Online Machine Learning Algorithms Review and Comparison in Healthcare

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dedication...

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Abstract

Currently, the healthcare industry uses Big Data for essential patient care information. Electronic Health Records (EHR) store massive data and are continuously updated with information such as laboratory results, medication, and clinical events. There are various methods by which healthcare data is generated and collected, including databases, healthcare websites, mobile applications, wearable technologies, and sensors. The continuous flow of data will improve healthcare service, medical diagnostic research and, ultimately, patient care. Thus, it is important to implement advanced data analysis techniques to obtain more precise prediction results.

Machine Learning (ML) has acquired an important place in Big Healthcare Data (BHD). ML has the capability to run predictive analysis, detect patterns or red flags, and connect dots to enhance personalized treatment plans. Because predictive models have dependent and independent variables, ML algorithms perform mathematical calculations to find the best suitable mathematical equations to predict dependent variables using a given set of independent variables. These model performances depend on datasets and response, or dependent, variable types such as binary or multi-class, supervised or unsupervised.

The current research analyzed incremental, or streaming or online, algorithm performance with offline or batch learning (these terms are used interchangeably) using performance measures such as accuracy, model complexity, and time consumption. Batch learning algorithms are provided with the specific dataset, which always constrains the size of the dataset depending on memory consumption. In the case of incremental algorithms, data arrive sequentially, which is determined by hyperparameter optimization such as chunk size, tree split, or hoeffding bond. The model complexity of an incremental learning algorithm is based on a number of parameters, which in turn determine memory consumption.

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Chapter 1

Introduction

The healthcare industry records large datasets which are essential for patient care, determining preventive diagnostic methods, compliance, and regulatory requirements. Electronic health records (EHRs) store massive data digitally through various software such as *Pediatric Therapy EMR*, *NextGen Healthcare*, and *athenaClinicals*. EHRs contain patient information that may include demographics, medical history, laboratory results, medication, clinical events, personal statistics like age and weight, and billing information. The Internet of Things (IoT) has increased the growth and scope of healthcare data with features such as internet-enabled blood pressure monitors, mHealth apps, and wearable technologies.

1.1 Big Data in Healthcare

Big Healthcare Data (BHD) refers to complex datasets that have some unique characteristics, beyond their large size, that both facilitate and convolute the process of extraction of actionable knowledge about an observable phenomenon. According to a recent study published by Market Research Future, the global market of Big Data in healthcare is forecast to reach approximately $35 billion by 2021, at a striking rate of CAGR ; during the forecast period 2016−2021. There is has been an exponential increase observed in the Big Data size and complexity; however, the lifespan of the data rapidly decays at an exponential rate (Figure 1.1).

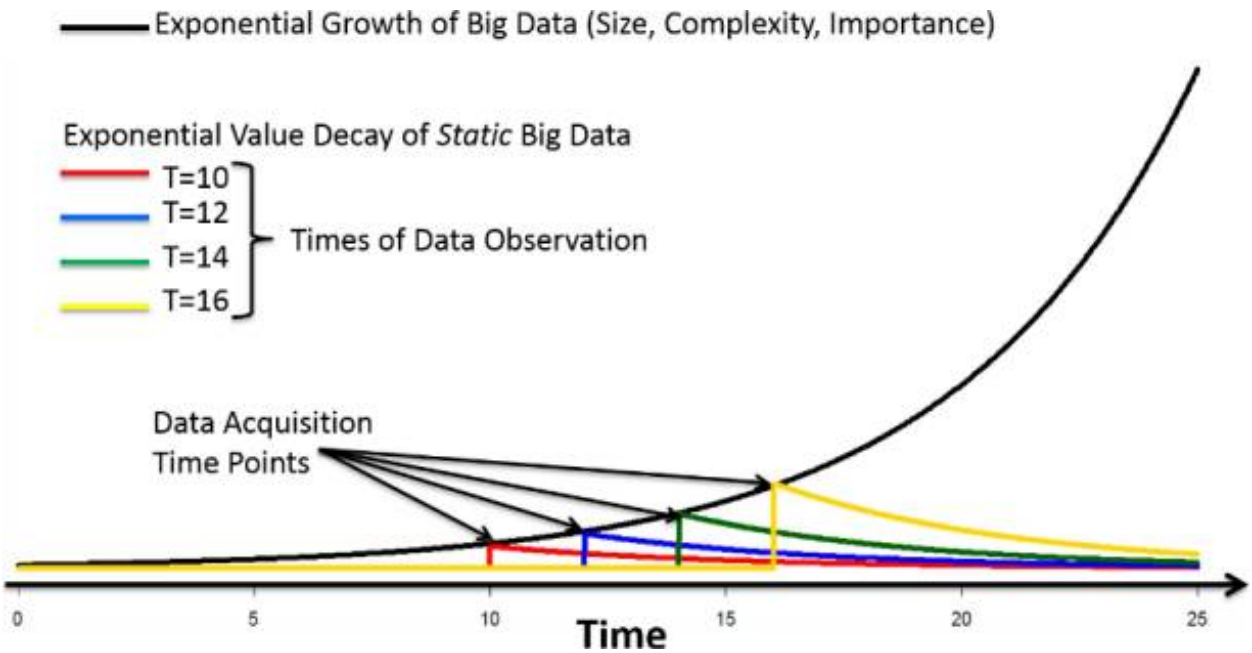


Figure 1.1: Exponential growth in data [8].

Increasing BHD faced with various challenges such as resource cost, precision of diagnostic or preventive prediction to improve patient care, and use of data considering rapid decrease of its lifespan. As healthcare organizations are moving towards real-time data analytics with the aim to gain actionable insights and personalized services, challenges remain how to harness the ever growing data generated continuously.

Model-based techniques have a fixed number of parameters and postulate explicitly their probability distributions, whereas non-parametric methods relax the a priori beliefs of the parameter distributions and allow varying number of parameters, relative to the amount of training data [8].

BHD is often unstructured data which can be produced through EHR, wearable device, social media. An initial analysis may involve taking care of missing data, identifying redundant information, classifying data for desired prediction. Another challenge of sharing EHR data is a concern with patient privacy, has to be a high priority in order to comply with the EU Directive 95/46/CE and the HIPAA privacy rule [14].

While researchers are still debating the definitions and boundaries of Big Data in health, benefits of health-related Big Data have been demonstrated in three areas so far, namely to

1) prevent disease, 2) identify modifiable risk factors for disease, and 3) design interventions for health behavior change [14].

1.2 Predictive analytics in Big Healthcare Data / Big Data Analytics

Various machine learning algorithms are used in Big Healthcare Data analytics for making decisions using predictive analysis (Figure 1.2). Google has recently developed machine learning algorithm to help detect cancer with 98% accuracy.

In an incremental predictive analysis, BHD can be used as a hypothesis for the new data rather than as a firm prediction. Recently, incremental or online machine learning algorithms have played a growing role in various big data applications such as healthcare, e-commerce, and social media; the healthcare industry in particular accesses a tremendous amount data recorded electronically and with cloud-computing services. With increasing compliance and regulatory requirements and a mounting patient care load, this massive data must be used to obtain more accurate diagnostic predictions.

The current discussion analyzes different offline and online classification and regression techniques. Modern-day predictive analytic techniques are useful in forecasting trends using retrospective and current data by recognizing adverse events or deteriorating patient conditions or behaviors before the actual events and identifying unusual patterns in the data. Traditional offline, or batch learning, is limited in memory size, time, and cost.

1.2.1 Predictive modeling process

In data mining given data, $\mathcal{D}_i = (x_i, y_i)$ is divided first for predictive modeling into three sets:

- **Training set -** In which observations are used to train the model with one or more algorithm.
- **Validation set -** In which validation data is used to predict the model and find best model. This process is also known as *tuning*.

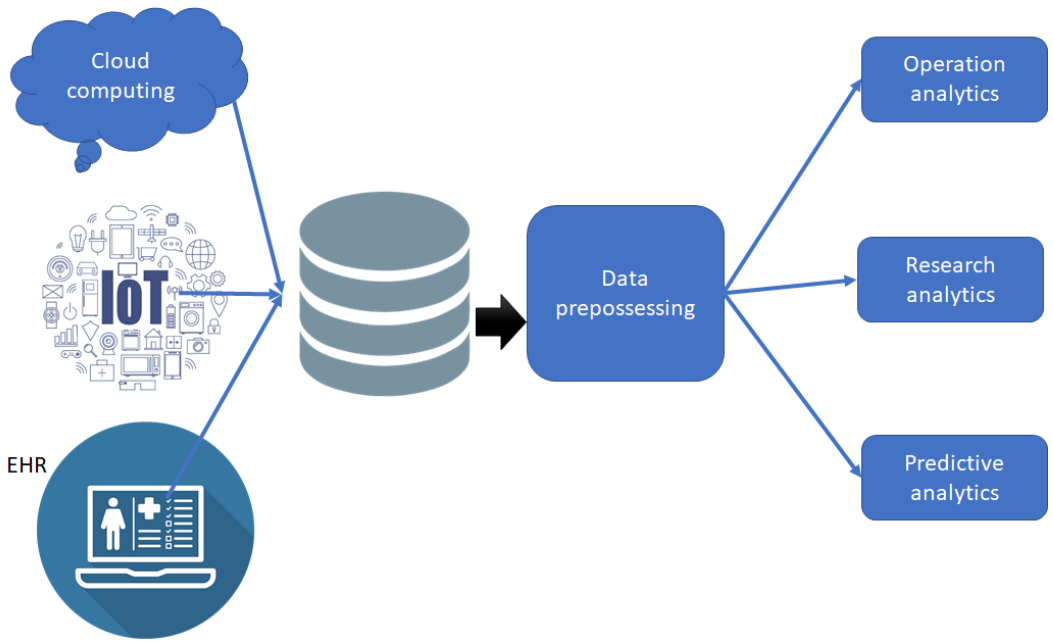


Figure 1.2: Big Data Predictive analytic process.

- **Testing set -** This set is used to predict final model performance.

There are various techniques to split the data such as even/odd, venetian blinds, random, and visual inspection. In this paper, data analyzed is healthcare data so random split technique is utilized to define train, validation, and test datasets.

1.2.2 Predictive analysis using batch learning

A batch algorithm develops a decision model on the entire sequence at once (Figure 1.3). The predictive model (aka machine learning) is a statistical process that forecasts the outcome of a particular event occurrence which is response or dependent variable using independent or predictor variables from the dataset. In machine learning, classification of the model can be either supervised or unsupervised. Supervised learning can evaluate observations using training set predictor variables; unsupervised learning uses clustering as classification procedure. The current study analyzed supervised healthcare data. For instance, a response variable $y_i \in 1,..,c$ given as set of features $X_i = (x_{i,1}, x_{i,2},...,x_{i,p}) \in \mathbb{R}^p$. The response variable can be multi-class or binary $\{0,1\}$.

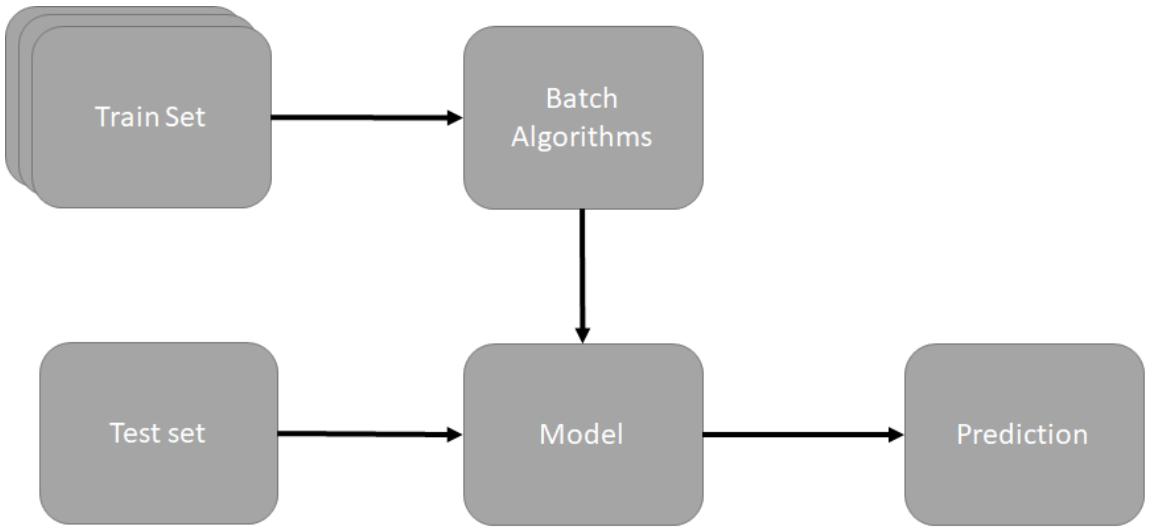


Figure 1.3: A representation of the batch machine learning scheme

1.2.3 Predictive analysis using incremental learning

Large dataset batch learning is not cost effective; also, in most cases one day's data sequence arrives over time (Figure 1.4). In order to keep the model updated with changes in data and features, incremental machine learning applications are used. For instance, in sequential supervised data: arrive $\{(x_i,y_i)\}_{i=1}^{t}$ and t be set of sequences. Each sequence contains (x_i,y_i) where $x_i = \langle\ x_{i,1},\ x_{i,2},\ ...,x_{i,N}\ \rangle$ and $y_i = \langle\ y_{i,1},\ y_{i,2},\ ...,y_{i,N}\ \rangle$. The goal is to construct the classifier h to predict label y_t for given x. The loss function $\mathcal{L}(\hat{y},\ y)$ is determined for each model. Then prediction of final t model can be formulated as $\hat{y}_t = h_{t-1}(x_t)$.

The online accuracy of model at time t is given by [22]:

$$E(S) = \frac{1}{t}\sum_{i=1}^{t} 1 - \mathcal{L}(h_{i-1}(x_i), y_i) \tag{1.1}$$

1.3 Challenges in batch learning

The batch learning algorithm has limitations when it comes to non-stationary datasets. The data flow is continuous in healthcare applications; however, batch learning algorithms can not offer dynamic adaption of the model based on when new data arrives [30]. Streaming of the new data may have time-varying domain, and it may vary in terms of probabilistic

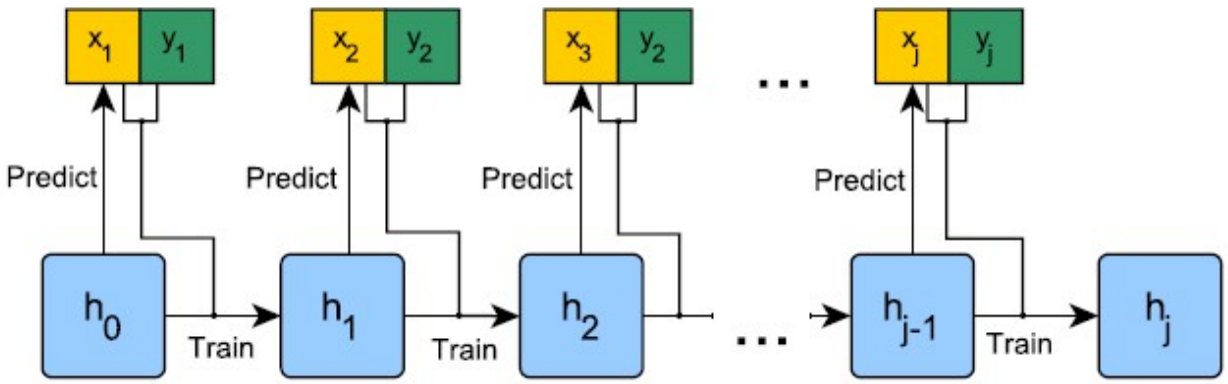


Figure 1.4: The online learning scheme [22].

distribution of the arrival data. This makes batch learning even more complex and requires more computation resources. Batch learning has inconsistency over the data. Subsequent models in batch learning are unrelated [6]. The high volume of data takes time and memory with batch learning and may also lead to an outdated model.

1.4 Challenges in incremental learning

1.4.1 Concept drift and data distribution change

Incremental algorithms with large data can result in time inefficiency, for instance distribution frequency sometime has error bound. Such a problem can be solved using sampling. This process stream error is within the space of computational resources in data stream system management error margins. There is always a trade-off between accuracy and amount of memory [28]. However, certain batch learning models, such as C4.5, work in linear time, whereas incremental models increase computation efforts. The incremental cost can be more than the overall batch learning computational cost [6]. Changes in data distribution over time are referred to as *concept drift*. As a learner is unable to predict arriving data distribution, concept drift is unpredictable [19]. The section 2.5 explains SMOTE (*Synthetic Minority Oversampling Technique*) algorithm employed to overcome concept drift challenge in the incremental model.

1.4.2 Catastrophic Forgetting

As new data arrives, incremental algorithms create a new decision model and forget the old in order to meet memory and time constraints,. In some situations, maintaining a decision model may be preferable. This behavior of incremental learning is known as *catastrophic forgetting* [26]. As discussed above, there are always trade-off dilemmas when working with accurate prediction and computational resource limitations for artificial or biological learning systems, which is known as a *stability-plasticity dilemma*. One way to deal with this problem is a just-in-time (JIT) classifier or online/offline hybrid algorithm; concept drift offers a partial remedy for this problem [12]. In neural networks standard back propagation is one way to deal with catastrophic forgetting *catastrophic forgetting* [10].

1.4.3 Model Complexity

If new data is unknown in the case of incremental data arrival, it is difficult to measure model complexity. Model complexity is critical factor when it comes to resource limitation. This topic is elaborated in section 4.3

1.4.4 Performance Evaluation and model benchmarking

In general, incremental learning data arrive in infinite sequences, S=(s_1,s_2,s_3, ...,s_t,...) with data (x_i,y_i) and a corresponding sequence of hypothesis model h_1,h_2,h_3, ...,h_t,...Therefore, accuracy in an incremental learning model is always evaluated on the model h_t on the test set.Unlike incremental learning, batch learning takes on a whole data at once, and the the prediction is with hypothesis h on the test set. Smaller datasets results are more precise with batch learning. In incremental learning it is useful to see how results improve over time. Learning from large datasets may be more effective when using algorithms that place greater emphasis on bias management.

Chapter 2

Literature Review

Healthcare data requires continuous monitoring of the vital health parameters of patients and encounters major challenges for healthcare organization in applying offline machine learning methods to tremendous amounts of data. Incremental learning aims to gain actionable insights and personalized services, but challenges remain regarding how to harness the ever-increasing data continuously generated. The term *incremental learning* refers to learning from streaming data where data arrive sequentially and the model uses limited learning without sacrificing accuracy.

The bottleneck in data analysis is in raising the most appropriate clinical questions and using suitable data and analysis techniques to obtain clinically relevant answers. Batch learning has limitations in big data such as cost and memory usage. A offline or batch learning algorithms receive the entire dataset in contrast to online algorithms, which receive data in sequence. In batch learning, data are given prior to training, hence meta-parameter optimization and model selection can be based on the full dataset, and training can rely on the assumption that the data and its underlying structure are static [12].

Incremental learning has recently gained more popularity in healthcare systems due to the rapidly increasing amount of data accumulation in health monitoring. The effectiveness of an online algorithm may be measured by its competitive ratio. Initial results show that machine learning holds great promise for addressing a variety of pressing healthcare issues such as clinical risk assessment, patient safety, and readmission.

2.1 Machine learning in healthcare

In healthcare, EHRs contain valuable patient informations. Various machine learning applications are used to determine the efficacy of the data. Data analysis of this data can overcome the gap between theoretical application of the nursing knowledge and decision making based on research analytics [13]. In addition, machine learning application in biomedical and healthcare data enables critical scientific discoveries and facilitates evidence based clinical solutions [15]. The biomedical field and healthcare data have various hurdles such as imbalanced datasets, unstructured data stored in data warehouse, noisy and ambiguous labeling, and missing data. [15]. Batch learning predictive analysis are performed using naive bayes (NB), linear regression (LR), support vector machine (SVM), neural network (NN), random forest (RF) etc. All these algorithms are describes in section 2.3.1, 2.3.2 and in chapter 3.

Zheng et al. proposed batch learning algorithm to predict Type 2 Diabetes Mellitus. Paper shows among, LR, NB, RF, kNN, and SVM; linear regression provide accuracy of 0.99 whereas RF and SVM provide 0.98. However, LR, kNN, NB achieve (near) perfect sensitivity [38]. In machine learning the so-called *"no free lunch"* theorem states that no one algorithm works perfect with different datasets. In the work of Zheng et al., high level accuracy is achieved without hyperparameter optimization.

In another study done by Sigurdardottir, Jonsdottir, & Benediktsson in their paper used decision tree J48 classifier to analyze which factors contribute to improvement in glycemic control in educational interventions [34]. Initial data analysis found that improving incongruity between designing and motivating self-care in diabetic patients can be done by adequately defined user care.

Batch predictive modeling encounters primary issues in data volume, non-linearity, time-series data, and computation cost [4]. Incremental learning overcomes these challenges across various applications applied to healthcare data.

2.2 Online machine learning applications

Real-time streaming of Big Data in healthcare should be analyzed with online machine learning. Embedded machine learning that can analyze real-time data, data of similar patients from multiple hospital locations, and data arriving from continuous monitoring wearable systems is going to enhance efficacy and cost of patient care. Mazilu et al. [24] analyzed the "freezing of gait" deficit using online machine learning from a wearable assistant, composed of an android smart phone and wearable accelerometer. Random forest and AdaBoost provided approximately 99.8% accuracy. This study also observed that detection performance more or less maintained the same levels in 1s and 4s windows. Additionally, the window size of data flow was measured using minimum sensitivity and specificity of classifier. In fact, based on detection parameters, window size increased from 0.5s to 3s. Thus,incremental learning produces flexibility of data ingestion according to the application.

In a similar study, Raghuraman, Senthurpandian, Shanmugasundaram, and Vaidehi [31] wdetected anomalies and predicted health parameters obtained from wearable sensor devices. In this analysis a Kalman filter [27] was applied in input data to reduce the noise.

2.3 Offline Machine learning Methods

Various offline methods are available for predictive modeling, and a few offline algorithms are used for comparison in this discussion.

2.3.1 Linear Regression

Regression is a data mining technique used to predict a value; the rate of success for patient treatment can be predicted using regression techniques. Regression takes a numeric dataset and develops a mathematical formula to fit the data, and a regression task begins with a dataset of known target values. In a case where data has an input variable x such a that $x_i \in \mathbb{R}^n$ and y is response variable, such a that $y_i \in \mathbb{R}$ for i = 1,...,m, a general ordinary least square regression would use the following model [16]:

$$y = X\beta + \varepsilon \tag{2.1}$$

where, β is the estimated coefficient matrix of predictor variable and ε is the vector of prediction error. The standard approach is to approximate β, which can also be defined as $\beta = (X^T X)^{-1} X^T Y$.

2.3.2 Support Vector Machine (SVM)

SVMs are supervised learning models in which data is analyzed using classification and regression techniques. There are two ways of implementing SVMs. The first involves mathematical programming, and the second technique employs kernel functions. If data can not be separated linearly (e.g., straight line or hyperplane), then it can be transformed into feature space or linearizing space using kernel function [2]. SVM solves the problem of interest indirectly, without solving the more difficult problem. The Support Vector Machine presents a partial solution to the bias variance trade-off dilemma. When kernel functions are used, a SVM focuses on dividing the data into two classes, P and N, corresponding to y_i =+1 and y_i = -1, respectively. The support vector classification searches for an optimal separating surface, a hyperplane, which is equidistant from each of the classes. This hyperplane has many important statistical properties and kernel functions are non-linear decision surfaces [2].

If training data are linearly separable, then a pair (w, b) exists such that:

$w^T x_i + b \geq 1$ for all $x_i \in$ P

$w^T x_i + b \leq -1$ for all $x_i \in$ N

where w is a weight vector and b is a bias. The prediction rule is shown as:

f = sign(<w.x>)+ b

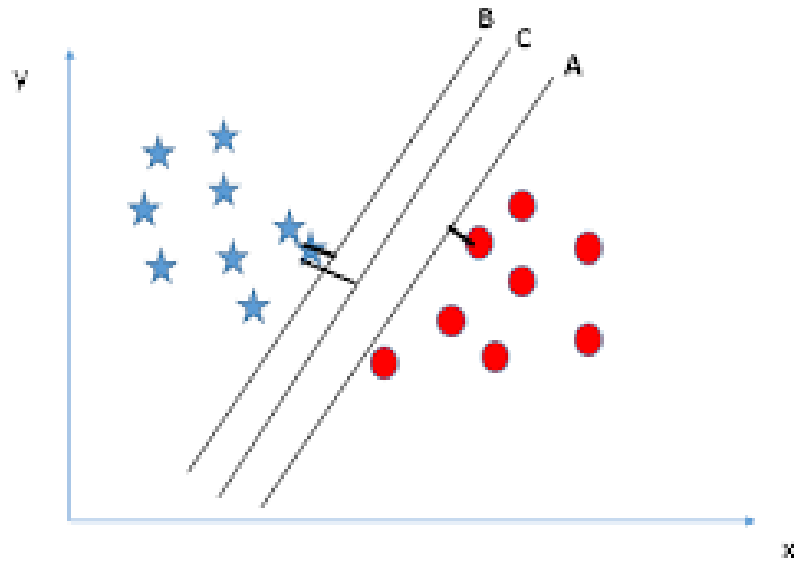


Figure 2.1: SVM algorithm representation

2.4 Online Machine learning Algorithm

Incremental learning refers to online learning strategies that work with limited memory resources. Potential infinite sequence S = (s_1,s_2,...,s_t,...) of data s_i = (x_i,y_i) arrive one after other.

Incremental Support Vector Machine (ISVM) is the most popular exact incremental version of the SVM. A limited number of examples, candidate vectors, is maintained in the set of support vectors. The smaller the set of candidate vectors, the higher is the probability of missing potential support vectors [22].

On-line Random Forest (ORF) by Saffari et al., is combination of online and extreme random forest [32]. Online bagging is modeled by sequential data arrival based on a Poisson distribution [32]. The minimum number of trees and minimum gain in Gini Index is predefined. The split value optimizing the Gini index is based on minimum number of samples available through sequential data within one leaf.

Mondrian Forest (MF) is based on the mondrian process, which is a stochastic process over binary hierarchical axis aligned partitions. Mondrian forest is faster and more accurate than online the random forest method [20]. The predictive performance of online mode is equal to that of a batch mode. A mondrian forest classifier samples independent trees T_1,..., T_m so called Mondrian trees. known as Mondrian trees; each tree is based on a predefined number of samples, and λ the complexity parameter.

2.5 Concept Drift

In online learning data is non-stationary when its statistical characteristics change over time; in machine learning, whose distribution at certain point of time is characterized by the joint distribution $p(x, w)$, where is x is input variables and w represent the class. The environment whose joint distribution changes over time is a non-stationary environment. The change in input distribution is referred as *virtual concept drift* or covariate shift whereas change in the functionality itself referred to as *real concept drift*.

Virtual concept drift generally occurs due to class imbalance over time. Class imbalance occurs when a dataset does not have (approximately) equal numbers. Under sampling of majority class or over sampling of minority class data is one technique to overcome imbalance data problem. The *Synthetic Minority Oversampling Technique* (SMOTE) algorithm is another popular technique for imbalance class data.

SMOTE (1) populates the minority class feature space by strategically placing a line segment connecting two minority instances.

2.6 Competitive Ratio

The effectiveness of an online algorithm is measured by its competitive ratio, defined as the worst-case ratio between its cost and that of a hypothetical offline algorithm that knows the entire sequence of the request in advance [16].

Algorithm 1 smote

Require: Minority Data $D = x_i \in$ X where i = 1,2,...,T Number of minority instances(T), SMOTE percentage (N), Number of nearest neighbors (k)

```
for i= 1,2,...,T do
    find k nearest minority neighbors of x_i
    N̂ =[N/100]
    while N̂ ≠ 0 do
        select one of the k nearest neighbor, x̄
        select random number α ∈ [0,1]
        x̂ = x_i + α(x̄-x_i)
        Append x̂ to S
        N̂= N̂ -1
output : Synthetic data S
```

Chapter 3

Algorithm

The current study compared various offline and online algorithms on two different datasets. This chapter describes the basic machine learning algorithm used.

3.1 Offline or batch learning algorithm

Five different offline machine learning algorithm are analyzed on both datasets.

1. Naive Bayes' is selected to understand simple probabilistic model performance.
2. Logistic Regression is chosen as it is a generalized linear model.
3. Neural Network one of the important algorithms used in image processing in various field. Deep learning plays critical role in healthcare analytics.
4. Random Forest is one of the robust classifiers in predictive analytics. In online machine learning, an incremental random forest model is analyzed in the current study.
5. Adaptive Boosting is boosting approach combines decision tree as a weak classifier to create a highly accurate predictive classifier. Additionally, in the current study Learn++, an incremental algorithm is analyzed for comparison which is inspired by Adaptive Boosting.

3.1.1 Naive Bayes : NB

In machine learning, Naive Bayes' model is simple probabilistic classifier based on Bayes' theorem and very suitable for data with high dimensionality. The Naive Bayes' theorem is given as :

$$P(A|B) = P(A) * \frac{P(B|A)}{P(B)} \tag{3.1}$$

Naive Bayes' is simple probabilistic theorem and can be redefined for binary dependent variable as:

$$P(y = 1|X = k) = P(y = 1) * \frac{P(X = k|y = 1)}{P(X = k)} \tag{3.2}$$

3.1.2 Logistic Regression: LR

Logistic regression is generalized linear model serve to predict binary classification. The linear regression model is discussed in the section 2.3.1. Both the datasets used for analysis have a binary response variable i.e. $y \in 0, 1$. If $\mathrm{P}(x_i) = \mathrm{P}(y = 1|x_i)$, that is considered to be the probability of certain event occurring for an instance; the logistic regression model can be written as 3.3:

$$z_i = \ln\left(\frac{P(x_i)}{1 - P(x_i)}\right) = \beta_0 + \beta_1 x_{i,1} + ... + \beta_n x_{i,q} + \varepsilon \tag{3.3}$$

The log-likelihood function i.e. [25, 18] is used to estimate maximum likelihood

$$l(\beta) = \sum_{i=1}^{n} y_i \ln\left(\frac{P(x_i)}{1 - P(x_i)}\right) - \ln\left[1 + \left(\frac{P(x_i)}{1 - P(x_i)}\right)\right] \tag{3.4}$$

Over fitting of logistic regression model is avoided using forward, backward or both direction propagation. This method eliminates correlated variables from predictive variables. A better and more efficient way to cope with over fitting is regularization. Regularization keeps all the variables in the model and shrinks the coefficients towards zero. Lasso estimator $\hat{\beta}$ is given by [37]:

$$\hat{\beta} = argmin\Big(- l(\beta) + \lambda \sum_{q=0}^{Q} |\beta_{i,q}|\Big) \tag{3.5}$$

Algorithm 2 Logistic regression

Require: : training set S, β
  $\beta_0 = argmin\hat{\beta}$
  for q= 1,2,...,Q **do**
    if $|X(y - p_q)| \leq \lambda$ **then**
      $\beta_q = 0$
    else
      $\beta_0 = argmin\hat{\beta}$
  Repeat until convergence criteria is met

3.1.3 Back-propagation Neural Network : NN

Neural network model is loosely based on human brain, and is designed to recognize the pattern. It consists of several nodes, which are also called as *neuron*. There are three nodes (1) input node (2) hidden node and (3) output node. Hidden node are latent variable, which is weighted sum of input variables [7, 1].

$$\alpha_j = \sum_{i=1}^{n} w_{ij} * x_i + b_{ij} \tag{3.6}$$

Here, $i = 1, 2, ..., n$ is number of input variables and $j = 1, 2, ..., s$ are neurons in hidden layer. w is weight and b is bias(intercept). This output of hidden layer is used to calculate output variable using sigmoid function as below [7, 1, 33].

$$f(\alpha_j) = \frac{1}{1 + \exp^{\alpha_j}} \tag{3.7}$$

A node may consist of multiple layers, and an optimal number of layers can be computed using a cross-validation technique. In this study, R programming was used to analyze a neural network model where parameters such as size of hidden layers, initial random weight range, and weight decay were tuned to obtain optimal results. NN uses L2-norm regularization parameter unlike logistic regression which uses L1-norm. In L1-norm, the weight shrinks in a constant progression, whereas in L2-norm weight shrinks proportionately to its weight.

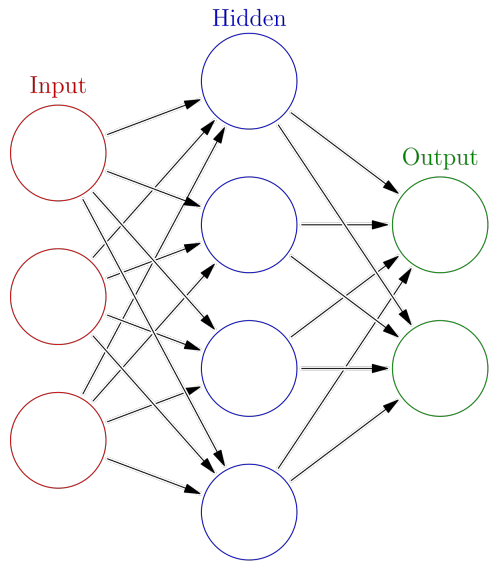


Figure 3.1: A representation of Neural Network classifier.

Algorithm 3 Neural Network

Require: : training set S, w_{ij} , test set, hidden layer size, weight decay, weight range
  Random Generate(w_{ij}) withing weight range defined
  set error ϵ value (generally 0.5)
  for i= 1,2,...,n **do**
    for j= 1,2,...,s **do**
      compute $\hat{y}_i = f(\alpha_j), using formula-, 3.6, \&, 3.7$
      $\epsilon_i = y_i - \hat{y}_i$
      if $\epsilon_i \leq 0.5$ **then**
        End
      else
        Adjust the weight w_{ij} using weight decay multiplier & recalculate error

3.1.4 Random Forest

Random Forest is one of the robust and optimal performance ensemble method for classification. The trees are built using the classification and regression trees methodology (CART) [5].In constructing the ensemble of trees, RF uses two types of randomness: first, each tree is grown using a bootstrapped version of the training data; a second level of randomness is added when growing the tree by selecting a random sample of predictors at each node to choose the best split. The number of predictors selected at each node and the number of trees in the ensemble are the two main parameters of the RF algorithm. The RF developers have reported that the method does not require much tuning of the parameters,

and the default values often produce good results. Once the forest is built, assigning a new instance to a class is accomplished by combining the trees, using a majority vote. When using a bootstrap sampling of the training data, around one-third of the samples are omitted when building each tree. These are the so-called out-of-the-bag (OOB) samples that can be used to assess the performance of the classifier and to build measures of importance [5]. A random forest algorithm [21] as shown in algorithm 4.

Algorithm 4 Random Forest

Require: : training set S, test set, n_tree = T
  T bootstrap samples from given training set S
  for i= 1,2,..., T **do**
    Develop classification & regression tree $rpart_i$ with node size m
    for j= 1,2,...,m **do**
      Random sample $m_{try} = p$ (number of variables) ⟨ In R programming minimum m_{try} = $\sqrt[2]{p}$ ⟩
    $\epsilon_i = y_i - \hat{y}_i$ on test data
  Estimate ϵ = mean(ϵ_i)

3.1.5 Adaptive Boosting (AdaBoost)

Boosting is an algorithm that combines many weak classifiers to generate a strong ensemble. This boosting is also known as stochastic boosting. The AdaBoost algorithm is given as [11]:

1. Given :(x_1, y_1), (x_2, y_2),..., (x_m, y_m) where $x_i \in$ X And $y_i \in$ Y = -1,+1
2. Initially, equal weights are assigned to all m instances. w_i = 1/m
3. For model, t = 1,...T repeat below process.
   - Based on the weight distribution generate bootstrap sample.
   - Fit the classifier to the bootstrap sample and make a prediction $P_m(x) \in$ [0,1]
   - Fit weak classifiers to the data set and select the one with the lowest weighted classification error. Compute accuracy of the model, α_m
   - Calculate the weight for weak classifier

$$f_m(x) = \frac{1}{2} \ln \frac{P_m(x)}{(1 - P_m(x))} \tag{3.8}$$

- Update the weights for each data points as:

$$w_i = w_i \exp(-y f_m(x_i)) \tag{3.9}$$

4. Normalize α_m

5. Compute the weighted sum of the predictions of the different models:

$$\hat{y} = \sum_{t=1}^{T} \alpha_m P_m(x) \tag{3.10}$$

3.2 Online or Incremental Learning Algorithm

In current study, three different classifier are analyzed.

1. Learn++ is an adaption of AdaBoost algorithm.

2. An incremental random forest is an adaption of an offline random forest to analyze sequential data arrival.

3. Hoeffding tree has sound guarantees of performance compare to other incremental decision tree learner.

3.2.1 Learn++

Learn++ is an incremental learning algorithm based on the AdaBoost(adaptive boosting) algorithm, which uses multiple classifiers to allow the system to learn incrementally; this is described in section 3.1.5.

In this algorithm, samples arrive in chunks with a predefined size. For each chunk an ensemble of base classifiers is trained and combined through weighted majority voting to an "ensemble of ensembles" [22]. Fig. 3.2 show general algorithm for Learn++ [22].

Algorithm Learn++

Input: For each database drawn from $\mathcal{D}_k$ $k=1,2,\ldots,K$

- Sequence of m training examples $S=[(x_1,y_1),(x_2,y_2),\ldots,(x_m,y_m)]$.
- Weak learning algorithm WeakLearn.
- Integer T_k, specifying the number of iterations.

Do for $k=1,2,\ldots,K$:

Initialize $w_1(i) = D(i) = 1/m,\ \forall i$, unless there is prior knowledge to select otherwise.

Do for $t = 1,2,\ldots,T_k$:

1. Set $\boldsymbol{D}_t = \mathbf{w}_t \Big/ \sum_{i=1}^{m} w_t(i)$ so that $\boldsymbol{D}_t$ is a distribution.
2. Randomly choose training TR_t and testing TE_t subsets according to $\boldsymbol{D}_t$.
3. Call WeakLearn, providing it with TR_t.
4. Get back a hypothesis $h_t : X \rightarrow Y$, and calculate the error of h_t : $\varepsilon_t = \sum_{i:h_t(x_i)\neq y_i} D_t(i)$ on $S_t = TR_t + TE_t$. If $\varepsilon_t > ½$, set $t = t-1$, discard h_t and go to step 2. Otherwise, compute normalized error as $\beta_t = \varepsilon_t/(1-\varepsilon_t)$.
5. Call weighted majority, obtain the composite hypothesis $H_t = \arg\max_{y\in Y} \sum_{t:h_t(x)=y} \log(1/\beta_t)$, and compute the composite error $E_t = \sum_{i:H_t(x_i)\neq y_i} D_t(i) = \sum_{i=1}^{m} D_t(i)[\![H_t(x_i)\neq y_i]\!]$

   If $E_t > ½$, set $t = t-1$, discard H_t and go to step 2.
6. Set $B_t = E_t/(1-E_t)$ (normalized composite error), and update the weights of the instances:

$$w_{t+1}(i) = w_t(i) \times \begin{cases} B_t, & if\ \ H_t(x_i) = y_i \\ 1, & otherwise \end{cases}$$
$$= w_t(i) \times B_t^{1-[\![H_t(x_i)\neq y_i]\!]}$$

Call weighted majority on combined hypotheses H_t and **Output** the final hypothesis:

$$H_{final} = \arg\max_{y\in Y} \sum_{k=1}^{K} \sum_{t:H_t(x)=y} \log\frac{1}{B_t}$$

Figure 3.2: Learn++ algorithm from [22]

3.2.2 Incremental Random Forest

In the current study, incremental random forest is an adaption of batch algorithm, the random forest classifier is updated with new data. First, percentile (here 25%) of an old data or validation dataset is combined with a new dataset. Then, based on the F-score of the old and new datasets, a percentile (here 5%) of bottom tree are dropped from the old dataset and the same amount of top trees is added from new dataset (Figure 3.3). The prediction of the new test set is then stored for further computation.

3.2.3 Hoeffding Tree

The Hoeffding Tree (HT) learner is utilized for inducing decision trees (such as ID3, C4.5, CART) in streaming data. This algorithm does not store the examples; only small amount of the data is used to decide the split of the decision tree. HT has sound guarantees of performance compared to other incremental decision tree learners. Unlike the batch decision tree algorithm, once the root best split is achieved, the example is passed down to the leaves to define new split [9]. In this learner, each node contains tests for attribute/predictor variables, each node branch corresponds to possible outcomes, and each leaf contains class/response variable predictions [9]. A batch tree learner stores all data points in the memory, thus limiting the number of data points learned. In HT, the number of examples necessary to obtain the best split at each node is decided by *Hoeffding Bound* (or additive Chernoff Bound), which is calculate by the formula 3.11

$$\epsilon = \sqrt{\frac{R^2 \ln(\frac{1}{\delta})}{2n}} \tag{3.11}$$

Here, n are independent variables with range R and mean $\overline{r}$. The Hoeffding bound states that with a probability of $1 - \delta$ the true mean of the variable is at least $\overline{r} - \epsilon$ [9].

FOr example, assuming $G(X_i)$ is a heuristic measure to choose test attributes for example Gini index in case of the CART (*Classification And Regression Trees*). With the X_a attribute observed highest $\overline{G}$ with n number of examples, and X_b as the second best. If the difference between the heuristic measures, is $\triangle G > \epsilon$, it can be said that X_a is a better split [23]. HT generic algorithm is as in figure 3.4 [9, 35].

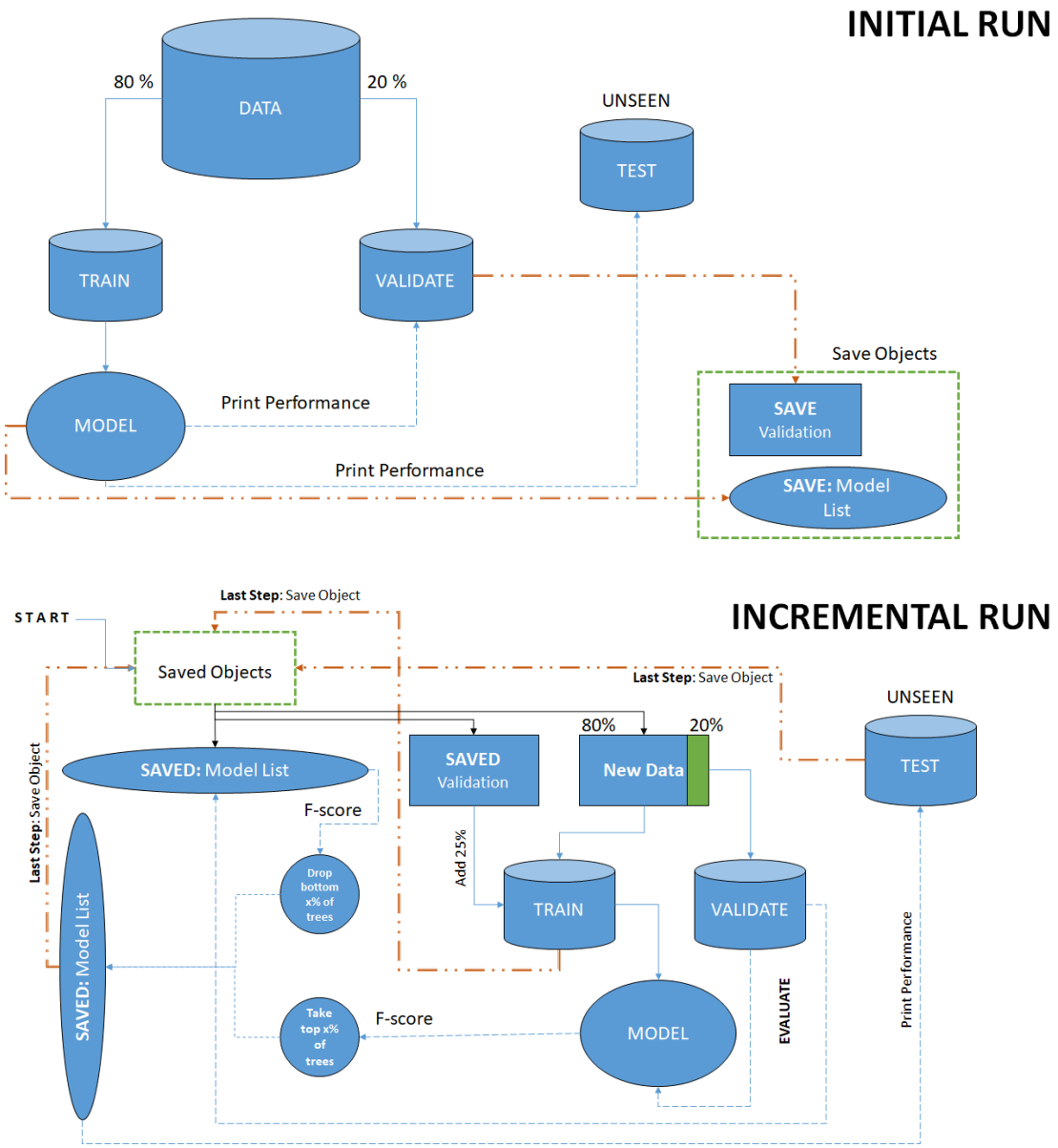


Figure 3.3: Incremental random forest flow diagram

Inputs:	S	is a sequence of examples,
	$\mathbf{X}$	is a set of discrete attributes,
	$G(.)$	is a split evaluation function,
	δ	is one minus the desired probability of choosing the correct attribute at any given node.
Output:	HT	is a decision tree.

Procedure HoeffdingTree $(S, \mathbf{X}, G, \delta)$
Let HT be a tree with a single leaf l_1 (the root).
Let $\mathbf{X_1} = \mathbf{X} \cup \{X_\emptyset\}$.
Let $\overline{G}_1(X_\emptyset)$ be the $\overline{G}$ obtained by predicting the most frequent class in S.
For each class y_k
  For each value x_{ij} of each attribute $X_i \in \mathbf{X}$
    Let $n_{ijk}(l_1) = 0$.
For each example $(\mathbf{x}, y_k)$ in S
  Sort $(\mathbf{x}, y)$ into a leaf l using HT.
  For each x_{ij} in $\mathbf{x}$ such that $X_i \in \mathbf{X}_l$
    Increment $n_{ijk}(l)$.
  Label l with the majority class among the examples seen so far at l.
  If the examples seen so far at l are not all of the same class, then
    Compute $\overline{G}_l(X_i)$ for each attribute $X_i \in \mathbf{X}_l - \{X_\emptyset\}$ using the counts $n_{ijk}(l)$.
    Let X_a be the attribute with highest $\overline{G}_l$.
    Let X_b be the attribute with second-highest $\overline{G}_l$.
    Compute ϵ using Equation 1.
    If $\overline{G}_l(X_a) - \overline{G}_l(X_b) > \epsilon$ and $X_a \neq X_\emptyset$, then
      Replace l by an internal node that splits on X_a.
      For each branch of the split
        Add a new leaf l_m, and let $\mathbf{X_m} = \mathbf{X} - \{X_a\}$.
        Let $\overline{G}_m(X_\emptyset)$ be the $\overline{G}$ obtained by predicting the most frequent class at l_m.
        For each class y_k and each value x_{ij} of each attribute $X_i \in \mathbf{X_m} - \{X_\emptyset\}$
          Let $n_{ijk}(l_m) = 0$.
Return HT.

Figure 3.4: Hoeffding Tree algorithm from [9]

RMOA (R Massive Online Analysis)

MOA is the most popular open source framework for data stream mining (Figure 3.5), with a very active growing community. MOA is written in Java. Data streaming in MOA has various requirement:

1. Process an example at a time, and inspect it only once (at most)
2. Use a limited amount of memory
3. Work in a limited amount of time
4. Be ready to predict at any time

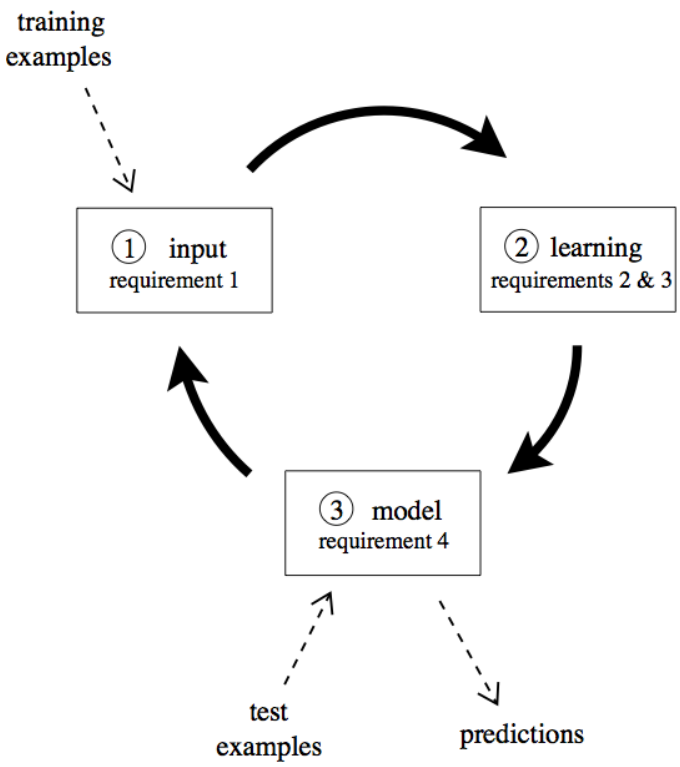


Figure 3.5: Data stream classification cycle in MOA

In the current study, HT code used an MOA framework in R programming language.

Chapter 4

Experiment

The purpose of experiment is to compare offline and online algorithms in different healthcare datasets. This comparison is based on different parameters such as performance of model, model complexity, time, and the memory consumption of algorithm.

4.1 Datasets

This study analyzed two different healthcare datasets (table 4.1). Details of the variables are explained in 4.1.1 & 4.1.2.

Table 4.1: The evaluated Datasets and their characteristics

Datasets	Train obs.	Test obs.	Features	Class
Mortality	8382	932	37	2
Diabetic Burnout	92808	10313	9	2

4.1.1 Mortality Data

This dataset contain information about patient mortality, with 9314 observations and 37 predictor variables (Table 4.2). For analysis, Encounter ID and Admitted Date was excluded from predictor variables; overall there are 37 independent variable and one binary response variable in this dataset.

Table 4.2: Mortality Data

Variable Name	Variable Descrption
x_1	Encounter ID
x_2,x_3,x_4,x_5	Heart rate for 24 hrs(min, max, std, mean)
x_6,x_7,x_8,x_9	respiratory rate for 24 hrs(min, max, std, mean)
x_{10},x_{11},x_{12},x_{13}	temperature for 24 hrs(min, max, std, mean)
x_{14},x_{15},x_{16},x_{17}	WBC for 24 hrs(min, max, std, mean)
x_{18},x_{19},x_{20},x_{21}	Heart rate ratio for 24 hrs(min, max, std, mean)
x_{22},x_{23},x_{24},x_{25}	respiratory rate ratio for 24 hrs(min, max, std, mean)
x_{26},x_{27},x_{28},x_{29}	temperature ratio for 24 hrs(min, max, std, mean)
x_{30},x_{31},x_{32},x_{33}	WBC ratio for 24 hrs(min, max, std, mean)
x_{34}	Age
x_{35}	Gender
x_{36}	Race
x_{37}	Marital status
x_{38}	Admitted Date
x_{39}	Payer Code
x_{40}	Expired

4.1.2 Diabetic burnout Data

The diabetic burnout dataset was acquired from the Cerner Healthcare System. This dataset contains the diabetic patient information from UT's health services. This research used predictive analysis to estimate patient *burnout* conditions, patients *burnout* is the feeling of exhaustion that causes patients to discontinue their self-care. This dataset contain 103121 observations and 9 predictor variables (Table 4.3). Overall there are 9 independent variables and one binary response variable in this dataset; the response variable is patient burnout condition. Diabetes mellitus codes are identified according to the International Classification of Diseases, ICD-9 and ICD-10-CM. The compliance description from the ER diagram of health facts data warehouse defines "patient condition" as understanding whether he or she is taking the medication prescribed.

4.2 Data preparation & Model Evaluation

Few actions mentioned below needed to perform before performing predictive analysis:

Table 4.3: Diabetic burnout Data

Variable Name	Variable Descrption
x_1	Age (years)
x_2	Total Charges ($)
x_3	Race
x_4	Gender
x_5	Marital Status
x_6	Diagnosis Code
x_7	Discharge disposition code
x_8	Payer Code
x_9	Result Indicator
x_{10}	Patient burnout condition

- Detection of missing data and outliers
- Identify imbalance data.
- To get more robust performance measure cross validation of the data

4.2.1 Performance Evaluation

Both the datasets have a binary variable; performance measures used are accurate. An accuracy of model is measured using *Area Under Receiver Operating Characteristic* (AUC (ROC)) . The ROC curve illustrates the diagnostic ability of the binary classifier system. ROC is created by plotting the true positive rate or sensitivity against (1-specificity) or false positive rate (Equations 4.1 & 4.2 respectively). The Area under the curve is calculated using formula 4.3.

$$TPR = \frac{\sum \text{True positive}}{\sum \text{Condition positive}} \tag{4.1}$$

$$FPR = \frac{\sum \text{False positive}}{\sum \text{Condition negative}} \tag{4.2}$$

$$AUC = \int (TPR)(FPR)' \tag{4.3}$$

In incremental random forest , the F-score is measured to evaluate each tree performance. F1-score or F-score or F-measure depend on the precision and sensitivity of the model:

$$precision = \frac{\sum \text{True positive}}{\sum \text{predicted condition positive}} \tag{4.4}$$

$$F_1 = 2.\frac{\text{precision.sensitivity}}{\text{precision} + \text{sensitivity}} \tag{4.5}$$

4.2.2 Cross Validation

The cross validation technique is used to optimize the performance of model due to unbalanced data. Here the k-fold cross validation scheme is applied to both datasets. The k-fold cross validation technique randomly cuts the original sample into k-equal subsamples. Out of k subsamples, one sample is consider as a test set for validation and testing of the data. And k-1 samples are used to train the model. In this study, 10fcv was used, meaning 9 subsamples were used as a training set, and one subsample was used as a test set. Figure 4.1 show cross validation process.

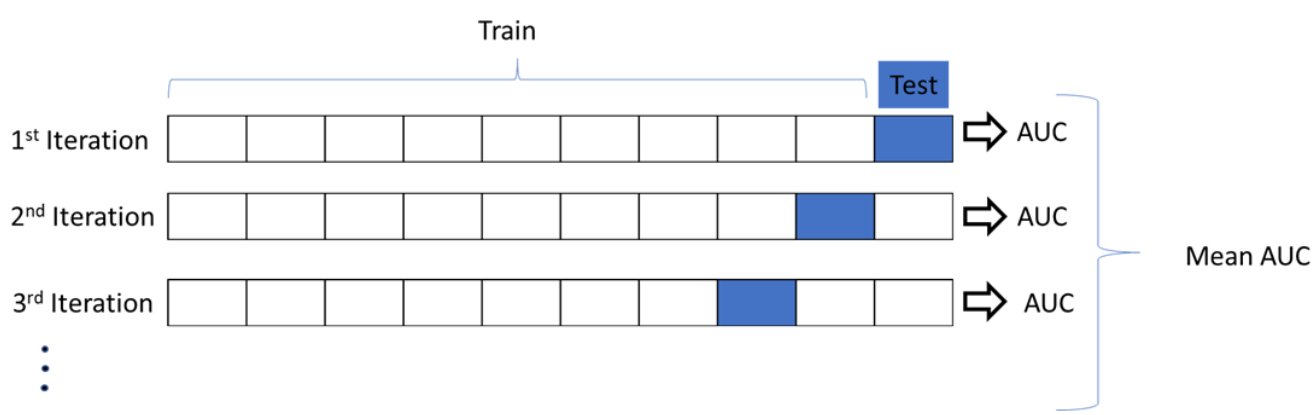


Figure 4.1: Cross Validation

In the case of an offline algorithm, cross validation performance datasets are combined to the mean of all performance measures (AUC). On the other hand, the same cross validation datasets are fed to the model as sequential data. The final performance measure of the online algorithm is then compared with the offline model.

4.2.3 Bootstrap and Bagging

The bootstrap sampling method samples n instances from the dataset without replacement. The probability of any instance not chosen is $(1 - \frac{1}{n})^n \approx \exp(-1) \approx 0.368$. Equation 4.6 show accuracy estimation of bootstrap training samples, m from dataset of n instances given that α_i for sample i [17].

$$\alpha_{boot} = \frac{1}{m}\sum_{i=1}^{m}(0.632.\alpha_i + 0.368.\alpha_{train}) \tag{4.6}$$

where α_{train} is the accuracy of the training set.

Algorithms like random forest and adaptive boosting use the bagging ensemble method to enhance model accuracy. The ensemble model is an aggregate prediction of multiple base models [29]. Decision trees are very sensitive to small changes in data; random forest and adaptive boosting learners build multiple trees and aggregate their performance. Bagging is also used to estimates generalized error and correlation of ensemble trees [5]. Bagging reduce the variance of unstable model. Bagging and bootstrap algorithm 5 [3] :

Algorithm 5 Bagging

Require: : training set S, Inducer I, integer T (number of bootstrap samples).
  for i= 1,2,...,T **do**
    S' = bootstrap from sample S
    $C_i = I$(S')
  C*$(x) = argmax \sum_{i=y} 1$
  output : Synthetic data S

4.3 Hyper-parameters and Model Complexity

The model selection in offline or incremental learning is dependent on hyper- parameters, which are crucial in determining model properties such as model complexity, regularization, and learning rate. In batch learning, hyper-parameters are defined prior to training. Some examples of hyper-parameters used in different models are number of leaves or depth of tree, learning rate, and chunk size. In general, model complexity determines model error, if training and testing errors are similar, which indicates higher complexity. In offline learning,

a cross-validation technique is used to optimize hyper-parameters [36]. Higher variance or over-fitting problems of the model can be optimized with an ensemble technique. Bagging, random forest, and adaptive boosting algorithms in this study used an ensemble model by aggregating.

In incremental learning, model complexity is variable as it is impossible to estimate model complexity for the variable in advance. Training and run time are measures of model complexity in incremental learning. However, it varies for different programming languages [22]. In this analysis, R and Matlab programming language were used for various algorithms.

4.4 Results

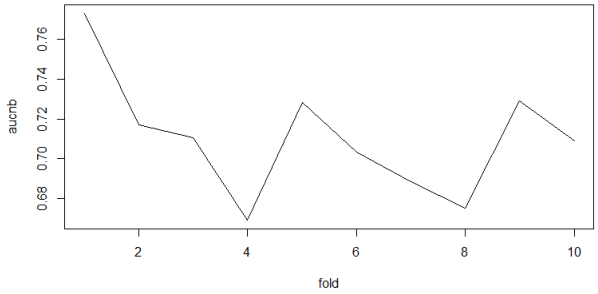
Model performance accuracy was measured in this study by using AUC (Table 4.4).

Table 4.4: Model accuracy comparison

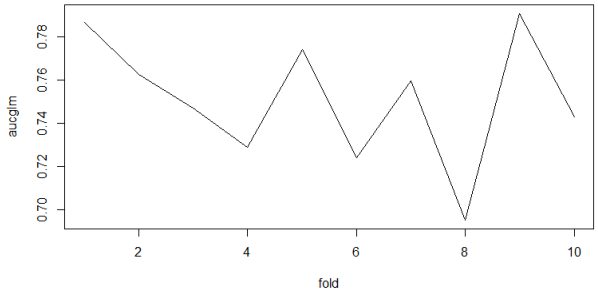
Datasets	off-line accuracy				
	NB	LR	NN	RF	AdaBoost
Mortality	0.71	0.75	0.75	**0.76**	**0.76**
Diabetic Burnout	0.72	0.74	0.89	**0.98**	0.95
	on-line accuracy				
	ORF	Learn++	Hoeffding tree		
Mortality	**0.98**	0.88	-		
Diabetic Burnout	**0.98**	**0.97**	0.74*		

4.4.1 Batch/off-line learning results

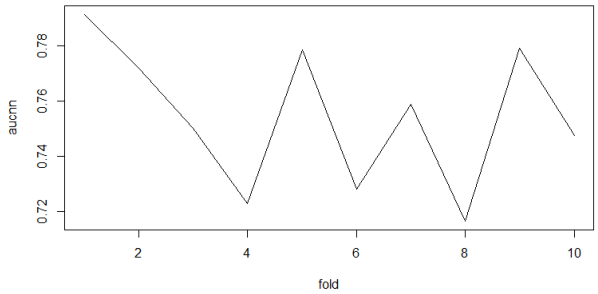
It can be interpreted that accuracy in the dataset for prediction of mortality improved through incremental learning when accuracy for cross-validation offline learning algorithm on mortality dataset. and for the diabetic burnout dataset are plotted (Figure 4.2, 4.3, and Table 4.4). However, diabetic burnout data incremental predictive analysis has no improvement over batch random forest learner.



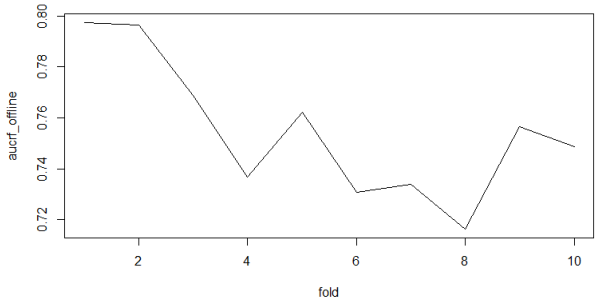
(a) Naive Bayes for mortality data



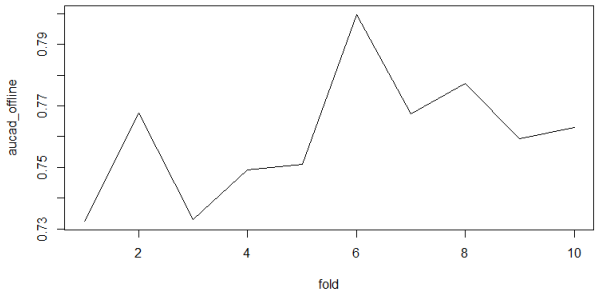
(b) Logistic Regression for mortality data



(c) Neural Network for mortality data

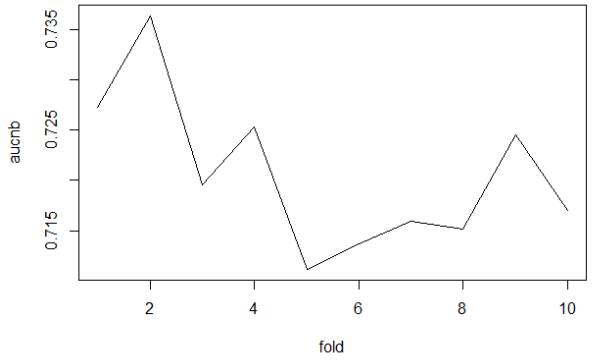


(d) Random Forest for mortality data

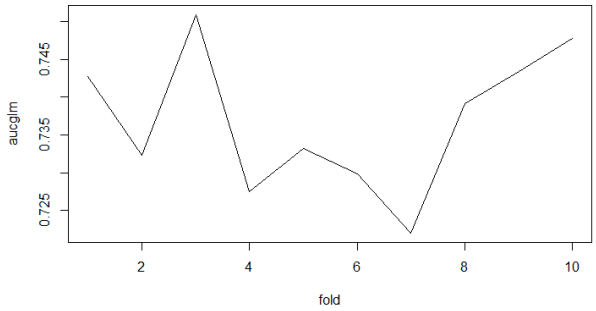


(e) Adaptive Boosting for mortality data

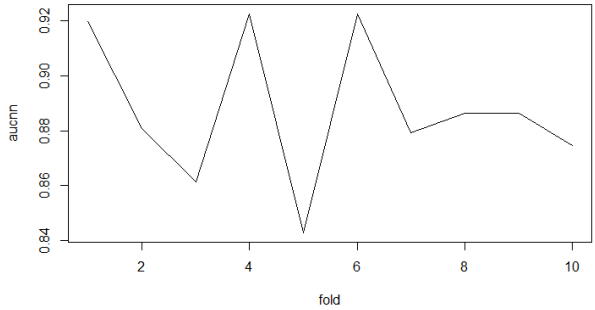
Figure 4.2: Cross-validation results of offline learning accuracy vs fold mortality dataset.



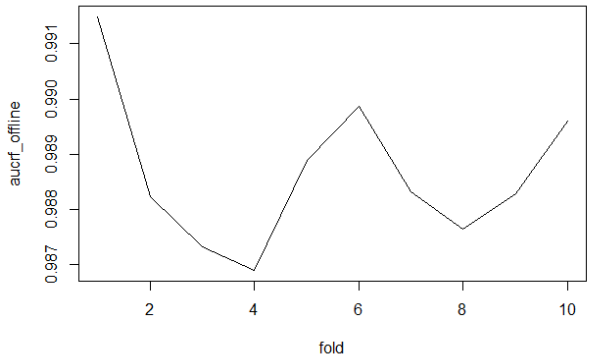
(a) Naive Bayes for diabetic data



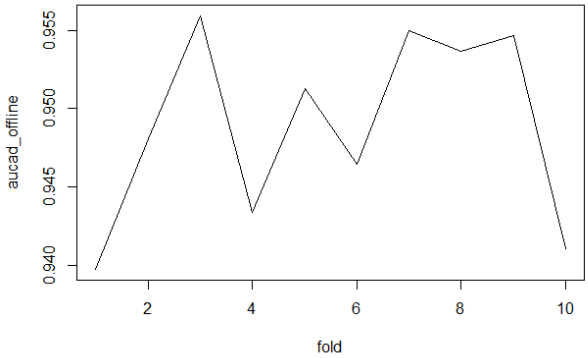
(b) Logistic Regression for diabetic data



(c) Neural Network for diabetic data



(d) Random Forest for diabetic data



(e) Adaptive Boosting for diabetic data

Figure 4.3: Cross-validation results of offline learning accuracy vs fold on diabetic dataset.

Random Forest

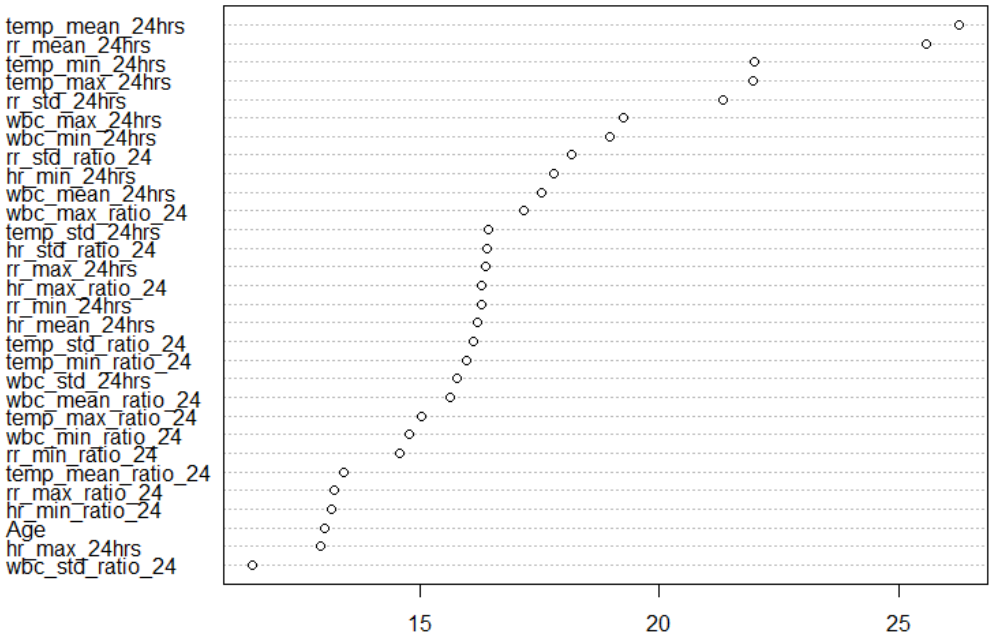
The top plot (Figure 4.4) measure is computed from permuting OOB (out-of-bag) data i.e. prediction error (error rate of classification, mean square error for regression) of predictor variables, $(x_1, x_2..., x_n)$ are recorded for each tree then the same is done after permuting. The difference of two is then averaged over all trees. Another plot in fig. 4.4 measure is total decrease node impurity measure in Gini Index. Gini index of the split s of the parent node τ (Equation 4.7) [32]:

$$\Delta(s, \tau) = p_\tau(1 - p_\tau) - \left(\frac{\tau_L}{\tau} p_{\tau_L}(1 - p_{\tau_L}) + \frac{\tau_R}{\tau} p_{\tau_R}(1 - p_{\tau_R}) \right) \tag{4.7}$$

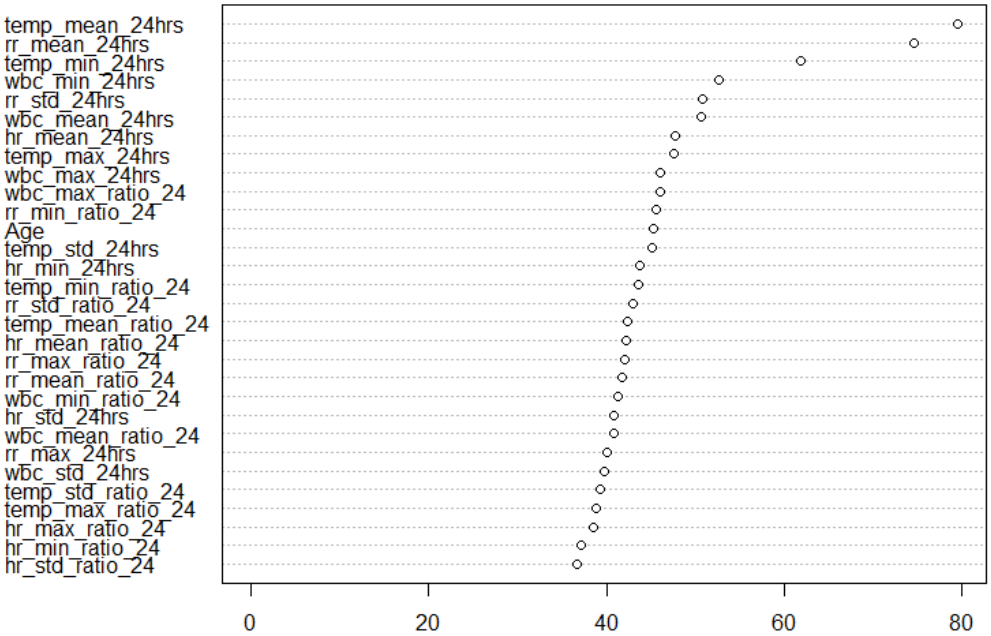
Here, τ_L and τ_R are left and right node of split s. The plot 4.4 demonstrates that variables temperature (mean, min, and max) and respiratory rate (mean) play vital role in mortality prediction.

Similarly, variables age, total charges, and diagnosis code (i.e. type of diabetes) contribute significantly in predictions of patient's burnout condition (Plot 4.5).

The AdaBoost variable importance plot for diabetic and mortality show similar variable importance in prediction analysis.

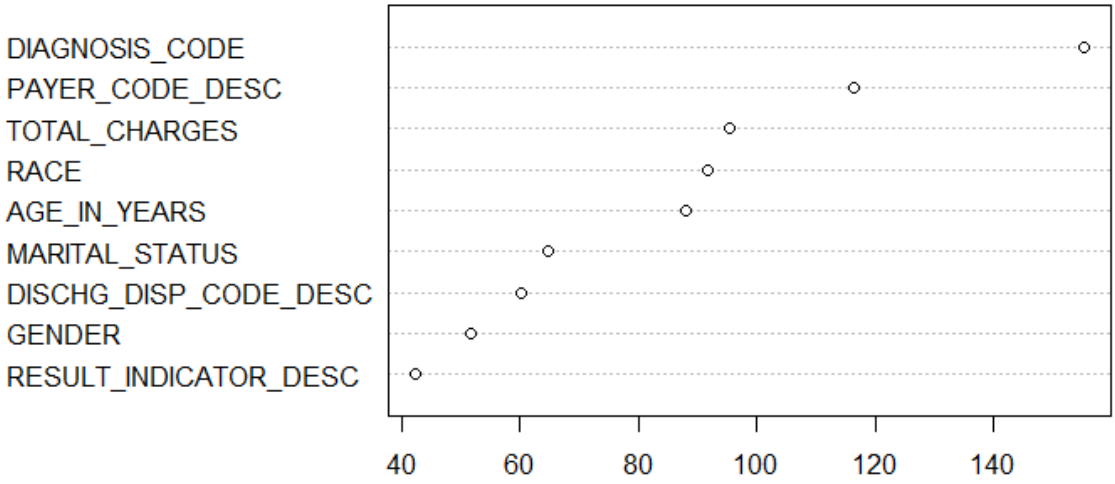


(a) Mean Decrease Accuracy for motality data

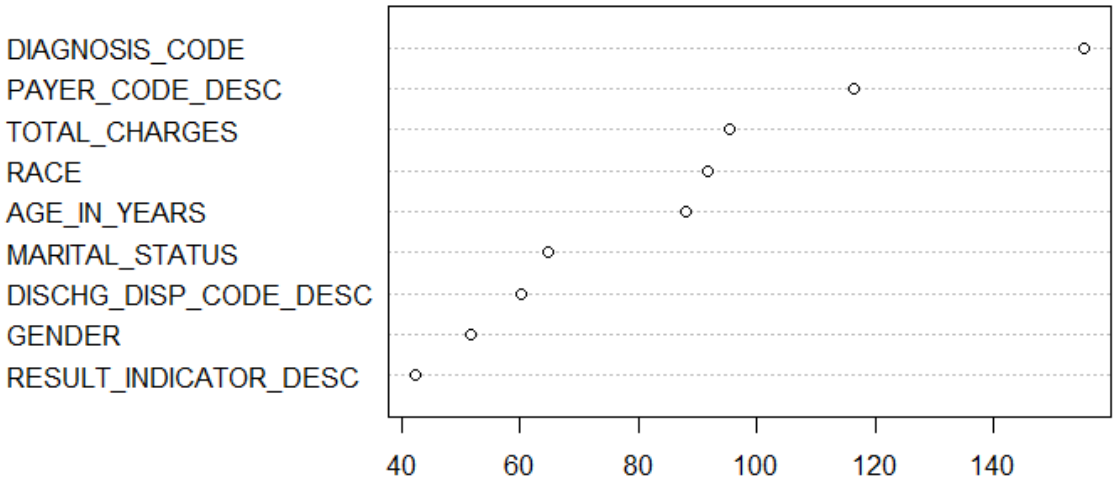


(b) Mean Decrease Gini for motality data

Figure 4.4: Random forest variable importance for Mortality dataset.



(a) Mean Decrease Accuracy for diabetic data



(b) Mean Decrease Gini for diabetic data

Figure 4.5: Random forest variable importance for Mortality dataset.

4.4.2 Incremental/on-line learning results

Learn++

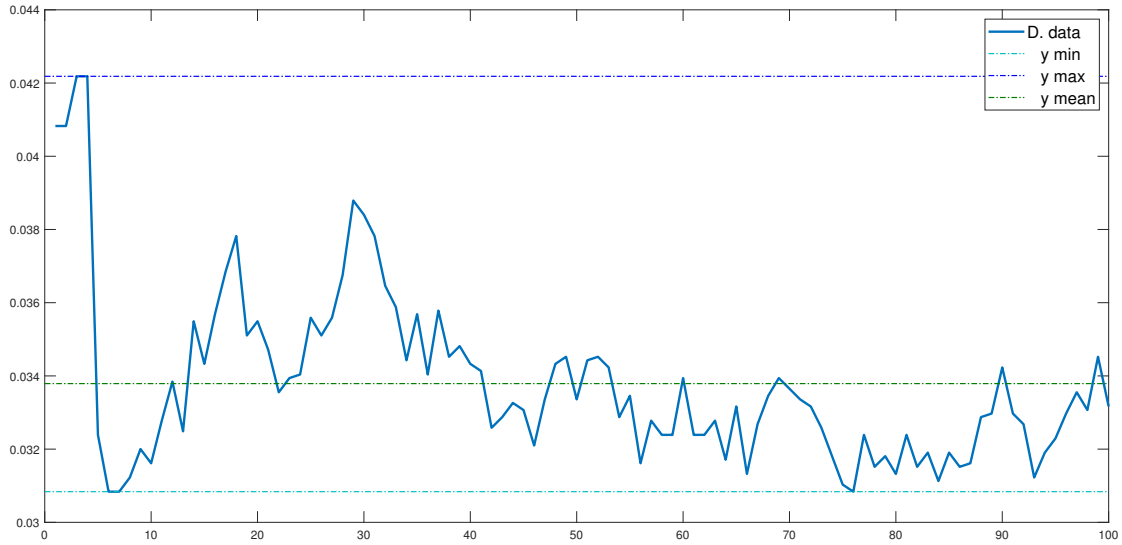
Error has been improved over the iteration with iterations using the incremental Learn++ algorithm on mortality and diabetic burnout dataset respectively (Figure 4.6). For mortality dataset there is 12.6% accuracy improvement over the iteration; however, it is 1.14% for diabetic burnout.

Hoeffding Tree

HT is an algorithm is based on the RMOA framework, which converts a data frame into streaming data; chunk size then defines data arrive every classification cycle. Massive data algorithm example size of less than 10,000 generally causes over-fitting of the model. Cross-validation datasets were not used in this study, thus *Mortality Data* has only 9,314 data points. For this reason, only diabetic burnout dataset was analyzed using Hoeffding tree learner.

Diabetic burnout data was divided into train (90% of samples) and test sets using the random method. The train set was converted to streaming data: 10,3121 examples arrive sequentially in a chunk size of 1,000 samples. The test set is then predicted in the final model.

(a) Mortality data Learn++ error



(b) Diabetic burnout data Learn++ error

Figure 4.6: Learn++ algorithm error graph

Chapter 5

Conclusions and Future Research

In this study, the same data was analyzed with batch and incremental learning algorithms. To simulate incremental learning, 10-fold cross-validation data was used as a new arrival sequence. Experimental results on the mortality dataset shows that incremental learning vastly improves performance accuracy. The batch learning algorithm AUC is higher for the random forest, and the AdaBoost learner is followed by a neural network in the case of diabetic burnout data. However, in diabetic burnout there is no improvement in incremental learning over the batch algorithm. The Random forest and AdaBoost variable importance plots indicate that temperature and respiratory rate are critical parameters in mortality prediction. Variables such as age, total charges, and type of diabetes contribute significantly to patient burnout condition. In future research, various other incremental learning algorithms can be analyzed on real-time data. This study applied incremental random forest, but online random forest (Saffari et al.) and Mondrian Forest are more effective in predictive analysis. Additionally, machine learning algorithm adaption is required to access real-time data from an actual database, for example MySQL, NoSQL, and SQL developer.

Depending on predictive or descriptive analytics requires that arrival data point be optimized. Computational efficiency depends on model complexity, which in turn is based on hyperparameter optimization. Concept drift is an important phenomenon in cases of healthcare Big Data as data distribution is not constant with time periods. Anomaly

detection is one of important area for research in healthcare analytics. Incremental learning can be applied to various wearable devices or sensors to track improvement in patient health.

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Appendices

A Summary of Equations

On-line accuracy of model at time t is given by [22]:

$$E(S) = \frac{1}{t}\sum_{i=1}^{t} 1 - \mathcal{L}(h_{i-1}(x_i), y_i) \tag{A.1}$$

General ordinary least square regression

$$y = X\beta + \varepsilon \tag{A.2}$$

Naive Bayes' theorem :

$$P(A|B) = P(A) * \frac{P(B|A)}{P(B)} \tag{A.3}$$

Naive Bayes' theorem for binary classification :

$$P(y = 1|X = k) = P(y = 1) * \frac{P(X = k|y = 1)}{P(X = k)} \tag{A.4}$$

Logistic Regression model :

$$z_i = \ln\left(\frac{P(x_i)}{1 - P(x_i)}\right) = \beta_0 + \beta_1 x_1 + ... + \beta_n x_n \tag{A.5}$$

The log-likelihood function :

$$l(\beta) = \sum_{i=1}^{n} y_i \ln\left(\frac{P(x_i)}{1 - P(x_i)}\right) - \ln\left[1 + \left(\frac{P(x_i)}{1 - P(x_i)}\right)\right] \tag{A.6}$$

Logistic Regression Lasso estimator formula :

$$\hat{\beta} = argmin\Big(- l(\beta) + \lambda \sum_{q=0}^{Q} |\beta_{i,q}|\Big) \tag{A.7}$$

Neural Network Model :

$$\alpha_j = \sum_{i=1}^{n} w_{ij} * x_i + b_{ij} \tag{A.8}$$

Sigmoid function :

$$f(\alpha_j) = \frac{1}{1 + \exp^{\alpha_j}} \tag{A.9}$$

AdaBoost weight calculation for weak classifier :

$$f_m(x) = \frac{1}{2} \ln \frac{P_m(x)}{(1 - P_m(x))} \tag{A.10}$$

AdaBoost weights for each data point :

$$w_i = w_i \exp(-y f_m(x_i)) \tag{A.11}$$

AdaBoost Compute the weighted sum of the predictions of the different models :

$$\hat{y} = \sum_{t=1}^{T} \alpha_m P_m(x) \tag{A.12}$$

Hoeffding bound :

$$\epsilon = \sqrt{\frac{R^2 \ln(\frac{1}{\delta})}{2n}} \tag{A.13}$$

True positive rate or sensitivity:

$$TPR = \frac{\sum \text{True positive}}{\sum \text{Condition positive}} \tag{A.14}$$

False positive rate :

$$FPR = \frac{\sum \text{False positive}}{\sum \text{Condition negative}} \tag{A.15}$$

Area Under Curve :

$$AUC = \int (TPR)(FPR)' \tag{A.16}$$

Precision of model :

$$precision = \frac{\sum \text{True positive}}{\sum \text{predicted condition positive}} \tag{A.17}$$

F_1 score of model :

$$F_1 = 2.\frac{\text{precision.sensitivity}}{\text{precision} + \text{sensitivity}} \tag{A.18}$$

Accuracy of bootstrap model :

$$\alpha_{boot} = \frac{1}{m}\sum_{i=1}^{m}(0.632.\alpha_i + 0.368.\alpha_{train}) \tag{A.19}$$

B Summary of Code

All the software programming codes are available on the GitHub link: Machine Learning code

C Summary of Confusion Matrix

C.1 Offline machine learning

Confusion matrix is calculated on the 10th dataset of cross-validation (Tables C.2, C.3, C.5, C.6, C.8, C.9, C.11, C.12).

Table C.1: Naive Bayes' algorithm confusion matrix

Table C.2: Mortality Data NB

	Actual	
predicted	0	1
0	702	80
1	111	39

Table C.3: Diabetic Data NB

	Actual	
predicted	0	1
0	6661	250
1	2961	440

Table C.4: Logistic regression algorithm confusion matrix

Table C.5: Mortality Data LR

	Actual	
predicted	0	1
0	803	110
1	5	14

Table C.6: Diabetic Data LR

	Actual	
predicted	0	1
0	9631	652
1	6	23

Table C.7: Random forest algorithm confusion matrix

Table C.8: Mortality Data RF

	Actual	
predicted	0	1
0	811	103
1	8	10

Table C.9: Diabetic Data RF

	Actual	
predicted	0	1
0	9536	179
1	131	466

Table C.10: AdaBoost algorithm confusion matrix

Table C.11: Mortality Data AdaBoost

	Actual	
predicted	0	1
0	804	117
1	4	7

Table C.12: Diabetic Data AdaBoost

	Actual	
predicted	0	1
0	9618	644
1	0	50

C.2 Online machine learning

In this study, confusion matrix is computed on final classifier of online algorithms (Tables C.14, C.15, C.17, C.18, C.19).

Table C.13: Learn++ algorithm confusion matrix

Table C.14: Mortality Data Learn++

	Actual	
predicted	0	1
0	794	120
1	4	13

Table C.15: Diabetic Data Learn++

	Actual	
predicted	0	1
0	9481	117
1	246	468

Table C.16: Incremental random forest algorithm confusion matrix

Table C.17: Mortality Data IRF

	Actual	
predicted	0	1
0	815	102
1	1	14

Table C.18: Diabetic Data IRF

	Actual	
predicted	0	1
0	9608	157
1	98	449

Table C.19: Hoeffding tree algorithm confusion matrix on Diabetic data

	Actual	
predicted	0	1
0	9548	344
1	110	310

Vita

Nikhil Mukund Jagirdar was born in Aurangabad, a city in the state of Maharashtra, India. In 2005 he completed a B.E. in Mechanical Engineering from the College of Engineering, Pune, India. He spent more than 10 years working in product design and development department for automotive industries in India. In 2016, Nikhil joined the graduate program in Industrial & System Engineering Department of the University of Tennessee, Knoxville. Currently, he is working as a graduate assistant under the guidance of Dr. Xueping Li in Industrial & System Engineering Department. Nikhil will graduate with an MS in Industrial Engineering with a Statistics minor in December 2018.