Predictive Modelling in Life Insurance.

By

Juliana Tula Talai (juliana.talai@aims.ac.rw)

Supervised by: Dr. Yabebal Fantaye

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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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Student: Juliana Tula Talai

[illegible]

Supervisor: Dr. Yabebal Fanataye

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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 predicting risk as compared to Random Forest.

Contents

1. Introduction

Insurance is a contract between an individual (insured) and the insurance company (insurer) to pay the individual a specific sum once the loss being covered occurs. The individual in turn pays a specific amount of payment periodically, premium, during the contract term. Traditionally, insurance companies estimated the appropriate fees to charge or determined the cost of insurance by analysing a single factor such as age of the insured. Basically, the process of determining risk depended on how accurately the insurance company is able to forecast a policy's ultimate cost, how to price its products to maximize profits and in turn avoid losses. 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 make expert decisions in claim management, premium audit, underwriting and fraud detection Mike Batty, 2017.

1.0.1 Definition. Predictive modelling 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. It 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, a process known as rate making and avoid adverse selection Frees et al. (2014).

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.

The stated drawbacks above can be eliminated if the modeller has a deep understanding of the stated problem, a clear visualization of the relevant data and how to adequately preprocess the data after having an intuition of of how the data is structured as stated by Kuhn and Johnson (2013)

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 Macedo (2009). 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.

The requirements for building a predictive model as stipulated by Mike Batty, 2017 are: Efficiently rich data set where there is a strong relationship between the predictor variables and the data, a well designed model that can be transformed to business plans, a wide range of predictors to develop the model such that underlying relationships between the target and the observations can be understood and quantified and lastly a well defined target variable.

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). To clearly understand the challenges faced in life insurance, we compare life underwriting and auto underwriting (Mike Batty, 2017).

It is easier for auto insures to make corrections in case of rate changes in the renewal of policies. This id because the frequency of claim in auto insurance is high usually over a six month contract, which is the target variable. In life insurance, contracts are long term usually 10 or 20 years. Therefore life insurers must correctly rate and price the insurance contracts from the start of the contract.

Underwriting data required for modelling is not present in life insurance due to inadequate and proper storage of the data. The data documented too is inconsistent making the modelling process a challenge.

Life underwriting is subject to psychological biases and inconsistencies of human decision-making thus predictive models help to curb this challenge.

Modelling insurance claims requires a large sample of loss events which is not available in the life insurance sector as the claims have low frequency as compared to auto insurance where the frequency of claim is high due to the short contract term of the policies.

From the discussion above, it is clear that the target variable and the amount of data in life insurance is a concern. Therefore, modellers have turned to using underwriting decisions like risk as they have valuable information 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

1.3.1 Definition. Underwriting 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).

Here we describe the traditional method of life insurance. A proposal form bearing information on relevant risk factors like age, occupation, health history etcetera is provided. The insured then fills the form depending on the type of policy they require. This helps ascertain the risk level of the insured. The process of underwriting helps to establish if additional premium is required for the insured based on the risk factors they are exposed to Dickson, Hardy, and Waters (2013).

Disadvantages of Underwriting.

1. There is the risk of adverse selection where the insurance company has different information from the insured. This bears a negative impact in life insurance as the company may not be able to the best decision when the loss occurs.
2. The underwriting process is usually lengthy and costly.
3. Utmost good faith is a principle of insurance where the insured and the insurer act honestly without withholding critical information from one another. In case this principle is breached, the sum assured may not be fully paid if the loss occurs.

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:

1. 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.

2. 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 this work entails.

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

1.4.1 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.

1.4.2 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.

1.4.3 Regression versus 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 advanced methods are trees, random forests, support vector machines and boosting Gareth, Daniela, and Trevor (2014).

1.4.4 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.

1.5 Classifiers

We introduce some of the most commonly used classifiers.

1.5.1 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;

$$\frac{p(X)}{1 - p(X)} = \exp(\beta_0 + \beta_1 X) \tag{1.5.1}$$

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

$$log\left(\frac{p(X)}{1 - p(X)}\right) = \beta_0 + \beta_1 X \tag{1.5.2}$$

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

1.5.2 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).

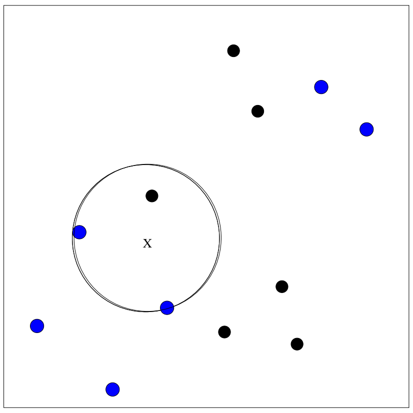


Figure 1.1: KNN approach using K=3.

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).

1.5.3 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

In this classifier, observations are grouped into N different classes such that $N \geqslant 2$, and the categorical response variable variable Y takes on N different and ordinal values.

Bayes theorem is given by:

$$P_n(X) = Pr(Y = n/X = x) = \frac{\pi_n f_n(x)}{\sum \pi_i f_i(x)} \tag{1.5.3}$$

$f_n = Pr(X = x/Y = n)$: This is defined as the density function of X for observations in the n^{th} class.

π_n: This is defined as the prior probability that an observation chosen randomly is from class n given a response variable Y.

$P_n(x)$: This is the probability that a given sampled observation $X = x$ is from the n^{th} class.

The prior probability is computed from the random samples of Y^s from the population by computing the fraction of observations which belong to the n^{th} class while $f_k x$ is approximated. A classifier that approximates the bayes classifier is thus developed.

Linear Discriminant Analysis for $p = 1$.

When $p = 1$, the model has only one predictor. As stated earlier, we estimate $f_n(x)$ that we plug into the posterior probability equation (1.5.3) so as to estimate $p_n(x)$. An observation is then classified to the class for which the posterior distribution is greatest.

The following assumptions are made inorder to estimate $f_n(x)$.

1. $f_n(x)$ is normal.

$$f_n(x) = \frac{1}{\sqrt{2\pi}\sigma_n} \exp\left(-\frac{1}{2\sigma_n^2}(x - \mu_n)^2\right) \tag{1.5.4}$$

   where μ_n and σ_n^2 are the mean and variance respectively for the observations in the n^{th} class.

2. Shared variance term across all n classes, $\sigma_1^2 =, ..., = \sigma_N^2$

Plugging the density function of X (1.5.4) into the posterior distribution (1.5.3), we have:

$$p_n(x) = \frac{\pi_n \frac{1}{\sqrt{2\pi}\sigma} \exp\left(-\frac{1}{2\sigma^2}(x - \mu_n)^2\right)}{\sum_{i=1}^{K} \pi_i \frac{1}{\sqrt{2\pi}\sigma} \exp\left(-\frac{1}{2\sigma^2}(x - \mu_i)^2\right)} \tag{1.5.5}$$

Taking the logs gives the posterior equation as:

$$\delta_n(x) = x\frac{\mu_n}{\sigma^2} - \frac{\mu_n^2}{2\sigma^2} + log(\pi_n) \tag{1.5.6}$$

The bayes classifier is estimated by first approximating the parameters $\mu_1, ..., \mu_K$, σ^2 and $\pi_1, ..., \pi_K$. The outputted estimates for the mean, variance and prior distribution are plugged into equation (1.5.6).

The following equations give the estimates for μ_n and σ^2

$$\hat{\mu_n} = \frac{1}{m_n} \sum_{i:y_i=n} x_i \tag{1.5.7}$$

$$\hat{\sigma} = \frac{1}{m-N} \sum_{N=1}^{N} \sum_{i:y_i=n} (x_i - \hat{\mu})^2 \tag{1.5.8}$$

m: The total number of training observations.

m_n: The total number of training observations that belong to class N.

μ_k is the mean of all training observations from class n.

$\hat{\sigma}^2$: This is the weighted average of the sample variances of the n classes.

The prior probability, π_n is computed as a fraction of the training observations belonging to the n^th class.

$$\pi_n = \frac{m_n}{m} \tag{1.5.9}$$

Having the estimates for the mean and variance from equation (1.5.8) and equation (**??**), we plug these estimates into (1.5.6) and the classifier assigns an observation to the class for which the posterior distribution given by

$$\hat{\delta}_k(x) = x\frac{\hat{\mu_k}}{\hat{\sigma}^2} - \frac{\hat{\mu}_k^2}{2\hat{\sigma}^2} + log(\hat{\pi}_k) \tag{1.5.10}$$

is largest Gareth, Daniela, and Trevor (2014).

2. 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, which is calculated by kaggle once the submission of predictions is made to the website. 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.

2.1 Quadratic weighted kappa metric

This metric 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 Web (Accessed March 2017b).

Calculation of quadratic weighted kappa metric.

1. An $M \times M$ histogram matrix P is formed where P_{ij} corresponds to the number of applications that got a rating i by A and j by B. Rater A is the actual risk and rater B, the predicted risk. An $M \times M$ matrix of weights, w, is formed based on the difference between the rater's score that is the difference between the score by rater A and the score by rater B.

$$w_{ij} = \frac{(i-j)^2}{(M-1)^2} \tag{2.1.1}$$

2. An $M \times M$ histogram matrix, E, which is a matrix of expected of ratings is formed. An assumption is made here that there is no association between the rating scores A and B.

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

$$\frac{1 - \sum_{ij} w_{ij} p_{ij}}{\sum_{ij} w_{ij} E_{ij}} \tag{2.1.2}$$

   The metric works well for a highly imbalanced classification task. The metric varies from 0 which is 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.

2.2 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.

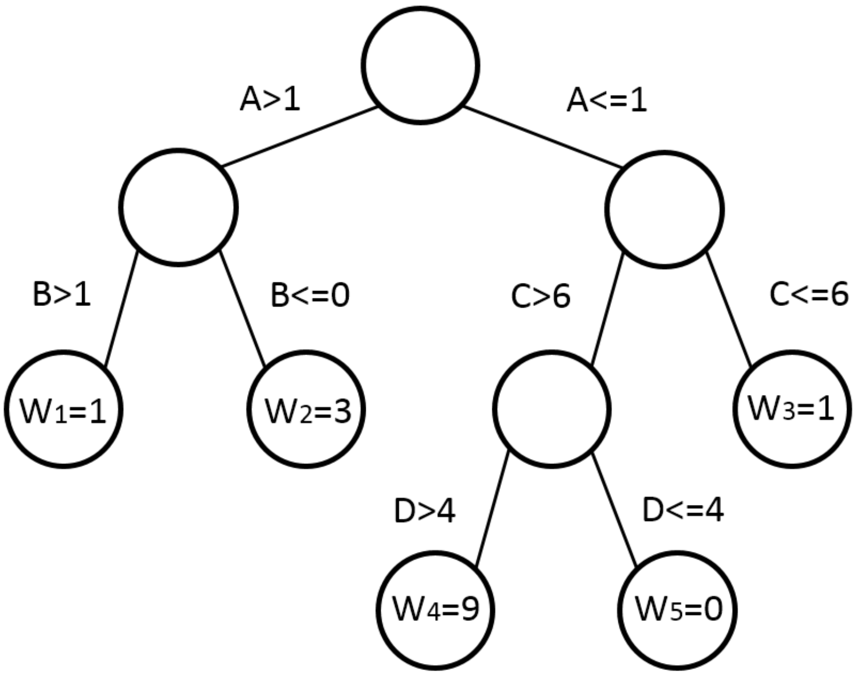


Figure 2.1: Structure of a decision tree He (2015).

The internal nodes split the flow of the data points by one of the features where the condition on the edge specifies what data can flow through. Data points which reach to a leaf will be assigned a weight. The weight is the prediction. Every time a split is made, we convert a leaf to an internal node.

2.2.1 Bagging.

Bagging and Random Forests use trees to build more accurate models Gareth, Daniela, and Trevor (2014).

A bootstrap sample is achieved through randomly sampling observations with replacement from the N known observations. This is called a bootstrap sample as we allow for replacement and this sample may not be identical to the original sample. We denote the training set by $Z = (Z_1, Z_2, ..., Z_N)$ where $z_i = (x_i, y_i)$. The idea here is to draw datasets randomly with replacement from the training data having each sample the same size as the original training set. This has the overall effect of reducing the variance of the learning method. This is done B times producing B bootstrapped datasets Hastie, Tibshirani, et al.

Consider the set of n independent observations denoted by $D_1, D_2, ..., D_n$ each with variance σ^2. Therefore the variance of the mean $\bar{Z}$ of the observation is given by $\frac{\sigma^2}{n}$ Hastie, Tibshirani, et al. To reduce the variance and increase the overall prediction accuracy of the learning method in the case of regression trees, 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 learning model given as:

$$\hat{f}_{avg}(x) = \frac{1}{B}\sum_{b=1}^{B} \hat{f}^b(x) \tag{2.2.1}$$

Since we cannot have multiple training sets, 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:

$$\hat{f}_{bag}(x) = \frac{1}{B}\sum_{b=1}^{B} \hat{f}^{\star b}(x) \tag{2.2.2}$$

This procedure of continuously fitting bootstrapped samples of the observations is called bagging in regression trees. Averaging the trees from the bootstrapped samples reduces the variance and the trees are grown deep and are not pruned therefore creating a low bias, high variance model. Therefore, given a training set $X = x_1, ..., x_n$ 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.

Bagging can also 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).

2.2.2 Out of Bag Error Estimation.

As discussed, we construct the model using bootstrap samples from the training set, the result is then aggregated to form a bagged predictor. Each bootstrap sample leaves out about $\frac{1}{3}$ of the observations. These left out samples are then used to improve the predictions and the test error in decision trees and are called out of bag observation. The remaining $\frac{2}{3}$ is used to fit bagged trees.

To predict the i^{th} observation's response, we use each of the trees in which that observation was out of bag. This will yield around $\frac{B}{3}$ predictions for the i^{th} observation. The majority vote of the predicted responses are obtained to obtain a single prediction giving a single OOB prediction for the i^{th} observation. This is done for the n observations and the classification error is computed. Gareth, Daniela, and Trevor (2014).

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

2.2.3 Variable importance measures.

Random Forests can output a list of predictor variables that are important in predicting the outcome. Having a large number of bagged trees makes it difficult to represent and understand the tree learning model. Despite the fact that Random Forests lacks interpretability, they have good prediction power. The overall summary of the importance of each predictor is obtained using the gini index Hastie, Tibshirani, et al..

At every split in the tree, the improvement in how the node is split is the measure of the importance attributed to the splitting variable and then accumulated over all the trees for each variable separately.

2.2.4 Definition. Gini index 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).

2.2.5 Random Forests.

Random Forest is a better approach over bagged trees by providing restrictions to the system that decorrelates the trees in an attempt to improve the prediction accuracy and reduce the variance. In building the decision trees, a random sample of n predictors is chosen as split candidates from the set of p predictors, which is the total number of predictors in the data, each time a split in a tree is considered. The split is allowed to use only one of those n subset of predictors.

We ensure that a new sample of n predictors is taken at each split and the number of predictors considered at each split is approximately equal to the square root of the total number of predictors, $n \approx \sqrt{p}$.

Suppose there is one very strong predictor in the dataset and a number of other moderately strong predictors. Random Forest has the tendency of using the strong predictors in the top split in the collection of the bagged trees leaving out the less important predictors. Thus, all of the bagged trees will look quite similar to each other and therefore the predictions from the bagged trees will be highly correlated Gareth, Daniela, and Trevor (2014).

This problem is overcome by ensuring that each split considers only a subset of the predictors. Averagely, $\dfrac{(p-n)}{p}$ of the splits will therefore not consider the strong predictor and the other less important predictors predictors will have a chance to participate in the splitting, a process referred to as decorrelating the trees.

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

Random Forest therefore uses fully grown decision trees (low bias, high variance). It manages the error reduction task by reducing the variance. The trees are made uncorrelated so as to maximize the decrease in variance, but the algorithm cannot reduce bias (which is slightly higher than the bias of an individual tree in the forest). Hence the need for large unprunned trees so that the bias is as low as possible. High variance is due to the correlation in the predictors. Bagging therefore succeeds in smoothing out the variance resulting to a reduction in the test error leading to improved predictions.

2.3 Implementing the Random forest algorithm

We describe how we preprocessed the raw data to achieve a good model score.

2.3.1 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.

2.3.2 Data preprocessing. This is the procedure carried out on raw data to prepare the data for modelling. 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.

2.3.3 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.

The following scikit learn parameters were tuned to achieve the best score (Web, Accessed May 2017).

n_estimators: This is the number of trees in the forest we want to build. The maximum vote is taken in the case of classification or average the predictions in the case of regression trees. A higher value of n_estimators increases the prediction accuracy and makes the model more stable.

Criterion: "gini", measures the relevance of the features in the data. The features are selected based on the gini importance.

max_depth: This parameter describes how deep we want to grow our trees. The deeper the tree, the less the bias error. If the value is none, all the trees are grown until all the leaves are pure.

Min_samples_split: This is the minimum number of samples needed to split at a node.

Min_samples_leaf: The minimum number of samples in the leaf nodes. This parameter reduces the chance of overfitting.

Max_features: This is the maximum number of features in a tree in Random Forest. There are a variety of oprions but in our model, we used sqrt(n_features). This option takes the square root of the total number of features at each split.

Max_leaf_nodes: This parameter specifies the total number of leaf nodes in the model and takes on integer values.

Min_impurity_split: This is the threshold subjected to a node. A node splits if the impurity is above a set threshold

Bootstrap: It takes on boolean with default =True. The model samples the observations randomly with replacement ensuring that the sample is the same size as the training data. It has the overall effect of reducing the variance.

Oob_score: This parameter estimates the test error of a model without the need of cross validation. In the case of classification, it finds out the maximum vote score for each observation based on only the trees that do not use a specific observation to train.

n_jobs: Default=1. This feature is responsible for the model speed. It tells the computer how many processors it is allowed to use. If it takes the value 1, then only one processor is used and -1 means there is no restriction.

Random state: Given similar training data and parameters, this parameter outputs the same results it therefore makes the replication of solutions easy.

Verbose: Default=0. Controls the information on the tree building process.

Warm_start: bool, (default=False). This parameter reuses the previous solution of the call to fit function when set to true.

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.

2.4 Overview of Xgboost Algorithm

The full name is eXtreme Gradient Boosting. It is an improved and efficient implementation 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 responsible for ranking, classification of qualitative data 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.

2.4.1 Boosting. Combines the outputs of many weak classifiers to produce powerful classifiers in an iterative fashion. A weak classifier is a classifier whose error rate is better than random guessing. Boosting therefore applies weak classification algorithm sequentially to repeatedly modified versions of the data, producing a sequence of weak classifiers. Classifiers are then trained on weighted versions of the dataset and combined to produce a final prediction. These predictions are then combined to produce a final prediction Hastie, Tibshirani, et al. Boosting has three tuning parameters: The number of trees which controls over fitting in that larger trees tend to overfit, the shrinkage parameter that controls the learning rate and the number of splits in each tree that controls the complexity of the model Gareth, Daniela, and Trevor (2014)

2.4.2 Gradient boosting. Uses the direction of quickest improvement (pseudo gradient). A decision tree is picked as close as possible to the pseudo gradient and added to the model. Here, we are picking the decision tree to be an improvement in the direction we can consider the best way to improve the overall loss function. Gradient boosting has shrinkage and regularization built in making it a very efficient method Li (2016).

2.4.3 Regularization. This is defined as adding additional information so as to control overfitting. Besides the size of constituent trees, the number of boosting iterations reduces the training risk such that for large number of iterations, this risk is minimized. In the context of boosting, shrinkage is scaling the contribution of each tree by a factor $0 < v < 1$ when training the algorithm. Smaller values of v implies more shrinkage and more training risk for the same number of iterations. Therefore, v, which controls the learning rate, and the number of iterations parameter control the prediction risk on the training data. These parameters are dependent on each other in that smaller values of v for the same training risk yield larger values of the number of iterations. It was found that smaller values of v yield better test error results and large values for the number of iterations are required.

The strategy is thus to set v to be small $(v < 0.1)$ and choose the number of iterations by early stopping, which is provided in XGBoost. Hastie, Tibshirani, et al.

2.4.4 Features of Xgboost.

Customization: Xgboost supports customized objective function required for ranking, classification and regression. In addition, a variety evaluation metrics are provided by the algorithm.

Sparcity: Xgboost accepts sparse input for both the tree and linear booster. It has a specified method of filling in missing values present in the data.

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 compared to different algorithms.

2.4.5 XG Boost parameters.

The parameters can be grouped into He (2015):

General parameters: Under general parameters we have number of threads. nthread is defined as the number of parallel threads.

Booster parameters: Under booster parameters we have the Stepsize and Regularization parameters.

1. gblinear: linear function.
2. gbtree: tree based model.

Task parameters: Here we have the objective and the evaluation metric.

2.4.6 Model Specification.

Training objective.

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

$$\sum_{k=1}^{K} f_k. \tag{2.4.1}$$

With all the prediction trees, the predictions are given by:

$$\hat{y_i} = \sum_{k=1}^{K} f_k(x_i) \tag{2.4.2}$$

x_i: Corresponds to the feature vector of the i^th data point.

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

$$\hat{y_i t} = \sum_{k=1}^{t} f_k(x_i) \tag{2.4.3}$$

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

1 Rooted mean squared error for regression.

$$-L = \frac{1}{N}\sum_{i=1}^{N}(y_i - \hat{y}_i)^2. \tag{2.4.4}$$

2 Logloss for binary classification.

$$-L = -\frac{1}{N}\sum_{i=1}^{N}(y_i log()p_i) + (1 - y_i)log(1 - p_i). \tag{2.4.5}$$

3 mlogloss for multi-classification.

$$-L = -\frac{1}{N}\sum_{i=1}^{N}\sum_{j=1}^{M} y_{i,j} log(p_{i,j}). \tag{2.4.6}$$

The regularization parameter, being an important term, controls the complexity of the model thereby preventing over fitting.

$$\Omega = \gamma T + \frac{1}{2}\lambda\sum_{j=1}^{T} wj^2. \tag{2.4.7}$$

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.

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

$$obj = L + \Omega. \tag{2.4.8}$$

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

2.4.7 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:

1. Prepossessed training data.
2. Missing values.
3. 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).

2.5 Implementing the XGBoost algorithm

We describe how we transformed the raw data by preprocessing and describe the parameters we tuned to achieve a good score.

2.5.1 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).

2.5.2 Applying offsets. An offset is a model variable with a specified coefficient. Modelling is affected by the real-world fact that insurance data is often incomplete, generally dirty and inconsistently coded. Due to this, important variables thst are useful in prediction are left out. This will bias the estimate of the model if this omitted variables correlate with the target variable. This is known as omitted variable bias Yan, Guszcza, Flynn, and Wu (2009). To curb this phenomenon, we incorporate the effect of omitted variables in the model design. A common way to approach 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.

2.5.3 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.

The following scikit learn parameters were tuned to achieve the best score He (2015):

1. "reg:linear": default option, Linear regression. The XGBoost algorithm uses regression trees to classify.
2. "binary: Logistic": Outputs probability. It performs logistic regression for binary classification.
3. "multi:softmax": Uses the softmax objective to classify predictions that are categorized into different classes.

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 and reduces the prediction risk. Eta is the stepsize shrinkage used to prevent overfitting and is in the range of [0,1], the default is usually 0.3.

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

The tree building process will stop further partitioning if the tree partition process results in a leaf node with the sum of instance weight less than the specified 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 needed to form 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 where 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. Therefore, the modeller should tune this parameter to obtain the optimum score. The range is from $[1,\infty]$, the default is given as 6.

We train the model by specifying the number of times to train the model. We then predict the target variable on the test data provided, submit the result to the kaggle website and the accuracy score is calculated.

3. Results and discussions

In this chapter, we give a brief description of the data and visualize the different features of the data with plots. We present the results and outline some key points on the XGBoost algorithm.

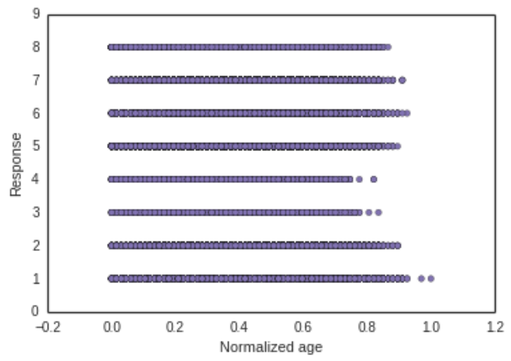
3.1 Data description

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.

3.1.1 Data visualization.

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

Figure 3.1: Scatter plot of Age vs Response

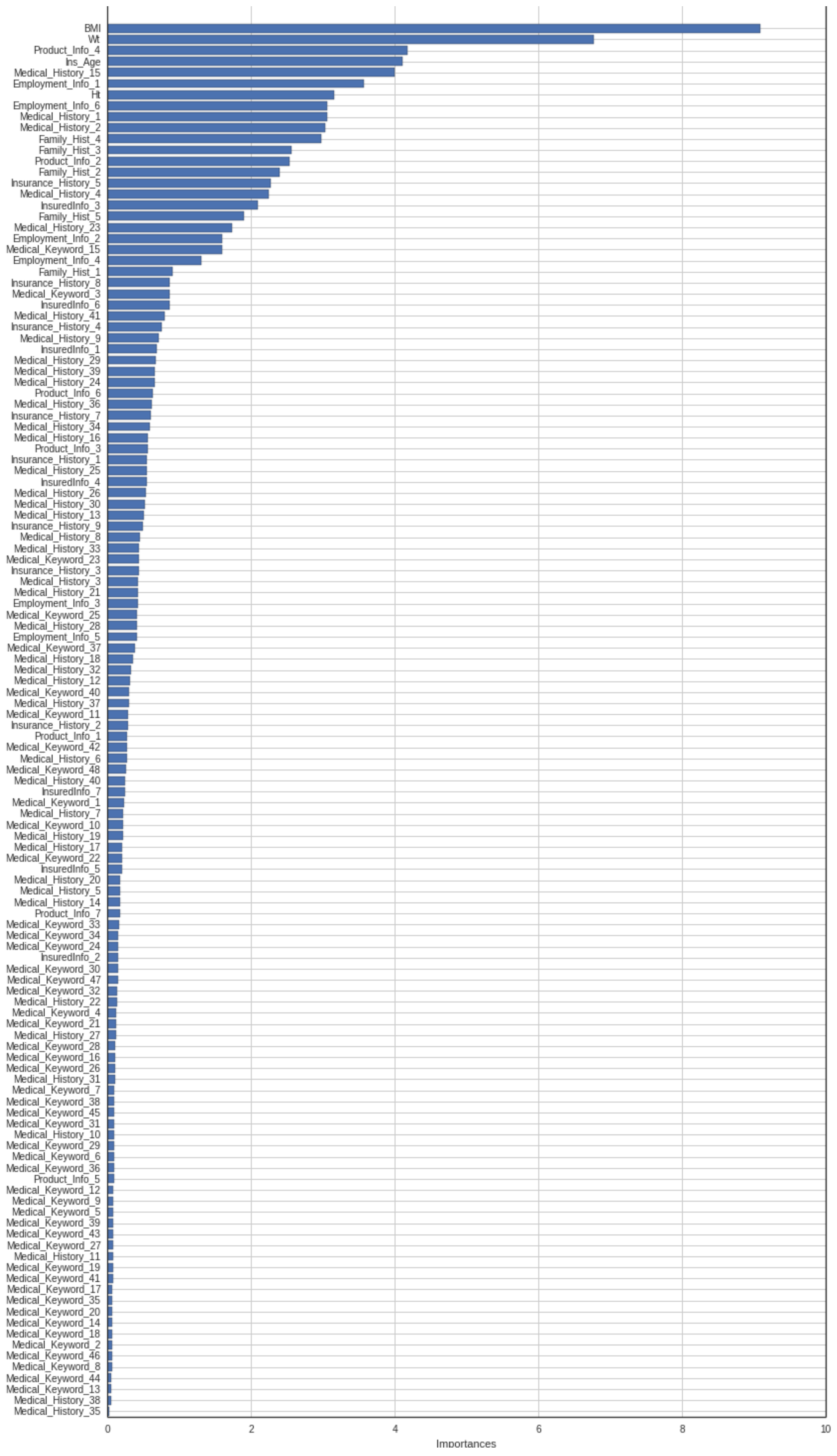


The risk prediction classes are almost evenly distributed across the ages of the clients with a few outliers. Clients across the ages almost experience similar types of risks.

Variable importance plot: 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.

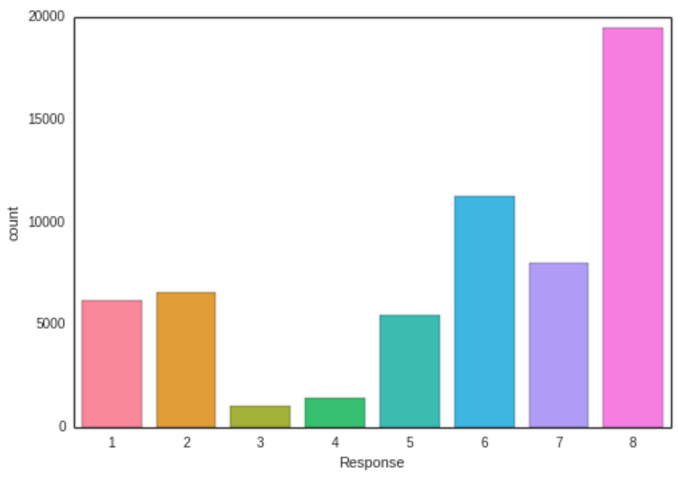
Figure 3.2: Feature importance plot



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_Keyword_13	0.000551
Medical_Keyword_44	0.000612
Medical_Keyword 8	0.000622

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 while the least number of clients fall under the risk class 3.

Class imbalance: Data classification is difficult because of the 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).

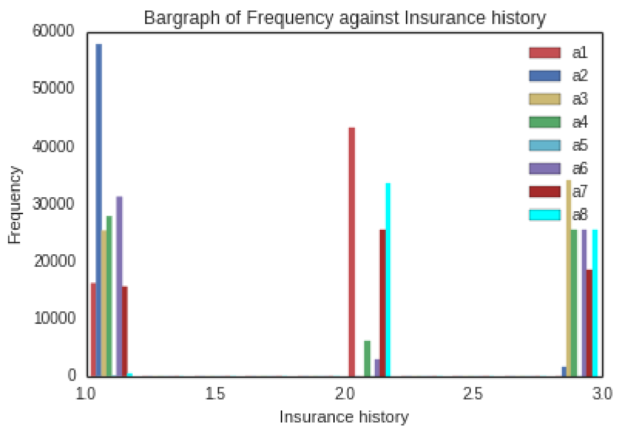
Threshold metrics help to curb the class imbalance problem. These metrics have a threshold level such that examples above the threshold are predicted as positive and the rest are negative. We used the quadratic weighted kappa metric which works well with unbalanced datasets by measuring the agreement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

Descriptive analysis of the Response feature.

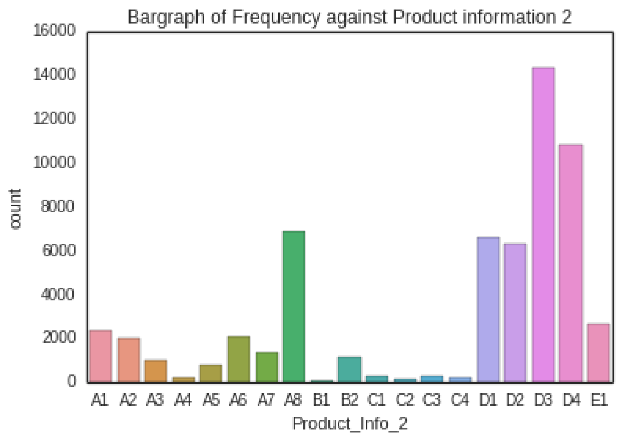
count	59381.000000
mean	5.636837
std	2.456833
min	1.000000
25 %	4.000000
50 %	6.000000
75 %	8.000000
max	8.000000

The mean risk prediction is roughly 6.

Feature bar plots: We plot the frequency of different features against the values.



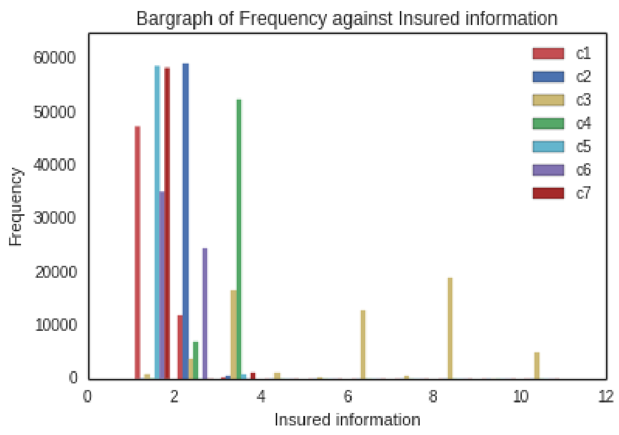
(a) Insurance history plot



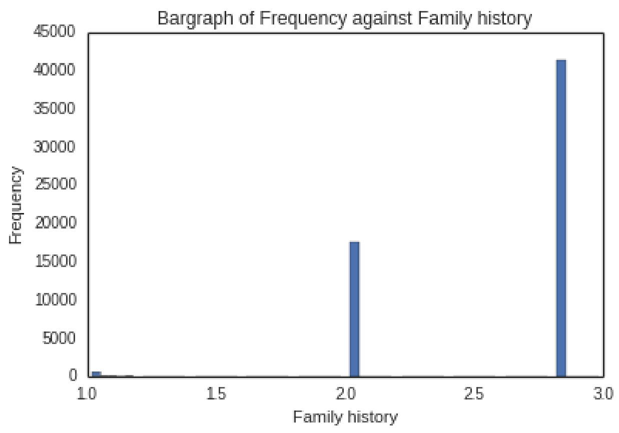
(b) Product Information 2

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.



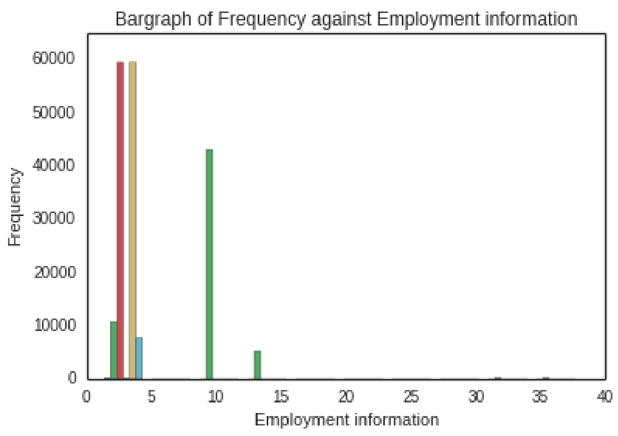
(a) Insurance information plot



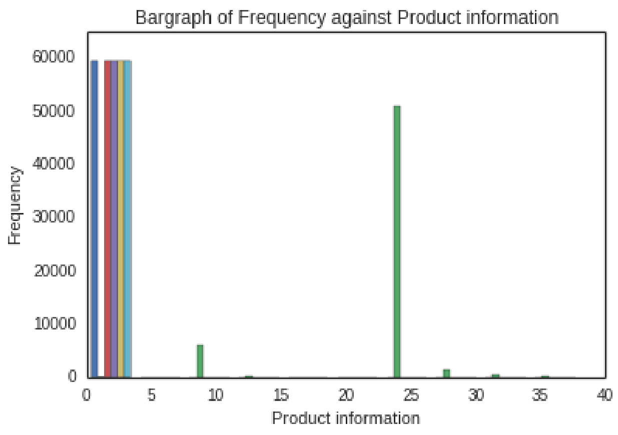
(b) Family history plot

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 take the values (2, 3). InsuredInfo_5 and 7 take 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 and InsuredInfo_3 takes the highest value of the variable 8 while 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 respectively. 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

1. Random forest may overfit noisy datasets: If the number of variables is large and the number of relevant variables small, this algorithm then tends to perform poorly with small n. At each split the chance can be small that the relevant variables will be chosen Hastie, Tibshirani, et al..

2. 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

3.3.1 Guide on parameter tuning.

Tuning 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. Therefore, parameters have to be tuned to achieve good results.

3.3.2 Key points on parameter tuning.

1. To control over fitting where over fitting is a scenario where an algorithm fits well on the training data but is less accurate on unseen or the test data.

2. To deal with imbalanced data where one class has more samples than the other.

3.3.3 Definition. Bias-variance trade off is the concern of continuously reducing two sources of error, the bias and variance, that makes it difficult for algorithms to generalize beyond the training data. Bias is the problem 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 algorithm to generalize unseen data (Sethu, 2007).

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).

3.3.4 How to 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).

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

3.3.5 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) thereby helping 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 and tune the model appropriately.

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

3.3.6 How to build a winning algorithm in a kaggle competition.

To score highly on kaggle, one needs to consistently focus on He (2015):

1. Parameter tuning.
2. Model ensembling which is combining two or more models so as to achieve a more accurate prediction and reduce the prediction risk.
3. Feature engineering which is defined as generating addition relevant features from the raw data so as to improve the predictive power of an algorithm.

3.3.7 Why XGBoost is the winning algorithm for kaggle competitions..

The following are the reasons why XGBoost is a winning algorithm (He, 2015).

1. It is efficient as it allows for parallel computing and can be run on a cluster.
2. It is accurate: It outputs good results for most datasets.
3. Feasibility: It provides a platform for tunable parameters.
4. 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, making XGBoost a superior algorithm to Random Forest.

The difference between boosting and Random Forest is that boosting takes into account the other trees that have already been grown when growing a particular tree. Smaller trees are sufficient and easy to interpret.

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:

1. Submission files.
2. Stacked generalization/blending.

4.1.1 Creating ensembles from submission files.

This method ensembles kaggle csv submission files. It is a faster way of ensembling already existing model predictions as one only needs the predictions on the test set and the model.

Model ensembling reduces the error rate because 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.

4.1.2 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

5.1 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)
```

5.2 XGBoost algorithm

The following code used in generating the best score was adapted from the kaggle website on this site: https://www.kaggle.com /zeroblue/xgboost-with- optimized-offsets/code

```
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)
```

5.3 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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