PREDICTIVE MODELLING IN LIFE INSURANCE.

By

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June 2017

AN ESSAY PRESENTED TO AIMS RWANDA IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR THE AWARD OF MASTER OF SCIENCE IN MATHEMATICAL SCIENCES

AIMS | African Institute for Mathematical Sciences RWANDA

DECLARATION

This work was carried out at AIMS Rwanda in partial fulfilment of the requirements for a Master of Science Degree.

I hereby declare that except where due acknowledgement is made, this work has never been presented wholly or in part for the award of a degree at AIMS Rwanda or any other University.

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ACKNOWLEDGEMENTS

I would like to express my sincere appreciation to my supervisor, Dr. Yabebal Fantaye for his unending support through the course of this work. His guidance and advise assisted me in compiling this essay.

I also thank my tutor, Marie Yvonne Uwera for her continuous support and insightful comments through the course of my work.

In addition, I would like to thank my fellow student, Catherine Moraa, for her brilliant idea in the course of the essay.

Lastly, I thank my parents for their unending support and encouragement.

Abstract

The predictive modelling concept is a commonly accepted framework for building insurance models. It involves using data in forecasting future unseen events, capturing and exploiting the relationships between the explanatory variables and the target variable, which we intend to predict. The introduction sheds light on the conditions and setbacks that have made predictive modelling in life insurance lag behind other insurance sectors.

The aim of this research is to understand the steps involved in building a predictive model and make a comparison between two known algorithms, the Random Forest and the XGBoost. We then explore why XGBoost is a better algorithm in prediction as compared to random forest.

Contents

1. Introduction

Initially, insurers guessed the appropriate premiums to charge or determined premiums by analysing a single factor such as age of the insured. Basically, traditional underwriting depended on how accurately an insurer is able to forecast a policy's ultimate cost, how to price its products to maximize profits and in turn avoid adverse selection. With changing technology, insurance operations have become more advanced and analysis methods have shifted from univariate analysis to multivariate analysis where several factors like characteristics of the area where the risk is located, what other policies the insured has, medical history among others are used to determine appropriate premiums Nyce and CPCU (2007).

Modern day insurers use predictive analytics to determine additional information that may correlate with a potential insurance outcome. This has been made possible due to the large quantity of data generated by insurers. The scientific guidance from predictive models has assisted insurers to make expert decisions in claim management, premium audit, underwriting and fraud detection Mike Batty, 2017.

The advantages of predictive analytics are: new premium growth, improved underwriting efficiency, accurate pricing, reduction of fraud and improved customer retention. However, this technique entails some disadvantages like cost of implementation is too high, the need for clean, accurate data, inadequate preprocessing of the data, over fitting the model to the existing data and inadequate model validation.

To overcome this problem, the foundation for an effective predictive model has been laid down by Kuhn and Johnson (2013). They include: Deep knowledge of the problem context, relevant data, intuition, adequate techniques for data preprocessing, visualization as well as modelling tools for handling a range of possible scenarios.

1.1 Problem Statement

Risk management is one of the fundamental tasks of insurance companies. The insurance industry should constantly adopt new technologies to address new risk types and trends affecting people's lives. We depend on insurance for several reasons but it all scales down to the basic principle: minimizing risk in that clients pay a fee, and in exchange, insurers cover any costs that could arise with future calamities.

Clients provide extensive information to identify risk classification and illegibility, including scheduling medical exams, family medical history, credit history, behavioural risk factors, and so on, making the whole insurance process lengthy. The outcome is that the clients are turned off. This constitutes the main reason why majority of the households do not own individual life insurance.

Life underwriting has its own modelling challenges making insurers to turn to predictive analytics to curb the problems. It is worth noting that auto underwriting has achieved remarkable success with predictive modelling unlike life underwriting where modelling is a new skill (Mike Batty, 2017).

Predictive modeling: It is defined as the process of developing models such that the model's prediction accuracy on future or unseen data can be understood and quantified. Therefore, predictive modelling is a combination of machine learning, pattern recognition and data mining Kuhn and Johnson (2013).

Predictive modelling has its roots in actuarial science where analysts seek to determine the right price for the right risk, aprocess known as rate making and avoid adverse selection Frees et al. (2014).

Mike Batty, 2017 Building a predictive model requires:

- The availability of a sufficiently rich dataset where the predictive variables that correlate with the target can be identified.
- An application by which results from the model are translated to business actions.
- A clearly defined target variable.
- A large number of observations to build the model so as surfacing relationships can be separated from random noise.

The above requirements are easily met with auto insurance. To clearly understand the challenges faced in life insurance, we compare life underwriting and auto underwriting (Mike Batty, 2017).

- Auto insurers can make underwriting corrections if mistakes are made through rate increases in subsequent renewals of policies whereas life insurers must price policies appropriately from the outset.
- For the auto insurer, the amount of insurance loss of a six-month contract is a target variable for the model. Life insurance is sold through long duration contracts, usually over a period of 10, 20 or more years. Due to the fact that the contribution of a given risk factor to mortality could change with time, it is not sufficient to analyse mortality experience over a short period of time.
- Accessing historical data that can be used in modelling life insurance is a challenge. Not all life insurers record underwriting data in an electronic format; The available underwriting data that has been implemented in recent years is not available electronically or in a machine readable form. Even when such data has been captured for years, the content of the older data may be different from the data gathered for current applicants.
- Life underwriting is subject to psychological biases and inconsistencies of human decision-making thus predictive models help to curb this challenge.
- Life insurance claims have low frequency compared to auto insurance claims. Modelling statistically significant variation in either auto claims or mortality requires a large sample of loss events. Therefore auto insurers have ample data to build robust models using loss

data while life insurers will find the data recorded in at similar times frames insufficient for modelling.

Given that the target variable and data volume in life insurance is a concern, insurers are utilizing underwriting decisions as the target variable as they contain a lot of information, expert judgement, do not require long developing periods as in insurance claims and are abundant in supply.

1.2 Objective

We are working on data from Prudential Life Insurance where the challenge is trying to make purchasing of life insurance easier by understanding the algorithms and procedures used in building a predictive model that accurately classifies risk using a more automated approach. We compare the Random Forest and XGboost algorithms. The data we are working on is from kaggle which is a platform for data science competitions. The host provides raw data and a description of the problem. Those participating in the competition then train algorithms where highly performing models can be adopted for predicting similar trends in the future.

1.3 Trends in Insurance

Underwriting

This is the process of understanding and evaluating risk in insuring a life or property. This ability is gained not only through theoretical study but also as a result of years of experience dealing with similar risks and mastering the art of paying claims on those risks. It is the traditional way of pricing and classifying risks in insurance (Macedo, 2009).

An insurance life office will have a premium rate schedule for a given type of policy. This rates depend on **the size of the policy and rating factors**. To establish an applicants risk level, a proposal form giving information on relevant rating factors such as age, gender, any dangerous hobbies, occupation, smoking habits, and health history is filled. The purpose of underwriting is to classify potential policy holders into homogeneous risk categories and assess what additional premium would be appropriate if risk factors indicate that standard premium rates would be too low Dickson, Hardy, and Waters (2013) .

Disadvantages

- There is the risk of adverse selection by policy holders if the underwriting is not strict. This means that very high-risk individuals will buy insurance in disproportionate numbers leading to excessive losses.
- The underwriting process could be lengthy and costly.

- Both the insurer and policy holder may assume 'utmost good faith' such that in case of loss and important information was held back or false, then the full sum assured may not be paid by the insurer in case the client claims from the insurance.

Thus, the use of predictive models makes the underwriting process faster, more economical, more efficient and more consistent when the model is used to analyze a set of underwriting requirements.It is also worth noting that models are not subject to bias in the same way that underwriters ,who do not always act with perfect consistency or optimally weigh disparate pieces of evidence, are.

1.4 Overview of Predictive Modelling

In predictive modelling, two situations arise:

- One is required to fit a well-defined parametrized model to the data using a learning algorithm that can find parameters on the large dataset without over-fitting. In this case, lasso and elastic-net regularized generalised linear models are a set of modern algorithms which meet this need because they are fast, work on huge datasets and avoid over-fitting automatically.
- One needs to accurately predict a dependent variable. A learning algorithm that automatically identifies the structures, interactions and relationships in the data is needed. In this case, ensembles of decision trees (known as 'Random Forests') have been the most successful algorithm in modern times and basically this is what my work entails.

Learning problems can be roughly categorized as either supervised or unsupervised (Berry and Linoff, 1997).

Supervised learning: For each observation of the predictor measurement(s) $x_i, i = 1, 2, ..., n$, there is an associated response measurement y_i Gareth, Daniela, and Trevor (2014). We fit a model that relates the response to the predictors, with the aim of accurately predicting the response for future observations(predictions) and understand the relationship between the response and the predictors. Traditional statistical learning methods such as linear regression and logistic regression as well as modern approaches such as boosting and support vector machines work in the supervised learning domain.

Unsupervised learning: For every observation $i = 1, 2, ..., n$, we observe a vector of measurements x_i but no associated response y_i. A linear regression model cannot be fit because there is no response variable to predict. In this case we seek to find the relationship between the variables. One statistical tool that can be used is cluster analysis. Clustering ascertains whether the observations fall into distinct groups.

Supervised learning can be grouped into **Regression** and **Classification** problems.

Regression Vs Classification Problems

Variables can be grouped into quantitative or qualitative(categorical) Gareth, Daniela, and Trevor (2014). Quantitative variables take on numerical values eg. height while qualitative variables take on values in one of the different classes eg. gender.

Problems with a quantitative response are referred to as regression problems while those involving a qualitative response are referred to as classification problems. Predicting a qualitative response for an observation is called classifying the observation since it involves assigning the observation to a class. Three of the most widely-used classifiers: logistic regression, k-nearest neighbors and Linear Discriminant Analysis. More computer-intensive methods are trees, random forests, support vector machines and boosting Gareth, Daniela, and Trevor (2014).

Machine Learning: This is a method of teaching computers to improve and make predictions based on data. It is teaching a program to react to and recognize patterns through analysis, self training, observation and experience (Hackeling, 2014).

In the classification setting, we have a set of training observations $(x_1, y_1), ..., (x_n, y_n)$ that we can use to build a classifier. We want our classifier to perform well not only on the training data, but also on test observation not used to train the classifier. Here, I introduce some of the most commonly used classifiers.

Logistic Regression

Models the probability that Y, the dependent variable belongs to a particular category (one of two categories eg. 'yes' or 'no').

The model

Modelling the relationship between $P(X) = Pr(Y = 1/X)$ and X. For convenience we use the generic coding 0 and 1 for the response. To use linear regression to represent this probabilities we have, $p(X) = \beta_0 + \beta_1 X$ which gives the left hand side of the logistic function.

However, there is a problem with this approach in that predicting of values close to zero would yield negative probabilities and if we were to predict large values, we would get probabilities bigger than 1 which defies the law of probability that probability values should fall between 0 and 1.

To prevent this, we model $p(X)$ using the logistic function that gives outputs between 0 and 1 for all values of X.

$$p(X) = \frac{\exp(\beta_0 + \beta_1 X)}{1 - \exp(\beta_0 + \beta_1 X)}$$

We notice that for lower values, we now predict the probability of default as close to but never below 0. Likewise for high values, we predict a default probability close to but, never above 1.

Manipulating the equation gives;

$$\frac{p(X)}{1 - p(X)} = \exp(\beta_0 + \beta_1 X) \tag{1.4.1}$$

where the LHS is called odds and takes values between 0 and ∞. Taking the logarithms on both sides yields:

$$log\left(\frac{p(X)}{1-p(X)}\right) = \beta_0 + \beta_1 X \tag{1.4.2}$$

The LHS is called the log-odds or logit which is linear in X.

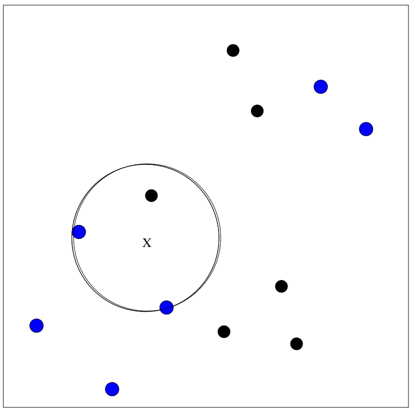
K-nearest Neighbors

KNN can handle both binary and multi-class data.

Consider having N training objects, each of which is represented by a set of attributes X_n and a label Y_n. Suppose we want to classify new objects X_{new}, we first find the K training points closest to X_{new}. Y_{new} is then set to be the majority class amongst these neighbors.

The figure below provides an illustrative example of the KNN approach Gareth, Daniela, and Trevor (2014).

Figure 1.1: KNN approach using K=3.



The goal is to predict the point labelled X. Suppose we choose $K = 3$, KNN will first identify the three observations closest to X, as shown in the diagram. The point consists of two blue points and a black point resulting in estimated probabilities of $\frac{2}{3}$ for the blue class and $\frac{1}{3}$ for the black class. KNN will predict that the point X belongs to the blue class.

One draw back of KNN is the issue of ties: Two or more classes having equal number of ties. Therefore, for binary classification, a good solution is to always use an odd number of neighbors.

Choosing K: If K is too small, the classification is heavily influenced by mislabelled points(noise). This problem is rectified by increasing K which regularises the boundary.

What about if K is too big? As we increase K, we are using neighbours further away from X_{new} which is useful upto a certain point as it has a regularizing effect that reduces the chances of over-fitting. However, when we go too far, we loose the true pattern of the data we are attempting to model. Therefore, to find the best value of K, we use cross validation Gareth, Daniela, and Trevor (2014).

Linear Discriminant Analysis

Linear Discriminant Analysis is used when we have more than two response classes Gareth, Daniela, and Trevor (2014).

Using bayes' theorem for classification

Suppose we wish to classify an observation into K classes, where $K \geqslant 2$ and the qualitative response variable Y can take on K distinct ordered values.

π_k: Denotes the prior probability that a randomly chosen observation comes from class K of the response variable Y.

$f_k = Pr(X = x/Y = k)$: Denote the density function of X for an observation from class K.

Bayes theorem states that:

$$P_k(X) = Pr(Y = k/X = x) = \frac{\pi_k f_k(x)}{\sum \pi_i f_i(x)} \tag{1.4.3}$$

$P_k(x)$: Posterior probability that an observation $X = x$ belongs to class K.

π_k is computed if we have a random sample of Y_s from the population. We therefore compute the fraction of training observations that belong to class K. $f_k(x)$ is estimated so we can develop a classifier that approximates the bayes classifier.

Linear Discriminant Analysis for $p = 1$. (We have only one predictor)

We are required to find an estimate for $f_k(x)$ that we can plug into (1.4.3) inorder to estimate $p_k(x)$. We then classify an observation for which $p_k(x)$ is greatest. Gareth, Daniela, and Trevor (2014) To estimate $f_k(x)$ the following assumptions are made:

- $f_k(x)$ is normal.

$$f_k(x) = \frac{1}{\sqrt{2\pi}\sigma_k} \exp\left(-\frac{1}{2\sigma_k^2}(x - \mu_k)^2\right) \tag{1.4.4}$$

  μ_k and σ_k^2 are the mean and variance parameters for class k.

- Shared variance term across all K classes, $\sigma_1^2 =, ..., = \sigma_K^2$

Plugging equation (1.4.4) to equation (1.4.3) yields:

$$p_k(x) = \frac{\pi_k \frac{1}{\sqrt{2\pi}\sigma} \exp\left(-\frac{1}{2\sigma^2}(x-\mu_k)^2\right)}{\sum_{i=1}^{K} \pi_i \frac{1}{\sqrt{2\pi}\sigma} \exp\left(-\frac{1}{2\sigma^2}(x-\mu_i)^2\right)} \tag{1.4.5}$$

Taking the logs of equation (1.4.5) and rearranging the terms gives:

$$\delta_k(x) = x\frac{\mu_k}{\sigma^2} - \frac{\mu_k^2}{2\sigma^2} + log(\pi_k) \tag{1.4.6}$$

It is not possible to calculate the bayes classifier in real-life. We still need to estimate the parameters $\mu_1, ..., \mu_K, \pi_1, ..., \pi_K$ and σ^2. LDA method approximates the bayes classifier by plugging the estimates for π_k, μ_k and σ^2 into equation (1.4.6).

The following estimates are used:

$$\hat{\mu_k} = \frac{1}{n_k}\sum_{i:y_i=k} x_i \tag{1.4.7}$$

$$\hat{\sigma} = \frac{1}{n-K}\sum_{K=1}^{K}\sum_{i:y_i=k}(x_i - \hat{\mu})^2 \tag{1.4.8}$$

$$\tag{1.4.9}$$

n: Number of training observations n_k: Total number of training observations in class k where μ_k is the average of all training observations from class k.

$\hat{\sigma}^2$: Weighted average of the sample variances for each of the k classes.

In the case where additional information is not present, LDA estimates π_k using the proportion of training observations that belongs to the k^{th} class.

$$\pi_k = \frac{n_k}{n} \tag{1.4.10}$$

LDA classifier plugs the estimates equation (1.4.8) and equation (1.4.9) into equation (1.4.6), assigning an observation $X = x$ to the class for which

$$\hat{\delta}_k(x) = x\frac{\hat{\mu_k}}{\hat{\sigma}^2} - \frac{\hat{\mu}_k^2}{2\hat{\sigma}^2} + log(\hat{\pi}_k) \tag{1.4.11}$$

is largest.

The classifier is linear due to the fact that the discriminant functions $\hat{\delta}_k(x)$ are linear functions of x Gareth, Daniela, and Trevor (2014).

We will use random forest and the XGBoost algorithms for analysis which we will discuss in depth in the subsequent chapter.

2. The Second Chapter

2.1 Methodology

We employed the Random Forest and XGboost algorithm to predict the risk classes of the test data. The evaluation metric used to score how accurately the models were able to classify the risk classes is the quadratic weighted kappa metric.

2.2 Quadratic weighted kappa metric

Web (Accessed March 2017b) It can be used to quantify the amount of agreement between the predictions from an algorithm and some trusted labels of the same objects in machine learning. It is a chance adjusted index of agreement and measures the agreement between two ratings.

Calculation of quadratic weighted kappa metric.

- We construct an $N \times N$ histogram matrix O. O_{ij} corresponds to the number of applications which received a rating i by A and j by B.

- We calculate an $N \times N$ matrix of weights, w, based on the difference between the rater's score.

$$w_{ij} = \frac{(i-j)^2}{(N-1)^2} \tag{2.2.1}$$

- An $N \times N$ histogram matrix of expected ratings, E, is calculated, making the assumptions that there is no correlation between the rating scores. This is calculated as the outer product between each rater's histogram vector of ratings and normalized such that E and O have the same sum.

- The quadratic weighted kappa is calculated from these three matrices as:

$$\frac{1 - \sum_{ij} w_{ij} o_{ij}}{\sum_{ij} w_{ij} E_{ij}} \tag{2.2.2}$$

The metric works well for a highly imbalanced classification task. The metric varies from 0 (random agreement) to 1 (complete agreement). In case there is less agreement between the raters than expected by chance, this metric may go below 0. The data has 8 possible ratings and each application is characterized by a tuple (ea, eb), that corresponds to the scores by rater A, actual risk and rater B, predicted risk.

2.3 Overview of Random Forest

Random forests are a combination of tree predictors such that each tree depends on the values of a random vector sampled independently and with the same distribution for all trees in the forest (Breiman,2001). The goal of Random forest is creating a predictive model that predicts the value of a target variable based on given input variables where one of the input variable is represented by each interior node and the values of the input variable is represented by edges.

Bagging and Random forests

Bagging and random forests use trees as building blocks to constructing more powerful models Gareth, Daniela, and Trevor (2014).

Bootstrap: It is a widely used statistical tool used to quantify uncertainty associated with given estimators. It can easily be applied to a wide range of statistical learning methods even those whose measure of variability is difficult to obtain.

Bootstrap aggregation / Bagging: This is the basic principle behind the training algorithm for random forests which reduces the variance of a statistical learning method.

Consider the set of n independent observations denoted by $C_1, C_2, ..., C_3$ each with variance σ^2. Therefore the variance of the mean $\bar{Z}$ of the observation is given by $\dfrac{\sigma^2}{n}$. Averaging a set of observations reduces the variance. To reduce the variance and increase the prediction accuracy of a statistical learning method, we sample many training sets from the population, build a separate prediction model and average the resulting predictions. Therefore, calculate $\hat{f}^1(x), \hat{f}^2(x), ..., \hat{f}^B(x)$ using B separate training sets and average them so as to obtain a single low-variance statistical model given as:

$$\hat{f}_{avg}(x) = \frac{1}{B}\sum_{b=1}^{B}\hat{f}^b(x) \tag{2.3.1}$$

However, this is not practical because we cannot have multiple training sets so the bootstrap approach is used where repeated samples from the single training dataset are sampled.In this method, B different bootstrapped training datasets are generated and we train our method on the b^{th} bootstrapped training set to obtain $\hat{f}^{\star b}(x)$ and then average all the predictions to obtain:

$$\hat{f}_{bag}(x) = \frac{1}{B}\sum_{b=1}^{B}\hat{f}^{\star b}(x) \tag{2.3.2}$$

This is called bagging. (When trees are repeatedly fit to bootstrapped subsets of the observations)

So given a training set $X = x_1, ..., x_2$ with responses $Y = y_1, ..., y_n$, bagging repeats B times and selects random samples **with replacement** of the training set and fits trees to the sample. Trees are grown deep and are not pruned therefore each individual tree has high variance but low bias. Finding the average of the B trees reduces the variance.

How can bagging be extended to a classification problem where Y is qualitative? Given a test observation, a predicted class can be recorded by each of the B trees and a majority vote is recorded. The overall prediction is the most commonly occurring class among the B predictions Gareth, Daniela, and Trevor (2014).

Out of Bag Error Estimation

This is a method of estimating the test error of a bagged model without the need of cross validation. Averagely, each bagged tree makes use of around $\frac{2}{3}$ of the observation and the other $\frac{1}{3}$ of the observation is not used to fit a bagged tree. This observations are referred to as out of bag observation. The response for the i^th observation can be predicted using each of the tree in which that observation was out of bag which will yield around $\frac{B}{3}$ predictions for the i^th observation. To obtain a single prediction for the i^th observation, we take a majority vote of the predicted responses. This gives a single OOB prediction for the i^th observation.

The OOB prediction is obtained for the n observations and the classification error is computed. The OOB error is an estimate for the test error for the bagged model since each of the observation has the response predicted using only the trees that were not fit using that observation Gareth, Daniela, and Trevor (2014). Therefore, the OOB method for test error estimation is convenient when bagging on large datasets.

For each observation $Z_i = (x_i, y_i)$ we build a random forest predictor by averaging the trees corresponding to bootstrap samples in which z_i did not appear. The training is terminated when the error stabilizes.

Variable importance measures

When a large number of trees are bagged, it is no longer possible to represent the statistical learning procedure using a single tree, and it is not also clear which variables are most important to the procedure. Although the collection of bagged trees is difficult to interpret than a single tree, an overall summary of the importance of each predictor can be obtained using the gini index for bagging classification trees. At every tree split, the improvement in the split criterion is the measure of importance attributed to the splitting variable and is then accumulated over all the trees for each variable separately Hastie, Tibshirani, et al..

Gini index: This is the expected error rate of the system. Calculating the gini index for each attribute helps one to get the splitting attributes. The 'best' split according to the Gini gain criterion is the split with the largest Gini gain Strobl, Boulesteix, and Augustin (2007).

Random Forests

Random forest is an improvement over bagged trees by providing a small adjustment to the system that decorrelates the trees. In building the decision trees, **a random sample of m predictors is chosen as split candidates from the set of p predictors** each time a split in a tree is considered. The split is allowed to use only one of those m predictors.

The number of predictors considered at each split is approximately equal to the square root of the total number of predictors, $m \approx \sqrt{p}$. A new sample of m predictors is taken at each split.

Suppose there is one very strong predictor in the dataset and a number of other moderately strong predictors. Then most or all of the predictors will use the strong predictors in the top split in the collection of the bagged trees. Consequently, all of the bagged trees will look quite similar to each other and therefore the predictions from the bagged trees will be highly uncorrelated. Bagging will not lead to a reduction in the variance over a single tree in this setting Gareth, Daniela, and Trevor (2014).

How does random forest overcome this problem? By ensuring that each split considers only a subset of the predictors. Averagely, $\dfrac{(p-m)}{p}$ of the splits will not consider the strong predictor and the other predictors will have a chance. This is referred to as decorrelating the trees. This approach makes the average of the resulting trees less variable and more reliable.

The main difference between bagging and Random Forest is the choice of the predictor subset size m. If a random forest is built using $m = p$, this amounts to bagging. Random Forest using $m = \sqrt{p}$ leads to a reduction in test error and OOB over the bagging technique. It is helpful to use a small value of m when building a random forest if we have a large number of uncorrelated predictors. Random forest does not overfit just like bagging if we increase B Gareth, Daniela, and Trevor (2014).

Implementing the Random forest algorithm

Before implementing the algorithm, we need to understand the data structure so as to preprocess the data accordingly.

(a) **Exploring the data**: We are provided with two sets of data, a training set and a test set. The training set comprises of the data we will use to build the model while the test or validation set is used for evaluating the performance of a final set of candidate model. The test set is composed of 59,381 observations and 128 predictors or independent variables. The test data comprises of 19,765 observations and 127 features. The aim here is to predict the dependent variable or the response of the test data. The risk predictions range from 1 to 8. To clearly understand the data, we explore the structure and missing predictors as shown in the codes (appendix).

(b) **Data splitting**: This is how data is allocated to model building (train set) and performance evaluation (test set). The core interest is to predict the risk of new clients by not using the same population as the data used to build the model. In other words, we are testing how well the model extrapolates to a different population. A small test set would have limited utility as a judge of performance. If the size of the test set is small, the test set may not have sufficient precision to make reasonable judgement.

In this model, the training and testing sets are homogeneous, therefore random sampling techniques are used to create similar data sets. To split the train data, a random sample is chosen from the data. The function model selection from sklearn is used to split the data into train and test in the proportion of 60%to 40%respectively.

(c) **Data preprocessing**.

- Centering and scaling: To center a predictor variable, we take the mean of that predictor value and subtract from all the values of that predictor. Due to centering, the predictor has 0 mean. This result is the divided by the standard deviation of the predictor. Scaling the data makes the predictor values have a common standard deviation of 1. These transformations improve the numerical stability of the calculations. In this data, some predictors like weight and height have been normalized. The only disadvantage of normalizing is the loss of interpretability as the values are no longer in the original units.

- Missing values: In the data, some predictors have missing values. Missing values are more often than not related to predictor variables than the sample. Due to this, the amount of missing could be concentrated in a subset of predictors rather than occurring randomly across the predictors.

  To deal with with missing values, we use the (Predictive) Value Imputation (PVI) where estimated values are imputed where missing values occur before the model is applied (Saar-Tsechansky and Provost, 2007). The widely used approach is to replace the missing value with the predictor's mean value or mode value if the attribute is categorical. These values are estimated from the training set and imputed along the columns. The strategy we used in our data is to impute the missing values with the mean value of the predictor where missing values occur (where the value reads Nan). The categorical predictors have no missing values.

- Factorize string variable: Product_Info_2 is a string categorical variable, we transform this feature to enumerate type using the factorize function. The factorize functions returns a list of unique values (or categorical labels) in the product_Info_2 column.

(d) **Model performance**: To prepare the data for modelling, we drop the features 'Id' and 'Response', assign the response and explanatory variables to a numpy array then we train the model using the train data and evaluate the performance of the model on the test data.

Description of the parameters that were tuned to achieve the best score (Web, Accessed May 2017).

n_estimators: The number of trees in the forest.

Criterion: "gini", measures the quality of a split.

max_depth: The maximum depth of the tree. Takes on integer values or none. If the value is none, then all nodes are expanded until all leaves are pure.

Min_samples_split: Minimum number of samples required to split an internal node.

Min_samples_leaf: The minimum number of samples required to be at a leaf node.

Max_features: Number of features to consider when looking for the best split. If it is auto, then the max features is equal to the sqrt(n_features).

Max_leaf_nodes: This parameter grows trees with max leaf nodes in the best first fashion.

Min_impurity_split: This is the threshold for early stopping in the tree growth. A node will split if its impurity is above the threshold, otherwise it is a leaf.

Bootstrap: It takes on boolean with default =True. If true, the algorithm makes use of bootstrap samples when building the trees.

Oob_score: It takes on boolean with default =True. If true, the algorithm uses the out of bag samples to estimate the generalization accuracy.

n_jobs: Default=1. The number of jobs that should run in parallel for bothfit and predict. If -1, then the number of jobs is set to the number of cores.

Random state: If none, it means that the random number generator is the random state instance used by np.random.

Verbose: Default=0. Controls the verbosity of the tree building process. That is if the verbose is set to a higher number, more information about the tree building process will be seen.

Warm_start: bool,(default=False). When set to true,the solution of the previous call to fit and add more estimators to the ensemble is reused. Otherwise, just fit a whole new forest.

- Fit the Random Forest classifier on the train data.
- Then predict the response feature for the test data that was split using the model selection code.
- The same feature transformations are done on the test data provided by kaggle. This is the data we are supposed to predict the response variable and evaluate the score using the quadratic weighted kappa metric.

Overview of Xgboost Algorithm

The full name is eXtreme Gradient Boosting. It is a variant of gradient boosting, a tree based supervised learning algorithm. It includes an efficient linear model solver and a tree learning algorithm that supports a variety of objective functions including ranking, classification and regression Chen and He (2015). This boosting approach learns slowly unlike fitting a large decision tree to the data which likely amounts to overfitting the data.

Features of Xgboost

- Customization: Xgboost supports customized objective function and evaluation function.
- Sparcity: Xgboost accepts sparse input for both the tree and linear booster, and is optimized for sparse input.
- Input type: Xgboost takes several types of input data. The recommended type is xgb.Dmatrix.
- Speed: It can automatically do parallel computation and faster than gradient boosting machine.
- Performance: Has better performance on different datasets.

XG Boost parameters

The parameters can be grouped into (He (2015)):

1 General parameters.

Under general parameters we have number of threads.

2 Booster parameters.

- Stepsize.
- Regularization.

3 Task parameters.

- Objective.
- Evaluation metric.

Model Specification

Training objective.

This model is a collection of decision trees. Supposing we have K trees, the model is given by He (2015):

$$\sum_{k=1}^{K} f_k. \tag{2.3.3}$$

With all the prediction trees, we predict by:

$$\hat{y}_i = \sum_{k=1}^{K} f_k(x_i) \tag{2.3.4}$$

x_i: Feature vector of the i^th data point.

The prediction at the t^th step can be defined as:

$$\hat{y_i t} = \sum_{k=1}^{t} f_k(x_i) \tag{2.3.5}$$

To train the model, we need to optimize a loss function He (2015). We use;

- Rooted mean squared error for regression.

$$-L = \frac{1}{N}\sum_{i=1}^{N}(y_i - \hat{y}_i)^2. \tag{2.3.6}$$

- Logloss for binary classification.

$$-L = -\frac{1}{N}\sum_{i=1}^{N}(y_i log()p_i) + (1 - y_i)log(1 - p_i). \tag{2.3.7}$$

- mlogloss for multi-classification.

$$-L = -\frac{1}{N}\sum_{i=1}^{N}\sum_{j=1}^{M} y_{i,j}log(p_{i,j}). \tag{2.3.8}$$

Regularization is an important part of the model. The regularization term controls the complexity of the model thereby preventing over fitting.

$$\Omega = \gamma T + \frac{1}{2}\lambda\sum_{j=1}^{T} wj^2. \tag{2.3.9}$$

λ: Regularization parameter.

γ: Minimum loss reduction required to make a further partition on a leaf node of a tree.

T: The number of leaves.

wj^2: The score of the j^th leaf.

Combing the loss function and the regularization function, we get the objective function of the model.

$$obj = L + \Omega. \tag{2.3.10}$$

where the loss function controls the predictive power and regularization controls the simplicity He (2015).

General parameters.

- nthread: Number of parallel threads.
- Booster:

- gblinear: linear function.
- gbtree: tree based model.

xgb.Dmatrix: This is the data structure used by the XGBoost algorithm. XGBoost prepossess the input data and labels it into an xgb.Dmatrix object before implementing it to the training algorithm.

An xgb.DMatrix contains:

- Prepossessed training data.
- Missing values.
- Data weight.

If the training process is to be repeated on the same data set, the xgb.DMatrix works well as it saves on the prepossessing time He (2015).

Implementing the XGBoost algorithm

1. **Data preprocessing.**

- Factorize string variables: Just like the Random Forest, we transform Product_info_2, a string variable into numeric variables.

- Adding an Interaction term: Interaction is defined as how the overall effect on the response of one explanatory variable is dependent on the level of one or more explanatory variables (Fitzmaurice, 2000). That is interaction occurs when the effect of one explanatory variable is dependent on a certain level of another explanatory variable .

  If no interaction is observed between two explanatory variables, then the overall effect of one explanatory variable is constant across all values of the other. BMI is related to age in that a higher BMI is found among the older age group and lower among the young age group, reducing thereafter in younger age groups Yanai, Kon, Kumasaka, and Kawano (1997). Therefore, there is an interaction between age and BMI on the response variable. We therefore include the interaction term in the data.

  Using a combination of predictors can be more effective than using the individual values. More often than not, data engineering is informed by the modeller's understanding of the data and problem and not derived from any mathematical technique Kuhn and Johnson (2013).

2. **Applying offsets**: An offset is a model variable with a pre-specified coefficient. Modelling is affected by the real-world fact that insurance data is often incomplete, generally dirty and inconsistently coded. Due to this, modellers are forced to exclude variables that are important in predicting. This will bias the estimate of the model if this omitted variables correlate with the target variable and one or more of the other modelling variables. This is known as **omitted variable bias** Yan, Guszcza, Flynn, and Wu (2009). To curb this phenomenon, we accommodate the effect of omitted variables in the model design. A

traditional approach to this problem is to adjust the model's target variable. It is therefore important to consider an offset when performing multivariate analysis so as to avoid the omitted variable bias. The offsets are generated after optimization by the fmin_Powell function which determines the minimum numeric value between arguments.

3. **Model performance**: To prepare the data for modelling, we drop the features 'Id' and 'Response'. We train the model using the train data and evaluate the performance of the model on the test data.

   Description of the parameters that we tuned to obtain the best score:

   - "reg:linear": default option, Linear regression.
   - "binary: Logistic": Outputs probability. It performs logistic regression for binary classification.
   - "multi:softmax": Uses the softmax objective for multiclass classification.

   Eta/Learning rate: We can directly get weights of new features after each boosting step. Eta shrinks the feature weights and makes the boosting process more conservative. Eta is the stepsize shrinkage used in update to prevent overfitting. It is in the range of [0,1], the default is 0.3.

   Min_child_weight: This is the minimum sum of instance weight needed in a child. It ranges from $[0,\infty]$ and the default is 1.

   The tree building process will give up further partitioning if the tree partition step results in a leaf node with the sum of instance weight less than the Min_child_weight.

   Subsample: It is the subsample ratio of the training instance. Setting it to 0.5 means that XGBoost randomly samples half of the data instances and grows trees thus prevents overfitting. It ranges from (0,1], the default value being 1. This parameter makes the model more robust and avoids overfitting.

   colsample_bytree: This is the subsample ratio of columns when constructing each tree. The range is (0,1] and the default is 1. Both subsample and colsample_bytree cannot be set to 0.

   Silent: The default=0. 0 means printing running messages, 1 means silent mode.

   max_depth: This is the maximum depth of a tree. Increasing the max_depth value makes the model more complex and more likely to overfit. The range is from $[1,\infty]$, the default is 6.

3. Third Chapter

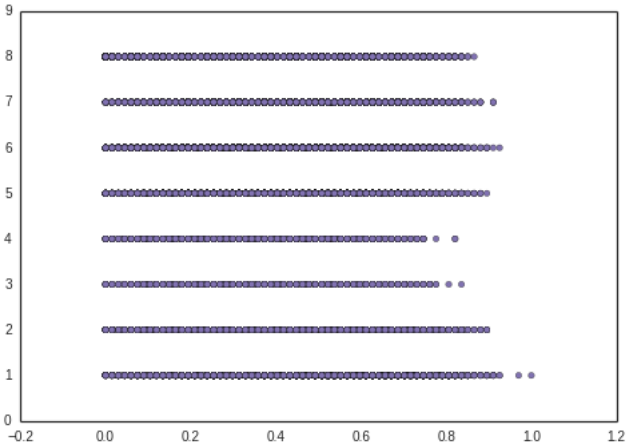
3.1 Data description

The data provided is divided into train and test data set (Web, Accessed March 2017a). There is a sample submission file that gives instructions on how predictions are submitted on the kaggle website. The train data is composed of 53,381 entries(clients) and a response variable. The total number of features is 128. The test data is composed of 19,765 entries(clients) and a total of 127 features. The predictions range from 1 to 8 where 1 represents the lowest risk level and 8 represents the highest risk level.

Data visualization

The scatter plot below shows the relationship between the various responses and the normalized Ins Age.

Figure 3.1: Scatter plot of Age vs Response



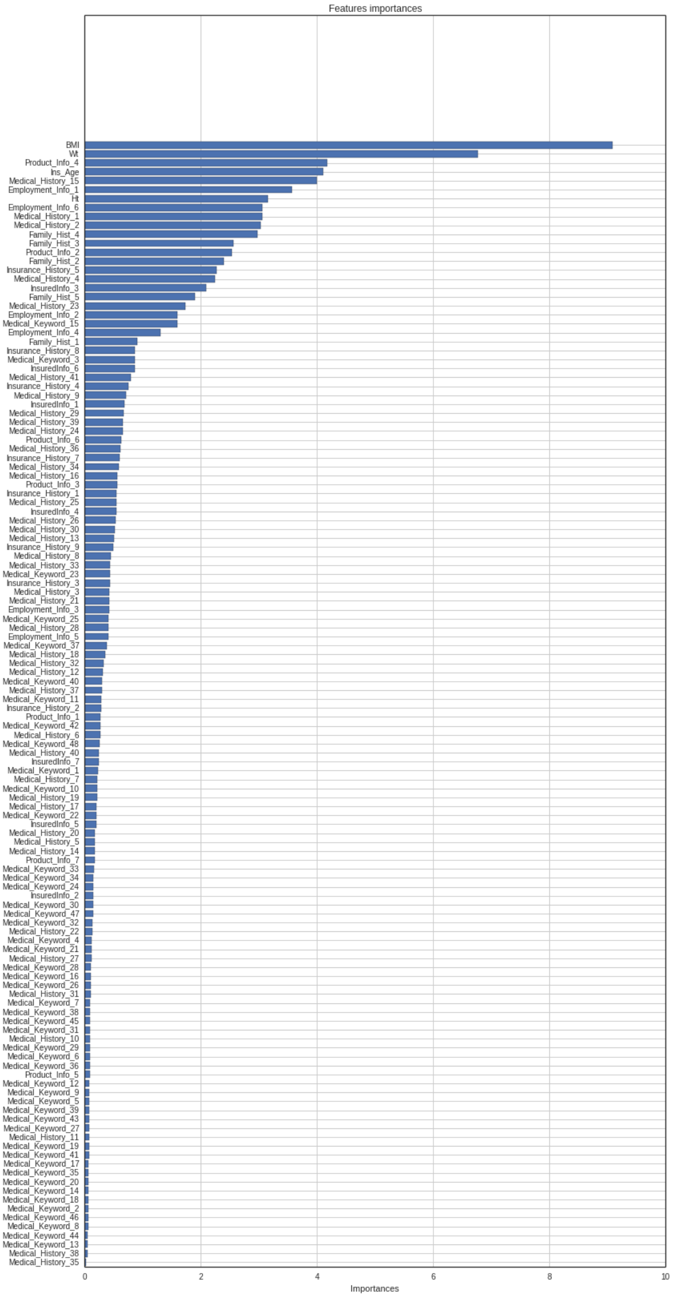
The risk prediction classes are evenly distributed across the ages of the clients with a few outliers.

The plot of the feature importances lists the most important features in descending order.

The figure below is a variable importance plot for the insurance data. Variable importance is computed using the mean decrease in the gini index and expressed relative to the maximum. Variable importance is the overall quantification of the relationship between the predictor and the outcome. With a large number of predictors, the exploratory analysis of the predictors may not be feasible and may concentrate on those with strong relationships with the outcome. We therefore rank predictors so as to sift through large amounts of data. A substantial drop in the performance of the model indicates that an important feature has been dropped.

The subsequent table lists the five most important features and the five least important features.

Figure 3.2: Feature importance plot

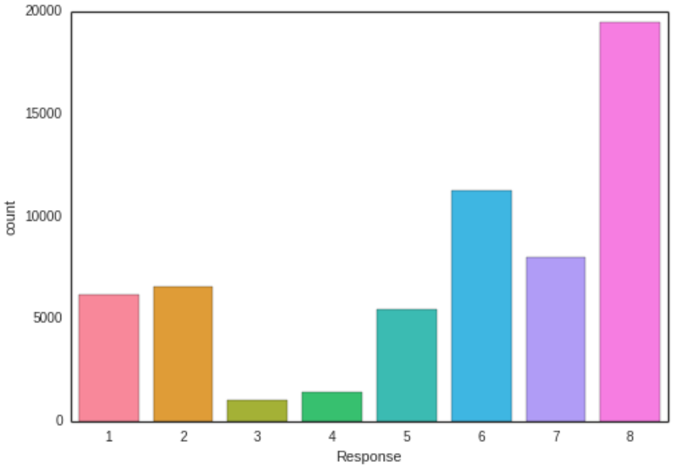


The first 5 important predictors	
BMI	0.089700
Wt	0.068185
Product_info_4	0.041591
Ins_Age	0.040372
Medical_History_15	0.039763
The last 5 less important predictors	
Medical_History_35	0.000219
Medical_History 38	0.000512
Medical_History_13	0.000551
Medical_History_44	0.000612
Medical History 8	0.000622

627

The response classes are imbalanced as shown in the plot below.

Figure 3.3: Class Imbalance of the response variable



Most clients fall under the risk class 8.

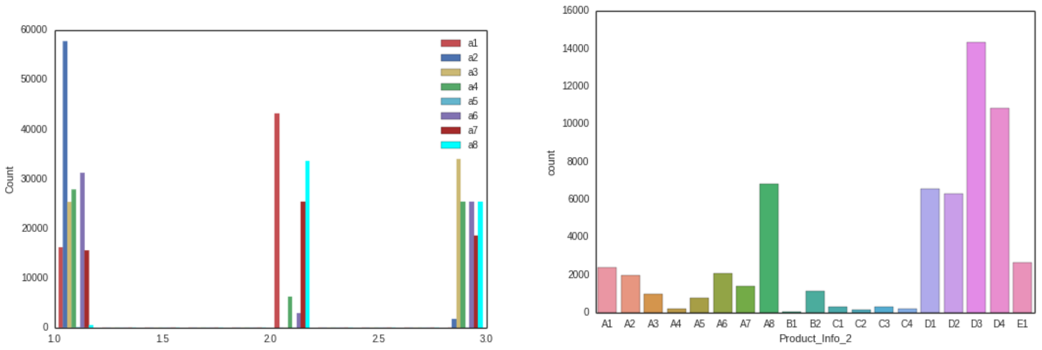
Class imbalance: Data classification is difficult because of unbounded size and the imbalanced nature of the data. Class imbalance occurs where one of the classes has more samples than other classes. This leads to most algorithms ignoring or misclassifying the minority sample(those that rarely occur but are very important) and focussing on the classification of major samples. A dataset is said to be highly skewed if samples from one class is higher than the other Longadge and Dongre (2013).

Threshold metrics help to curb the class imbalance problem. These metrics have a threshold level such that examples above the threshold are predicted as positive and the rest are negative. We used the quadratic weighted kappa metric which works well with unbalanced datasets by measuring the among observers Jeni, Cohn, and De La Torre (2013).

Descriptive analysis of the Response feature.

count	59381.000000
mean	5.636837
std	2.456833
min	1.000000
25 %	4.000000
50 %	6.000000
75 %	8.000000
max	8.000000

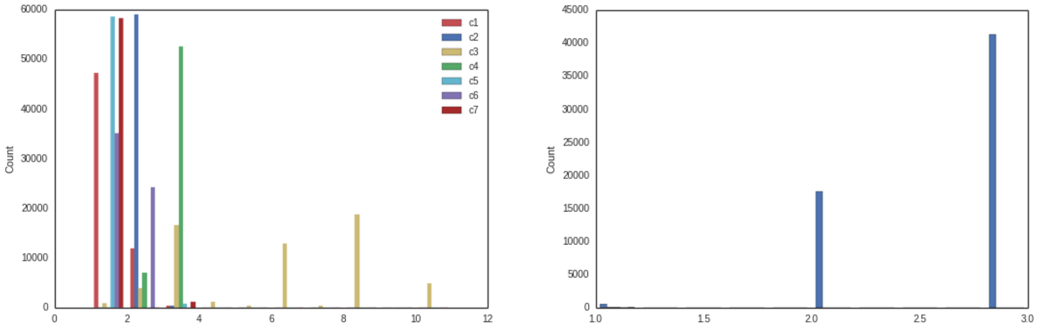
The mean risk prediction is a roughly 6.



(a) Insurance_history plot (b) Product_Info_2

Figure 3.4: Plots of count against insurance history and product information 2 showing the distribution of the two features.

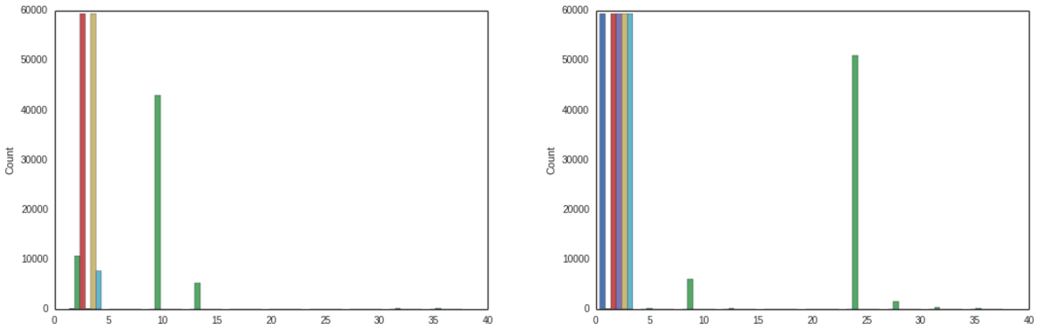
Plot(a): Insurance_History_2, 3, 4, 7, 8 and 9 take on the categorical values 1, 3, 2. Insurance_History_1 takes on the categorical values (1, 2) while Insurance History_5 takes on a range of values almost close to 0. Insurance_History_2, 1 and 3 have the highest distribution of the categorical variable 1, 2 and 3 respectively while Insurance_History_8, 7 and 2 have the lowest distribution of the categorical variable 1, 2 and 3 respectively. Plot(b) shows the distribution of the categorical variable Product_Info_2 where the product D3 was highly preferred.



(a) Insurance information plot (b) Family history plot

Figure 3.5: Plots of count against insurance information and family history showing the distribution of the two explanatory variables.

Plot(a) InsuredInfo_1 takes on the categorical values (1, 2, 3), InsuredInfo_2 and 4 takes the values (2, 3). InsuredInfo_5 and 6 takes the values (1, 3). InsuredInfo_6 takes the values (2, 1). InsuredInfo_3 takes on a range of values. InsuredInfo_1, 5 and 6 take on the highest values of the categorical variable 1 while InsuredInfo_3 takes the highest value of the variable 8 and InsuredInfo_4 takes on the highest value of categorical variable 3. Plot(b) Family_Hist_1 takes on the values (2, 3, 1) while the rest of the features take on values close to 0. The highest value for Family_Hist_1 was recorded for the categorical variable 3.



(a) Employment information plot

(b) Product Information plot

Figure 3.6: Plots of count against employment information and product information showing the distribution of the two features.

Plot(a): Employment_Info_3 and 5 take on categorical values (1, 3) and (3, 2) respectively. Employment_Info_1, 2, 4 and 6 have no unique values. Employment_Info_3 and 5 have the highest values as the categorical variables 1 and 2. Employment_Info_2 takes on the highest value as 9. Plot(b): Product_Info_1, 5, 6, and 7 takes on the categorical variables (1, 2), (2, 3), (1, 3) and (1, 3, 2) respectively. Product_Info_3 and 4 take on different values. Product_Info_1, 5, 6 and 7 take on the highest values of the categorical variables 1, 2, 3 and 1 respectively. Product_Info_3 takes on the highest value as 26.

3.2 Model evaluation

Using the random forest algorithm to predict the risk levels of the test data, the model scored 0.53074 as evaluated by the quadratic weighted kappa metric.

Weakness of Random forest

- Random forest may overfit noisy datasets: If the number of variables is large and the fraction of relevant variables small, this algorithm tends to perform poorly with small m. At each split the chance can be small that the relevant variables will be chosen Hastie, Tibshirani, et al..
- Having a large number of trees makes the algorithm slow for real time prediction

To improve my score on kaggle, I employed the Xgboost algorithm whose full name is eXtreme Gradient Booosting. It is a variant of gradient boosting, which is a tree model based supervised learning algorithm. Unlike fitting a single large decision tree to the data, which could amount to overfitting, the boosting approach instead learns slowly. It includes an efficient linear model solver and a tree learning algorithm.

XGBoost proved to be a reliable large scale tree boosting system as the model scored 0.66289 using the quadratic weighted kappa metric, an improvement from Random forest algorithm.

3.3 Key points on XGboost

Guide on parameter tuning

Tuning: It is defined as choosing the best parameters to optimize the performance of an algorithm.

It is really not possible to give a universal set of accepted parameters that can optimize an algorithm. Parameters have to be tuned to achieve good results.

Key points on parameter tuning

- To control overfitting.
- To deal with imbalanced data.
- To trust the cross validation.

The bias-variance trade off is the most important concept in controlling overfitting and applies to both classification and regression problems. This trade off elaborates why we have no universal optimal learning method for algorithms. Basically, finding an optimal bias-variance tradeoff is difficult. Despite this, acceptable solutions can be found, e.g., use of cross validation or regularization (Sethu, 2007).

Bias-variance trade off: This is the difficulty experienced in reducing sources of error arising from erroneous assumptions in the algorithm resulting to missing out of relevant relationships between the target variable and the features whereas variance is the error arising from the sensitivity and small fluctuations in the training sets which causes overfitting. The two types of errors makes it difficult for a supervised learning to generalize unseen data (Sethu, 2007).

How do we counter the bias-variance trade off in XGBoost?

We can group the booster specific parameters as below and tune the given parameters accordingly (He, 2015).

- To control the model complexity: max_depth, min_child_weight and gamma.
- Robust to noise: subsample, colsample_by tree.

How to deal with imbalanced data among classes.

If one is interested in a model that can only predict the right probability, then the dataset cannot be rebalanced and therefore set the parameter max_delta_step to a finite number (say 1). This will help in convergence.

On the other hand, if one is interested in a model that ranks, then balance the negative and positive weights by the scale_pos_weight parameter and use the "auc" as the evaluation metric.

Use early.stop.round to detect if the model is continuously getting worse on the test set.

Reduce the step size eta and increase nround simultaneously if overfitting is observed (He, 2015).

How does one build a winning algorithm in a kaggle competition?

To score highly on kaggle, one needs to consistently focus on:

- Parameter tuning.
- Model ensembling.
- Feature engineering.

(He, 2015) Why XGBoost is the winning algorithm for kaggle competitions.

- It is efficient as it allows for parallel computing and can be run on a cluster.
- It is accurate: It outputs good results for most datasets.
- Feasibility: It provides a platform for tunable parameters.
- XGBoost is easy to use and install with a highly developed R and python interface.

4. Conclusion

We first showed the procedure used in building a predictive model which include: pre-processing the predictor data, estimating the model parameters, selecting predictors for the model, evaluating the model performance and fine tuning the class prediction rules.

We then make a comparison between the Random Forest and the XGBoost algorithms. Despite Random Forest being an efficient algorithm on large datasets, handling thousands of variables without variable deletion, it has been observed to over fit datasets with noisy classification. On the other hand, XGBoost has proved to build higher accuracy models due to its regularization feature which reduces over fitting. Additionally, XGBoost offers a randomization parameter used to decorrelate the individual trees and in turn reduce the overall variance of the additive tree model. XGBoost also has an inbuilt method of handling missing values. The modeller is required to initialize a different value different from other observations and pass it as a parameter. XGBoost then learns which path to take for missing values in future data. The computing time in Random Forest algorithm is longer as compared to XGBoost. In conclusion, XGBoost is an algorithm that carefully takes into account the bias-variance tradeoff in every aspect of the learning process.

4.1 Future outlook.

To increase the accuracy of a machine learning algorithm, model ensembling is a vital technique.

Ensemble methods are learning algorithms that construct a set of classifiers and then classifies new data points by taking a (weighted) vote of their predictions. Recent algorithms include error-correcting output coding, bagging and boosting.

Ensembles can be created from:

- Submission files.
- Stacked generalization/blending.

Creating ensembles from submission files.

This method ensembles kaggle csv submission files. It is a quick way of ensembling already existing model predictions as one only needs the predictions on the test set and the model is not retrained.

Model ensembling reduces the error rate. Ensembling low correlated model predictions works better that is, there is an increase in the error-correcting ability if there is a lower correlation between model members.

Creating ensembles from stacking multiple learning models.

This is an ensemble method where models are combined using another machine learning algorithm eg logistic regression, train the machine learning algorithm with the training dataset thereby generating a new dataset using these models. The new generated dataset is used as the input for the combiner machine algorithm.

It is worth noting that the same training dataset is not used for prediction. So to overcome this, the training dataset is split before training the base algorithm. Stacking reduces the generalization error/ out-of-sample error which is a measure of how accurately unseen data can be predicted by an algorithm.

5. Appendix

Random forest algorithm.

```
raw_data1=pd.read_csv('train.csv')  #loading the train data
test2=pd.read_csv('test.csv')  #loading the test data

test2.shape
(19765, 127)

raw_data1.columns.values

raw_data['Product_Info_2'] = pd.factorize(raw_data['Product_Info_2'])[0]
raw_data['Product_Info_2']

imp=Imputer(missing_values='NaN', strategy='mean', axis=0)
imp.fit_transform(raw_data,y='Response')

train_raw, test_raw=model_selection.train_test_split(raw_data,
test_size=0.4, random_state=100)

t1=train_raw.drop(0,axis=1)    #Train_raw dataset
t2= test_raw.drop(0,axis=1)     #Test_raw dataset
t1=t1.drop(127,axis=1)
t2=t2.drop(127,axis=1)

ob=list(t1.columns)
def choose_columns(data):
    ret_X= np.array(data.loc[:,ob]) #Explanatory variables
    ret_Y=data.values[:,-1]
    return ret_X, ret_Y

import sklearn.ensemble as en
RF= en.RandomForestClassifier(n_estimators= 250, criterion='gini',
   max_depth=None,min_samples_split=2, min_samples_leaf=1,max_features='auto',
   max_leaf_nodes=None, min_impurity_split=1e-08,bootstrap=True,
   oob_score=False,n_jobs=1, random_state=None, verbose=0,warm_start=True)
```

XGBoost algorithm

```
def eval_wrapper(yhat, y):
    y = np.array(y)
    y = y.astype(int)
    yhat = np.array(yhat)
    yhat = np.clip(np.round(yhat), np.min(y), np.max(y)).astype(int)
    return quadratic_weighted_kappa(yhat, y)

def get_params():

    params = {}
    params["objective"] = "reg:linear"
    params["eta"] = 0.05
    params["min_child_weight"] = 360
    params["subsample"] = 0.85
    params["colsample_bytree"] = 0.3
    params["silent"] = 1
    params["max_depth"] = 7
    plst = list(params.items())

    return plst

def apply_offsets(data, offsets):
    for j in range(num_classes):
        data[1, data[0].astype(int)==j] = data[0, data[0].astype(int)==j] +
        offsets[j]
    return data

# global variables
columns_to_drop = [’Id’, ’Response’]
xgb_num_rounds = 720
num_classes = 8
missing_indicator = -1000

train = pd.read_csv("train.csv")
test = pd.read_csv("test.csv")

all_data = train.append(test)
all_data.shape

all_data[’Product_Info_2_char’] = all_data.Product_Info_2.str[0]
all_data[’Product_Info_2_num’] = all_data.Product_Info_2.str[1]
```

```
all_data['Product_Info_2'] = pd.factorize(all_data['Product_Info_2'])[0]

all_data['Product_Info_2_char'] =pd.factorize(all_data['Product_Info_2_char'])[0]

all_data['Product_Info_2_num'] = pd.factorize(all_data['Product_Info_2_num'])[0]

all_data['BMI_Age'] = all_data['BMI'] * all_data['Ins_Age']

med_keyword_columns=all_data.columns[all_data.columns.str.startswith('Medical_Keyword_

all_data['Med_Keywords_Count'] = all_data[med_keyword_columns].sum(axis=1)


all_data.fillna(missing_indicator, inplace=True)
all_data['Response'] = all_data['Response'].astype(int)


train = all_data[all_data['Response']>0].copy()
test = all_data[all_data['Response']<1].copy()


 xgtrain = xgb.DMatrix(train.drop(columns_to_drop, axis=1),
            train['Response'].values, missing=missing_indicator)
xgtest = xgb.DMatrix(test.drop(columns_to_drop, axis=1),
            label=test['Response'].values,missing=missing_indicator)



 plst = get_params()
model = xgb.train(plst, xgtrain, xgb_num_rounds)



train_preds = model.predict(xgtrain)
print('Train score is:', eval_wrapper(train_preds, train['Response']))
test_preds = model.predict(xgtest)


offsets=np.array([-1.5,-2.6,-3.6,-1.2,-0.8,-0.1,0.6,3.6])
offset_preds = np.vstack((train_preds, train_preds, train['Response'].values))
offset_preds = apply_offsets(offset_preds, offsets)
print('Offset Train score is:', eval_wrapper(offset_preds[1], train['Response']))


def score_offset(data, bin_offset, sv, scorer=eval_wrapper):
    data[1, data[0].astype(int)==sv] = data[0, data[0].astype(int)==sv] +
    bin_offset
    score = scorer(data[1], data[2])
    return score
```

```
from scipy.optimize import fmin_powell
opt_order = [0,1,2,3,4,5,6,7]
for j in opt_order:
    train_offset = lambda x: -score_offset(offset_preds, x,j)
    offsets[j] = fmin_powell(train_offset, offsets[j], disp=False)
    print (offsets[j])

# apply offsets to test
data = np.vstack((test_preds, test_preds, test['Response'].values))
data = apply_offsets(data, offsets)

final_test_preds = np.round(np.clip(data[1], 1, 8)).astype(int)
```

5.1 Data description.

Variable	Description
Id	A unique value associated with an application.
Product_Info_1-7	A set of normalized variables relating to the product a client applied for
Ins_Age	Normalized age of applicant
BMI	Normalized BMI of applicant
Wt	Normalized weight of applicant
Ht	Normalized height of applicant
InsuredInfo_1-6	Normalized variables providing information about the applicant.
Employment_Info_1-6	Normalized variables relating to the employment history of the applicant.
Family_Hist_1-5	Normalized variables relating to the family history of the applicant.
Insurance_History_1-9	Normalized variables relating to the insurance history of the applicant.
Medical_Keyword_1-48	Dummy variables relating to the presence of/absence of a medical keyword being associated with the application.
Medical_History_1-41	Normalized variables relating to the medical history of the applicant.
Response	This is the target variable, an ordinal variable relating to the final decision associated with an application

The following variables are all categorical (nominal):

Product_Info_1, Product_Info_2, Product_Info_3, Product_Info_5, Product_Info_6, Product_Info_7, Employment_Info_2, Employment_Info_3, Employment_Info_5, InsuredInfo_1, InsuredInfo_2, InsuredInfo_3, InsuredInfo_4, InsuredInfo_5, InsuredInfo_6, InsuredInfo_7, Insurance_History_1, Insurance_History_2, Insurance_History_3, Insurance_History_4, Insurance_History_7, Insurance_History_8, Insurance_History_9, Family_Hist_1, Medical_History_2, Medical_History_3, Medical_History_4, Medical_History_5, Medical_History_6, Medical_History_7, Medical_History_8, Medical_History_9, Medical_History_11, Medical_History_12, Medical_History_13, Medical_History_14, Medical_History_16, Medical_History_17, Medical_History_18, Medical_History_19, Medical_History_20, Medical_History_21, Medical_History_22, Medical_History_23, Medical_History_25, Medical_History_26, Medical_History_27, Medical_History_28, Medical_History_29, Medical_History_30, Medical_History_31, Medical_History_33, Medical_History_34, Medical_History_35, Medical_History_36, Medical_History_37, Medical_History_38, Medical_History_39, Medical_History_40, Medical_History_41

The following variables are discrete:

Medical_History_1, Medical_History_10, Medical_History_15, Medical_History_24, Medical_History_32

Medical_Keyword_1-48 are dummy variables.

The following variables are continuous:

Product_Info_4, Ins_Age, Ht, Wt, BMI, Employment_Info_1, Employment_Info_4, Employment_Info_6, Insurance_History_5, Family_Hist_2, Family_Hist_3, Family_Hist_4, Family_Hist_5

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