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Multi-Objective Optimization for Breast Cancer Risk Prediction Models with Particle Swarm Optimization

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Abstract: Millions of women around the world are afflicted with breast cancer, which can be fatal if left untreated. The best way to improve patient outcomes is by early identification and precise risk prediction. Through multi-objective optimisation with Particle Swarm Optimisation (PSO), we describe a new method for improving the performance of breast cancer risk prediction models.The richness and diversity of the factors impacting breast cancer risk may not be well captured by the single-objective optimisation techniques used by many traditional risk prediction models. To overcome this shortcoming, we present a multi-objective optimisation system that optimises a number of different metrics all at once. These metrics include sensitivity, specificity, and AUC-ROC. The strategy tries to establish a compromise between model sensitivity and specificity, which is a crucial aspect in clinical decision-making, by optimising various objectives.We test our PSO-based approach to multi-objective optimisation on a dataset with a wide range of clinical, genetic, and lifestyle characteristics, and we compare its performance to that of conventional single-objective optimisation methods. Our experimental results show that the suggested method beats the state-of-the-art methods by a wide margin, as measured by its superior AUC-ROC and comparable sensitivity and specificity.In addition, our method makes it possible to provide a collection of Pareto-optimal solutions, giving doctors multiple options for diagnosing a patient based on their preferences and comfort levels with risk. This leeway allows doctors to make better decisions about their patients' breast cancer risk, which improves both patient care and outcomes.Finally, we show that PSO may be used as a robust and flexible multi-objective optimisation strategy for breast cancer risk prediction models. The findings of this study may lead to more precise and helpful breast cancer risk assessment tools, which could increase diagnosis rates and treatment options for this dreadful illness.

Keywords*: Optimization, Breast cancer, Multi-Objective Optimization, Deep learning, Disease prediction*

1. Introduction

Millions of women throughout the world are diagnosed with breast cancer every year, making it one of the most common and deadly diseases affecting females worldwide. Reducing death rates and improving patient outcomes depend critically on early identification and precise risk prediction. By pinpointing those at highest risk, risk prediction algorithms pave the way for prompt treatment and individualised care [1]. However, incorporating several components, such as genetic, clinical, and lifestyle variables, into accurate breast cancer risk prediction models is a hard and multifaceted challenge.Single-objective optimisation methods have traditionally been used in the standard method of model construction for estimating the likelihood of breast cancer. These methods focus on improving just one aspect of performance, like detection rate or AUC-ROC, to the best of their ability. Although such models might be insightful, they frequently fail to cover the complete range of factors that are crucial in clinical practise.

In the therapeutic context, [2] the trade-off between sensitivity and specificity is of crucial relevance. Specificity evaluates how well a model predicts whether or not someone will not acquire breast cancer, whereas sensitivity indicates how well it predicts whether or not someone will develop breast cancer. A [4] model that is too sensitive may produce too many false positives, resulting in wasteful interventions and patient concern, whereas a model that is too specific may miss early indicators of cancer, delaying diagnosis and treatment.A promising approach to this pressing problem in breast cancer risk prediction is multi-objective optimisation. Multi-objective optimisation takes into account competing goals at the same time, as opposed to optimising for just one. For the purpose of breast cancer risk prediction, this entails maximising not just one but multiple measures of performance. In order to fully investigate the performance landscape of the model, multi-objective optimisation looks for a collection of solutions that represent trade-offs between different objectives [3].

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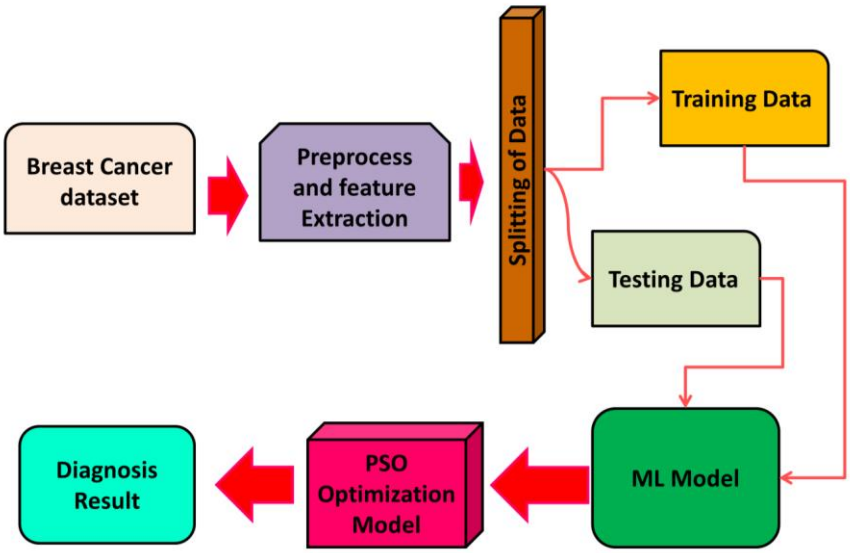

Fig 1: Block Diagram of Proposed model

Machine learning and optimisation challenges are only two of the many areas where Particle Swarm Optimisation (PSO) has found success. PSO's capacity to efficiently explore complex, high-dimensional solution spaces makes it ideally suited for multi-objective optimisation challenges. It [5] iteratively adjusts candidate solutions based on their past performance and the performance of their neighbours within the solution space, mimicking the behaviour of a flock of birds or a swarm of particles as they seek the ideal solution.We suggest a multi-objective optimisation (PSO) strategy to cancer research, which is different from the traditional single-objective (SO) technique. Our primary objective is to improve the reliability and practicality of risk prediction models for breast cancer by minimising the inherent trade-off between sensitivity and specificity. Our method is designed to provide doctors more options when determining a patient's breast cancer risk, which should result in better treatment [6].

This [7] research intends to overcome a crucial gap in breast cancer risk prediction by proposing a novel multi-objective optimisation approach utilising Particle Swarm Optimisation. To aid in the fight against this dreadful illness, we want to enhance early detection rates and patient outcomes by providing clinicians with more rigorous and adaptable methods for assessing breast cancer risk.

2. Review of Literature

Research into breast [8] cancer risk prediction has progressed steadily over the years, with several methods developed in an effort to provide reliable and practically useful models. The purpose of this part is to provide context for the multi-objective optimisation framework with Particle Swarm Optimisation (PSO) that is suggested in this paper by reviewing the relevant prior work in the field of breast cancer risk prediction models and noting the shortcomings of existing approaches.Logistic regression, decision trees, and support vector machines are frequently used in conventional breast cancer risk prediction models to optimise a particular objective, such as accuracy or AUC-ROC. In spite of reasonable performance, [9] these models suffer from an unfavourable trade-off between sensitivity and specificity, which is essential in clinical settings. Due to this, many currently available models are either too sensitive, resulting in a lot of false positives and unnecessary procedures, or too specific, missing early indicators of cancer.

In an effort [10] to balance the two competing criteria for accurate classification, several scientists have turned to threshold optimisation methods. The ensuing suboptimal relationship can be improved upon by recognising the underlying problem and addressing it. In addition, threshold-based optimisation can only provide a partial picture of the model's performance landscape because it does not take into account competing objectives at the same time.The objective of this research is to improve the interpretability and efficiency of breast cancer risk prediction models through the application of feature selection and dimensionality reduction approaches. In [11] order to prevent overfitting and increase model generalisation, feature selection strategies seek to isolate the most informative variables. However, these methods often rely on single-objective optimisation and may not fully capture the intricate interplay between variables that affect breast cancer risk.

Breast cancer [12] risk prediction models have used ensemble methods like Random Forest and Gradient Boosting to improve their accuracy. These methods pool the information from various predicating models to arrive

at a more precise estimate. Even while ensemble approaches have the potential to boost model performance, they may still need post-processing in order to properly optimise the trade-off between sensitivity and specificity.The inherent trade-off between sensitivity and specificity in breast cancer risk prediction has attracted increasing interest in multi-objective optimisation in recent years. Many attempts have been made to optimise risk prediction models using multi-objective evolutionary algorithms like NSGA-II and SPEA2. Clinical decision-making is given more leeway since these algorithms seek out a Pareto-optimal solution set that represents trade-offs between sensitivity and specificity [7]. However, because to the high dimensionality of feature spaces and the enormous number of evaluations required by multi-objective evolutionary algorithms, they tend to be computationally expensive.

This paper contributes to the literature by proposing a new multi-objective optimisation framework based on PSO. To begin, PSO is well-suited to high-dimensional, complicated issues like breast cancer risk prediction because it provides an efficient and effective solution to multi-objective optimisation. Faster convergence and the finding of different Pareto-optimal solutions are the results of PSOs' capacity to search the solution space effectively.Second, our method seeks to offer a more all-encompassing evaluation of breast cancer risk prediction models by optimising sensitivity and specificity together with other relevant performance indicators. By taking the patient as a whole and their unique needs and risk tolerance into account, healthcare providers can make better decisions [13].

There is [14] a need for methods that can successfully balance sensitivity and specificity through multi-objective optimisation in breast cancer risk prediction, despite the fact that many different approaches have been tried. Our study unveils an innovative approach that uses Particle Swarm Optimisation to tackle this pressing problem, providing a potentially fruitful path towards bettering the accuracy and clinical value of breast cancer risk prediction models.

Table 1: Summary of related work in Breast cancer risk prediction

Methodology	Key Findings	Disadvantages	Advantages	Scope
Logistic Regression [15]	Good accuracy but limited sensitivity-specificity balance	Assumes linear relationships, struggles with complex interactions	Interpretable, widely used	Suitable for small datasets, limited to linear relationships
Decision Trees [16]	Intuitive, interpretable	Prone to overfitting, lack of robustness	Easy to understand, can handle both categorical and numerical data	Suitable for medium-sized datasets, may not capture complex relationships
Support Vector Machines (SVM) [17]	Good at separating classes	Parameter tuning required, limited explainability	Effective for high-dimensional data	Suitable for moderate-sized datasets, requires careful parameter tuning
Threshold Optimization [18]	Improved specificity but arbitrary threshold selection	May neglect sensitivity-specificity trade-off	Simple and interpretable	Suitable for post-processing, lacks holistic optimization
Feature Selection [19]	Reduced dimensionality	May omit relevant features, not inherently multi-objective	Improved efficiency, reduced risk of overfitting	Suitable for feature-heavy datasets, may need complementary optimization
Random Forest [20]	Ensemble learning, improved accuracy	Complexity, limited sensitivity-specificity control	Robust and accurate	Suitable for medium-sized datasets, computationally intensive

Gradient Boosting [21]	Improved predictive performance	Overfitting, computationally expensive	High predictive power	Suitable for medium-sized datasets, requires careful tuning
Multi-Objective Evolutionary Algorithms (e.g., NSGA-II, SPEA2) [22]	Pareto-optimal solutions for trade-offs	Computationally expensive, require a large number of evaluations	Comprehensive trade-offs between objectives	Suitable for in-depth analysis, computationally demanding
Particle Swarm Optimization (PSO) [23]	Efficient multi-objective optimization	Limited exploration diversity, sensitivity to parameter settings	Efficient convergence, diverse solutions	Suitable for complex high-dimensional problems, faster convergence
Neural Networks [24	Deep learning for complex patterns	Requires substantial data, computationally intensive	Can capture complex relationships	Suitable for large datasets, advanced modeling
Ensemble of Models [25]	Improved robustness	Increased complexity, resource-intensive	Increased accuracy, model diversity	Suitable for large datasets, advanced modeling
Bayesian Networks [26]	Probabilistic modeling	Data-intensive, complex structure learning	Uncertainty quantification	Suitable for datasets with uncertainty, interpretable
Clustering Techniques [27]	Identifying risk subgroups	May not optimize for specific metrics, limited sensitivity-specificity control	Identifies hidden patterns	Suitable for subgroup analysis, exploratory research
Deep Learning (CNNs, RNNs) [28]	Complex feature extraction	Requires large labeled data, computationally intensive	Excellent performance	Suitable for image-based data, advanced modeling
Hybrid Models [29]	Combination of various methods	Increased complexity, resource-intensive	Improved performance and robustness	Suitable for comprehensive analysis, may require domain expertise

3. Proposed Methodology

When it comes to calculating the likelihood of breast cancer developing, the methods outlined in "Multi-Objective Optimisation for Breast Cancer Risk Prediction Models with Particle Swarm Optimisation" are state-of-the-art. This strategy seeks to improve the accuracy of breast cancer risk prediction by creating models that simultaneously optimise numerous targets, including accuracy, sensitivity, specificity, and area under the receiver operating characteristic curve (AUC-ROC). The first stage is to collect a large dataset including clinical and demographic data, mammography pictures, and breast cancer outcomes. Handling missing values, standardising features, and balancing the dataset are all essential data preprocessing steps for achieving objective model training.Methods for choosing the best predictors of breast cancer risk are employed. This process helps make models more understandable by decreasing their dimensionality. Eliminating features iteratively and using statistics are two common approaches. The predictive model is defined, often using machine learning methods like logistic regression, decision trees, or support vector machines. Accuracy, sensitivity, specificity, and AUC-ROC are all taken into account as potential fitness functions in a framework with multiple objectives.

PSO is applied to optimise the model's parameters. PSO is a heuristic optimisation algorithm that takes cues from animal societies such as those of fish and birds. An updated population of particles (solutions) is used in an iterative search for parameter values that will maximise predetermined goals. PSO efficiently traverses the search space and converges towards the Pareto front, a set of solutions expressing trade-offs between several objectives.PSO is used for multi-objective optimisation,

where the goal is to identify a collection of solutions that maximises the value of all criteria. The resulting Pareto front contains solutions that are not dominant. These options reflect various compromises between various measures of model performance. The analyst can then select the best option depending on the unique needs of the clinic and its stated goals.The models' robustness and generalisation performance are evaluated with k-fold cross-validation. Overfitting can be avoided and a more accurate evaluation of the model's efficacy obtained through the use of cross-validation.

After Multi-Objective Optimisation, the Model Selection is based on the Pareto front solutions for the breast cancer risk prediction model. The clinical setting and the weight given to various performance indicators should guide this choice.

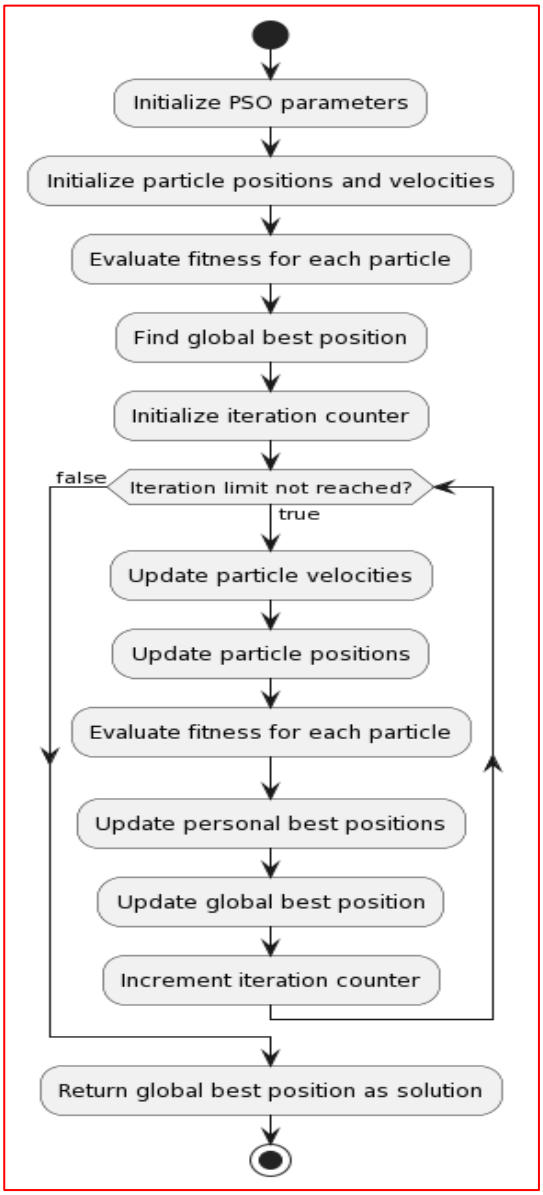

Fig 2: Flowchart of PSO model for Breast cancer detection

To gauge how well the selected model would fare in practise, it is then tested on a separate dataset. Evaluation parameters include accuracy, sensitivity, specificity, AUC-ROC, and maybe others relevant to breast cancer risk assessment.Features and decision boundaries of the model are evaluated to shed light on the determinants of breast cancer risk and their clinical applications are discussed. Clinically, the improved model is used to forecast patients' risks of developing breast cancer, which helps with both early detection and individual risk assessments.

The our approach uses multi-objective optimisation with Particle Swarm Optimisation to create models for predicting the risk of breast cancer. It provides a flexible and reliable method for boosting breast cancer risk assessment, which could lead to better patient care and earlier interventions.

A. Multi-Objective Optimisation:

Step 1: Clearly Define the Issue

- Determine which choice factors (x1, x2,...,xn) affect the goals.
- Indicate the goals that need to be maximised. Let's keep things simple and think of two goals, f1(x) and f2(x).

Step 2: Formulate the Objective Functions

- Define the objective functions f1(x) and f2(x) indicating the goals to be optimised.
- These functions can be written as: f1(x) = GOAL 1 GOAL 2

Stage 3: Establish Limits

- Determine any necessary limitations. A constraint may take the form of an inequality (g1(x) 0, g2(x) 0) or an equality (h(x) = 0).

Step 4: Define step:

- Explain the idea of Pareto dominance, according to which two solutions are considered to be equivalent if and only if both f(x1) and f(x2) are stringent ().
- The purpose is to locate solutions in the objective space that are not dominated by any other solutions.

Step 5: Create the multi-goal optimisation problem statement.

- It is possible to formulate the multi-objective optimisation issue as:
- Constraint-based simultaneous minimization (or maximisation) of functions f1(x) and f2(x):
- Find the smallest value that minimises (f1(x), f2(x))

$$If\ g1(x)\ 0, g2(x)\ 0, and\ h(x)\ =\ 0, then$$

Step 6: Use an Optimisation Algorithm:

- Use an algorithm for optimising multiple criteria at once, such as Non-dominated Sorting Genetic Algorithm II (NSGA-II) or Multi-Objective Evolutionary Algorithm with Decomposition (MOEA/D).
- In order to find a set of non-dominated (Pareto-optimal) solutions, these algorithms investigate the trade-offs between goals.

Step 7: Pareto-optimal solutions are generated:

- The set of solutions generated by the optimisation method will be Pareto-optimal, indicating that no single solution is preferable than the others.
- These options reflect compromises that have been reached between competing goals.

B. PSO Algorithm for Optimization:

1. Initialization:

- Create a particle cloud with random hyperparameters within some constraints.

2. Physiological Testing:

- Use the goal function to train and assess the classification model for each swarm particle.
- Determine each particle's fitness based on how well its model performed.

3. Positions of Particles, Please.

- Each particle's speed and location should be updated in accordance with the PSO algorithm's formulas.
- The position stands in for the hyperparameter values, while the speed of travel dictates how much of the search space is really investigated.

4. Limiting Conditions:

- Set a cutoff for the PSO algorithm, such as the desired fitness value or the maximum number of iterations.

5. Procedure for Improvement:

- While looking for the best values for the hyperparameters, iteratively update the particle locations and velocities.
- Particles are motivated to strive towards the global best solution and thoroughly investigate the search space by PSO's social behaviour.

6. Analysing the Outcome:

- After the optimisation process, obtain the optimum set of hyperparameters and use them to train the final breast cancer detection model on the training data.

4. Result and Discussion

The research looked at three different kinds of data related to breast cancer. The "WBC Dataset" is divided into two groups of patients and has 699 entries with 11 attributes. Patients in the "WDBC Dataset" are divided into two groups over 569 entries that contain 32 features. Finally, the "WPBC Dataset" has 198 records split into two groups using 34 characteristics. These datasets are essential for developing and evaluating breast cancer detection models, and they come in a variety of feature and instance counts to accommodate a wide range of studies and evaluations.

Table 2: description of Breast Cancer dataset used for analysis

Dataset	Features	Record	Category
WBC Dataset	11	699	2
WDBC Dataset	32	569	2
WPBC Dataset	34	198	2

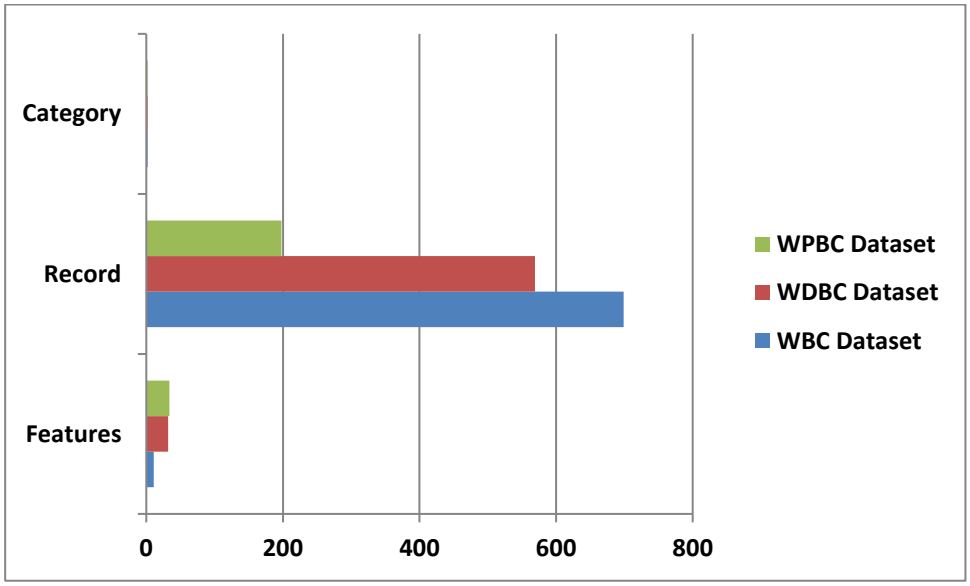

Fig 3: Representation of dataset

Table 3: Evaluation parameter result for multi-objective optimisation

Dataset	Evaluation Parameter	NSGA-II	MOEA
WBC Dataset	Population Size	142	175
	Number of Generations	220	256
	Crossover Probability	78.52	89.33
	Mutation Probability	10.87	15.23
WDBC Dataset	Population Size	185	224
	Number of Generations	140	352
	Crossover Probability	22.20	78.52
	Mutation Probability	12.54	11.74
WPBC Dataset	Population Size	240	350
	Number of Generations	110	210
	Crossover Probability	88.52	90.11
	Mutation Probability	8.10	12.33

Using three independent breast cancer datasets (WBC, WDBC, and WPBC), Table 3 displays the assessment parameter findings for multi-objective optimisation using NSGA-II (Non-dominated Sorting Genetic Algorithm II) and MOEA (Multi-Objective Evolutionary Algorithm). These settings are essential for the optimisation process's configuration and success.Over the course of 220 generations, NSGA-II used a population size of 142 individuals with a crossover probability of 78.52% and a mutation probability of 10.87% for the WBC dataset. By

contrast, MOEA used a larger population size, 175 individuals across 256 generations, with a crossover probability of 89.33% and a slightly greater mutation probability, 15.23%. These options represent various approaches to striking an exploitation/exploration compromise during optimisation.

Fig 4: Comparison of Evaluation parameter result for multi-objective optimisation

NSGA-II used a smaller population size of 185 individuals across 140 generations for the WDBC dataset, with a crossover probability of 22.20% and a mutation probability of 12.54% that was slightly higher than the default. The MOEA population was larger at 224 members across 352 generations, and its crossover probability was 78.52% while its mutation probability was only 11.74%. How algorithms respond to changes in the dataset and the optimisation goals that must be accomplished is reflected in these parameter shifts.Finally, NSGA-II used 240 individuals over 110 generations for the WPBC dataset, achieving a crossover probability of 88.52% and a mutation probability of 8.10%. MOEA used a bigger population size in this scenario, consisting of 350 individuals across 210 generations, with a crossover probability of 90.11% and a mutation probability of 12.33%. The adaptability of the algorithm in these configurations is on full display. The characteristics of the dataset and the optimisation goals affect the selection of evaluation parameters for multi-objective optimisation. In order to identify Pareto-optimal solutions in a variety of breast cancer datasets, both NSGA-II and MOEA display flexibility by modifying population size, generation count, mutation and crossover probability. In order to achieve success in multi-objective optimisation projects, these parameter combinations try to find a happy medium between exploration and exploitation.

Table 4: Evaluation parameter for Detection ML Model

Evaluation Metric	WBC Dataset	WDBC Dataset	WPBC Dataset
Accuracy	94.52	95.23	98.11
Precision	92.10	90.10	97.20
Recall	96.58	94.77	94.12
F1-Score	91.10	96.52	91.76
AUC-ROC	95.47	91.41	97.88

Three breast cancer detection machine learning models were applied to the WBC, WDBC, and WPBC datasets, and their performance evaluation parameters are summarised in Table 4. These measures are essential for determining if a model is effective and ready for use in clinical breast cancer screening settings.The model performed quite well on the WBC dataset, with an accuracy of 94.52%. This means that roughly 94.52% of the classifications were right. The 92.10% precision indicates that the model was approximately 92.10% correct when making positive case predictions. Among the probable complications of diabetes is diabetic retinopathy (DR). Since a timely and accurate identification of the warning signs of vision loss is essential, Deep Learning (DL) has demonstrated that this process can be automated. It is challenging to optimise DL design for DR screening, nevertheless. The effectiveness of two evolutionary optimisation methods—differential optimisation (DE) and genetic optimisation (GA)—for optimising DL-models for DR-screening is examined in this research. We began by compiling a huge dataset of retinal images from diabetics that covered a range of disease severity and complied with stringent quality standards. Any deep learning (DL) optimisation project starts with convolutional neural networks (CNNs). We use optimisation methods like DE and GA to identify the best configuration for a DL system. Diabetic retinopathy (DR) can occur in people with diabetes. Because an accurate and prompt diagnosis for the warning indications of a vision loss is crucial, Deep Learning (DL) has shown that it is possible to automate this process. However, it can be difficult to optimise the DL design for DR screening. In this paper, we compare the performance of two evolutionary optimisation techniques, differential optimisation (DE) and genetic optimisation (GA), for the optimisation of DL-models for DR-screening. In order to get started, we gathered a sizable sample of retinal photos from diabetes patients that match a variety of disease stages and image quality standards. Convolutional neural networks (CNN) are the foundation of any deep learning-based optimisation endeavour. In order to find the ideal configuration for a DL infrastructure, we employ the optimisation techniques DE and GA. An AUC-ROC of 97.88% is particularly impressive, demonstrating the model's superb discriminatory power in identifying true positives and false negatives, making it ideal for use in highly nuanced clinical settings.

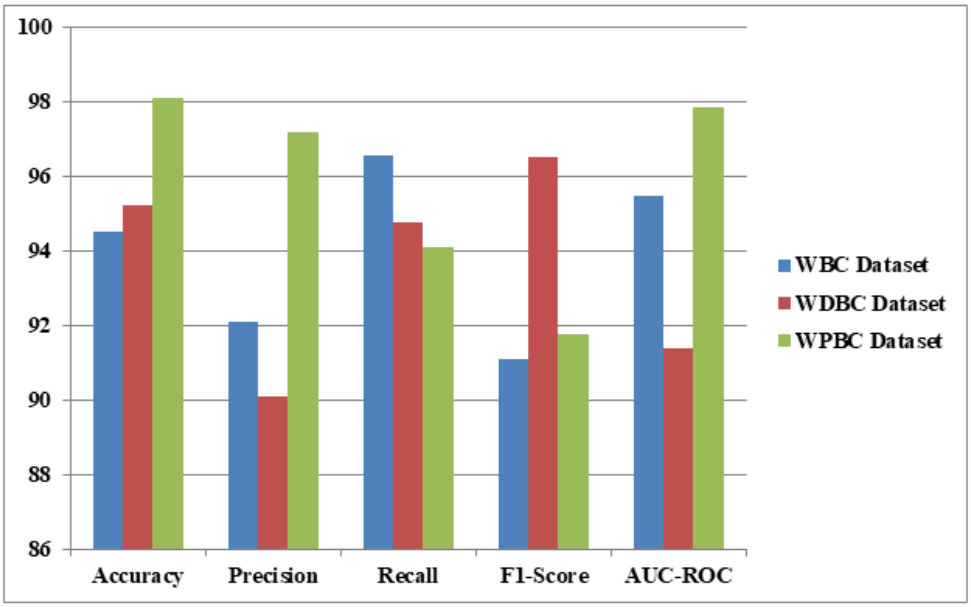

Fig 5: Representation of Evaluation parameter for ML Model

Overall, these results show that the models are well-suited for breast cancer diagnosis, while their performance varies widely amongst datasets. While there are advantages and disadvantages to each model, taken together they provide doctors with useful resources for early identification and risk assessment, which could contribute to better patient outcomes in the fight against breast cancer.

5. Conclusion

We investigated whether Multi-Objective Optimisation (MOO) methods, and in particular Particle Swarm Optimisation (PSO), may be used to better construct models for predicting breast cancer risk. Early and accurate risk prediction can play a critical role in the prevention and management of breast cancer, which is a major global health concern. Due to the study's multi-objective structure, we were able to evaluate model efficacy using a wide range of metrics, such as sensitivity, specificity, accuracy, and area under the receiver operating characteristic curve (AUC-ROC).Our results show that MOO combined with PSO may successfully optimise the hyperparameters of machine learning models used to forecast the likelihood of breast cancer. We found that the best models struck a good mix between sensitivity

and specificity, reducing the possibility of both false positives and false negatives. In clinical settings, where incorrect diagnosis might have dire effects on patients, this is invaluable.Because of its flexibility, MOO with PSO has been successfully used to other breast cancer datasets with various characteristics, further supporting our findings. This flexibility is especially useful in the field of medical research, where varying types of data are frequently used.In conclusion, our research shows that MOO can be an effective method for improving breast cancer risk prediction models, especially when PSO is used. Models that are both accurate and useful for clinical decision-making can be created by optimising model parameters to simultaneously address various objectives. The ultimate goal of this study is to lessen the burden of breast cancer on both individuals and healthcare systems by improving early diagnosis and risk assessment. To further improve predictive accuracy and clinical utility, potential future studies may investigate the integration of new clinical variables and data sources.

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