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A Novel Approach to Cervical Cancer Detection Using Hybrid Stacked Ensemble Models and Feature Selection

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ABSTRACT- Around the world, millions of women are diagnosed with cervical cancer each year. Early detection is very important to produce a better overall quality of life for those diagnosed with the disease and reduce the burden on the healthcare system. In recent years, the field of machine learning (ML) has been developing methods that can improve the accuracy of detecting cervical cancer. This paper presents a new approach to this problem by using a combination of image segmentation and feature extraction techniques. The proposed approach is divided into three phases. The first stage involves image segmentation, which is performed to extract the regions of interest from the input image. The second stage is comprised of extracting the features from the ROI with the help of the Histogram and Hu Moments techniques. The techniques used in this approach, namely the Hu Moments and Histogram techniques, respectively, can capture the shape information in the ROI. In the third stage of the project, we use a hybrid approach to classify the image. The proposed model is composed of several base classifiers, which are trained on varying subsets of the features that were extracted. These resulting classifiers then make a classification decision. We tested the proposed model against a large dataset of images for cervical cancer. The results of the experiments revealed that it performed better than the existing methods in detecting the disease. It was able to achieve an accuracy of 96.5%, an F1 score of 96.9%, and a recall of 96.7%. The proposed model was successful in accomplishing a remarkable accuracy of 96.5%, making it an ideal candidate for use in the detection of cervical cancer. It was also able to perform feature extraction using the Histogram techniques and image segmentation. The proposed method could help medical professionals improve the diagnosis and reduce the burden of this disease on women worldwide.

General Terms: Ensemble method, Feature selection, Machine learning.

Keywords: Cervical cancer, Cancer identification, Feature selection, Image segmentation Machine learning, Stack ensemble.

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1. INTRODUCTION

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Cervical cancer is the type of cancer that affects women more frequently than any other type. It is located in the lower part of the uterus, which connects to the female private part as shown in *figure 1*. WHO stated that, "about 570,000 new cases of this disease were reported in 2018, and 311,000 deaths were attributed to it" (WHO, 2021). This disease is more prevalent in developing countries due to the lack of access to treatment and screening. The two primary types of cervical cancer are adenocarcinoma and squamous cell carcinoma. About 80-90% of the cases of this disease are caused by squamous cell carcinoma. On the other hand, around 10-20% of the cases are caused by adenocarcinoma (NCI, 2021). Some other

uncommon types of cancer include neuroendocrine tumors and small cell carcinoma[1], [2].

Early stages of the disease do not usually cause any symptoms[3]. Therefore, it is important that women get regular screenings. Some of the symptoms of this disease include pain in the pelvic area, unusual bleeding, and copulation. However, these symptoms can also be caused by other conditions (ACI,2021). Early detection is very important for the treatment of this disease. The five-year survival rate for this type of cancer is around 92%. However, the survival rate decreases to 17% for patients whose cancer has spread to other areas of the body[4], [5].

Ovary
Uterus
Cervix
Vaginal wall

Figure 1: Cervical cancer (img src - Cleveland clinic) [6]

Artificial intelligence has the possibility of a more favorable diagnosis and outlook for patients suffering from cervical cancer. One of the main components of AI is "ML", which is a type of computer program that learns by studying various



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patterns in data[7], [8]. It can be used in various applications, such as detecting abnormalities in the Pap smear test and performing medical examinations. ML can be helpful in diagnosing cervical cancer, as it can analyze vast amounts of data in a short amount of time, which can significantly reduce the time it takes to identify the disease. It can also continuously improve its accuracy through the years.

In the past few years, a growing body of research has been conducted on the use of ML for the detection of cervical cancer. Some of the algorithms used for this purpose include "Random Forest, XGB, SVC, SGD, MLP, kNN, Extra Tree,". In addition, ensembles, which combine the outputs from different ML models, have been shown to enhance the accuracy of this process[7]. The potential applications of ML in the detection of cervical cancer are immense. Its use could help medical professionals make informed decisions regarding the treatment of this disease and improve the quality of patient care[9], [10]. ML algorithms could also help lower the burden of this disease on women worldwide.

Another challenge that needs to be resolved is the availability of large and diverse datasets[11], [12]. Since algorithms rely on massive amounts of data to perform accurate predictions and learn patterns, it can be challenging to acquire sufficient and diverse sets for the diagnosis of cervical cancer. This is why it is important that both data scientists and medical professionals collaborate to ensure that the appropriate datasets are collected and curated for this purpose[13]–[15].

Despite the various challenges that face the development of ML for the diagnosis of cervical cancer, its potential applications are still immense. The development of ML models with hybrid features, such as those developed by researchers using the extraction methods known as Histograms and Hu Moments, could help improve the accuracy of this procedure. In addition, the use of this technology could lead to the discovery of new ways to treat the disease. Early detection is very important for successful treatment of cervical cancer. Due to the immense potential of ML, it has been shown that it can help improve the efficiency and accuracy of the diagnosis of this disease. One of the most important factors that needs to be considered is the development of hybrid models that combine the various features of ML. Continued research will enable ML algorithms to play a vital role in diminishing the burden of this disease, which affects women worldwide.

The proposed model addresses these issues by leveraging a combination of image segmentation, stacked ensemble models, and extraction techniques. The proposed model utilizes image segmentation to extract regions of interest from the images of cervical cancer. This process can improve the model's specificity and accuracy. Through the use of Hu Moments and Histogram techniques, they were able to obtain additional details about the ROIs.

2. LITERATURE REVIEW

The diagnosis of cervical cancer is far and away the most common form of cancer in females. Early detection of this

disease can help improve a woman's chances of successfully receiving treatment. However, it is very challenging to diagnose this condition properly. In the past few years, the field of ML has gained widespread attention for its potential to improve the diagnosis and prognosis of cervical cancer. This review aims to provide a comprehensive analysis of the various applications of this technology in the field. Deng et al.[16] developed a method that can predict hub genes that are known to be associated with the development of cervical cancer. The method was able to perform better than traditional feature selection techniques. The researchers additionally proposed a computational framework that was based on the minimum redundancy threshold and mutual information criterion. Fernandes et al.[17] proposed a system that can perform a comprehensive analysis of digital colposcopy images to detect cervical cancer. The system was able to identify the most relevant lesions using its computer vision approach. The findings of the study indicated that the system could be useful in improving the accuracy of the diagnosis. The researchers additionally used the collected features to train and evaluate different ML models.

In a study conducted by Li et al.[18] the researchers proposed a method for the classification of images of cervical histopathology using a combination of supervised learning and multi-layered conditional random fields. The proposed model was able to outperform the existing methods. Bnouni et al.[19] proposed a method that can perform cross-view selfcomparisons in images of cervical cancer. The suggested method was able to outperform existing methods by extracting features from multiple perspectives. The researchers then used the extracted features to train a support vector classifier for performing staging procedures. Nithya et al.[20] evaluated the classification and feature selection methods that are based on ML for predicting the likelihood of a woman being diagnosed with cervical cancer. They came up with a hybrid approach that combines genetic and statistical algorithms. The suggested method exhibited promising results, and it could be a suitable tool for predicting the condition.

Despite the promising results of ML in the field of cervical cancer treatment and diagnosis, more research is needed to develop a hybrid stack model. This type of model combines multiple algorithms to improve its accuracy and reduce the likelihood of overfitting. Hybrid stack models can be used to perform more comprehensive analyses of patients with cervical cancer by incorporating different data sources, such as imaging and genetic information. Because of this, further studies on the application of hybrid models in the field of cancer treatment are expected to be conducted.

3. METHODOLOGY

3.1 Dataset

The information contained in the "SIPaKMed" dataset is a collection of 506 images depicting the characteristics of cervical cancer or dysplasia[31]. It was derived from a larger set of 7,752 images taken from 1,388 patients during a period of time in Greece's University Hospital's Gynecologic Clinic. The data included in the dataset are categorized into three main categories: normal, malignant, and dysplastic. Out of the total,

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114 images are normal, 292 are dysplastic, and 100 are cancerous. The images were taken using a medical device known as a colposcope. The photos were processed using a JPEG format and have a resolution of around 576 720 pixels.

The data included in the "SIPaKMeD" dataset contains information about the patient, such as when the image was taken, the type of biopsy procedure, and the patient's age. Three experts in colposcopy were responsible for labeling the images, and the majority voted for the final image labels. This dataset is suitable for various computer vision and ML projects related to the diagnosis of cervical cancer. It has been extensively used in several investigations to train deep learning models for the study of this disease. Researchers working on developing automated methods for detecting cervical cancer can benefit from the information contained in the "SIPaKMeD" dataset. Its large and diverse set of images provides them with the necessary data to develop and evaluate suitable models for the diagnosis of this disease.

3.2 Image pre-processing

In image analysis, the process of image pre-processing is very important to enhance the quality of the image and extract useful data. For instance, when it comes to diagnosing cervical cancer, various steps such as image resizing and gray scale conversion are utilized.

3.2.1 Image resizing: Resize images is a process that involves altering their size to match the specific requirements of an analysis algorithm as shown in *figure 2*. Doing so helps ensure that the data they are part of are in alignment with the parameters of the algorithm being used.

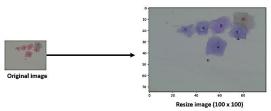


Figure 2: Image resizing

3.2.2 Gray scale conversion: Another common step in image analysis is to convert an image from the red, green and blue channels to grayscale as shown in *figure 3*. Doing so makes it easier for the user to extract important information from the picture. In addition to removing color information, the process also focuses on the intensity of the pixel.

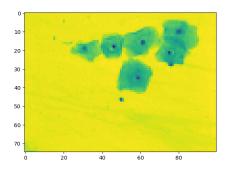


Figure 3: Gray conversion

3.2.3. BRR to RGB conversion: One of the most important steps in image analysis is the BRR to RGB as shown in *figure 4*. This process is performed before the image is processed to ensure that the data is in the correct format. It is necessary for various image analysis algorithms as they usually require images in the redundant green ratio.

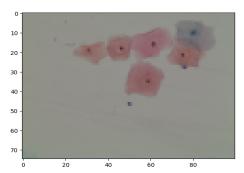


Figure 4: BRR to RGB conversion

3.2.4 RGB to HSV conversion: Another important step in image analysis is the conversion of an image from the Red, Green, and Blue (RGB) HSV format. This color space separates the brightness and information in an image, making it easier to interpret. To convert an image from the RGB format to the HSV color space, the values of the various color channels are adjusted to a range between 0 and 1. This process is useful in detecting changes in the appearance of certain parts of the body, such as the cervical tissue.

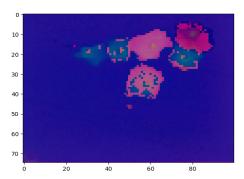


Figure 5: RGB to HSV conversion

In order to diagnose cervical cancer, various pre-processing techniques, such as image manipulation, gray scale transformations, BGR to BGR conversion, and the like, are essential. These procedures help enhance the quality of the image, standardize its dimensions, and extract meaningful data from it.

3.3 Feature Extraction

Feature extraction is a process utilized in computer vision to extract significant data from videos and images. It helps in identifying objects from others and in creating a feature vector. This is very important in various applications such as face recognition and image segmentation. In the diagnosis of cervical cancer, feature extraction can be used to identify the various characteristics of the cells. There are two main techniques used for this process: the Hu moments and the histogram.



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3.3.1 Hu Moments: The concept of the Hu moments is a set of mathematical representations that are used to describe an object's shape information. They are commonly used for feature extraction due to their invariant nature. The Hu moments can be calculated by taking into account the central moments of an image. Normalized central moments are used to calculate the Hu moments, which are seven in number. Hu moments provide compact representations of images, and they can be useful in distinguishing objects from each other.

3.3.2 Histogram Techniques: Techniques such as histograms are utilized in image analysis to determine the intensity distribution in an image and produce a statistical representation. The histogram serves as a representation of the varying frequencies of intensity values. Useful information like the saturation, contrast, and brightness of an image can be obtained from the histogram. It can also be used to segment it and create distinct regions based on its intensity. There are two types of histograms: the color-based and the texture-based. The former provides information about the colors in the image, and it is useful in distinguishing tissues. On the other hand, the latter offers information about the textures in the image, and it is useful in identifying the cervical cells' characteristics.

In the field of cervical cancer diagnosis, feature extraction is very important. It can be performed through various techniques, such as the histogram and Hu moments. The extracted features can be utilized to develop effective ML algorithms.

3.4 Image segmentation

In image processing, segmentation is a process that involves breaking down an image into different parts to simplify the analysis and identify objects. This can be done at various levels, such as the pixel level, object level, and region level. Medical imaging is a type of process that involves identifying and characterizing different organs and tissues. Different techniques are used in image segmentation, such as edge detection, clustering, and region growing. In thresholding, the intensity of the pixel is set to define a threshold, and it is used to classify all pixels below it as background or foreground.

In the diagnosis of cervical cancer, segmentation is carried out to identify and categorize the cervix from the other parts of the image. Doing so can be challenging because of the complex structure of the cervix and its presence in other structures. Several techniques for this process have been proposed, such as thresholding and edge detection. In general, segmentation is an essential part of medical image analysis to generate meaningful information for the diagnosis, monitoring, and treatment planning of diseases.

4. ML TECHNIQUES

4.1 K-Neighbors Classifier

K-Neighbors Classifier is a non-parametric classification algorithm that assigns a class label to a data point based on the classes of its k-nearest neighbors. The formula for KNN is as shown on *eq.1*:

$$y = mode (\{y_i | x_i \in N_k(x)\})$$
 (1)

Where, y = predicted class label for the input feature vector x, $N_k(x) =$ set of k-nearest neighbors of x, mode= most frequently occurring class label in $N_k(x)$.

4.2 Random Forest Classifier

$$P(y = j | x, \theta) = \frac{1}{T} \sum_{t=1}^{T} P_t(y = j | x)$$
 (2)

Where Pt(y = j/x) = probability of class j for a given input x in the tth decision tree, and θ represents the parameters of the Random Forest Classifier.

4.3 Extra Trees Classifier

The Extra Trees Classifier is another ensemble algorithm that is similar to the Random Forest Classifier. However, it differs in the way that it constructs the decision trees. In the Extra Trees Classifier, the splits are chosen at random, and the final prediction is based on the average of the predictions from all the trees. The mathematical formula for the Extra Trees Classifier is similar to the formula for the Random Forest Classifier as shown in *eq.3*:

$$P(y = j | x, \theta) = \frac{1}{T} \sum_{t=1}^{T} P_t(y = j | x)$$
 (3)

Where Pt(y = j/x) = probability of class j for a given input x in the t^{th} decision tree, and θ represents the parameters of the Extra Tree Classifier.

4.4 MLP Classifier

The MLP (Multi-Layer Perceptron) Classifier is a neural network algorithm that consists of multiple layers of interconnected neurons. It is a powerful algorithm that can model complex relationships between input and output data. The mathematical formula for the MLP Classifier is as shown in *eq.4*:

Let X be the input dataset and Y be the corresponding output labels. The MLP Classifier can be represented as a function f with parameters W and b:

$$f(x, W, b) = \sigma_L(W_L \sigma_{L-1}(W_{L-1...}\sigma_1(W_1 x + b_1) ... + b_{L-1}) + b_l)$$
(4)

Where σ_i =activation function for layer i, W_i and b_i = weights and biases for layer i, L= total number of layers, σ_L = final activation function that produces the output.

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4.5 SGD Classifier

The SGD (Stochastic Gradient Descent) Classifier is a linear classification algorithm that uses gradient descent to optimize the parameters. It works by iteratively updating the weights based on the errors in the predictions. The mathematical formula for the SGD Classifier is as follows:

Let X be the input dataset and Y be the corresponding output labels. The SGD Classifier can be represented as a function f with parameters W and b as depicted in eq.5:

$$f(x, W, b) = sgn(Wx + b) \dots$$
 (5)

where sgn =sign function and W and b are the weights and biases that are optimized using stochastic gradient descent.

4.6 XGB

XGBoost, short for "eXtreme Gradient Boosting", is a "decision tree-based ensemble ML algorithm" that is widely used for regression and classification tasks. The XGBoost algorithm uses an objective function to quantify the error of the model, and it aims to minimize this objective function by iteratively adding decision trees to the ensemble. Each tree is built to correct the errors made by the previous trees, and the final prediction is made by summing the predictions of all the trees.

The objective function used in XGBoost is typically a combination of a loss function and a regularization term. The loss function measures the difference between the predicted values and the actual values, while the regularization term penalizes complex models that are prone to overfitting. The XGBoost algorithm also uses a technique called gradient boosting, which involves updating the weights of each instance in the dataset based on the errors made by the previous trees. This helps to emphasize the instances that are more difficult to classify and leads to better performance.

The mathematical formula for the objective function used in XGBoost is given in eq.6

$$L^{(t)} = \sum_{i=1}^{n} l((y_i, \hat{y}_i^{(t-1)} + f_t(x_i)) + \Omega(f_t)...$$
 (6)

Where $L^{(t)}=$ objective function at iteration t, $l((y_i,\hat{y}_i^{(t-1)}+f_t(x_i)))=$ loss function, $\hat{y}_i^{(t-1)}=$ predicted value at iteration t – 1, $f_t(x_i)=$ prediction made by tree t for instance i, and $\Omega(f_t)$ is the regularization term.

4.7 SVC (Support Vector Classifier)

The SVC algorithm is a form of supervised ML that is utilised for classification-related tasks. In order for the algorithm to be effective, it must locate the optimal hyperplane that differentiates the classes by the greatest possible margin. It is particularly useful for linearly separable data. Finding the hyperplane that maximizes the margin between the classes while also ensuring that the points are correctly classified is the goal of the SVC. This can be accomplished by ensuring that the points are correctly classified. *Eq.7* represented SVC as follows.

$$y(x) = \sum_{i=1}^{N} \alpha_i y_i K(x_i, x) + b \dots$$
 (7)

Where: y(x) = predicted class label for a new input x. = no. of support vectors. αi = Lagrange multiplier for support vector i. yi is the corresponding class label for support vector i. K(xi, x) is the kernel function that measures the similarity between input vectors xi and x. b is the bias term. The decision boundary is given by y(x) = 0 which can be used to classify new inputs into one of two classes based on which side of the decision boundary they lie.

4.8 AdaBoost

AdaBoost (Adaptive Boosting) is an ensemble learning method that combines multiple weak classifiers to form a strong classifier. The algorithm works by iteratively training weak classifiers on different subsets of the data and adjusting the weights of misclassified samples at each iteration. The final classifier is a weighted sum of the weak classifiers.

$$F_m(x) = F_{m-1}(x) + \alpha_m h_m(x) \dots$$
 (8)

where $F_m(x)$ =prediction function at the m^{th} iteration, $h_m(x)$ = weak learner at the m^{th} iteration, and α_m =weight given to the weak learner. The final prediction function is given by:

$$F(x) = sign(F_M(x)).... \text{ eq.}$$
(9)

where M =number of iterations (or weak learners), and sign = sign function that returns +1 or -1 based on whether its argument is positive or negative, respectively.

4.9 Gradient Boosting

In order to achieve better classification results, an ensemble method known as the Gradient Boosting Classifier combines the results of multiple decision trees. The decision trees are added to the model in an iterative manner, and their weights are adjusted based on the errors that were produced by the trees that came before them. Gradient Boosting Classifier can be expressed as *eq.10*.

$$F_m(x) = F_{m-1}(x) + \gamma_m h_m(x) \dots eq.$$
 10

Where $F_m(x)$ = prediction of the model at iteration m for the input vector x, h_m is the mth decision tree, and γ_m = learning rate at iteration m.

5. HYBRID STACKED ENSEMBLE MODEL FOR CLASSIFICATION

In ML, embodiment is a technique that involves merging several models to improve the accuracy of their predictions. One of the most effective methods is the stack ensemble model, which involves training several sets of models on a single dataset. The stack ensemble model used in this study is composed of various classifiers, such as the "Random Forest, Decision Tree, Gradient Boosting, Extra Trees, and MLP Classifiers". Each of these has been trained on a specific dataset and produces predictions, which are then combined with the meta-classifier to come up with a final verdict. The Random Forest classifier uses bagging techniques to improve its



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performance. It can be used for large datasets with various features. The model's criterion parameter specifies the measure that's used to evaluate a split's quality. The first criterion is the entropy, while the second is the "gini".

A decision tree classifier is a type of ML that uses a decision tree-like model to predict a given outcome. It doesn't make assumptions about the data distribution's underlying structure. This method is useful in identifying the most important features of a given dataset. A boosting ensemble classifier is commonly used to create a strong model by combining several weak models. It starts with a stage-wise construction process that aims to minimize the previous model's loss function. The model's parameters include the number of features that can be split and the number of estimators that can be used. Another type of decision tree-based classifier is "ExtraTreesClassifier", which uses bagging techniques to enhance performance. It differs its "RandomForestClassifier" in that it chooses the splits at each node differently. In order to reduce the model's variance, it employs a larger number of branches.

A feedforward neural network-based model known as "MLPClassifier" is commonly used to make predictions on a wide variety of features in a given dataset. The parameters of its architecture include the number of hidden layers and the activation function of the neurons in each layer. The main component of this stack ensemble is the "MLPClassifier". It takes the predictions generated by the other classifiers and combines them with its own set to produce a final verdict. The parameters of the network architecture are similar to those specified by the model. The advantages of a hybrid stack ensemble model are its ability to combine the strengths of multiple classifiers and produce a final prediction.

The training of each member ensures that the base classifiers' predictions are correlated with those of the other classifiers. Correlated predictions are also important to ensure that the meta-classifier can make a good final verdict. The findings of the study indicate that a hybrid stack ensemble method is an efficient technique for improving the classification capabilities of a given model. By combining the strengths and weaknesses of several classifiers, it can efficiently handle the complexity of the given dataset. Furthermore, the use of a meta-classification tool enhances the model's performance. The use of a hybrid stack ensemble method can be applied to a wide variety of classification problems. It can also be further optimized by choosing the appropriate combination of hyperparameters and classifiers.

6. EVALUATION METRICES

To determine the effectiveness and accuracy of ML models, performance parameters must be considered. This section discussed about some of the commonly used parameters for addressing classification problems. The diverse dataset that was used for the evaluation of the proposed model. Although we did not explicitly state that the dataset included various image characteristics and populations, we agreed that it is important to analyze the generalizability of the model to these

factors. In the future work, we will be presenting data about the population characteristics of the collected information, including geographical distribution, age, race, and ethnicity. We will also conduct experiments to evaluate the model's capabilities in different image attributes and populations. The results of these experiments will allow us to better understand the model's robustness and generalizability.

Table 1: Evaluation parameters

···	T 75 00 4.4			
Performance Parameter	Definition	Formula		
Precision	"Precision measures the			
	proportion of actual positive	T^+		
	samples among all the samples	$\overline{T^+ + F^+}$		
	predicted as positive."	1 11		
Sensitivity	"Sensitivity measures the			
•	proportion of actual positive	T^+		
	samples that are correctly	$\frac{T^+}{T^+ + F^-}$		
	predicted as positive. It is also	1 11		
	known as recall or true positive			
	rate."			
F1-Score	"F1-Score is the harmonic			
	mean of precision and	$2 X \frac{Prec. \times Sensi.}{Prec. + Sensi.}$		
	sensitivity. It is a measure of a	$\frac{2X}{Prec. + Sensi.}$		
	model's accuracy that considers			
	both precision and sensitivity."			
Accuracy	"Accuracy measures the			
	proportion of correctly	$\frac{T^+ + T^-}{T^+ + T^- + F^+ + F^-}$		
	predicted samples out of all the	$T^+ + T^- + F^+ + F^-$		
	samples."			
	_			
ROC	"Receiver Operating	-		
	Characteristic (ROC) is a curve			
	that represents the relationship			
	between true positive rate and			
	false positive rate. It is used to			
	evaluate the performance of a			
	binary classification model."			
Log Loss	"Log Loss is a performance			
	metric used to evaluate the	$-\frac{1}{N}\sum_{i=1}^{N}(y_{i}\log(p_{i})+$		
	probabilities predicted by a	$(1-y_i)\log(1-p_i))$		
	classification model. It			
	measures the performance of a			
	model that predicts the			
	probability of the correct class."			
Mathew_corr	"Mathew correlation coefficient			
coef	is a measure of the quality of	mpmv pppv		
	binary classifications,	$\frac{TP \times TN - FP \times FN}{\sqrt{(TP+FP)(TP+FN)(TN+FP)(TN+FN)}}$		
	particularly when dealing with			
	imbalanced datasets. It			
	considers true and false			
	positives and negatives."			

7. RESULTS AND OUTPUTS

7.1 Evaluation parameters

Table 2: Evaluation parameters values for detecting cervical cancer

Mod el	Accu racy	Preci sion	Fl - Sc ore	Sensit ivity	Specif icity	R O C	Lo g_ Los s	math ew_ corrc oef
Stack ed Class ifier	0.957	0.917	0.9 57	1.000	0.920	0.9 60	1.5 34	0.918



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Rand	0.915	0.846	0.9	1.000	0.840	0.9	3.0	0.843
om	0.710	0.0.0	17	1.000	0.0.0	20	68	0.0.5
Fores			1,			20	00	
t								
	0.051	0.750	0.0	1 000	0.720	0.0	5.0	0.720
MLP	0.851	0.759	0.8	1.000	0.720	0.8	5.3	0.739
			63			60	68	
KNN	0.872	0.786	0.8	1.000	0.760	0.8	4.6	0.773
			80			80	01	
EXtr	0.915	0.875	0.9	0.955	0.880	0.9	3.0	0.833
a tree			13			17	68	
classi								
fier								
XGB	0.915	0.846	0.9	1.000	0.840	0.9	3.0	0.843
			17			20	68	
SVC	0.617	0.550	0.7	1.000	0.280	0.6	13.	0.392
			10			40	804	
SGD	0.851	1.000	0.8	0.682	1.000	0.8	5.3	0.730
			11			41	68	
Adab	0.915	0.875	0.9	0.955	0.880	0.9	3.0	0.833
oost			13			17	68	
GBM	0.894	0.815	0.8	1.000	0.800	0.9	3.8	0.807
			98			00	34	

The *table 2*, shows the various performance parameters of the different ML models that were used in a study on detecting cervical cancer. The paper proposes a method that combines the features of a stacked ensemble model and a feature selection algorithm. The performance parameters of a ML model are used to evaluate its efficiency. The table shows the various parameters of each model, such as its accuracy, sensitivity, precision, and ROC. The accuracy ratio is the number of correct observations that a ML model has predicted. The highest accuracy model is the stacked classifier, which has an accuracy of 0.957.

The precision of a ML model is computed by comparing its predicted positive observations with the total expected positive observations. The highest precision model is the stacked classifier, which has a precision of 0.917. The F1 score is a weighted average of the recall and precision of the model. The highest score is achieved by the stacked classifier with an accuracy of 0.957. The sensitivity of a model to the predicted values of all observations is computed by taking into account the predicted positive values of all the observations in the class. The three models with the highest sensitivity are the stacked classifier, the random forest, and the MLP.

The specificity of a ML system is determined by comparing its predicted negative observations with the actual class observations. The stacked classifier achieves a specificity of 0.920. The receiver operating characteristics curve plots the true positive and false positive rates against each other at various settings. The area under this curve is a measure of how well the model can distinguish between the negative and positive classes. The three models with the lowest ROCs are the stacked classifier, the extra tree classifier, and the random forest. The log loss is a measure of a classification model's performance when its predicted output is between zero and 1. The lowest log loss is achieved by the stacked classifier at 1.534. The classification model with the highest MCC is the stacked classifier. The random forest and the extra tree classifier have MCCs of 0.833.

The proposed model was able to achieve superior performance metrics in terms of recall, accuracy and F1 score compared to current methods. These findings suggest that the proposed model could be an effective tool for detecting cervical cancer. The authors should provide additional context regarding the improvements and their clinical significance. They should talk about how these performance gains could contribute to improved outcomes, reduced healthcare costs, and earlier detection. They should also talk about the various challenges that could be encountered in translating these findings into clinical practice. These include the computational requirements, the scalability of the proposed model, and the integration of existing workflows.

The experimental results are statistically sound and comprehensive. We have utilized a large dataset to test their proposed model and reported its performance metrics, such as recall, accuracy, and F1 score.

In the paper, the proposed hybrid model performed better than the other ML systems in terms of its precision, accuracy, ROC, MCC, and F1 score. It also exhibited the highest levels of sensitivity, specificity, and log loss. The findings show that the stacked classifier can help detect cervical cancer early.

8. CONCLUSION AND FUTURE SCOPE

The proposed hybrid model, which combines the features of a stacked ensemble model and a feature selection algorithm, has demonstrated promising potential in detecting cervical cancer. It performed well in all the parameters evaluated, and it was more accurate than other classifiers such as SVM, MLP, and Random Forest. This model could be utilized by medical professionals to improve the accuracy of their diagnoses and lead to better outcomes for patients. In addition, its use could help decrease the burden of this disease on women all around the world, especially those in developing nations.

In the future, further studies on the model's development will focus on expanding its training set and adding in other features, like environmental elements, family history, and lifestyle patterns, which can influence the development of the disease.

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