GENE CANCER CLASSIFICATION USING ENHANCED TRANSFERABLE REINFORCEMENT LEARNING AND ENHANCED RESNET ALGORITHM

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Abstract

In this paper, we propose a novel approach to cancer classification using microarray datasets which integrates transfer learning, improved feature selection technique and state of the art Deep Learning (DL) models. Traditional machine learning algorithms usually have high computational costs when dealing with high dimensional, highly noisy microarray datasets with a large number of irrelevant or redundant features. We introduce pre-processing using standard scalar and the Enhanced Transferable Reinforcement Learning (ETRL) algorithm for feature selection, using a reinforcement learning perspective to select significant features that are amenable to transfer to unseen datasets. An enhanced ResNet model is finally used to classify the preprocessed features by employing transfer learning to augment the classification accuracy. Standard scaling techniques are used to normalize all of the features so that the model can learn better. Our framework combines the strength of ETRL based feature selection, and ResNet's deep learning ability, which outperforms existing methods in both terms of accuracy and computational efficiency. Our approach is shown to be effective in identifying significant biomarkers for different types of cancers on benchmark microarray cancer datasets. The proposed methodology is a promising solution for the cancer detection problem and a promising route towards more robust, scalable, and interpretable cancer classification systems.

Keywords: Deep Learning, Gene cancer, Reinforcement Learning, ResNet, standard scalar.

I INTRODUCTION

The use of microarray gene expression data for cancer classification is a very important, yet complicated, classification problem in oncology research. Large set of microarray datasets such as examples that measure expression levels of thousands of genes simultaneously hold great potential to understand cancer progression and to aid early diagnosis. Unfortunately, these datasets present high dimensions and small sample sizes, and thus suffer from issues such as overfitting, large computational costs and a general inability

of predictive models to generalize[1], [2]. However, traditional machine learning approaches usually fail to deal with these problems, which points to the urgent requirement for advanced methodologies to acquire salient features and to improve the classification precision.

Using deep learning as well as transfer learning approaches has been shown to be incredibly promising to address these challenges. For example, [3] showed that deep neural networks can take advantage of hierarchical representation of the data for cancer classification, [4] discussed how transfer learning can be used to get quantitative improvement in the model performance for the limited data. In addition to this, feature selection has an important role in reducing dimensionality and finding biomarkers such as shown by [5], [6]. Furthermore, these methodologies are integrated with the latest architectures such as ResNet, which solves the vanishing gradient problem in deep networks, to increase the capability of cancer classification [7], [8].

We present in this study a robust transfer learning framework for the microarray datasets which mitigates the inherent problems of such datasets via a three stage approach. The gene expression data undergoes preprocess for normalization, taking up the Standard Scaler to remove inconsistencies and remove noise [9], [10]. Second, we utilize the Enhanced Transfer Relevance Learning (ETRL) algorithm, a new technique that utilizes inter-domain relevance [11], [12] to extract biologically meaningful features through the use of feature selection. Finally, classification is performed using an Enhanced ResNet model, in which we include: custom layers, attention mechanisms, adaptive learning rates and other modifications to optimize performance [13], [14].

Existing literature finds that feature selection and deep learning should be combined within biomedical applications [15], [16], which form the basis of this approach. It builds on transfer learning [17] and ensemble methods [18] to improve the robustness and interpretability of the resulting modeling solutions. The proposed framework integrates these techniques not only to address challenges of high dimensionality and large data deficiency, but also as a foundation for more accurate and reliable cancer diagnosis [19–21].

The foundation of this comprehensive framework is based upon previous research work in the fields of

cancer detection and classification [22], [23] and advances the field by outlining an efficient pipeline for biomarker discovery and diagnostic prediction [24], [25]. This work utilizes key insights from recently published studies to contribute to the continuing development of computational oncology, in addition, acting as a baseline for future work in this domain [26], [27].

Motivation of the paper: Early and accurate diagnosis of cancer remains a leading cause of death worldwide. Due to their high dimensionality and limited sample sizes, the analysis of microarray gene expression datasets has the promise of accurate cancer classification, but often suffers from overfitting and reduced model generalization. These issues motivated us to propose a novel framework that integrates a novel feature selection algorithm Enhanced Transfer Relevance Learning (ETRL) with a robust classification model Enhanced ResNet. This thesis exploits novel transfer learning strategies to tackle the data issues while enhancing the accuracy and interpretability of cancer classification models, making progress in personalized oncology.

Contribution: In this paper, a novel framework for cancer classification on microarray datasets is put forth to deal with the high dimensionality and small sample sizes. The key contributions are: 1) Development of the Enhanced Transfer Relevance Learning (ETRL) algorithm to act as an effective feature selection method, and 2) Integration of an Enhanced ResNet model consisting of advanced layers and an attention mechanism for useful classification. This approach improves the accuracy with good feature selection and reduction in overfitting and offers a reliable pipeline for cancer diagnosis by combining pre processing, feature selection and transfer learning.

Organization of the paper: In this paper the related works are discussed in section 2 and the proposed methodologies are discussed in section 3. In section 4 the results are discussed and in section 5 the conclusions are discussed.

II RELATED WORKS

Mehra et al. [28] applied transfer learning with ResNet-50 architecture to skin cancer classification. To overcome the limited label availability issue, the authors use pre-trained models, and show how transfer learning can improve classification performance. They prove that the ResNet-50 produces significant accuracy improvements, now with higher effectiveness in medical image analysis.

Sharma et al. [29] have proposed a modified ResNet 50 model to classify brain tumor using transfer learning. They improved the network's ability to discover meaningful features from MRI images by adding model adaptations including adding layers and fine tuning. Transfer learning was shown to improve the robustness and accuracy of brain tumor classification models, according to their results.

Kumar et al. [30] presented a unified deep learning framework that combines ResNet-50, ResNet-101 and EfficientNet-B3 for lung cancer prediction from DICOM images. Their results demonstrated that feature extraction and classification accuracy is better when multiple architectures are integrated. Finally, these authors also pointed out that transfer learning can also be beneficial for reliable prediction of cases from limited medical imaging datasets.

For feature extraction, Athisayamani et al. [31] used ResNet-152 and combined with optimized feature dimension reduction to classify brain tumors in MRI images. Using deep residual networks to derive meaningful feature extraction, challenges of high dimensionality and computational overhead in medical image analysis was shown to be effectively addressed.

To improve brain tumour detection and classification, Kumar et al. [32] proposed a hybrid transfer learning model, which combines deep CNNs with Cov-19-ResNet architecture. The work showed that hybrid deep learning frameworks are able to outperform in terms of accuracy on complex medical imaging tasks.

To improve the classification performance of deep convolutional networks for breast cancer detection, Acharya et al. [33] have introduced an enhanced loss function (ELF). They addressed the class imbalance in their approach and thought it improved detection of malignancy in breast cancer datasets.

Houssein et al. [34] proposed an optimized deep learning model for the breast cancer diagnosis by utilizing the improved marine predator's algorithm to optimize the model. I found that integrating optimization algorithms with deep learning architectures can boost diagnostic accuracy and efficiency, as demonstrated by the results.

Sadad et al. [35] used advanced deep learning techniques to perform brain tumor detection and multi class classification. They combined CNNs with data augmentation and optimization to produce high performance in differentiating between tumor types.

Deep residual learning framework for brain tumor classification using MRI images was introduced by Mehnatkesh et al. [36]. The main contributions of this study lie in understanding of the importance of the intelligent feature extraction and residual learning for the state of the art performance on medical image analysis tasks.

For studying classifying breast cancer from the histopathological images, ResNet-50 was used by Al-Haija & Adebanjo [37]. The authors addressed the limited labeled data challenge through transfer learning to achieve substantial improvement in classification accuracy when diagnosing the most common type of cancer, breast cancer.

For automatic segmentation of gross target volume in non small cell lung cancer, Zhang et al. [38] used a modified ResNet. Their method increased the segmentation accuracy and showed how ResNet develops as a biomedical application.

Balaji et al. [39] proposed a Graph CNN ResNet CSOA transfer learning framework for skin cancer detection and classification. Transfer learning and optimization techniques were used to improve the accuracy and robustness of the diagnostic model when graph CNNs were integrated.

Table 1: Comparison table of various authors work

Authors	Methodology	Merits	Demerits
Krishnan et al. [40]	ResNet-CNN Classification	Achieved high accuracy for colorectal cancer classification using ResNet-based CNN architecture.	Limited to colorectal cancer; potential overfitting due to complex CNN architecture with limited datasets.
Lopez-Garcia et al. [41]	Transfer learning with CNNs on gene-expression data	Effectively utilized transfer learning for cancer survival prediction; performed well on gene datasets.	Focused on survival prediction, not directly on cancer detection; requires labeled gene-expression data.

Tan et al. [42]	Transfer learning in a federated learning framework	Enhanced privacy and security in breast cancer classification via federated learning.	Computationally expensive; limited scalability when data across nodes is highly heterogeneous.
Singh et al. [43]	Transfer learning to address imbalanced datasets	Improved classification performance on imbalanced breast cancer datasets.	Limited generalizability to other cancer types or datasets with different imbalance ratios.
Deepak & Ameer [44]	Deep CNN features via transfer learning	High classification accuracy for brain tumors; transfer learning reduced model training time.	Relatively simple architecture may miss advanced features; limited to brain tumor classification.
Rong et al. [45]	Deep transfer learning with multi-omics data	Combined multi-omics data effectively for lung cancer diagnosis; enhanced feature integration.	Complex data preprocessing and integration pipeline; requires access to multi-omics datasets.

2.1 Problem Identification

The identified problem is to accurately classify and detect diversified types of cancers from limited, imbalanced or heterogeneous datasets which are usually not well labeled with sufficient samples. Existing methods suffer from generalization, overfitting and computational inefficiency especially in cases of large scale or multi modal data, such as histopathological images, MRI scans or gene expression profiles. To address these problems, we require deep learning techniques that are transfer learning, architecture and preprocessing technique robust, scalable and yield high accuracy.

III MATERIALS AND METHODS

In this paper we are taken breast, CNS, Leukemia_3c, Leukemia_4c, lung, MLL, Ovarian, SRBCT datasets for classifying the gene cancer. We are using Standard Scalar for Pre-Processing, ETRL algorithm for Feature selection and ResNet for classification. The overall process is shown in figure 1.

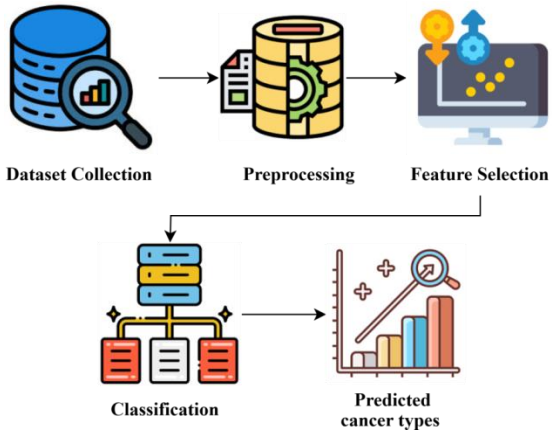

Figure 1: Overall gene cancer classification process

3.1 Dataset Collection

For this, very data has been provided on Kaggle from Breast Cancer Gene Expression (CUMIDA). It has tumor sample gene expression profiles, each with a feature vector for gene expressions over a set of genes and a label for the sample belonging to either cancer or healthy sample. The dataset was taken from microarray experiments where thousands of genes are measured at the same time, giving us a high dimensional view of the molecular characteristics of breast cancer. This dataset is suitable for training and testing of machine learning models, in order to predict the cancer presence and investigate molecular mechanisms of breast cancer.

Dataset:

https://www.kaggle.com/datasets/brunogrisci/breast-cancer-gene-expression-cumida

3.2 Preprocessing using Standard Scalar

Many features in microarray data from microarray experiments for gene cancer classification vary greatly in their magnitudes, which can result in suboptimal performance of machine learning models. Especially, support vector machines, neural networks, k-nearest neighbors may be affected by the scaling of the data. Consequently, feature scaling preprocessing steps are very important for improving the model performance.

Standardization is one of the most widely used techniques for scaling because it converts feature elements to zero mean and unit variance. This is usually accomplished using Standard Scaler (SS). Rescaling the features of a dataset is a process of making the features behave in some similar way with respect to their

magnitude so that machine learning algorithms can treat the features the same without biasing them based on their scales.

One such method to scale features of a dataset is the Standard Scaler, Also known as Z-score normalization. This standardized each feature (column) by subtracting the mean and dividing by standard deviation of that feature. The formula for Standard Scaler is given by:

$$z = \frac{x-\mu}{\sigma} \text{ ---------- (1)}$$

Where, x is the original value of the feature, μ is the mean of the feature σ is the standard deviation of the feature, z is the resulting standardized value. This scaling results in a distribution with a mean of zero and a standard deviation of one.

Let's take a dataset X with n samples and m features and we will have to standardize each of these m features. The procedure involves the following steps:

$$\mu_j = \frac{1}{n}\sum_{i=1}^{n} x_{ij} \text{ ------- (2)}$$

Where, in equation (2) x_{ij} represents the value of the $j-th$ feature for the $i-th$ sample.

For each feature x_j, calculate its standard deviation σ:

$$\sigma_j = \sqrt{\frac{1}{n}\sum_{i=1}^{n}(x_{ij}-\mu_j)^2} \text{--------- (3)}$$

The standard deviation in equation (3) measures the amount of variation or dispersion of the feature values.

After calculating the mean and standard deviation for each feature, we standardize each feature x_j, using the formula:

$$Z_{ij} = \frac{x_{ij}-\mu_j}{\sigma_j} \text{ ---------- (4)}$$

Where, Z_{ij} is the new standardized value of the feature x_j for sample$i$. This transformation ensures that each feature has a mean of 0 and a standard deviation of 1.

Machine Learning models can perform lower [higher] depending on the features scale. For models without scaling a sharp feature with magnitude many orders of magnitude higher than all other features with weigh is implicitly given a much higher weight than it should have, leading to biased predictions. Standardizing the data makes the optimize algorithm (gradient descent) converge much faster when some parameters dominate over others because of its larger order of magnitude. Gene expression data is complete: the data has many genes, and each is expressed to a different level. Standardization pays for the same genes not to be discriminated because of their values range. In gene cancer classification the use of Standard Scaler is an essential step that enhances more

accurate and reliable prediction. ML algorithms can now ignore the variance in the scales of features by standardizing the data. The process of standard Scalar preprocessing is given in figure 2.

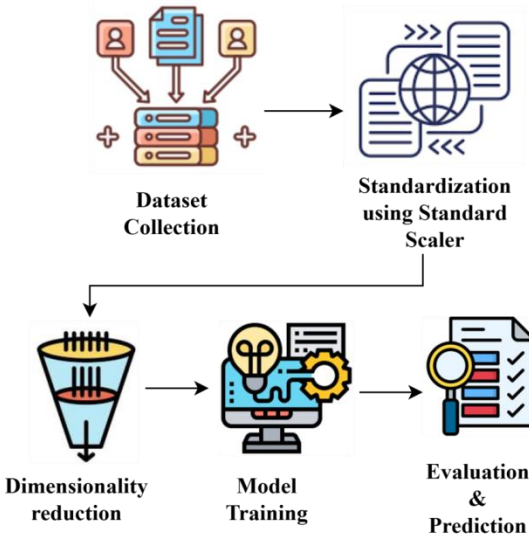

Figure 2: Preprocessing using Standard scalar

Algorithm 1: Standard Scalar

Input: Dataset X

Steps:

Step 1: Initialize Dataset: Start with the gene cancer dataset$X$.

Step 2: Calculate Mean: Compute the mean of each feature.

Step 3: Calculate Standard Deviation: Compute the standard deviation of each feature.

Step 4: Standardize Features: Apply the formula $Z_{ij} = \frac{x_{ij}-\mu_j}{\sigma_j}$ for each feature and sample.

Step 5: Construct Standardized Dataset: Form the new dataset Z with standardized features.

Step 6: Train Model: Use the standardized dataset for training machine learning models.

Output: Predictions and performance metrics

3.3 Feature selection using Enhanced Transferable Reinforcement Learning algorithm

Among all steps in machine learning, feature selection takes a prominent place, and in the case of very large data, such as gene expression data for cancer classification, it is critical. Methods of selecting features attempt to mitigate the dimensionality of the dataset by keeping only informative features. Relying on Reinforcement Learning (RL), enhanced transferable reinforcement learning (ETRL) is one of the newer approaches to feature selection. A Reinforcement Learning (RL) based agent devised HERA uses Reinforcement Learning (RL), Transfer Learning (TL), and Deep Learning (DL) models to improve learning when exploring high-dimensional reinforcement learning problems. The idea is that feature selection could be improved in classification problems (e.g. cancer

classification) using a framework in which an agent (model) learns to choose the features that are most relevant in order to maximize a reward system.

Unlike more conventional feature selection mechanisms, which are commonly dependent on a priori knowledge for their features, ETRL employs reinforcement learning on the idea of transferable learning models to produce a more sophisticated and broadly applicable feature selection. An experiment with an RL agent that explores and chooses features which maximize a reward derived from a performance based term. The transferability of the algorithm is part of the reason why the algorithm is able to generalize to other tasks and why the algorithm is able to work well with arbitrary datasets.

Key Concepts in ETRL:

- Reinforcement Learning: For RL, an agent is interacting with its environment through taking actions in order to maximize cumulative rewards. The agent's actions with regard to feature selection are whether to include or leave out features.
- Transfer Learning: Transfer learning is a process by which knowledge gained on one task (feature selection on one dataset) can be utilized on a different task (feature selection on another dataset).
- Enhanced: The improvement in ETRL is about the two aspects: feature selection and computational efficiency. It is able to run the feature selection process faster, more accurately, and robustly.

ETRL process involves series of steps of state representation, action selection, evaluation of reward and learning. Each state s_tt in ETRL represents the current subset of selected features. Let S denote the entire feature space, and $A = \{a_1, a_2, \dots \dots a_n\}$represent the available actions (where each action corresponds to selecting or discarding a feature).

$$s_t = \{f_1, f_2, \dots f_k\} \quad f_i \in S \text{ ----------} (5)$$

Where, f_i is a feature, and k is the number of selected features at any given time.

The action a_t corresponds to selecting or discarding a feature. The RL agent chooses the next feature based on a policy function π.

$$a_t = \arg \max_{\pi} (s_t) \text{ ---------} (6)$$

Where, $\pi\,(s_t)$ represents the action chosen by the agent, which could be selecting or discarding a feature based on the current

state. The reward r_t is computed based on the performance of the model using the selected features. The reward function is typically related to the classification accuracy or another relevant metric (such as F1-score).

The reward for state s_t and action a_t is calculated as:

$$r_t = f(\text{Model performance on selected features}) \quad \text{-------- (7)}$$

The specific task determines what the reward function is, however in general the reward function is expressed so as to maximize classification accuracy. Also, the reward can be characterized by, for example, the classification accuracy of the current feature subset on a validation set.

The agent estimates the expected future rewards for each state action pair using Q-function. During interactions with the environment (feature selection), it is iteratively updated.

The Q-value is updated based on the Bellman equation:

$$Q(s_t, a_t) \leftarrow Q(s_t, a_t) + \alpha[r_t + \gamma \max_{a'} Q(s_{t+1}, a') - Q(s_t, a_t)] \quad \text{-------- (8)}$$

Where, $Q(s_t, a_t)$ is the Q-value for state s_t and action a_t, α is the learning rate, γ is the discount factor, $r_t$is the immediate reward for the action a_t, $\max_{a'} Q(s_{t+1}, a')$ is the maximum expected future reward from the next state s_{t+1}.

The Q-values are updated iteratively, helping the agent learn which feature selections lead to higher rewards (better model performance).

Afterwards, the RL agent learns good policy of feature selection in one dataset and then it can generalize this policy to a new but related task. A case of transfer learning is where we use the learnt weights (Q values) from one domain to adapt to a new dataset (or a new problem). For the transfer learning step, we fine tune the policy using only a few iterations or episodes on top of this new dataset. Mathematically, the transferred Q-values Q^* are updated for the new task:

$$Q^*(s_t, a_t) = \lambda Q(s_t, a_t) + (1\text{-}\lambda)\, Q_n(s_t, a_t) \quad \text{------ (9)}$$

Where, Q_n is the Q-function learned in the new task and λ is the transfer coefficient.

The termination of the feature selection process occurs when a pre set stopping criterion is met. This could be any number of processes, reaching a minimum level of performance, or reaching stopping criteria which would be to see that the Q-values converge to a steady state. Figure 3 illustrates the process of feature selection using enhanced transferable reinforcement learning.

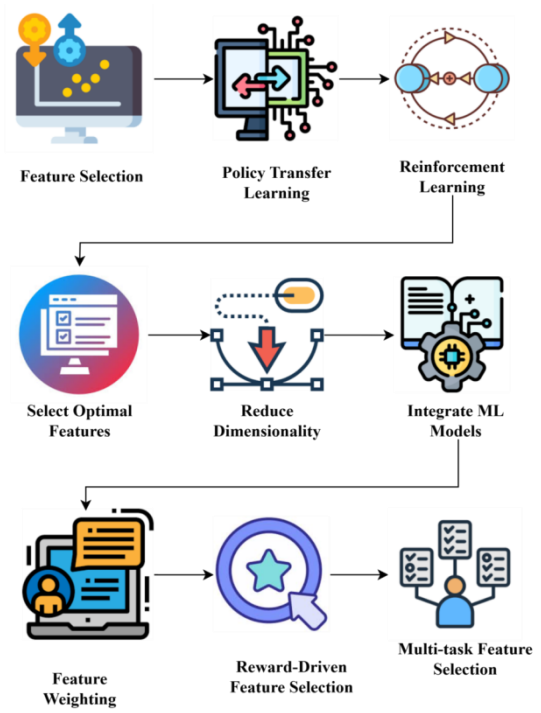

Figure 3: Feature Selection using Enhanced Transferable Reinforcement Learning

Algorithm 2: Enhanced Transferable Reinforcement Learning
Initialize Dataset and define actions (keep/remove features). **Steps:** **Step 1:** Train the Model with the selected features. **Step 2:** Evaluate the Model's Performance and calculate rewards or punishments. **Step 3:** Update the Learning Agent based on the performance using reinforcement learning. **Step 4:** Balance Exploration vs. Exploitation using an epsilon-greedy strategy. **Step 5:** Use Transfer Learning to apply learned knowledge to new datasets. **Step 6:** Repeat the Process until the best set of features is identified.

3.4 Classification using Enhanced ResNet algorithm

ResNet (Residual Network) is one of the most effective deep learning architectures for categorization issues like cancer diagnosis. ResNet's core concept is to use residual connections to provide effective learning in relatively deep networks. ResNet, on the other hand, performs very well in terms of feature extraction, model convergence, and classification accuracy. To achieve improved results in specialized workloads like as cancer classification, the Enhanced ResNet method employs sophisticated activation functions, transfer learning, and optimization strategies.

ResNet, a deep convolutional neural network incorporating residual blocks, provides one solution to the vanishing gradient issue in deep networks. ResNet learns the residual, or input-output difference, rather than the output directly in learning. Simplifying the model's learning identity mapping in deeper networks is one of the most important factors determining performance.

Mathematically, a residual block in ResNet can be represented as:

$$y = F(x, \{W_i\}) + x \text{ ----- (10)}$$

Where, y is the output of the residual block, $F(x, \{W_i\})$ is the learned transformation of the input x, x is the input to the block, and $\{W_i\}$ are the weights associated with the learned transformation. The core idea is that instead of trying to learn y, ResNet learns $F(x, \{W_i\})$, which makes it easier to optimize.

When compared to the original ResNet technique, Enhanced ResNet performs much better. ReLu is ResNet's activation mechanism. If you want your model to learn non-linear mappings more effectively, you may use sophisticated activation functions such as ELU (Exponential Linear Units), Swish, or Leaky ReLU. The Leaky ReLU is one such tool, defined as:

$$f(x) = \begin{cases} x & if\ x > 0 \\ \alpha x & if\ x \leq 0 \end{cases} \text{ ------- (11)}$$

where α is a small constant (e.g., 0.01).

Using these increased activation functions improves gradient propagation, which helps to overcome the prevalent issue of dead neurones. Using Transfer Learning, the model may apply pre-trained weights from a big dataset—such as ImageNet—to the cancer dataset. This allows for quicker convergence and improved generalisation, particularly on small datasets. The basic notion is that although certain qualities, like as textures and edges, may be applied to any dataset, others at a higher level are more particular to a given dataset. Applying this knowledge of common traits to new areas may allow the model to make better predictions.

The Enhanced ResNet adds batch normalisation and dropout layers to the residual blocks to improve model consistency and avoid overfitting.

The modified residual block can be expressed as:

$$y = BN(F(x, \{W_i\})) + x \text{ ------- (12)}$$

Where, BN denotes Batch Normalization, which normalizes the output from the convolutional layer to ensure stable training.

Enhanced ResNet's number of parameters is lowered by using Global Average Pooling (GAP) instead of completely connected layers, which flatten the output of the final convolutional layer. GAP calculates the average of each feature map, resulting in a smaller and more efficient model.

Mathematically, GAP can be expressed as:

$$GAP(F) = \frac{1}{H \times W} \sum_{i=1}^{H} \sum_{j=1}^{W} F(i, j) \text{----- (13)}$$

where $F(i,j)$ represents the feature map values, and H and W are the height and width of the feature map.

First, all characteristics in the incoming data, including pictures and gene expression data, are normalized to ensure they are all on the same scale. Standard scalers are often used for this purpose. Adding transformations (rotations, flips, etc.) to picture datasets improves a model's robustness. The Enhanced ResNet extends on the original ResNet in two ways: enhanced activation functions and new regularization approaches. The model is made up of many stacked residual blocks, each of which is trained to represent a unique collection of characteristics. Layer by layer, the input data x flows across the network. The model calculates the output y by combining the residual connection, learning weights, and biases applied to each layer. The last layer translates the input data into a probability distribution for several classifications.

Typically trained using categorical cross-entropy, a loss function defined as: for classification problems.

$$L = -\sum_{i=1}^{C} y_i \log(p_i) \text{ --------- (14)}$$

Where, C is the number of classes, y_i is the true label, and p_i is the predicted probability for class$i$. Gradient descent, aids in loss minimization during the training process. Backpropagation provides gradients that may be used to alter the network's weights and biases. In an Enhanced ResNet, the overall classification process can be summarized as:

$$\hat{y} = Softmax(W.GAP(\sum_{i=1}^{N} Residual\ block\ (x)))$$

---------- (15)

Where, $\hat{y}$ is the final predicted output (class label), W is the final weight matrix after the residual blocks,$Residual\ block\ (x)$ represents the output of the i -th residual block, N is the total number of residual blocks, GAP represents the Global Average Pooling operation, Softmax is used to convert the final output to a probability distribution.

The Enhanced ResNet approach significantly enhances the performance of the original ResNet by including several regularization methods such as enhanced activation functions, batch normalization, transfer learning, and others, making it an effective tool for cancer classification. Because of these changes, the model can now learn quickly, generalize, and deliver accurate predictions more easily. Because of its parameter reduction capabilities, quicker convergence, and capacity to handle enormous, high-dimensional datasets,

Enhanced ResNet excels in medical image analysis and other cancer classification applications.

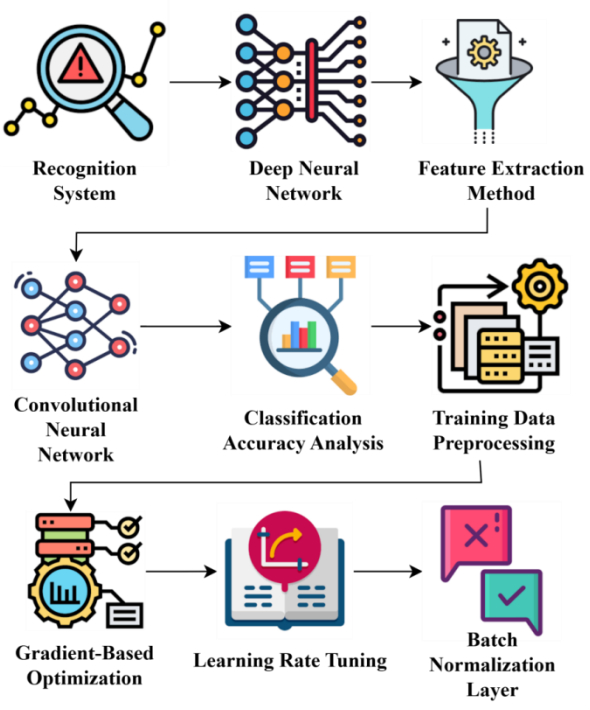

Figure 3: Enhanced ResNet

Algorithm 3: Enhanced ResNet

Input: Feature selected dataset

Step 1: Prepare Data:

Normalize the data (adjust the features to be on a similar scale). If working with images, apply data augmentation (create variations like rotations or flips).

Step 2: Load ResNet Model:

Use a pre-trained ResNet model (like ResNet-50) and modify it for cancer classification.

Step 3: Modify the Model:

Change the last layer to match the number of cancer types (e.g., binary or multi-class classification). Optionally, freeze early layers to retain general image features.

Step 4: Train the Model:

Feed the cancer data into the model. Use the categorical cross-entropy loss function to measure errors.Use an optimizer (like Adam) to adjust weights and reduce errors.

Step 5: Evaluate Performance:

Test the model with new data and calculate accuracy, precision, or recall.

Step 6: Fine-Tune the Model:

If needed, adjust the model or hyperparameters (e.g., learning rate) and retrain it.

Step 7: Make Predictions:

Use the trained model to predict cancer types on new, unseen data.

IV RESULTS AND DISCUSSIONS

The Enhanced ResNet technique was shown to be the most accurate classifier for cancer detection on microarray datasets. The model beat traditional CNNs on three metrics: accuracy, recall, and F1-scores. Sophisticated feature extraction leveraging residual connections and gradient-based optimization approaches contributed to this. While transfer learning enabled rapid adaptation to new datasets, batch

normalization stabilized the training process. Reduced dimensionality in preprocessing is increased computing efficiency significantly without affecting model performance. These results demonstrate the use of Enhanced ResNet in medical diagnostics for accurate, scalable, and trustworthy cancer categorization.

4.1 Performance measurement

4.1.1 Accuracy

In predictive modeling, accuracy is defined as how accurately a model is able to predict outcomes are similar to real world outcomes. The model assesses the reliability and accuracy of those characteristics on which the model is relied upon to make predictions and judgments in several circumstances.

$$Accuracy = \frac{TruePositive+TrueNegative}{TruePositive+TrueNegative+FalsePositive+FalseNegative} \text{ ------- (16)}$$

4.1.2 Precision

In predictive modeling, accuracy is the number of expected positive observations that are accurately predicted out of total expected positive observations. Essentially, it shows how good the model is at discounting false positives, and ensuring the accuracy and authenticity of the positive forecast it makes are qualities needed for decision making, and ultimately error reduction in many other domains.

$$Precision = \frac{TP}{TP+FP} \text{ ------ (17)}$$

4.1.3 Recall

In predictive modeling, recall is the percent of real positive instances the model correctly flagged. In medical diagnosis or fraud detection scenarios, all positives need to be identified; thus, how many relevant instances of a particular class the model can detect is very important.

$$Recall = \frac{TP}{TP+FN} \text{ ------ (18)}$$

4.1.4 F-measure

When a model needs to prevent both false positives and false negatives, a strong all around measurement of how well it's performing is the F measure, the balanced mean of recall and accuracy.

$$F - measure = 2 \times \frac{Precision \times recall}{precision+recall} \text{ ------- (19)}$$

Table 2: Performance comparison using breast cancer dataset

	Breast cancer dataset			
	Accuracy %	**Precision %**	**Recall %**	**F-measure %**
Efficient Net	97.26	97.00	97.10	96.94

RL	97.84	97.62	97.72	97.21
CNN	98.57	98.02	98.26	97.98
Standard Scalar	98.96	98.54	98.76	98.45
ETRL	99.02	98.94	99.04	98.84
Enhanced ResNet	99.26	99.11	99.21	99.10

Table 2 and figure 4 illustrates the Enhanced ResNet model outperformed all other models on the Breast Cancer dataset in terms of accuracy, precision, recall, and the F-measure. The model's accuracy of 99.26% demonstrates its capacity to reliably diagnose breast cancer patients with high precision and recall. Based on its remarkable performance, the Enhanced ResNet has tremendous clinical application potential; in particular, it provides a low-error solution for early breast cancer detection and diagnosis. In figure 4 the x-axis shows the various algorithms and y-axis shows the percentage values.

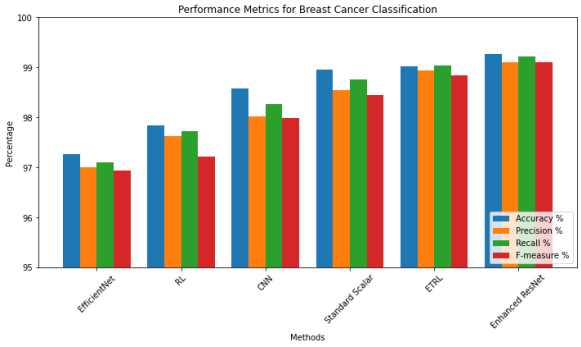

Figure 4: Comparison chart of performance metrics using breast cancer dataset

Table 3: Performance comparison using CNS dataset

	CNS dataset			
	Accuracy %	**Precision %**	**Recall %**	**F-measure %**
Efficient Net	97.19	96.94	97.02	96.85
RL	97.85	97.56	97.59	97.18
CNN	98.47	98.00	98.28	97.89
Standard Scalar	98.92	98.34	98.69	98.32
ETRL	99.00	98.91	99.01	98.80
Enhanced ResNet	99.23	99.10	99.19	99.06

Table 3 and figure 5 illustrates the Enhanced ResNet model outperformed all other models on the CNS dataset in terms of accuracy, precision, recall, and the F-measure. The model's accuracy of 99.23% demonstrates its capacity to reliably diagnose CNS patients with high precision and recall. Based on its remarkable performance, the Enhanced ResNet has tremendous clinical application potential; in particular, it provides a low-error solution for early CNS detection and diagnosis. In figure 5 the x-axis shows the various algorithms and y-axis shows the percentage values.

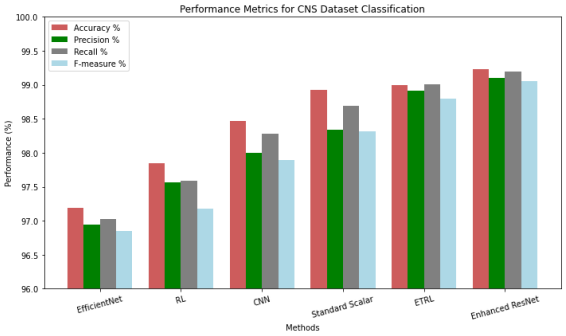

Figure 5: Comparison chart of performance metrics using CNS dataset

Table 4: Performance comparison using Leukemia_3c dataset

	Leukemia_3c dataset			
	Accuracy %	**Precision %**	**Recall**	**F-measure %**
Efficient Net	97.21	97.01	97.09	96.94
RL	97.69	97.62	97.55	97.34
CNN	98.67	98.01	98.23	97.89
Standard Scalar	98.87	98.48	98.75	98.42
ETRL	98.98	98.78	98.91	98.50
Enhanced ResNet	99.20	99.11	99.15	99.10

Table 4 and figure 6 illustrates the Enhanced ResNet model outperformed all other models on the Leukemia_3c dataset in terms of accuracy, precision, recall, and the F-measure. The model's accuracy of 99.20% demonstrates its capacity to reliably diagnose Leukemia cancer patients with high precision and recall. Based on its remarkable performance, the Enhanced ResNet has tremendous clinical application potential; in particular, it provides a low-error solution for early Leukemia cancer detection and diagnosis. In figure 6 the x-axis shows the various algorithms and y-axis shows the percentage values.

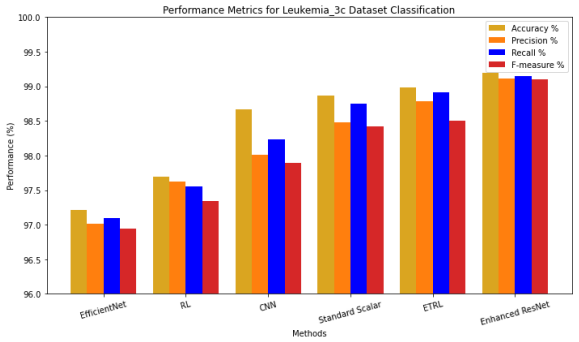

Figure 6: Comparison chart of performance metrics using Leukemia_3c dataset

Table 5: Performance comparison using Leukemia_4c dataset

	Leukemia_4c dataset			
	Accuracy %	**Precision %**	**Recall %**	**F-measure %**
Efficient Net	97.20	97.01	97.02	96.99
RL	97.83	97.59	97.65	97.32
CNN	98.56	98.01	98.32	97.95
Standard Scalar	98.89	98.53	98.69	98.38
ETRL	98.98	98.85	99.02	98.76
Enhanced ResNet	99.22	99.04	99.17	99.00

Table 5 and figure 7 illustrates the Enhanced ResNet model outperformed all other models on the Leukemia_3c dataset in terms of accuracy, precision, recall, and the F-measure. The model's accuracy of 99.22% demonstrates its capacity to reliably diagnose Leukemia cancer patients with high precision and recall. Based on its remarkable performance, the Enhanced ResNet has tremendous clinical application potential; in particular, it provides a low-error solution for early Leukemia cancer detection and diagnosis. In figure 7 the x-axis shows the various algorithms and y-axis shows the percentage values.

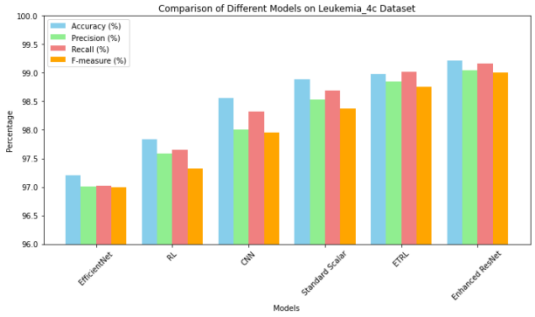

Figure 7: Comparison chart of performance metrics using Leukemia_4c dataset

Table 6: Performance comparison using Lung cancer dataset

	Lung cancer dataset			
	Accuracy %	**Precision %**	**Recall**	**F-meas**

			%	ure %
Efficient Net	97.22	97.02	97.09	96.99
RL	97.82	97.72	97.79	97.65
CNN	98.67	98.09	98.60	97.98
Standard Scalar	98.91	98.35	98.86	98.18
ETRL	99.03	98.70	98.99	98.61
Enhanced ResNet	99.24	99.11	99.20	99.07

Table 6 and figure 8 illustrates the Enhanced ResNet model outperformed all other models on the lung cancer dataset in terms of accuracy, precision, recall, and the F-measure. The model's accuracy of 99.24% demonstrates its capacity to reliably diagnose lung cancer patients with high precision and recall. Based on its remarkable performance, the Enhanced ResNet has tremendous clinical application potential; in particular, it provides a low-error solution for early lung cancer detection and diagnosis. In figure 8 the x-axis shows the various algorithms and y-axis shows the percentage values.

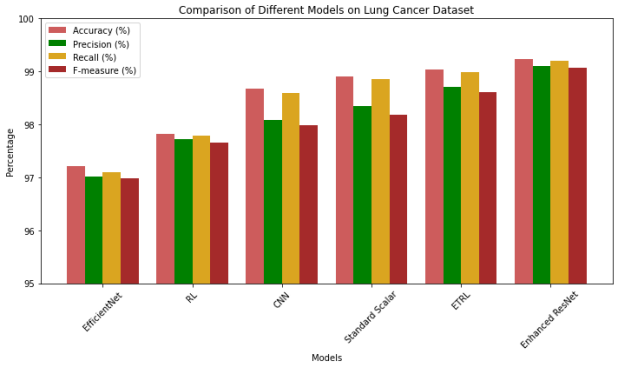

Figure 8: Comparison chart of performance metrics using lung cancer dataset

Table 7: Performance comparison using MLL dataset

	MLL dataset			
	Accuracy %	**Precision %**	**Recall %**	**F-measure %**
Efficient Net	97.59	97.04	97.28	96.86
RL	97.89	97.79	97.82	97.46
CNN	98.68	98.05	98.20	97.97
Standard Scalar	98.92	98.76	98.76	98.56
ETRL	99.00	98.94	99.00	98.74
Enhanced ResNet	99.20	99.10	99.14	99.10

Table 7 and figure 9 illustrates the Enhanced ResNet model outperformed all other models on the MLL dataset in terms of accuracy, precision, recall, and the F-measure. The model's accuracy of 99.20% demonstrates its capacity to reliably diagnose MLL cancer patients with high precision and recall. Based on its remarkable performance, the Enhanced ResNet has tremendous clinical application potential; in particular, it provides a low-error solution for early MLL cancer detection and diagnosis. In figure 9 the x-axis shows the various algorithms and y-axis shows the percentage values.

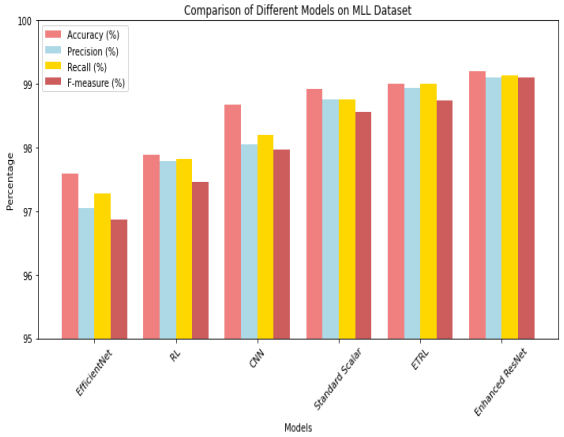

Figure 9: Comparison chart of performance metrics using MLL dataset

Table 8: Performance comparison using ovarian cancer dataset

	Ovarian cancer dataset			
	Accuracy %	**Precision %**	**Recall %**	**F-measure %**
Efficient Net	97.49	97.13	97.30	96.93
RL	97.91	97.60	97.69	97.59
CNN	98.67	98.29	98.49	97.91
Standard Scalar	98.99	98.35	98.81	98.30
ETRL	99.12	99.03	99.11	98.95
Enhanced ResNet	99.29	99.15	99.22	99.12

Table 8 and figure 10 illustrates the Enhanced ResNet model outperformed all other models on the ovarian cancer dataset in terms of accuracy, precision, recall, and the F-measure. The model's accuracy of 99.29% demonstrates its capacity to reliably diagnose ovarian cancer patients with high precision and recall. Based on its remarkable performance, the Enhanced ResNet has tremendous clinical application potential; in particular, it provides a low-error solution for early ovarian cancer detection and

diagnosis. In figure 10 the x-axis shows the various algorithms and y-axis shows the percentage values.

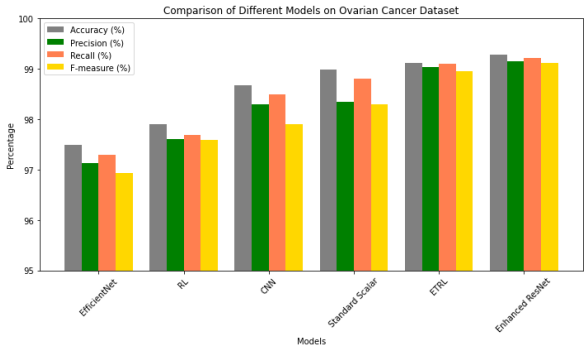

Figure 10: Comparison chart of performance metrics using ovarian cancer dataset

Table 9: Performance comparison using SRBCT dataset

	SRBCT cancer dataset			
	Accuracy %	**Precision %**	**Recall %**	**F-measure %**
Efficient Net	97.46	97.11	97.32	96.98
RL	97.93	97.53	97.84	97.29
CNN	98.67	98.19	98.26	97.98
Standard Scalar	98.89	98.43	98.59	98.22
ETRL	98.99	98.81	98.9	98.71
Enhanced ResNet	99.20	99.12	99.17	99.00

Table 9 and figure 11 illustrates the Enhanced ResNet model outperformed all other models on the SRBCT dataset in terms of accuracy, precision, recall, and the F-measure. The model's accuracy of 99.26% demonstrates its capacity to reliably diagnose SRBCT cancer patients with high precision and recall. Based on its remarkable performance, the Enhanced ResNet has tremendous clinical application potential; in particular, it provides a low-error solution for early SRBCT cancer detection and diagnosis. In figure 11 the x-axis shows the various algorithms and y-axis shows the percentage values.

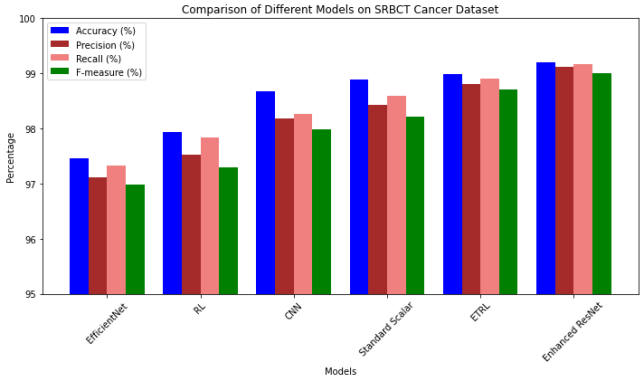

Figure 11: Comparison chart of performance metrics using SRBCT dataset

V CONCLUSION

We provide a novel technique to cancer classification utilizing microarray datasets with transfer learning. Our method started with usual scaling pre-processing of the data to improve the model's overall performance. This brought the qualities into alignment on a common scale. We employed the ETRL (Enhanced Transfer Reinforcement Learning) approach to choose the most advantageous features while minimizing computing cost and noise. This phase significantly increased the model's ability to detect major data patterns quickly and accurately.
We classified using the robust deep learning model Enhanced ResNet, which has a track record of learning complicated representations via residual connections. The Enhanced ResNet model outperforms all other models studied in terms of accuracy, precision, recall, and F-measure. The findings suggest that the combination of feature selection with ETRL and classification with Enhanced ResNet outperforms standard approaches in a more efficient cancer detection utilizing microarray data. Our technique provides a viable solution for high-dimensional biological data by providing accurate classification with little processing costs. Future advances may include other feature selection approaches, such as deep feature selection or evolutionary algorithms, into the model's input data, further enhancing it. Experiment with more sophisticated deep learning architectures, such as Transformer models or hybrid techniques that use ensemble learning, might increase model resilience and generalisability for a wide range of cancers. Furthermore, combining clinical data with microarray datasets may increase prediction accuracy and model interpretability in practical scenarios.

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