Machine Learning Models for Prostate Cancer Identification

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Keywords: Prostate Cancer, Data Analysis, Machine Learning, Prediction, Ensemble Models, SMOTE.

Abstract: In the present research paper, we focused on prostate cancer identification with machine learning (ML) techniques and models. Specifically, we approached the specific disease as a 2-class classification problem by categorizing patients based on tumour type as benign or malignant. We applied the synthetic minority oversampling technique (SMOTE) in our ML models in order to reveal the model with the best predictive ability for our purpose. After the experimental evaluation, the Rotation Forest (RotF) model overcame the others, achieving an accuracy, precision, recall, and f1-score of 86.3%, and an AUC equal to 92.4% after SMOTE with 10-fold cross-validation.

1 INTRODUCTION

The prostate is a small gland that produces and stores a component of male sperm. It is located under the bladder and surrounds the urethra, which is why even in the case of a significant increase in size, urination problems are caused. A common result is prostate cancer (Verze et al., 2016; Mottet et al., 2015).

Prostate cancer is nowadays one of the dominant health problems faced by the male population. It is the most frequent cancer in men in the Western world and the second leading cause of death after lung cancer. It usually develops slowly and is initially limited to the prostate gland. Some forms of prostate cancer can be very aggressive and metastasize rapidly. If detected in time, it has good prospects for effective treatment (Pernar et al., 2018; Rawla, 2019).

In addition, it is already known that the risk factors for the occurrence of prostate cancer are age, family history, the existence of metabolic syndrome, arterial hypertension, increased waist circumference, obesity, diabetes, smoking and high alcohol consumption. Prostate cancer can appear on many faces and evolve at different rates. Thus, there are men with prostate cancer with no symptoms, while others present with urination, ejaculation disorders, erectile dysfunction, frequent urge to urinate, especially at night, bleeding or even bone pain (Perdana et al., 2017; Leitzmann and Rohrmann, 2012).

This disease mainly concerns older men and is relatively rare in men under 40 years of age. The diagnosis of prostate cancer is made by a competent doctor, who is the urologist-andrologist. Clinical examination and imaging testing with digital rectal examination and Prostate Specific Antigen (PSA) testing via blood test are required. If necessary, an additional ultrasound check, prostatic tissue sample collection - biopsy and magnetic resonance imaging are performed (Bechis et al., 2011; Descotes, 2019).

Reduced intake of saturated fatty acids (red meat), increased consumption of vegetables and dietary intake of vitamins E and D, selenium, lycopene, soy proteins and fish oils have been proven to have a protective effect. In addition, choosing a Mediterranean diet based on fruits and vegetables, exercising regularly, and maintaining a stable and healthy body weight are contributing factors to avoiding the occurrence of prostate cancer (Gandaglia et al., 2021; Matsushita et al., 2020).

As mentioned above, early diagnosis plays a key role in prevention. ML now plays a decisive and, at the same time, a complementary role towards this direction. Medical science has an important tool for better and more accurate prediction of various diseases such as diabetes (as classification (Fazakis et al., 2021b; Dritsas and Trigka, 2022a) or regression task for continuous glucose prediction (Dritsas et al., 2022a; Alexiou et al., 2021)), cholesterol (Fazakis et al., 2021a; Dritsas and Trigka, 2022c), hyper-

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Dritsas, E., Trigka, M. and Mylonas, P.
Machine Learning Models for Prostate Cancer Identification.
DOI: 10.5220/0012236800003598
In *Proceedings of the 15th International Joint Conference on Knowledge Discovery, Knowledge Engineering and Knowledge Management (IC3K 2023) - Volume 1: KDIR*, pages 421-428
ISBN: 978-989-758-671-2; ISSN: 2184-3228

tension (Dritsas et al., 2021a; Dritsas et al., 2022d), chronic obstructive pulmonary disease (Dritsas et al., 2022c), covid-19 (Dritsas and Trigka, 2022f), stroke (Dritsas and Trigka, 2022e), chronic kidney disease (Dritsas and Trigka, 2022d), cardiovascular diseases (Dritsas and Trigka, 2023a; Trigka and Dritsas, 2023a; Dritsas et al., 2022b), sleep disorders (Konstantoulas et al., 2021; Konstantoulas et al., 2022), lung cancer (Dritsas and Trigka, 2022b), liver disease (Dritsas and Trigka, 2023b), breast cancer (Dritsas et al., 2023), metabolic syndrome (Dritsas et al., 2022e; Trigka and Dritsas, 2023b), etc.

This study was based on a publicly available dataset that provides morphological descriptions to discriminate the type of prostate tumour and facilitate the classification process. These data were exploited to build high-performance ML models. More specifically, a key step of the adopted methodology was the application of SMOTE (Chawla et al., 2002) for training ensemble ML models on class-balanced data. The models were evaluated in terms of accuracy, precision, recall, f1-score and AUC. The model which overcame the others in the aforementioned metrics was the Rotation Forest. Finally, a discussion on related works in the same concept is presented.

The rest of this paper is organized as follows. In Section 2 the main parts of the methodology for prostate cancer identification are noted. In particular, in Section 3 a discussion of the results and related works for the subject under consideration are provided. Finally, in Section 4 the conclusions are outlined.

2 METHODOLOGY

In this section, we note the dataset's characteristics in which our ML models were evaluated. Also, we describe the adopted methodology, and finally, we capture the ensemble models we experimented with, as well as the metrics for their evaluation.

2.1 Dataset Description

The dataset (Dat,) on which our experimental evaluation was performed contains information on 100 patients suffering from prostate cancer. Each sample is represented by eight independent variables - predictors (radius, texture, area, perimeter, compactness, smoothness, fractal dimension, symmetry) and one dependent variable that captures the diagnosis result. The class output takes two values: "B" for benign tumours and "M" for malignant tumours.

Table 1: Statistical analysis of the dataset.

Attribute	Description		
	Min	Max	Mean±stdDev
radius	9	25	16.85±4.879
texture	11	27	18.23±5.193
perimeter	52	172	96.78±23.676
area	202	1878	702.88±319.711
smoothness	0.07	0.143	0.103±0.015
compactness	0.038	0.345	0.127±0.061
symmetry	0.135	0.304	0.193±0.031
fractal_dimension	0.053	0.097	0.065±0.008

2.2 Data Processing and Analysis

Following an exploratory data analysis, a statistical description of the features in the whole dataset is given in Table 1. Also, for each feature, their values among the involved patients are shown in Figure 1.

Moreover, the Pearson correlation coefficient is used to estimate the degree of linear association between the features including the target class. Table 2 demonstrates the outcomes of this coefficient based on the equation of (Liu et al., 2020) defined as follows:

$$\rho_{X,Y} = \frac{E\left[(X-\mu_x)(Y-\mu_y)\right]}{\sigma_X \sigma_Y},$$

where X, Y are the variables that capture the compared features values, $E[\cdot]$ denotes the expectation operator and μ_x, σ_x and μ_y, σ_y are the mean values and variances of the X, Y, respectively. Based on this coefficient, the features' importance is ordered as: "perimeters, area, compactness, symmetry, smoothness, radius (the minus shows a negative correlation with the class variable), texture and fractal dimension". Also, it was observed that the features of area and perimeter indicated the highest positive linear association. From a medical point of view, the considered features are necessary for concretely representing the tumour type and thus the patient's status. So, all of them will be considered for the models' training and evaluation.

The application of SMOTE is an important step in the process to ensure that the employed ML models will be trained on data with uniform class distribution (Dritsas et al., 2021b). Algorithm 1 provides the steps that SMOTE considers exploiting the K-Nearest Neighbours method with K equal to 5 (default parameter in the WEKA environment where we worked) (Dritsas and Trigka, 2022f). The use of SMOTE was combined with 10-fold cross-validation since the size of the dataset is quite limited; it consists of 100 samples, where 62 belong to the "Malignant" class and 38 to the "Benign" class. The ML models were trained and evaluated in each fold, and the outcomes from both classes and all folds were averaged to obtain the final prediction (or, else, classification performance).

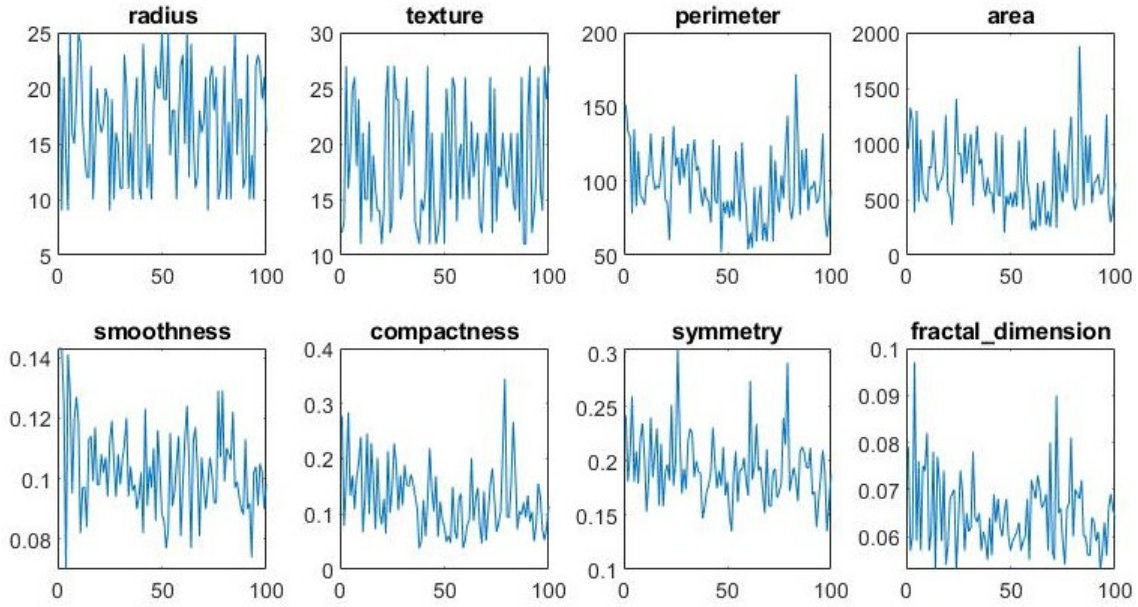

Figure 1: The clinical features evolution among the patients.

Table 2: Pearson Correlation Coefficient $\rho_{X,Y}$ among the features (including the class variable).

	radius	**texture**	**perimeter**	**area**	**smoothness**	**compactness**	**symmetry**	**fractal**	**class**
radius	1.0000	0.1002	-0.2382	-0.2509	-0.1271	-0.1915	-0.0397	-0.0291	-0.1770
texture	0.1002	1.0000	-0.1135	-0.1137	0.1023	0.0324	0.0779	0.1392	0.0707
perimeter	-0.2382	-0.1135	1.0000	0.9766	0.2694	0.5275	0.1955	-0.1954	0.6075
area	-0.2509	-0.1137	0.9766	1.0000	0.2084	0.4249	0.1104	-0.2743	0.5624
smoothness	-0.1271	0.1023	0.2694	0.2084	1.0000	0.4657	0.4242	0.3696	0.1976
compactness	-0.1915	0.0324	0.5275	0.4249	0.4657	1.0000	0.6811	0.6480	0.5122
symmetry	-0.0397	0.0779	0.1955	0.1104	0.4242	0.6811	1.0000	0.5686	0.2330
fractal	-0.0291	0.1392	-0.1954	-0.2743	0.3696	0.6480	0.5686	1.0000	0.0082
class	-0.1770	0.0707	0.6075	0.5624	0.1976	0.5122	0.2330	0.0082	1.0000

Algorithm 1: SMOTE.

Input: T (number of minority class samples, N (% ratio of synthetic minority samples for class balancing), K (number of nearest neighbours);
Choose randomly a subset $\mathcal{S}$ of the minority class data of size $S = \frac{N}{100}T$ (synthetic minority class samples) such the classes are uniformly distributed;
for all $s_i \in \mathcal{S}$ **do**
(1) Find the K nearest neighbours.;
(2) Calculate the distance $d_{i,k}$ between the one randomly selected NN among K and the sample s_i.;
(3) The new synthetic sample is generated as $s_n = s_i + rand(0-1)d_{i,k}$ ($rand(0-1)$ generates a random number between 0 and 1).;
end for
Repeat steps number 2–3 until the desired proportion of minority class is met.

2.3 Machine Learning Models and Performance Metrics

The assessment of ML models was conducted in WEKA (WEK,), free software which contains tools for data pre-processing, classification, regression, clustering, visualization, etc. The experiments were performed on a computer system with the following specifications: Apple MacBook Pro 13.3", Retina Display (M2/ 16GB RAM/ 256GB SSD). As for the ML methodology, we applied ensemble techniques (Sagi and Rokach, 2018) that combine multiple models to make predictions rather than individual ones. From the family of ensemble techniques, the following methods were considered:

1. Bagging (Ngo et al., 2022) – It creates a different training subset from sample training data with replacement and the final output is based on majority voting.
2. AdaBoost (Ying et al., 2013) – An Adaptive

Boosting method combines weak learners into strong ones by creating sequential models such that the final model has the highest accuracy.

3. Stacking (Pavlyshenko, 2018) - It trains different base learners on the same data and combines their predictions using a meta-classifier that is trained with the outcomes of the base models to learn the class label.
4. Voting (Mushtaq et al., 2022) - It trains different base learners on the same data and finds the final prediction by applying soft voting. The soft voting scheme classifies input data by averaging the probabilities of all the predictions made by different classifiers. The winning class is the one with the highest average probability.
5. Random Forest (RF) (Palimkar et al., 2022) - It selects a random subset of data records and a subset of features for constructing each decision tree. Individual decision trees are built for each sample, generate output and the final decision is derived based on majority voting.
6. Rotation Forest (RotF) (Rodriguez et al., 2006) - It is an ensemble classification method similar to Random Forests. Data rotation is a key processing step in RotF and is performed internally prior to training the base classifiers (trees are commonly used) using Principal Component Analysis (PCA). Therefore, base classifiers can divide the decision space into the feature axes and directions generated after the rotation. This feature makes it much more powerful than other traditional ensemble techniques.

Comparing bagging, boosting and stacking techniques, each one fulfils a different purpose. Bagging reduces the overfitting or variance of the model while boosting reduces underfitting or bias. Finally, stacking increases predictive accuracy. The benefit of stacking is that it can harness the capabilities of a range of well-performing models on a classification task and obtain better predictions than any single model in the ensemble. Here, the Bagging, AdaBoost and RotF methods considered RF as a base classifier. Stacking and Voting exploited as base classifiers the RF and Naive Bayes (NB) (Leung et al., 2007) and, especially Stacking, as meta-classifier the Logistic Regression (LR) (Maalouf, 2011).

To evaluate the ML models, we relied on metrics (Hossin and Sulaiman, 2015) commonly used in the ML field, namely accuracy, precision, recall, f1-score and AUC. It should be noted that the ultimate value in each metric was derived by averaging the outcomes of both classes from all folds. The definition of these metrics was based on the confusion matrix consisting of the elements true-positive (Tp), true-negative (Tn), false-positive (Fp) and false-negative (Fn). Hence, the aforementioned metrics were computed as follows:

$$\text{Accuracy} = \frac{\text{Tn}+\text{Tp}}{\text{Tn}+\text{Fn}+\text{Tp}+\text{Fp}},$$

$$\text{Precision} = \frac{\text{Tp}}{\text{Tp}+\text{Fp}}, \text{Recall} = \frac{\text{Tp}}{\text{Tp}+\text{Fn}},$$

$$\text{F1}-\text{score} = 2\frac{\text{Precision}\times\text{Recall}}{\text{Precision}+\text{Recall}}.$$

In addition to the above metrics, in the assessment of ensemble techniques the AUC metric was used. The values of this metric should vary between 0 and 1 and show the models' ability to discriminate the samples into "Benign" and "Malignant" classes, respectively. The closer to 1 the higher the models' separation capacity. In the worst case, when AUC ≈ 0.5, the model has no capacity to distinguish between the "Benign" class and the "Malignant" class. Finally, the AUC ROC curve is used to depict the performance of the ensemble classification models. This curve plots the True Positive Rate - TPR (or Recall) in terms of False Positive Rate - FPR defined as $\frac{\text{Fp}}{\text{Fp}+\text{Tn}}$ for different cut-off points.

3 RESULTS AND DISCUSSION

In this section, we analyse the results acquired by experimenting with the ensemble models RF, RotF, Stacking, Bagging, Voting and AdaBoost trained to classify a patient as "Benign" or "Malignant" and thus, predict the type of prostate cancer. Also, a short description of related works for prostate cancer identification is presented.

3.1 Ensemble Models Results

Focusing on Table 3, the selected ensemble models were compared in terms of accuracy, precision, recall, f1-score and AUC. Also, in the context of our analysis, the selected models were evaluated before and after the application of class balancing using the SMOTE technique. As the outcomes revealed, the use of SMOTE for the models' training increased their predictive performance. RotF (after SMOTE) was the dominant model indicating an accuracy, precision, recall, and f1-score of 86.3% and an AUC of 92.4%. The voting scheme noted the second proximal accuracy, precision, recall, and f1-score of 86.1% and an AUC equal to 90.7%. The rest models noted lower performance than RotF but proximal to each other.

In Figure 2, the ROC curves are depicted. Comparing the behaviour of the selected models, it seemed

Table 3: Experimental Results without and with applying class balancing using SMOTE.

Ensemble Models	Accuracy - %		Precision		Recall		F1 Score		AUC	
	No SMOTE	SMOTE	No SMOTE	SMOTE	No SMOTE	SMOTE	No SMOTE	SMOTE	No SMOTE	SMOTE
RF	82	83.1	0.820	0.831	0.820	0.831	0.820	0.831	0.882	0.912
RotF	85	86.3	0.850	0.863	0.850	0.863	0.850	0.863	0.887	0.924
Stacking	82	83.9	0.820	0.839	0.820	0.839	0.820	0.839	0.899	0.909
Bagging	82	83.1	0.820	0.831	0.820	0.831	0.820	0.831	0.895	0.915
Voting	85	86.1	0.850	0.861	0.850	0.861	0.850	0.861	0.888	0.907
AdaBoost	82	82.5	0.820	0.825	0.820	0.825	0.820	0.825	0.885	0.914

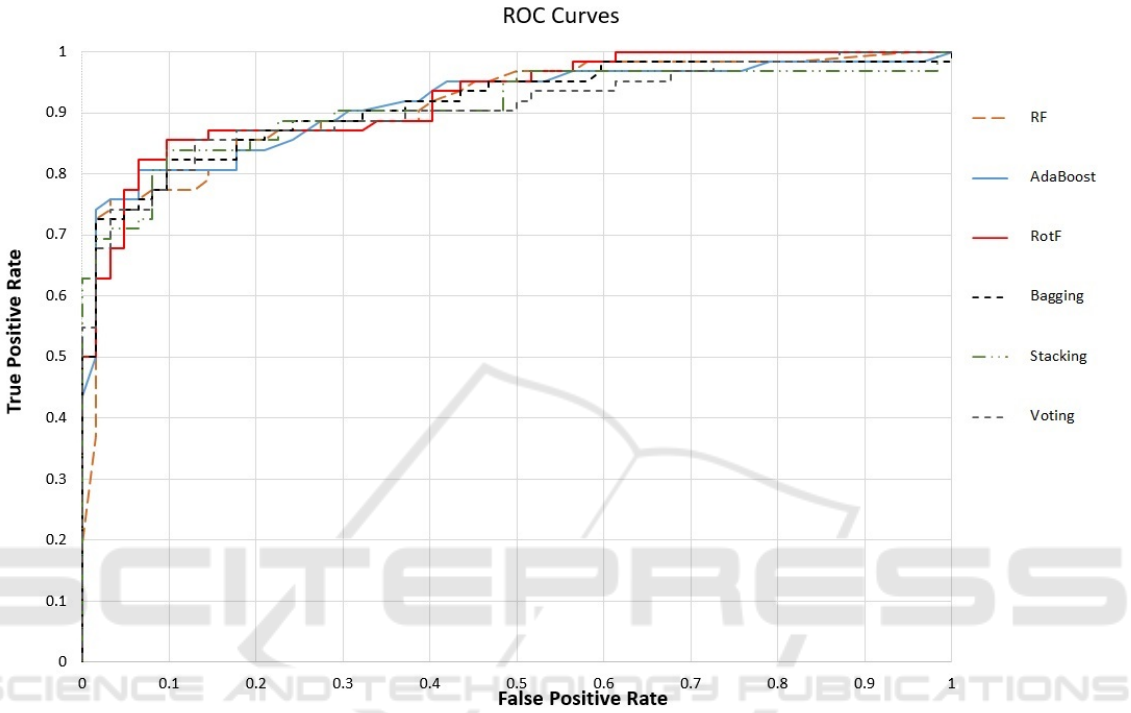

Figure 2: ROC Curves of ML models.

again that RotF was the classifier that indicated the lowest classification error. This curve and the corresponding AUC values showed that RotF with the selected bio-makers (namely, features) had the highest predictive ability to discriminate "Malignant" from "Benign" patients.

3.2 Results on Related Works for Prostate Cancer Prediction

In (Alam et al., 2020), a modified LR classifier is proposed and implemented on patients who are susceptible to prostate cancer, achieving accuracy, sensitivity and specificity equal to 96.86%, 95.50% and 98.39%, respectively. Moreover, in (Wen et al., 2018), the authors compared and evaluated four ML models, namely Artificial Neural Network (ANN), NB, Support Vector Machine (SVM) and Decision Tree (DT), for the prediction of prostate cancer survivability. The results showed that ANN had the best predictive ability with an accuracy of 85.64%.

Similarly in (Wang et al., 2018), the authors experimented with ML models SVM, Least Squares SVM, ANN, and RF, to detect prostate cancer cases using the available biopsy information. ANN achieved the highest accuracy of 0.9527 and an AUC value of 0.9755. RF outperformed the other three models in classifying benign, significant, and insignificant cases of prostate cancer, with an accuracy of 0.9741 and an f1-score of 0.8290.

Huljanah et al. (Huljanah et al., 2019) experimented with RF to detect prostate cancer. Feature selection and the use of 85% of the data for the models' training reached the best accuracy and precision of 100%. Finally, in (Laabidi and Aissaoui, 2020), the authors experimented with the same dataset as the present research paper keeping the same features. They applied scaling and no scaling techniques to the dataset, and proposed the Recurrent Neural Network (RNN) model, as it achieved better results. Specifi-

cally, the RNN model without (with) scaling achieved accuracy, AUC, f1-score, precision, and recall equal to 81% (81.3%), 0.866 (0.866), 0.809 (0.802), 0.798 (0.802) and 0.810 (0.813). Comparing the outcomes without scaling with the ones derived from the current study, it was observed that our proposed model, i.e. RotF, presented constantly more stable performance than RNN in all metrics.

4 CONCLUSIONS

Prostate cancer is the most common health condition in elderly men (with limited occurrence in men under 40 years old) and the second leading cause of death after lung cancer. Early diagnosis plays a contributing role in prevention. In this research paper, we based on a publicly available dataset, which provides morphological descriptions in order to discriminate the type of prostate tumour and facilitate the identification process. We applied the SMOTE technique for training ensemble ML models, namely, Stacking, Bagging, Voting, AdaBoost, Rotation Forest and Random Forest on uniform distribution class data to categorize patients based on tumour type as benign or malignant. The models were evaluated and compared in accuracy, precision, recall, f1-score and AUC. The RotF prevailed over the other models, achieving an accuracy, precision, recall, f1-score of 86.3%, and an AUC equal to 92.4% after SMOTE with 10-fold cross-validation. Finally, we aim to investigate an alternative methodology for prostate cancer detection by applying Deep Learning models and techniques to data generated from tumour X-rays.

ACKNOWLEDGEMENTS

This research was funded by the European Union and Greece (Partnership Agreement for the Development Framework 2014-2020) under the Regional Operational Programme Ionian Islands 2014-2020, project title: “Indirect costs for project “Smart digital applications and tools for the effective promotion and enhancement of the Ionian Islands bio-diversity” ”, project number: 5034557.

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