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PPH (Postpartum Hemorrhage) is defined as blood loss greater than or equal to 1000 ml following delivery. PPH is among the leading causes of maternal death; however, the existing predictive mechanism used by UNC-CH hospital is oversensitive by flagging too many patients as high risk and is generally abandoned by medical providers. This study is aimed to applying the trending machine learning classifying models to better predict the risk of PPH. Actual dataset was extracted and integrated from EHRS (Electronic Health Record System) with 12 variables considered to be highly relevant to PPH occurrence. Six machine learning models including Logistic Regression, Decision Trees, Random Forest, KNN, SVM and ANN (a deep learning model) were tried and compared in terms of their predicting accuracy and other metrics such as precision and recall. Random Forest stood out as the best model with the accuracy being 89%.

Headings:

Machine Learning

Predictive Model Building

Postpartum Hemorrhage Risk Factors

Exploratory Data Analysis

COMPARATIVE STUDY OF MACHINE LEARNING MODELS TO PREDICT PPH

by
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BACKGROUND

Blood loss in the immediate postpartum period is expected for all women; however, an excessive amount can have serious consequences and is among the leading causes of maternal mortality globally (Say L et al., 2014). There is no consensus regarding what constitutes excessive blood loss. The most cited definition is specified by the World Health Organization (WHO), defining PPH as ≥ 500 ml blood loss within 24 hours of a vaginal birth and ≥ 1000 ml blood loss following a cesarean birth (WHO, 2012; Arulkumaran, Mavrides and Penney, 2009). The criteria of PPH was formed in the 1950s and 1960s, when articles provided rationale for the 500 ml threshold (De Boer, 1955; Newton, Egli, Gifford and Hull, 1961; Pritchard, 1965; Theobald, 1950). However, there is little published evidence indicating that this amount can result in PPH-related morbidity (Kerr, 2017) and evidence from studies that treated women at later thresholds of bleeding (e.g. 700 ml) suggests that many women who bleed 500 ml may be fine without intervention (Blum et al., 2010; Winikoff et al., 2010). Notably, in many scenarios all over the world, the 500 ml definition continues to be a guiding norm that is used in clinical practice guidelines, program evaluation approaches and research studies. Nonetheless, the American College of Obstetricians and Gynecologists (ACOG) published their definition of PPH to be “blood loss greater than or equal to 1000 ml or blood loss accompanied by signs or symptoms of hypovolemia”(Menard, Main, and Currihan, 2014). Thus, in our project, we will use 999 ml as the threshold to define PPH and label the datapoints

Thanks to advances in the management of postpartum bleeding (e.g, uterotonic medications and transfusion medicine), maternal death from PPH trended downward between 1994 and 2006 (Callaghan, Kuklina and Berg, 2008). Despite the lives saved, PPH remains a major contributor to maternal morbidity (Callaghan, Kuklina and Berg, 2010), but there is evidence this tragedy can be prevented. In case reviews of near-miss and severe maternal morbidity within one perinatal network of U.S. hospitals, experts concluded that 54% of cases were potentially preventable. In particular, the panel pointed out that 43% of the preventable cases involved a ‘delay in diagnosis.’ (Berg et al., 2005) Another review of pregnancy-related deaths conducted by an expert panel showed that maternal deaths involving hemorrhage were mostly preventable (Glover 2003).

On Jul. 26 2018, an investigative series titled “Deadly Deliveries” was published by USA Today (<https://www.usatoday.com/deadly-deliveries/interactive/how-hospitals-are-failing-new-moms-in-graphics/>). One article in the series highlighted several NC hospitals who are not adequately preventing PPH, so this is a very visible patient safety issue. UNC Medical Center (UNCMC) currently uses a risk assessment tool embedded in Epic to assess hemorrhage risk for every patient, which follows the recommendation of the Alliance for Innovation on Maternal Health (AIM). This tool is based on guidance from the PPH project (pphproject.org) conducted by AWHONN (Association of Women’s Health, Obstetric and Neonatal Nurses). Based on the tool’s assessed risk of the patient, clinical decisions are made and ‘anticipatory interventions’ are recommended for those patients deemed high risk. Examples of ‘anticipatory interventions’ are: blood sample type and cross match, heightened postpartum assessment surveillance (requiring

increased nursing workload), insertion of second large bore IV, and preparing the OR team.

MOTIVATION

Having a reliable PPH risk assessment tool is the first step in decreasing rate of maternal deaths from hemorrhage, as well as reducing blood transfusions, length of stay, and ICU admissions.

Nevertheless, providers perceive the AWHONN Method to be doubtful because it is oversensitive, flagging too many of the patients as high risk; they assert that overreacting to false positives leads to overutilization of resources, since implementing ‘anticipatory interventions’ for patients who are improperly flagged as high risk leads to tremendous waste (blood bank time and cost, nursing time, etc.) and causes ‘alarm fatigue,’ as clinicians are less likely to heed the warning of an over-sensitive system. Another reason providers are doubting the predictive capability of the current AWHONN tool in Epic is because it indicates a sharp drop in risk acuity immediately after delivery: about half of high risk patients suddenly become low risk. When queried, an AWHONN representative stated, “Since some factors remain constant and others involve interventions that occur during the trajectory of intrapartum and postpartum care, transitioning from high to low risk is not uncommon.” Clinicians are skeptical of this response, since conventional wisdom indicates that risk for hemorrhage is cumulative throughout admission and should not reduce. Clinicians would prefer to use resources already in place and in the EHRS workflow (via Epic) to explore a stand-alone tool or module outside of Epic - and this paper explores the use of Machine Learning for prediction of PPH.

Machine learning (ML) based prediction of clinical outcomes can be used for appropriate decision making and can lead to better patient care. Machine learning prediction model can accurately predict the risk of PPH as categorized into three classes, namely, ‘no’, ‘low risk’ and ‘high risk’. ML also has advantages compared with traditional statistical models in terms of high power and accuracy to predict disease. However, there is no specific algorithm that performs better for the prediction model. We, therefore, conducted most commonly used algorithms and compared their performance in the prediction of PPH.

METHOD

Data Collection

Data was collected from EPIC Clarity, Epic’s relational database for analytical reports that was created via ETL(Extract, Transform and Load) from EPIC Chronicles (Epic’s LIVE hierarchical database). Records of patients who delivered their babies from “NC Women’s Hospital” at UNC-CH Medical Center in Chapel Hill, NC during Dec. 2018 to May 2019 inclusive was extracted and de-identified. As to which variables should be queried and retrieved from the database, professional opinions from medical providers from UNC-CH Women’s Hospital were consulted and published papers in this regard were reviewed (Kramer et al., 2013; Oyelese and Ananth, 2010; Briley et al., 2014; Stones, Paterson and Saunders, 1993; Tessier and Pierre, 2004). The following variables are included in the dataset thus retrieved:

- Mom_ID: masked ID for Mom
- race: mom’s race(Latino, NL White, NL Black, NL Asian, NL Other)
- age: mom’s age at delivery

- gravida: the total number of confirmed pregnancies that a woman has had, regardless of the outcome.
- para: the number of births that a woman has had after 20 weeks gestation.
- PUS(prior_uterine_surgery): 1 (=yes) or 0 (=no) [obtained if CS_Indications includes “Prior Uterine Surgery”]
- multiple: 0 (=no, or singleton) or 1 (=yes to multiple, twins or triplets or more)
- MBP(mom_bmi_pg): mom’s BMI pre-gravida
- prev_cs: 0 (=no previous C-Section) or 1 (=yes, mom had at least one previous C-Section)
- DSLC(days_since_last_cs): days since last C-Section
- GA: gestational age (if multiples, is max ga) – it has a couple of NULLs
- deltype: delivery type (if multiples, C-Section if one of the deliveries was a C-Section, Vaginal otherwise)
- induction: 0 (=no induction was performed on delivery) or 1 (=yes for induction)
- BL_total= Blood Loss Total – it is the sum of BL_surgery and BL_flowsheet_EBL

Machine Learning

The primary objective of this study is to select potential prognostic factors to predict

PPH. To this end, the entire prediction model building was divided into four steps:

First, the raw data was preprocessed. This process consisted of EDA, data cleaning,

missing data handling, data integration, data transformation, and data reduction. Second,

I identified the most relevant variables which can augment the effectiveness of the predictive model. Third, the models were built. Finally, the classification models were evaluated using confusion matrices, ROC, precision, recall, f1 score, and cross validation score.

EDA(Exploratory Data Analysis)

As is demonstrated by Figure 1, there are 1988 instances in the dataset, which means that it is fairly small by Machine Learning standards, but it's perfect to get started. More datapoints will be available along with the progress of ETL effort and this study is meant to test the performance of various machine learning classifying algorithms in preparation for the final model building that can make prediction of PPH risks against streamlined dataset. Notice that the para and ga attributes have null values, which necessitates dropping null values.

All attributes are numerical, except the race and deltype fields. Their type is object, so it could hold any kind of Python object, but since they are loaded from a CSV file so they must be a text attribute. Most machine learning algorithms prefer to work with numbers, so the text labels will be converted to numerical ones using LabelEncoder, a transformer from python library Scikit-Learn.

```

1 data.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1988 entries, 0 to 1987
Data columns (total 13 columns):
race          1988 non-null object
age           1988 non-null int64
gravida       1988 non-null int64
para          1987 non-null float64
PUS           1988 non-null int64
multiple      1988 non-null int64
MBP           1988 non-null float64
prev_cs       1988 non-null int64
DSLCL         1988 non-null int64
GA            1982 non-null float64
deltypes      1988 non-null object
induction     1988 non-null int64
BL_total      1988 non-null float64
dtypes: float64(4), int64(7), object(2)

```

Figure 1: Data information

Figure 2 illustrates the summary of the numeric attributes. The count, mean, min, and max rows are self-explanatory. Note that the null values are ignored. The std row shows the standard deviation, which measures how dispersed the values are. The 25%, 50%, and 75% rows show the corresponding percentiles: a percentile indicates the value below which a given percentage of observations in a group of observations falls.

All fields on the data set are for the current delivery except: PUS, prev_cs, DSLC. It is worth mentioning that DSLC will be 0 when the woman never had a C-Section, which does not make sense as this attribute measures the extent of recovery from the previous C-Section; thus the bigger the number is, the healthier the patient is supposed to be. This being the case, zero may be interpreted as extremely poor physical condition on the part of the patient as if the patient had received C-Section the day before the delivery. The remedy of this issue is as follows: transform the zero values to the maximum number of

this variable, since those who have never had C-Section should be considered the sturdiest ones, thus assigned the largest number.

The target variable is BL_total, which is originally a continuous number recording the actual amount of PPH. According to the definition of PPH published by the ACOG, we split the cases of this field into two classes, namely, PPH (1) with values greater than or equal to 1000 ml and none-PPH (0) with values less than 1000 ml.

	age	gravidita	para	PUS	multiple	MBP	prev_cs	DSLCL	GA	induction	BL_total
count	1988.000000	1988.000000	1987.000000	1988.000000	1988.000000	1988.000000	1988.000000	1988.000000	1982.000000	1988.000000	1988.000000
mean	29.926559	2.725855	2.170106	0.007545	0.027666	19.700201	0.189135	360.924044	38.143794	0.384809	449.087676
std	5.955432	1.759808	1.293820	0.086557	0.164055	14.507455	0.391714	950.097456	3.036877	0.486673	578.158804
min	14.000000	1.000000	1.000000	0.000000	0.000000	0.000000	0.000000	0.000000	16.000000	0.000000	0.000000
25%	26.000000	1.000000	1.000000	0.000000	0.000000	0.000000	0.000000	0.000000	38.000000	0.000000	130.000000
50%	30.000000	2.000000	2.000000	0.000000	0.000000	22.700000	0.000000	0.000000	39.000000	0.000000	300.000000
75%	34.000000	4.000000	3.000000	0.000000	0.000000	29.100000	0.000000	0.000000	40.000000	1.000000	565.500000
max	50.000000	12.000000	10.000000	1.000000	1.000000	91.000000	1.000000	6686.000000	42.000000	1.000000	8649.000000

Figure 2: Summary of each numeric attribute

Another quick way to get a feel of the type of data you are dealing with is to plot a histogram for each numerical attribute. A histogram shows the number of instances (on the vertical axis) that have a given value range (on the horizontal axis).

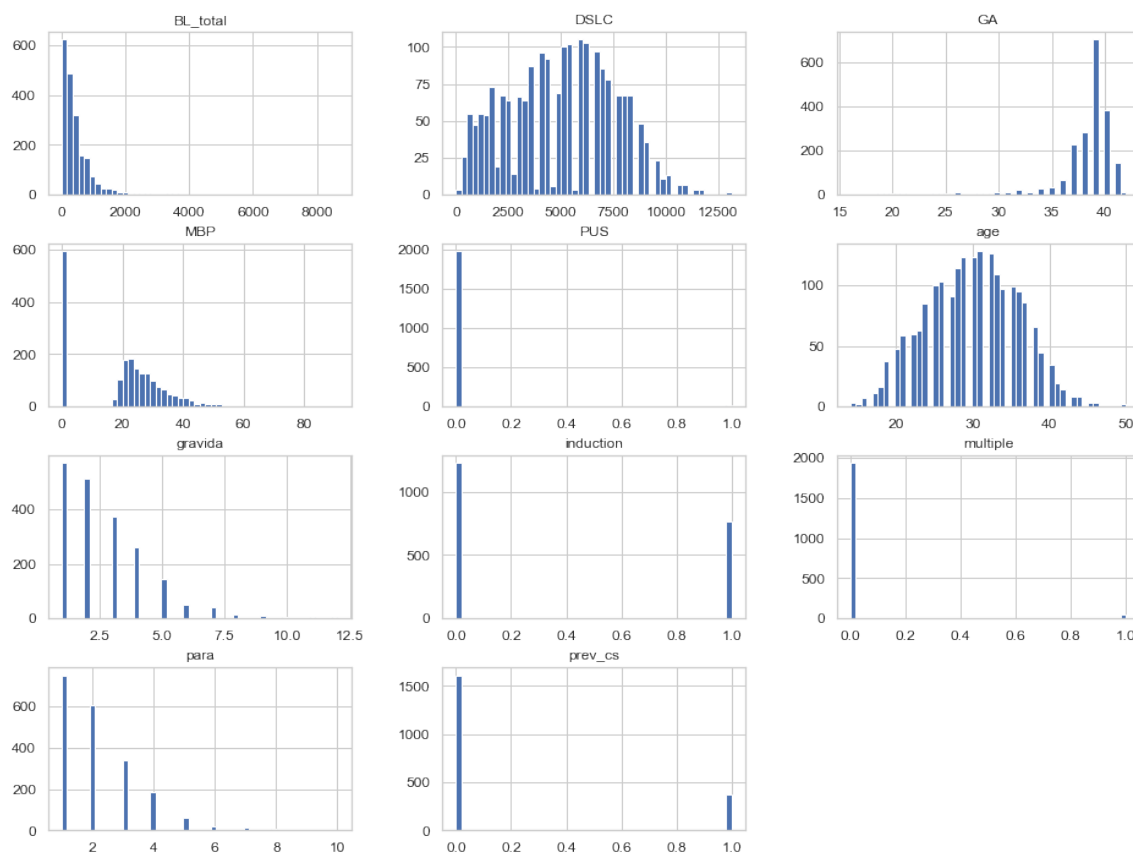


Figure 3: The histogram of each numeric attribute

From Figure 3, we can see that these attributes have very different scales. With few exceptions, Machine Learning algorithms don't perform well when the input numerical attributes have very different scales. This is the case for the PPH data: the total number of DSLC ranges from about 312 to 6687, while the age only range from 14 to 50. Note that scaling the target values is generally not required.

There are two common ways to get all attributes to have the same scale: *min-max scaling* and *standardization*.

Min-max scaling (many people call this *normalization*) is quite simple: values are shifted and rescaled so that they end up ranging from 0 to 1. We do this by subtracting the min

value and dividing by the max minus the min. Scikit-Learn provides a transformer called `MinMaxScaler` for this. It has a `feature_range` hyperparameter that lets you change the range if you don't want 0–1 for some reason.

Standardization is quite different: first it subtracts the mean value (so standardized values always have a zero mean), and then it divides by the standard deviation so that the resulting distribution has unit variance. Unlike min-max scaling, standardization does not bound values to a specific range, which may be a problem for some algorithms (e.g., neural networks often expect an input value ranging from 0 to 1). However, standardization is much less affected by outliers. Scikit-Learn provides a transformer called `StandardScaler` for standardization.

Standardization is employed in our study to normalize the data in light of the fact that for some variables such as DSLC, a majority of values are of great difference with the other values.

Another outstanding finding from Figure 3 is that there are many zeros in the MBP attribute, which doesn't make sense. After consulting the data manager, it turned out that these zeros are actually missing values. I will use median value of this variable to fill these missing ones, as is the common practice of data preprocessing for machine learning algorithms.

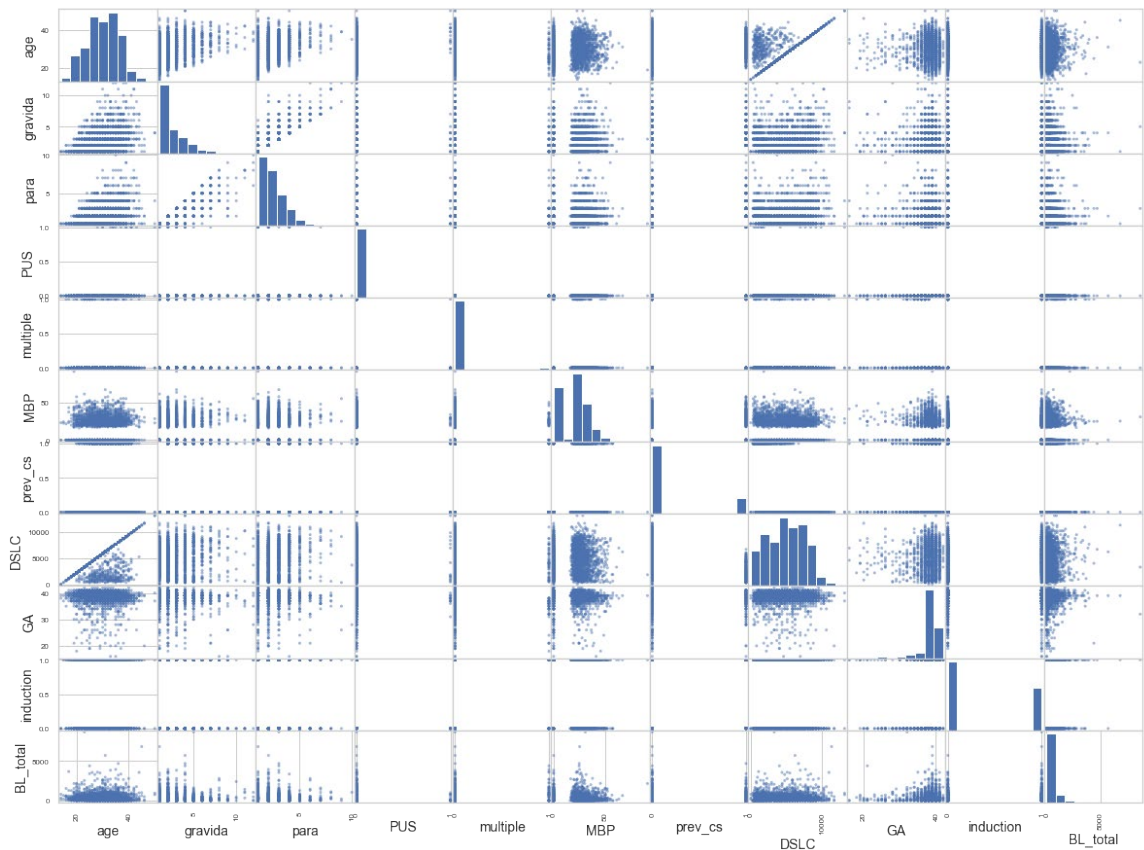


Figure 4: Scatter matrix of correlation among attributes

One essential task of EDA is to explore the correlation of each attribute to others. The main diagonal (top left to bottom right) would be full of straight lines if Pandas plotted each variable against itself, which would not be very useful. So instead Pandas displays a histogram of each attribute, as is shown in Figure 4. The less dispersed the points are, the more correlated the two variables are. From this figure, we can see that the most promising variable to predict PPH are age and DSLC. Notably, para and gravida are the least correlated with other features, which means they are the variables that contribute new information not being captured by other variables.

However, categorical features are not included in this figure, so the next step is to convert the categorical variables into numeric using get_dummies function from python. After the dummification, more in-depth analysis can be conducted.

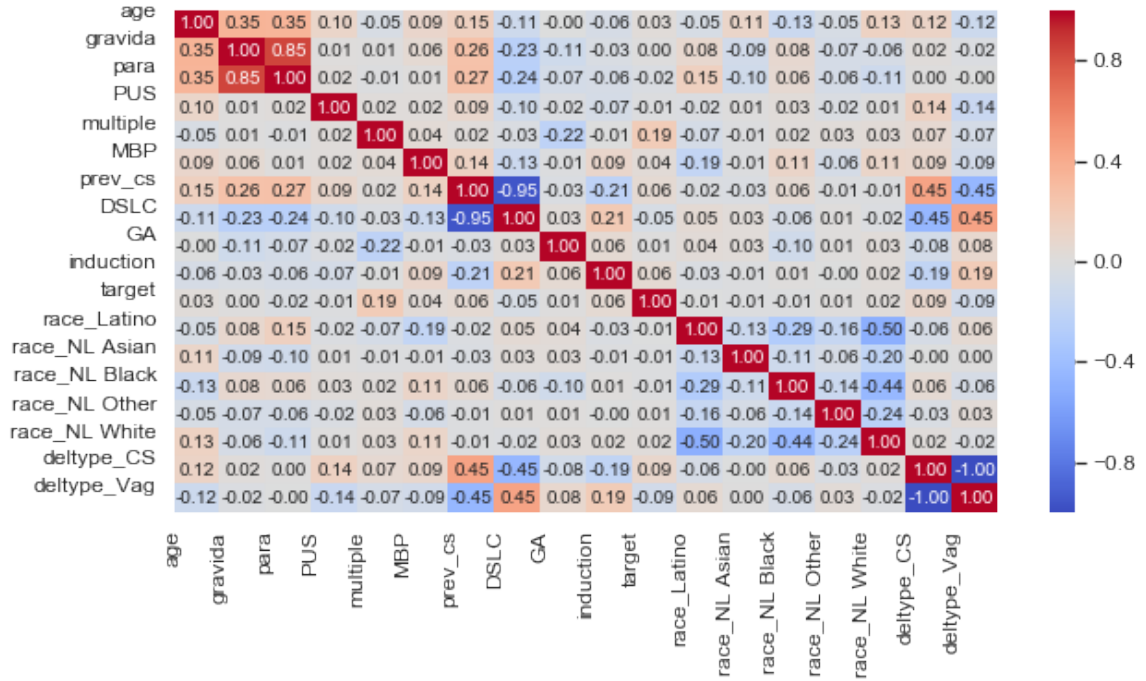


Figure 5: Correlation between each attribute



Figure 6: Correlation between each attribute based on chi-square/chi-contingency

Figure 5 depicts the correlation based on the *standard correlation coefficient* (also called *Pearson's r*) between every pair of attributes using the `corr()` method. The correlation coefficient ranges from -1 to 1 . When it is close to 1 , it means that there is a strong positive correlation. When the coefficient is close to -1 , it means that there is a strong negative correlation. Finally, coefficients close to zero mean that there is no linear correlation. The attribute `target` is transformed from `BL_total`, splitting the continuous values into two classes based on the definition of PPH stipulated by ACOG.

To plot Figure 6, I have created a function that returns correlation value based on *chi-square/chi-contingency*, this ranges from 0 to 1 . Generally, *chi-square* is a non-parametric test that is used to show association between two qualitative variables (like

deltypes and race); while correlation (*Pearson's r*) is used to test the correlation between two real-valued variables (like BMI and age).

It can be clearly seen from the two heat maps that variables generally have low correlation scores with the target variable, with the highest ones being 0.19 and 0.22, which doesn't bode well for the later machine learning results. Nonetheless, it has to be pointed out that the above correlation coefficients only measure linear correlations ("if x goes up, then y generally goes up/down"). It may completely miss out on nonlinear relationships (e.g., "if x is close to zero then y generally goes up").

Data preprocessing

Data cleaning: All variables will be removed that contained missing values accounting for more than 50% of the entire data points. If the variable contains missing values, occupying less than 5% of the number of datapoints, we will fill it up with median value - this is used as a common approach when dealing with missing data in machine learning (Peng and Lei, 2005). Scikit-Learn provides a handy class to take care of missing values: *SimpleImputer*. We can fit the imputer instance to the dataset using the `fit()` method. The imputer has simply computed the median of each attribute and stored the result in its `statistics_` instance variable. Then, we can use this "trained" imputer to transform the dataset by replacing missing values by the learned medians.

Oversampling using SMOTE:

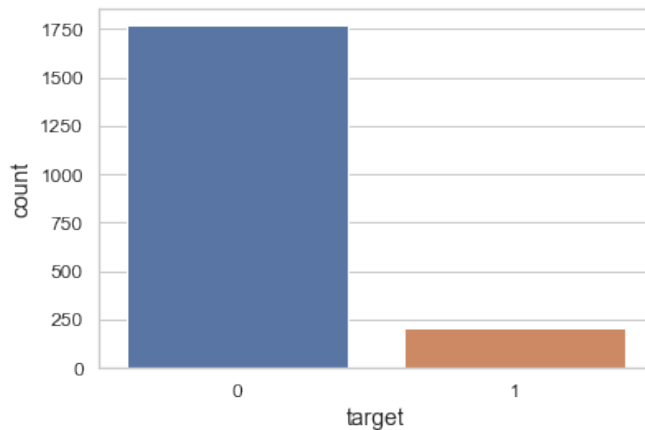


Figure 7: Unbalanced target attribute

As is illustrated by Figure 7, the target variable is imbalanced, which could affect the correlation between variables and affect the result. We can balance the data through undersampling or oversampling.

Undersampling is reducing the larger class (target=0) and bring it equal to smaller class (target=1). Oversampling is randomly generating samples of minority class(1 here) and bring it equal to majority class (0 in our dataset). This can be achieved through SMOTE (Synthetic Minority Over-sampling Technique).

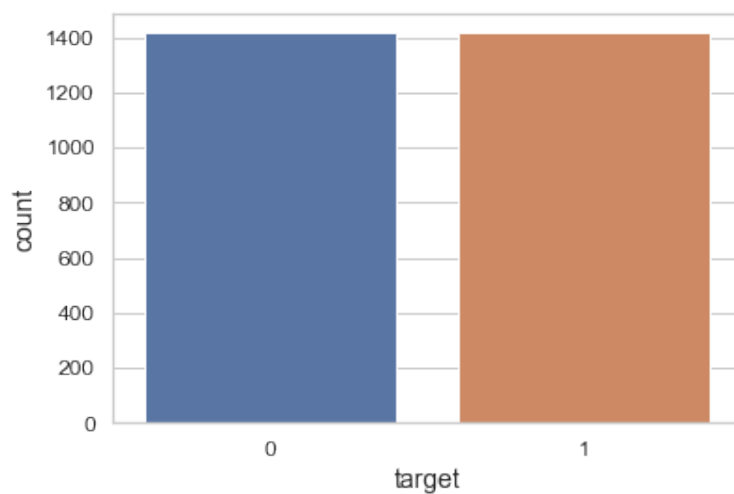


Figure 8: Balanced dataset after SMOTE

Now we have a perfect balanced data. I over-sampled only on the training data, because by oversampling only on the training data, none of the information in the test data is being used to create synthetic observations, therefore, no information will bleed from test data into the model training.

Recursive Feature Elimination (RFE): Recursive Feature Elimination (RFE) is based on the idea to repeatedly construct a model and choose either the best or worst performing feature, setting the feature aside and then repeating the process with the rest of the features. This process is applied until all features in the dataset are exhausted. The goal of RFE is to select features by recursively considering smaller and smaller sets of features. It is worth mentioning that RFE was only applied to measuring the performance of features from the training data, not the test data,

Dummification: For better visualization and more in depth analysis, we need to convert these categorical variables into numeric using `get_dummies` function. This function create different columns for each category and mark the category used to create column as 1 and rest other as 0.

Model building

Six classification models, namely, Random forest (RF), artificial neural network (ANN), Decision tree (DT), support vector machine (SVM), logistic regression (LR), and K-nearest neighbors (KNN) were used to predict PPH risks. These models are commonly used to conduct classifications for supervised machine learning.

Cross-validation

The model validation technique, 10-fold cross-validation was used assessed models performance and estimation of general error during the whole machine process. In this process, entire dataset was divided into equal 10 folds which are approximately the same number of events. Nine-folds was used as the training set, and the remaining 1 fold as the test set. It continued until each fold was used once for evaluation. The results from 10 times validation models were then combined to provide a measure of the overall performance.

Statistical analysis

Descriptive characteristics of the study population were provided including continuous variables as a mean \pm standard deviation. The ROC (Receiver-Operating Curve) was used to assess the performance of these models. Python software (version 3.6) was used to analyze the basic statistical problem and to construct the ANN prediction model. All statistical tests were two-tailed and $p < 0.05$ will be considered significant.

Model evaluation

Confusion matrix: the confusion matrix has been widely used for summarizing the performance of the classification model.

Accuracy: Accuracy of a model is defined as the total positive instances of the model are divided by the total number of instances. Accuracy parameter provides the percentage of correctly classified instances. The accuracy of model is defined as

$$Accuracy = \frac{TP+TN}{TP+FP+TN+FN}$$

Precision: This parameter is used to determine the degree of the attribute to correctly classify the person with risk of PPH and is defined as

$$Precision = \frac{TP}{TP+FN}$$

Recall: This parameter is used to determine the degree of the attribute to correctly classify the person with non-PPH and is defined as

$$\text{Recall} = \text{TN} / (\text{TN} + \text{FP})$$

F-measure (F1 score): Since we have two measures (Precision and Recall) it helps to have a measurement that represents both of them. We calculate an F-measure which uses *Harmonic Mean* in place of *Arithmetic Mean* as it punishes the extreme values more. The F-Measure will always be nearer to the smaller value of Precision or Recall.

$$\text{F1 score} = 2 * (\text{Precision} * \text{Recall}) / (\text{Precision} + \text{Recall})$$

The precision, recall and F1 score are also known as quality parameters and used to define the quality of the predicted class. To determine the goodness of the medical diagnosis model, basically four parameters are used, these three parameters are accuracy, precision, recall and F1.

RESULTS

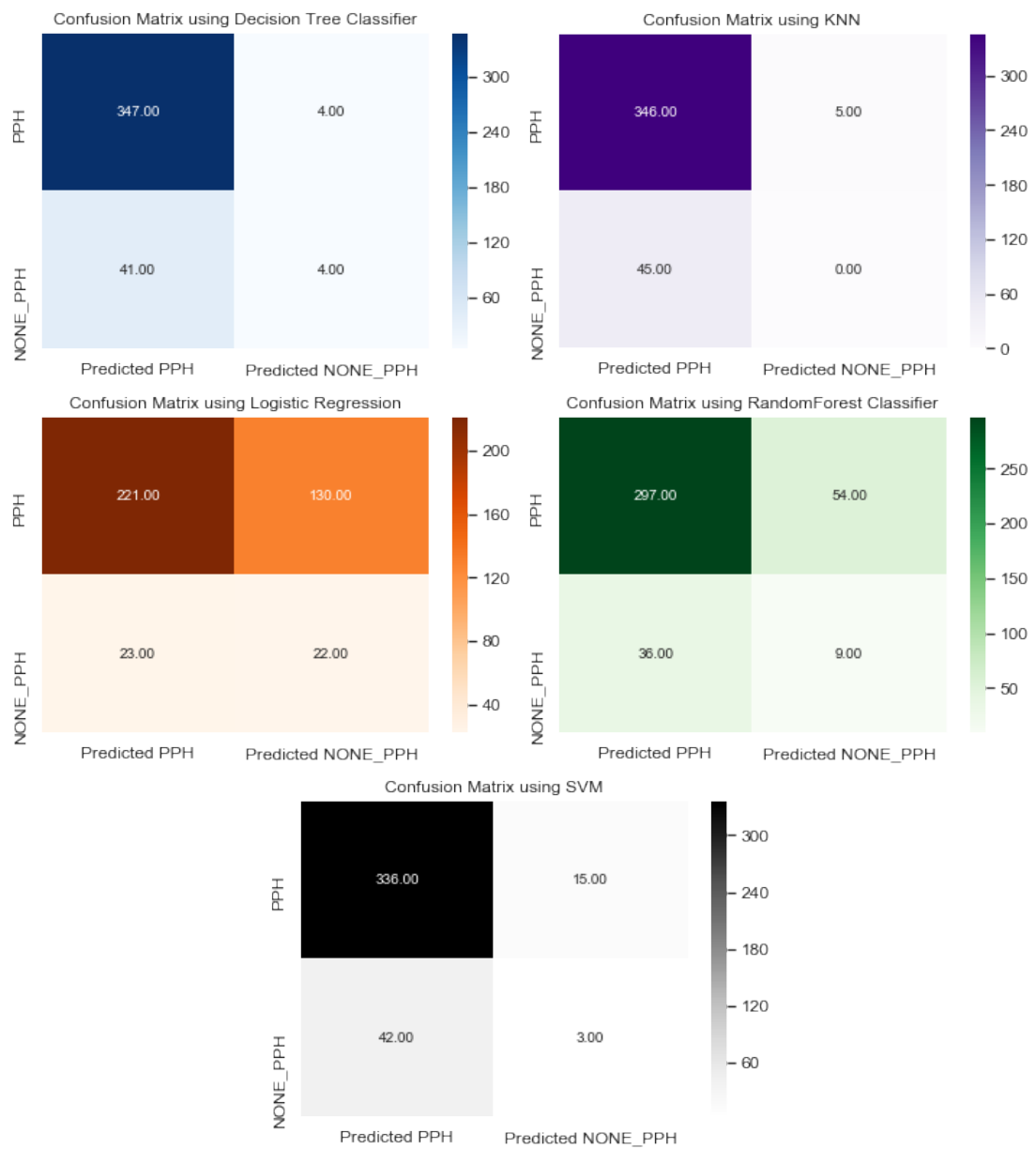


Figure 9: Confusion Matrices

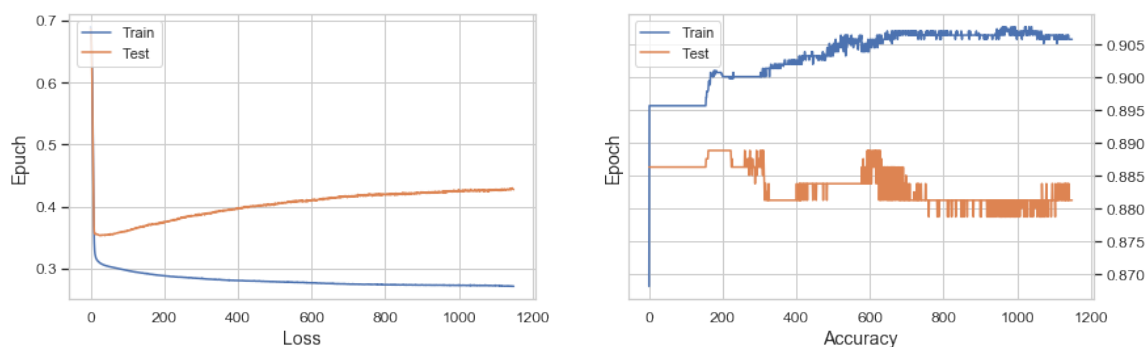


Figure 10: Results from ANN model

Based on Figure 9 and Figure 10, Table 1 and Figure 11 summarize the metrics of the performance of the six models.

Models	Average CV Accuracy (10 folds)	Accuracy	Precision	Recall	F1 Score
Logistic Regression	0.56	0.61	0.82	0.61	0.68
Decision Trees	0.88	0.77	0.81	0.77	0.79
Random Forest	0.93	0.89	0.85	0.89	0.85
KNN	0.75	0.87	0.78	0.87	0.83
SVM	0.69	0.86	0.81	0.86	0.83
ANN	NA	0.88	NA	NA	NA

Table 1: Metrics of each model

Given that the data is skewed towards non-PPH, the accuracy of a degenerate baseline that always predicts non-PPH is calculated as 0.88 by assuming all the predictions are zeros.

High recall, low precision: This means that most of the positive examples are correctly recognized (low FN) but there are a lot of false positives.

Low recall, high precision: This shows that we miss a lot of positive examples (high FN) but those we predict as positive are indeed positive (low FP)

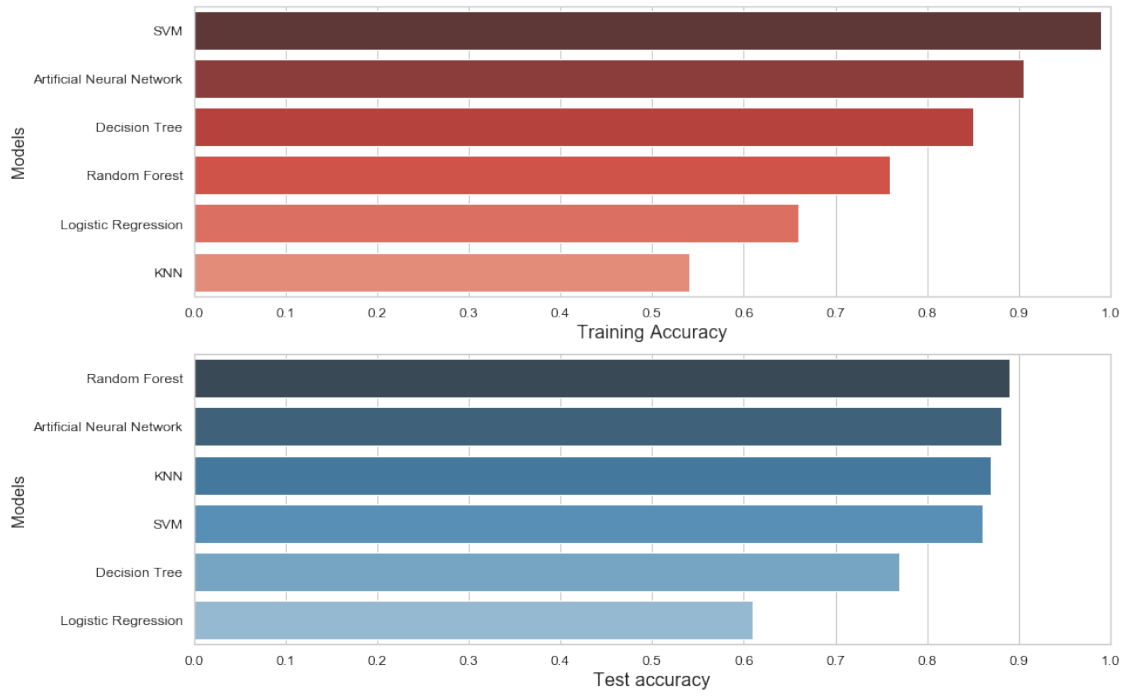


Figure 11: Comparison of the accuracy of each model

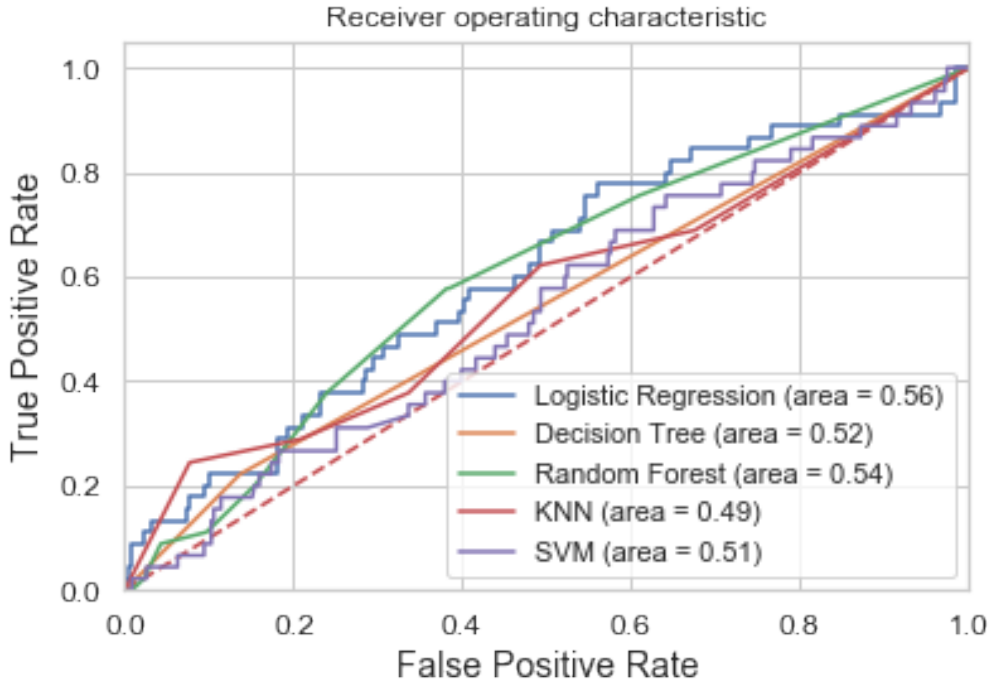


Figure 12: ROC Curve

ROC is plot of True positive Rate (Recall) vs False Positive Rate. The farther the line is above the red dotted line the better is our prediction. The more area we have under ROC curve, the better the fit.

DISCUSSION

PPH is a major public health concern worldwide. A major impediment to timely recognition and management of PPH is the ineffective mechanism to predict it. Early diagnosis and timely screening would help to increase the quality of a patient's care. Therefore, there is a great need for the ability to predict the treatment outcome to be used in the proper and timely treatment decision. However, there is no exact tool in the clinical setting that is designed to distinguish PPH and non-PPH patients with higher accuracy. In this study, I developed and assessed prediction models which are based on the machine learning algorithms and data were collected from actual EHRS records. Nine variables are used to predict the target value, which is the high risk PPH with the total blood loss equal to or greater than 1000 ml. Recursive Feature Elimination (RFE) finds all the variables relevant to the prediction of PPH and heatmap of correlations indicate that traditionally important factors such as age, BMI, number of babies carried, days before the last C-Section and induction are of great significance to the potential risk of PPH. Of all the models, Random Forest stands out as the best one in terms of accuracy, precision, recall, f1 score and cross validation score. It is worth noting that ANN, as a deep learning algorithm, generated the second best accuracy with a slight difference (0.01) with the one of Random Forest.

Random forest won for the following reasons. First, it reduces overfitting problem in decision trees and also reduces the variance and therefore improves the accuracy by creating as many trees on the subset of the data and combining the output of all the trees. Besides, it handles non-linear variables better than other algorithms and is robust to outliers. In our case, the variables are mostly not linearly correlated, as is shown by Figure 4 and Figure 3 demonstrates that values of most variables are immensely unbalanced.

ANN churned out the second best result also because, as Random Forest, it is more capable of exploiting interactions between features, as is described by Figure 13 and Figure 14.

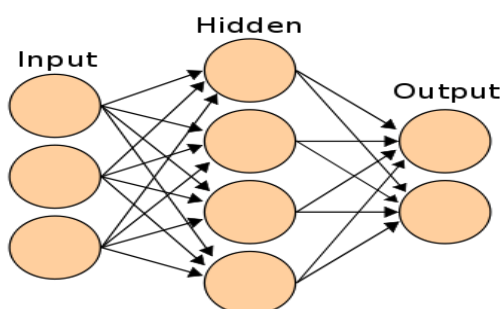


Figure 13: Artificial Neural Network

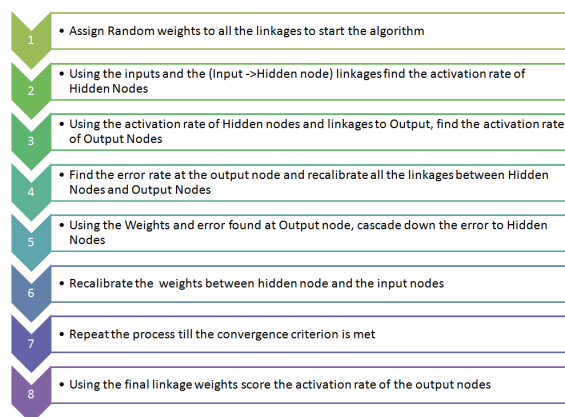


Figure 14: ANN flow chart

Another important observation is that the accuracy is not an ideal metric to evaluate the predictive ability of these models. The chief reason behind this statement is that though we balanced the training dataset using SMOTE, the test dataset is extremely unbalanced, skewing toward the non-PPH cases. Plus, the relatively small size of the entire dataset worsens this problem to the extent that the accuracy of most models didn't exceed the baseline. We may as well abandon accuracy as a metric; however, since our goal is to

compare the models in predicting PPH against the currently available data, this accuracy carries information in this respect and will definitely be more able to differentiate the models when more datapoints are available.

LIMITATIONS

PPH Measurement

After a vaginal delivery, the patient's blood loss is routinely assessed and recorded as part of the medical record. In the delivery room, the patient's blood often saturates medical supplies like laparotomy sponges ("laps"), pads, and sheets. Spills on the floor are also normal. The standard practice for determining the volume of blood loss is a provider's subjective visual estimate. Visual estimation of blood loss (VEBL) is widely known to be inaccurate, with several studies finding a 30-50% underestimation of blood losses, especially at higher volumes. Another quantification tool is the calibrated collector bag, which can be placed under the patient's buttocks to collect lost fluid. The bags are calibrated and marked with volume lines that serve as an objective guide for the provider. Measurement via calibrated collector bags can be falsely elevated when amniotic fluid, urine, or sponges fall into the collector bag during delivery (Shields et al., 2011).

The University of North Carolina Hospitals in Chapel Hill, NC is a tertiary care hospital with a busy labor and delivery (L&D) unit. Currently, it does not quantify blood loss as standard practice after vaginal deliveries. Instead, blood loss during delivery is collected in a clear, non-calibrated collector bag. At the end of each delivery encounter, blood loss is visually estimated by looking at blood-soaked supplies and contents of the collector bag. UNC uses three criteria for the diagnosis of postpartum hemorrhage after a vaginal

delivery: (1) estimated blood loss of greater than 500 mL, (2) significant vital sign changes (includes $HR > 110$, $BP < 90/60$, O_2 saturation $< 95\%$), or (3) three uterotonic medications given. When one of these is met, the provider initiates Stage 1 of the OB hemorrhage protocol, which requires quantification of blood loss every 5-10 minutes with gravimetric measurement of blood-soaked supplies (“UNC”, 2017). However, this portion of the current protocol is not uniformly applied by all providers, partly due to the subjectivity of blood loss estimation. In light of this, the target value of the dataset that feeds the machine learning models is intrinsically inaccurate.

Data Quality

Only 1988 datapoints from the time range of half an year were collected. The size of dataset is far from ideal to feed machine learning models, especially for ANN, a deep learning model which favors large datasets. That is also one of the major reasons behind the fact that the accuracy of all the models tested are not far beyond the accuracy of the degenerate baseline. Another limitation is that there are many missing values for the variable DSLC (Days Since Last C-Section) and BMI, which are among the most important risk factors contributing to PPH. Again, more datapoints will solve the this problem, making the proportion of missing values insignificant.

CONCLUSION:

This study is aimed to compare the performances of various machine learning models in predicting the risk of PPH using the actual EHRS data from UNC-CH Women’s hospital. Five machine learning models (Logistic Regression, Decision Trees, Random Forest,

KNN, SVM) and one deep learning model (ANN) are tried and their performances are evaluated by cross validation and performance metrics including accuracy, precision, recall, f1 score and ROC curve. Random forest stands out as the best model with the accuracy of 0.89 and ANN the second best with 0.88. The small size of the dataset is the culprit of the low accuracy compared with the accuracy of the degenerate baseline (0.88).

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