm with Logistic Regression, K Nearest Neighbors, Support Vector Machine (linear), Support Vector Machine, Gaussian, Decision Tree and Random Forest along with ensemble learning algorithms such as Bagged Trees, Subspace discriminant and RUSBoosted Trees are implemented with 30 attributes. Comparison of performance metrices indicates that random forest performs better. Then, feature selection of 14 attributes is attained through heat map. With minimal features, the above set of algorithms is implemented and their corresponding performance indices such as accuracy, misclassification cost, prediction speed, training time, predicted class, true class, positive predict value, sensitivity, specificity, precision, F1 score, Area Under the Curve and Receiver Operating Characteristic Curve are obtained. In this, random forest performs better and in addition, the performance of 14 attributes is almost exhibiting closer performance as that of 30. However, feature selection is mandate and can be eliminated if the algorithm is implemented through deep learning model. The model consists

of many hidden layers which performs binary classification on the given dataset to predict whether a person is malignant or benign.

"WARM: a new breast masses classification method by weighting association rule mining" by Mohammad Reza Keyvanpour, Mehrnoush Barani Shirzad, Leyli Mahdikhani, Springer, January 20, 2022.

A new method is designed for mass detection and classification based on weighted association rule mining (WARM). The main purpose of this study is to focus on the segmentation and classification and to provide a solution to optimize the accuracy of detection and classification of masses in mammography images to classify the masses in mammography images into two classes, benign and malignant. The results show proposed model in terms of accuracy, sensitivity and specificity achieved superior in comparison with several baselines.

2.2 LIMITATIONS IN THE EXISTING SYSTEM

- Diagnosis of diseases especially of cancer types deals with heterogeneous data and hence very difficult.
- More number of features for better accuracy leads to high computation and space complexity.
- High dimensionality data on micro array dataset (unordered data without label and group).
- Imbalanced class distribution on medical datasets.
- Appropriate anthropometric measures not focused such has genetic metric.
- Low clarity of imaging data causes high error rate.
- High time complexity to select quality of features.

CHAPTER 3: PROPOSED SYSTEM

3.1 PROPOSAL

In our model, we are going to use association rule mining and GIANT feature selection to detect breast cancer. Association rule mining is used to generate the rule conditions from the image dataset. In feature selection, whose priority of their feature vector is gathered by GIANT (Genetic Investigation of Anthropometric Traits) feature selection, the lower level value of feature vector are neglected from data frame. The high priority features from the data are identified by feature selection to improve time complexity and reduce memory space and time required. Finally whether the cancer is malignant or benign and the performance of our proposed system is found by convolutional neural network. Our proposed system has the following main modules.

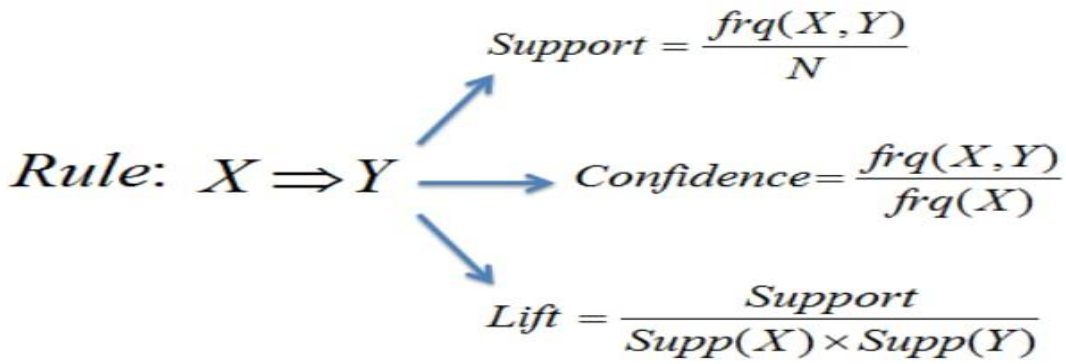
- Association Rule Mining
- GIANT Feature Selection
- Convolutional Neural Network

3.2 MAIN MODULES

3.2.1 Association Rule Mining

The Apriori Algorithm is applied to the dataset to implement association rule mining. The Apriori Algorithm, used for the first phase of the Association Rules, is the most popular and classical algorithm to mine frequent processes and relevant association rules. The algorithm properties and data are evaluated with Boolean Association Rules. In this algorithm, there are product clusters that pass frequently, and then strong relationships between these products and other products are sought. The importance of an Association

Rules is be determined by three parameters support, confidence and lift that are used to identify the strength of the algorithm. Let X and Y represent the data and N represents the total number of data.



- Support: Probability of an event to occur (frequency of an item's occurrence).
- Confidence: Measure of conditional probability
- Lift: Probability of all items occurring together divided by the product of antecedent and consequent occurring as if they are independent of each other (measure of importance of a rule).
- The IF component of an association rule is known as the antecedent. The THEN component is known as the consequent. The antecedent and the consequent are disjoint; they have no items in common.
- Leverage computes the difference between the observed frequency of X and Y appearing together and the frequency that would be expected if X and Y were independent. A leverage value of 0 indicates independence.
- Conviction compares the probability that X appears without Y if they were dependent with the actual frequency of the appearance of X without Y. Unlike confidence, conviction factors in both P(X) and P(Y) and always has a value of 1 when the relevant items are completely unrelated.

Association Rule Mining is:

- Discovering interesting relations between variables in large databases, which is given in the form of rules to user.
- Rule mining structure can be expressed in the form of

  IF <Conditions> THEN < class >
- The IF part is said to be rule antecedent which contains a set of conditions connected by using logical conjunction operator (AND). Rule condition are refers as a term 1, 2.., n, so that the rule antecedent is a logical conjunction of terms in the form of IF term1 AND term2 AND ...infinity, Each term is a triple <attribute, operator, value>, such as <Gender = female>.
- The THEN part is said to be rule consequent specifies the class predicted for cases whose predictor attributes satisfies the terms specified in the rule antecedent.

3.2.2 GIANT Feature Selection

- Our implemented scheme present the anthropometric traits for the filtration of the best features by measuring the dimensionality of the features (gene) *shape, size* based on the action of gene by computing the feature set.
- Here the term gene represents the features.
- The highest priority sets are selected as the best optimal features to diagnose the cancer.

Objective 1: GIANT – FS to identify biomarkers

- ✓ The Genetic Investigation of anthropometric trait Feature Selection (GAINT-FS) overcome the challenges of overfitting classes (gene) and identify the unique biomarker based on the gene action to diagnosis the cancer disease.
- ✓ GAINT-FS decreases the dimensionality of biomarker feature and improves the prediction performances, transparency, compactness and improve efficiency by decreasing human errors.

1. Initialize the process
2. Partition Class dependent and Class independent
3. Apply Anthropometric trait to select the features
4. Identification of Biomarkers with GA(Genetic Algorithm)
    - Initial Population, Fitness function, Parent selection, Crossover, mutation

Objective 2: Genetic Algorithm with Suppressor Mutation – GIANT

- ✓ Genetic algorithm with a newly proposed genetic operator named suppressor mutation (GA-SM), to suppress the activity of genes which are over expressive in nature i.e. to suppress the useless attributes from the rules. By using this new operator in association rule mining techniques, it generates a smaller number of rules for diagnosing diseases.

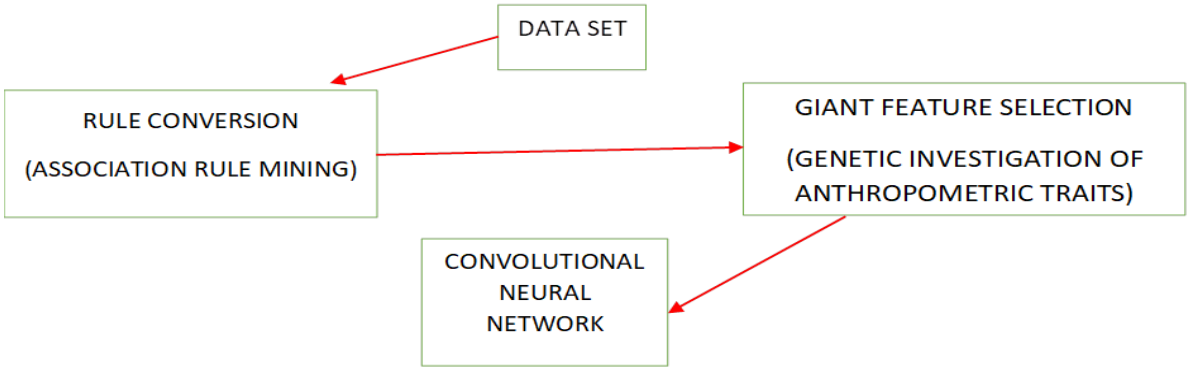
3.2.3 Convolutional Neural Networks

- A Convolutional neural network (CNN) is a neural network that has one or more convolutional layers and is used mainly for image processing, classification, segmentation and also for other auto correlated data.
- A convolution is essentially sliding a filter over the input.

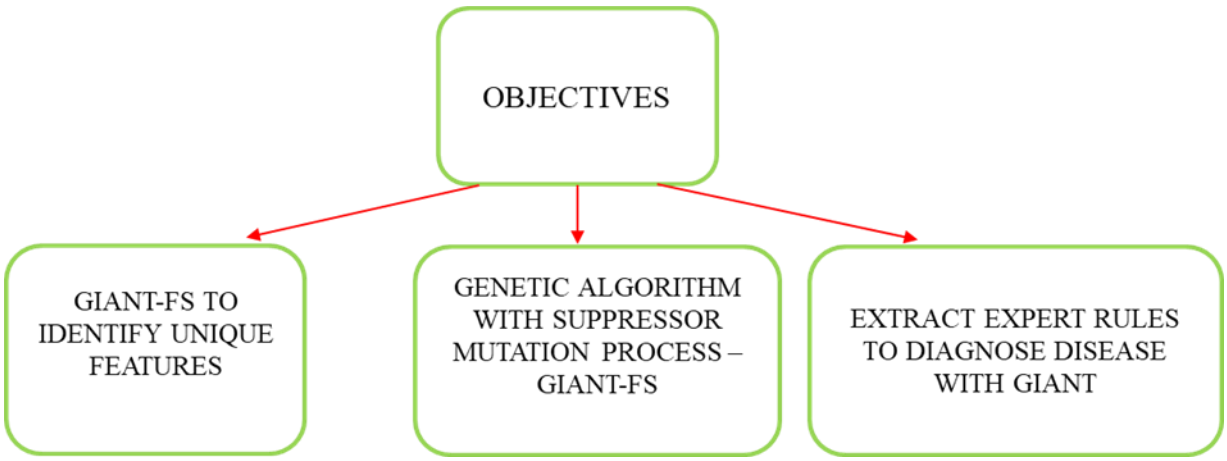
- A filter is used to detect the presence of specific features or patterns present in the input.
    - INPUT layer : holds the input
    - CONV layer : computes the dot product
    - RELU layer : applies an activation function
    - POOL layer : reduces the number of parameters
    - FC (Fully-Connected): computes the class score
- It is used to find the performance of the proposed system.

3.3 DESIGN DIAGRAM OF THE PROPOSED SYSTEM

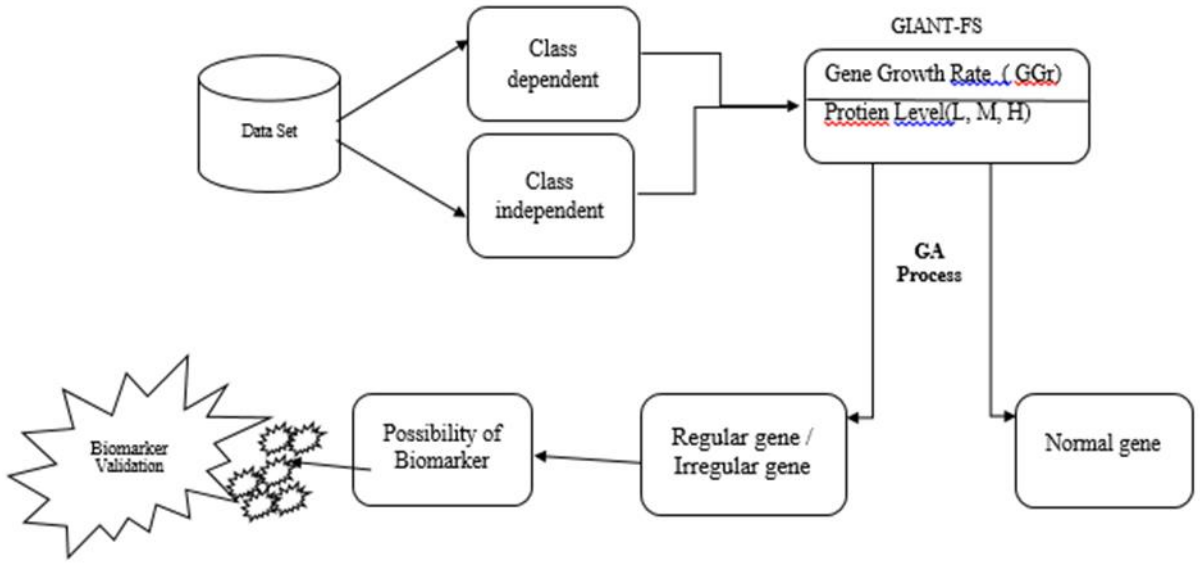
3.3.1 General Design Diagram:



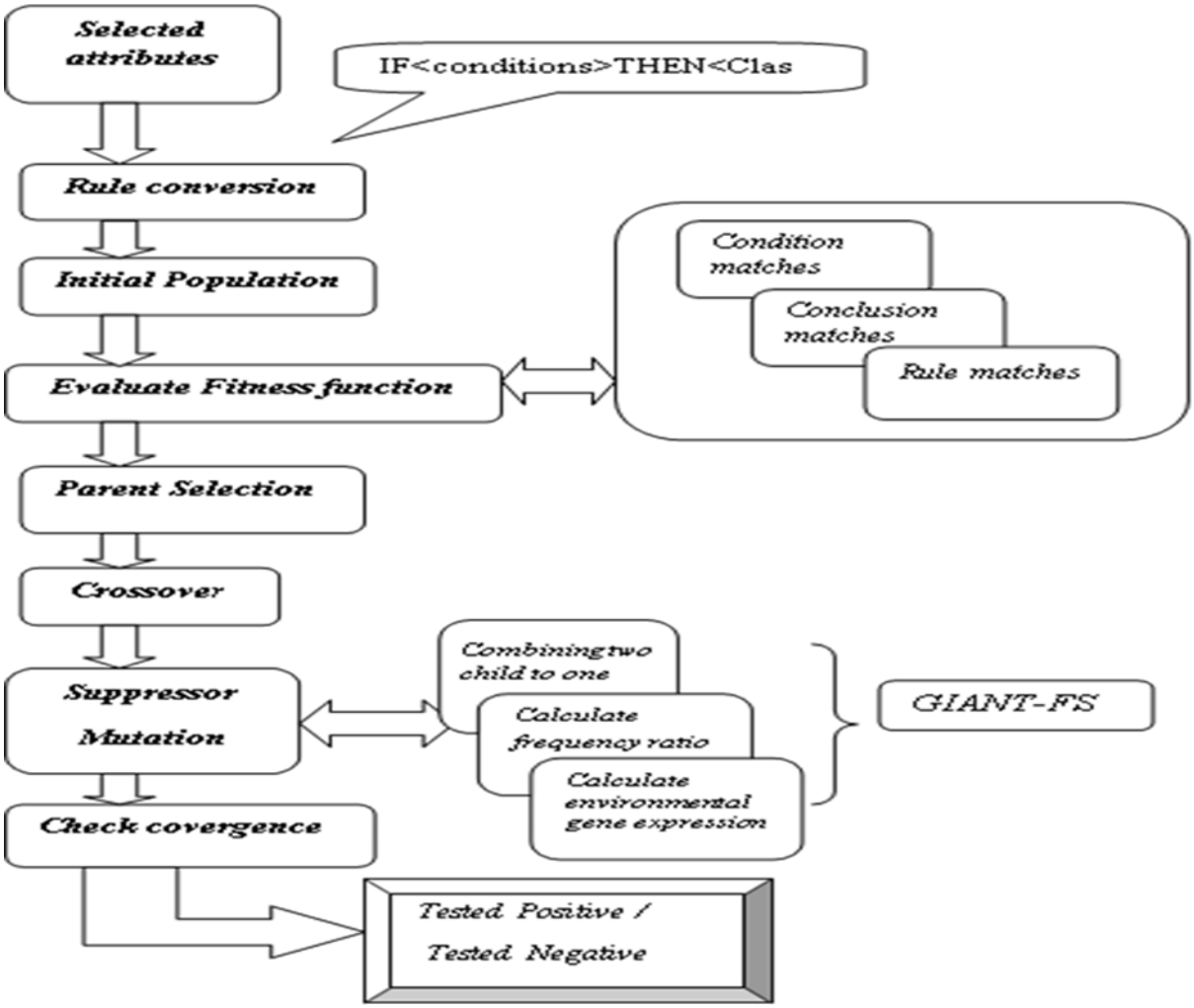
3.3.2 Objectives of GIANT – FS Module:



3.3.3 Work Flow of GIANT - FS:



3.3.4 Flow diagram of GA – SM to extract expert rules:



CHAPTER 4: SYSTEM SPECIFICATION

4.1 MINIMUM SYSTEM REQUIREMENTS

Clock speed	:	1.80 GHz
RAM	:	8 GB
Hard disk capacity	:	80 GB
Compact Disk	:	650 MB
Internet connection	:	Broadband/4mps speed
Browsers	:	Chrome*36+

4.2 MINIMUM SOFTWARE REQUIREMENTS

Operating system	:	WINDOWS 11
Coding Language	:	Python 3.9
Tools used	:	Google Colab

CHAPTER 5: IMPLEMENTATION OF MODULES WITH RESULT SCREENSHOTS

The breast cancer dataset is downloaded from UCI Machine Learning Repository (https://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+(Original)?msclkid=ed5fedf4c14011ecb516983a83c5483e). The dataset has 699 instances, 11 attributes and 2 classes. The 11 attributes are id, clump thickness, uniformity of cell size, uniformity of cell shape, marginal adhesion, single epithelial cell size, bare nuclei, bland chromatin, normal nuclei, mitosis and class. The breast cancer dataset is of 2 classes, benign and malignant. Since the id column is unique for each data, it is dropped out from the dataset before applying association rule mining, GIANT feature selection and convolutional neural networks.

5.1 RESULT SCREENSHOTS

DATASET DOWNLOADED FROM UCI MACHINE LEARNING REPOSITORY

	id	Clump Thickness	Uniformity of Cell Size	Uniformity of Cell Shape	Marginal Adhesion	Single Epithelial Cell Size	Bare Nuclei	Bland Chromatin	Normal Nucleoli	Mitoses	Class
0	1000025	5	1	1	1	2	1	3	1	1	2
1	1002945	5	4	4	5	7	10	3	2	1	2
2	1015425	3	1	1	1	2	2	3	1	1	2
3	1016277	6	8	8	1	3	4	3	7	1	2
4	1017023	4	1	1	3	2	1	3	1	1	2

DATATYPE OF COLUMNS IN THE DATASET

```
RangeIndex: 699 entries, 0 to 698
Data columns (total 11 columns):
 #   Column                       Non-Null Count  Dtype
---  ------                       --------------  -----
 0   id                           699 non-null    int64
 1   Clump Thickness              699 non-null    int64
 2   Uniformity of Cell Size      699 non-null    int64
 3   Uniformity of Cell Shape     699 non-null    int64
 4   Marginal Adhesion            699 non-null    int64
 5   Single Epithelial Cell Size  699 non-null    int64
 6   Bare Nuclei                  699 non-null    object
 7   Bland Chromatin              699 non-null    int64
 8   Normal Nucleoli              699 non-null    int64
 9    Mitoses                     699 non-null    int64
 10  Class                        699 non-null    int64
dtypes: int64(10), object(1)
memory usage: 60.2+ KB
```

DATASET AFTER DROPPING THE ID COLUMN

	Clump Thickness	Uniformity of Cell Size	Uniformity of Cell Shape	Marginal Adhesion	Single Epithelial Cell Size	Bare Nuclei	Bland Chromatin	Normal Nucleoli	Mitoses	Class
0	5	1	1	1	2	1	3	1	1	2
1	5	4	4	5	7	10	3	2	1	2
2	3	1	1	1	2	2	3	1	1	2
3	6	8	8	1	3	4	3	7	1	2
4	4	1	1	3	2	1	3	1	1	2
...	...	...	...	...	...	...	...	...	...	...
694	3	1	1	1	3	2	1	1	1	2
695	2	1	1	1	2	1	1	1	1	2
696	5	10	10	3	7	3	8	10	2	4
697	4	8	6	4	3	4	10	6	1	4
698	4	8	8	5	4	5	10	4	1	4

699 rows × 10 columns

5.1.1 Module 1: Association Rule Mining

FREQUENT ITEMSETS

	support	itemsets
0	0.071531	(Clump Thickness_2)
1	0.154506	(Clump Thickness_3)
2	0.114449	(Clump Thickness_4)
3	0.185980	(Clump Thickness_5)
4	0.098712	(Clump Thickness_10)
5	0.074392	(Uniformity of Cell Size_3)
6	0.095851	(Uniformity of Cell Size_10)
7	0.084406	(Uniformity of Cell Shape_2)
8	0.080114	(Uniformity of Cell Shape_3)
9	0.082976	(Uniformity of Cell Shape_10)
10	0.082976	(Marginal Adhesion_2)
11	0.082976	(Marginal Adhesion_3)
12	0.078684	(Marginal Adhesion_10)
13	0.552217	(Single Epithelial Cell Size_2)
14	0.103004	(Single Epithelial Cell Size_3)
15	0.188841	(Bare Nuclei_10)
16	0.237482	(Bland Chromatin_2)
17	0.236052	(Bland Chromatin_3)
18	0.104435	(Bland Chromatin_7)
19	0.087268	(Normal Nucleoli_10)
20	0.344778	(Class_4)
21	0.108727	(Clump Thickness_3, Single Epithelial Cell Siz...
22	0.085837	(Clump Thickness_4, Single Epithelial Cell Siz...
23	0.103004	(Clump Thickness_5, Single Epithelial Cell Siz...
24	0.098712	(Class_4, Clump Thickness_10)
25	0.095851	(Uniformity of Cell Size_10, Class_4)
26	0.082976	(Class_4, Uniformity of Cell Shape_10)
27	0.077253	(Marginal Adhesion_10, Class_4)
28	0.184549	(Bland Chromatin_2, Single Epithelial Cell Siz...
29	0.160229	(Single Epithelial Cell Size_2, Bland Chromati...
30	0.184549	(Bare Nuclei_10, Class_4)
31	0.094421	(Class_4, Bland Chromatin_7)
32	0.087268	(Normal Nucleoli_10, Class_4)

RULES

	antecedents	consequents	antecedent support	consequent support	support	confidence	lift	leverage	conviction
0	(Clump Thickness_3)	(Single Epithelial Cell Size_2)	0.154506	0.552217	0.108727	0.703704	1.274324	0.023406	1.511266
1	(Single Epithelial Cell Size_2)	(Clump Thickness_3)	0.552217	0.154506	0.108727	0.196891	1.274324	0.023406	1.052776
2	(Clump Thickness_4)	(Single Epithelial Cell Size_2)	0.114449	0.552217	0.085837	0.750000	1.358161	0.022636	1.791130
3	(Single Epithelial Cell Size_2)	(Clump Thickness_4)	0.552217	0.114449	0.085837	0.155440	1.358161	0.022636	1.048536
4	(Clump Thickness_5)	(Single Epithelial Cell Size_2)	0.185980	0.552217	0.103004	0.553846	1.002949	0.000303	1.003651
5	(Single Epithelial Cell Size_2)	(Clump Thickness_5)	0.552217	0.185980	0.103004	0.186528	1.002949	0.000303	1.000674
6	(Class_4)	(Clump Thickness_10)	0.344778	0.098712	0.098712	0.286307	2.900415	0.064679	1.262851
7	(Clump Thickness_10)	(Class_4)	0.098712	0.344778	0.098712	1.000000	2.900415	0.064679	inf
8	(Uniformity of Cell Size_10)	(Class_4)	0.095851	0.344778	0.095851	1.000000	2.900415	0.062804	inf
9	(Class_4)	(Uniformity of Cell Size_10)	0.344778	0.095851	0.095851	0.278008	2.900415	0.062804	1.252298
10	(Class_4)	(Uniformity of Cell Shape_10)	0.344778	0.082976	0.082976	0.240664	2.900415	0.054367	1.207666
11	(Uniformity of Cell Shape_10)	(Class_4)	0.082976	0.344778	0.082976	1.000000	2.900415	0.054367	inf
12	(Marginal Adhesion_10)	(Class_4)	0.078684	0.344778	0.077253	0.981818	2.847680	0.050125	36.037196
13	(Class_4)	(Marginal Adhesion_10)	0.344778	0.078684	0.077253	0.224066	2.847680	0.050125	1.187365
14	(Bland Chromatin_2)	(Single Epithelial Cell Size_2)	0.237482	0.552217	0.184549	0.777108	1.407251	0.053408	2.008970
15	(Single Epithelial Cell Size_2)	(Bland Chromatin_2)	0.552217	0.237482	0.184549	0.334197	1.407251	0.053408	1.145260
16	(Single Epithelial Cell Size_2)	(Bland Chromatin_3)	0.552217	0.236052	0.160229	0.290155	1.229204	0.029877	1.076219
17	(Bland Chromatin_3)	(Single Epithelial Cell Size_2)	0.236052	0.552217	0.160229	0.678788	1.229204	0.029877	1.394040
18	(Bare Nuclei_10)	(Class_4)	0.188841	0.344778	0.184549	0.977273	2.834496	0.119441	28.829757
19	(Class_4)	(Bare Nuclei_10)	0.344778	0.188841	0.184549	0.535270	2.834496	0.119441	1.745440
20	(Class_4)	(Bland Chromatin_7)	0.344778	0.104435	0.094421	0.273859	2.622293	0.058414	1.233321
21	(Bland Chromatin_7)	(Class_4)	0.104435	0.344778	0.094421	0.904110	2.622293	0.058414	6.833027
22	(Normal Nucleoli_10)	(Class_4)	0.087268	0.344778	0.087268	1.000000	2.900415	0.057180	inf
23	(Class_4)	(Normal Nucleoli_10)	0.344778	0.087268	0.087268	0.253112	2.900415	0.057180	1.222047

RULES WITH ANTECEDENT LENGTH

]

	antecedents	consequents	antecedent support	consequent support	support	confidence	lift	leverage	conviction	antecedent_len
0	(Single Epithelial Cell Size_2)	(Clump Thickness_3)	0.552217	0.154506	0.108727	0.196891	1.274324	0.023406	1.052776	1
1	(Clump Thickness_3)	(Single Epithelial Cell Size_2)	0.154506	0.552217	0.108727	0.703704	1.274324	0.023406	1.511266	1
2	(Clump Thickness_4)	(Single Epithelial Cell Size_2)	0.114449	0.552217	0.085837	0.750000	1.358161	0.022636	1.791130	1
3	(Single Epithelial Cell Size_2)	(Clump Thickness_4)	0.552217	0.114449	0.085837	0.155440	1.358161	0.022636	1.048536	1
4	(Single Epithelial Cell Size_2)	(Clump Thickness_5)	0.552217	0.185980	0.103004	0.186528	1.002949	0.000303	1.000674	1
5	(Clump Thickness_5)	(Single Epithelial Cell Size_2)	0.185980	0.552217	0.103004	0.553846	1.002949	0.000303	1.003651	1
6	(Class_4)	(Clump Thickness_10)	0.344778	0.098712	0.098712	0.286307	2.900415	0.064679	1.262851	1
7	(Clump Thickness_10)	(Class_4)	0.098712	0.344778	0.098712	1.000000	2.900415	0.064679	inf	1
8	(Class_4)	(Uniformity of Cell Size_10)	0.344778	0.095851	0.095851	0.278008	2.900415	0.062804	1.252298	1
9	(Uniformity of Cell Size_10)	(Class_4)	0.095851	0.344778	0.095851	1.000000	2.900415	0.062804	inf	1
10	(Class_4)	(Uniformity of Cell Shape_10)	0.344778	0.082976	0.082976	0.240664	2.900415	0.054367	1.207666	1
11	(Uniformity of Cell Shape_10)	(Class_4)	0.082976	0.344778	0.082976	1.000000	2.900415	0.054367	inf	1
12	(Class_4)	(Marginal Adhesion_10)	0.344778	0.078684	0.077253	0.224066	2.847680	0.050125	1.187365	1
13	(Marginal Adhesion_10)	(Class_4)	0.078684	0.344778	0.077253	0.981818	2.847680	0.050125	36.037196	1
14	(Single Epithelial Cell Size_2)	(Bland Chromatin_2)	0.552217	0.237482	0.184549	0.334197	1.407251	0.053408	1.145260	1
15	(Bland Chromatin_2)	(Single Epithelial Cell Size_2)	0.237482	0.552217	0.184549	0.777108	1.407251	0.053408	2.008970	1
16	(Single Epithelial Cell Size_2)	(Bland Chromatin_3)	0.552217	0.236052	0.160229	0.290155	1.229204	0.029877	1.076219	1
17	(Bland Chromatin_3)	(Single Epithelial Cell Size_2)	0.236052	0.552217	0.160229	0.678788	1.229204	0.029877	1.394040	1
18	(Class_4)	(Bare Nuclei_10)	0.344778	0.188841	0.184549	0.535270	2.834496	0.119441	1.745440	1
19	(Bare Nuclei_10)	(Class_4)	0.188841	0.344778	0.184549	0.977273	2.834496	0.119441	28.829757	1
20	(Class_4)	(Bland Chromatin_7)	0.344778	0.104435	0.094421	0.273859	2.622293	0.058414	1.233321	1
21	(Bland Chromatin_7)	(Class_4)	0.104435	0.344778	0.094421	0.904110	2.622293	0.058414	6.833027	1
22	(Class_4)	(Normal Nucleoli_10)	0.344778	0.087268	0.087268	0.253112	2.900415	0.057180	1.222047	1
23	(Normal Nucleoli_10)	(Class_4)	0.087268	0.344778	0.087268	1.000000	2.900415	0.057180	inf	1

RULES OF ANTECEDENT LENGTH >= 1, CONFIDENCE > 0.75, LIFT > 1.2

	antecedents	consequents	antecedent support	consequent support	support	confidence	lift	leverage	conviction	antecedent_len
7	(Clump Thickness_10)	(Class_4)	0.098712	0.344778	0.098712	1.000000	2.900415	0.064679	inf	1
9	(Uniformity of Cell Size_10)	(Class_4)	0.095851	0.344778	0.095851	1.000000	2.900415	0.062804	inf	1
11	(Uniformity of Cell Shape_10)	(Class_4)	0.082976	0.344778	0.082976	1.000000	2.900415	0.054367	inf	1
13	(Marginal Adhesion_10)	(Class_4)	0.078684	0.344778	0.077253	0.981818	2.847680	0.050125	36.037196	1
15	(Bland Chromatin_2)	(Single Epithelial Cell Size_2)	0.237482	0.552217	0.184549	0.777108	1.407251	0.053408	2.008970	1
19	(Bare Nuclei_10)	(Class_4)	0.188841	0.344778	0.184549	0.977273	2.834496	0.119441	28.829757	1
21	(Bland Chromatin_7)	(Class_4)	0.104435	0.344778	0.094421	0.904110	2.622293	0.058414	6.833027	1
23	(Normal Nucleoli_10)	(Class_4)	0.087268	0.344778	0.087268	1.000000	2.900415	0.057180	inf	1

5.1.2 Module 2: GIANT Feature Selection

SELECTING FEATURES WITH GIANT ALGORITHM

```
Selecting features with genetic algorithm.
gen    nevals  avg                                 std                                 min                                 max
0      400     [ 0.189728  5.31      0.073531] [ 0.163894  2.846735  0.038738] [-0.075035  1.        0.008323] [  0.616671  10.        0.21099 ]
1      244     [-1674.730063     7.855     1675.080086]      [ 3734.337869     3.057609  3734.180863]      [-10000.          0.          0.008323]      [    0.62143    17.      10000.    ]
2      223     [-1249.639193     7.98      1250.099508]      [ 3307.325513     2.620038  3307.151529]      [-10000.          1.          0.0171]        [    0.62143    19.      10000.    ]
3      230     [-1974.604274     8.685     1975.098546]      [ 3981.32367      2.51113   3981.078465]      [-10000.          3.          0.023331]      [    0.63872    18.      10000.    ]
4      237     [-1874.5641       8.7275    1875.098914]      [ 3903.333149     2.333076  3903.076233]      [-10000.          3.          0.032975]      [    0.659871   18.      10000.    ]
5      220     [-1274.498383     8.565     1275.101561]      [ 3335.514078     2.158883  3335.283499]      [-10000.          4.          0.039467]      [    0.666998   16.      10000.    ]
6      260     [-1699.50026      8.765     1700.094557]      [ 3756.554162     2.252726  3756.285201]      [-10000.          3.          0.017423]      [    0.695334   17.      10000.    ]
7      232     [-1749.484314     9.0425    1750.089133]      [ 3799.908546     2.209229  3799.629987]      [-10000.          4.          0.051876]      [    0.70394    21.      10000.    ]
8      243     [-2174.498315     9.3275    2175.083203]      [ 4125.719016     2.222666  4125.410655]      [-10000.          4.          0.060539]      [    0.70394    18.      10000.    ]
9      250     [-2249.49601      9.57      2250.080382]      [ 4176.09483      2.189772  4175.779961]      [-10000.          5.          0.056297]      [    0.70394    19.      10000.    ]
10     241     [-2449.502325     9.665     2450.076886]      [ 4301.155506     2.204036  4300.828206]      [-10000.          4.          0.056297]      [    0.70394    18.      10000.    ]
11     239     [-2424.494515     9.78      2425.075026]      [ 4286.236891     2.04245   4285.908436]      [-10000.          5.          0.053312]      [    0.70415    17.      10000.    ]
12     237     [-2324.482989     9.78      2325.074892]      [ 4224.544849     1.944634  4224.21907 ]      [-10000.          5.          0.050347]      [    0.715309   18.      10000.    ]
13     249     [-2524.492014     9.825     2525.072049]      [ 4344.76011      1.956879  4344.422994]      [-10000.          5.          0.053932]      [    0.727878   18.      10000.    ]
14     266     [-2549.489665     9.89      2550.071321]      [ 4358.910735     1.727107  4358.570438]      [-10000.          6.          0.051082]      [    0.727878   16.      10000.    ]
15     249     [-2849.506119    10.055     2850.068555]      [ 4514.456249     1.793593  4514.101155]      [-10000.          6.          0.053932]      [    0.727878   17.      10000.    ]
16     216     [-2324.467274     9.94      2325.071757]      [ 4224.553498     1.873873  4224.220796]      [-10000.          5.          0.053932]      [    0.736918   19.      10000.    ]
17     233     [-2574.47917     10.0325    2575.066566]      [ 4372.87747      1.853765  4372.531553]      [-10000.          5.          0.053932]      [    0.736918   17.      10000.    ]
18     258     [-2724.48652     10.155     2725.061499]      [ 4452.771448     2.020142  4452.419548]      [-10000.          5.          0.053932]      [    0.736918   19.      10000.    ]
19     242     [-2174.442929     9.99      2175.061325]      [ 4125.748216     1.763491  4125.422189]      [-10000.          7.          0.047793]      [    0.736918   17.      10000.    ]
20     231     [-2374.452782    10.165     2375.056485]      [ 4255.816535     1.828326  4255.479609]      [-10000.          7.          0.047793]      [    0.736918   18.      10000.    ]
21     247     [-2524.459699    10.28      2525.051182]      [ 4344.778892     1.797665  4344.435122]      [-10000.          5.          0.047793]      [    0.736918   19.      10000.    ]
22     240     [-2374.446029    10.385     2375.04986 ]      [ 4255.820304     1.732563  4255.483306]      [-10000.          7.          0.047793]      [    0.736918   19.      10000.    ]
23     229     [-2324.439777    10.465     2325.048145]      [ 4224.568633     1.630575  4224.233791]      [-10000.          8.          0.047793]      [    0.736918   19.      10000.    ]
24     221     [-2399.442901    10.505     2400.04628 ]      [ 4271.144364     1.504983  4270.805293]      [-10000.          8.          0.047793]      [    0.736918   18.      10000.    ]
25     238     [-2524.450089    10.7       2525.044555]      [ 4344.784477     1.601562  4344.438974]      [-10000.          9.          0.047793]      [    0.736918   18.      10000.    ]
26     238     [-1974.406894    10.5925    1975.047498]      [ 3981.420595     1.456518  3981.10379 ]      [-10000.          9.          0.047793]      [    0.736918   17.      10000.    ]
[False False False False False False  True  True  True False False False
 False False False False False False False False False False False False
 False False False False False False False False False False False False
  True False False False False False False False False False False False
 False  True False  True  True  True False False False False False False
 False False False False False False  True False False False False False
  True False False False False False False False False]
```

COLUMNS

```
Index(['Clump Thickness_2', 'Clump Thickness_3', 'Clump Thickness_4',
       'Clump Thickness_5', 'Clump Thickness_6', 'Clump Thickness_7',
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       'Single Epithelial Cell Size_8', 'Single Epithelial Cell Size_9',
       'Single Epithelial Cell Size_10', 'Bare Nuclei_2', 'Bare Nuclei_3',
       'Bare Nuclei_4', 'Bare Nuclei_5', 'Bare Nuclei_6', 'Bare Nuclei_7',
       'Bare Nuclei_8', 'Bare Nuclei_9', 'Bare Nuclei_10', 'Bare Nuclei_?',
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       'Bland Chromatin_5', 'Bland Chromatin_6', 'Bland Chromatin_7',
       'Bland Chromatin_8', 'Bland Chromatin_9', 'Bland Chromatin_10',
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       'Normal Nucleoli_5', 'Normal Nucleoli_6', 'Normal Nucleoli_7',
       'Normal Nucleoli_8', 'Normal Nucleoli_9', 'Normal Nucleoli_10',
       ' Mitoses _2', ' Mitoses _3', ' Mitoses _4', ' Mitoses _5',
       ' Mitoses _6', ' Mitoses _7', ' Mitoses _8', ' Mitoses _10'],
      dtype='object')
```

FINAL FEATURES SELECTED

```
6
7
8
36
49
51
52
53
66
72
```

5.1.3 Module 3: Convolutional Neural Networks

EPOCHS DURING FEATURE SELECTION

```
Epoch 1/250
33/33 [==============================] - 5s 9ms/step - loss: 0.3305 - accuracy: 0.8732
Epoch 2/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1942 - accuracy: 0.9264
Epoch 3/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1915 - accuracy: 0.9407
Epoch 4/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1674 - accuracy: 0.9448
Epoch 5/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1852 - accuracy: 0.9427
Epoch 6/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1670 - accuracy: 0.9427
Epoch 7/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1666 - accuracy: 0.9448
Epoch 8/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1595 - accuracy: 0.9468
Epoch 9/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1565 - accuracy: 0.9468
Epoch 10/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1400 - accuracy: 0.9448
Epoch 11/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1579 - accuracy: 0.9509
Epoch 12/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1860 - accuracy: 0.9448
Epoch 13/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1531 - accuracy: 0.9427
Epoch 14/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1418 - accuracy: 0.9571
Epoch 15/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1532 - accuracy: 0.9407
Epoch 16/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1399 - accuracy: 0.9489
```

```
Epoch 17/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1468 - accuracy: 0.9468
Epoch 18/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1370 - accuracy: 0.9509
Epoch 19/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1577 - accuracy: 0.9468
Epoch 20/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1586 - accuracy: 0.9468
Epoch 21/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1372 - accuracy: 0.9509
Epoch 22/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1384 - accuracy: 0.9571
Epoch 23/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1490 - accuracy: 0.9468
Epoch 24/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1250 - accuracy: 0.9591
Epoch 25/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1430 - accuracy: 0.9509
Epoch 26/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1427 - accuracy: 0.9509
Epoch 27/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1485 - accuracy: 0.9468
Epoch 28/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1174 - accuracy: 0.9591
Epoch 29/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1504 - accuracy: 0.9448
Epoch 30/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1379 - accuracy: 0.9509
Epoch 31/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1302 - accuracy: 0.9530
Epoch 32/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1306 - accuracy: 0.9530
Epoch 33/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1526 - accuracy: 0.9509
Epoch 34/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1467 - accuracy: 0.9468
Epoch 35/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1474 - accuracy: 0.9468
Epoch 36/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1377 - accuracy: 0.9509
Epoch 37/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1417 - accuracy: 0.9530
Epoch 38/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1296 - accuracy: 0.9530
Epoch 39/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1392 - accuracy: 0.9509
Epoch 40/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1370 - accuracy: 0.9530
Epoch 41/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1539 - accuracy: 0.9530
Epoch 42/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1294 - accuracy: 0.9571
Epoch 43/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1395 - accuracy: 0.9489
Epoch 44/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1365 - accuracy: 0.9489
Epoch 45/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1347 - accuracy: 0.9571
Epoch 46/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1344 - accuracy: 0.9509
Epoch 47/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1430 - accuracy: 0.9468
Epoch 48/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1359 - accuracy: 0.9530
Epoch 49/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1273 - accuracy: 0.9509
Epoch 50/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1333 - accuracy: 0.9489
Epoch 51/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1362 - accuracy: 0.9530
Epoch 52/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1362 - accuracy: 0.9550
Epoch 53/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1522 - accuracy: 0.9468
Epoch 54/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1404 - accuracy: 0.9468
Epoch 55/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1467 - accuracy: 0.9509
Epoch 56/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1276 - accuracy: 0.9530
Epoch 57/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1363 - accuracy: 0.9448
Epoch 58/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1271 - accuracy: 0.9509
Epoch 59/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1315 - accuracy: 0.9530
Epoch 60/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1394 - accuracy: 0.9509
Epoch 61/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1367 - accuracy: 0.9571
```

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Epoch 62/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1359 - accuracy: 0.9530
Epoch 63/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1272 - accuracy: 0.9571
Epoch 64/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1406 - accuracy: 0.9571
Epoch 65/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1371 - accuracy: 0.9509
Epoch 66/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1333 - accuracy: 0.9509
Epoch 67/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1284 - accuracy: 0.9509
Epoch 68/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1322 - accuracy: 0.9591
Epoch 69/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1322 - accuracy: 0.9571
Epoch 70/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1339 - accuracy: 0.9509
Epoch 71/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1304 - accuracy: 0.9489
Epoch 72/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1268 - accuracy: 0.9571
Epoch 73/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1334 - accuracy: 0.9489
Epoch 74/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1302 - accuracy: 0.9509
Epoch 75/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1256 - accuracy: 0.9530
Epoch 76/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1295 - accuracy: 0.9530
Epoch 77/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1532 - accuracy: 0.9530
Epoch 78/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1575 - accuracy: 0.9366
Epoch 79/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1302 - accuracy: 0.9509
Epoch 80/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1332 - accuracy: 0.9489
Epoch 81/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1379 - accuracy: 0.9530
Epoch 82/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1345 - accuracy: 0.9550
Epoch 83/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1311 - accuracy: 0.9530
Epoch 84/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1266 - accuracy: 0.9530
Epoch 85/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1275 - accuracy: 0.9468
Epoch 86/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1346 - accuracy: 0.9530
Epoch 87/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1271 - accuracy: 0.9550
Epoch 88/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1287 - accuracy: 0.9489
Epoch 89/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1250 - accuracy: 0.9530
Epoch 90/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1323 - accuracy: 0.9509
Epoch 91/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1346 - accuracy: 0.9509
Epoch 92/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1299 - accuracy: 0.9571
Epoch 93/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1349 - accuracy: 0.9550
Epoch 94/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1291 - accuracy: 0.9530
Epoch 95/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1302 - accuracy: 0.9550
Epoch 96/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1253 - accuracy: 0.9509
Epoch 97/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1309 - accuracy: 0.9509
Epoch 98/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1343 - accuracy: 0.9489
Epoch 99/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1343 - accuracy: 0.9509
Epoch 100/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1343 - accuracy: 0.9530
Epoch 101/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1313 - accuracy: 0.9550
Epoch 102/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1249 - accuracy: 0.9509
Epoch 103/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1369 - accuracy: 0.9489
Epoch 104/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1391 - accuracy: 0.9468
Epoch 105/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1259 - accuracy: 0.9509
Epoch 106/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1344 - accuracy: 0.9530
Epoch 107/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1264 - accuracy: 0.9530
Epoch 108/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1292 - accuracy: 0.9530
Epoch 109/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1307 - accuracy: 0.9489
Epoch 110/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1276 - accuracy: 0.9550
Epoch 111/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1252 - accuracy: 0.9571
Epoch 112/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1221 - accuracy: 0.9550
Epoch 113/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1232 - accuracy: 0.9550
Epoch 114/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1303 - accuracy: 0.9509
Epoch 115/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1504 - accuracy: 0.9448
Epoch 116/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1305 - accuracy: 0.9509
Epoch 117/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1310 - accuracy: 0.9489
Epoch 118/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1288 - accuracy: 0.9550
Epoch 119/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1295 - accuracy: 0.9489
Epoch 120/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1295 - accuracy: 0.9550
Epoch 121/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1234 - accuracy: 0.9550
Epoch 122/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1310 - accuracy: 0.9489
Epoch 123/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1323 - accuracy: 0.9530
```

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Epoch 124/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1298 - accuracy: 0.9530
Epoch 125/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1274 - accuracy: 0.9489
Epoch 126/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1325 - accuracy: 0.9509
Epoch 127/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1248 - accuracy: 0.9550
Epoch 128/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1316 - accuracy: 0.9509
Epoch 129/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1289 - accuracy: 0.9571
Epoch 130/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1294 - accuracy: 0.9509
Epoch 131/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1182 - accuracy: 0.9530
Epoch 132/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1424 - accuracy: 0.9530
Epoch 133/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1282 - accuracy: 0.9530
Epoch 134/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1305 - accuracy: 0.9509
Epoch 135/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1270 - accuracy: 0.9530
Epoch 136/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1254 - accuracy: 0.9509
Epoch 137/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1323 - accuracy: 0.9550
Epoch 138/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1258 - accuracy: 0.9509
Epoch 139/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1218 - accuracy: 0.9509
Epoch 140/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1251 - accuracy: 0.9530
Epoch 141/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1251 - accuracy: 0.9530
Epoch 142/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1292 - accuracy: 0.9509
Epoch 143/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1360 - accuracy: 0.9489
Epoch 144/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1266 - accuracy: 0.9509
Epoch 145/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1291 - accuracy: 0.9468
Epoch 146/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1221 - accuracy: 0.9530
Epoch 147/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1233 - accuracy: 0.9550
Epoch 148/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1208 - accuracy: 0.9530
Epoch 149/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1317 - accuracy: 0.9509
Epoch 150/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1256 - accuracy: 0.9509
Epoch 151/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1315 - accuracy: 0.9530
Epoch 152/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1322 - accuracy: 0.9550
Epoch 153/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1237 - accuracy: 0.9530
Epoch 154/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1294 - accuracy: 0.9489
Epoch 155/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1255 - accuracy: 0.9468
Epoch 156/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1209 - accuracy: 0.9550
Epoch 157/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1260 - accuracy: 0.9509
Epoch 158/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1217 - accuracy: 0.9550
Epoch 159/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1228 - accuracy: 0.9509
Epoch 160/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1207 - accuracy: 0.9489
Epoch 161/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1359 - accuracy: 0.9509
Epoch 162/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1290 - accuracy: 0.9407
Epoch 163/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1268 - accuracy: 0.9509
Epoch 164/250
33/33 [==============================] - 0s 4ms/step - loss: 0.1263 - accuracy: 0.9530
Epoch 165/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1346 - accuracy: 0.9530
Epoch 166/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1252 - accuracy: 0.9550
Epoch 167/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1233 - accuracy: 0.9550
Epoch 168/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1298 - accuracy: 0.9509
Epoch 169/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1316 - accuracy: 0.9550
Epoch 170/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1248 - accuracy: 0.9550
Epoch 171/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1269 - accuracy: 0.9489
Epoch 172/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1225 - accuracy: 0.9509
Epoch 173/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1196 - accuracy: 0.9509
Epoch 174/250
33/33 [==============================] - 0s 5ms/step - loss: 0.1266 - accuracy: 0.9530
Epoch 175/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1215 - accuracy: 0.9550
Epoch 176/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1265 - accuracy: 0.9509
Epoch 177/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1248 - accuracy: 0.9530
Epoch 178/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1193 - accuracy: 0.9550
Epoch 179/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1273 - accuracy: 0.9489
Epoch 180/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1280 - accuracy: 0.9509
Epoch 181/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1244 - accuracy: 0.9530
Epoch 182/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1256 - accuracy: 0.9468
Epoch 183/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1196 - accuracy: 0.9509
Epoch 184/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1251 - accuracy: 0.9550
Epoch 185/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1250 - accuracy: 0.9530
```

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Epoch 186/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1203 - accuracy: 0.9509
Epoch 187/250
33/33 [==============================] - 0s 10ms/step - loss: 0.1249 - accuracy: 0.9550
Epoch 188/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1216 - accuracy: 0.9530
Epoch 189/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1297 - accuracy: 0.9489
Epoch 190/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1258 - accuracy: 0.9550
Epoch 191/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1255 - accuracy: 0.9509
Epoch 192/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1320 - accuracy: 0.9571
Epoch 193/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1221 - accuracy: 0.9571
Epoch 194/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1324 - accuracy: 0.9530
Epoch 195/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1369 - accuracy: 0.9530
Epoch 196/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1286 - accuracy: 0.9550
Epoch 197/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1242 - accuracy: 0.9509
Epoch 198/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1294 - accuracy: 0.9468
Epoch 199/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1487 - accuracy: 0.9448
Epoch 200/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1499 - accuracy: 0.9448
Epoch 201/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1259 - accuracy: 0.9530
Epoch 202/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1326 - accuracy: 0.9509
Epoch 203/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1265 - accuracy: 0.9571
Epoch 204/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1283 - accuracy: 0.9550
Epoch 205/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1294 - accuracy: 0.9530
Epoch 206/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1247 - accuracy: 0.9509
Epoch 207/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1342 - accuracy: 0.9509
Epoch 208/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1265 - accuracy: 0.9571
Epoch 209/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1390 - accuracy: 0.9509
Epoch 210/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1260 - accuracy: 0.9509
Epoch 211/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1224 - accuracy: 0.9509
Epoch 212/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1224 - accuracy: 0.9550
Epoch 213/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1218 - accuracy: 0.9550
Epoch 214/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1278 - accuracy: 0.9530
Epoch 215/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1232 - accuracy: 0.9509
Epoch 216/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1272 - accuracy: 0.9489
Epoch 217/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1249 - accuracy: 0.9509
Epoch 218/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1242 - accuracy: 0.9550
Epoch 219/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1231 - accuracy: 0.9550
Epoch 220/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1256 - accuracy: 0.9530
Epoch 221/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1288 - accuracy: 0.9489
Epoch 222/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1226 - accuracy: 0.9530
Epoch 223/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1242 - accuracy: 0.9530
Epoch 224/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1292 - accuracy: 0.9448
Epoch 225/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1260 - accuracy: 0.9550
Epoch 226/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1274 - accuracy: 0.9591
Epoch 227/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1264 - accuracy: 0.9489
Epoch 228/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1249 - accuracy: 0.9489
Epoch 229/250
33/33 [==============================] - 0s 6ms/step - loss: 0.1186 - accuracy: 0.9530
Epoch 230/250
33/33 [==============================] - 0s 7ms/step - loss: 0.1203 - accuracy: 0.9550
Epoch 231/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1269 - accuracy: 0.9509
Epoch 232/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1303 - accuracy: 0.9509
Epoch 233/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1231 - accuracy: 0.9530
Epoch 234/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1260 - accuracy: 0.9530
Epoch 235/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1221 - accuracy: 0.9489
Epoch 236/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1247 - accuracy: 0.9509
```

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Epoch 237/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1311 - accuracy: 0.9530
Epoch 238/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1208 - accuracy: 0.9509
Epoch 239/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1225 - accuracy: 0.9591
Epoch 240/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1380 - accuracy: 0.9550
Epoch 241/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1258 - accuracy: 0.9550
Epoch 242/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1252 - accuracy: 0.9509
Epoch 243/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1295 - accuracy: 0.9530
Epoch 244/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1296 - accuracy: 0.9509
Epoch 245/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1313 - accuracy: 0.9530
Epoch 246/250
33/33 [==============================] - 0s 9ms/step - loss: 0.1214 - accuracy: 0.9571
Epoch 247/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1355 - accuracy: 0.9489
Epoch 248/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1213 - accuracy: 0.9550
Epoch 249/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1269 - accuracy: 0.9489
Epoch 250/250
33/33 [==============================] - 0s 8ms/step - loss: 0.1292 - accuracy: 0.9530
```
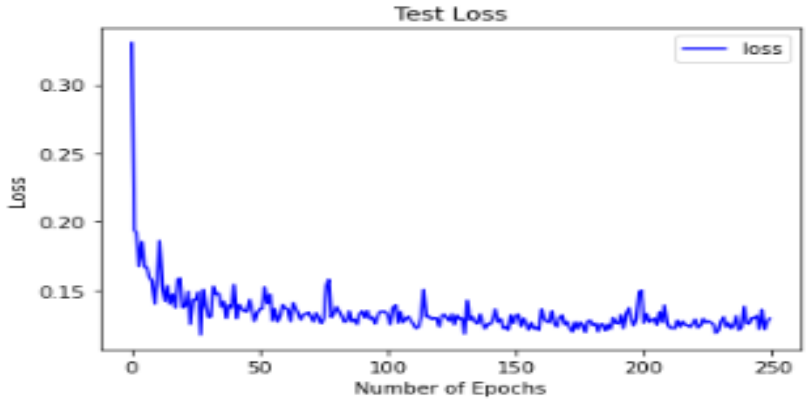
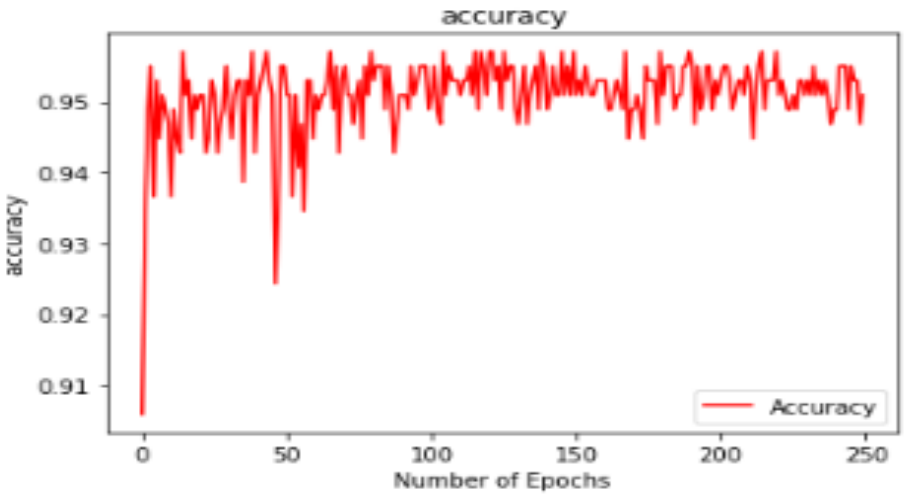

TEST LOSS DURING FEATURE SELECTION



ACCURACY WHEN FEATURE SELECTION IS DONE



EPOCHS WHEN ALL FEATURES ARE CONSIDERED

```
Epoch 1/250
28/28 [==============================] - 1s 2ms/step - loss: nan - accuracy: 0.6038
Epoch 2/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 3/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 4/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 5/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 6/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 7/250
28/28 [==============================] - 0s 1ms/step - loss: nan - accuracy: 0.6587
Epoch 8/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 9/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 10/250
28/28 [==============================] - 0s 1ms/step - loss: nan - accuracy: 0.6587
Epoch 11/250
28/28 [==============================] - 0s 3ms/step - loss: nan - accuracy: 0.6587
Epoch 12/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 13/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 14/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 15/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 16/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 17/250
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Epoch 18/250
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Epoch 24/250
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Epoch 25/250
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Epoch 26/250
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Epoch 27/250
28/28 [==============================] - 0s 3ms/step - loss: nan - accuracy: 0.6587
Epoch 28/250
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Epoch 29/250
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Epoch 30/250
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Epoch 51/250
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Epoch 52/250
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Epoch 179/250
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28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 232/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 233/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 234/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 235/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
```
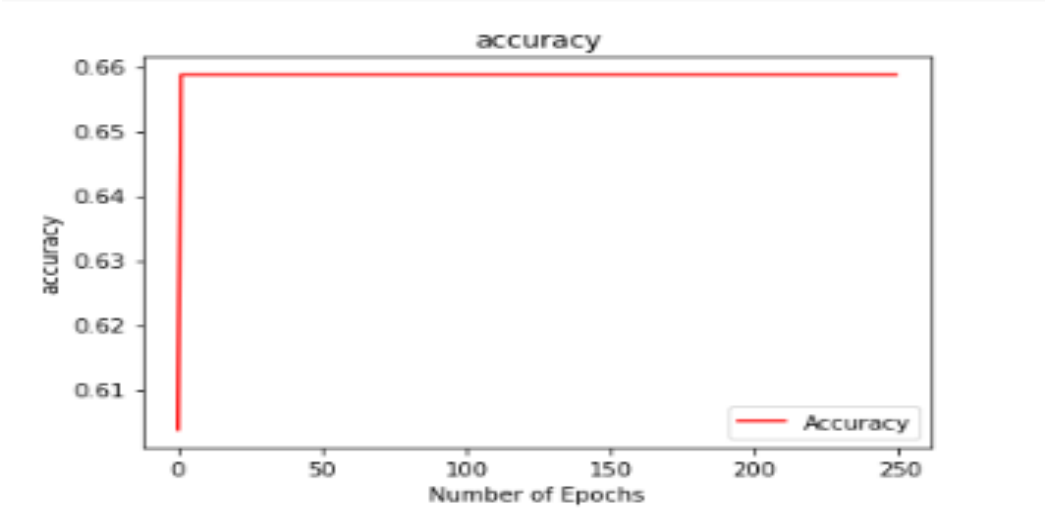
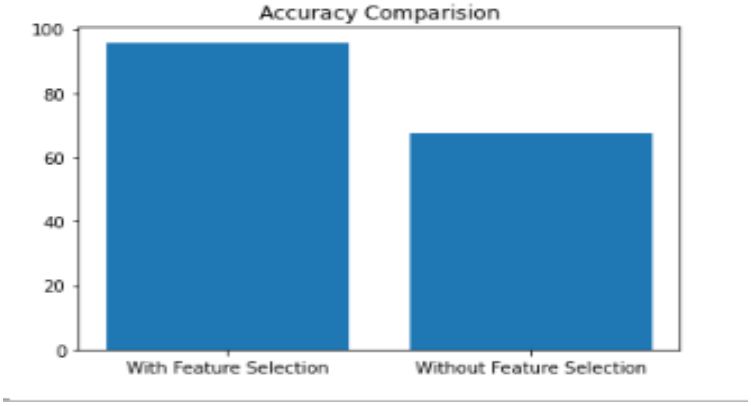

```
Epoch 236/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 237/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 238/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 239/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 240/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 241/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 242/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 243/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 244/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 245/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 246/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 247/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 248/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 249/250
28/28 [==============================] - 0s 2ms/step - loss: nan - accuracy: 0.6587
Epoch 250/250
28/28 [==============================] - 0s 1ms/step - loss: nan - accuracy: 0.6587
```

ACCURACY WHEN ALL FEATURES ARE CONSIDERED

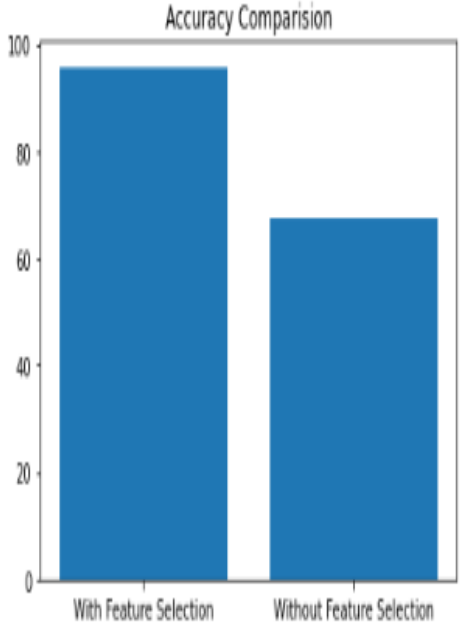


COMPARISON OF ACCURACIES WHEN FEATURE SELECTION IS DONE AND WHEN ALL FEATURES ARE CONSIDERED



5.2 EVALUATION OF RESULTS

- All the rules from the dataset are mined using Association Rule Mining and the rules of antecedent length >= 1, confidence > 0.75 and lift > 1.2 are considered.
- The features that are of highest relevance are extracted using GIANT Feature Selection. The final features selected are 6, 7, 8, 36, 49, 51, 52, 53, 66, 72.
- Convolutional Neural Networks is used to find the accuracy of the proposed system.
    - Accuracy when all features are considered = 0.6587 (or) 65.87%
    - Accuracy when feature selection is done = 0.9530 (or) 95.3%



CHAPTER 6: CONCLUSION AND FUTURE ENHANCEMENTS

6.1 CONCLUSION

A feature selection method based on Genetic Investigation of Anthropometric Traits-Feature Selection GIANT-FS for classifying the classes, selecting the relevant features and to identify biomarkers to diagnose breast cancer is implemented. This gives a better prognosis of the cancer. The association rule mining provides the necessary conditions for the diagnosis. We applied Convolutional Neural Networks to find the performance of the implemented model. This proposed system gives a better performance due to less number of features, reduced time and memory space. The performance is measured on the basis of accuracy. When feature selection is done by GIANT Feature Selection, the accuracy achieved is 95.3%. This is a better outcome as the accuracy achieved when all the features are considered is only 65.87%.

6.2 FUTURE ENHANCEMENTS

Future works will focus on approaches where more features could be extracted from the breast cancer datasets. Another possibility for future improvement is including real time retraining and evaluation capability. Time complexity of the proposed system can be improved. In future, we will use other features selection algorithms along with other data sets of breast cancer for further improvement in breast cancer detection. Additionally, other deep learning models will also be applied for the detection of breast cancer.

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1. Dalal Bardou, Kun Zhang and Sayed Mohammad Ahmad, “Classification of Breast Cancer Based on Histology Images Using Convolutional Neural Networks”, IEEE ACCESS, May 24, 2018.
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PUBLICATION

1. Ellen Daniel, Manigandan G, Sushma T, Thamizhselvi E and Geetha V, "A Survey on the Recent Feature Selection Methods used for the Detection of Breast Cancer", 12th Internationnal Conference on Science and Innovative Engineering 2022 (12 ICSIE 2022), June 05, 2022 with Paper ID: ICSIE201066 will be published in Journal IJARBEST.

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