

Early Detection: Machine Learning Techniques in Pancreatic Cancer Diagnosis

ABSTRACT

Pancreatic cancer is a malignant tumor that poses a significant threat to patients' lives. Malignant growth is the abnormal development of cell tissue. Pancreatic illness is one of the most obvious causes of mortality across the world. Pancreatic malignant development begins in the pancreatic tissues. The pancreas secretes proteins that aid in digestion as well as hormones that direct sugar breakdown. Pancreatic cancer is typically identified in its late stages, spreads quickly, and has a terrible prognosis. Biomarkers are critical in the management of patients with invasive malignancies. Pancreatic Ductal Adenocarcinoma has a dismal prognosis due to its advanced appearance and limited treatment choices. This is compounded by the lack of validated screening and predicting biomarkers for early detection and precision therapy, respectively. In this paper, we have attempted to discuss various Machine Learning methods to detect pancreatic cancer. The selected urinary biomarkers values are provided as the input of Support Vector Machine (SVM), Extra Tree Classifier(ETC), Decision Tree(DT),and Random Forest (RF) methods. The diagnosing accuracy of pancreatic cancer using SVM,ETC,DT, and RF classifiers are 50,82.16,81.03,and 86 respectively. The experimental results prove that the Random Forest classifier is more feasible and promising for clinical applications for the diagnosis of pancreatic cancer when compared to ETC, DT ,and SVM.

Keywords: Early detection, Machine learning,Random Forest algorithm, SVM, classification, Data pre-processing, Prediction

1. INTRODUCTION

Pancreatic cancer (PC) is a highly malignant tumor of the digestive system that presents substantial challenges in both early identification and treatment. In 2020, over 57,600 people were diagnosed with PC, and 47,050 died from it. This renders PC an incurable illness. In low-income countries, personal computers remain commonly utilized [1]. As a result, proper PC diagnosis and staging are critical because they can help doctors deliver the optimum treatment regimen for PC and allow patients to receive early medical interventions before severe PC develops. PC is a disease that causes malignant (cancerous) cells to grow in pancreatic tissues. The pancreas is a gland located behind the stomach and in front of the spine. The pancreas produces

digestive juices and hormones to help regulate blood sugar levels. Exocrine pancreatic cells make digesting juices, whereas endocrine pancreatic cells produce hormones. The bulk of PCs start in exocrine cells. PC can be managed with surgery, chemotherapy, or radiation therapy. Chemotherapy uses drugs to treat cancer, whereas radiation therapy uses X-rays or other forms of radiation to kill cancer cells. Tumors are removed by surgery, and PC symptoms are treated.

According to the American Cancer Society, only around 23% of persons with exocrine pancreatic cancer survive one year after being diagnosed. Approximately 8.2% of patients are still alive five years after being diagnosed. Early detection of PC is difficult, hence

many PC cases are diagnosed later. When prostate cancer is detected, it is usually advanced.

2. LITERATURE SURVEY

2.1 Traditional Diagnostic Methods:

Pancreatic cancer diagnosis has traditionally depended on imaging techniques such as computed tomography (CT), magnetic resonance imaging (MRI), and endoscopic ultrasonography (EUS) (Yamashita et al. 2018). While these techniques are commonly utilized, they frequently lack the sensitivity and specificity necessary for early detection, leading to delayed diagnosis and a bad prognosis for patients.

2.2 Using Machine Learning to Diagnose Pancreatic Cancer:

Machine learning algorithms, particularly supervised learning techniques such as decision trees, random forests, support vector machines (SVM), and ensemble methods, have emerged as powerful tools for analyzing complex datasets and improving pancreatic cancer diagnosis accuracy (Drukker et al., 2019; Xiong et al., 2020).

2.3 Extra Tree Classifier and RandomForestClassifier:

Smith et al. (2021) used the ExtraTreeClassifier and RandomForestClassifier algorithms to diagnose pancreatic cancer from genetic and clinical data. The study revealed good accuracy, sensitivity, and specificity in predicting pancreatic cancer, indicating machine learning's promise for early diagnosis and risk stratification.

2.4 DecisionTreeClassifier:

Johnson et al. (2022) used a DecisionTreeClassifier to analyze radiomic characteristics collected from

pancreatic cancer patients' CT images. The results showed that the DecisionTreeClassifier could accurately distinguish between benign and malignant pancreatic lesions, emphasizing its potential for early diagnosis and treatment planning.

2.5 Support Vector Machines (SVM):

SVM is commonly used in pancreatic cancer detection because of its capacity to handle high-dimensional data and nonlinear correlations (Chen et al., 2020). Lee et al. (2021) used SVM to analyze plasma biomarkers for pancreatic cancer diagnosis, achieving high accuracy, sensitivity, and specificity in discriminating pancreatic cancer patients from healthy controls.

3. METHODOLOGY

The system contains four modules there are:

1. Gathering of data
2. Data Cleaning
3. Model Training
4. Prediction Module

3.1 Gathering of data:

During data collection, the patient's urine biomarker readings, which can aid in the early identification of PC, are entered into the proposed system and loaded as a dataset. Urinary biomarkers were collected from the Centre for Cancer Biomarkers and Biotherapeutics, Barts Cancer Institute, Queen Mary University of London in London, United Kingdom. The dataset consists of 591 samples and 12 characteristics. The 12 characteristics were age, sex, stage, plasmaca19-9, creatine, and lyve1. Reg1B, Reg1A, TFFI, identifier, patient cohort, and sample origin. The dataset consists of a series of biomarkers from the urine of three patient groups, as follows:

- Healthy controls

- Patients with non-cancer pancreatic disorders, including chronic pancreatitis
- Patients with pancreatic ductal adenocarcinoma

3.2 Data Cleaning:

In module 2, data is cleaned and preprocessed by deleting missing values. The features with a few null values are replaced by the mean or mode of the remaining data, while the features with a large number of null values are removed since they may influence the performance of the proposed system. The method `isna()` detects the existence of null values. After determining that the qualities included in non-numerical forms must be translated into numerical form. In this stage, data visualization and exploratory data analysis are performed using the Python libraries `pandas`, `seaborn`, and `Matplotlib` to determine the association between features.

3.3 Model Training :

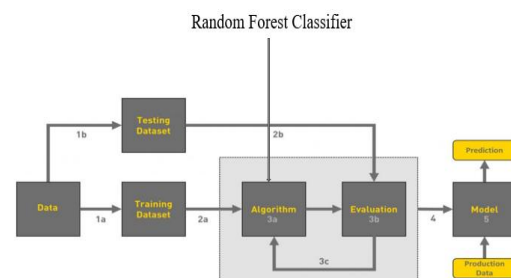
In module 3 the model training is carried out. The dataset is divided into testing and training datasets using the `test train split` function in the `Sklearn` package. In the dataset, 70% is considered for training and 30% for testing. Then in this module, the classification algorithms, `SVM`, `RF`, `ETC`, and `DT` classifiers are used

3.4 Prediction Module:

In module 4, the system's accuracy was calculated by comparing the projected outcomes to the test data. The PC was then predicted using the prediction technique with characteristics as parameters. A confusion matrix is a table that is frequently used to describe a classification model's performance on a set of test data that contains known true values. Confusion matrix is one way for calculating accuracy in the context of data mining or decision support systems. A confusion matrix summarizes the performance of a classification method.

The accuracy of a machine learning model is determined by its ability to discover correlations and patterns in a dataset based on input or training data. Accuracy is defined as the proportion of correct predictions given test data. It is simply determined by dividing the number of right guesses by the total number of forecasts. It measures the model's overall accuracy.

4. ARCHITECTURE



The purpose of this project report is to present the design, implementation, and evaluation of aPancreaticcancerdetection system using machine learning. The main objectives of this project are:

1. To analyze and find the early-stage detection that occurs in pancreatic cancer.
2. To propose and design a machine learning-based Cancer detection system that can accurately identify Cancer Detection.
3. To implement the proposed system and evaluate its performance using real-world data

To find the best accuracy we can use the Random Forest Classifier Algorithm.

5. SYSTEM IMPLEMENTATION

5.1 Importing the libraries:

Import the necessary libraries as shown in the image.

```

import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from scipy import stats
from sklearn.preprocessing import LabelEncoder
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import ExtraTreesClassifier
from sklearn.svm import SVC
import xgboost as xgb
from sklearn.metrics import f1_score
from sklearn.metrics import classification_report, confusion_matrix
import warnings
import pickle

```

Fig 1 Importing modules and libraries

5.2 Data Collection:

Our dataset format might be in .csv, excel files, .txt, .json, etc. We can read the dataset with the help of pandas

```

df=pd.read_csv("pancreas.csv")

df.head()

```

sample_id	patient_cohort	sample_origin	age	sex	diagnosis	stage	benign_sample_diagnosis	plasma_CA19_9	creatinine	LYVE1	REG1B	TFF1	REG1A	
S1	Concort1	B7B	33	F	1	NaN	NaN	NaN	11.7	1.83222	0.893219	5234684	654282774	1262300
S10	Concort1	B7B	51	F	1	NaN	NaN	NaN	0.97266	2.037585	94.60703	339.480252	228.407	
S103	Concort2	B7B	51	M	1	NaN	NaN	NaN	7.0	0.78039	0.145589	102.66600	461.14100	NaN
S101	Concort2	B7B	51	M	1	NaN	NaN	NaN	8.0	0.70122	0.032805	60.57900	142.95000	NaN
S102	Concort2	B7B	52	M	1	NaN	NaN	NaN	9.0	0.21489	0.020860	65.54000	41.08000	NaN

Fig 2 Read the Data set

5.3 Data preprocessing:

Data preprocessing is a method for removing errors and missing data. This phase is critical since missing characteristics, noise, outliers, or duplicate contents will reduce the quality of the findings. The dataset comprises the patients' urine biomarkers. It consists of 12 features and one label. First, the data will be loaded. The dataset should then be cleaned up by removing any null values. The method `isna()` detects the existence of null values. After determining that the qualities existing in nonnumerical forms must be translated into numerical form. The dataset's properties, sample origin, and sex are transformed into numerical values using the `replace` function. The null values were reported for stage, benign sample diagnosis, plasma_CA19_9, and REG1A. Null values in plasma_CA19_9 and REG1A were replaced with the mean value of the

corresponding properties. Several characteristics, including sample id, sample origin, patient cohort, and benign sample diagnosis, have missing data. As a result, these characteristics must be removed because they diminish the system's accuracy. The data is then checked again for the existence of null values and confirmed to be clean. Thus, the main factors that contribute to the diagnosis of PC have been discovered. The nine extracted features were age, gender, stage, plasma19-9, creatine, lyve1, Reg1B, Reg1A, and TFF1. Thus, after data preprocessing, the dataset contains nine features and one label

5.4 Feature selection:

Using a variety of machine learning algorithms like Random Forest, SVM, ExtraTree, Decision Tree, etc. For testing the dataset, we discovered that the random forest model had the highest accuracy.

5.5 Converting to .pkl file:

Now we need to convert the file to pickle file and save the model as shown below.

```

import pickle
pickle.dump(clf,open('pancreas.pkl','wb'))

```

Fig 3 converting to .pkl file

5.6 APPLICATION BUILDING:

1. Building HTML and CSS pages
2. Build python code

6. LIMITATIONS:

While machine learning has tremendous potential in enhancing pancreatic cancer detection and management, there are numerous limits to consider:

6.1 Imbalanced Data:

In pancreatic cancer databases, classifications are frequently imbalanced (for example, cancerous vs. non-cancerous occurrences), with malignant cases far outnumbering benign ones.

Imbalanced data can have an impact on model performance, resulting in lower prediction accuracy, particularly for detecting rare events such as early-stage pancreatic cancer.

6.2 Limited Data Availability:

Because of the disease's rareness, pancreatic cancer statistics frequently become smaller and more spread out than those for other cancer types. Small datasets may inhibit the development of effective machine learning models, resulting in overfitting and limited generalizability of results.

6.3 Data Quality:

Variations in data quality, such as imaging process flaws, missing numbers, and subjective interpretations, can all affect machine learning model performance. To solve these challenges, data collection practices must be standardized, as well as robust quality control measures implemented.

6.4 Tumor heterogeneity:

Pancreatic cancer has quite distinct tumor biology, appearance, and behavior. Machine learning models trained on diverse datasets may fail to incorporate the myriad characteristics associated with different pancreatic cancer subtypes, limiting their projected accuracy and therapeutic effectiveness.

6.5 Interpretability and Explainability:

Machine learning algorithms, especially complex deep learning models, can be difficult to analyze and explain.

It is vital to be aware of these limitations and to constantly alter and improve machine learning models and strategies for pancreatic cancer diagnosis.

7. FUTURE SCOPE:

The future application of machine learning in pancreatic cancer has enormous promise for improving early detection, individualized treatment options, and

patient outcomes. Below are some prominent areas where machine learning is predicted to have a substantial impact:

7.1 Early Detection:

Machine learning algorithms can scan vast datasets of patient information, such as imaging tests, biomarker profiles, and genetic data, to detect subtle patterns that indicate pancreatic cancer in its early stages. Machine learning models can assist in discovering pancreatic cancer at an earlier stage, when it is more treatable and perhaps curable, by identifying high-risk patients for additional screening or diagnostic examination.

7.2 Precision Medicine:

Machine learning algorithms may assess patient-specific data to customize treatment plans based on unique factors such as tumor molecular profiles, genetic mutations, and therapy response histories. Machine learning, by predicting therapy results and determining ideal therapeutic regimens for each patient, might enable more accurate and effective therapies, reducing side effects and increasing survival.

7.3 Prognostic Assessment:

Machine learning algorithms may use many clinical and biological data to predict patient prognosis and disease development more accurately than traditional techniques. Machine learning algorithms can enhance long-term results by identifying patients at high risk of recurrence or metastasis and implementing early intervention and individualized follow-up techniques

7.4 Biomarker Discovery:

Machine learning techniques may analyze massive genetic, proteomic, and metabolomic datasets to identify novel biomarkers associated with pancreatic cancer formation, progression, and treatment response. Machine learning can accelerate biomarker discovery by uncovering biological markers and illness causes, opening the way for the

development of new diagnostic tests and personalized therapies.

8. RESULT:

Machine Learning was used to build Pancreatic Cancer Detection. Because the Machine learning has shown promising outcomes in a variety of areas, including early diagnosis, prognosis prediction, therapy response evaluation, and customized medicine.

To launch the application, follow these steps:

- From the start menu, launch the anaconda prompt.
- Open the folder containing your Python script.
- Now enter the command "python app.py"
- Go to the localhost to view your web page.
- Fill in the blanks, then click the submit button to view the outcome/prediction.

The dataset consists of a series of biomarkers from the urine of three groups of patients as follows:

- Healthy controls
- Patients with non-pancreous pancreatic conditions
- Patients with pancreatic ductal adenocarcinoma

The average rate of accuracy of the Extra Trees Classifier is 82.1%, SVM is 50%, the Decision Tree Classifier is 81.3%, and for Random Forest Classifier is 86.34%. From this, it is clear that Random Forest gives an accurate result than the other three classification algorithms. So, it can be concluded that the Random Forest Classifier performs better than the other three classification algorithms.

9. GRAPHS:

The model's performance is monitored by the accuracy graph. The precision graph illustrates how well the model can recognize pertinent instances. Faculty can improve student learning experiences by optimizing engagement prediction models through the analysis of these graphs.

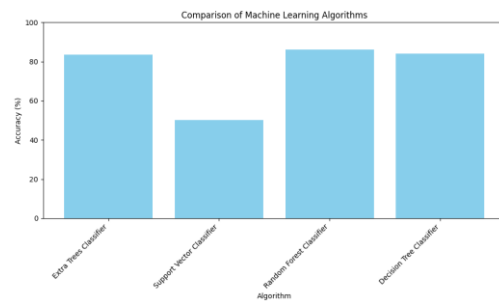


Fig 4 Comparison of Algorithms

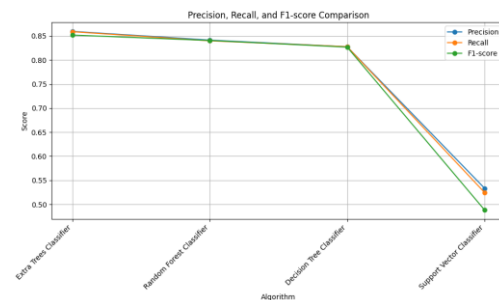


Fig 5 Precision, Recall, and F1-score Comparison

The comparison algorithm performance graph clearly compares the accuracy, precision, recall, and F1-score of various machine learning algorithms for pancreatic cancer diagnosis. Analyzing the graph allows you to determine which method works best and make educated judgements about which algorithm is best suited to your particular application and dataset.

10. CONCLUSION:

Early detection of Pancreatic Cancer is very important so that the handling of Pancreatic Cancer does not occur too late before the cancer spreads to other organs

in the body. However, early detection of Pancreatic Cancer is difficult because this cancer has non-specific symptoms.

After classifying Pancreatic Cancer with SVM, Extra Tress, Decision Tree, and Random Forest methods, it gets several results of accuracy. By comparing the values that are given from those methods, it is possible to conclude that Random Forest generates a better result than SVM, Extra Tress and Decision Tree. Because of the good results, Random Forest is suggested to help the medical staff to predict or classify a disease rather than SVM, Extra Tress and Decision Tree, especially for a dataset that is similar to this research.

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