FETAL HEALTH PREDICTION USING CARDIOTOCOGRAPHIC DATA

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Abstract

The Goal 4 of many goals of Millennium Development, which is aiming to reduce under-five mortality by 2/3 rd in all over the world, could not efficiently reach its goal. The death of children in their first month of their birth is a prominent contributor to under-five mortality. One of the leading and main causes of perinatal mortality is intrapartum difficulties. CTGs (fetal cardiotocographs) are a type of monitoring device that can be used to detect the mothers with high-risk during the time of giving birth. The goal of this project is to see how accurate some machine learning algorithm techniques are in identifying high-risk fetuses using CTG data. The University of California Irvine Machine Learning Repository provided CTG data for two thousand and one hundred and twenty-six pregnant women of total. The data, which is contained in a Comma separated values file, includes baseline readings, accelerations, uterine contractions, and light decelerations, among other things. We have taken the dataset from the Kaggle. We are going to train our dataset using different machine learning classification models using CTG data. To forecast normal, suspect, and pathological fetal states, the sensitivity, precision, and F1 score for each class, as well as the overall accuracy of each model, will be calculated or determined. The models which we are going to use are K-Nearest Neighbors Classifier, Decision Tree Classifier, Random Forest Classifier, Gradient Boosting Classifier, XGBoost Classifier. The model that performs the best on the particular metrics will be finally chosen further. As a result, we anticipate that our initiative will aid in the classification of fetal health, hence reducing the infant and mother mortality.

Keywords: K-Nearest Neighbors Classifier, Decision Tree Classifier, Random Forest Classifier, Gradient Boosting Classifier, XGBoost Classifier, Python, Anaconda

1. Introduction

Children dying in their first month of life are a key contributor to under-five mortality. The Millennium Development Goal 4, which aimed to reduce mortality among children under the age of five by two-thirds globally, was not met. One of the primary drivers of perinatal death is intrapartum complications. We use CTG data to detect fetal health. CTGs are a type of foetal cardiotocograph that can be used to detect high-risk mothers during birth.Preterm birth complications (thirty-five percent), intrapartum events (twenty-five percent), and infections are the predominant causes of death in this population (e.g., sepsis or meningitis in 15 percent). Pakistan has one of the highest infant death rates in the world, at fort six per thousand live births, according to the UNICEF 2018

report. Cardiotocograph (CTG) can be classified (multi-class classifications) as normal, suspect, or pathological depending on the fetal heart rate (FHR), heart rate variability, accelerations, and decelerations, according to the International Federation of Gynaecology and Obstetrics (FIGO) recommendations.

Machine learning is not new to cancer research. Artificial neural networks (ANNs) and decision trees (DTs) have been used in cancer detection and diagnosis for nearly 20 years (Simes 1985; Maclin et al. 1991; Ciccheti 1992). Today machine learning methods are being used in a wide range of applications ranging from detecting and classifying tumors via X-ray and CRT images (Petricoin and Liotta 2004; Bocchi et al. 2004) to the classification of malignancies from proteomic and genomic (microarray) assays (Zhou et al. 2004; Dettling 2004; Wang et al. 2005). According to the latest PubMed statistics, more than 1500 papers have been published on the subject of machine learning and cancer. However, the vast majority of these papers are concerned with using machine learning methods to identify, classify, detect, or distinguish tumors and other malignancies. In other words machine learning has been used primarily as an aid to cancer diagnosis and detection (McCarthy et al. 2004). It has only been relatively recently that cancer researchers have attempted to apply machine learning towards cancer prediction and prognosis. As a consequence the body of literature in the field of machine learning and cancer prediction/prognosis is relatively small (<120 papers)

The fundamental goals of cancer prediction and prognosis are distinct from the goals of cancer detection and diagnosis. In cancer prediction/prognosis one is concerned with three predictive foci: 1) the prediction of cancer susceptibility (i.e. risk assessment); 2) the prediction of cancer recurrence and 3) the prediction of cancer survivability. In the first case, one is trying to predict the likelihood of developing a type of cancer prior to the occurrence of the disease. In the second case one is trying to predict the likelihood of redeveloping cancer after to the apparent resolution of the disease. In the third case one is trying to predict an outcome (life expectancy, survivability, progression, tumor-drug sensitivity) after the diagnosis of the disease. In the latter two situations the success of the prognostic prediction is obviously dependent, in part, on the success or quality of the diagnosis. However a disease prognosis can only come after a medical diagnosis and a prognostic prediction must take into account more than just a simple diagnosis (Hagerty et al. 2005)

Indeed, a cancer prognosis typically involves multiple physicians from different specialties using different subsets of biomarkers and multiple clinical factors, including the age and general health of the patient, the location and type of cancer, as well as the grade and size of the tumor (Fielding et al. 1992; Cochran 1997; Burke et al. 2005). Typically histological (cell-based), clinical (patient-based) and demographic (populationbased) information must all be carefully integrated by the attending physician to come up with a reasonable prognosis. Even for the most skilled clinician, this is not easy to do. Similar challenges also exist for both physicians and patients alike when it comes to the issues of cancer prevention and cancer susceptibility prediction. Family history, age, diet, weight (obesity), high-risk habits (smoking, heavy drinking), and exposure to environmental carcinogens (UV radiation, radon, asbestos, PCBs) all play a role in predicting an individual's risk for developing cancer (Leenhouts 1999; Bach et al. 2003; Gascon et al. 2004; Claus 2001; Domchek et al. 2003). Unfortunately these conventional "macro-scale" clinical, environmental and behavioral parameters generally do not provide enough information to make robust predictions or prognoses. Ideally what is needed is some very specific molecular details about either the

tumor or the patient's own genetic make-up (Colozza et al. 2005).

With the rapid development of genomic (DNA sequencing, microarrays), proteomic (protein chips, tissue arrays, immuno-histology) and imaging (fMRI, PET, micro-CT) technologies, this kind of molecular-scale information about patients or tumors can now be readily acquired. Molecular biomarkers, such as somatic mutations in certain genes (p53, BRCA1, BRCA2), the appearance or expression of certain tumor proteins (MUC1, HER2, PSA) or the chemical environment of the tumor (anoxic, hypoxic) have been shown to serve as very powerful prognostic or predictive indicators (Piccart et al. 2001; Duffy 2001; Baldus et al. 2004). More recently, combinations or patterns of multiple molecular biomarkers have been found to be even more predictive than single component tests or readouts (Savage and Gascoyne 2004; Petricoin and Liotta 2004; Duffy 2005; Vendrell et al. 2005) If these molecular patterns are combined with macro-scale clinical data (tumor type, hereditary aspects, risk factors), the robustness and accuracy of cancer prognoses and predictions improves even more. However, as the number of parameters we measure grows, so too does the challenge of trying to make sense of all this information.

In the past, our dependency on macro-scale information (tumor, patient, population, and environmental data) generally kept the numbers of variables small enough so that standard statistical methods or even a physician's own intuition could be used to predict cancer risks and outcomes. However, with today's high-throughput diagnostic and imaging technologies we now find ourselves overwhelmed with dozens or even hundreds of molecular, cellular and clinical parameters. In these situations, human intuition and standard statistics don't generally work. Instead we must increasingly rely on nontraditional, intensively computational approaches such as machine learning. The use of computers (and machine learning) in disease prediction and prognosis is part of a growing trend towards personalized, predictive medicine (Weston and Hood 2004). This movement towards predictive medicine is important, not only for patients (in terms of lifestyle and quality-of-life decisions) but also for physicians (in making treatment decisions) as well as health economists and policy planners (in implementing large scale cancer prevention or cancer treatment policies). Given the growing importance of predictive medicine and the growing reliance on machine learning to make predictions, we believed it would be of interest to conduct a detailed review of published studies employing machine learning methods in cancer prediction and prognosis. The intent is to identify key trends with respect to the types of machine learning methods being used, the types of training data being integrated, the kinds of endpoint predictions being made, the types of cancers being studied and the overall performance of these methods in predicting cancer susceptibility or patient outcomes. Interestingly, when referring to cancer prediction and prognosis we found that most studies were concerned with three "predictive" foci or clinical endpoints: 1) the prediction of cancer susceptibility (i.e. risk assessment); 2) the prediction of cancer recurrence and 3) the prediction of cancer survivability. We also found that almost all predictions are made using just four types of input data: genomic data (SNPs, mutations, microarrays), proteomic data (specific protein biomarkers, 2D gel data, mass spectral analyses), clinical data (histology, tumor staging, tumor size, age, weight, risk behavior, etc.) or combinations of these three. In comparing and evaluating the existing studies a number of general trends were noted and a number of common problems detected. Some of the more obvious trends include a rapidly growing use of machine learning methods in cancer prediction and prognosis (Figure 1), a growing reliance on protein markers and

microarray data, a trend towards using mixed (proteomic + clinical) data, a strong bias towards applications in prostate and breast cancer, and an unexpected dependency on older technologies such as artificial neural networks (ANNs). Among the more commonly noted problems was an imbalance of predictive events with parameters (too few events, too many parameters), overtraining, and a lack of external validation or testing. Nevertheless, among the better designed and better validated studies it was clear that machine learning methods, relative to simple statistical methods, could substantially (15- 25%) improve the accuracy of cancer susceptibility and cancer outcome prediction. In other words, machine learning has an important role to play in cancer prediction and prognosis.

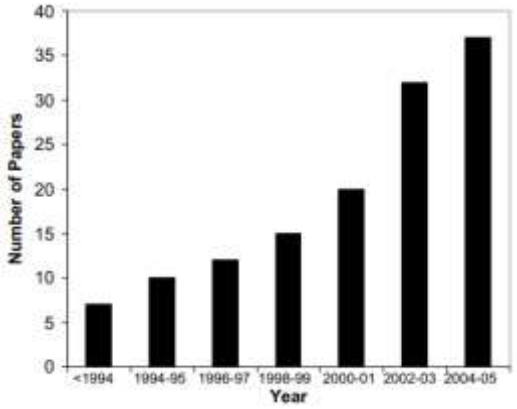


Figure 1. A histogram showing the steady increase in published papers using machine learning methods to predict cancer risk, recurrence and outcome. The data were collected using a variety of keyword searches through PubMed, CiteSeer, Google Scholar, Science Citation Index and other online resources. Each bar represents the cumulative total of papers published over a two year period. The earliest papers appeared in the early 1990's.

2. LITERATURE SURVEY

[1]A medical issue in the mother (such as diabetes or high blood pressure) or a disease that may impact the baby's health or development can complicate some pregnancies. An accurate test that could be utilised throughout pregnancy could be advantageous if these infants with potential issues could be detected and if there were appropriate measures to enhance the outcomes. Cardiotocography (CTG) is an ultrasound transducer implanted on the mother's abdomen [2] that provides a continuous computerised record of the baby's heart rate. [3] 'Electronic fetal monitoring' is another name for it (EFM).[4] In a recent Cochrane study, Grivell et al. found that computerised CTG (related risk: 0.20, 95 percent confidence interval [CI]: 0.04–0.88) reduced perinatal mortality significantly more than traditional CTG (relative risk: 0.20, 95 percent confidence interval [CI]: 0.04–0.88). The researchers wanted to determine if utilising CTG throughout pregnancy could help newborns have better outcomes by identifying individuals who had abnormalities. It looked for trials that included women who were at high risk of problems as well as those who were at low risk. Six studies were included in the review, with all of the women being at a higher risk of problems. Four of the investigations were conducted in the 1980s, while the other two were completed in the late 1990s [5]. The studies that were included were of poor quality. Although the findings seemed encouraging when computerised interpretation of the CTG trace was applied, no changes in outcomes were detected (low/very low-quality evidence). CTG monitors, associated technologies, and the way midwives and obstetricians treat women with various pregnancy problems have all evolved over time. This indicates that more research is needed to establish if antenatal CTG, particularly computerised CTG, can improve outcomes for newborns at higher risk of problems.

[6] Use of Machine Learning Algorithms for Prediction of Fetal Risk using Cardiotocographic Data" from Department of Paediatrics and Child Health, The Aga Khan

University, Department of Artificial Intelligence, Ephlux Pvt Ltd., Karachi, Pakistan, Cardiology Care for Children, Pennsylvania, USA was published in 2019.

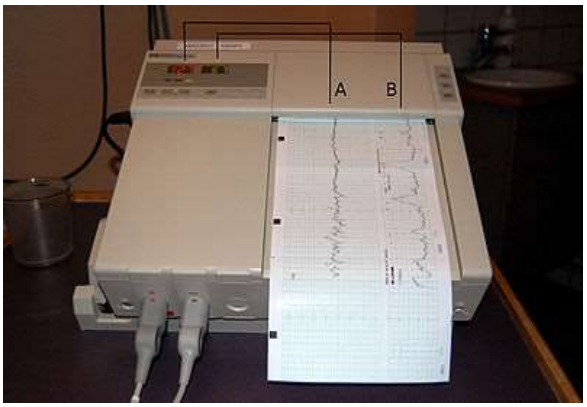
Same dataset, CTG data of two thousand and one hundred and twenty-six pregnant women were collected from the University of California Irvine Machine Learning Repository has been used.

Various ML algorithms were trained with CTG data present in dataset and model's highest accuracy which was received was ninety two percent. The percentage of time with attributes such as abnormal short term variability, percentage of time with abnormal long term variability, number of accelerations per second (AC), mean value of short term variability, and uterine contractions were the most prominent risk factors depicted by their all ten machine learning models, according to their research. These five criteria out of twenty-one were found to have the most influence on foetal state prediction.

In recent years several factors have been identified that have been regarded as indicators of disease progression in breast cancer. Since the original observation by that tumor dissemination to axillary lymph nodes and the number of nodes involved are related to breast cancer prognosis, tumor size and cellularity, its location, histological differentiation, the status of steroid and growth factor receptors, among others, have been used as indicators of tumor progression and prognosis. The detection of tumor dissemination to the regional lymph nodes is of paramount importance in the management of the disease. Several surrogates for histological assessment of axillary lymph nodes are currently available which are able to predict nodal metastasis with varying degrees of success. Nonetheless, histological assessment has remained as the accepted standard method, and node positive (even one node positive) patients are generally offered chemotherapy, the case for this in the node negative patients being far less. DNA ploidy has been described as an independent prognostic factor in ovarian cancer and nondiploid status has been correlated with early recurrence of endometrial carcinomas, as well as with the degree of myometrial invasion by the tumor Diploid DNA has been associated with less aggressive carcinomas of the pancreas, and higher DNA ploidy correlated with decreased median survival This has also been demonstrated in colorectal cancer [7] and hepatocellular carcinoma [8]. Azua et al. [9] have shown that DNA quantification possesses considerable predictive value for patient survival in prostatic adenocarcinoma. Equally, several studies may be cited where no prognostic value has been attributed to DNA ploidy. Thus in carcinoma of the gall bladder DNA ploidy correlated with neither tumor stage nor survival [10]. It possessed no prognostic value in lung cancer [11]. More pertinent to this study is the report by. [12] which relates to the measurement of DNA ploidy in fine-needle aspirates (FNA's) of breast cancer patients. They found DNA quantification to be significantly related to survival times. In another study of a large series of breast cancer, DNA ploidy did relate to lymph node metastasis and early death [13]. In that study oestrogen receptor (ER) negative status correlated even more significantly. However, when the patients were stratified according to ER status, the correlation with DNA ploidy was reduced markedly, suggesting that it is not an independent prognostic indicator. Numerous other investigations on the prognostic values of DNA content have been reviewed and a consensus statement has been published by [14], which confirm that there is no evidence for regarding DNA aneuploidy as an independent prognostic factor. While this has been confirmed in other studies [15], [16],

an increased incidence of aneuploidy and higher Sphase fractions are associated with oestrogen and progesterone receptor negative tumors, and tumors from patients with metastatic disease in axillary lymph nodes [15]. This study also reported that S-phase fraction (SPF) and DNA ploidy in combination with other prognostic markers were powerful predictors of early relapse. Indeed, DNA hyperdiploidy has been found to correlate with favorable prognosis in childhood lymphoblastic leukemia [17]. There is also some disagreement with regard to the significance of the size of the SPF as a prognostic factor. Camplejohn et al. [16] have stated that SPF was a significant marker for overall survival, relapse-free survival and survival after disease relapse as well. SPF in their view is an independent prognostic marker. However, SPF has not been regarded as a significant prognostic factor in some tumor types but in others

it is associated with higher DNA ploidy and other features such as mitotic index, Ki67 staining and p53 expression status [18]–[20]. The divergence of opinion concerning the prognostic significance of these cellular features could be attributed to the degree of sophistication of statistical techniques employed and the difficulties associated with assigning weighting to individual cellular attributes or dissecting out specific features in



order to assess their individual merits as prognostic factors. We demonstrated in previous studies that artificial neural networks (ANN's) are capable of predicting lymph node

Figure 2. Traditional CTG

metastasis in breast cancer patients using measurements relating to the expression of specific markers [21], [22]. Here we show that cellular features such as DNA ploidy, size of the S-phase fraction (SPF), cell cycle distribution, and nuclear pleomorphism of breast cancer FNA cells measured by image cytometry, can be analyzed using ANN's and successfully used to predict subclinical metastatic disease. During pregnancy and childbirth, cardiotocography (CTG) is a technique for examining the fetal heartbeat and uterine contractions. A cardiotocograph is the machine that performs the monitoring.

Cardiotocography (CTG) is a procedure that involves placing an ultrasound transducer on the mother's abdomen and continuously measuring the fetal heart rate. CTG is commonly used to check fetal well-being during pregnancy, especially in pregnancies with a higher risk of problems.

Currently existing models are good and efficient at forecasting the pathological state of the fetus, but they aren't very efficient at predicting the suspicious state. So that is something which we want to introduce in our proposed system.

4 Methodology

The goal of our proposed method is to create a machine learning model that can detect high-risk foetuses (both suspicious and pathological) with the same accuracy as highly educated medical professionals.

Our framework uses computerized CTG.

In a recent Cochrane study, Grivell et al. found that computerised CTG (related risk: 0.20, 95 percent confidence interval [CI]: 0.04–0.88) reduced perinatal mortality significantly more than traditional CTG (relative risk: 0.20, 95

percent confidence interval [CI]: 0.04–0.88). [3] However, because the trials were of moderate quality, more research is needed to determine the influence of CTG on perinatal outcomes.

When computerised CTG was compared to traditional CTG, perinatal mortality was found to be much lower with computerised CTG (RR 0.20, 95 percent CI 0.04 to 0.88, two studies, 0.9 percent versus 4.2 percent, 469 women, moderate quality evidence). To make a diagnosis, AI/ML will make use of the mathematical algorithms and a number of data points from the human body. These models have been used to in large number of projects, like increase the accuracy of forecasting cancer recurrence and death, cardiovascular risk prediction, and the diagnostic accuracy of radiological investigations like Computed tomography scans which are also known as CT scans and Magnetic resonance imaging (mri). Experts of medical and engineering have been working to automate this CTG interpretation, culminating in less errors in outcome classification.

6 Results

6.1. Description of the data:

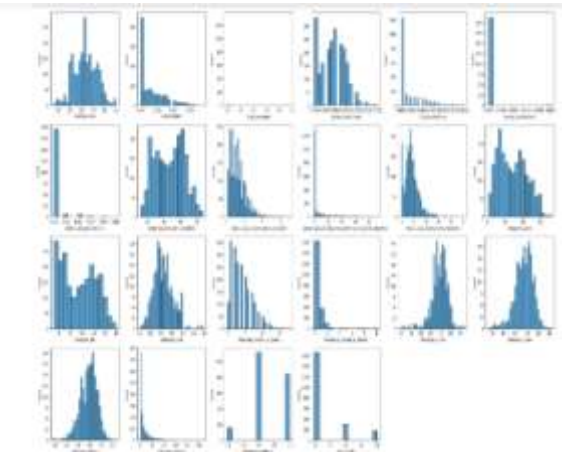


Figure 3. Description of data

We have 21 features and One Label column.

6.2. Boxplot

Below images shows our data before and after removing outliers.

Initially our dataset contains lot of outliers. After performing removeOutlier function, outliers have been decreased.

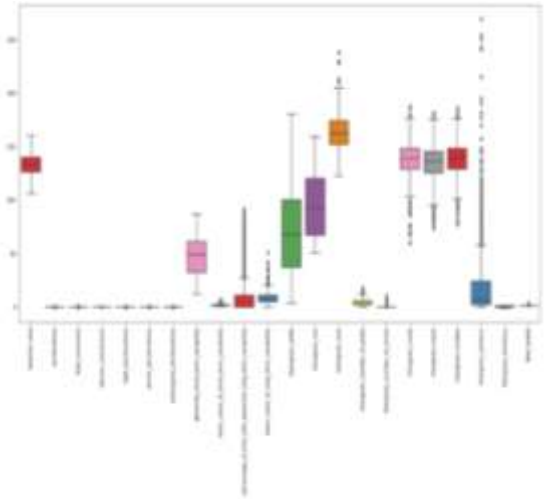


Figure 4. Data with outliers

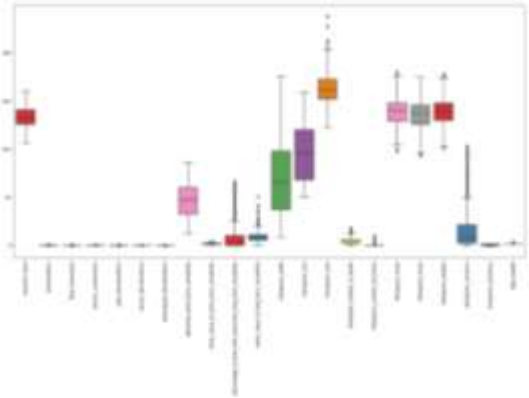


Figure 5. Data after removing outliers

6.3. Correlation Heatmap:

We can see that the below features from dataset shows the positive correlation:

baseline_value

abnormal_short_term_variability

prolongued_decelerations,

percentage_of_time_with_abnormal_long_term_variability

histogram_min

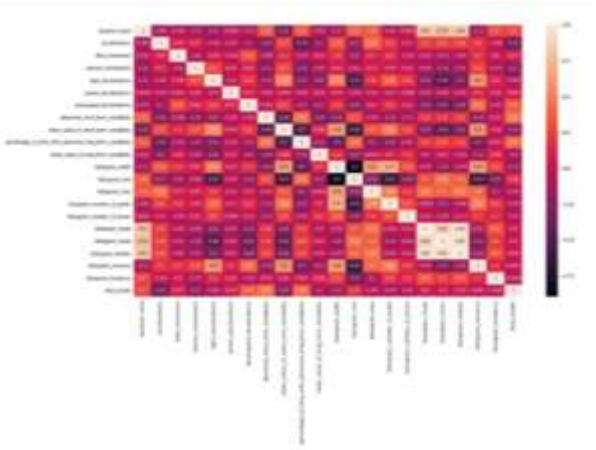


Figure 6. Correlation Heatmap

6.4. Comparision of accuracies for following models can be seen below:

KNN scores
0.9547325102880658

	precision	recall	f1-score	support
1.0	0.98	0.90	0.94	421
2.0	0.91	0.97	0.94	396
3.0	0.97	1.00	0.99	398
accuracy			0.95	1215
macro avg	0.96	0.96	0.95	1215
weighted avg	0.96	0.95	0.95	1215

[[379 36 6]
[8 383 5]
[0 0 398]]
****
****
****

DT scores
0.9777777777777777

	precision	recall	f1-score	support
1.0	1.00	0.94	0.97	421
2.0	0.95	1.00	0.97	396
3.0	0.99	1.00	0.99	398
accuracy			0.98	1215
macro avg	0.98	0.98	0.98	1215
weighted avg	0.98	0.98	0.98	1215

[[395 22 4]
[1 395 0]
[0 0 398]]
****
****
****

RFC scores
0.9843621399176955

	precision	recall	f1-score	support
1.0	1.00	0.96	0.98	421
2.0	0.96	1.00	0.98	396
3.0	0.99	1.00	1.00	398
accuracy			0.98	1215
macro avg	0.98	0.98	0.98	1215
weighted avg	0.98	0.98	0.98	1215

[[403 16 2]
[0 395 1]
[0 0 398]]
****
****
****

GBC scores
0.9703703703703703

	precision	recall	f1-score	support
1.0	0.98	0.95	0.96	421
2.0	0.95	0.97	0.96	396
3.0	0.98	0.99	0.99	
accuracy			0.97	1215
macro avg	0.97	0.97	0.97	1215
weighted avg	0.97	0.97	0.97	1215

[[399 17 5]
[7 384 5]
[0 2 396]]
****
****
****

XGB scores
0.9868312757201646

	precision	recall	f1-score	support
1.0	1.00	0.96	0.98	421
2.0	0.98	1.00	0.99	396
3.0	0.99	1.00	0.99	398
accuracy			0.99	1215
macro avg	0.99	0.99	0.99	1215

weighted avg 0.99 0.99 0.99 121
5
[[406 10 5]
[0 395 1]
[0 0 398]]
****
****
****

6.5. Table shows accuracies of all models in descending order.

	Model	Accuracy	Train_acc
4	XGB	0.986831	0.999725
2	RFC	0.984362	0.999725
1	DT	0.977778	0.999725
3	GBC	0.970370	0.986271
0	KNN	0.954733	0.971993

Figure 7. Accuracies

6.6. XGB Classifier:

This is the classification report of the XGB classifier.

We can see the confusion matrix.

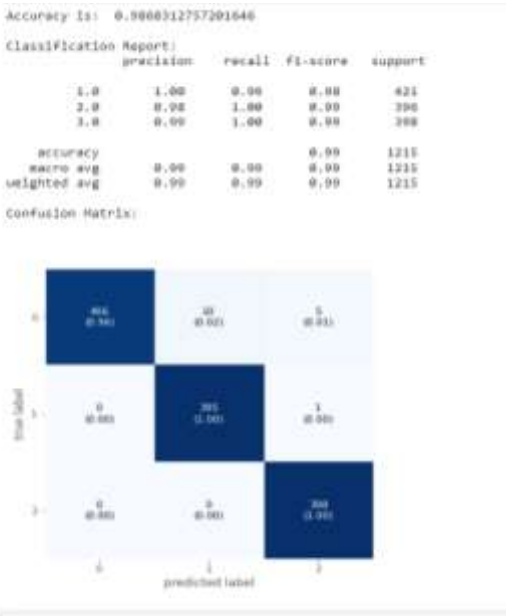


Figure 8. Classification report of XGB

6.7. Random Forest classifier:

Random forest helps in getting the feature importance. Figure 19 shows the classification report of random forest classifier and it shows the confusion matrix of the same.

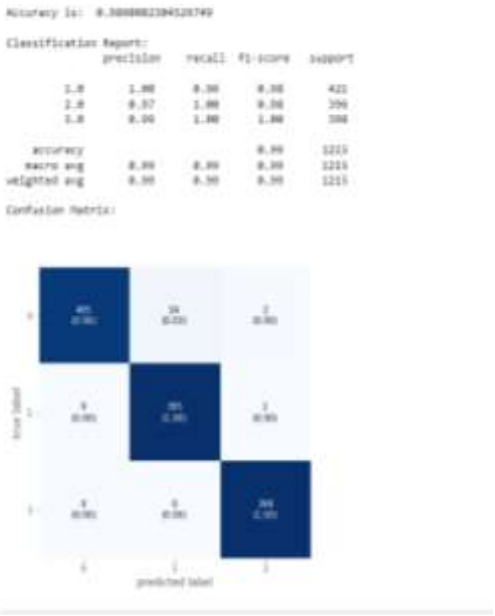


Figure 9. Classification Report of Random Forest

6.8. Feature importance

There are 21 features in total in our dataset Below image shows the importance of all 21 features in identifying the fetal health.

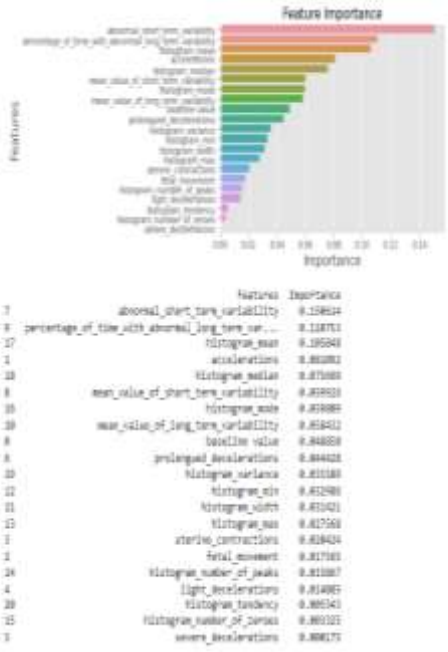


Figure 10. Feature importance

6.9. Detecting fetal health by giving input.

We pass an array as input. Array contains values of all 21 features. Based on those features we can predict the fetal health. We can

predict whether fetal health is Normal/Suspect/Pathological.

Figure 11. Prediction of fetal health.

Conclusion

The classification model developed using XGBoost technique had the highest prediction accuracy for an adverse fetal outcome. This project deploys various ML algorithms to predict fetal health from the cardiotocographic (CTG) data by labelling the health state into normal, suspect, and pathology. Our project aim is to remove all the outliers in the data which will boost the accuracy. This tool can be used to decrease perinatal mortality. Our framework helps in reducing mortality of the fetus, which is more prevalent in developing and underdeveloped countries.

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